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Ecology of Fish Community: Niche Modeling Based on Fish Morphological Parameters

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Introduction

This book is a monograph deconstructing morphological models of river fish communities. It provides a new method for studies of fish community niches and addresses morphological modeling, software analysis, and applications.

Over long-term evolution, fish interactions with their environment have led to the formation of new species, the exploitation of various ecological niches, and the development of species communities. Although organisms can be dated from fossils, the niche composition of fish communities 200 years ago remains unknown. The lack of data on the evolution of ecosystem structure and function affects studies of ecology. The purpose of this book is to establish a systematic method for determining niches based on species morphology and the morphological characters of fish communities, as well as to discuss the niche composition of community species through historical records of "qualitative" species. This book attempts to provide a method to clarify community species structure in a given ecosystem and to establish a standard for evaluating ecosystem changes based on community species structure. This book may provide a community structure reference system for river ecosystem assessment and restoration based on natural attributes. Using fish morphological data, we establish a model for fish community studies based on morphological characters. This book also examines the relationships between fish species in communities from the perspective of ecological niches, and it attempts to establish a fish community research tool for the ecological restoration of rivers.

This integrative, cross-disciplinary book, which is both deeply theoretical and has strong practical value, is a rich source of basic information and research content. This book should be useful to researchers, teachers, and students of higher education as a reference for ecological river management, environmental protection, and fishery resource management.

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Foreword

Rivers, an important part of the earth's ecological system, can be described as the basis of life and biological growth. Rivers, which predate human beings, support life on earth, and human survival and development depend on rivers. For example, the Chinese civilization originated in the Yellow River valley, the ancient Egyptian civilization originated in the Nile Valley, the Indian civilization originated in the Ganges valley, and the ancient Babylonian civilization originated in the Tigris and Euphrates valleys.

River water supports life. Water content differs among biological species but is generally 60%–97%. Water is the basis of life activities. The water content of the human body is about 65%. Fresh water is the basic material that drives the activity of the human body. Although water covers 71% of the earth, with a total water volume of 1.386 billion km^3, freshwater accounts for only 2.53% of the total water resources, and 87% of the freshwater is in the form of polar ice caps, Alpine glaciers, and permafrost. River water, lake water, and shallow groundwater are the main freshwater resources that can be utilized by human beings, and this only accounts for 0.26% of the earth's total water. Globally, about 9000 km^3 of freshwater resources can be used effectively per year.

There are more than 1500 rivers in China, with a basin area of more than 1000 km^2. China's water resources are about 2680 km^3/yr, which is equivalent to 5.8% of the total global runoff, ranking fourth in the world. In total river runoff, China ranks sixth in the world. China's per capita runoff is 2530 km^3, about a quarter of the world's total per capita runoff. It is clear that China is a water-poor country, while China's water resources maintain the survival and reproduction of 1.4 billion people.

Ecology is the state which defined the existence and development of living things in a certain natural environment. When we close our eyes and think about it, the ecological environment that unfolds in our minds is a picturesque landscape of clear water and green mountains. However, as a result of human economic and social

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activities, rivers have been divided by numerous dams, natural waters have been occupied, and freshwaters have been polluted. Yet, we live in this environment as if unaware of the destruction of aquatic ecology. Human activities are also unwittingly exacerbating the destruction of nature.

Fish are some of the most advanced organisms in the aquatic ecosystem, interacting with other aquatic organisms and the aquatic environment to maintain the dynamic equilibrium of the ecosystem. However, as society and the economy have developed, anthropogenic influences on river ecosystems have become increasingly severe, and fish communities have suffered serious environmental stress. Species extinction, loss of diversity, and declining resources are common problems facing the river environment worldwide. Fish already suffer, and humans would also be affected by the stress that fish are suffering. Fortunately, our society and government pay attention to ecological problems and have put forward new requirements for an ecological civilization. Rivers are expected to return to their natural states, our living environments will gradually improve, and man and nature will return to harmonious coexistence. However, we have to work together to make this happen.

Under the background of ecological protection, we wonder about the nature of river ecology. What kind of relationship exists between organisms and the environment in an aquatic ecosystem? What can we do to protect aquatic ecosystems? It is necessary to report to society our ideas and findings, which are based on the results of multi-year research, in order to clarify the direction of our work with respect to aquatic ecological protection and to better support ecological protection activities. To those thinking, we have decided to publish the "River Ecology Series."

The "River Ecology Series" relies on several platforms, such as the Pearl River Fishery Resources Observation and Experimental Station of the Ministry of Agriculture and Rural Areas; the Pearl River Basin Fishery Ecology Environmental Monitoring Center of the Ministry of Agriculture and Rural Areas; the Key Laboratory of Fishery Resources and Environment Diversity Protection and Utilization of the Chinese Academy of Aquatic Sciences; the Pearl River Fishery Resources Survey and Evaluation Innovation Team; and the Pearl River Fisheries Research Institute of the China Academy of Aquatic Sciences. During the development of this discipline, a team was established to study hydrochemistry, toxicology, plankton, benthos, fish, and biodiversity conservation. The work of this team revealed the characteristics of river water quality, the composition of biological communities, and the evolution of food chains under environmental stress. A quantitative sampling method called the "River Section Control" method, was used to monitor floating fish eggs and larvae and to improve the quantitative assessment of fish resources in rivers. An observation system for locating and monitoring early floating fish resources was established, which provided data for studies of fish population dynamics. The relationships between environmental factors and larval species, river structure, and river volume with respect to drifting larvae were interpreted over various time scales. The regularity of occurrence and annual variations in early fish resources were determined. The research platform "Ecological information database of floating fish eggs and larvae in the Pearl River" was established. Our long-term data on early fish resources can be used to expand basic research in various fields, including hydrology and meteorology, for transdisciplinary studies. With respect to the research of alga, a monitoring and analysis system for long-term and high-intensity sampling has been established, which expands the research scope for elucidating the current state and succession of river ecology. Some frameworks for the protection of river fish biodiversity, the restoration of fish resources, and ecological restoration engineering have also been developed. These efforts have gradually exhibited our team's work in the understanding, research, and service of river ecosystems. The "River Ecology Series" will focus on fishery resources and ecological domains, constructing a framework for the series from the perspective of the relationship between fish and the environment in an aquatic ecosystem.

With respect to the river ecosystem itself, this series will publish the team's exploratory research, including discussions of the characters of the water environment, changes in the water environment, the structure of the food chain, the relationship between the food chain and the environment, and certain problems and solutions for the river ecosystem. The "River Ecology Series" began with two books about studies of fish, including "The Pearl River system fish primary color atlas (Guangdong section)" and the "Hainan freshwater and estuarine fish primary color atlas," and the five books in the observations of the changes and succession of fish resources, including "Floating fish eggs and larvae monitoring diary (2006) in the Zhaoqing section of the Pearl River," "Floating fish eggs and larvae monitoring diary (2007) in the Zhaoqing section of the Pearl River," "Floating fish eggs and larvae monitoring diary (2008) in the Zhaoqing section of the Pearl River," "Floating fish eggs and larvae monitoring diary (2009) in the Zhaoqing section of the Pearl River," and "Floating fish eggs and larvae monitoring diary (2010) in the Zhaoqing section of the Pearl River." We also exhibit our understanding of fish distributions in the book of "The distribution of the main fishery resources in the Pearl River", and the changes in river ecosystem structure and function in the water areas in the book "A study of the aquatic ecological characteristics of the river network in the Pearl River Delta", the mechanisms of fish resources in key river ecological units and an evaluation system for river ecosystems based on the number of early fish resources in the book of "Early river fish resources", and the theory and method of functional management of spawning grounds for the functional evaluation system for spawning grounds in the book of "Studies on spawning grounds of river fishes". This series aims to improve the management of river fishery resources and river ecosystem management through the ecosystem and fish community construction theory.

Through the publication of the "River Ecology Series," we express our understanding of river ecology to the reader. We hope that our ideas in this book series can inspire thinkings in river ecology and are useful to the reader.

More than 14 950 species of freshwater fish worldwide (Tedesco *et al.*, 2017) belong to 47 orders, 209 families, and 2298 genera (Richard van der Laan, 2017). Fish in a given ecosystem form communities based on the functional characteristics of the food web and the ecological niche, in this way, completing the river ecosystem energy cycle in different environments. The fish community evolves with changes in the environment.

Due to the impact of human activities on the environment, the changes in fish communities are exacerbated and lead to changes in the aquatic ecosystem. Fish are the key organismal group in the food chain of the river ecosystem, determining the state of energy output. River systems influenced by human disturbance are generally in a state of eutrophication. Fish play an important role in the water purification process, performing energy and nutrient output functions in the water. When water quality becomes a strategic demand for a human being, it is necessary to study the relationships within the fish community in order to maintain the optimal energy output of the river fish community.

Over long-term evolution, fish interactions with their environment can lead to the occurrence of new species, the exploitation of different ecological niches, and the development of species communities. Although organisms can be dated from fossils, the niche composition of fish communities 200 years ago remains unknown. The lack of data on the evolution of ecosystem structure and function obstructs the studies of ecology. The purpose of this book is to establish a systematic method for determining niches based on species morphology and the morphological characters of fish communities and to discuss the niche composition of species communities using historical records of "qualitative" species. This monograph attempts to provide a method to clarify community species structure in a given ecosystem and to establish a standard for evaluating ecosystem changes based on community species structure. This work may provide a community structure reference system for river ecosystem assessment and restoration based on natural attributes. Using fish morphological data, we established a model for fish community studies based on morphological characters. This paper also examines the relationships among fish species and fish communities from the perspective of the ecological niche and attempts to establish a fish community research tool for the ecological restoration of rivers. This book is part of the "River Ecology Series."

The book is supported by the Fishery Administration Bureau of the Ministry of Agriculture and Rural Areas, the Yangtze River Basin Fisheries Administration Bureau of the Ministry of Agriculture and Rural Areas, the Science and Technology Agency, and the Department of Agriculture and Rural Areas of Guangdong Province. I would like to express our heartfelt thanks to the experts who have encouraged and supported the authors in the preparation of this book.

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In October 2022, Ecology of Fish Community: Niche Modeling Based on Fish Morphological Parameters was published in Chinese by Science Press (Li X.-H., *et al.*, 2022). Readers can scan the QR code in the book to download Chinese version of Niche Modeling software (http://fmodel.prfri.ac.cn). The authors would like to express their gratitude to Science Press and EDP Sciences for publishing the English edition of Ecology of Fish Community: Niche Modeling Based on Fish

Morphological Parameters. This book is mostly base on the published Chinese edition except for removing the chapter to introduce the Chinese version of Niche Modeling software.

This integrative, cross-disciplinary book, which is both deeply theoretical and strongly practical significance, is a rich source of basic information and research content. The book can be used by scientific workers, teachers, and students at colleges and universities as a reference for ecological river management, environmental protection, and fishery resource management. Due to the limitations of time and scope, there are inevitable omissions in this book. We hope that readers will make valuable suggestions for future improvements.

Prof. Xinhui LI

May 31, 2020

Chapter 1

Fish Communities and River Ecosystems

A biological community refers to the distribution of organisms in a certain time and space, usually including animals, plants, microorganisms, and other species populations. Biological communities are the living parts of an ecosystem. Biological communities depend on the environment; usually, each environment has a corresponding specific biological community. Therefore, the ecological environment includes the biological community and the biological habitat. More complex environmental conditions imply that the biological community has a more complex structure and higher species richness, with a greater number of ecological niches and a lower intensity of competition among organisms within the community. Therefore, complex environments generally have relatively stable community structures, while less complex environments generally have more unstable communities.

The word "niche" first appeared in 1910 in the ecology treatise of the American scholar R. H. Johnson. The early concept of "niche" applied to the species distributions of flora. In 1924, Grinnell applied "niche" to the concept of "space." In 1927, Elton defined an animal's niche as its place in the environment, including the relationship between food and predators. In this way, "niche" includes a conception of "function." In 1957, Hutchinson described "niche" as a multidimensional space in which all non-biological and biological species elements existed, using the phrase "basic niche." Under this concept, a species niche may become a "niche" without boundaries or a natural niche. A "natural niche" contains all of the elements of the survival of species or communities and is as well a system, a concept of the whole, and an ideal ecological space. However, due to competition among species in nature, each species can only occupy a part of the basic niche, which is known as the actual niche. Niche represents the minimum threshold of habitat that is necessary for each organism to survive in an ecosystem. Therefore, what is usually studied is the relative niche. By means of artificial segmentation, the main conditions for the survival of interacting species are separated from the natural niche and become a bounded niche space; the relative niche is a part of the natural niche. In fact, the niche varies with the environment. For example, when the main food source is scarce, an animal will increase its prey species and tend to expand its feeding habits, broadening the

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niche; when the food sources are rich, the number of prey species will probably decrease and feeding habits will tend to become more specialized, narrowing the niche. Consequently, the same food source faces different predators, which is considered niche overlap.

The basic characteristics of a biological community include species diversity, community growth form and structure, dominant species, relative abundance, and nutrition structure. In response to the specific ecological conditions, the community spatial structure includes different horizontal and vertical structures. In the community, there are dominant species, and the species in the community often change over time. These species are constantly interacting with each other, so the niche is in a dynamic state. Any organism in a given community has both competitive and mutually beneficial aspects, and the balance between these aspects should be one of the main characteristics of an ecosystem. Currently, community studies focus on competition, predation, mutualism, and abiotic stress relationships among species (Bruno *et al.*, 2003). As human development is increasingly dependent on ecosystem services, future community research will focus on the functional needs of ecosystems, and functional communities of organisms will become the tools that help the ecosystem to achieve its functional goals. The mechanisms of functional community construction not only provide a theoretical system for restoring ecosystem function but also lay a foundation for the shaping of functional communities.

Ecological environmental elements constitute the spatial dimension of the community. Different species occupy special positions in the community. Species diversity corresponds to the multi-spatial dimension of the community ecosystem, which is the basis of the niche concept. A niche refers to the space occupied by species in the system and reflects the functions of species in the system, the relationships among species in the community, and the functional state of the ecosystem. The morphological characters of individuals can reflect the niche status of a species. In the ecosystem, the sizes of individuals within a species can reflect differences in living space and energy utilization, while variations in the sharpness of animal teeth can reflect differences in food lineages and feeding niches. Differences in leaf morphology indicate differences in energy absorption, which correspond to differences in energy niches.

Taxonomy adds a temporal dimension to species in a community, reflecting the response of “niches” to environmental evolution. The community is in a multi-dimensional system, which shapes the morphological and biological characteristics of different species. All aspects of life phenomena can provide features for classification, including physiology, biochemistry, proteins, genes, and mating behaviors. The evolution of organisms into different species is usually described based on species characteristics or attributes, but the most intuitive classification method is morphological classification, especially based on external morphology. People recognize species based on morphological characteristics, and morphology refers to the appearance of things, or, under certain conditions, a reflection of gene expression. Morphology is the basis for species classification. Through the analysis of the characteristics of species diversity, all of the species in a community sample can be distinguished based on the average “distance” among species. This is the simplest character measure, and its association with phylogenetic and functional diversity forms the analytical framework for systematic classification (Clarke and Warwick, 1999). Abellán *et al.* (2006) argued that environmental changes or human activities cannot change the taxonomic properties of species. Organisms have many characteristics. In morphological classification, characters are divided into morphological characters and quantitative characters. The morphological characters are extracted into taxonomic characters to identify species. By using a large number of numerical classification features to form a data matrix, a biodiversity index of classification features (Leonard *et al.*, 2006) can be established on a computer operating system and used to study community structure and species relationships. By constructing a digital dataset of morphological characters comparable among species, a multi-dimensional system can be formed to characterize species and environments. This system can be used to study the interactions among species, as well as the stability and evolutionary trends of the community.

Species classification and taxonomic data can correspond to sequential changes in interspecies order and reflect the evolution of species communities. Therefore, the morphological data for a given organism include information about adaptation, niche, and system evolution. Community characteristics are the result of the adaptation of a species to environmental change, including changes in the niches of various species. Because the number of factors involved in the theoretical niche has no boundary, it is difficult to establish a standard niche to evaluate community status. In model analysis, many environmental factors have uncertain aspects, including variable boundary, data quantity, analysis statistics, model, and theory. It is difficult to establish a standard for assessing the status of communities and niches.

Freshwater fish are fish inhabiting rivers, lakes, reservoirs, and other freshwater water bodies. There are about 32 500 species of fish worldwide, of which more than 15 000 live in freshwater. Less than 10% of all migratory fish species migrate between freshwater and marine habitats. Fish community characteristics include regional specificity, systematic correlation, relative stability, and interspecific relationships such as mutualism, competition, parasitism, and predation. The number of species comprising a community can vary greatly depending on the abundance of nutrients. Over the past half-century, freshwater fish in China have become steadily more threatened. Compared with the 1980s, the fish resources in the Yangtze River and the Pearl River have decreased by more than 60%, and more than one-third of the fish species in these communities have experienced substantial succession. The decline of fish resources affects the food chain in the river ecosystem, resulting in insufficient energy and material circulation in the water body. Guaranteed water quality has become an important problem to be solved in social development. Water quality assurance, the restoration of fish resources, and the rebuilding of fish communities have become integral issues in the restoration of river ecosystems. Fish community status is closely related to the environment, and fish communities differ with respect to species diversity, biomass, and function.

The communities discussed in this book are fish in river ecosystems. Fish are aquatic vertebrates that breathe through their gills, swim by wiggling their tails and trunks in coordination with their fins, and feed by opening and closing their jaws. Fish make up about 53% of all vertebrate species, and about a third of all fish live in freshwater. Fish are active consumers. Fish may be carnivorous, herbivorous, or omnivorous. In studying fish, we assumed that the boundary was an ecological unit in a section of a river, in which a community is composed of many species of fish. The "biomass" of each species and the "biomass" of the total community were regarded as the niche of the corresponding species. That is, "biomass" was used to represent the spatial niche occupied by fish in the water body. The quality of fish in a river ecosystem is affected by the environment, and the degree of interannual quality change can reflect the degree of environmental change. In the analysis model of species morphological characteristics, the influence of environmental factors on species can be determined by taking the biomass abundance of species as the adaptive variable to the environment. The results of the morphological character analysis model included the comprehensive effects of the community species' response to environmental change. The results of this niche analysis indirectly introduced environmental factors. Before the introduction of the model, this chapter reviews the basic characteristics of fish and their role in river ecosystems.

1.1 Species

A species is a group of closely related organisms in which males and females mate and produce fertile offspring. Species are the basic units of biological reproduction, and each species maintains a series of ancestral characteristics. There are obvious differences between species, and hybrids that cannot mate or copulate cannot reproduce. Species are the basic unit of biological classification. Each species has unique characteristics. No two species are identical. Each species has a taxonomic status; the boundary, phylum, class, order, family, and genus can reflect the evolutionary history of the species.

Natural fossil records of prokaryotic bacteria and cyanobacteria date back more than 3 billion years, while eukaryotes, such as gold algae and green algae, have been found in strata dated between 1.4 billion and 1.5 billion years ago. The diversity of life on Earth is so great that there are thought to be at least 6–14 million species on the planet, including animals, plants, and microbes. Others think that there are around 30 million species. About 1.75 million species have been identified. As the planet evolves, the species in biological communities are constantly changing: some species go extinct, and some new species emerge.

1.1.1 Species Classification

Classification dissects the parts of an individual of a given species to establish identification indexes from the features of various parts, such as body shape and organ structure (including anatomy, histology, and organology), the cell, the tissues, the organ process, and other parts of the organism. Based on the similarities and differences among systematic characteristics, biological groups are classified using a category-based system (*i.e.*, boundary, phylum, class, order, family, genus, and species).

There are millions of species living on Earth. Species classification means to classify, rank, and name living things according to certain rules. Humans have long identified and named species. Erya, a book written in the Early Han Dynasty of China, describes animals in four categories: insects, fish, birds, and beasts. J. Ray used genera and species to distinguish plants in 1682. In 1753, Carl Linnaeus divided nature into plants, animals, and microorganisms. He then organized animals and plants into a hierarchal system using boundaries, classes, orders, genera, and species. Each species occupies a place in the taxonomic system, forming a ranking system for species identification. In 1859, with the publication of Darwin's On the Origin of Species, the taxonomic system was established. Taxonomy is the elucidation of the historical origins of species, such that the classification system reflects evolutionary history. Taxonomy sets boundaries between species, analogous to the "bits" that define a species.

1.1.2 Fish

Fish are aquatic vertebrates that breathe using gills. Fish have a head, trunk, and tail with fins on the back, thorax, and abdomen. Fish swim in the water by moving the tail and trunk in coordination with the fins. The mouth is at the front or lower end of the head, and the fish feeds by closing the upper and lower jaws. Fish belong to the subphylum Vertebrata in the phylum Chordata. About 32 000 species of fish are found worldwide, distributed in the oceans and freshwater. Two-thirds of all fish live in the oceans, and the remainder inhabits freshwater.

1.1.3 Morphological Characters for Classification

Form refers to the appearance of things, or, under certain conditions, the form of expression. The body part of a species is a state that can be grasped, perceived, or understood. Morphological characteristics can also include the appearances and structures of organs, cells, and tissues, as well as the characteristics of organogenesis. Species morphology is the result of interactions within species communities during niche competition, which is determined by the relationships among species and between species and the environment. The morphological characters of species reflect competition, mutual benefit, and balance among species, as well as the regional habitat or environment. The morphological characteristics of species represent the characteristics reflected by the best niche in which the species is located.

1.1.3.1 Fish Morphology

1.1.3.1.1 Fusiform

Fusiform fish have spindle-shaped bodies that are slightly flattened. The head–tail axis is the longest, followed by the dorsal–ventral axis and the left–right axis. Fusiform fish swim well because their whole body is streamlined or slightly flattened to reduce drag as they move through the water. The basic fish body is spindle-shaped; this body type is shared among a number of different fish taxa, including carp, crucian carp, and sharks.

1.1.3.1.2 Oblate Sides

In fish with oblate sides, the left–right axis is the shortest, with the head–tail axis about the same length as the dorsal–ventral axis, forming a symmetrical flat shape from left to right. These fish live in the middle and lower layers of the water and are less able to swim than spindle-shaped fish. Fish with oblate sides include butterfish, bitterlings, and species in the genus *Acheilognathus.*

1.1.3.1.3 Club Type

Club-type fish have particularly long head–tail axes, with very short left–right and dorsal–ventral axes of nearly equivalent length. Thus, the body of the fish resembles a club or rod. Club-type fish, such as eels, are stronger swimmers than flat-sided or flat fish and often inhabit subaqueous holes in soil or sandstone.

1.1.3.1.4 Flat Type

Flat-type fish are sluggish because they have a particularly long left–right axis and a particularly short dorsal–ventral axis. Flat fish are benthic and include rays and flounder.

1.1.3.2 Body Composition

The body of a fish consists of a head, a trunk, and a tail. One of the differences between fish and land vertebrates is that the head and trunk of the fish are joined and thus cannot rotate with respect to one another. The dividing line between the head and the trunk is the posterior edge of the operculum in teleost fish or the hindmost pair of gill lobes in the Chondrichthyes. The trunk and tail are generally demarcated by the posterior edge of the anus or the beginning of the anal fin.

1.1.3.2.1 Spine

The spine joins the head and tail to form the trunk that supports the body. The spine consists of the vertebral body, vertebral arch, medullary spine, transverse process of the vertebral body, anterior articular process, and posterior articular process. The number of vertebrae from head to tail is one of the characteristics used in morphological classification.

1.1.3.2.2 Fins

Fish fins consist of skin and spines. There are three types of fin spines: soft spines, hard spines, and soft-hard mixed spines. The positions of the fins vary and include dorsal fins, pectoral fins, ventral fins, anal fins, and caudal fins. Fins also may have a variety of shapes. There are two kinds of fins, odd fins, and even fins. Odd fins are unpaired and include the dorsal fins, caudal fins, and anal fins. Paired fins include the pectoral and pelvic fins and correspond to the fore and hind limbs of terrestrial vertebrates. Each fish has a maximum of one pair of each type of paired fin. The basic functions of the dorsal and anal fins are to maintain balance, prevent tilting and rocking, and assist swimming. The caudal fin acts as a rudder, controlling the direction and propelling the fish forward. Fins with hard spines can also be used in attack or defense. In general, fish have five types of fins: pectoral, ventral, dorsal, anal, and tail. However, there are a few exceptions to this rule. For example, Monopterus albus has no even fins and has degenerated odd fins, Anguilla japonica has no abdominal fins, and Electrophorus electricus has no dorsal fins. Fin shape and quantity differ among fish taxa.

1.1.3.2.3 Scales

Scales, a class of skin derivatives, are a biological feature of certain fish and reptiles, as well as a small number of mammals and birds. Scales are generally flaky and have a protective effect. According to their origin, scales can be divided into bony scales (dermal scales) and cuticular scales.

1.1.3.3 Measurable Characters

Measurable characters are traits that can be measured. Measurable characters include plant or animal height or length. Measurable characters are easily influenced by the environment. Individual differences within a population generally fall along a continuous normal distribution, and it is thus difficult to group these differences. There are no qualitative differences among continuously varying individuals in a population, only quantitative differences.

1.1.3.3.1 Full Length

The full length refers to the length measured from the rostral end to the tail fork.

1.1.3.3.2 Body Length

Body length refers to the length measured from the rostral end to the junction of the trunk and the caudal fin.

1.1.3.3.3 Body Height

Body height refers to the height measured from the abdomen to the highest point of the dorsal fin.

1.1.3.3.4 Body Width

Body width refers to the thickness of the fish's body when placed flat.

1.1.3.3.5 Lips Length

The lip length of the fish is the distance between the front tip of the mouth and the mouth slit.

1.1.3.3.6 Eye Distance

Eye distance refers to the minimum distance between the two eyes.

1.1.3.3.7 Eye Diameter

The eye diameter refers to the diameter of the orbit.

1.1.3.3.8 Scale Formula

Scale form describes the characteristics of the scales covering the fish's body. The lateral line scales are a series of regular concave scales from the operculum to the tail stalk. The upper scale number refers to the complete scale number between the beginning of the dorsal fin and the lateral line. The under-scale number refers to the complete scale number between the beginning of the anal fin and the lateral line. Most fish have obvious lateral line scales, but some fish lack lateral line scales entirely.

1.1.3.3.9 Fin Formulas

Fin patterns are described using certain patterns of letters, numbers, and symbols. In most cases, the first letter of the English name for each fin is used to represent the fin category. For example, "D" corresponds to the dorsal fin, "A" corresponds to the anal fin, "P" corresponded to the pectoral fin, and "C" corresponds to the caudal fin. To avoid confusion, "V" is used for pelvic fin. Roman numerals in capital letters represent the number of hard spines and Arabic numerals indicate the number of soft spines. The apostrophe (‘) indicates the range of quantitative variation in the spines or soft spines. Hard spines connected to soft spines are denoted using a dash (-); hard spines not connected to soft spines are denoted using a comma (,).

For example, the fins of *Cyprinus carpio* (Linnaeus, 1758) are described as follows: DIII-IV-17-22; PI-14-16; VII-8-9; AIII-5-6; C20-22. This pattern indicates that *C. carpio* has a dorsal fin with three to four hard spines and 17–22 soft spines; a pectoral fin with one hard spine and 14–16 soft spines; a ventral fin with two hard spines and eight to nine soft spines; an anal fin with three hard spines and five to six soft spines; and a caudal fin with 20–22 soft spines.

1.2 Community

The biological community refers to all of the living things in a specific environment, including animals, plants, microorganisms, and other species. Typically, a "community" refers to organisms existing in a certain range of time and space. Biological communities have certain basic characteristics and can be described based on features such as species diversity, a form of community growth (including species types and growth state), community structure (including spatial structure, time composition, and species structure), dominant species (species in the community that play a decisive role in the community due to physical size, abundance, or activity), relative abundance (the relative proportions of different species in the community), and nutrition structure.

1.2.1 Composition

Composition describes the species composition of a biological community. Species composition is an important feature of a community, and habitat status affects community composition. The abundance of nutrients is an important indicator of environmental status, which affects species composition and diversity in a given community.

1.2.2 Proportion

Proportion refers to the quantitative spatial relationships among all of the conspecific individuals in a given community. These characteristics include proportion density, age structure, sex ratio, immigration rate, emigration rate, birth rate, mortality rate, spatial features, and other quantitative characteristics. Of these, proportional density is the most fundamental quantitative proportional characteristic and refers to the number of individuals per unit area or volume.

1.2.3 Structure

Community structure has spatial properties. Community structure is influenced by ecological conditions such as light intensity, temperature, humidity, and interspecific relationships. Each population in the community lives at the structural level corresponding to the most suitable ecological conditions for that particular population. Therefore, the specific ecological conditions determine the biological populations comprising the community. More complex community structures imply that the organisms use the resources in the ecosystem more fully. For example, the utilization rate of light energy in the forest ecosystem is much higher than that in the farmland and grassland ecosystems. The more complex the community structure, the more complex the environmental conditions and the more stable the community.

Community structures can be divided into horizontal and vertical structures. For example, the vertical stratification of trees, shrubs, and ground herbs is closely related to light availability, as is the stratification of underground and aquatic organisms. With respect to horizontal structure, different organisms may congregate in certain areas on the horizontal plane due to similarities among environmental requirements or interdependence. Community characteristics are usually determined by a number of dominant species.

1.2.4 Community Habitat

Community habitat is the spatial extent of abiotic factors in an ecosystem. Over evolutionary time, organisms gradually develop requirements for certain physical conditions and chemical components in the environment, such as air, light, water, heat, and inorganic salts. The life-form composition of a given community can reflect environmental characteristics, and the community habitat is the synthesis of the interactions between species and the environment.

1.2.5 Environment

The environment describes the overall living conditions, including energy, atmosphere, water, and soil. Due to mutualism, competition, parasitism, and predation among species in the community, the environmental factors pertinent to some species also include the biological environment formed by other species. Each population in a community requires specific ecological conditions, such as light intensity, temperature, humidity, food, and interacting species.

1.2.6 Ecological Characters

Ecological characteristics usually refer to the conditions necessary for the survival of a species. All living things need materials and energy and adapt to different physical and chemical conditions. The longer a community evolves, and the more favorable and stable its environment is, the more species it will contain. Therefore, the ecological character of a biological community is a complex system character.

1.2.7 Spatial Pattern

Spatial pattern refers to the distribution of species in space. For survival, activity, and reproduction, living things need a certain amount of space, material, and energy. In quantitative analyses, three types of distribution are often used to express the positional relationships of an individual in space: the uniform distribution describes the spatial pattern produced by the uniform distribution of individuals over a certain distance; the random distribution states that the likelihood of the appearance of an individual at a certain point in the space is random, and the position of one individual does not affect the distribution of other individuals; and the cluster distribution corresponds to an uneven distribution of biological individuals in space, with individuals often appearing in dense groups, clusters, or patches.

1.2.8 Temporal Characteristics

Different species inhabit different environments. Therefore, environmental conditions determine community composition. The community was in a state of dynamic stability during the evolution of the earth's environment, which was accompanied by species formations, lineage differentiation, population formation, and species extinction. The species' numbers in a community often change with time. For example, some flowers bloom and animals are active following a circadian rhythm, while the overall temperate and polar communities have obvious seasonal rhythms. Therefore, descriptions of community status must be accompanied by specific time ranges.

1.3 Niche

In nature, to avoid competition, closely related species, or species with very similar needs and habits, are often found in different geographical areas or different habitats within the same area; some such species may also adopt alternative lifestyles to avoid competition. For example, species may utilize different food sources or may be active at different times of the day or season. Organisms form niches according to the following principles: the principle of adaptation, the principle of competition, the principle of development, and the principle of balance. The adaptation principle states that an organism seeks a suitable ecological niche due to instinctive need. This adaptation behavior describes the constant change in resources needed by the organism. The competition principle occurs during the competition between different organisms for the same resources or environment. The principle of colonization refers to constant colonization and occupation of all of the available spare niches by organisms. The principle of balance states that, in open ecosystems, niche potential (*i.e.*, the competition-driven gap between the ideal niche and the actual niche) tends to decrease over time, because a system with too much ecological potential is unstable.

Niche content includes the region scope and the function of the organism itself in the ecosystem. In the natural environment, there are different biological communities in different ecological environments. The better the ecological environment, the more species make up the community and *vice versa*. Community habitat is the living space of community organisms, which together constitute the ecosystem. There are different kinds of living things in each particular position, and the activities and interactions of a given organism depend on its particular structure, physiology, and behavior. Therefore, each organism has a unique niche. The relationships among species and between species and the environment develop through niche competition. The concept of niche not only refers to living space but also emphasizes the function and status of the organism itself within the community, especially the nutritional relationship of a given species with other species.

Organisms in a community are constantly interacting. For example, organisms acquire nutrients *via* complex food relationships; plants photosynthesize, animals feed, and microorganisms capture nutrients through their body surfaces. Species relationships can be competitive or symbiotic, depending on the mutual interests of each species (*i.e.*, parasitic, partial symbiosis, and mutually beneficial). If two species utilize the same resources (niche overlap), they must compete, and one species will be excluded. However, if the resource demands of one species change (niche differentiation), the two species may coexist.

1.3.1 Ideal Niche

Ideally, species occupy a given niche without competition or disturbance. A niche has systematic characteristics that are measured based on its position in space, which is a portion of the position occupied by a given species in the total community space. Species account for the total energy demand of a community. Due to the multi-channel nature of species energy (for example, the energy of predatory species can be obtained from other species), niche relationships among species are complicated by energy space. Similar to time, air, water, and energy, it is difficult to determine the boundaries of space.

1.3.2 Real Niche

The ecological niche occupied by the environmental resources needed by a given species in a natural state under competition pressure is usually represented by variations in the breadth of a given species' niche as the environment changes. Niche studies usually focus on a certain time and space background. The conditions of the survival needs of a given species within the ecosystem are defined in the minimum threshold analysis.

1.3.3 Conservation

The niche is conserved because the community includes phylogenic characters. Therefore, when fish from the same family or genus inhabit the same community, the niches of neighboring species often differ (Cavender-Bares *et al.*, 2006). This is consistent with speciation characteristics: for every new species formed, a new niche is created within the community.

1.3.4 Multidimensionality

Niche is a combination of the physical environment (*e.g.*, energy, water, and habitat) and the biological environment (*e.g.*, mutualism, competition, parasitism, and predation). Each environmental factor becomes a dimension, meaning that the conceptual niche space is an N-dimensional hypervolumic space.

1.3.5 Overlap

Niche overlap refers to the phenomenon when two or more species with similar niches share or compete for common resources when they inhabit the same space. Competition among niche-overlapping species always leads to reductions in the degree of overlap, which may be affected by inhabiting or foraging in different spatial positions.

1.3.6 Niche Breadth

Niche breadth corresponds to the sum total of the different resources utilized by species. In the absence of any competition or other enemies, the total resources utilized are called the "original" niche. Owing to interspecific competition, it is impossible for an organism to utilize all of the resources of the ideal niche, and thus organisms occupy only the actual niche. The niche breadth of a species varies with the environment. Niche breadth is usually defined within the axis of an ecological factor.

1.3.7 Ecological Equivalents

Two organisms with similar functional niches, but distributed in different geographical regions, can be considered in some senses ecological equivalents. However, a given species will have a different niche in different communities. The niche of a species is determined by its diet and habitat.

1.3.8 Coincident Species

Scale form describes the characteristics of the scales covering the fish's body. The lateral line scales are a series of regular concave scales from the operculum to the tail stalk. The upper scale number refers to the complete scale number between the beginning of the dorsal fin and the lateral line. The under-scale number refers to the complete scale number between the beginning of the anal fin and the lateral line. Most fish have obvious lateral line scales, but some fish lack lateral line scales entirely.

1.3.9 Species Evolution and Niche

Species consist of groups of organisms with the same genetic characteristics. Individuals mate with one another to form populations with small genetic differences, aiming to maximize energy utilization and each occupying certain niches within the community. Species have an inherent tendency toward continuous differentiation, which drives the continuous subdivision of the earth's ecological niches. Due to competition for energy, populations differentiate into new species that make use of the original share of energy but do not compete with each other, forming new, complementary niches with the original species and becoming new members of the community. However, because each niche has a fixed energy capacity, species differentiation is restricted by an energy threshold. That is, the niche space cannot accommodate unlimited new species. As a result, species differentiation, population formation and extinction, and species niches within a community form a "stable" but dynamic equilibrium.

1.4 River Ecosystem Elements

A natural ecosystem is the unified composition of organisms within a specific environment. In an ecosystem, organisms interact with their environment and with each other in a state of dynamic equilibrium. Ecosystems are open systems. To maintain stability, the ecosystem must continuously input energy, and many basic materials in the ecosystem are continuously recycled. The total volume of the earth's water is 1.386 billion km, of which 96.53% is in the sea. Fresh water accounts for only 2.53% of the total volume of water resources, and 87% of the freshwater is in polar ice caps, Alpine glaciers, and permafrost. Rivers, freshwater lakes, and shallow groundwaters account for only 0.26% of the earth's total water volume, about 9000 cubic kilometers per year.

"Aquatic ecosystem" is a general term for the various aquatic ecosystems on the surface of the earth. The organisms in an aquatic ecosystem consist of autotrophs (*e.g.*, algae and aquatic plants), heterotrophs (*e.g.*, various invertebrates and vertebrates), and decomposers (*e.g.*, various microorganisms). All types of biological communities interact with the aquatic environment to maintain a specific materials cycle and energy flow; together, these communities constitute a complete ecological unit. The river ecosystem describes the ecosystem of a river water body ecosystem, which is a type of flowing water ecosystem.

1.4.1 Water Chemistry

Water, which is composed of hydrogen and oxygen, is a colorless, odorless, transparent liquid under normal temperature and pressure. In rivers and lakes, the ions naturally dissolved in the water are primarily potassium, sodium, calcium, magnesium, chlorine, sulfate, hydrogen carbonate, and carbonate ions, as well as micronutrients such as bromine, iodine, and manganese. River-water composition depends on the types of rocks and soil in the area over which the water flows and on the source of recharge. The degree of river mineralization is generally lowest with rainwater recharge, slightly higher with snowmelt recharge, and highest with groundwater recharge. There are more dissolved substances in groundwater than in surface water, and dissolved substances in groundwater are only weakly mixed. In general, rivers worldwide are moderately mineralized, with the exception of inland areas that receive little rainfall. Groundwaters are mostly weakly acidic, neutral, or weakly alkaline, with typical pH values of 5–9. The chemical composition of groundwater changes from shallow to deep groundwater: salinity gradually increases and the hydrochemical makeup of the water shifts from bicarbonate to sulfate/chloride.

1.4.2 Water Quality

Water quality is an index system that describes the quality of water containing dissolved substances. Considering the ecological function of the water, the contents of dissolved substances in the water are divided into different grades to indicate water quality, forming a water quality index. The quality of water is expressed by physical, chemical, and biological indices. Physical indicators of water quality include smell, temperature, turbidity, transparency, and color. There are four types of chemical indexes: (a) the non-specific indexes, including conductivity, pH value, hardness, alkalinity, and inorganic acidity; (b) the inorganic indexes, including toxic metals, toxic quasi-metals, nitrate, nitrite, and phosphate; (c) the non-specific organic indicators, including total oxygen consumption, chemical oxygen consumption, biochemical oxygen consumption, total organic carbon, the potassium permanganate index, and the phenolic index; and (d) the biological indicators, including the total number of bacteria, the number of coliform bacteria, and the number of algae. Radioactivity indicators include α-rays, β-rays, uranium, radium, and thorium. Some single indicators correspond to a physical parameter or the concentration of an expressed substance, such as temperature, pH, or dissolved oxygen. Other indicators reflect the shared characteristics of groups of substances that are indicators of water quality. Such indicators are known as composite indicators. For example, biochemical oxygen demand is an indicator of the level of biodegradable organic compounds in the water, while total hardness indicates the water content of inorganic salts, such as calcium and magnesium.

1.4.3 Aquatic Life

"Aquatic organisms" is a general term for organisms that inhabit various types of water bodies. Aquatic organisms are diverse, ranging from microorganisms and algae to aquatic vascular plants, invertebrates, and vertebrates. Aquatic organisms also have various lifestyles and may float, swim, be sessile, or dwell in caves.

1.4.3.1 Aquatic Bacteria

Aquatic bacteria are microorganisms that grow in water bodies. There are several types of aquatic bacteria, including cocci, bacilli, vibrios, and spirochetes. Bacteria have a simple structure, including a cell wall, plasma membrane, cytoplasm, and nucleus. Bacteria reproduce rapidly and divide once every 20–30 min. Bacteria have a wide distribution. The abundance of aquatic bacteria in a given water body is closely related to the fertility and quality of the water. Aquatic bacteria are part of the aquatic food chain and provide inorganic salts (*e.g.*, phosphates and nitrates), carbon dioxide, and water to plants by breaking down organic matter, including dead organisms. Autotrophic bacteria are primary producers, consuming nutrients for growth.

1.4.3.2 Phytoplankton

The term "phytoplankton," which refers to tiny aquatic, planktonic plants living in the water, is usually used for planktonic algae, such as the Cyanophyta, Chlorophyta, diatoms, Chrysomyta, Xanthophyta, dinoflagellates, cryptoalgae, and Gymnophyta. Changes in phytoplanktonic species composition, community structure, and abundance directly affect water quality, energy flow, material flow, and biological resources. Phytoplankton is also globally important for carbon and nitrogen fixation. The total amount of carbon and nitrogen fixed by phytoplankton in the oceans and freshwaters is seven times that of terrestrial plants. Phytoplankton fixes about 170 million tons of nitrogen each year. The world produces about 100 billion tons of carbon dioxide annually, about 50% of which is taken up by phytoplankton. Phytoplankton is not only the most important primary producers in aquatic ecosystems, but these organisms are also the main providers of aquatic dissolved oxygen. Phytoplankton plays a vital role in energy flow, material circulation, and information transmission in aquatic ecosystems.

1.4.3.3 Zooplankton

Zooplankton is heterotrophic invertebrates and notochordates found in the water column. Zooplankton includes a wide variety of species, including protozoans, coelenterates, ctenophores, rotifers, crustaceans, gastropods, uropods, benthos, fish larvae, and fish juveniles. Zooplankton is important components of aquatic ecosystems that not only feed on phytoplankton, bacteria, and organic detritus but also are preyed on by fish and aquatic animals.

1.4.3.4 Aquatic Plants

Aquatic plants are plants that grow in water. Aquatic plants absorb aquatic nutrients and water through their roots and fix nitrogen through photosynthesis in their leaves. These plants are an important part of the global energy cycle, as well as a major source of food for terrestrial and aquatic organisms. Generally, aquatic plants can be grouped into emergent plants, floating plants, submerged plants, and hydrophytes.

1.4.3.5 Benthos

The benthic fauna is aquatic animals that spend most or all of their life at the bottom of a water body. The organisms of the benthos are typically invertebrates, including mollusks, arthropods, crustaceans, and flatworms. Protozoans, such as common worms, benthic crustaceans, and bivalve mollusks, can use dissolved oxygen directly from the water. The secondary benthos mainly includes various aquatic insects and mollusks. Zoobenthos feed mainly on plankton and sediment.

1.4.4 Organic Detritus

Organic detritus includes the materials into which organisms decompose after death, the organic detritus formed by aquatic organisms, and the organic detritus imported from land, as well as large volumes of dissolved organic matter and its aggregates. Organic detritus is derived from intermediate products during the decomposition of dead organisms by bacteria (the final stage is inorganic), from food residues that are not fully ingested and digested, from the low-molecular-weight extracellular organic matter produced by phytoplankton during photosynthesis, and from the particulate organic matter imported from terrestrial ecosystems. Organic detritus can be used directly as food by certain organisms.

1.4.5 Productivity of Water Bodies

Productivity indicates the number of organisms produced by the water body per unit of time. It can be expressed as the rate at which solar energy is fixed by chloroplasts or the rate at which organic matter is produced by photosynthesis. Productivity units vary and include the weight of organic carbon/unit surface (body) product/unit time, and heat/unit face (body) product/unit of time. Primary productivity is the rate at which the total energy or total organic matter is produced by chloroplasts per unit surface product per unit time. Primary consumers transform primary productivity into their own material and energy, which is called secondary productivity. And so on for the third level of productivity, etc. The final production link in the food chain is referred to as ultimate productivity. The process of productivity is essentially a process of energy transformation and organic matter cycling for all of the levels of nutrients in an ecosystem.

1.4.6 Trophic Level

A trophic level refers to the level of an organism in the food chain of an ecosystem. The food energy flow in an ecosystem is graded according to an organism's position in the food chain. In an ecosystem, chloroplasts and other autotrophs are classified as the first trophic level and the starting point of the food chain; animals feeding on chloroplasts and autotrophs are classified as second trophic level (herbivores); carnivores that feed on herbivores are classified as the third trophic level; and carnivores that feed on carnivores are classified into higher trophic levels, such as the fourth and fifth trophic levels.

The nutritional relationship between the senior consumer and the underlying producers is called the food chain, which is both a material chain and an energy chain. Organisms located on the same link in the food chain are classified into the same trophic level, which simplifies the structure of the food web. Organism interactions are a form of food restriction, with chloroplast energy and nutrients derived from photosynthesis transferred up the food chain. However, only about 10% of photosynthesis-derived energy and nutrients are transferred to upper trophic levels; about 90% of the energy is returned to the environment as heat dissipation, which is known as Lindemann's 10th law.

1.4.7 Natural Balance

The natural balance refers to a state in which the relationship between the living and nonliving elements of a system is highly adaptive, coordinated, and unified. Within an ecosystem, producers, consumers, decomposers, and the abiotic environment maintain a relatively stable state of dynamic input and output of energy and matter within a certain period of time. External interference cannot disrupt the equilibrium among the proportional components of the system.

1.4.8 Water Pollution

Water pollution refers to poor sensory characteristics (*e.g.*, pungent smell and changes in watercolor), inorganic pollutants, organic pollutants, microorganisms, radioactivity, and five other categories of abnormality indicators. Pollutants can poison or affect aquatic organisms, leading to the reduction or extinction of organisms and resulting in ecological imbalance.

1.4.9 Algal Blooms

Algal blooms are a type of water pollution caused by excessive amounts of nitrogen and phosphorus in water bodies including rivers, lakes, and reservoirs. Nutrients in the water cause the rapid multiplication of algae and other plankton. This rapid increase in algal/plankton abundance cannot be supported by the food chain, leading to reductions in the dissolved oxygen content of the water. Thus, algal blooms can cause the die-off or extinction of algae, plankton, plants, fish, and other aquatic life, leading to the deposition of many dead aquatic organisms on the water bottom. During the decomposition of these organisms by microorganisms, large amounts of dissolved oxygen are consumed, further deteriorating water quality and accelerating the eutrophication of the water body in a vicious cycle.

1.5 Freshwater Fish

Freshwater fish are those that inhabit freshwater bodies such as rivers, lakes, and reservoirs. Freshwater fish also include migratory fish that migrate back and forth between freshwater and marine habitats. The migration of fish from the ocean to fresh water for reproduction is called anadromous migration (for example, *Acipenser sinensis*), and the migration from fresh water to the ocean for reproduction is called catadromous migration (for example, that of *Anguilla marmorata*). There are about 32 500 known fish species worldwide, of which about 15 000 are freshwater and about 10% are migratory.

1.5.1 Global Freshwater Fish Communities

There are a great variety of fish species worldwide, with Tedesco *et al.* (2017) reporting 14 953 species of freshwater fish belonging to 47 orders, 209 families, and 2298 genera (Richard van der Laan, 2017). Community composition ranges from simple to complex and is related to the watershed area (see table 1.1). Islands usually form in one of three ways: separation from the mainland, underwater volcanic eruptions, or marine corals that grow into reefs. Studies of freshwater fish species on small islands show that the fish community composition progresses from simple to complex; invasive alien species also impact the evolution process. For example, there are seven species of fish in the Azores, of which only one is indigenous and the remaining six are alien (see table 1.1). The composition of the fish community is simple (https://www.fishbase.de/2021,0810). It is also possible for native fish to differentiate into new species, such as the two species of Goby (*Awaous stamineus* and *Lentipes concolor*; Fishbase) found in Hawaii. In addition, there are 1603 freshwater fish species in China's interior, which are distributed in the Yangtze River, the Pearl River, and other water systems. Fish community composition differs strongly among river systems, reflecting differences in the ecological environment of each river basin. In nature, fish must form their own niche according to the function of the food web, thus developing a distinctive fish community and completing the same energy cycle functions in different river ecosystems.

The indigenous species in the community constantly adapt to changes in the environment and differentiate into new species. Simultaneously, the invasion of alien species also impacts the structure of the original community. Fish communities are constantly changing to adapt to changes in the environment, reflecting the characteristics of community structure constrained by space and time.

Tab. 1.1 – Fish community composition in some inland waters (Fishbase).

	Native species	Endemic species	Total species	Alien species
Azores	1Order 1Family 1Species	0Order 0Family 0Species	5Order 6Family 7Species	6
Hawaii (US)	3Order 4Family 7Species	2Order 2Family 4Species	14Order 24Family 60Species	53
New Zealand	8Order 12Family 42Species	6Order 6Family 21Species	12Order 16Family 62Species	21
Australia	27Order 56Family 349Species	6Order 16Family 136Species	32Order 67Family 379Species	30
South Africa	20Order 36Family 152Species	2Order 4Family 32Species	23Order 43Family 180Species	28
Angola	14Order 27Family 353Species	5Order 7Family 68Species	14Order 27Family 355Species	2
Zimbabwe	15Order 23Family 127Species	0Order 0Family 0Species	19Order 29Family 144Species	17
France	18Order 23Family 73Species	2Order 2Family 3Species	20Order 30Family 99Species	26
USA (North America)	27Order 43Family 896Species	2Order 8Family 370Species	34Order 60Family 963Species	67
Philippines	22Order 49Family 286Species	3Order 6Family 87Species	28Order 69Family 337Species	51
Malaysia	22Order 75Family 605Species	4Order 13Family 50Species	24Order 79Family 625Species	20
Vietnam	26Order 70Family 709Species	0Order 0Family 0Species	29Order 75Family 729Species	20
Thailand	27Order 75Family 806Species	3Order 9Family 19Species	29Order 82Family 828Species	22
Cambodia	25Order 72Family 462Species	1Order 1Family 1Species	26Order 75Family 475Species	13
China	24Order 74Family 1576Species	6Order 18Family 124Species	27Order 82Family 1603Species	27

1.5.2 Community Characteristics of Freshwater Fish in China

China is among the countries with the greatest number of rivers worldwide. Fishbase indicates that 1603 species of freshwater fish are found in China's inland waters. Zhang and Zhao (2016) studied the functional diversity of 1384 species of fish, while Xing *et al.* (2016) and Nelson *et al.* (2016) described more than 1000 species of freshwater fish endemic to China. The composition of the fish community in each river system reflects the adaptation of each species to the environment (see table 1.2).

The composition of the fish community varies from river to river. However, there are some fish taxa in larger rivers that are widely distributed, including *Mylopharyngodon piceus* (Richardson, 1846), *Ctenopharyngodon idella* (Valenciennes, 1844), *Elopichthys bambusa* (Richardson, 1845), *Squaliobarbus curriculus* (Richardson, 1846), *Hemiculter leucisculus* (Basilewsky, 1855), *Parabramis pekinensis* (Basilewsky, 1855), *Xenocypris argentea* (Günther, 1868), *Hypophthalmichthys molitrix* (Valenciennes, 1844), *Hypophthalmichthys nobilis* (Richardson, 1845), *Cyprinus carpio* (Linnaeus, 1758), *Carassius auratus* (Linnaeus, 1758), *Pelteobagrus fulvidraco* (Richardson, 1846), and *Siniperca chuatsi* (Basilewsky, 1855). Some fish species are widespread due to crust movements, which distributed homologous species to different areas. Others were introduced by human activities, and the number of these fish is increasing in the major rivers of the country. These species became important factors influencing local river ecosystems.

1.5.2.1 Cold Temperate Zone

The main families of fish in Heilongjiang waters are hardy species, such as three species of lampreys in the class Cyclostomata, 10 species of Salmonidae, two species of Aniseiidae, one species of Camelidae, and one species of Cyprinidae in the order Osmeriformes, *Lota lota* (Linnaeus, 1758), *Acipenser schrenckii* (Brandt, 1869), *Huso dauricus* (Georgi, 1775), and *Gasterosteus aculeatus* (Linnaeus, 1957). The cold temperate zone is characterized by a variety of fish, such as *Coregonus chadary* (Dybowski, 1869), *Esox reicherti* (Dybowski, 1869), *Phoxinus phoxinus phoxinus* (Linnaeus, 1758), *Rhynchocypris percnurus* (Pallas, 1814), *Gobio cynocephalus* (Dybowski, 1869), *Cyprinus carpio* (Linnaeus, 1758), *Carassius auratus auratus* (Linnaeus, 1758), *Silurus asotus* (Linnaeus, 1758), *Culter alburnus* (Basilewsky, 1855), *Hemibarbus labeo* (Pallas, 1776), and *Chanodichthys mongolicus mongolicus* (Basilewsky, 1855) (Zhang Chunguang *et al.*, 2020; Dong Chongzhi, 1996a, 1996b).

1.5.2.2 Mesothermal Zone

In China, much cold-water fish inhabit northeastern Mongolia and northern Xinjiang. Some of the fish here are characteristic of European waters, for example *Acipenser baeri* (Brandt, 1869), *Lucioperca lucioperca* (Linnaeus, 1758), *Thymallus arcticus arcticus* (Pallas, 1776), *Leuciscus idus* (Linnaeus, 1758), *Esox lucius* (Linnaeus, 1758), and *Perca fluviatilis* (Linnaeus, 1758), In addition, local species

Tab. 1.2 – Distribution of endemic fish species in the main rivers of China.

	Fish species	Endemic fish species	References	Author
The Yangtze	426	175	Freshwater fishes of China: species richness, endemism, threatened species and conservation [J]. Diversity and Distribution	Xing *et al.*, 2016
The Yellow	127	30		
The Pearl	682	243		
The Heilongjiang	124	9		
The Lancang River	890	202		
The Yili	21	2	Xinjiang ICHTHYOLOGY	Institute of Zoology, Chinese Academy of Sciences, etc., People's Publishing House, 1979
The Tarim	12	4		
The Irtysh River	16	4		
Nandu River	85	10	Freshwater and Estuarine ichthyography of Hainan Island Olor map of freshwater and estuarine fishes of Hainan Island	Pearl River Fisheries Research Institute, Chinese Academy of Aquatic Sciences, 1986; Xinhui Li *et al.*, 2020f

include *Coregonus ussuriensis* (Berg, 1906), *Osmerus mordax* (Mitchill, 1814), *Hypomesus* spp. (Gill, 1862), *Abramisbrama orientalis* (Berg, 1949), *Gobio acutipnnatus* (Men'shikov, 1939), *Brachymystax lenok lenok* (Pallas, 1773), *Hucho taimen* (Pallas, 1773), *Lota lota* (Linnaeus, 1758), *Pseudogobio vaillanti* (Sauvage, 1878), *Oncorhynchus keta* (Walbaum, 1792), *Cyprinus carpio* (Linnaeus, 1758), *Carassius auratus auratus* (Linnaeus, 1758), *Culter alburnus* (Basilewsky, 1855), *Hemibarbus labeo* (Pallas, 1776), and *Chanodichthys mongolicus mongolicus* (Basilewsky, 1855) (Cai Lingang *et al.*, 2017; Li Guogang *et al.*, 2017; Ren *et al.*, 2002; Li Shuguo *et al.*, 2000; Mu-Lian *et al.*, 1998; Dong Chongzhi, 1996a, 1996b).

1.5.2.3 Warm Temperate Zone

The warm temperate zone includes the Tarim River system, the Yellow River, the Yangtze River, the Hai River, and the Huai River. There is much warm temperate fish, including *Lampetra reissneri* (Dybowski, 1869), *Coregonus chadary* (Dybowski, 1869), *Rhynchocypris lagowskii* (Dybowski, 1869), *Cyprinus carpio* (Linnaeus, 1758), *Gymnocypris przewalskii* (Kessler, 1876), *Silurus lanzhouensis* (Chen, 1977), *Carassius auratus auratus* (Linnaeus, 1758), *Squaliobarbus curriculus* (Richardson, 1846), *Parabramis pekinensis* (Basilewsky, 1855), *Hypophthalmichthys molitrix* (Valenciennes, 1844), and *Hypophthalmichthys nobilis* (Richardson, 1845) (Li Sizhong, 2015; Cai Wenxian, 2013).

1.5.2.4 Subtropical Zone

The subtropical region, which includes the Yangtze River system and the Pearl River system, has the most abundant fish species. Many fish are characteristic of subtropical regions, such as *Acipenser sinensis* (Gray, 1834), *Acipenser dabryanus* (Dumeril, 1868), *Anguilla japonica* (Temminck and Schlegel, 1846), *Abbottina obtusirostris* (H. W. Wu and Ki. Fu. Wang, 1931), *Abbottina rivularis* (Basilewsky, 1855), *Acheilognathus* sp. (Bleeker, 1860), *Acrossocheilus fasciatus* (Steindachner, 1892), and species in the Culterinae. In the Yangtze River system, both the abundance and the richness of species in the Cyprinidae are very high, and this system can be regarded as the germplasm resource center for Cyprinidae in Asia. The main taxa characteristic of the Pearl River water system includes the Cyprinidae, Danioninae, Labeoninae, Barbinae, and the Siluriformes (*e.g.*, the families Akysidae, Cranoglanididae, Siluridae, Clariidae, Pangasiidae, Schilbeidae, and Amblycipitidae). The fish in the Lancang River system include species of Labeoninae, the loach genus in the loach family, the flat fin family, the Bagrid family, the catfish family, the finless eels in the Lamibranchia, and *Channa argus.* These fish are also found elsewhere in Asia, while the species of Schizostominae and loach are also found in the Northwest Plateau Region. Fish species from the Lancang River system are mixed with those from Asia and the Northwest Plateau Region. The fish taxa found in Lancang River and elsewhere in Asia include the Labeoninae, the Botiidae in Cobitidae, the Balitoridae, the Bagridae, *Silurus* (Linnaeus, 1758) in Siluridae, *Monopterus albus* (Zuiew, 1793), and *Channa argus* (Cantor, 1842). Similar to the

Northwest Plateau Region, there are also some species in the Schizostominae and Noemacheilinae.

1.5.2.5 Tropical Zone

The tropical regions of China are located in southern Yunnan, Leizhou Peninsula, southern Taiwan Province, and Hainan Province. Some of these fish, including species in the Labeoninae and Botiinae, are also found in India, Burma, Vietnam, and Thailand. Some fish in the Schizothoracinae are also found in the Northwest Plateau. The composition of the fish fauna is similar to that of Vietnam, Thailand, Myanmar, and India, with taxa including the Cyprinidae, Danioninae, Labeoninae, Barbinae, and various families in the Siluriformes (*e.g.*, Akysidae, Cranoglanididae, Siluridae, Clariidae, Pangasiidae, Schilbeidae, and Amblycipitidae).

1.5.2.6 Plateau Zone

The southern and southeastern parts of the Qinghai-Tibet plateau have dense river networks and are the source of many famous rivers in Asia, such as the Yangtze River, Yellow River, Salween River, Lancang River, Yarlung Tsangpo River, Ganges River, and Indus River. The well-known fish characteristic of the plateau includes the Schizothoracinae, Sisoridae, and *Triplophysa* (Rendahl, 1933) (China Digital Science and Technology Museum https://www.cdstm.cn; Qinghai-Tibet Plateau Fish Database, Institute of Northwest Plateau Biology, Chinese Academy of Sciences; http://ptsc.nwipb.cas.cn/lxwm/).

Chapter 2

Fish Morphological Models and Mechanisms

The natural environment is constantly changing as organisms adapt to and change with the environment. The species composition of the ecosystem community is restricted by time and space. Speciation changes with the environment, and when the change goes beyond the dimension of the species, new species, and new communities are formed.

Changes in species distribution and abundance are the key processes of niche evolution, but most previous studies do not address these areas (Gaston, 1996, 2009). Niche is affected by biotic and abiotic factors, so it is difficult to establish the system boundary. The species niche is affected by the size of the geographical range and the environmental changes over time (Gaston, K. J.; Fuller, R. A.). Species diffusion and habitat heterogeneity are the determinants of species distributions, and the need to reduce environmental uncertainties are well recognized (Wright *et al.*, 2006). Genetic isolation, genetic differentiation, individual or population variation, biological invasion, climate, and other scale factors have been proposed as the boundaries of species distributions (Sexton *et al.*, 2009), but reducing the influence of environmental uncertainties is still a challenge for community studies. Therefore, the applicability of the species distribution model (SDMS) to interspecific relationships still needs to be improved (Elith and Leathwick, 2009). Clarke and Warwick (1999) defined the length of the path as the distance between two species and the sum of the relationships between species and their environment. In this way, expressing the relationship between species is also essentially the embodiment of the community relationship. According to Hirzel *et al.* (2002), the niche theory of Hutchinson SA is indispensable for the establishment of models that objectively reflect the niche relationships of communities. Václavík and Meentemeyer (2009) stated that models of species distribution must solve the problems of questionable systematic data, uncertain systematic boundaries, and doubtful system representativeness. Many factors seem to be considered in studies of niche, but the "environmental factor" has no boundary, and artificial values tend to be subjective.

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The ecological niche of a species in a community is influenced by the complexity of the environment. However, within the same geographical region, the environmental conditions of each community species are the same, so the environmental factors are similar. Under such a conceptual background, the establishment of a model purely of interspecific relationships can avoid the problem of "environmental factors" without boundaries and can be used for community niche research. The morphological characters of a species are formed due to the interactions between species and the environment as well as among species. These traits also contain evolutionary information, reflecting the phylogeny of species (that is, information about environmental factors). Due to the differences among classification characters, species size, and food habits, the food chain has complementary ecological niches that are formed by energy utilization, and these differences reflect the ecological functions of the community. Morphological characters can also reflect the migration ability of a species, as well as the spatial characters or range of its habitat, such as air, land, water, and different water layers. We believe that characters with species-specific attributes are the key to deciphering the niche.

The river is a zonal ecosystem. Only fragmentary data can be collected at small scales, and the heterogeneity of the large-scale environment is so great that it is difficult to establish a research model that can systematically reflect the spatial niche relationships among fish. To solve the problem of environmental factors, we aim to characterize the niche relationships among species in the fish community based on morphological characteristics. In this study of fish communities, it is assumed that the morphological characters of species are a direct reflection of the interactions between species and the environment. Because "characters" are the result of interactions between species and environment, the term "integrated morphological character" is used to record "niche" information. In this book, the morphological characters of each species recorded in rivers are digitized, and a data information matrix for all of the species in the community is established. After character digitization, the recorded information includes the time and space boundaries of the system as well as the spatiotemporal dimension of the community, which solves the problem of determining community boundaries. In this type of community model, the defined species determine the boundary of the research system. Changes in the species community indicate that the studied system has changed. For example, species extinctions or speciation events are spatiotemporal changes in the system.

Over evolutionary time, a certain "trait" is determined by the "initiation" of a new niche formed by another species as part of its adaptation to the environment. It can be said that the characters of all of the species in the community include the "initial" characteristics when the niche is formed. Therefore, the "initial" characteristics present when communities were formed can be obtained. These results also give rise to the concept of the "initial" niche in interspecific relationships among communities. This concept should be compared with the "initial" reference frame in the context of drastic changes in the present environment. The results of this comparison might serve as the "initial niche" frame of reference.

Characteristic features are the basis of taxonomy, and community research reveals systems. The quantitative characteristics of the systematic morphology of a species reflect the evolution of that species in the community. By means of the quantitative transformation of traits into data that can be analyzed with a computer, trait data are transformed into image data, combining the theoretical niche hypothesis with real niche analysis and the image-information space transformation method to determine the species composition of the theoretical niche in the studied community and to provide an analytical method for evaluating community evolution and community species construction. Through the application of computer technology, data for n fish species are used to form a community data matrix describing "species + taxonomic characters." This matrix is transformed using multivariate statistics, reducing the dimensions of Galway's information to a "projection" in the Cartesian coordinate system. After model implementation, the n species in the community are distributed in the two-dimensional plane in the form of a niche (scattered points). The n sites in the plane reflect the fixed relationships among species in the community. In a community composed of n species of fish, the niche summation value of each species of fish is equal to "1." It is difficult to disassemble the niche quantitation value of n species of fish from "1." It is difficult to disassemble the niche quantitation value of n species of fish from "1."

It is assumed that the positions in the Cartesian coordinate system reflect the ecological spatial relationships among the species in the community and that these species have quantitative attributes that are key to the quantification of relative community species abundance. Thus, when deriving the niche value, if the niche value assigned to n species of fish is Xi ($i = 1, 2, 3, \ldots, n$), then $\sum \text{Xi} = 1$. In the digital matrix describing the morphological traits of n species, the number sequence of the numerical group Xi (which is a random number sequence that is a variable factor in the matrix) is newly introduced as the assumed niche value of each species (a random number or the measured abundance ratio of each species in the community) to construct a new matrix including "species (assumed n species) + taxonomic traits + assumed niche value." At this point, in the two-dimensional graph of the model analysis, in addition to the original n species of fish, a site "A" is identified, where "A" corresponds to the sequence of variable numbers that varies with the number of species in the studied community in the data matrix. In the following 19 fish examples, "A" is the number "20" in the two-dimensional graph studied, and the distance between "A" and the origin of the coordinates is defined as the niche deviation. The farther "A" is from the origin of the coordinates, the more unbalanced the niche of n species in the community. In contrast, when the deviation value is "0," the ecological niche of each species in the community is in the most reasonable relationship equilibrium among species. Therefore, the deviation value can be used as a measure of the adaptation of a community of species to environmental changes.

The matrix analysis model of morphological parameters, which integrates the essential taxonomic features, expands the application of character difference analysis in the quantitative community niche. A high-dimensional analysis model of morphological parameters was established to study community composition from the perspective of spatial niche. The random sample analysis method avoided the concept of species boundaries in reality and was especially suitable for the analysis of community standards and for community reconstruction. In this study, only the characteristics of species were used to study community structure, which eliminated the disruptive effects of uncertainty with respect to environmental factors and revealed the community-species relationships more clearly.

In this model, the two-dimensional coordinates "species + taxonomic characters" were used as the reference frame. By "correcting" the "A" value (usually deviating from the origin of the coordinates) in the "Species + taxonomic traits + assumed niche" value ("A") to "0," the niche value "A" of each species in the community (total value "1") was obtained. The result of this iteration corresponding to "A" was regarded as the proportional abundance of the fish in the community and the niche value of the fish in the community. Under this analysis model, the value of the "vector" (actually the scalar) of each fish in the two-dimensional graph was iterated, and the value of the niche of each fish was adjusted, such that the "A" point approached the origin of the coordinates, generating the "A" result. The "A" results reflect the proportion of species in the study community, that is, the estimated value of the natural niche.

Taking the species in a fish community as a unit, the method for examining interspecific relationships was established with taxonomic parameters as variables. The boundary of this research system is determined by the species, and the most suitable niche relationships among species in the community are defined by the positional relationships among species in the model and are equivalent to the ideal niche relationship. Under the ideal niche state, the proportion of each species in the community (*e.g.*, space, abundance, and biomass) is in the most reasonable state. That is, at the state of maximum utilization of energy in the ecosystem, the comprehensive value of the antagonistic rate among species was "0." Due to abrupt changes in the environment, niche imbalance is reflected in variations in species niches, which are in turn reflected in variations in abundance and biomass. Niche imbalance leads to an imbalance among species proportions in the community, and the absolute value of the comprehensive antagonism rate among species will be greater than "0." Therefore, niche deviations between "0" and an absolute value greater than "0" identified by the model can be used to establish a control system to evaluate community status (or to reconstruct community species) and thus to solve the difficult problem of evaluating community change. In this chapter, we introduce the method used to establish a quantitative model to evaluate the niche of a species within a community.

2.1 Multivariate Statistics

Multivariate statistical analysis (MSA) can be used to analyze the characteristic rules of multiple interrelated objects and indexes. If each individual has multiple observations that can be represented as a p-dimensional Euclidean space, the data are called multivariate data, and the statistical method for analyzing multivariate data is called multivariate statistical analysis.

Multivariate statistical analyses can be divided into narrow-sense and broad-sense methods. The narrow-sense multivariate statistical analysis assumes that the data distribution is a multivariate normal distribution; otherwise, the data are referred to as generalized. Narrow-sense multivariate analyses are widely used. There are several important classifications of multivariate methods that are based on the nature of the practical problems handled.

2.1.1 Regression Analysis

Regression analysis is a statistical analysis method that quantifies the interdependence between two or more variables. Based on the number of dependent variables involved, regression analyses are divided into univariate regression analyses and multiple regression analyses. If the relationship between an independent variable and a dependent variable can be expressed in an approximately straight line, the regression analysis is called a univariate regression analysis. A regression analysis is said to be a multiple regression analysis if it includes two or more dependent variables in a linear relationship. The relationships between independent and dependent variables can be divided into univariate regression analysis and multiple regression analysis.

2.1.2 Linear Discriminant Analysis

Certain classification conditions of various eigenvalues can be used to determine the type of research object. The basic principle is to establish one or more discriminant functions according to certain discriminant criteria, to use a large amount of data about the object to discriminate the undetermined coefficients in the functions, and to calculate the discriminant indexes. Thus, it is possible to determine the classification of the sample. Sample classification methods can be divided into parametric and non-parametric methods, as well as qualitative and quantitative data discriminant analyses. Based on the number of discriminant data sets, discriminant analyses can be divided into two-group and multi-group discriminant analyses; based on the mathematical model used in the discriminant analysis, discriminant analyses can be divided into linear and non-linear discriminant analyses; and based on the method used to process variables, discriminant analyses can be divided into step-by-step and sequential discrimination analyses.

2.1.3 Cluster Analysis

Cluster analysis, which is also called group analysis, groups sets of physical or abstract objects into classes composed of similar objects and classifies the data sources into different clusters by measuring the similarity among different data sources. Cluster analysis is an exploratory analysis for classification; because it is not necessary to give the classification criteria in advance, it is possible to perform automatic classification starting from the sample data. Using different cluster analysis methods will often generate different clusters. Thus, researchers must determine whether the analysis results are applicable.

2.1.4 Principal Component Analysis (PCA)

PCA is a multivariate statistical analysis method, in which several variables are transformed into a few representative variables by a linear transformation. The process aims to recombine the original variables into a new set of independent composite variables. Based on the research object, as few comprehensive variables as possible can be used to reflect the original variable. PCA is also a method used in mathematics to reduce the dimensions used.

2.1.5 Correspondence Analysis

Correspondence analysis is also called association analysis and R-Q factor transformation analysis. The associations between variables were revealed by analyzing the interaction summary table of samples and variable composition. If the subject is a sample, then Q-type factor analysis is used; namely, the factor analysis for finding the common factor for the sample. If the subject is a variable, then R-type factor analysis is used; namely the factor analysis for finding the common factor for the variable. Correspondence analysis can reveal the differences among different categories of the same variable and the corresponding relationships among different categories of different variables. Correspondence analysis can also reduce the dimensions of many samples and many variables simultaneously on the same graph according to the internal relationships of the factor R- and Q-type data. In this analysis, the categories and attributes of the samples are directly and clearly shown on the graph. Correspondence analysis not only classifies samples directly, but it can also indicate the main parameters (main factors) and reveal the basis for classification. Correspondence analysis can omit complicated mathematical operations as well as intermediate processes such as factor selection and factor axis rotation.

2.1.6 Factor Analysis

Factor analysis refers to the extraction of common factors from the group of variables to find hidden representative factors. Grouping variables of the same nature into a single factor reduces the number of variables and tests hypotheses of relationships among variables.

2.1.7 Canonical Correlation Analysis

Canonical correlation analysis is the study of the correlation between two groups of random variables. In the two groups of variables, the representative comprehensive variables U_1 and V_1 (the linear combination of the variables in the two groups of variables) are extracted, and the correlation between the two comprehensive variables is used to reflect the overall correlation between the two groups of indicators.

2.2 Morphological Data Model

It is difficult to include complete community species data in the model or actual evaluation, which results in an incomplete model analysis. Species with small distributions are difficult to monitor due to their small niche and small population, and it is difficult to integrate such species into the model system. The species data for historical communities can be used to accumulate recorded species distribution data based on systematic data. These data can reflect the relationships within the species community, as well as the structure and function of the ecosystem. The origin and development of species interactions in contemporary ecosystems can also be revealed through the comparative analysis of phylogenetic community structure. Studies of the phylogenetic structures of communities, including different species and trophic levels across various spatial and phylogenetic scales, also contribute to our understanding of trait evolution (Vamosi *et al.*, 2009).

In nature, speciation, competition among species, mutual benefit, and relationships with the environment are essential elements of the community. Relationships among species affect community status, and community composition is related to geographical range (Anderson and Raza, 2010). This indicates that determining how to select the "community" and the "species distribution area" is critical for modeling studies, and the "boundary" of a community is difficult to determine in reality. Macroscopically, all of the species in a community inhabit the same environment, and the results are "fair" to all of the species in the model when the same factors are removed for examinations of the community niche. The results of such studies of interspecific relationships among communities may be purer. Moreover, in community studies, the corresponding species, with the exception of the target species, can be considered part of the environmental conditions, and the taxonomic characters of each species are the result of the interactions between the species and the environment as well as among species. Therefore, pure biological traits actually contain "environmental" information and objectively do not exclude "environmental factors."

Fish characters can reflect the ecological function of the fish, and the trophic level of the fish corresponds to its special functional morphology. For example, *Siniperca kneri* (Garman, 1912) has a large, high head, a forward dorsal fin, and large, upturned eyes, while *Ancherythroculter lini* (Luo, 1994) and *Ochetobius elongatus* (Kner, 1867) have fusiform bodies, rearward dorsal, and caudal fins, deeply forked tails, long, narrow caudal handles, and small heads, all of which are favorable for hunting with speed. The intestine of herbivorous fish is longer than that of carnivorous fish, which is related to the energy acquisition process and the energy niche of the species. The size, eye position, eye diameter, mouth position, and mouth beard are related to predation and niche. The functional process of the fish in the ecosystem is embodied by the food chain, in which each species is a basic functional unit. Because species are related to characters, species characters are in turn related to species' function in the ecosystem. Different fish have different characters, which represent species characters. The model of community characters can be used to analyze the species relationships in a community. This book uses taxonomic morphological characters to study community characteristics. The same environmental factors are not considered in the model. The model adopts the correspondence analysis method of multivariate statistics.

2.2.1 Data Source

Based on the morphological characters used in fish taxonomy (Guangxi Zhuang Autonomous Region Institute of Aquaculture, 2006; Zhu Jiang Institute of Aquaculture, Chinese Academy of Aquatic Sciences, 1986, 1991; Chu *et al.*, 1989, 1990; Wu *et al.*, 1963, 1964, 1989; Zheng, 1989; Hunan Provincial Institute of Aquatic Sciences, 1977; Zhang, 1960), a total of 59 traits used to identify fish species were extracted as candidate modeling factors. Morphological traits were digitized into distinguishable values. Qualitative traits, such as "mouth position," are usually described as "mouth superior," "mouth inferior," and "mouth end" in fish taxonomy, and these three types can be digitized as "1," "2," and "3," respectively. Similar features, such as "caudal fin obtuse," "caudal fin pointed," "caudal fin circular," and "caudal fin forked" were distinguished using the numerical values "1," "2," "3," and "4," respectively. The numerical values of quantitative traits can be presented directly in a matrix table. The values of the 59 taxonomic characters are shown in table 2.1.

2.2.2 Data Matrix

To model the inter-species relationships in the fish community, it is necessary to record fish community sample data and construct a matrix of quantitative taxonomic characters. The n lines (from 1 to n in formula 2.1 represent the species in the studied fish community (that is, the sample for the statistical analysis of the model). P is a data column (from 1 to p) used to identify the taxonomic traits (*i.e.*, the variables for the statistical analysis of the model) of each species in the community; column p contains both qualitative and quantitative data.

A data matrix with n samples, p factors, and a target (column p + 1), where each sample corresponded to the factor data Xij and target data Yi (where the software runs and the model does not need a target factor, but still adds a dummy value), was constructed as follows:

$$\begin{pmatrix} \mathrm{X}_{11}, \mathrm{X}_{12}, \ldots\ldots \mathrm{X}_{1\mathrm{p}}, \mathrm{Y}_{1} \\ \mathrm{X}_{21}, \mathrm{X}_{22}, \ldots\ldots \mathrm{X}_{2\mathrm{p}}, \mathrm{Y}_{2} \\ \ldots\ldots \\ \mathrm{X}_{\mathrm{n}1}, \mathrm{X}_{12}, \ldots\ldots \mathrm{X}_{\mathrm{np}}, \mathrm{Y}_{\mathrm{n}} \end{pmatrix}_{\mathrm{n}(\mathrm{p}+1)} \tag{2.1}$$

Formula 2.1 Model data matrix.

Tab. 2.1 – Morphological classification parameters and differences among several fish*.

I: Fish, II Morphological classification parameters, III Character numbers	III II I	*Mylopharyngodon piceus* (Richardson, 1846)	*Misgurnus anguillicaudatus* (Cantor, 1842)	*Rhinogobius giurinus* (Rutter, 1897)
1	Mouth position	3	3	3
2	Caudal fin character	3	2	1
3	Number of air bladders	2	2	0
4	Upper jaw/lower jaw	1.5	1.5	0.1
5	Gill raker I	0	0	0
6	Gill raker II	18	36	9
7	Lingual tooth	0	0	0
8	Hypopharyngeal teeth I1	4	0	0
9	Hypopharyngeal teeth I2	0	0	0
10	Hypopharyngeal teeth I3	0	0	0
11	Hypopharyngeal teeth II1	5	0	0
12	Hypopharyngeal teeth II2	0	0	0
13	Hypopharyngeal teeth II3	0	0	0
14	Dorsal fin spine I	3	3	6
15	Dorsal fin spine II	0	0	1
16	Dorsal fin branched rays	7	8.5	8.5
17	Hard spine of anal fin	3	2	1
18	Anal fin branched rays	8	5	7.5
19	Hard spine of pectoral fin	1	1	0
20	Pectoral fin branched rays	16	12.5	18.5
21	Hard spine of ventral fin	1	1	1
22	Ventral fin branched rays	8	7	5
23	Body length/body height I	3.7	3.6	4.2
24	Body length/body height II	3.8	4.05	4.6
25	Body length/body height III	3.9	4.5	5

TAB. 2.1 – (Continued).

I: Fish, II Morphological classification parameters, III Character numbers	III II I	*Mylopharyngodon piceus* (Richardson, 1846)	*Misgurnus anguillicaudatus* (Cantor, 1842)	*Rhinogobius giurinus* (Rutter, 1897)
26	Body length/head length I	3.5	3.5	2.9
27	Body length/head length II	3.65	3.55	3
28	Body length/head length III	3.8	3.6	3.1
29	Head length/length of lips I	4	2	2.8
30	Head length/length of lips II	4.3	2.25	2.95
31	Head length/length of lips III	4.6	2.5	3.1
32	Head length/eye diameter I	5.2	4.5	4.9
33	Head length/eye diameter II	5.4	5.2	5
34	Head length/eye diameter III	5.6	5.9	5.1
35	Head length/interorbital width I	2.3	3.6	6.5
36	Head length/interorbital width II	2.35	4.2	7
37	Head length/interorbital width III	2.4	4.8	7.5
38	Tail stalk length/tail stalk height	1.38	1.08	2.25
39	Lateral line I	42	0	0
40	Scale above lateral I	6	0	0
41	Scale above lateral II	6	0	0
42	Scale above lateral III	6	0	0
43	Scale below lateral I	4	0	0
44	Scale below lateral II	4	0	0
45	Scale below lateral III	4	0	0
46	Lateral line II	43	0	0
47	Anterior dorsal fin scale I	15	0	20
48	Anterior dorsal fin scale II	16	0	45
49	Anterior dorsal fin scale III	17	0	70
50	Coccygeal scale I	16	0	12

TAB. 2.1 – (continued).

51	Coccygeal scale II	16.5	0	19
52	Coccygeal scale III	17	0	26
53	Mouth length/eye diameter	1.4	2.5	1.8
54	Maxillary barbel	0	1	0
55	Mouth barbel (a pair)	0	2	0
56	Dorsal fin position I	2	2	1
57	Dorsal fin position II	2	3	4
58	Shape of dorsal fin	1	1	2
59	Number of ventral fins	5	5	3

[*] "0" indicates no such trait was present.

2.2.3 Principles of the Correspondence Analysis Model

Correspondence analysis is a combination of R-type factor analysis and Q-type factor analysis. By transforming the matrix data, the relationship between each row and column in the data table is represented by a low-dimensional graph that reveals the differences among different categories of the same variable and the corresponding relationships among different categories of different variables. This analysis is also known as correlation analysis or R-Q factor transformation analysis (Yu and Ren, 1999; Luo *et al.*, 1986). This analysis mainly reflects the internal relationships between the factors and the different sides of the sample as a whole. To reflect the factor information, as well as the samples and the relationships between factors and samples, on a two-dimensional surface, the model combined R-factor analysis and Q-factor analysis statistically. The results of the Q-type factor analysis were obtained directly from the R-type factor analysis. Between these steps, we used transition matrix Z to find covariance matrix A of the variable and covariance matrix B of the sample. Then, we determined the eigenvalues of A and the eigenvectors of B. Finally, the load matrix of the R factor and the Q factor was obtained, such that factor and sample information was available in the same two-dimensional plane.

To determine the covariance matrix of variable A, we first find the covariance matrix of the i and j variables as well as W_{pn} (where p is the factor number and n is the sample number). For example,

$$Z_{pn} = W_{pn}. \tag{2.2}$$

The covariance matrix of the variable is

$$A = Z', \text{where } Z' \text{ is the transposed matrix of } Z\ldots \tag{2.3}$$

In variable R factor analysis, the factor axis F_α is the product of the eigenvector of matrix A and the square root of its corresponding eigenvalues, namely,

$$\begin{gathered} F_\alpha = (u_{1\alpha}, u_{2\alpha}, \ldots, u_{p\alpha})' \sqrt{\lambda_\alpha} \\ (\alpha = 1, 2, \ldots, m, m < p), \end{gathered} \tag{2.4}$$

where λ_α is the eigenvalue of matrix A (and the contribution of the α factor to the total variance) and $(u_{1\alpha}, u_{2\alpha}, \ldots, u_{p\alpha})'$ is the eigenvector corresponding to λ_α.

Using the same method, we can find the covariance matrix B of the sample, which is

$$B = Z'Z. \tag{2.5}$$

The number of principal factors and the load matrix of the R-type factor are calculated as follows: According to the theorems of linear algebra, both the A and B matrices have the same characteristic non-zero root. Thus, the result of the Q-type can be obtained directly from the R-type factor analysis. We then use $A = ZZ'$ to find the result of $\lambda_1 \geq \lambda_2 \geq \cdots \lambda_p$. When the cumulative variance contribution rate to $(\lambda_1 + \lambda_2 + \cdots + \lambda_m)/(\lambda_1 + \lambda_2 + \cdots + \lambda_p) \geq 70\%$–$85\%$ (the lower limit is 70% when $m \geq 10$, and 85% when m is less than 10%), m is the number of main factors.

After choosing the m of $\lambda_1 + \lambda_2 + \cdots + \lambda_m$ and the corresponding unit of U_1, U_2, ..., U_m, we can obtain the R-type factor load matrix as follows:

$$F = (u_{i\alpha}\lambda_\alpha)_{pm} \tag{2.6}$$

The load matrix of the Q-factor is determined as follows: Because $B = Z'Z$, the preceding eigenvalues are $\lambda_1 \geq \lambda_2 \geq \cdots \lambda_m$, and the corresponding unit eigenvectors are $V_1 = Z'U_1$, $V_2 = Z'U_2$, ..., $V_m = Z'U_m$. Therefore, the load matrix of the Q factor is

$$G = (V_{j\alpha}\lambda_\alpha)_{nm}. \tag{2.7}$$

Using the load of the R-factor and Q-factor, the reduced-dimensional diagram of the variable (factor) and the sample point can be positioned on the plane of the two-factor axis.

2.2.4 Contribution to Variance

In multivariate statistical analysis, it is necessary to transform the m original variables linearly and to construct m new variables (called principal factors or principal components). Each new variable contains m information about the original variables, but the new and original variables are independent of one another. When calculating the eigenvalues λ_i and the eigenvectors of each principal component, the first principal component has the largest variance, the second principal component has the second largest variance, and the last principal component has the smallest variance. The ratio of the variance each principal component to the total variance (referring to each of principal axis in the reduced dimension graph) is the variance contribution ratio, which also reflects the relative total information contained in each principal axis in the reduced-dimensional graph. The variance contribution rate can be understood as the proportion of information: higher contribution rates indicate more important principal components. The contribution to the variance of the first principal component is

$$\lambda_i/(\lambda_1 + \lambda_2 + \lambda_3 + \cdots + \lambda_m). \tag{2.8}$$

In multivariate statistical analysis, it is necessary to know the variance contribution rate of each principal axis. The higher the variance contribution rate of the principal axis, the higher the information occupancy rate and the stronger the objectivity and reliability of the analysis. When the high-dimensional data information in the matrix is reduced to a two-dimensional graph, the cumulative variance contribution rates of the first and second principal axes represent the credibility measures of the graph interpretation. If the variance contribution rate of the first and second axes is more than 75% (if the dimension is higher, this accumulated-value requirement can be reduced appropriately), the total information contained in the two-dimensional graph is more than 75%. The selection of model parameters should carefully consider the variance contribution rate and its cumulative value. The larger the variance contribution rate and its cumulative value, the higher the information credibility of the two-dimensional graph. In general, the variance contribution of the first principal axis is greater than that of the second principal axis, in which case the position of the sample (or variable) point on the horizontal axis is more important than the position of the second principal axis. Thus, the influence of the sample (or variable) point on the absolute value of the first principal axis is usually greater than that on the absolute value of the second principal axis.

In the two-dimensional graph of the fish community model, adjacent sample points were closely related and were regarded as generally similar sample points. These factors were also assumed to have a similar influence on the sample points and were classified into the same class. The closer the relationship between the sample and the factor, the greater the influence of the factor on the sample. However, in the study of point-to-point relationships, it is also necessary to pay attention to the difference in the variance contribution rate of the different axes (information ratio) and its impact on the results.

2.2.5 Graph Representation of the Interspecific Relationships Within Fish Communities

The results of the inter-species relationship model of fish communities were represented as a two-dimensional graph. In other words, the different coordinates (values) of the x- and y-axes on the plane map were used to study the relationship between different community types (samples) and various common characters (variables). According to the information provided by the matrix, the points were distributed in the two-dimensional plane in a way that could be distinguished during model operation. The numbers marked on the four corners of the plane map were the maximum and minimum values of the coordinate axis of the interspecific relationship within the community. The line between the origin of the two-dimensional graph and the locus of the sample or variable reflected the vector (length) of the sample or variable, and this vector was regarded as a measure of the spatial relationships within the community. Three kinds of two-dimensional distribution graphs were obtained *via* model analysis.

2.2.5.1 Relationships Between Species and Traits

The results of the correspondence analysis of the species-character matrix of the community were shown on a two-dimensional plane. The species and traits were represented by graph points, and the black circle represented the species; these were numbered according to the sequence in the matrix. The red circle represented the character, and the numbers corresponded to the "character sequence number + maximum number of species" from the matrix (*i.e.*, if the number of species was 1, 2, 3,…, 10, then the character number 1 was "1 + 10" in the graph or character number 11, and character number 2 was 12). The line connecting the circle (red or black) to the origin of the coordinates (red or black) indicated the positional relationship between the species or trait and the coordinate system, the value of which is determined by the value of the x- and y-axes indicated by the graph angle (see figure 2.1).

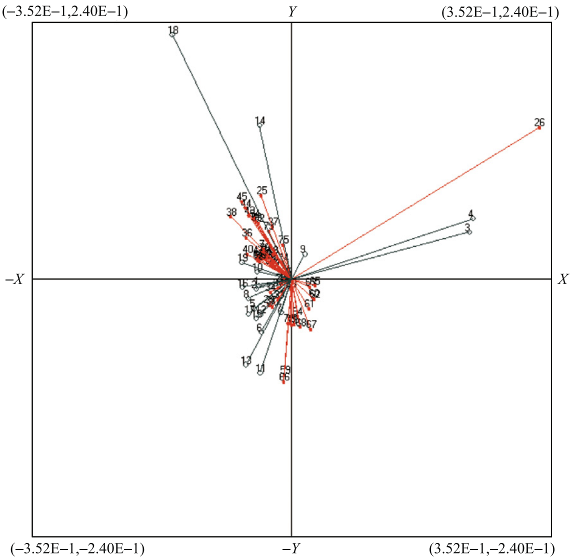


Fig. 2.1 – The two-dimensional graph of the 19 species × 59 trait matrix, showing the sample-character relationships.

Figure 2.1 shows the result of the model analysis of the 19 × 59 matrices composed of 19 fish species as communities and the 59 taxonomic characters listed in the table (see table 2.1). The numbers 1–19 represented 19 different species of fish, as follows: “1,” *Mylopharyngodon piceus* (Richardson, 1846); “2,” *Ctenopharyngodon idella* (Valenciennes, 1844); “3,” *Hypophthalmichthys molitrix* (Valenciennes, 1844); “4,” *Hypophthalmichthys nobilis* (Richardson, 1845); “5,” *Megalobrama terminalis* (Richardson, 1846); “6,” *Parabramis pekinensis* (Basilewsky, 1855); “7,” *Xenocypris argentea* (Günther, 1868); “8,” *Squaliobarbus curriculus* (Richardson, 1846); “9,” *Cirrhinus molitorella* (Valenciennes, 1844); “10,” *Cyprinus carpio* (Linnaeus, 1758); “11,” *Elopichthys bambusa* (Richardson, 1845); “12,” *Ochetobius elongatus* (Kner, 1867); “13,” *Siniperca kneri* (Garman, 1912); “14,” *Sinibotia pulchra* (Wu, 1939); “15,” *Hemiculter leucisculus* (Basilewsky, 1855); “16,” *Squalidus argentatus* (Sauvage and Dabry de Thiersant, 1874); “17,” *Pseudolaubuca sinensis* (Bleeker, 1865); “18,” *Lcucosoma chinensis* (Osbeck, 1765); and “19,” *Rhinogobius giurinus* (Rutter, 1897). The numbers 20–78 represented different variables (*i.e.*, taxonomic parameters) in the order shown in table 2.1.

2.2.5.2 Interspecific Relationships

The results of the species-character matrix of the community were graphed on a two-dimensional plane. The species were represented by numbered circles, and the numbers were derived from the serial numbers of the species in the matrix. The line connecting each circle to the origin of the coordinate system indicated the positional relationship between the two coordinate systems. The value of the line was determined by the value of the x- and y-axes indicated by the graph angle. Figure 2.2 only shows the results of 19 species.

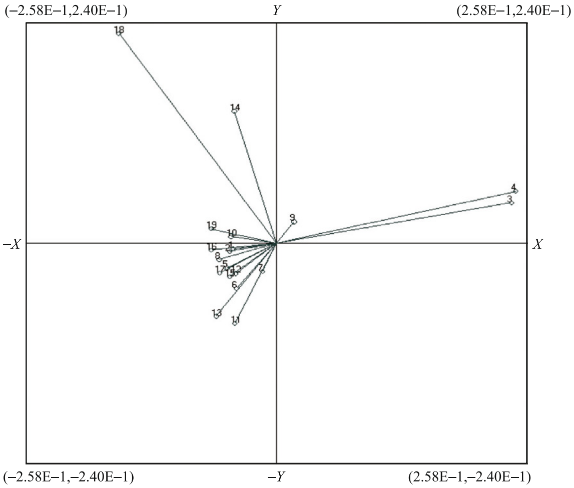


FIG. 2.2 – The two-dimensional graph of the 19 species × 59 traits matrix, showing the interspecific relationships.

2.2.5.3 Character Relationships

The results of the species-character matrix of the community were shown on a two-dimensional plane, with the red circles representing different characters. The characters were numbered following the "maximum number of species + character sequence number" in the matrix. Figure 2.3 shows the results of the variable such as the 59 different characters (numbers 20–78) in figure 2.1.

2.2.5.4 Coordinates

After reducing the dimensions of the inter-species relationships, each species corresponded to coordinates in the two-dimensional result map. In the same data matrix, changes in the position of a row (character factor) or column (fish sample) did not affect the two-dimensional coordinate value of each species in the community. That is, each coordinate was unique. Of course, different species and numbers, as well as different character factors and numbers, constitute different data matrices, showing that the coordinates of different fish differ. Table 2.2 shows the coordinate values for 19 species of fish based on the data in figure 2.1.

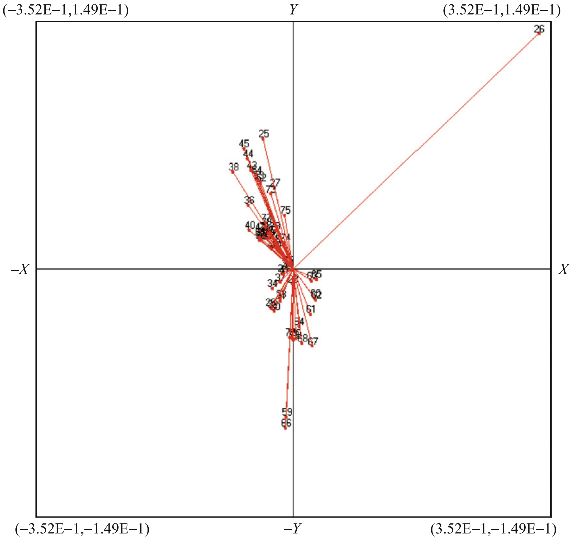


FIG. 2.3 – Two-dimensional graph of the 19 species × 59 character matrix, showing character relationships.

TAB. 2.2 – Coordinates of the 19 species shown in figure 2.2.

Number	Fish species	x-axis coordinates	y-axis coordinates
1	*Mylopharyngodon piceus*	−0.044874	−0.005854
2	*Ctenopharyngodon idella*	−0.048582	−0.008689
3	*Hypophthalmichthys molitrix*	0.240778	0.044257
4	*Hypophthalmichthys nobilis*	0.245318	0.057038
5	*Megalobrama terminalis*	−0.051155	−0.026847
6	*Parabramis pekinensis*	−0.041304	−0.048978
7	*Xenocypris argentea*	−0.014737	−0.0306
8	*Squaliobarbus curriculus*	−0.059231	−0.01754
9	*Cirrhinus molitorella*	0.017656	0.023696
10	*Cyprinus carpio*	−0.046981	0.007503
11	*Elopichthys bambusa*	−0.042912	−0.086624
12	*Ochetobius elongatus*	−0.042176	−0.032617
13	*Siniperca kneri*	−0.062285	−0.079371
14	*Sinibotia pulchra*	−0.043638	0.143961
15	*Hemiculter leucisculus*	−0.0485	−0.036018
16	*Squalidus argentatus*	−0.067134	−0.007238
17	*Pseudolaubuca sinensis*	−0.0586	−0.032028
18	*Lcucosoma chinensis*	−0.162126	0.228608
19	*Rhinogobius giurinus*	−0.067629	0.016062

2.2.5.5 Contribution to Variance

The variance contribution rate is the proportion of information of every dimension in the model analysis result. In a two-dimensional graph, only x and y are marked, but in system analysis, the background can reflect the proportional information associated with each dimension.

The dimension-reduction analysis of the 19 fish × 59-factor data matrix is shown in figure 2.1, while the information for each dimension is shown in figure 2.4. The sum of the variance contributions of all axes was "1." The variance contribution of the first axis was 0.44, the variance contribution of the second axis was 0.24, and the variance contribution of the third axis was 0.1. After the 14th axis, the variance contribution of each axis was too small to show. The variance contribution rate of the first and second axes was 68%, which indicated that the information rate of the two-dimensional graph derived from the model was 68%.

Fig. 2.4 – The variance contribution rates of each principal axis for the 19 species × 59 character matrix.

The variance test thus showed that the results of the model analysis were suitable for our analysis, and the species relationships in the two-dimensional graph met the analysis requirements.

2.3 The Model

In community-building, one theory states that species are in competitive relationships (Green, 1971), and that community composition is dominated by species groups; another theory states that species groups in a community are governed by chance (Hubbell, 2001) and that their total abundance corresponds to the total biomass of the community (de Mazancourt, 2001). Competition theory holds that species with similar ecological niches cannot coexist, while stochastic theory holds that species with similar ecological requirements can coexist. Ulrich *et al.* (2010) reported evidence of the co-occurrence of niche differentiation and speciation, reflecting the complexity of the biological composition of the ecosystem and the need for diversity to maintain the system. Therefore, species competition and niche-like species co-exist in the community. This is related to the need for system functions to meet the needs of adaptation to high environmental variability, which reflects the diversity or high buffer function of ecosystems. Niche is a basic concept in biology that states that species occupy a specific ecological space in the ecosystem (Vandermeer J H, 1972). Species distributions are governed by multidimensional space. Drake *et al.* (2006) constructed a model of nine environmental factors related to 106 plant species and their growth and characterized the niche of Hutchinson analyzed the relationship between phylogenetic distance and ecological similarity, explaining the mechanism of community structure based on the relationship between phylogenetic similarity and niche. The intensity of niche conservativeness (habitat filtration) and species interaction (competition or mutual benefit) affect community structure through phylogeny.

The study of biodiversity and ecosystems requires functional, community, and biogeographic studies, in conjunction with the development of an ecological and taxonomic approach to quantitative analysis (Naeem and Wright, 2003). A quantitative analysis method for extended population and community studies (Jacobson B and Peres-Neto P R, 2010) is also necessary, and quantitative research is needed for the development of ecology (Devictor *et al.*, 2010). The spatial variability within ecological communities is extremely complex, and the accuracy of the species distribution model is influenced by the sample size (Stockwell and Peterson, 2002). Quantitative spatial and environmental factors are one of the main objectives of community studies (Henriques-Silva *et al.*, 2013). The species niche is the core of many ecological applications. An understanding of the niche can help to analyze the evolutionary relationships among coexisting species from the perspective of species phylogenies, and the number of taxon nodes isolated from phylogeny can be used as an index of the phylogenetic correlations among species. From this, the phylogenetic structure of a species community can be understood, and the basis of the niche structure of a community and the evolutionary relationships among characters can be explored (Webb *et al.*, 2002).

The current biodiversity crisis is prompting ecologists and conservation biologists to develop models to predict the impact of human-induced natural resource transformation on species distributions and to try to understand the drivers of biodiversity patterns. Species niche distributions are related to the environment (Randin *et al.*, 2006). Environmental variables can explain the mechanisms of fish population construction, indicate the existence or function of a specific mechanism, and support hypotheses about this mechanism (Miller, 2007). Statistical models for predicting species distributions include the generalized linear model and generalized additive models (GAM), quantitative regression (QR), structural equation modeling (SEM), and geographically weighted regression (GWR) (Austin, 2007). The model needs to be explanatory, predictive, and provide a good balance of features that reduce overfitting of the model (Rangel and Loyola, 2012). Despite previous research efforts, it has gradually become recognized that the objects, models, and theories studied are local, limited, and difficult to encompass. The study of biological communities, like other fields of natural science, needs to take the best of each family, and to focus, as far as possible, on multi-angle observations and studies to develop a more comprehensive understanding of biological communities.

The niche concept of Hutchinson SA applies to the role of interspecific competition in the formation of species distribution patterns. Pulliam (2000) expressed the effects of niche breadth, habitat availability, dispersion, and interspecific competition by quantifying the temporal and spatial relationships between niche dimensions and specific populations. In this way, the relationship between species distributions and the availability of suitable habitats was observed. Jackson and Overpeck (2000) retraced environmental conditions and the forms of biological responses in a historical period using a model of community reorganization. If late quaternary climate changes continue to occur on a large time scale, then the magnitude of changes in biological communities will fluctuate over time. The responses of land, animal, and plant populations to habitat change may be migration or extinction, and these results also reflect the degree and speed of environmental change. Biomes are affected by spatial processes, and species in communities have their own spatial structural characteristics.

Interspecific relationships can be explored using quantitative trait analysis or genetic analysis. Clarke and Warwick (1999) hypothesized that species distance embodies the inter-species relationships in a community, as well as the summation of the relationships within species, among species, and between species and the environment. Elith *et al.* (2006) devised an analytical method to study species distribution and interspecific relationships using museum specimen data. Robert *et al.* (2010) argued that niche studies can yield objective results if they are framed in the right context and that the concept of "relative niche" allows further community analysis. All of that can be obtained by assessing taxonomic differences within ecosystems, such as the taxonomic characteristics of biodiversity (Leonard *et al.*, 2006), the relationships between biodiversity indicators and community structure, the relationships between traditional diversity and new concepts of diversity and richness, and the spatial niche of community composition (Shen *et al.*, 2015). Most commonly, communities are defined by interspecific relationships, also known as niche relationships, and it is important to develop methods to quantify community niches. The patterns of interspecific relationships and community species diversity are influenced by selection, drift, species formation, and diffusion, in which differences in species fitness reflect interspecific relationships, changes in abundance reflect drift, speciation events reflect the creation of new traits, and the movement of organisms across space reflects diffusion. The theory of community dynamics states that species are formed and added to a community, and the relative abundance of these species drives community dynamics through drift, selection, and sustained diffusion. The key to revealing the interspecific relationships within communities is a clear understanding of the spatial distributions of organisms or the spatial occupancy of species (Velend, 2010).

Speciation is the result of interactions between organisms and the environment. Although organisms are constantly adapting to the changing environment, the characteristics of the "species" (*i.e.*, the taxonomic characters) do not change. The "environment" here corresponds to the summation of other species and their conditions, as well as predation and the competition for food. Therefore, the morphological characteristics of a "species" record the information affected by the environment (*i.e.*, niche information). Taxonomic parameters quantify species characteristics and the differences among species in communities. Such data address the difficulty of quantifying the relationships among species in communities (*i.e.*, the problem of identifying a data source for the analysis of "niche"). The relationships between species and the environment are also generally considered a niche relationship, and the niche of a species can be represented by its spatial position. The "amount of space" for a "niche" can be expressed as a percentage of space occupancy (%). In the systematics concept category, the total niche occupied by each species in the community is "1."

2.3.1 Species Relationship Model

The relationships between ecosystem boundaries and species are a major concern of community studies because species respond differently to their environment at different geographic scales (Gotelli and Engstrom, 2003). The community function is ultimately reflected in changes in species composition, species richness, and taxonomic diversity (Heino *et al.*, 2005). Community formation across space, including uncertain dynamic processes, biological interactions, and community effects, is ultimately reflected in differences in species distributions and functional traits (Guisan and Thuiller, 2005).

There is a positive linear correlation between the size of the geographical boundaries and the individual sizes of the species in the community. However, in small-scale environments, the largest and smallest species occur less frequently and medium-sized species occur more frequently (Inostroza-Michael *et al.*, 2018). The geographical distributions of biological species vary by orders of magnitude from broad to narrow. For example, microbial species rarely occupy large ecological spaces but are characterized by local richness. Differences in microbial distribution range can be predicted by taxonomic characteristics, phenotypic traits, genomic attributes, and habitat preference (Choudoir *et al.*, 2018), which suggests that the community niche can be revealed by biological characteristics. Each community's environment is different, which reflects the different functional states of each ecosystem. The environment determines the species composition of the community. In studies of community niches, geological information about time dimensions and biological information about evolution can be used for analyses of community niche change (Marc Kéry *et al.*, 2010). Database data mining is important for the study of species relationship models (Dudei and Stigall, 2010).

Zintzen *et al.* (2011) studied fish communities along marine bathymetric gradients; the results demonstrated that the number of species in each bathymetric community was stable and did not change significantly with depth. However, taxonomic similarities in species composition among communities in different habitats along the environmental gradient decreased with depth, and there were no obvious patterns relating depth to the average taxonomic difference. Interestingly, taxon trees constructed for species from deeper samples had more variable path lengths than shallow samples. There were taxonomic differences associated with depth, and functionally similar species were found at similar depths, indicating that functional niches are formed in relatively stable extreme environments (*e.g.*, similar levels of darkness and water pressure). These results also showed that certain fish species occupy the community niche and fulfill ecosystem function, which is the basis of community functional ecology. Over large spatiotemporal scales, the species in an ecosystem are characterized by "traits." The disappearance of "traits" will lead to the disappearance of species, and the appearance of new "traits" will lead to the emergence of new species. In model studies, the "character" value of a given species is "fixed," and changes in the community are reflected by changes in species abundance. In communities with identical species compositions, species adjust their interspecific relationships *via* changes in abundance, realizing the niche balance.

In the mathematical analysis system, the relationships among species niches in a community are not an exclusive mechanism, and the rational distribution of energy in the system means that objects occupy the space on a "first come, first served" basis (Aarssen *et al.*, 2006). That is, later species always "squeeze" the space occupied by the original object to obtain corresponding positions. As a result, the space occupied by the early objects is large, but the space is then gradually squeezed by latecomers, and the space occupied by the position is gradually reduced.

A matrix analysis model of morphological parameters, which integrates the essence of taxonomic features and expands the analysis functions of character differences, is proposed by establishing a multidimensional model with characters as variables, community species as samples, and taxonomic characters as variables. Thus, the spatial relationships among species in a community can be studied using multi-dimensional mathematics. The spatial niche of a species in a community was defined by two-dimensional coordinates and vector double-positioning. Interspecific mutual benefit and competition are the key factors that determine niche and community formation. In the model, only the taxonomic characters of species were selected, and the concepts of species and environmental boundaries were avoided. This model is suitable for the analysis of pure species relationships within the community and can provide a reference for niche succession in a community in response to environmental change. The model is also suitable for community reconstruction, as it provides an analytical means for predicting niche relationships among species.

Species abundance is one of the key indicators of community species niche. In this study, "species + traits" were used to establish a "fish morphological model" for studying community species relationships. The positional relationships within the model community in space were solidified by coordinate demarcation, and these positions were identified as the ideal niche of each species in the community. Then, "species abundance" was introduced as a synthetic variable (which can be introduced randomly such that the sum of the values of "species abundance" equal "1"), and the variations in synthetic variables were compared with the "spatial positional relationships among solidified community species" in order to quantitatively study the niche based on proportional relationships among species abundance (comprehensive variable).

Based on multivariate statistical theory, the model "solidifies" the relationships between "species + traits" into spatial relationships among species in the community, obtains various two-dimensional coordinates and "vectors" for the community, and constructs a spatial ecological conformation to reveal the standard "ideal niche" pattern. The proportional "species abundance" (referred to as the "niche value" at the beginning of this chapter) was introduced as an indicator of niche value. It is assumed that the niche value of the ideal community should satisfy the "ideal niche pattern of the community," as calculated by the "species + traits" model. Using computer iterative positioning technology, the proportional "species abundance" in the community was adjusted, and the spatial positions of the species in the community tended toward the "ideal ecological position" (*i.e.*, the position determined by the two-dimensional coordinates and "vector" double positioning). The result of this iteration is the "ideal niche" species abundance ratio in the community, which is equivalent to the quantitative niche.

In the model, "species abundance" in the community was introduced as a comprehensive variable, and its vector (deviation degree) affected the species abundance ratio of the community. At the lowest vector values, the species abundance ratio of the community was the most reasonable. At larger vector values, the species abundance ratio was more unreasonable. Therefore, changes in the vector reflect changes in community species abundance, and the species model can be named the "fish community niche research model." This model can be used as a tool to transform interspecific relationships into quantitative niche relationships.

Little attention has been paid to the role of fish morphology in the functional mechanisms of fish communities and ecosystems (Zhang, 2005). Morphology provides a very promising indicator of biodiversity because morphological characters are multifunctional and do not just indicate taxonomy and phylogeny (Xiong *et al.*, 2015). One of the main theoretical hypotheses of ecomorphology is that the ecology of an organism is related to its morphology. Morphology can be used to understand the relationship between ecological factors (both physical and biological) and functional traits. The fish community niche model is not influenced by environmental factors, as it only considers fish and fish characters. Usually, all of the species in a community are in the same environment. Therefore, models ruled out that the same environmental conditions are "fair" to all species in the model, and the results are purer. Moreover, in community research, species besides the target species can be considered environmental conditions. The taxonomic characters of each species are the result of the interaction between species and the environment as well as among species. Therefore, pure biological traits actually contain "environmental" information and objectively do not exclude "environmental factors."

The theoretical underpinnings of this model are as follows:

I. Biodiversity (species richness) measurements are influenced by habitat type and complexity, and it is difficult to compare data from different habitats or habitat types. Taxonomic traits do not have this problem. There is no difference in sampling effort or rigor among workers, and the differences in taxonomic characters among species have been tested by history. Classification difference analysis has theoretical and mechanical advantages compared to the evaluation of many uncertain data measures (Warwick and Clarke, 1998).
II. Blackburn *et al.* (1997) studied species distributions and suggested that there is a fixed structural relationship among species within a community. Peterson *et al.* (1999) performed reciprocal geographic predictions of niche models for sister taxa of birds, mammals, and butterflies in southern Mexico and showed that niche conservativeness exceeds millions of years of independent evolution; this

conservation is reflected at the species level. Communities with similar structures live in similar habitats, and community structure has little relationship to species richness (Bellwood *et al.*, 2002). This conclusion also demonstrates that the "ideal niche" can be obtained from species community data.

III. Enquist *et al.* (2002) used biodata from different biogeographic regions, continents, and geological epochs to study the taxonomic and ecological characteristics of communities, as well as to reveal the mechanisms of species interactions. The results showed that the community species data reflected the environmental attributes.

IV. Multiple regression analysis and its generalized form (GLM) are very popular methods for species distribution modeling. Techniques such as neural networks, ranking and classification methods, Bayesian cognitive science, and local weighting methods (GAM), which are probabilistic in nature, can be used to support analyses of community characteristics and niches (Guisan and Zimmermann, 2000).

V. Hirzel *et al.* (2002) studied biological communities, and the first factor from the multidimensional space of ecological variables was extracted as the maximum range of activity of the target species. This factor was then defined as the optimal ecological distance between the species in the study area and the average habitat, and the feature vector was used to demarcate the suitable range map of the species' habitat. The feature vector can be used as a scalar to measure or distinguish species characteristics, thus determining the "niche scope" for species in the community.

Interspecific interactions are important for the maintenance of community status. In this book, we introduce the vector concept of the interspecific interaction force in our analysis of species' spatial effects. That is, we hypothesize that there is an interaction force among species in a natural biological community. When the community is in a state of natural stability, the resultant force of interaction among species is "zero." Otherwise, the community niche is not stable, or the community structure is in a state of environmental disturbance. The absolute value of the composite vector of a stable community is "0," and values between "1" and "0" reflect not only the state of the community but also the possible degree of environmental disturbance. Due to the changing environment of the species community, the absolute value of community resultant force cannot be "0" in reality.

In general, in the same ecological unit under study, the effects of environmental conditions on each species in the community can be regarded as equal, but different species respond differently to the environment. This difference results in the development of different taxonomic characters, which in turn leads to the formation of new species, which become members of a diverse community in an ecological unit. The variables in the fish community morphological model were quantified based on the morphological characters of each species, and the results of the morphological character analysis can be regarded as the theoretical niche.

As shown in figure 2.1, a simulated variable (A) representing the abundance of the 19 species was added to the hypothetical community matrix of 19 species × 59 traits. A new matrix, defined as "19 species × 59 characters + A" was formed,

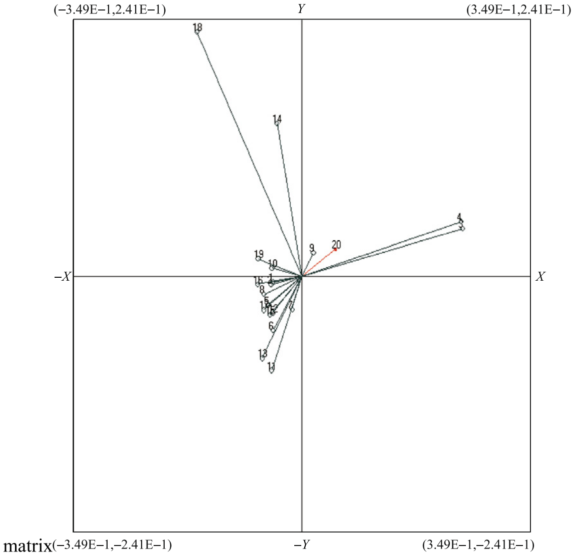


FIG. 2.5 – The position of "20" ("A") deviates from the origin of the coordinates, indicating that the community is disturbed.

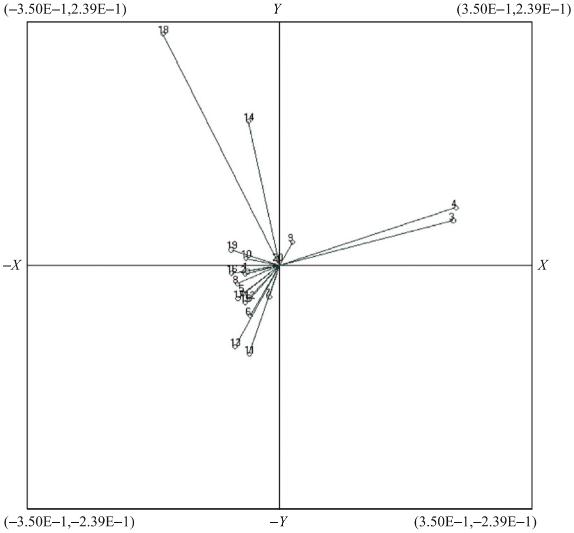


FIG. 2.6 – The position of "20" ("A") at the origin of the coordinates indicates that the community is a natural niche.

where A was numbered "20" and deviated from the central point (see figure 2.5). This indicated that the interspecific relationships in the community corresponded to a non-natural niche relationship. That is, our results indicated that the simulated community was disturbed. We then explored how the niche of 19 fish species in a simulated community might look in an undisturbed community. These results were obtained by adjusting the abundance ratios of each species. The result A = 0 was obtained by adjusting abundance relationships among the 19 fish species. Figure 2.6 shows the status of the "undisturbed community," which also could be considered the "ideal niche," after adjustment for the model parameter (A).

With the help of computer technology, the species abundance ratio was introduced into the morphological species model as the niche evaluation value, which can be applied to the study of the niche relationships of fish communities that include any combination of species. This model provides an analytical method for the study of fish community structure. Mutual benefit and competition are common phenomena. Understanding the relationships among different species in the community is the basis of community reconstruction. The interactions among adjacent species can reflect the response of these species to environmental change.

2.3.2 Character Fitness

Communities are constantly adapting to changes in their environment. This historical process is reflected in species' evolutionary trees. The adaptation of organisms to the environment is manifested not only in the change of niche but also in the change of characters. For example, the number of lateral scales varies across the range of a single fish species, as does the number of teeth across humans. These changes are the result of intraspecific differences and the adaptation of the population to environmental changes. Many of the changes in a species are also the basis for the emergence of new species. These changes can be applied to the niche model by systematically quantifying the characters of the species in the community using unified community variables and identifying characters that can be refined. For example, if tooth (T) is a characteristic trait that can be refined, and a species has 28–32 teeth, three characteristic variables can be refined: the minimum number of teeth (T_1), the average number of teeth (T_2), and the maximum number of teeth (T_3). In this way, the volume of data in the community species matrix can be increased, and the niche relationships obtained by the model will be more objective.

2.3.3 Applicability of New Species

According to Burns and Strauss (2011), we can understand the mechanisms of community construction by exploring the potential relationships between phylogenetic similarity and niche, with special consideration of the relationship between phylogenetic distance and ecological similarity. It is believed that niche conservation (habitat filtration) and species interactions (competition or promotion) are the basis of community formation and maintenance. The adaptation of biological communities to environmental change eventually leads to the formation of new species communities (*e.g.*, *via* species extinction, new species formation, and alien species invasion). In such cases, species change in the community, as well as species abundance (*i.e.*, quantity), is in a stable transition period. The model can be used to estimate the "rationality" of the niche community structure after new species formation and to predict the direction of changes in community abundance.

2.4 Examples of Model Application

Species change over evolutionary time, but the environment has changed dramatically in recent decades, and many species have gone extinct due to their inability to adapt to these sudden environmental changes. The loss of ecological species niches due to environmental change has become a common worldwide phenomenon that has disordered river ecosystem function and led to declines in an ecosystem service function. It has become gradually clear that water quality depends on fish, but more research is needed to explore the interspecific relationships and niche functions of fish communities in river ecosystems. The fields involved in ecologies, such as taxonomy, phylogeny, and biodiversity, are developing toward quantification (Devictor V *et al.*, 2010). Based on the concept that the ideal niche is related to the spatial composition of the species community, the proportional abundance of the species in the community was characterized. The fish community morphological model may thus provide a new method for niche research. Quantification of the ideal niche will provide a reference system for community succession analysis, which may help clarify fish morphological niches, leading to improvements in the restoration and guarantee of river ecosystem function, as well as the restoration and reconstruction of fish communities.

The distribution patterns of quantitative analyses help to clarify the processes that shape species distributions. In ecosystems, the range over which species are distributed is constrained by environmental conditions, and the niche patterns of species are regular. The ranges of genera, families, orders, and species of plants and animals usually vary by several orders of magnitude; these differences are related to changes in individual size, population density, dispersion patterns, latitude, altitude, and depth (in ocean systems). To analyze and evaluate changes in species communities, it is necessary to establish standards by which to judge change. The method of quantitative analysis of the "ideal niche" established in this study can quantify the "standard" model of the ideal niche for each species in fish communities composed of "any species," providing both a reference for the study of fish communities and an analysis platform for the exploration of the mechanisms of community species formation. In this section, the model of the Pearl River fish community is analyzed in order to specify the technical details of the model.

2.4.1 Characterization of Community Species Relationships

Taxonomic traits are the result of interactions between organisms and their environment over evolutionary time. These interactions lead to the development of "fixed" traits that distinguish individuals and species. Although organisms are constantly changing in the environment, the usual changes are not sufficient to change the characteristics of the species (that is, if the characteristics of the species are changed, it is generally believed that a new species has formed). Therefore, species characteristics can be regarded as "unchanged." In an investigation of fish resources in the middle and lower reaches of the Pearl River, we found that 19 species of fish accounted for more than 70% of the fishing resources (Li *et al.*, 2008, 2010, 2020a, 2020b, 2020c, 2020d, 2020e, 2021a, 2021b; Xu *et al.*, 2018; Tan *et al.*, 2010). This study of 19 species of fish, representing the target fish community, reflects certain information about species relationships in the studied section of the Pearl River. The parameters were selected from the 59 candidate morphological characters in table 2.2; in total, 24 morphological characters were selected for analysis. Fish abundance data were extracted every two days from the daily data collected by our laboratory in the Zhaoqing section of the Pearl River and corrected using cross-sectional runoff data. The total amount of early recruitment for each species was calculated and converted to the percentage of early recruitment for the 19 species. This value was used as a proxy for abundance data (niche space occupancy) for this group (see table 2.3).

Tab. 2.3 – Proportion of early floating fish resources in the Zhaoqing section of the Pearl River in 2012.

Number	Species	2012
1	*Mylopharyngodon piceus*	0.10
2	*Ctenopharyngodon idella*	1.13
3	*Hypophthalmichthys molitrix*	2.76
4	*Hypophthalmichthys nobilis*	1.15
5	*Megalobrama terminalis*	22.30
6	*Parabramis pekinensis*	0.56
7	*Xenocypris argentea*	9.32
8	*Squaliobarbus curriculus*	50.48
9	*Cirrhinus molitorella*	4.59
10	*Cyprinus carpio*	0.00
11	*Elopichthys bambusa*	0.68
12	*Ochetobius elongatus*	0.31
13	*Siniperca kneri*	0.15
14	*Sinibotia pulchra*	1.39
15	*Hemiculter leucisculus*	3.44
16	*Squalidus argentatus*	0.92
17	*Pseudolaubuca sinensis*	0.40
18	*Lcucosoma chinensis*	0.13
19	*Rhinogobius giurinus*	0.19
20	Accumulates	100.0

The sample serial numbers shown in table 2.3 were included in the matrix. The numbers 1–19 correspond to the fish (*e.g.*, 1 corresponds to *Mylopharyngodon piceus* and 2 corresponds to grass carp). Number 20 is a comprehensive variable representing measured species richness. Numbers 21–44 correspond to the dependent variables (traits): 21 corresponds to gill raker I; 22 corresponds to hypopharyngeal teeth I1; 23 corresponds to hypopharyngeal teeth I2; 24 corresponds to hypopharyngeal teeth II1; 25 corresponds to hypopharyngeal teeth II2; 26 corresponds to dorsal fin spine I; 27 corresponds to soft spine of dorsal fin; 28 corresponds to soft spine of anal fin; 29 corresponds to hard spine of anal fin; 30 corresponds to soft spine of pectoral fin; 31 corresponds to soft spine of ventral fin; 32 corresponds to body length/body height III; 33 corresponds to body length/head length III; 34 corresponds to head length/length of lips III; 35 corresponds to head length/eye diameter III; 36 corresponds to head length/interocular septum III; 37 corresponds to tail stalk length/tail stalk height; 38 corresponds to lateral line I; 39 corresponds to lateral scale III; 40 corresponds to lateral sale III; 41 corresponds to inferior lateral line; 42 corresponds to anterior dorsal fin scale III; 43 corresponds to coccygeal scale I; and 44 corresponds to maximum body length.

The model is a morphological analysis model of the fish community. The positional relationships among the 19 species of fish were determined using multi-dimensional relationship analysis and reduced to a two-dimensional graph. As shown in figure 2.7, 19 species of fish were distributed in the plane (black circles), and the spatial niche relationships of the 19 fish species (based on larvae measured in 2012) in the Pearl River reach were studied. As shown in table 2.4, each species corresponded to coordinates in the two-dimensional plane, reflected in the position of the x- and y-axes. The line between the origin of the coordinates and the fish distribution points is the vectors of the points.

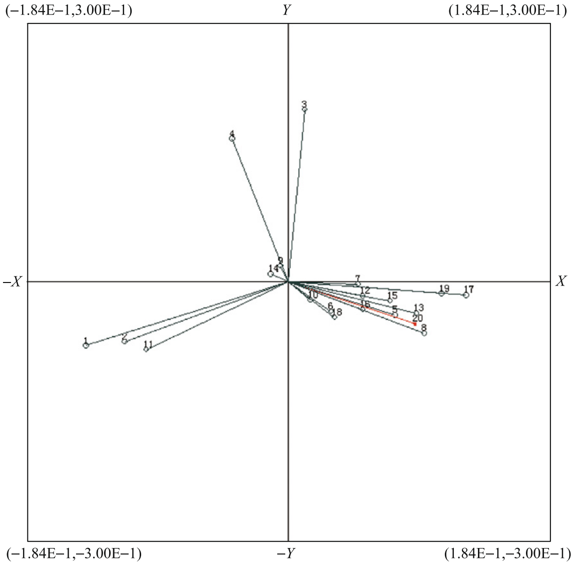


Fig. 2.7 – Community ecological map of 19 species of fish (fish abundance data based on larval measurements in 2012).

TAB. 2.4 – Coordinates of variables (19 species of fish) and independent variables (24 taxonomic traits) in the model analysis results.

Number	Fish	Characterization of the 24 taxonomic character parameters		Representing the measured larval abundance in 2012	
		x coordinate	y coordinate	x coordinate	y coordinate
1	*Mylopharyngodon piceus*	−0.151054	−0.046193	−0.142393	−0.073112
2	*Ctenopharyngodon idella*	−0.123994	−0.046818	−0.115161	−0.068696
3	*Hypophthalmichthys molitrix*	0.051495	0.193775	0.011141	0.200559
4	*Hypophthalmichthys nobilis*	−0.004695	0.169715	−0.039908	0.166425
5	*Megalobrama terminalis*	0.050262	−0.038226	0.074369	−0.037824
6	*Parabramis pekinensis*	0.027657	−0.043075	0.029563	−0.033252
7	*Squaliobarbus curriculus** (Representing the *Squaliobarbus*)	0.043327	−0.008284	0.048483	−0.002338
8	*Xenocypris argentea*	0.038162	−0.038585	0.095056	−0.058907
9	*Cirrhinus molitorella*	−0.00305	0.020642	−0.00588	0.01886
10	*Cyprinus carpio*	0.014746	−0.026327	0.015125	−0.020295
11	*Elopichthys bambusa*	−0.108723	0.060384	−0.099959	−0.077613
12	*Ochetobius elongatus*	0.052637	−0.029706	0.051985	−0.015654
13	*Siniperca kneri*	0.087724	−0.058959	0.089384	−0.035725
14	*Sinibotia pulchra*	−0.01003	0.011197	−0.012657	0.009464
15	*Pseudolaubuca sinensis*	0.067393	−0.036665	0.070946	−0.021377
16	*Hemiculter leucisculus** (Representing the *Hemiculter*)	0.047671	−0.043766	0.051766	−0.031513
17	*Squalidus argentatus* (Representing the *Squalidus*)	0.125002	−0.044006	0.124345	−0.014619

Tab. 2.4 – (continued).

18	*Lcucosoma chinensis*	0.028382	−0.050426	0.031993	−0.040283
19	*Rhinogobius giurinus** (Representing the GOBIES)	0.112105	−0.04279	0.107082	−0.012745
20	Abundance			0.08891	−0.047711

*Represented by dominant species.

The niche consists of species, geographical distribution, and abundance. According to the above hypothesis, if the variation reflecting the niche (abundance) deviates from the origin (the red circle in figure 2.7), then the community is disturbed by the environment. Table 2.4 shows that the community abundance variables representing the 19 species of fish were found at the x- and y-coordinates 0.08891 and −0.047711, respectively. It is thus obvious that this community niche is disturbed by the environment. The length of the red line is the deviation of the niche.

It is necessary to clarify the "ideal niche" of a simulated community of 19 species of fish. According to the assumptions described in the previous section, the ideal niche is the composite variable (a) representing species abundance that appears at the origin of the two-dimensional graph. The optimum species composition is used to adjust the comprehensive variable of species abundance to the origin of the coordinates, which can be achieved by adjusting the biological abundance of each of the 19 species of fish. In this way, the niche proportion of the specific attributes can also be obtained.

2.4.2 Determining the Ideal Niche

In the previous section of this book, we introduced the principle of the model: to analyze species relationships within a community based on the morphological classification parameters of fish. We also determined the niche of the community using the biomass abundance ratio. In other words, the synthetic vector of species abundance was taken as the hypothesized degree of disturbance in the niche. The proportion of community species abundance was adjusted using computer technology, and the "0" of the synthetic vector (*i.e.*, the synthetic variable at the coordinate origin of the two-dimensional graph) was realized in the course of iterative calculation. The proportion of species abundance should be consistent with the calculation of "1," allowing the "ideal niche" value of each species in the community to be obtained.

From 2006 to 2013, we conducted a long-term observation of the floating larvae in the Zhaoqing section of the Pearl River; in this study, the relative proportions of the annual early resources of the 19 species of fish were determined (Li Xinhui *et al.*, 2020a, 2020b, 2020c, 2020d, 2020e). The abundance ratios of the 19 fish species in the community differed across years, which indicated that the spatial niche of the 19 fish species changed dynamically and demonstrated that the environment of the fish habitat was changing. Table 2.5 shows the average proportion of the larval biomass of different species for each year, with the last column showing the multi-year average proportion of each species.

According to the records of the Pearl River fish resources over the last century (Guangxi Fisheries Research Institute, Report on the investigation of the natural resources of the Guangxi Zhuang Autonomous Region inland waters fishery, published by Guangxi Fisheries Research Institute, 1985; Pearl River Fishery Resources Survey Editorial Committee, Investigation report on fishery resources of Pearl River System, Pearl River Fishery Research, China Academy of Fishery Sciences, 1985),

Tab. 2.5 – Proportion of different species of early drifting fish in the Zhaoqing section of the Pearl River*.

Species	2006	2007	2008	2009	2010	2011	2012	2013	Average
Mylopharyngodon piceus	0.07	0.59	0.21	0.54	0.42	0.11	0.10	0.17	0.28
Ctenopharyngodon idella	2.15	0.29	1.14	1.28	1.19	2.10	1.13	0.94	1.28
Hypophthalmichthys molitrix	2.86	1.08	4.51	2.97	2.21	2.73	2.76	2.51	2.70
Hypophthalmichthys nobilis	1.14	0.12	0.51	0.78	0.57	0.96	1.15	0.82	0.76
Megalobrama terminalis	29.59	29.95	12.13	15.10	11.91	29.68	22.30	4.73	19.42
Parabramis pekinensis	1.21	1.39	1.57	0.57	0.74	1.14	0.56	0.37	0.94
Xenocypris argentea	22.02	19.32	10.44	8.91	26.53	21.89	9.32	6.45	15.61
Squaliobarbus curriculus	26.11	24.84	45.23	46.21	32.51	26.20	50.48	52.31	37.99
Cirrhinus molitorella	4.58	14.06	8.79	11.55	10.43	4.47	4.59	7.32	8.22
Cyprinus carpio	0.15	0.02	0.10	0.02	0.01	0.14	0.00	0.01	0.06
Elopichthys bambusa	0.32	0.25	0.62	0.40	0.42	0.50	0.68	0.27	0.43
Ochetobius elongatus	0.05	0.05	0.07	0.32	0.32	0.50	0.31	0.09	0.21
Siniperca kneri	0.34	0.09	0.37	0.23	0.20	0.34	0.15	0.09	0.23
Sinibotia pulchra	0.23	0.40	4.45	3.77	2.25	0.13	1.39	1.92	1.82
Hemiculter leucisculus	4.61	5.16	4.00	2.90	4.03	4.57	3.44	1.33	3.75
Squalidus argentatus	1.11	0.36	2.72	2.41	5.43	1.29	0.92	20.21	4.31
Pseudolaubuca sinensis	1.64	1.01	1.98	0.95	0.47	1.59	0.40	0.25	1.04
Lcucosoma chinensis	1.20	0.59	0.66	0.14	0.09	1.02	0.13	0.09	0.49
Rhinogobius giurinus	0.63	0.42	0.51	0.95	0.27	0.65	0.19	0.13	0.47
Total	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0

*Note: The relative proportions of the identified species.

the catch of the four major fish in the Pearl River section (*Mylopharyngodon piceus*, *Ctenopharyngodon idella*, *Hypophthalmichthys molitrix*, and *Hypophthalmichthys nobilis*) accounted for more than 40% of the total catch. Investigation of the early resources indicated that these four major fish were the dominant species; *Squaliobarbus curriculus* was less abundant, and the abundance of *Megalobrama terminalis* was less than 5%. In 2016–2018, our team conducted a sampling survey of inland fish catches in the Pearl River system. A total of 40 fishing boats were surveyed from five counties in the river waters of Guangdong Province for an average of 12.6 days from January to December, and 101.5 kg of samples were obtained daily. The catch of four major fish accounted for 10.5% of the total catch (see table 2.6).

TAB. 2.6 – Catch of the main species in the Pearl Rivers, Guangdong Province.

Number	Fish	Average share of each category from 2016 to 2018 (%)
1	Other Fishes	58.9
2	*Megalobrama terminalis* Richardson, 1846	10.7
3	*Ctenopharyngodon idella* Valenciennes, 1844	5.7
4	*Cirrhinus molitorella* Valenciennes, 1844	6.5
5	*Cyprinus carpio* Linnaeus, 1758	4.6
6	*Squaliobarbus curriculus* Richardson, 1846	2.7
7	*Pelteobagrus fulvidraco* Richardson, 1846	2.2
8	*Hypophthalmichthys molitrix* Valenciennes, 1844	2.4
9	*Hypophthalmichthys nobilis* Richardson, 1845	2.1
10	*Hemiculter leucisculus* Basilewsky, 1855	0.5
11	*Cichlidae*	1.1
12	*Parabramis pekinensis* Basilewsky, 1855	1.2
13	*Silurus asotus* Linnaeus, 1758	0.5
14	*Mylopharyngodon piceus* Richardson, 1846	0.2
15	*Siniperca kneri* Garman, 1912	0.2
16	*Hemibagrus guttatus* Lacepede, 1803	0.0
17	*Cranoglasis bouderius* Richardson, 1846	0.1
18	*Carassius auratus auratus*	0.1
19	*Ictalurus punctatus* Rafinesque, 1818	0.0
20	*Mastacembelus armatus* Lacepede, 1800	0.0
21	*Siniperca scherzeri* Steindachner, 1892	0.0
22	*Leiocassis longirostris* Gunther, 1864	0.0
23	*Elopichthys bambusa* Richardson, 1845	0.0
24	*Culter alburnus* Basilewsky, 1855	0.0
25	*Ptychidio jordani* Myers, 1930	0.0
26	*Culter recurviceps* Richardson, 1846	0.0
27	Total	100.0

Compared with the total biomass of the four major fish species, both tables 2.5 and 2.6 indicate that performance data are changing, but there is a lack of a uniform reference to measure the extent of changes in various species. It is necessary to establish a standard reference frame, especially a quantitative niche reference frame at the community structure level. This difficulty can be avoided by using the "ideal niche." Through comparison, the ratio of ideal niche to measured biomass as a comparison of ecological niche can understand the niche changes of various species in the community, which is of great significance for understanding the formation mechanism of fish communities. This is significant for an improved understanding of the mechanisms of fish community formation, predicting niche changes for fish reconstruction, and river ecological management. Figure 2.8 (see figures 2.8a–2.8c) shows the changes in the distributions of 19 fish species and the stage-by-stage presentation of the "niche" synthetic vector in the model. Table 2.7 shows that the vector representing the niche of 19 fish species approaches "0" and that the total relative abundance of the four major fish species with respect to the 19 fish species reached 57.46%. This was consistent with the data from the Pearl River Fish Resources Survey over the last century.

Historically, the Pearl River basin includes four major spawning grounds for fish: the Xijiang river system (Hongshui River and Xunjiang River), the Yujiang River system (Zuojiang River and Youjiang River), the Liujiang River system, and the Dongjiang River. After decades of cascading development, only the Xunjiang River in the Xi River system and the middle and lower reaches of the Liu River still retain spawning grounds. The few remaining spawning grounds are also threatened by habitat change. After this change in the river environment, the biomass of the fish community changed. About 170 000 tons of fish products were recorded in the Pearl River system in the 1980s, compared with 60 000 tons recorded by our team in

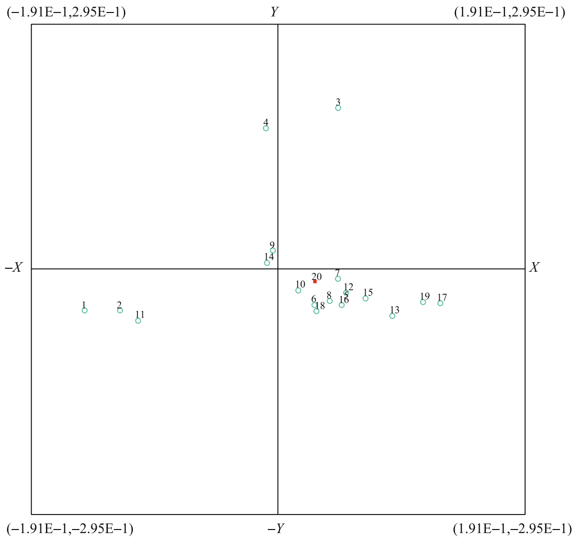


FIG. 2.8a – The "niche" vector (red number 20) deviates from the origin of the coordinates.

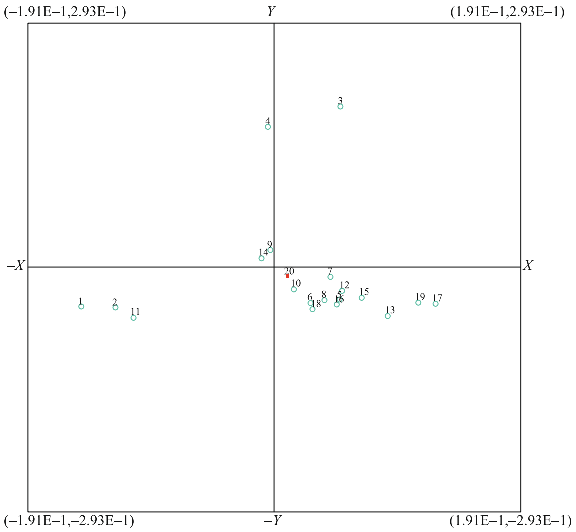


FIG. 2.8b – The "niche" vector (red number 20) was near the origin of the coordinates.

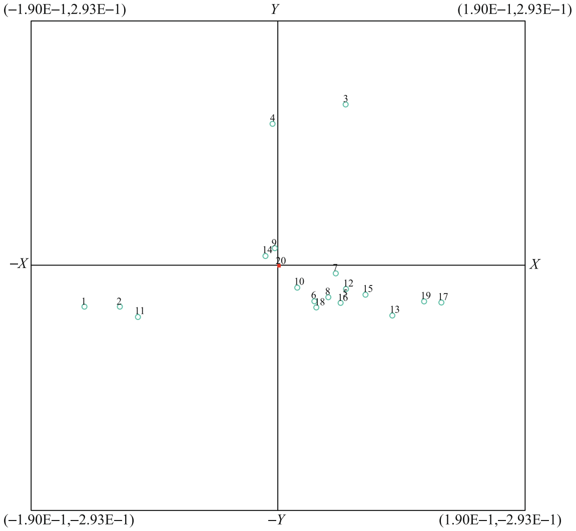


FIG. 2.8c – The "niche" vector (red number 20) coincides with the origin of the coordinates.

2016–18. This decrease in biomass suggested that the fish niche space decreased from 170 000 tons to 60 000 tons. The evaluation and restoration of the river ecosystem must be guided by the theory of the fish community niche.

Tab. 2.7 – Model-determined average relative biomass (*i.e.*, the total supplementary population) for each of the 19 fish communities and the corresponding coordinates in the Zhaoqing section of the Pearl River.

Number	Species	Annual quantity abundance from 2006 to 2013 (%)	Figure 2.8a			Figure 2.8b			Figure 2.8c		
			model-abundance (%)	x-coordinate	y-coordinate	model-abundance (%)	x-coordinate	y-coordinate	model-abundance (%)	x-coordinate	y-coordinate
1	*Mylopharyngodon piceus*	0.28	8	−0.149956	−0.049416	15.71	−0.150001	−0.046779	20.31	−0.150295	−0.045994
2	*Ctenopharyngodon idella*	1.28	7.7	−0.12276	−0.049483	11.78	−0.123255	−0.04719	10.31	−0.123619	−0.046702
3	*Hypophthalmichthys molitrix*	2.70	8.3	0.046492	0.194712	9.82	0.050867	0.193404	14.36	0.051264	0.193065
4	*Hypophthalmichthys nobilis*	0.76	7	−0.009414	0.169736	8.84	−0.005285	0.169548	12.48	−0.004722	0.169264
5	*Megalobrama terminalis*	19.42	10	0.052699	−0.037815	4.47	0.050272	−0.038067	3.90	0.05012	−0.0381
6	*Parabramis pekinensis*	0.94	5	0.028292	−0.042155	2.03	0.027418	−0.042614	3.80	0.027612	−0.042985
7	*Squaliobarbus curriculus*	15.61	15	0.046293	−0.008949	8.25	0.043555	−0.008631	0.06	0.043341	−0.0083
8	*Xenocypris argentea*	37.99	6.22	0.039798	−0.038001	6.11	0.038429	−0.038687	3.88	0.038036	−0.038445
9	*Cirrhinus molitorella*	8.22	3.6	−0.003775	0.02066	2.54	−0.003285	0.020812	0.07	−0.003055	0.020657
10	*Cyprinus carpio*	0.06	4	0.01551	−0.025996	1.33	0.01457	−0.026002	3.91	0.014695	−0.026216
11	*Elopichthys bambusa*	0.43	4.04	−0.108819	−0.061983	3.97	−0.109053	−0.060025	3.81	−0.108613	−0.060405
12	*Ochetobius elongatus*	0.21	2.9	0.052514	−0.02806	2.85	0.05244	−0.029344	3.90	0.052513	−0.029642
13	*Siniperca kneri*	0.23	4.55	0.088413	−0.05654	4.47	0.087591	−0.058565	3.91	0.087497	−0.058826
14	*Sinibotia pulchra*	1.82	4.8	−0.008631	0.010058	1.63	−0.010004	0.011166	0.03	−0.010065	0.011293
15	*Pseudolaubuca sinensis*	3.75	3.21	0.06769	−0.034819	3.15	0.067262	−0.036365	3.90	0.067165	−0.036542
16	*Hemiculter leucisculus*	4.31	4.67	0.049098	−0.042792	4.59	0.047819	−0.043723	3.89	0.04747	−0.04356
17	*Squalidus argentatus*	1.04	4.36	0.125567	−0.041018	4.28	0.124679	−0.043694	1.75	0.124769	−0.043919
18	*Lcucosoma chinensis*	0.49	2.39	0.02986	−0.049721	2.35	0.028573	−0.050238	3.89	0.028121	−0.049871
19	*Rhinogobius giurinus*	0.47	1.87	0.111975	−0.03964	1.84	0.111839	−0.042283	1.84	0.111706	−0.042578
20	Vector of "Niche"		Deviation from the center of coordinates	0.028583	−0.014448	Approaching the center of coordinates	0.009695	−0.009849	Coincidence	−0.000035	−0.000013

2.4.3 Iteration

In mathematics, iteration is the process of repeated computation with the goal of determining parameters. Each computation is called an "iteration," and the result of each iteration is used as the initial value of the next iteration. A computer has the characteristics of fast operation speed and is suitable for repetitive operations. It is possible to execute a set of instructions (or a certain step) repeatedly on the computer. After each instruction (or step) is completed, a new value of the variable is deduced from its original value, the final result is obtained by continuous calculation. This model studies the quantitative relationships among the niche values of species in a community, assuming that the abundance ratios representing the niche values of species in the community are not balanced. Thus, the abundance ratio values are used as variables. Because the vector of the comprehensive variables (referred to as "A") deviates from the origin, it is necessary to adjust the abundance ratio, and the "A" approach to the origin is the iterative goal under the two-dimensional species coordinate system. For example, in figure 2.9a serial number "20" ("A") approximates the center point through computer iteration, which involves the selection of various parameters and conditions in the software system.

2.4.3.1 Selection of the Iteration Target

Serial number "20," which is the abundance factor, can be located anywhere in the two-dimensional graph depending on the niche deviation of the species community (see figure 2.8a). The endpoint of the iteration is determined at any position by the values of the x- and y-coordinates according to the purposes of the study. If we want the "20" to approach the center point, we choose the x- and y-coordinates of the endpoint of the iteration as the origin (0, 0). If we need to study different niche relationships within the species community, we can also locate the endpoint of the iteration on any non-zero x- or y-coordinates. This process can also be used for community species restoration. Using the fish community shown in table 2.7 as an example, we can assume that the niche of *Mylopharyngodon piceus*, *Ctenopharyngodon idella*, *Hypophthalmichthys molitrix*, and *Hypophthalmichthys nobilis* had been disturbed and needs to be repaired to 50% of the theoretical value. In this case, the mean abundance of the damaged community from 2006 to 2013 (see table 2.7) can be used as the starting point. Using the theoretical 50% index of the four species, the theoretical niches of the other 15 fish species were obtained (see table 2.8). Thus,

TAB. 2.8 – Determination of the theoretical 50% niche of four fish species.

Number	Species	Current mean abundance	Model analysis abundance (%)	50% theoretical target (%)
1	*Mylopharyngodon piceus*	0.28	20.31	10.16
2	*Ctenopharyngodon idella*	1.28	10.31	5.16
3	*Hypophthalmichthys molitrix*	2.70	14.36	7.18
4	*Hypophthalmichthys nobilis*	0.76	12.48	6.24

following this principle, we can set the niche of any target in the community, obtain the theoretical niche quantity of other species by iteration, and provide the results of the morphological relationship model as a reference for community construction or restoration.

2.4.3.2 Coordinate Error of the Iteration End Point

Although we determine the end-point value of the iteration goal, it is not necessary for the computer to achieve 100% of the iteration location goal. With the premise that it is undesirable to affect the iteration result, it is acceptable that the end-point target (coordinate) of the iteration exhibits some error. In general, an absolute error of x or y in the range of 0.001–0.0001 satisfies the statistical requirements. If it is difficult to quickly iterate to the end result, the error precision can be increased to 0.005 or more, reducing the iteration time without affecting the result.

2.4.3.3 Determination of Iteration Step Size

When the computer iterates automatically, it must adjust the abundance ratio of each sample repeatedly. The value of each increment (or decrement) is called the "step length." The choice of step size is related to the accuracy of the result and the running time. Smaller step lengths correspond to higher precisions and longer running times, while larger step lengths correspond to lower precisions and shorter running times. Generally, we choose step lengths of 0.1–0.001.

2.4.3.4 Iterative Cycle Selection

The so-called small cycle iteration is applied to a sample in the data matrix: step size is increased or decreased repeatedly, such that the "abundance ratio factor" is set to the direction of the movement. The so-called large cycle iteration applied to each sample in the matrix was adjusted for the size of the abundance proportion values in the matrix until the abundance ratio was equivalent to the size of the adjustment of the iteration. Cycle iteration is essentially a statistical term that means to complete small and large loop iterations.

To move the "20" factor of figure 2.8a to the intended destination, the computer iterates by repeatedly adjusting the sample abundance ratios. The number of small loop iterations can be greater than or equal to 1. Greater numbers of small-cycle iterations will have a greater influence on iteration results on the sequence of sample iteration, and *vice versa*. We usually find that 1–5 times is most appropriate.

When the number of samples is large, the "20" factor in figure 2.8c is close to the requirements of the user. The proportional value of each sample is also basically determined. Therefore, the large-cycle number is set to five times in the system, which usually meets user requirements. When the destination has not been reached after five iterations, the computer will prompt the user to either continue the large cycle iteration or modify the iteration parameters. The user may make this decision according to the situation.

2.4.4 Sample Iteration Order

The order in which the samples are adjusted affects the results of abundance ratios when iterating over the sample. The model has three possible iteration types: in the first type, the samples are arranged in the order specified by the user, while in the other two types, the samples are arranged in either descending or ascending order according to the magnitude of the vector scalar value (*i.e.*, the content of the reference vector iteration method) associated with the samples in the two-dimensional graph.

During adaptation, organisms form a pattern of coexistence between large and small species, and the niche relationships among the species in a community are not an exclusive mechanism; niche relationships seem to be related to the maximum energy utilization in an ecosystem. A central objective of evolutionary ecology is to identify the general characteristics that maintain the diversity of species assemblages. By analyzing the classification and ecological characteristics of community species and studying the process mechanism of the coexistence and diversity of species, we found that the higher-scoring taxa species (with high abundance) were stronger than lower-scoring taxa species (with less abundance), and that regional communities were characterized by higher-scoring taxa (Enquist B J *et al.*, 2002).

The ecological niche of large trees was dominant, but there were gaps between trees that provided space for the survival of small species, and these spaces enabled the coexistence of large and small species (Aarssen L W *et al.*, 2006). In animal communities, the energy cycle requires the food chain, which constitutes the relationship between predator and prey. If the predator has an exclusive behavior in a given niche, there is no basis for its existence. Therefore, the "link" of the niche is the rational distribution of energy in the system, which provides the basic conditions for the coexistence of large and small species.

Large species use a larger proportion of the resources in the local ecosystem. Even though small species tend to have higher population densities, these high-density populations use lower levels of energy more efficiently. These types of relationships are common among birds, mammals, fish, and plants (Brown J H *et al.*, 1996). It is generally believed that several ecologically advantageous species monopolize more resources, and the resulting selection pressure may be the reason for the evolution of species in the direction of individual generality. This demonstrates that the energy utilization rate of a given species is related to its niche in the ecosystem.

Natural objects possess space on a "first come, first served" basis, and later species always obtain corresponding positions by "squeezing" the space occupied by the original objects. As a result, the space occupied by the early objects is large, and this space is gradually squeezed by latecomers such that the space occupied by the position is gradually reduced. Based on this principle, our model analysis procedure assumes that big species occupy the niche first. In this morphological model analysis system, the niche analysis program gives priority to the dominant species. It is possible to select a "large vector" to a "small vector" order iteration.

Communities are made up of species of different sizes, and the distribution of species follows certain rules. However, small species cannot be ignored. Based on observations of maximum plant height, leaf size, and seed size in several plant types, that the distribution of species sizes is universal, even at the intraspecies level, and that species distributions are the result of species self-adaptation during evolution. Thus, species distributions have nothing to do with the competitive ability of the species (traditionally, superior competitive ability requires a relatively large size/biomass production), and small species cannot be neglected in community studies. In the model analysis, the order of niche occupation by species in the community can be determined by the user according to the research goal.

2.4.5 Sample Iteration Constraints

Because iteration is a computer operation, it is necessary to give boundary values (*i.e.*, upper and lower limits) for the niche value of the species in the community as part of the program design. In this manner, the computer can automatically select the optimal niche value of a species in a community. This type of boundary value varies with different iterative methods and can be determined by the user or by the computer according to certain principles; these boundary values may be the same or different. It should be noted that the boundary values (upper and lower limits) of the iteration values may vary, and thus the final iteration results may vary.

2.4.6 Sample Normalization

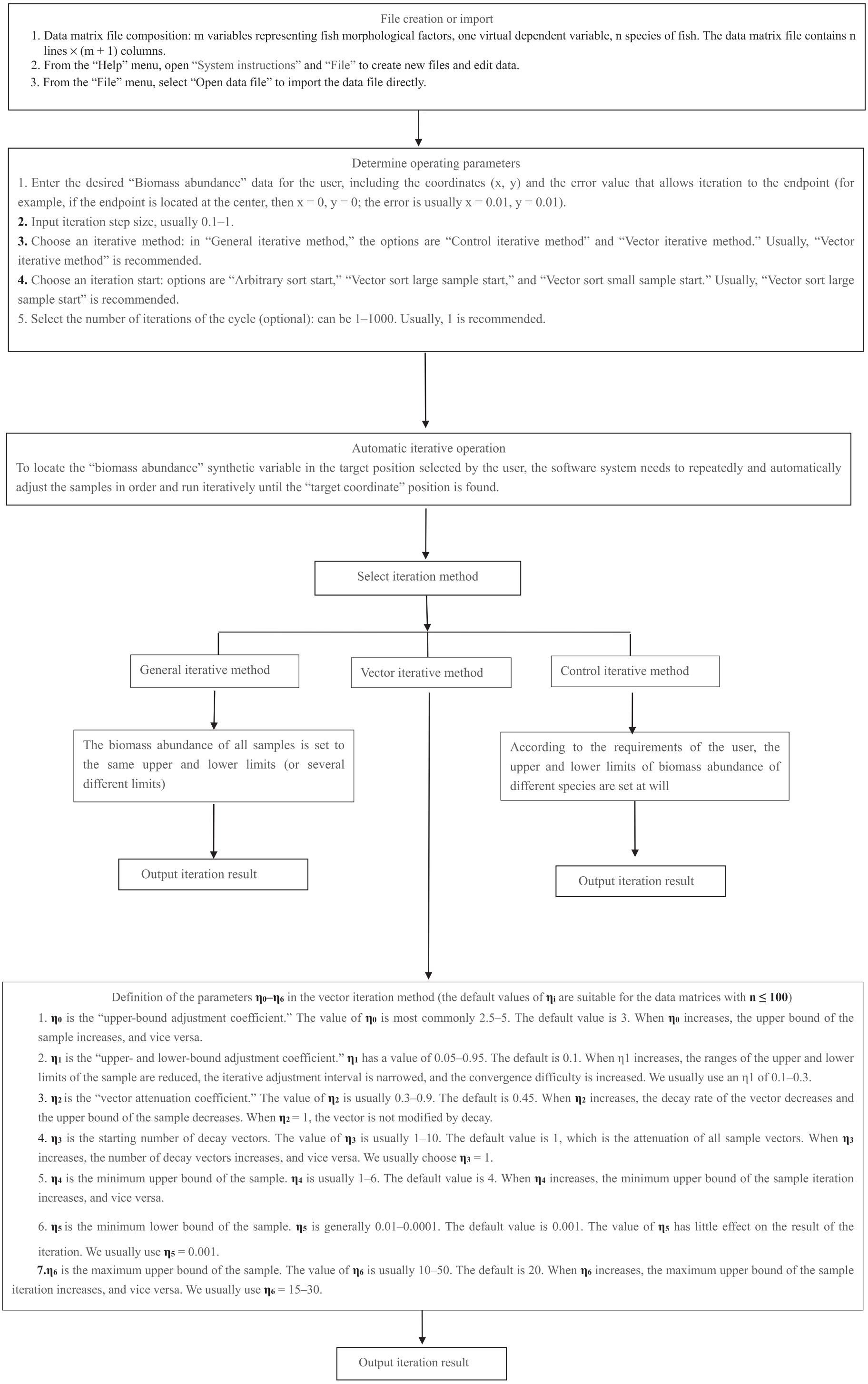
At the end of the automatic iteration, the sum of the relative niche values for all species in the community should be 100%. The normalized value is "1." Generally, only positive and negative errors less than 0.01 are allowed, with a range of 0.99–1.01. Otherwise, the normalization process should continue to operate until 100% is reached.

2.4.7 Model Checking

Any model study needs to be verified in practice. In model analysis, it is necessary to evaluate the analytical data (*e.g.*, the correlation coefficient and other parameters) to judge the accuracy and applicability of the model. This model uses the classification character parameter to identify the ecological space occupancy rate of the species community, as well as changes in this rate. Nonlinear multiple regressions were used to test the functional relationships between the measured biomass abundance data for the early fish resources and the coordinates of the corresponding species in the model. F-tests showed that the average confidence level was above 95%, while the average validation accuracy and average prediction accuracy of 19 species of fish biomass abundance were greater than 98% and 93%, respectively.

2.4.8 Model Workflow

System workflow diagram and explanations.



File creation or import

1. Data matrix file composition: m variables representing fish morphological factors, one virtual dependent variable, n species of fish. The data matrix file contains n lines × (m + 1) columns.
2. From the "Help" menu, open "System instructions" and "File" to create new files and edit data.
3. From the "File" menu, select "Open data file" to import the data file directly.

Determine operating parameters

1. Enter the desired "Biomass abundance" data for the user, including the coordinates (x, y) and the error value that allows iteration to the endpoint (for example, if the endpoint is located at the center, then x = 0, y = 0; the error is usually x = 0.01, y = 0.01).

2. Input iteration step size, usually 0.1–1.

3. Choose an iterative method: in "General iterative method," the options are "Control iterative method" and "Vector iterative method." Usually, "Vector iterative method" is recommended.

4. Choose an iteration start: options are "Arbitrary sort start," "Vector sort large sample start," and "Vector sort small sample start." Usually, "Vector sort large sample start" is recommended.

5. Select the number of iterations of the cycle (optional): can be 1–1000. Usually, 1 is recommended.

Automatic iterative operation

To locate the "biomass abundance" synthetic variable in the target position selected by the user, the software system needs to repeatedly and automatically adjust the samples in order and run iteratively until the "target coordinate" position is found.

The biomass abundance of all samples is set to the same upper and lower limits (or several different limits)

According to the requirements of the user, the upper and lower limits of biomass abundance of different species are set at will

Definition of the parameters $\boldsymbol{\eta_0}$–$\boldsymbol{\eta_6}$ in the vector iteration method (the default values of $\boldsymbol{\eta_i}$ are suitable for the data matrices with $\mathbf{n \leq 100}$)

1. $\boldsymbol{\eta_0}$ is the "upper-bound adjustment coefficient." The value of $\boldsymbol{\eta_0}$ is most commonly 2.5–5. The default value is 3. When $\boldsymbol{\eta_0}$ increases, the upper bound of the sample increases, and vice versa.

2. $\boldsymbol{\eta_1}$ is the "upper- and lower-bound adjustment coefficient." $\boldsymbol{\eta_1}$ has a value of 0.05–0.95. The default is 0.1. When η1 increases, the ranges of the upper and lower limits of the sample are reduced, the iterative adjustment interval is narrowed, and the convergence difficulty is increased. We usually use an η1 of 0.1–0.3.

3. $\boldsymbol{\eta_2}$ is the "vector attenuation coefficient." The value of $\boldsymbol{\eta_2}$ is usually 0.3–0.9. The default is 0.45. When $\boldsymbol{\eta_2}$ increases, the decay rate of the vector decreases and the upper bound of the sample decreases. When $\boldsymbol{\eta_2} = 1$, the vector is not modified by decay.

4. $\boldsymbol{\eta_3}$ is the starting number of decay vectors. The value of $\boldsymbol{\eta_3}$ is usually 1–10. The default value is 1, which is the attenuation of all sample vectors. When $\boldsymbol{\eta_3}$ increases, the number of decay vectors increases, and vice versa. We usually choose $\boldsymbol{\eta_3} = 1$.

5. $\boldsymbol{\eta_4}$ is the minimum upper bound of the sample. $\boldsymbol{\eta_4}$ is usually 1–6. The default value is 4. When $\boldsymbol{\eta_4}$ increases, the minimum upper bound of the sample iteration increases, and vice versa.

6. $\boldsymbol{\eta_5}$ is the minimum lower bound of the sample. $\boldsymbol{\eta_5}$ is generally 0.01–0.0001. The default value is 0.001. The value of $\boldsymbol{\eta_5}$ has little effect on the result of the iteration. We usually use $\boldsymbol{\eta_5} = 0.001$.

7. $\boldsymbol{\eta_6}$ is the maximum upper bound of the sample. The value of $\boldsymbol{\eta_6}$ is usually 10–50. The default is 20. When $\boldsymbol{\eta_6}$ increases, the maximum upper bound of the sample iteration increases, and vice versa. We usually use $\boldsymbol{\eta_6} = 15$–30.

2.4.9 Model Application and Limitations

The species itself carries information about many ecological categories. The species information model was used to map the distribution of resources. Recently, statistical methods in geographic information systems have become more widely used and the uses of biological and environmental data have expanded. Thus, in addition to its applications to biogeography, species evolution, and species distributions, the models including different types of species information are also widely used for research and decision-making in areas such as climate change, biological protection, biological invasions, disease transmission, and risk control (Miller J., 2010). In paleontology, the stability of the quantitative niche and the geographic species ranges can be studied using fossil parameter models, which reveal the effects of environmental change on species distributions. In such models, C3 is used as a reference time series in combination with GIS positioning techniques; the results of these models can reflect species distribution ranges in different geological eras and can also be used to infer processes of environmental change at different time nodes (Walls and Stigall, 2011).

The ecological and geographical distributions of *Rangifer tarandus* and *Cervus elaphus* during the last ice age were assessed by applying the niche model to historical fauna; this method also provided a means for the quantitative prediction of early biological distributions and community status (Svenning *et al.*, 2011). The use of trend surface analysis (TSA) to delineate regional range of species distributions, in conjunction with geographical criteria to delineate the regional range of species distributions, can reduce the impact of historical events on the parameterization of the model (Acevedo *et al.*, 2012). The main objective of species distribution modeling is to extract the important factors related to ecological models and to explain or predict changes in the development of ecological models. During the modeling process, the spatial structure data and the model parameters must be assumed, so all of the models have limitations in "distortion" and application scope; the scope of the model, as well as its autocorrelation behavior and non-stationarity, must be explained (Miller J. A., 2013).

The importance of using animal and plant data in species distribution modeling is clear, but the development of species distribution models is limited by methodology, research boundaries, and the effects of environmental factors. These factors affect the extrapolation and application functions of the model (Kéry *et al.*, 2010). The relationship between species and the environment is not a simple linear relationship. To establish a species distribution model, a clear theoretical system is necessary, including a conceptual framework for extracting data features, a mathematical analysis method (Austin, 2002; Walker and Cocks, 1991), and a method for identifying the data conditional factors and targets required for a species distribution model (Barbet-Massin *et al.*, 2012). In general, the precision of the model prediction increases with the number of samples, while prediction efficiency increases as the number of samples decreases (Stockwell and Peterson, 2002). It is also possible to develop a universal spatial modeling platform to extend the application of the model *via* the Internet (Stockwell and Peters, 1998). The taxonomy and regional distribution of a given organism are the basis of the niche of that species in the ecosystem (Batchelder *et al.*, 2002). This notion is the key to model evaluation (Peterson *et al.*, 2007). To maintain the most basic biological groups in the ecosystem, the ecosystem functions needed by human beings must probably be sustainable. The future development of science and technology is a powerful guarantee that ecosystem service functions will be changed and safeguarded.

The interpolation accuracy and transferability of the species distribution model are important features of this model. Of the models using machine learning, Maxent, the generalized Boosting method (GBM), and artificial neural networks (ANNs) show good transferability, while the genetic algorithm for rule-set prediction (GARP) and random forest (RF) models show significantly poorer extrapolation performance. Of the regression-based methods, generalized additive models (GAMs) and generalized linear models have good transferability. Three modeling techniques, Maxent, GBM, and GAM, have an ideal combination of prediction accuracy and portability (Heikkinen *et al.*, 2012).

The coexistence patterns among diverse forest species are determined by habitat-related factors and niche differentiation. In the community model, species distributions are not uniform at large spatial scales but are uniform at small spatial scales (Kraft and Ackerly, 2010). Competition theory holds that niche-like species cannot coexist; this corresponds to species classification. Instead, the concept of habitat filtering means that species with similar ecological requirements should coexist. In a real-world ecological environment, Ulrich *et al.* (2010) showed the aggregation of the species in the same genus, random species symbiosis, and cross-genus species isolation. The similar responses of congeneric species to environmental variables are the basis of stochastic symbiosis.

During the establishment of the fish community morphological model, we began with the ideal niche, considered the fish species and their taxonomic parameters in the community, and avoided many of the uncertain environmental factors involved in the actual niche. The multi-dimensional morphology of a given species was defined as the spatial conformation of the ideal niche of the species community. The spatial concept of niche and species "abundance" in the community was regarded as the ideal niche. Using the ideal niche value as a reference, the model was extended to analyze the actual niche and evaluate community succession. For example, figure 2.8 shows a two-dimensional graph of the results, with the ratio of the supplementary populations of different species as a variable based on the larval data collected in 2012. This figure shows that the "abundance" ratio factor deviates from the origin. We believe that this species' community is in an unbalanced ecological state. Although the analysis indicated that the fish community was disturbed, the analysis did not identify the target of the disturbance. Target identification requires further analysis of key factors associated with the environmental conditions of the fish habitat. Finally, matching results were obtained. These environmental factors can be further studied in a variable manner using this model. The river is a linear system, and disturbance events at certain nodes will affect the entire system. Therefore, it is important to master system information for further analysis.

Ecosystems are often disturbed at varying frequencies and intensities over time, and the niche of the species community is in a state of dynamic equilibrium during dynamic change. Community species structure in river systems is determined by species competition and niche allocation in time and space. Moore and Hunt (1988) studied regional species diversity, the structure of food webs, and the energy of habitats and food webs, and the results showed that communities may contain tightly coupled subunits whose numbers may increase with increasing diversity. As species diversity increases, interaction intensity decreases and the ecosystem stabilizes. Therefore, the community niche should also be in a state of dynamic equilibrium, and the occupancy rate of the species niche in the communities studied using this model should only be set to "dynamic equilibrium."

Elith and Leathwick (2009) proposed that model uncertainty could be resolved by strengthening studies of biological interactions. The species distribution model (SDMS) should be further developed to better consider biological interactions and model applications (Elith and Leathwick, 2009). The results of the basic niche and species distribution area model can be used as an indirect indicator for assessments of species distribution and abundances in response to environmental influences (Stanley and Royle, 2005). Theoretical and empirical support is necessary for ecological research (Chave, 2004). It is important to establish a standard system for ecological reconstruction, and theoretical systems must be used to guide the formation of cognitive communities. The application of phylogenetic and trait data in community studies is increasing (Ings *et al.*, 2009; Webb *et al.*, 2008).

2.5 The Modeling Software

The user interface dialog box appears on the main page of the "Morphological character niche analysis model" software. The home page of the "Help" feature includes comprehensive, systematic, and detailed guidance, as well as a description of the software.

2.5.1 Data File and Editing

2.5.1.1 Data File Format Requirements

The system has a variety of available statistical functions, and there are specific requirements for the format of the data file.

A list of the required fields follows:

Sample number (N), independent variable (factor) number (P), dependent variable (target) number (k), forecast Number (n)

Note that, for the purposes of the fish ecological research described herein, neither a target value nor a forecast number is needed, and both are thus set to 0. In addition, the forecast sample column values are not used. However, for other applications, values for these parameters may be input according to need.

"Independent Variable 1," "Independent Variable 2," "Independent variable 3," …, "Independent variable P"

"Dependent variable 1," "Dependent variable 2," "Dependent variable 3," …, "Dependent variable P"

"Goal 1," "Goal 2," "Goal 3," …, "Goal K"

"Sample 1," "Sample 2," "Sample 3," …, "Sample n"

"Forecast 1," "Forecast 2," "Forecast 3," …, "Forecast n"

The help notes included in the software give the exact representations of the factor data (Xij) and target data (Yi) needed for each sample in the data matrix.

2.5.1.2 Data File Generation

① Under the system "File" menu, select "New data file." Use the prompt box to find and edit the input data. If you do not wish to use the default factor name (or sample name), it can be changed by right-clicking the pop-up prompt.
② Use another editing software (such as Microsoft Word) to prepare the documents. Data files for six fish (samples), 22 factors, one target, and zero forecast samples follow. Please note that independent variables (factors) and dependent variables (targets) are strings and thus must be enclosed in quotation marks.

6, 22, 1, 0

"factor 1," "factor 2," ”factor 3," "factor 4," "factor 5," "factor 6", "factor 7", "factor 8", "factor 9", "factor 10", "factor 11", "factor 12", "factor 13", "factor 14", "factor 15", "factor 16", "factor 17", "factor 18", "factor 19", "factor 20", "factor 21", "factor 22", "target (%)"

"*Mylopharyngodon piceus*", "*Ctenopharyngodon idella*", "*Hypophthalmichthys molitrix*", "*Hypophthalmichthys nobilis*", "*Megalobrama terminalis*", "*Parabramis pekinensis*", "*Xenocypris argentea*", "*Squaliobarbus curriculus*", "*Cirrhinus molitorella*", "*Cyprinus carpio*", "*Elopichthys bambusa*", "*Ochetobius elongatus*", "*Siniperca kneri*", "*Sinibotia pulchra*", "*Hemiculter leucisculus*", "*Squalidus argentatus*", "*Pseudolaubuca sinensis*", "*Lcucosoma chinensis*", "*Rhinogobius giurinus*"

2,4.5,0.01,0.01,7,8,16,8,3.9,3.8,4.6,5.6,2.4,0.95,42,6,4,43,17,17,0.01,0.01, 12.2668657

2,2,4.5,0.01,7,8,16.5,8,4.3,3.8,4,7.1,2,0.85,39,7,5,41,18,18,0.01,0.01,13.9

2,4,0.01,0.01,7,13,17,8,3.3,3.7,4.4,7.2,2.4,1.43,108,32,19,120,75,43,0.01,0.01,13.6

2,4,0.01,0.01,7,12.5,17,8,3.5,3,3.4,6.8,2.1,1.25,98,27,17,106,66,45,0.01,0.01,12.3

2,2,3,4,10,11,16.5,10.5,6.2,4.2,3.4,8.4,3.8,1.55,107,19,6,112,56,32,0.01,0.01,7.0

1,0.01,0.01,0.01,13.5,8.5,15,5,3.5,2.7,4.1,6.9,10.8,1.35,85,9,20,98,20,40,0.01,0.01,4.8

2.5.1.3 Data Editing

Using the system "File" menu, it is possible to select different secondary functions and edit the data file.

2.5.2 Run

Click on the "Analysis" menu to select different operations and access various information.

2.5.2.1 Result Information

The menu "Correspondence analysis" can be used to obtain the correlation coefficient matrix, the R-type load matrix (*i.e.*, the scatter plot of independent variables), the Q-type load matrix (*i.e.*, the scatter plot of samples), and the eigenvalues (*i.e.*, the variance contribution rates of the principal axes).

2.5.2.2 Result Graph

Select "Eigenvalue map" to obtain the relative contribution of each principal axis (principal component or principal factor) to the variance.

2.5.2.3 "Graph Analysis" Function

After selecting "Graph analysis," four types of the two-dimensional graph can be selected: "Factor and sample graph," "Factor graph," "Sample graph," and "Composition (1) + sample graph." These data can be displayed using an origin, dot-line, or vector graph.

2.5.2.4 "Adjust" Function

The "Adjust" function can be used on a two-dimensional page. After selecting "Adjust," it is possible to modify the automatic pre-iteration parameters and iteration methods that are shown on the selection page. The user can input the coordinates of the endpoint of the iteration and parameters such as the error, step length, number of cycles, and the starting order of the iteration samples.

2.5.2.5 Select the Iteration Mode

When the "Enter adjust" function is selected, an iterative mode can be chosen from three options: the common method, the constraint method, and the vector method.

2.5.2.6 Iterative Effects

Due to a large number of calculations, the page will sometimes appear to hang or freeze. This is normal. Please wait patiently. If the calculations take too long, the program may be forced to close because the iteration method and iteration parameters are not properly selected.

After the system completes the auto-tuning iteration, the iteration results will display "Up to standard" or "Not up to standard." If the parameters are suitable, the program will exit and output the result. If the parameters are not suitable, the system will return to the "Adjust" page. At this point, changes can be made to factors such as the adjustment parameters and the iteration method. Parameters should be repeatedly adjusted until the "Up to standard" message is returned.

2.5.2.7 Parameter Specification

In order to get a good iterative result, it is very important to choose the proper working parameters. In particular, the vector method has several parameters (*e.g.*, $\boldsymbol{\eta}_1$–$\boldsymbol{\eta}_6$) that can be set by the user based on experience. For the convenience of the users, these parameters have default values.

Chapter 3

Relationship Between Community Structure and Species Succession

The function of an ecosystem is to keep organisms in harmony with their environment. In an ecosystem, the biological community occupies the ecological niche under a unified system of energy distribution. External energy (such as solar energy) and the internal energy of the earth drive the continuous circulation of the earth's material in the ecosystem, which includes the materials cycle in the environment, nutrient transfer among organisms, and material exchange between organisms and the environment. This cycle also includes conversions among material forms, such as the synthesis and decomposition of living matter. The materials cycle in the ecosystem is closely related to the composition of the biological community, and species composition and abundance in the biological community are in a stable and balanced equilibrium in an environment without mutation. Because the resources of the environment space are limited, only a certain number of organisms can be carried in the system. When the carrying biomass is close to saturation, if the number (density) of one species increases, the growth of other species in the system will be affected, causing a change in community structure until a new balance is achieved. Biological communities are composed of numerous species, which inevitably leads to competition, predation, abiotic stress, and mutually beneficial relationships among species (Bruno *et al.*, 2003). All of the species in a given biome are interdependent on other species. There are several common relationships.

One common relationship is the food chain. The survival of the predator depends on the prey, and the survival and abundance of the prey are controlled by the predator. These opposing forces remain relatively stable. The proportion of two species inhabiting the same space also remains relatively stable.

A second common relationship is a competition. Species often compete for the same resources. For example, plants compete for light, space, water, and soil nutrients, while animals compete for food and habitat. Over evolutionary time, competition has promoted the ecological differentiation of species. As a result, when competition relaxes, the community structures of species are stable. For example, fish are both sedentary and migratory in rivers; some fish species thrive in the upper water layers and some prefer to inhabit the lower layers; and fish can be herbivorous

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or predatory. Different types of organisms in the system are closely related, but each has its place.

A third common relationship is a mutualism. Species may be interdependent in a variety of ways, including the symbiotic relationship between bacteria and algae in lichens, as well as between microbes and their hosts in the gastrointestinal tract of animals. The disruption of this balance may lead to the reorganization of community structure, the permanent loss of a biological resource, or a change in ecosystem function. A mutually beneficial relationship is not just an attribute between two partners. Macroscopically, species relationships in stable communities are in a mutually beneficial state. There is a lack of studies on the interspecific relationships of a wide range of communities (Bronstein, 1994). Competition and predation are not the only functional forms among community species. All organisms have competitive and mutually beneficial relationships, and the balance between competition and mutual benefit is typically the main characteristic of an ecosystem. In both aquatic and terrestrial ecosystems, mutually beneficial relationships among species have been well studied. Mutually beneficial relationships are universal in biological communities and may involve specific taxa, combinations of taxa, or the relationship between the part and the whole systems (Bruno *et al.*, 2003).

In addition to the diversity index and the species abundance ranking method, indices of species composition, the average distance among species, and weight have also been used for community evaluation (Rochet and Trenkel, 2003). The stability of a community includes the balanced relationships of the spatial niche, in which the "niche" reflects the "quantity" of relationships a species possesses, and "quantity" relates to the amount of space occupied. The relationships among organisms may also be quantified in terms of energy allocation and material transport in the food chain, where biomass, or niche values, may be an important indicator of community stability.

The stability of an ecosystem is related to the composition of environmental resources and species. From the perspective of species composition, earlier studies suggested that simple ecosystems are less stable than complex ones, but later studies have come to the opposite conclusion (Pimm, 1984; Connell, 1978; Mcnaughton, 1978). The weak correlation between species diversity and functional diversity in communities is also reflected in river ecosystems. Rivers that are rich in species diversity may not have high functional diversity; overlapping relationships among species niches in communities, multiple complementarities in the construction of species niches, and community complexity may also increase the ecological buffer and guarantee the capacity of community functions, which may be a mechanism that safeguards the ecological functions of communities. Communities have a basic species composition, which is very important for the establishment of a fish community framework in an aquatic ecosystem.

In ecosystems, the degree of diversity is influenced by diffusion patterns and potential biological interactions. Biological community characteristics are characterized by higher taxa because higher taxa have greater biomass abundance than other taxa. In a given system, changes in diversity are determined by periodic changes in biomass allocation among community species (Enquist B J *et al.*, 2002). Species distributions in a community are characterized by the dominant species and the rare species. That is, most species occupy a small area, while only a few species occupy a large ecological position. Species survival decreases with the increase in geographic range; however, the relationships between range size and rates of speciation or population size increase are not significant (Castiglione *et al.*, 2017). Community structure is affected by regional environmental characteristics, and it is difficult to capture all of the information about the relationships among species in the ecosystem in general models, as these are restricted by a lack of data sources in the research system (Bowman, 1986). In the food chain, community species fall in a series from top to bottom. In studies of communities, it is important to clarify the species that are first to be impacted by environmental stress, as well as the environmental stress process and its effects on the community at large. In order to investigate these ecological questions, it is important to carefully choose the research object, and it is worth exploring whether the answer can be found by clarifying the niche relationships among community species.

Information on the niches of community species can be obtained from fossil specimen data (Elith *et al.*, 2006), which may include information about specific species in space and time based on specimen characteristics (Nic *et al.*, 2018). Fossils can also provide information about specific historical periods, and researchers can use fossils to study the relationship between the biome and the environment on a geological scale (Stigall, 2012). Niche data and regional species distributions reveal the interactions among species and with the environment. In addition, character changes reflect the differentiation and adaptability of species within the environment; this helps to clarify the spatial processes of ecology and the evolution of biological communities, as well as species range distributions in different periods. The impact of environmental processes on species distributions can also be inferred from fossil numbers (Walls and Stigall, 2011). Similarly, species data in the literature can be used to study succession in biological communities, restore the structural characteristics of biological communities at different times, and study community construction beyond the regional scope. Species data improve our understanding of community evolution and may help in ecosystem reconstruction (Gravel *et al.*, 2006). During ecosystem reconstruction, it is necessary to consider the fact that diverse species cannot occupy a large niche, and that widespread species have a "wide" niche, whereas individual species have a "narrow" niche; the niche width of individual large species is also "wide." Under environmental stress, the miniaturization of some species indicates that the spatial niche of the species also becomes smaller. Species composition in the community will change accordingly, and ecosystem functions will be rearranged. Predictive tools and methods are needed to characterize the relationships among community species.

This chapter presents the relationships among community species from the perspective of species succession. We selected 104 species found in China, representing 61 genera, for the establishment of a simulated community, and the model was used to study the loss of one species and changes in interspecific relationships. Modeling studies also highlighted the fish in the Pearl River system, as far as possible, to choose the morphological taxonomic species of the "genus." Specialized species were also included in the model analysis, such as *Schizothorax meridionalis* (Tsao, 1964) and *Sinocyclocheilus* spp. (Fang, 1936). These species, along with other special species, are closer to the real-world river fish community. Through this study, we can understand the relationship between "missing" species and other species. In addition, we can deduce changes in community species relationships and the mechanisms of niche succession. Using the 104 fish species described in the previous section, a species-by-species disappearance simulation was conducted to analyze the response of some fish species in the community to the disappearance of other species. The principle is that if the simulated species disappears and the niche occupation of a given fish decreases, these species are "mutually beneficial." If the simulated species disappears and the niche occupation of a given fish species remains unchanged, these species are "non-competitive." If the simulated species disappears and the niche occupancy of a certain fish increases, the disappeared species is judged as "competitive" with the species with the corresponding niche increase.

Cypriniforms are the main freshwater fish in China. Of the 89 species selected, 84 were species in Cyprinidae. We also included six species of the Perciformes, representing six families; seven species of the Siluriformes in the same family; and one species each from the Osmeriformes and Tetraodntiformes. In general, the simulation analysis showed that fish that were closely related taxonomically had different responses to the loss of the same fish and did not exhibit clustering patterns consistent with taxonomic classification. This result might be due to differences in various competitive or mutually beneficial attributes, with the result that the degree of influence on niche change rate was different.

In the analysis of interspecific relationships within simulated communities, irrespective of the specific fish removed, the niche of some fish increased obviously. The initial niche of these fish in the simulated community was small or missing. Thus, niche expansion was obvious. In the simulated community of 104 species of fish, there were two species of fish that were competitive with all other fish: *Cyprinus chilia* (Wu, 1963) and *Onychostoma ovalis rhomboides* (Tang, 1942). These two species of fish have small distributions and populations in the real-world Pearl River system. Irrespective of the specific fish that lost its niche, the niche of some fish decreased. The initial basal niche of these fish in the simulated community was small or missing, and the niche reductions were obvious. In the simulated community of 104 species of fish, only *Procypris merus* (Lin, 1933), which is distributed in the southwest river and has a small population, was mutually beneficial to all other fish. Species with moderate niche change may be more favorable for community stability, suggesting that more consideration should be given to the niches of "stable" species in artificial ecosystem construction. The niche relationships within fish communities may be closely related to the energy allocation in the food chain. By analyzing succession in a simulated community, we can increase our understanding of species relationships and provide a means for the pre-evaluation of species relationships when reconstructing fish communities.

3.1 Simulations of Species Removal

Schoener (1974) stated that the niche of a species in a community is related to the distribution of resources and that to study the niche, the establishment of a complete theoretical system, including models at the individual and group levels, is required. In addition, to analyze species relationships in the community, it is necessary to understand the relationships between dimension and niche, as well as interspecific niche boundaries and niche shapes, the number and abundances of the species in a biome, the number of interactions among species (mainly feeding and competition relationships), and the intensity of these interactions expressed in terms of the proportion of species pairs that interact directly. The interaction force varies with the number of species, and the intensity of the interaction usually decreases significantly as the number of species increases (Rejmanek and Stary, 1979). The changes in an interspecific niche can be understood by simulating the loss of species in the community. There were 104 species of fish in the simulated community, which represented five orders and 12 families.

3.1.1 Osmeriformes Lcucosoma chinensis (Osbeck, 1765)

The niche variation of *Lcucosoma chinensis* (Osbeck, 1765) ranged from 0% to 98% in the absence of different species (see figure 3.1). Among the 103 species of fish, 58 species were mutually beneficial to *Lcucosoma chinensis*. There were 34 species that had more than a 10% effect on the niche of *Lcucosoma chinensis*. Of these, in which the largest effect was 98% by *Hypophthalmichthys molitrix*. There were 45 species of fish in competitive relationships with *Lcucosoma chinensis*. There were 30 species that affected the niche of *Lcucosoma chinensis* by more than 10%, with which the biggest effect was 23%. An additional 39 species had less than a 10% effect on the rate of the niche variation of *Lcucosoma chinensis*.

3.1.2 Cypriniformes

3.1.2.1 Cobitidae

3.1.2.1.1 Micronemacheilus pulcher (Nichols and Pope, 1927)

The niche variation of *Micronemacheilus pulcher* (Nichols and Pope, 1927) ranged from 0% to 124% in the absence of different species (see figure 3.2). Among the 103 species of fish, 41 species were mutually beneficial to *Micronemacheilus pulcher*. There were 9 species that had more than a 10% effect on the niche of *Micronemacheilus pulcher*. Of these, in which the largest effect was 98% by *hypophthalmichthys molitrix*. There are 62 species of fish in competitive relationships with *Micronemacheilus pulcher*. There were 58 species that affected the niche of *Micronemacheilus pulcher* by more than 10%, and 124% of those fishes. An additional 36 species had less than a 10% effect on the rate of niche variation of *Micronemacheilus pulcher*.

3.1.2.1.2 Sinibotia pulchra (Wu, 1939)

The niche variation of *Sinibotia pulchra* (Wu, 1939) ranged from 0% to 230% in the absence of different species (see figure 3.3). Among the 103 species of fish, 45 species were mutually beneficial to *Sinibotia pulchra*. There were 3 species that had more than a 10% effect on the niche of *Sinibotia pulchra*. Of these, in which

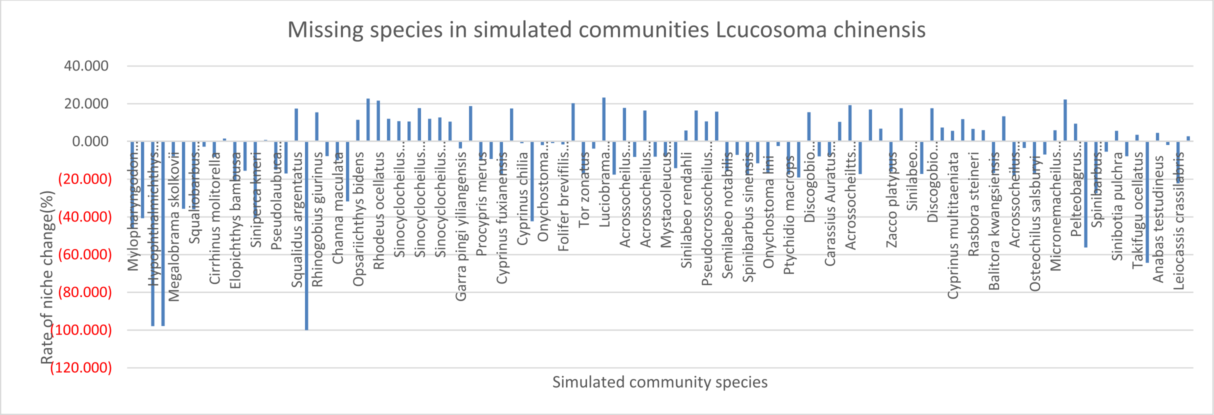

Fig. 3.1 – The responses of the niches of *Lcucosoma chinensis* to various missing fish in the simulated community.

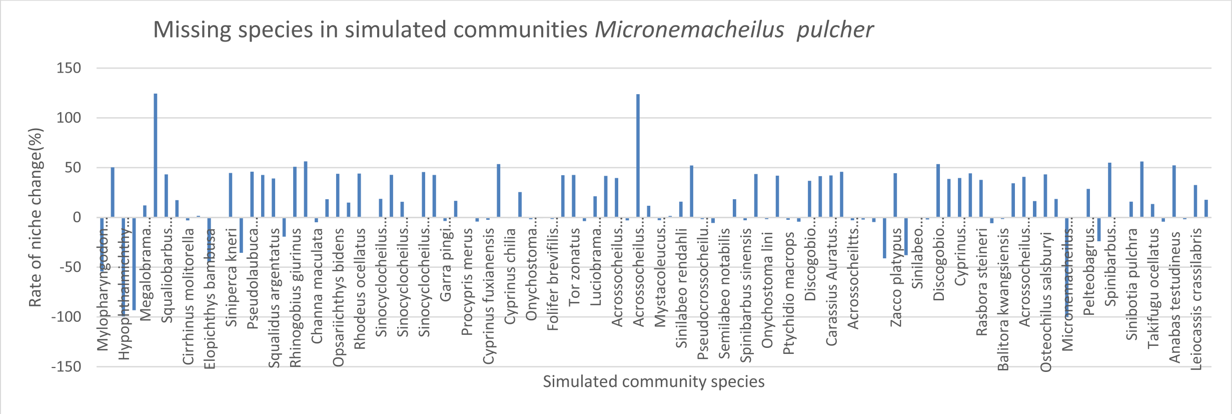

Fig. 3.2 – The responses of the niches of *Micronemacheilus pulcher* to various missing fish in the simulated community.

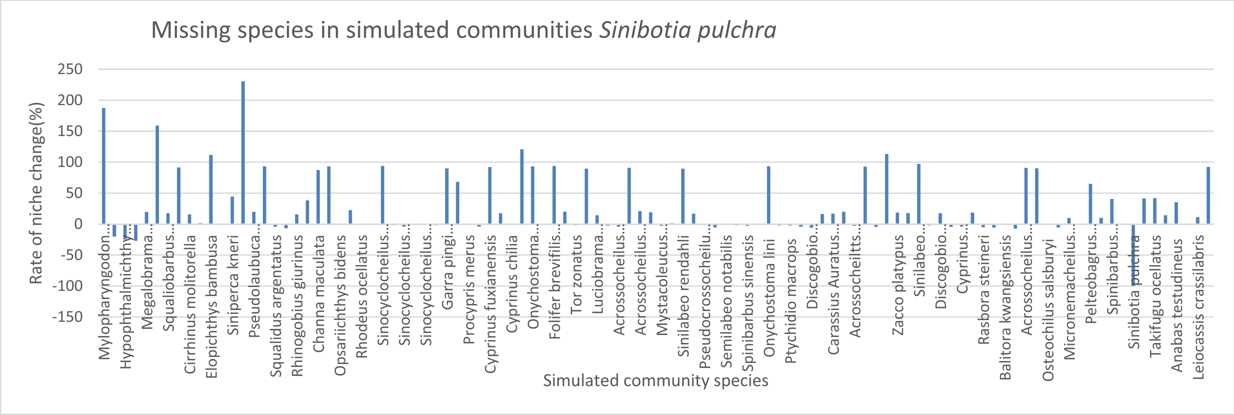

FIG. 3.3 – The responses of the niches of *Sinibotia pulchra* to various missing fish in the simulated community.

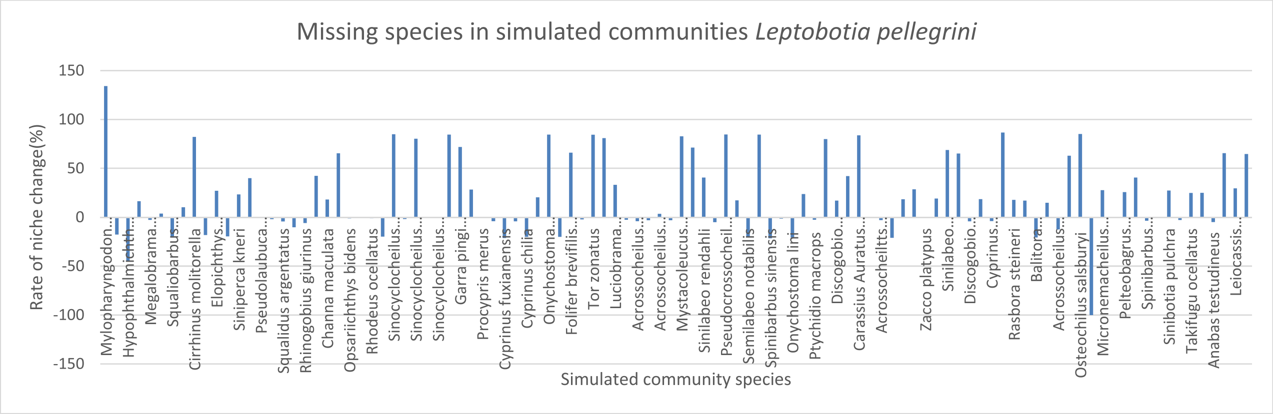

FIG. 3.4 – The responses of the niches of *Leptobotia pellegrini* to various missing fish in the simulated community.

the largest effect was 27% by *Hypophthalmichthys nobilis*. There were 58 species of fish in competitive relationships with *Sinibotia pulchra*. There were 54 species that affected the niche of *Sinibotia pulchra* by more than 10%, in which the biggest effect was 230% by *Misgurnus anguillicaudatus*. An additional 46 species had less than a 10% effect on the rate of the niche variation of *Sinibotia pulchra*.

3.1.2.1.3 Leptobotia pellegrini (Fang, 1963)

The niche variation of *Leptobotia pellegrini* (Fang, 1963) ranged from 0% to 134% in the absence of different species (see figure 3.4). Among the 103 species of fish, 46 species were mutually beneficial to *Leptobotia pellegrini*. There were 16 species that had more than a 10% effect on the niche of *Leptobotia pellegrini*. Of these, in which the largest effect was 27% by *Hypophthalmichthys molitrix*. There were 57 species of fish in competitive relationships with *Leptobotia pellegrini*. There were 53 species that affected the niche of *Leptobotia pellegrini* by more than 10%, with which the biggest effect was 134% by *Hypophthalmichthys molitrix*. An additional 34 species had less than a 10% effect on the rate of the niche variation of *Leptobotia pellegrini*.

3.1.2.1.4 Misgurnus anguillicaudatus (Cantor, 1842)

The niche variation of *Misgurnus anguillicaudatus* (Cantor, 1842) ranged from 0% to 63% in the absence of different species (see figure 3.5). Among the 103 species of fish, 58 species were mutually beneficial to the *Misgurnus anguillicaudatus*. There were 34 species that had more than a 10% effect on the niche of *Misgurnus anguillicaudatus*. Of these, in which the largest effect was 63% by *Hypophthalmichthys molitrix*. There were 19 species of fish in a competitive relationship with *Misgurnus anguillicaudatus*. There were 15 species that affected the niche of *Misgurnus anguillicaudatus* by more than 10%, and 51% of those were affected by *Lateolabrax japonicus*. An additional 73 species had less than a 10% effect on the rate of the niche variation of *Misgurnus anguillicaudatus*.

3.1.2.2 Cyprininae

3.1.2.2.1 Opsariichthys bidens (Günther, 1873)

The niche variation of *Opsariichthys bidens* (Günther, 1873) ranged from 0% to 63% in the absence of different species (see figure 3.6). Among the 103 species of fish, 91 species were mutually beneficial to *Opsariichthys bidens*. There were 87 species that had more than a 10% effect on the niche of *Opsariichthys bidens*. Of these, in which the largest effect was 87% by *Hemibagrus macropterus*. There were 12 species of fish in competitive relationships with *Opsariichthys bidens*. There were 2 species that affected the niche of *Opsariichthys bidens* by more than 10%, with which the biggest effect was 23% by *Megalobrama skolkovii*. An additional 39 species had less than a 10% effect on the rate of the niche variation of *Opsariichthys bidens*.

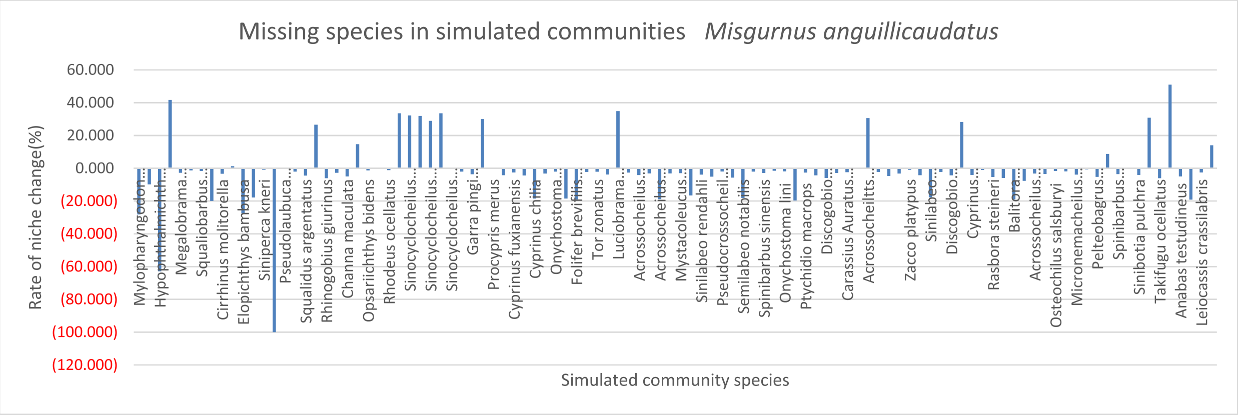

Fig. 3.5 – The responses of the niches of *Misgurnus anguillicaudatus* to various missing fish in the simulated community.

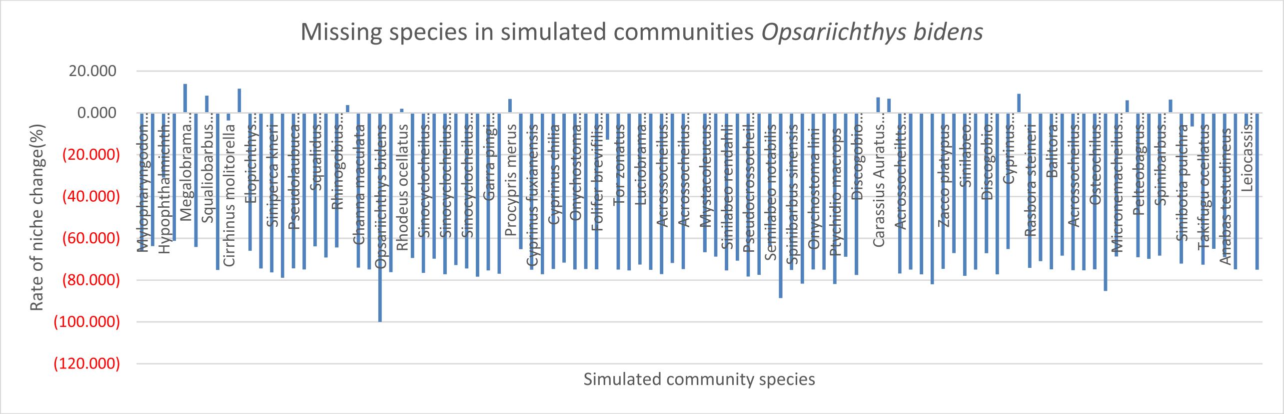

Fig. 3.6 – The responses of the niches of *Opsariichthys bidens* to various missing fish in the simulated community.

3.1.2.2.2 Rasbora steineri (Nichols and Pope, 1927)

The niche variation of *Rasbora steineri* (Nichols and Pope, 1927) ranged from 0% to 51% in the absence of different species (see figure 3.7). Among the 103 species of fish, 95 species were mutually beneficial to *Rasbora steineri.* There were 52 species that had more than a 10% effect on the niche of *Rasbora steineri.* Of these, in which the largest effect was 51% by *Semilabeo notabilis.* There were 8 species of fish in competitive relationships with *Rasbora steineri.* There were 2 species that affected the niche of *Rasbora steineri* by more than 10%, with which the biggest effect was 35% by *Hypophthalmichthys molitrix.* An additional 47 species had less than a 10% effect on the rate of the niche variation of *Rasbora steineri.*

3.1.2.2.3 Zacco platypus (Temminck and Schlegel, 1846)

The niche variation of *Zacco platypus* (Temminck and Schlegel, 1846) ranged from 0% to 116% in the absence of different species (see figure 3.8). Among the 103 species of fish, 47 species were mutually beneficial to *Zacco platypus.* There were 31 species that had more than a 10% effect on the niche of *Zacco platypus.* Of these, in which the largest effect was 81% by *Hypophthalmichthys molitrix.* There were 59 species of fish in competitive relationships with *Zacco platypus.* There were 46 species that affected the niche of *Zacco platypus* by more than 10%, in which the biggest effect was 116% by *Hypophthalmichthys molitrix.* An additional 47 species had less than a 10% effect on the rate of the niche variation of *Zacco platypus.*

3.1.2.2.4 Mylopharyngodon piceus (Richardson, 1846)

The niche variation of *Mylopharyngodon piceus* (Richardson, 1846) ranged from 0% to 629% in the absence of different species (see figure 3.9). Among the 103 species of fish, 91 species were mutually beneficial to *Mylopharyngodon piceus.* There were 3 species that had more than a 10% effect on the niche of *Mylopharyngodon piceus.* Of these, in which the largest effect was 12% by *Garra pingi pingi.* There were 12 species of fish in competitive relationships with *Mylopharyngodon piceus.* There were 3 species that affected the niche of *Mylopharyngodon piceus* by more than 10%, with which the biggest effect was 629% by *Hypophthalmichthys molitrix.* An additional 98 species had less than a 10% effect on the rate of the niche variation of *Mylopharyngodon piceus.*

3.1.2.2.5 Luciobrama macrocephalus (Lacepède, 1803)

The niche variation of *Luciobrama macrocephalus* (Lacepède, 1803) ranged from 12% to 1974% in the absence of different species (see figure 3.10). Among the 103 species of fish, 17 species were mutually beneficial to *Luciobrama macrocephalus.* All species had more than a 10% effect on the niche of *Luciobrama macrocephalus.* Of these, in which the largest effect was 55% by *Acrossocheilus iridescens iridescens.* There were 86 species of fish in competitive relationships with *Luciobrama macrocephalus.* All species affected the niche of *Luciobrama macrocephalus* by more than 10%, with which the biggest effect was 1974% by *Pelteobagrus vachellii.*

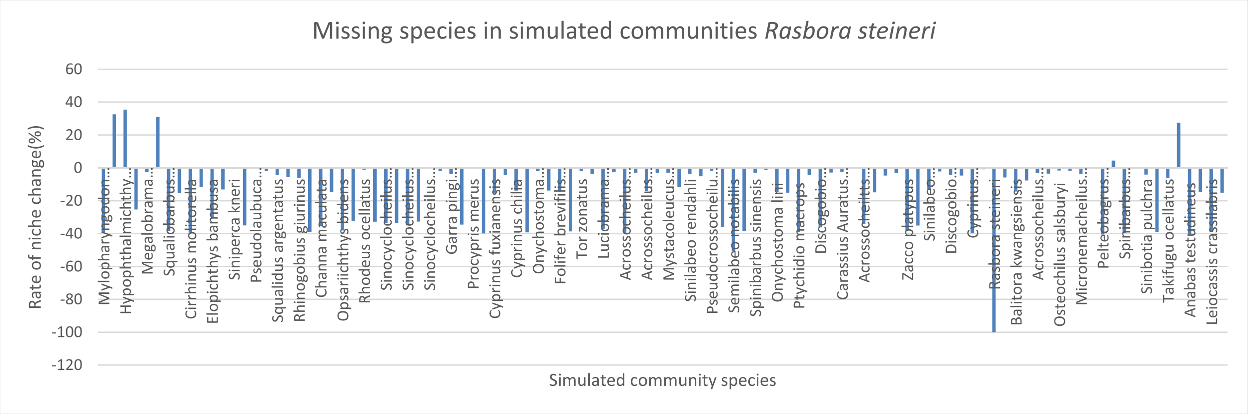

FIG. 3.7 – The responses of the niches of *Rasbora steineri* to various missing fish in the simulated community.

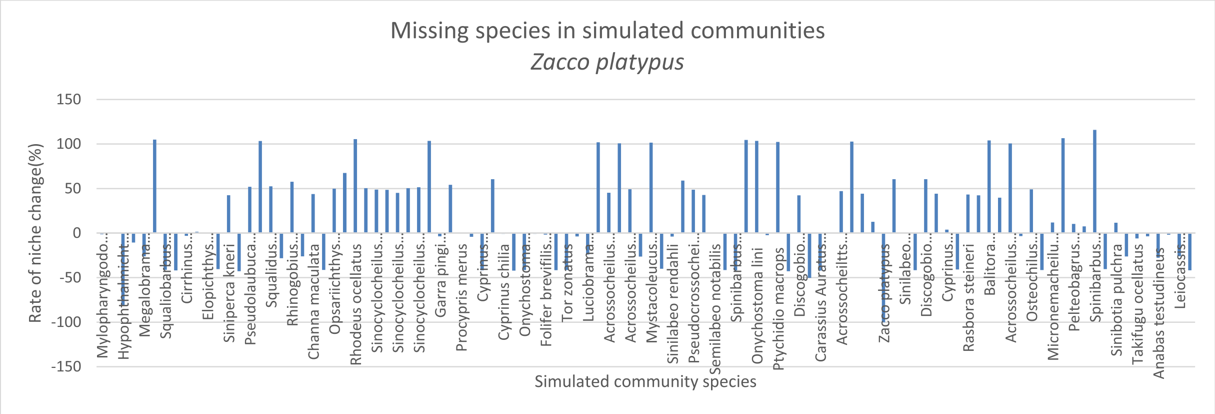

FIG. 3.8 – The responses of the niches of *Zacco platypus* to various missing fish in the simulated community.

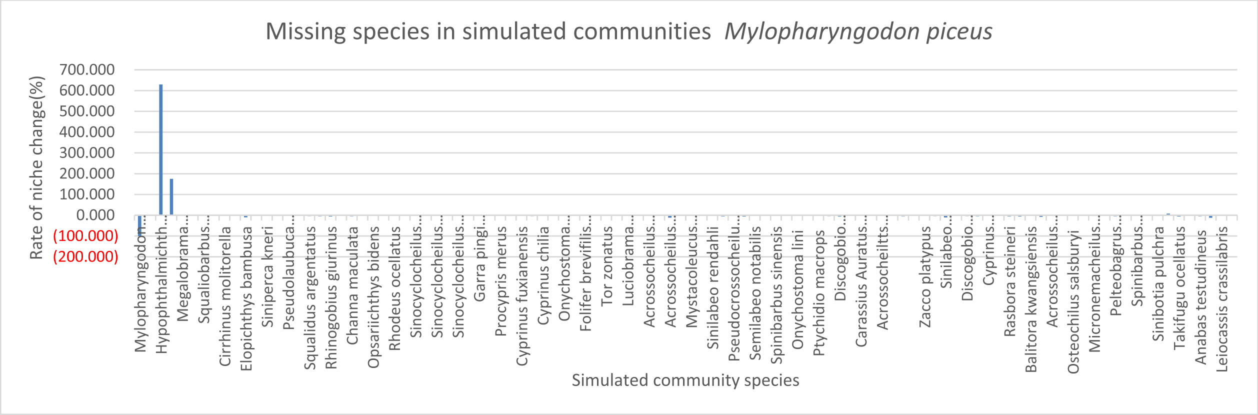

FIG. 3.9 – The responses of the niches of *Mylopharyngodon piceus* to various missing fish in the simulated community.

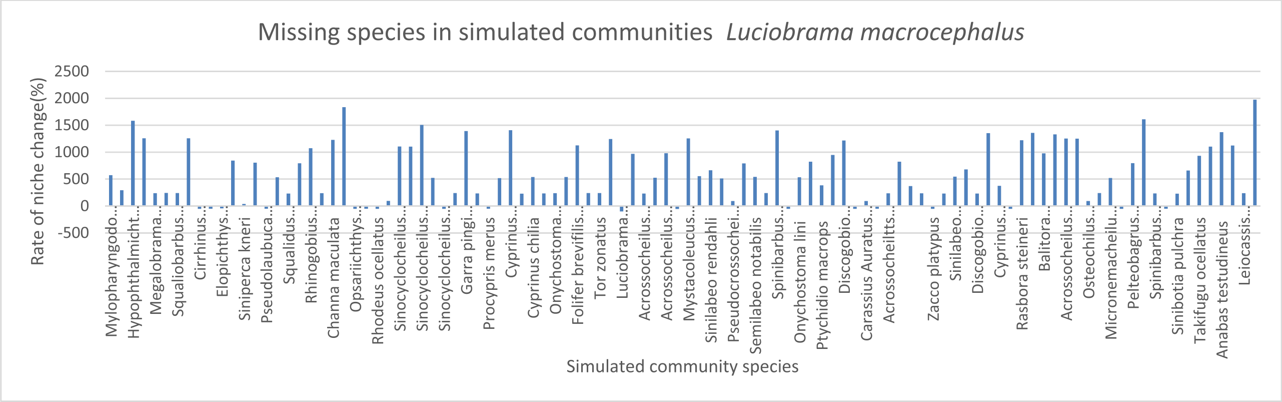

FIG. 3.10 – The responses of the niches of *Luciobrama macrocephalus* to various missing fish in the simulated community.

3.1.2.2.6 Ctenopharyngodon idella (Valenciennes, 1844)

The niche variation of *Ctenopharyngodon idella* (Valenciennes, 1844) ranged from 0% to 230% in the absence of different species (see figure 3.11). Among the 103 species of fish, 45 species were mutually beneficial to *Ctenopharyngodon idella*. There were 3 species that had more than a 10% effect on the niche of *Ctenopharyngodon idella*. Of these, in which the largest effect was 27% by *Hypophthalmichthys nobilis*. There were 58 species of fish in competitive relationships with *Ctenopharyngodon idella*. There were 54 species that affected the niche of *Ctenopharyngodon idella* by more than 10%, with which the biggest effect was 230% by *Misgurnus anguillicaudatus*. An additional 46 species had less than a 10% effect on the rate of the niche variation of *Ctenopharyngodon idella*.

3.1.2.2.7 Ochetobius elongatus (Kner, 1867)

The niche variation of *Ochetobius elongatus* (Kner, 1867) ranged from 0% to 395% in the absence of different species (see figure 3.12). Among the 103 species of fish, 11 species were mutually beneficial to *Ochetobius elongatus*. No species had more than a 10% effect on the niche of *Ochetobius elongatus*. Of these, in which the largest effect was 3% by *Luciocyprinus langsoni*. There were 92 species of fish in competitive relationships with *Ochetobius elongatus*. There were 87 species that affected the niche of *Ochetobius elongatus* by more than 10%, with which the biggest effect was 395% by *Hypophthalmichthys nobilis*. An additional 16 species had less than a 10% effect on the rate of the niche variation of *Ochetobius elongatus*.

3.1.2.2.8 Elopichthys bambusa (Richardson, 1845)

The niche variation of *Elopichthys bambusa* (Richardson, 1845) ranged from 0% to 213% in the absence of different species (see figure 3.13). Among the 103 species of fish, 95 species were mutually beneficial to *Elopichthys bambusa*. There were 7 species that had more than a 10% effect on the niche of *Elopichthys bambusa*. Of these, in which the largest effect was 25% by *Mylopharyngodon piceus*. There were 8 species of fish in competitive relationships with *Elopichthys bambusa*. Only one species affected the niche of *Elopichthys bambusa* by more than 10%, with which the biggest effect was 213% by *Hypophthalmichthys molitrix*. An additional 90 species had less than a 10% effect on the rate of the niche variation of *Elopichthys bambusa*.

3.1.2.2.9 Squaliobarbus curriculus (Richardson, 1846)

The niche variation of *Squaliobarbus curriculus* (Richardson, 1846) ranged from 0% to 98% in the absence of different species (see figure 3.14). Among the 103 species of fish, 13 species were mutually beneficial to *Squaliobarbus curriculus*. There were 8 species that had more than a 10% effect on the niche of *Squaliobarbus curriculus*. Of these, in which the largest effect was 45% by *Elopichthys bambusa*. There were 30 species of fish in competitive relationships with *Squaliobarbus curriculus*. There were 20 species that affected the niche of *Squaliobarbus curriculus* by more than 10%, with which the biggest effect being 199% by *Micronemacheilus pulcher*. An additional 60 species had less than a 10% effect on the rate of the niche variation of *Squaliobarbus curriculus*.

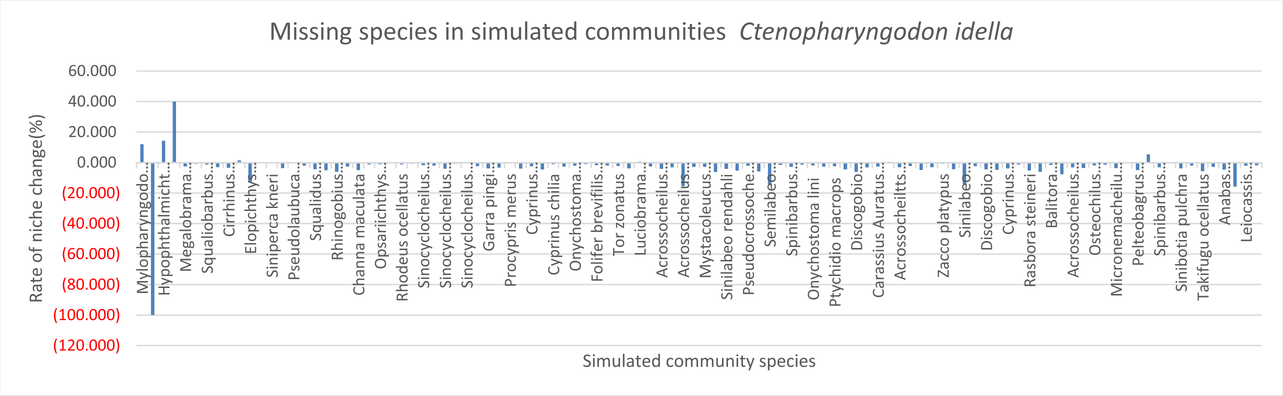

FIG. 3.11 – The responses of the niches of *Ctenopharyngodon idella* to various missing fish in the simulated community.

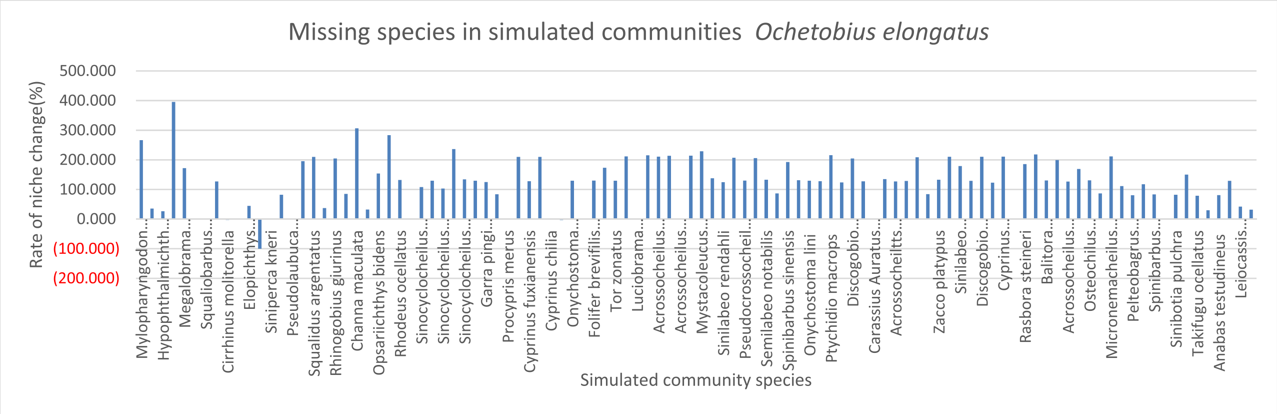

FIG. 3.12 – The responses of the niches of *Ochetobius elongatus* to various missing fish in the simulated community.

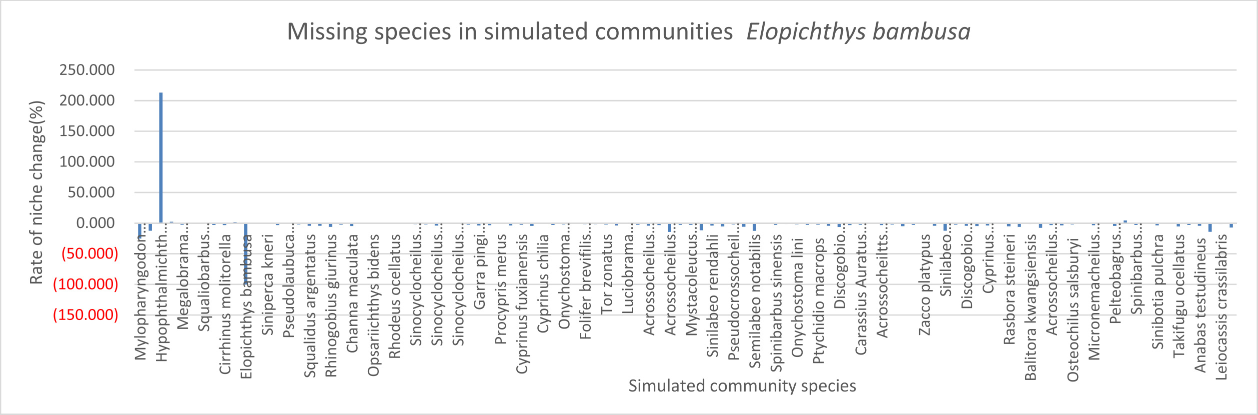

FIG. 3.13 – The responses of the niches of *Elopichthys bambusa* to various missing fish in the simulated community.

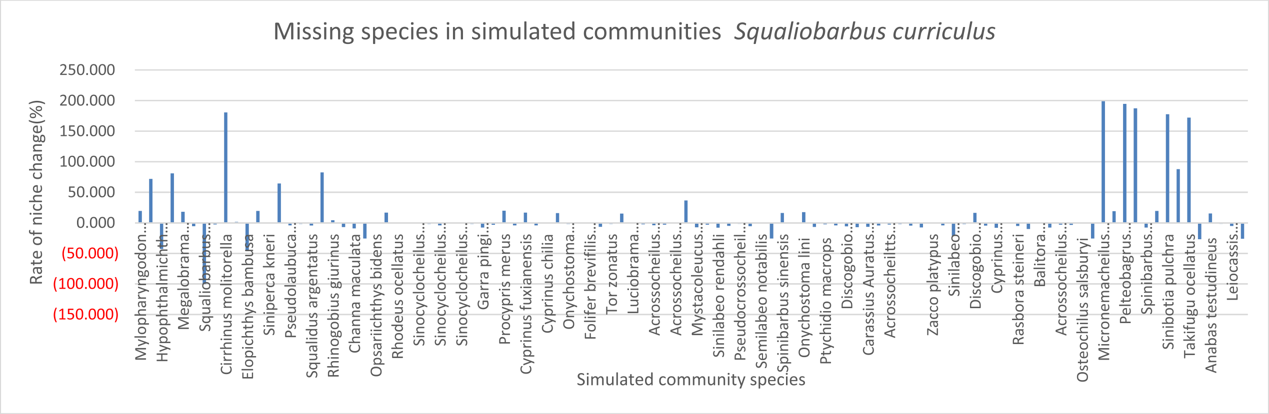

FIG. 3.14 – The responses of the niches of *Squaliobarbus curriculus* to various missing fish in the simulated community.

3.1.2.2.10 Ancherythroculter lini (Luo, 1994)

The niche variation of *Ancherythroculter lini* (Luo, 1994) ranged from 0% to 211% in the absence of different species (see figure 3.15). Among the 103 species of fish, 69 species were mutually beneficial to *Ancherythroculter lini*. There were 19 species that had more than a 10% effect on the niche of *Ancherythroculter lini*. Of these, in which the largest effect was 52% by *Hypophthalmichthys molitrix*. There were 34 species of fish in competitive relationships with *Ancherythroculter lini*. All of those species affected the niche of *Ancherythroculter lini* by more than 10%, with which the biggest effect was 211% by *Luciobrama macrocephalus*. An additional 50 species had less than a 10% effect on the rate of the niche variation of *Ancherythroculter lini*.

3.1.2.2.11 Pseudolaubuca sinensis (Bleeker, 1865)

The niche variation of *Pseudolaubuca sinensis* (Bleeker, 1865) ranged from 0% to 158% in the absence of different species see (figure 3.16). Among the 103 species of fish, 41 species were mutually beneficial to *Pseudolaubuca sinensis*. There were 4 species that had more than a 10% effect on the niche of *Pseudolaubuca sinensis*. Of these, in which the largest effect was 38% by *Hypophthalmichthys molitrix*. There were 62 species of fish in competitive relationships with *Pseudolaubuca sinensis*. There were 58 species that affected the niche of *Pseudolaubuca sinensis* by more than 10%, with which the biggest effect was 158% by *Hypophthalmichthys nobilis*. An additional 46 species had less than a 10% effect on the rate of the niche variation of *Pseudolaubuca sinensis*.

3.1.2.2.12 Parabramis pekinensis (Basilewsky, 1855)

The niche variation of *Parabramis pekinensis* (Basilewsky, 1855) ranged from 0% to 160% in the absence of different species (see figure 3.17). Among the 103 species of fish, 3 species were mutually beneficial to *Parabramis pekinensis*. There were 2 species that had more than a 10% effect on the niche of *Parabramis pekinensis*. Of these, in which the largest effect was 73% by *Hypophthalmichthys molitrix*. There were 99 species of fish in competitive relationships with *Parabramis pekinensis*. There were 98 species that affected the niche of *Parabramis pekinensis* by more than 10%, with which the biggest effect was 160% by *Leptobotia pellegrini*. An additional 2 species had less than a 10% effect on the rate of the niche variation of *Parabramis pekinensis*.

3.1.2.2.13 Hemiculter leucisculus (Basilewsky, 1855)

The niche variation of *Hemiculter leucisculus* (Basilewsky, 1855) ranged from 0% to 273% in the absence of different species (see figure 3.18). Among the 103 species of fish, 45 species were mutually beneficial to *Hemiculter leucisculus*. There were 3 species that had more than a 10% effect on the niche of *Hemiculter leucisculus*. Of these, in which the largest effect was 49% by *Hypophthalmichthys molitrix*. There were 37 species of fish in competitive relationships with *Hemiculter leucisculus*. There were 32 species that affected the niche of *Hemiculter leucisculus* by more than 10%, with which the biggest effect was 273% by *Carassius auratus auratus*. An additional 64 species had less than a 10% effect on the rate of the niche variation of *Hemiculter leucisculus*.

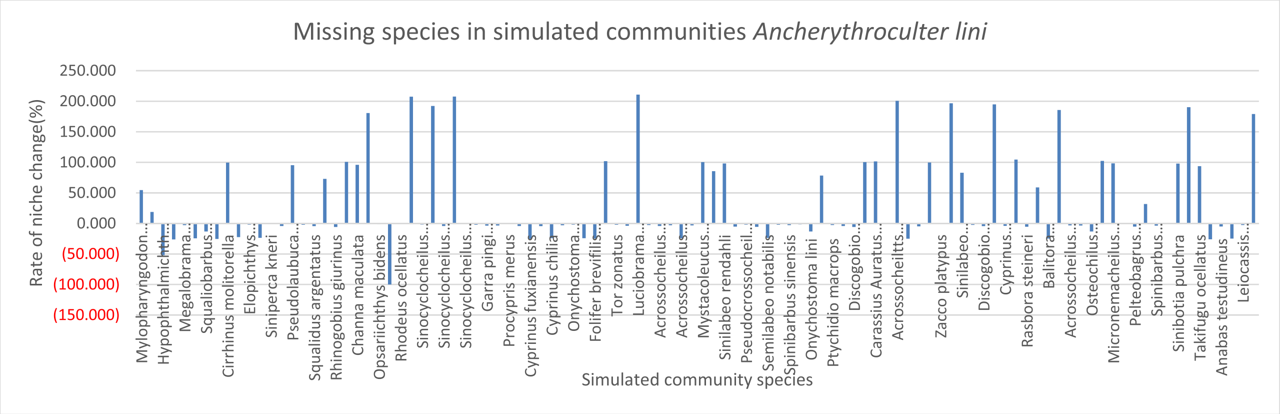

FIG. 3.15 – The responses of the niches of *Ancherythroculter lini* to various missing fish in the simulated community.

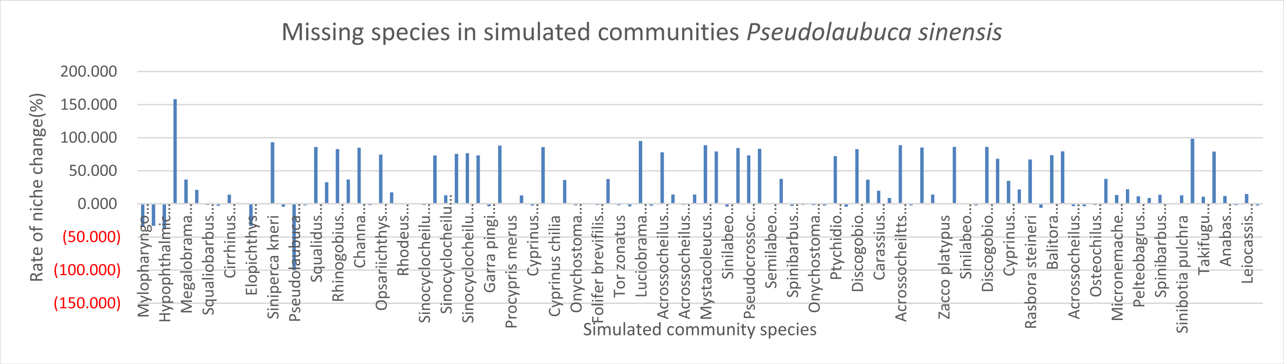

FIG. 3.16 – The responses of the niches of *Pseudolaubuca sinensis* to various missing fish in the simulated community.

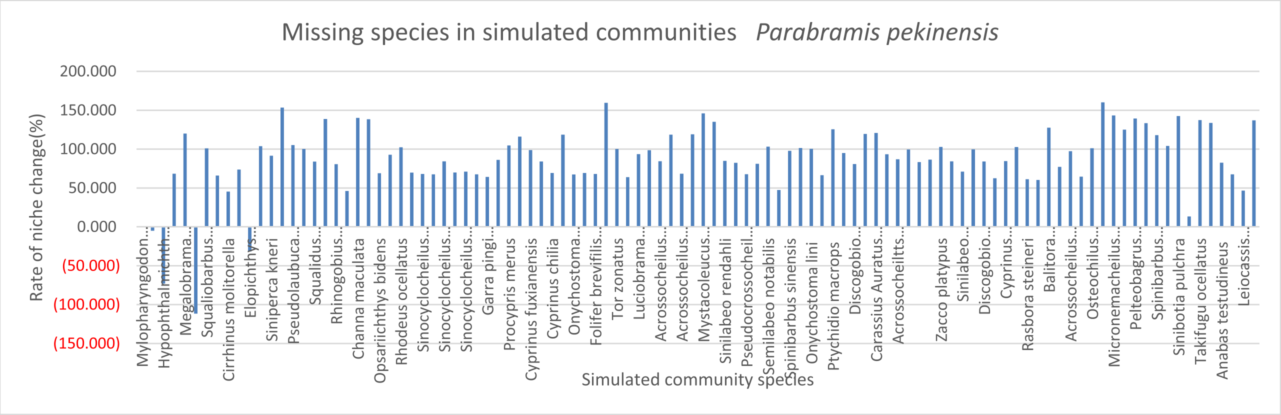

FIG. 3.17 – The responses of the niches of *Parabramis pekinensis* to various missing fish in the simulated community.

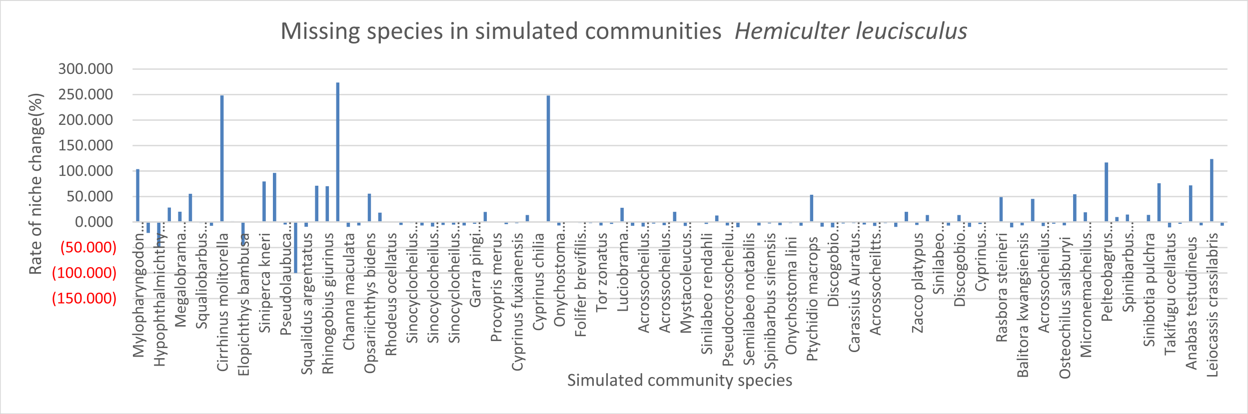

FIG. 3.18 – The responses of the niches of *Hemiculter leucisculus* to various missing fish in the simulated community.

3.1.2.2.14 Rasborinus lineatus (Pellegrin, 1907)

The niche variation of *Rasborinus lineatus* (Pellegrin, 1907) ranged from 0% to 193% in the absence of different species (see figure 3.19). Among the 103 species of fish, 30 species were mutually beneficial to *Rasborinus lineatus.* There were 12 species that had more than a 10% effect on the niche of *Rasborinus lineatus.* Of these, in which the largest effect was 52% by *Hypophthalmichthys nobilis.* There were 73 species of fish in competitive relationships with *Rasborinus lineatus.* There were 67 species that affected the niche of *Rasborinus lineatus* by more than 10%, with which the biggest effect was 193% by *Hypophthalmichthys nobilis.* An additional 46 species had less than a 10% effect on the rate of the niche variation of *Rasborinus lineatus.*

3.1.2.2.15 Megalobrama skolkovii (Dybowski, 1872)

The niche variation of *Megalobrama skolkovii* (Dybowski, 1872) ranged from 0% to 145% in the absence of different species (see figure 3.20). Among the 103 species of fish, 93 species were mutually beneficial to *Megalobrama skolkovii.* There were 74 species that had more than a 10% effect on the niche of *Megalobrama skolkovii.* Of these, in which the largest effect was 43% by *Hypophthalmichthys molitrix.* There were 10 species of fish in competitive relationships with *Megalobrama skolkovii.* There were 6 species that affected the niche of *Lcucosoma chinensis* by more than 10%, with which the biggest effect was 145% by *Anabas testudineus.* An additional 23 species had less than a 10% effect on the rate of the niche variation of *Megalobrama skolkovii.*

3.1.2.2.16 Xenocypris argentea (Günther, 1868)

The niche variation of *Xenocypris argentea* (Günther, 1868) ranged from 0% to 1704% in the absence of different species (see figure 3.21). Among the 103 species of fish, 24 species were mutually beneficial to *Xenocypris argentea.* Only one species had more than a 10% effect on the niche of *Lcucosoma chinensis* with an effect was 17% by *Mylopharyngodon piceus.* There were 79 species of fish in competitive relationships with *Xenocypris argentea.* There were 72 species that affected the niche of *Lcucosoma chinensis* by more than 10%, with which the biggest effect was 1704% by *Ctenopharyngodon idella.* An additional 39 species had less than a 10% effect on the rate of the niche variation of *Xenocypris argentea.*

3.1.2.2.17 Hypophthalmichthys molitrix (Valenciennes, 1844)

The niche variation of *Hypophthalmichthys molitrix* (Valenciennes, 1844) ranged from 0% to 10% in the absence of different species (see figure 3.22). Among the 103 species of fish, 93 species were mutually beneficial to *Hypophthalmichthys molitrix.* There were 10 species of fish in competitive relationships with *Hypophthalmichthys molitrix.* No species that affected the niche of No species by more than 10%, in which the biggest effect was 2% by *Sinilabeo discognathoides.* All of the species had less than a 10% effect on the rate of the niche variation of *Hypophthalmichthys molitrix.*

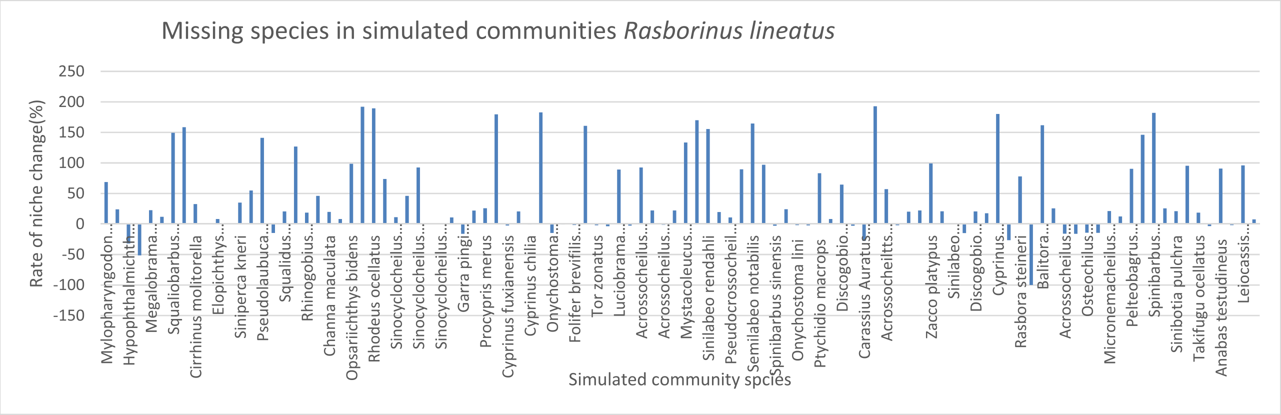

Fig. 3.19 – The responses of the niches of *Rasborinus lineatus* to various missing fish in the simulated community.

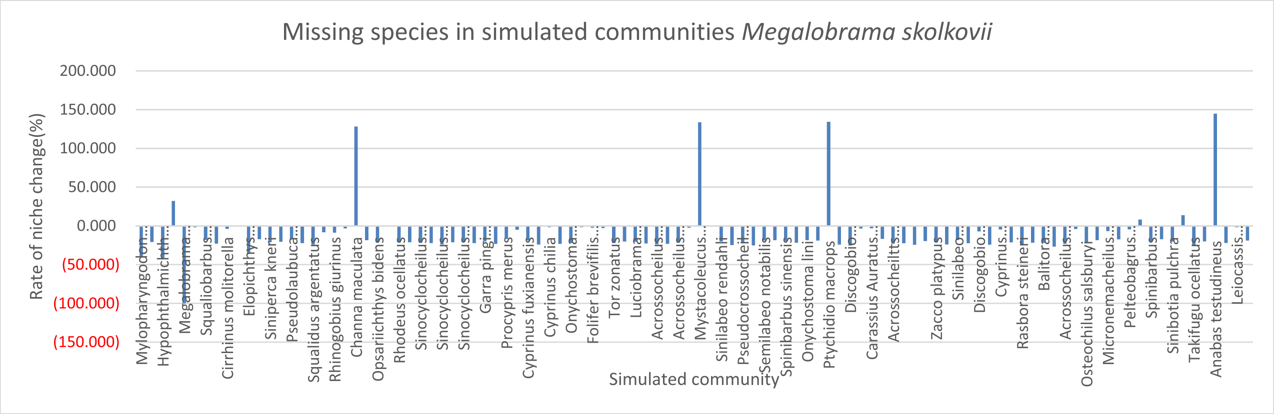

Fig. 3.20 – The responses of the niches of *Megalobrama skolkovii* to various missing fish in the simulated community.

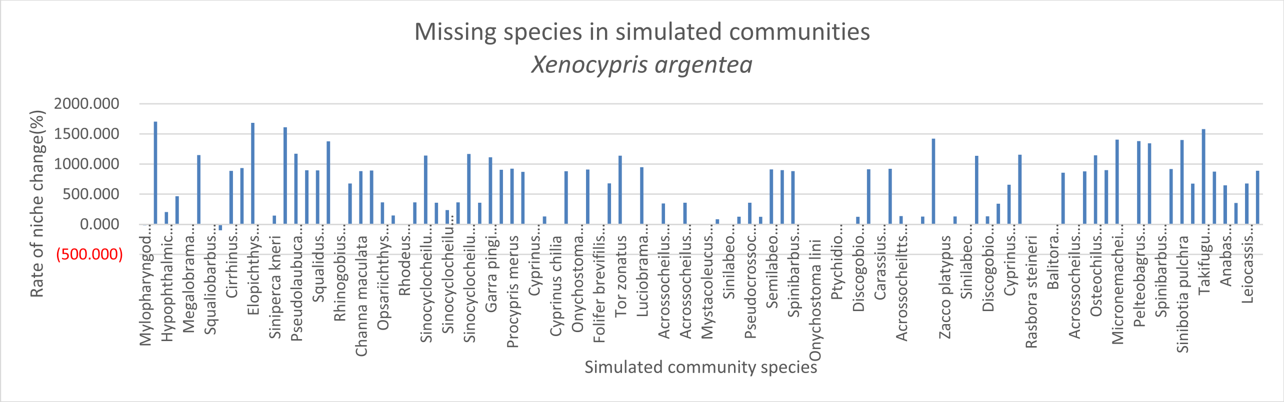

Fig. 3.21 – The responses of the niches of *Xenocypris argentea* to various missing fish in the simulated community.

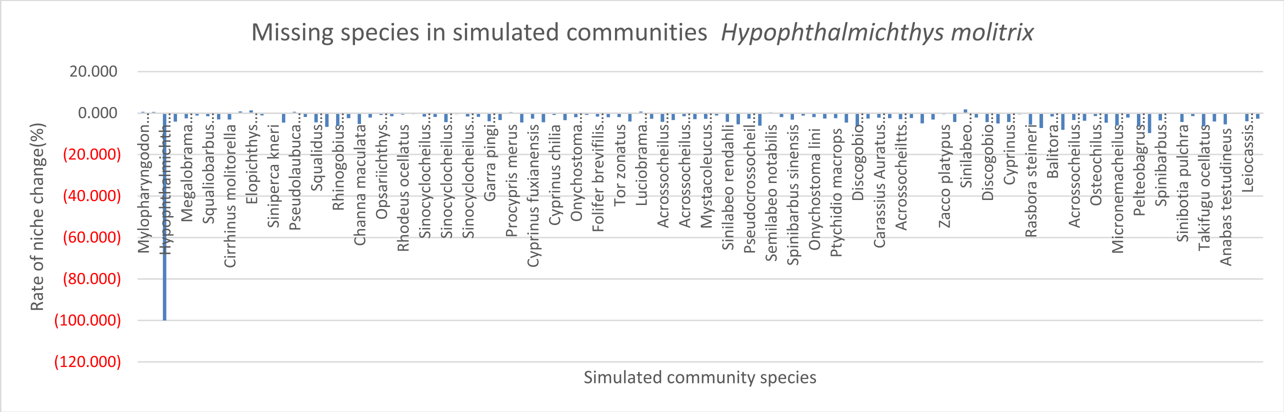

Fig. 3.22 – The responses of the niches of *Hypophthalmichthys molitrix* to various missing fish in the simulated community.

3.1.2.2.18 Hypophthalmichthys nobilis (Richardson, 1845)

The niche variation of *Hypophthalmichthys nobilis* (Richardson, 1845) ranged from 0% to 98% in the absence of different species (see figure 3.23). Among the 103 species of fish, 85 species were mutually beneficial to *Hypophthalmichthys nobilis*. There were 2 species that had more than a 10% effect on the niche of *Hypophthalmichthys nobilis*. Of these, in which the largest effect was 98% by *Hypophthalmichthys molitrix*. There were 18 species of fish in competitive relationships with *Hypophthalmichthys nobilis*. No species affected the niche of *Hypophthalmichthys nobilis* by more than 10%, with which the biggest effect was 2% by *Sinilabeo discognathoides*. An additional 46 species had less than a 10% effect on the rate of the niche variation of *Hypophthalmichthys nobilis*.

3.1.2.2.19 Pseudogyrinocheilus prochilus (Sauvage and Dabry, 1874)

The niche variation of *Pseudogyrinocheilus prochilus* (Sauvage and Dabry, 1874) ranged from 0% to 2319% in the absence of different species (see figure 3.24). Among the 103 species of fish, 36 species were mutually beneficial to *Pseudogyrinocheilus prochilus*. There were 10 species that had more than a 10% effect on the niche of *Pseudogyrinocheilus prochilus*. Of these, in which the largest effect was 20% by *Tachysurus argentivittatus*. There were 67 species of fish in competitive relationships with *Pseudogyrinocheilus prochilus*. There were 46 species that affected the niche of *Pseudogyrinocheilus prochilus* by more than 10%, with which the biggest effect being 2319% by *Pseudolaubuca sinensis*. An additional 47 species had less than a 10% effect on the rate of the niche variation of *Pseudogyrinocheilus prochilus*.

3.1.2.2.20 Squalidus argentatus (Sauvage and Dabry de Thiersant, 1874)

The niche variation of *Squalidus argentatus* (Sauvage and Dabry de Thiersant, 1874) ranged from 0% to 76% in the absence of different species (see figure 3.25). Among the 103 species of fish, 68 species were mutually beneficial to *Squalidus argentatus*. There were 32 species that had more than a 10% effect on the niche of *Squalidus argentatus*. Of these, in which the largest effect was 76% by *Hypophthalmichthys molitrix*. There were 35 species of fish in competitive relationships with *Squalidus argentatus*. There were 11 species that affected the niche of *Squalidus argentatus* by more than 10%, in which the biggest effect was 22% by *Hypophthalmichthys molitrix*. An additional 60 species had less than a 10% effect on the rate of the niche variation of *Squalidus argentatus*.

3.1.2.2.21 Rhodeus ocellatus (Kner, 1867)

The niche variation of *Rhodeus ocellatus* (Kner, 1867) ranged from 0% to 111% in the absence of different species (see figure 3.26). Among the 103 species of fish, 88 species were mutually beneficial to *Rhodeus ocellatus*. There were 71 species that had more than a 10% effect on the niche of *Rhodeus ocellatus*. Of these, in which 50 species affected *Rhodeus ocellatus* nearly 100%. There were 15 species of fish in competitive relationships with *Rhodeus ocellatus*. There were 9 species that affected the niche of *Rhodeus ocellatus* by more than 10%, with which the biggest effect was

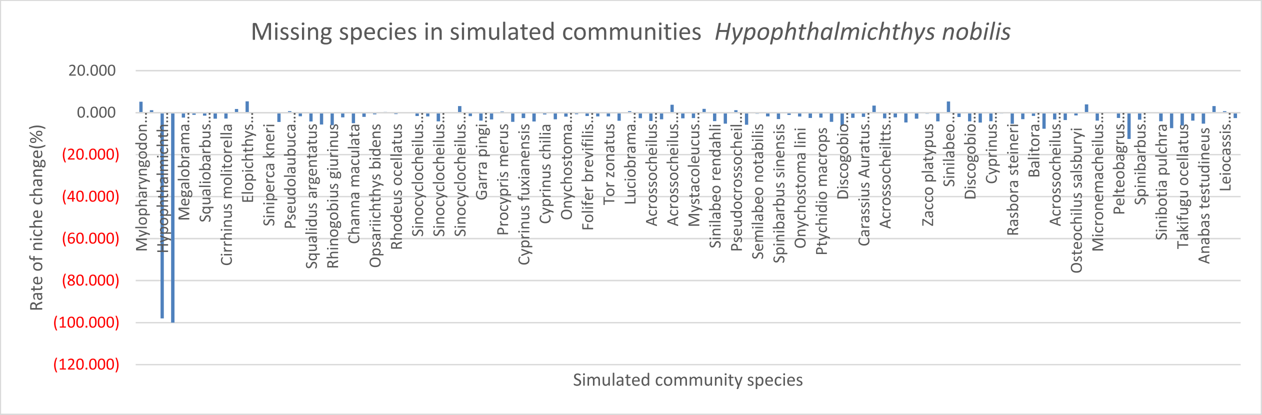

FIG. 3.23 – The responses of the niches of *Hypophthalmichthys nobilis* to various missing fish in the simulated community.

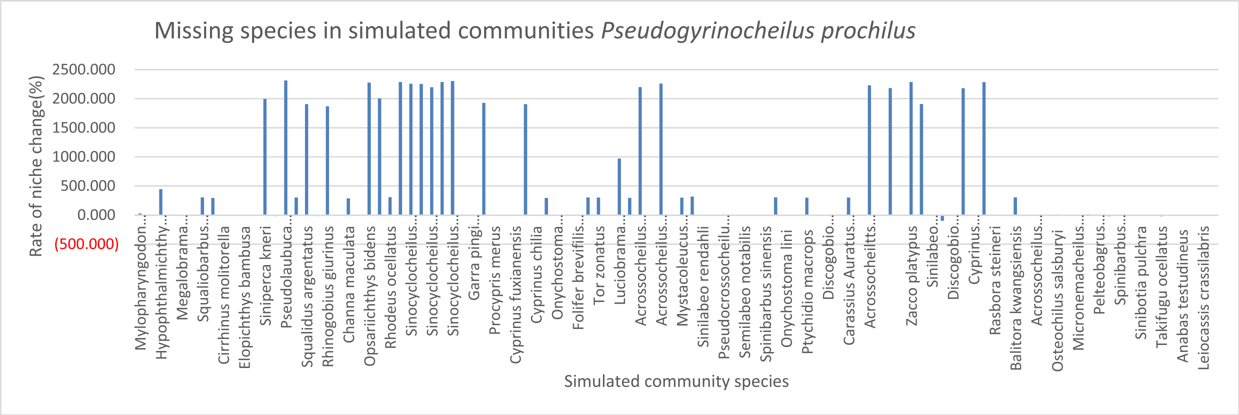

FIG. 3.24 – The responses of the niches of *Pseudogyrinocheilus prochilus* to various missing fish in the simulated community.

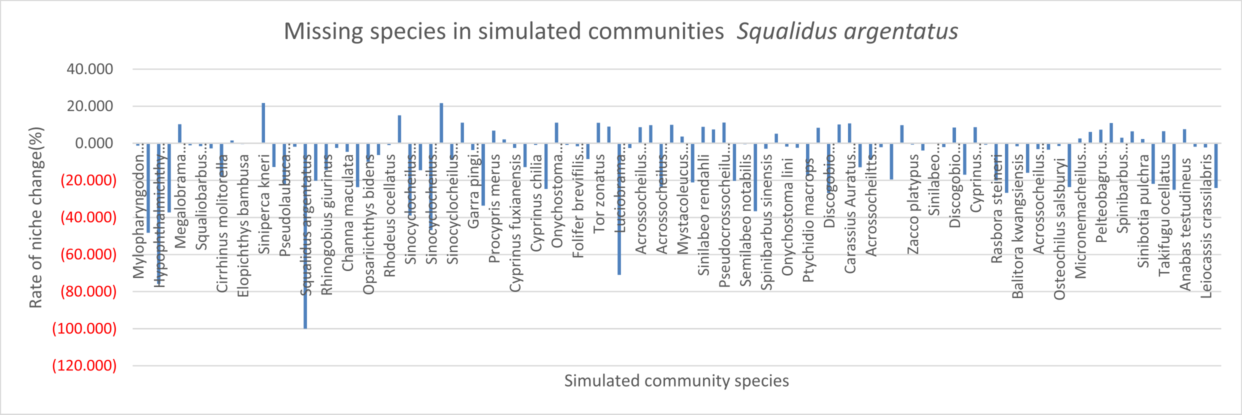

Fig. 3.25 – The responses of the niches of *Squalidus argentatus* to various missing fish in the simulated community.

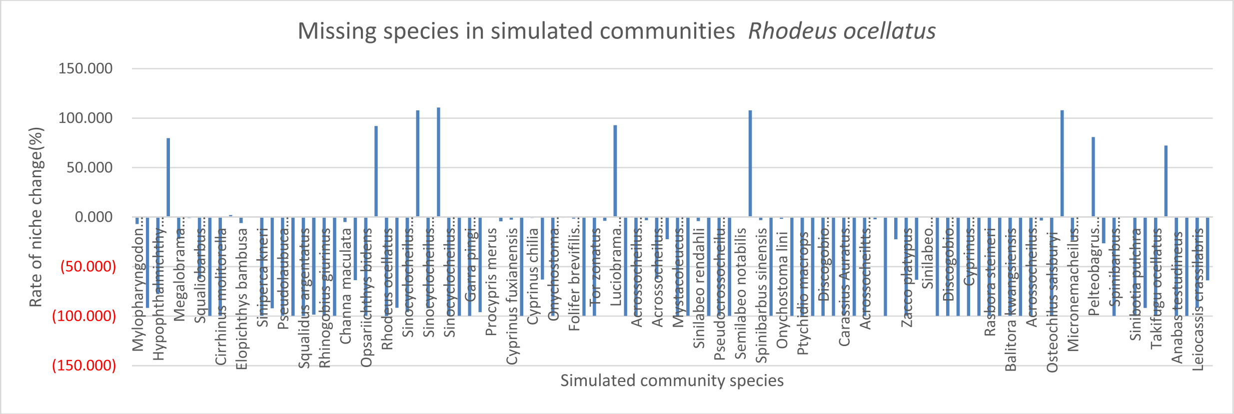

Fig. 3.26 – The responses of the niches of *Rhodeus ocellatus* to various missing fish in the simulated community.

111% by *Sinocyclocheilus anophthalmus*. An additional 23 species had less than a 10% effect on the rate of the niche variation of *Rhodeus ocellatus*.

3.1.2.2.22 Acheilognathus tonkinensis (Vaillant, 1892)

The niche variation of *Acheilognathus tonkinensis* (Vaillant, 1892) ranged from 0% to 842% in the absence of different species (see figure 3.27). Among the 103 species of fish, 33 species were mutually beneficial to *Acheilognathus tonkinensis*. There were 30 species that had more than a 10% effect on the niche of *Acheilognathus tonkinensis*. Of these, in which the largest effect was 87% by *Misgurnus anguillicaudatus*. There were 70 species of fish in competitive relationships with *Acheilognathus tonkinensis*. There were 67 species that affected the niche of *Acheilognathus tonkinensis* by more than 10%, with which the biggest effect was 842% by *Elopichthys bambusa*. An additional 6 species had less than a 10% effect on the rate of the niche variation of *Acheilognathus tonkinensis*.

3.1.2.2.23 Puntius semifasciolatus (Günther, 1968)

The niche variation of *Puntius semifasciolatus* (Günther, 1968) ranged from 0% to 77% in the absence of different species (see figure 3.28). Among the 103 species of fish, 20 species were mutually beneficial to *Puntius semifasciolatus*. There were 19 species that had more than a 10% effect on the niche of *Puntius semifasciolatus*. Of these, in which the largest effect was 77% by *Hypophthalmichthys nobilis*. There were 81 species of fish in competitive relationships with*Puntius semifasciolatus*. There were 7 species that affected the niche of *Puntius semifasciolatus* by more than 10%, with which the biggest effect was 11% by *Spinibarbus hollandi*. An additional 77 species had less than a 10% effect on the rate of the niche variation of *Puntius semifasciolatus*.

3.1.2.2.24 Spinibarbus hollandi (Oshima, 1919)

The niche variation of *Spinibarbus hollandi* (Oshima, 1919) ranged from 0% to 154% in the absence of different species (see figure 3.29). Among the 103 species of fish, 45 species were mutually beneficial to *Spinibarbus hollandi*. There were 22 species that had more than a 10% effect on the niche of *Spinibarbus hollandi*. Of these, in which the largest effect was 67% by *Hypophthalmichthys molitrix*. There were 58 species of fish in competitive relationships with *Spinibarbus hollandi*. There were 52 species that affected the niche of *Spinibarbus hollandi* by more than 10%, with which the biggest effect was 154% by *Hypophthalmichthys nobilis*. An additional 29 species had less than a 10% effect on the rate of the niche variation of *Spinibarbus hollandi*.

3.1.2.2.25 Spinibarbus sinensis (Bleeker, 1871)

The niche variation of *Spinibarbus sinensis* (Bleeker, 1871) ranged from 0% to 42% in the absence of different species (see figure 3.30). Among the 103 species of fish, 94 species were mutually beneficial to *Spinibarbus sinensis*. There were 64 species that had more than a 10% effect on the niche of *Spinibarbus sinensis*. Of these, in which the largest effect was 42% by *Puntius semifasciolatus*. There were 9 species of fish in competitive relationships with *Spinibarbus sinensis*. There were 5 species that affected the niche of *Spinibarbus sinensis* by more than 10%, with which the biggest

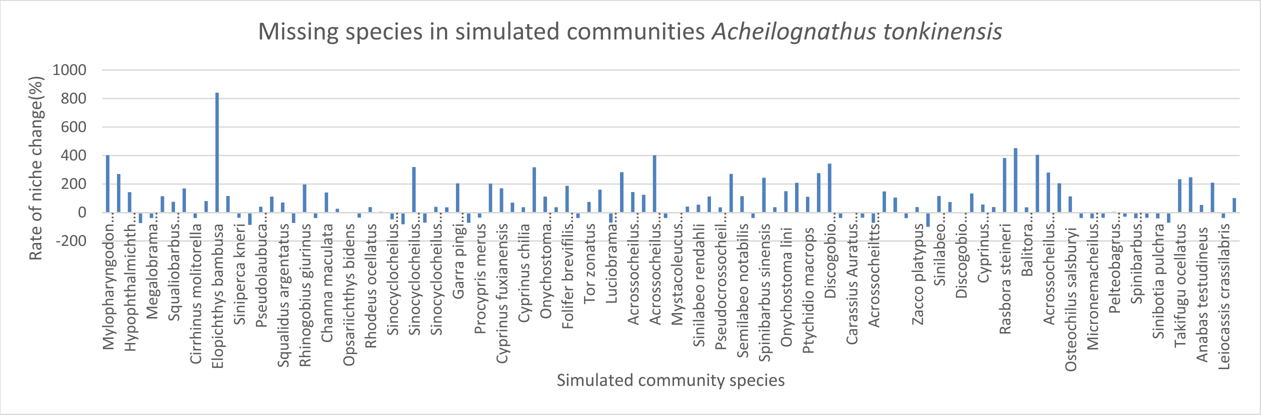

FIG. 3.27 – The responses of the niches of *Acheilognathus tonkinensis* to various missing fish in the simulated community.

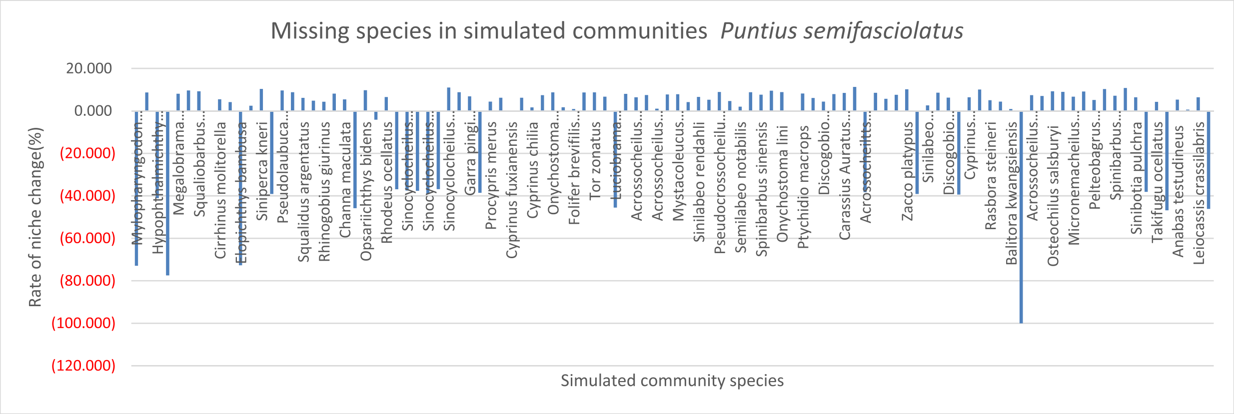

FIG. 3.28 – The responses of the niches of *Puntius semifasciolatus* to various missing fish in the simulated community.

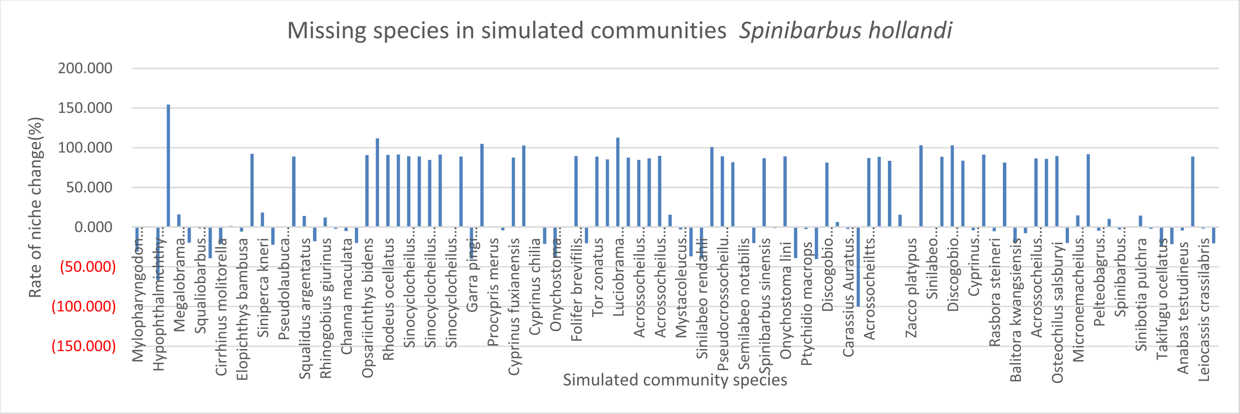

FIG. 3.29 – The responses of the niches of *Spinibarbus hollandi* to various missing fish in the simulated community.

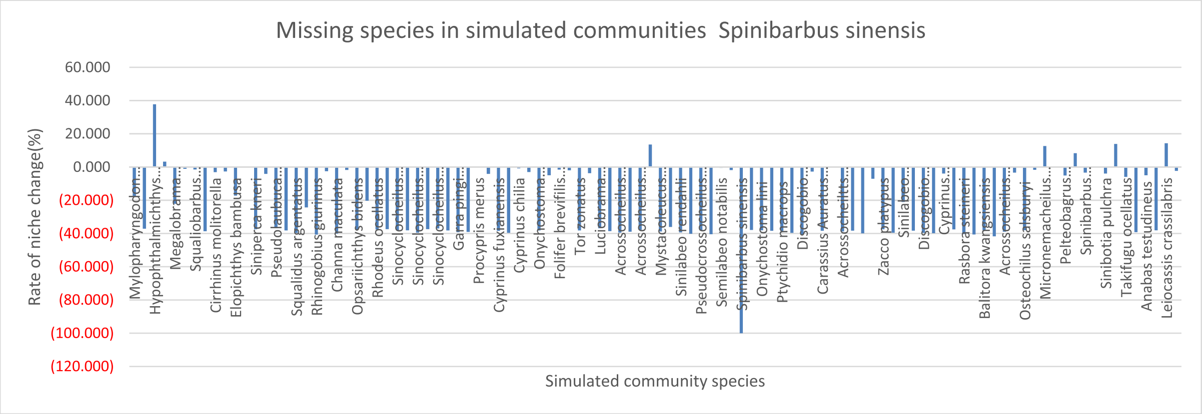

FIG. 3.30 – The responses of the niches of *Spinibarbus sinensis* to various missing fish in the simulated community.

effect was 38% by *Hypophthalmichthys molitrix.* An additional 34 species had less than a 10% effect on the rate of the niche variation of *Spinibarbus sinensis.*

3.1.2.2.26 Spinibarbus denticulatus denticulatus (Oshima, 1926)

The niche variation of *Spinibarbus denticulatus denticulatus* (Oshima, 1926) ranged from 0% to 66% in the absence of different species (see figure 3.31). Among the 103 species of fish, 88 species were mutually beneficial to *pinibarbus denticulatus denticulatus.* There were 57 species that had more than a 10% effect on the niche of *pinibarbus denticulatus denticulatus.* Of these, in which the largest effect was 66% by *Discogobiolongibarbatus.* There were 15 species of fish in competitive relationships with *pinibarbus denticulatus denticulatus.* There were 30 species that affected the niche of *pinibarbus denticulatus denticulatus* by more than 10%, with which the biggest effect was 17% by *Hypophthalmichthys nobilis.* An additional 45 species had less than a 10% effect on the rate of the niche variation of *pinibarbus denticulatus denticulatus.*

3.1.2.2.27 Sinocyclocheilus macrolepis (Wang, 1989)

The niche variation of *Sinocyclocheilus macrolepis* (Wang, 1989) ranged from 0% to 5117% in the absence of different species (see figure 3.32). Among the 103 species of fish, 2 species were mutually beneficial to *Sinocyclocheilus macrolepis.* There were 2 species that had more than a 10% effect on the niche of *Sinocyclocheilus macrolepis.* Of these, in which the largest effect was 93% by *Acrossocheilus iridescens iridescens.* There were 101 species of fish in competitive relationships with *Sinocyclocheilus macrolepis.* There were 97 species that affected the niche of *Sinocyclocheilus macrolepis* by more than 10%, with which the biggest effect was 5117% by *Cyprinus multitaeniata.* An additional 4 species had less than a 10% effect on the rate of the niche variation of *Sinocyclocheilus macrolepis.*

3.1.2.2.28 Sinocyclocheilus grahami tingi (Fang, 1936)

The niche variation of *Sinocyclocheilus grahami tingi* (Fang, 1936) ranged from 0% to 63% in the absence of different species (see figure 3.33). Among the 103 species of fish, 29 species were mutually beneficial to *Sinocyclocheilus grahami tingi.* There were 12 species that had more than a 10% effect on the niche of *Sinocyclocheilus grahami tingi.* Of these, in which the largest effect was 63% by *Luciobrama macrocephalus.* There were 74 species of fish in competitive relationships with *Sinocyclocheilus grahami tingi.* There were 4 species that affected the niche of *Sinocyclocheilus grahami tingi* by more than 10%, with which the biggest effect was 13% by *Tachysurus argentivittatus.* An additional 91 species had less than a 10% effect on the rate of the niche variation of *Sinocyclocheilus grahami tingi.*

3.1.2.2.29 Sinocyclocheilus yangzongensis (Tsu and Chen, 1982)

The niche variation of *Sinocyclocheilus yangzongensis* (Tsu and Chen, 1982) ranged from 0% to 13 293% in the absence of different species (see figure 3.34). Among the 103 species of fish, 29 species were mutually beneficial to *Sinocyclocheilus yangzongensis.* Only one species had more than a 10% effect on the niche of *Sinocyclocheilus yangzongensis.* Of which the largest effect was 40% by *Ptychidio macrops.*

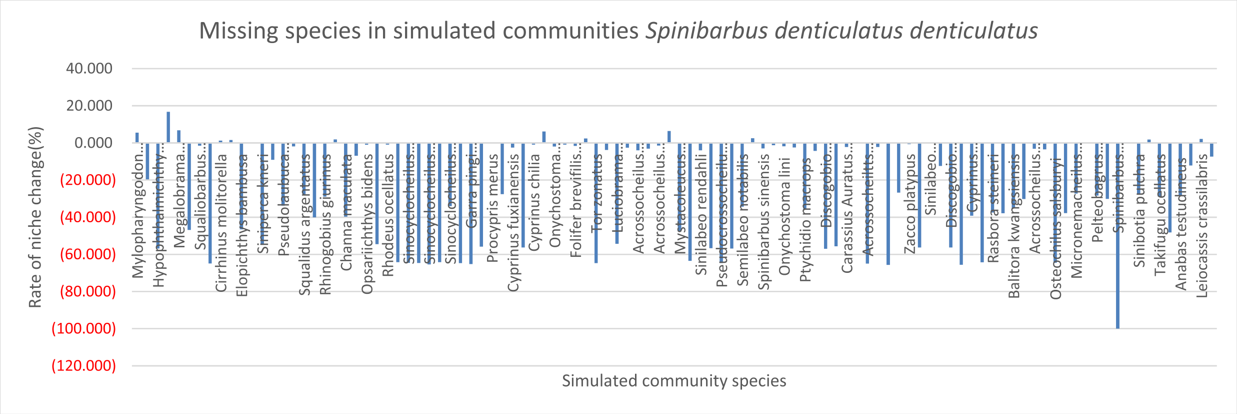

Fig. 3.31 – The responses of the niches of *Sinibarbus denticulatus denticulatus* to various missing fish in the simulated community.

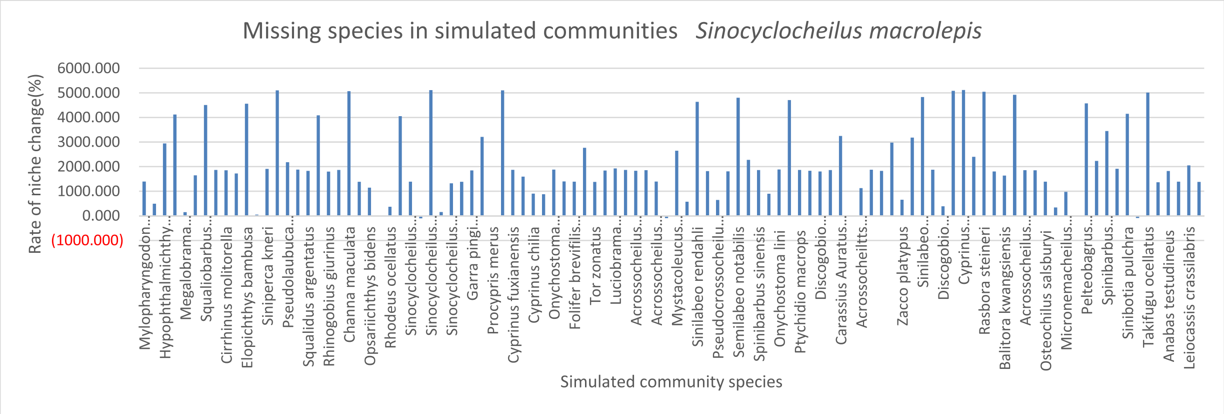

Fig. 3.32 – The responses of the niches of *Sinocyclocheilus macrolepis* to various missing fish in the simulated community.

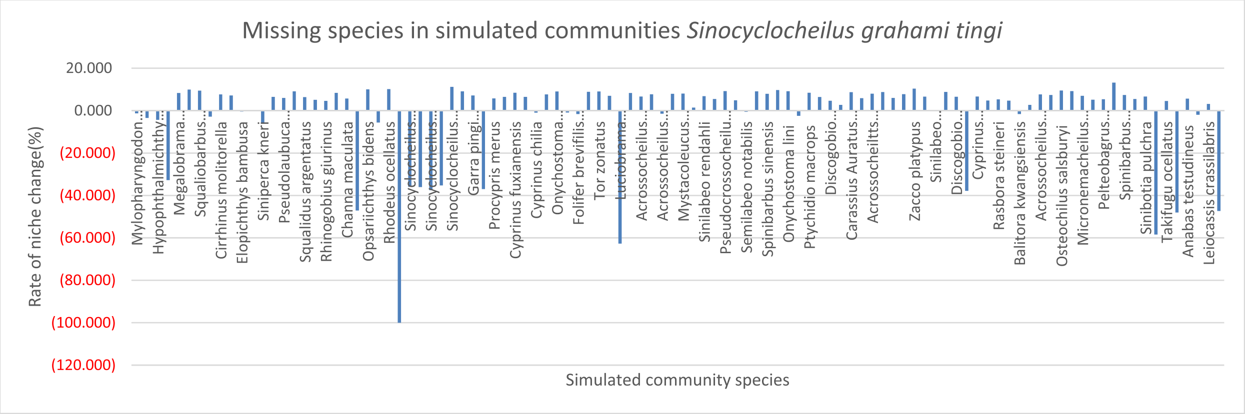

Fig. 3.33 – The responses of the niches of *Sinocyclocheilus grahami tingi* to various missing fish in the simulated community.

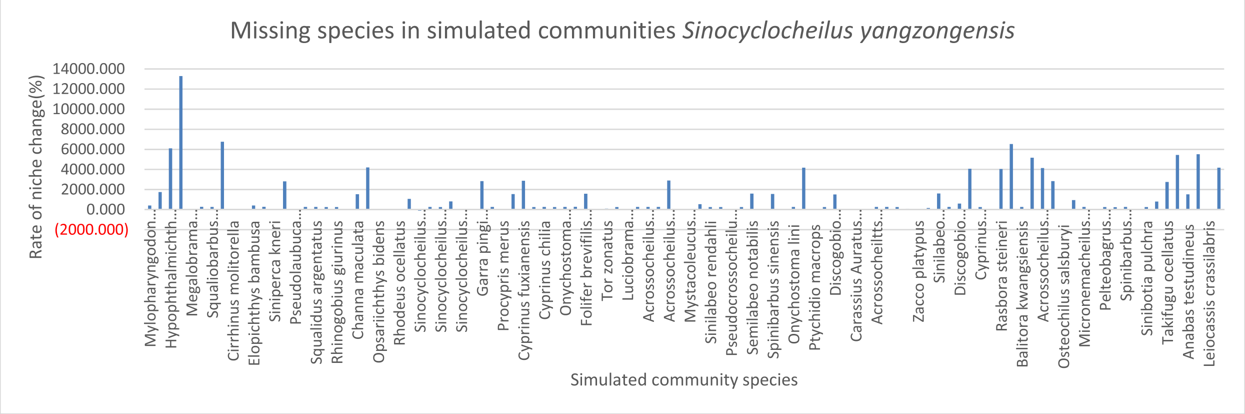

Fig. 3.34 – The responses of the niches of *Sinocyclocheilus yangzongensis* to various missing fish in the simulated community.

There were 74 species of fish in competitive relationships with *Sinocyclocheilus yangzongensis*. All of the species affected the niche of *Lcucosoma chinensis* by more than 10%, in which the biggest effect was 13 293% by *Hypophthalmichthys nobilis*. An additional 28 species had less than a 10% effect on the rate of the niche variation of *Sinocyclocheilus yangzongensis*.

3.1.2.2.30 Sinocyclocheilus anophthalmus (Chen and Chu, 1988)

The niche variation of *Sinocyclocheilus anophthalmus* (Chen and Chu, 1988) ranged from 0% to 2020% in the absence of different species (see figure 3.35). Among the 103 species of fish, 72 species were mutually beneficial to *Sinocyclocheilus anophthalmus*. There were 34 species that had more than a 10% effect on the niche of *Sinocyclocheilus anophthalmus*. Of these, in which the largest effect was 71% by *Xenocypris argentea*. There were 31 species of fish in competitive relationships with *Lcucosoma chinensis*. There were 15 species that affected the niche of *Sinocyclocheilus anophthalmus* by more than 10%, with which the biggest effect was 2020% by *Hypophthalmichthys nobilis*. An additional 54 species had less than a 10% effect on the rate of the niche variation of *Sinocyclocheilus anophthalmus*.

3.1.2.2.31 Sinocyclocheilus microphthalmus (Li, 1989)

The niche variation of *Sinocyclocheilus microphthalmus* (Li, 1989) ranged from 0% to 75% in the absence of different species (see figure 3.36). Among the 103 species of fish, 89 species were mutually beneficial to *Sinocyclocheilus microphthalmus*. There were 72 species that had more than a 10% effect on the niche of *Sinocyclocheilus microphthalmus*. Of these, in which the largest effect was 70% by *Lateolabrax japonicus*. There were 14 species of fish in competitive relationships with *Lcucosoma chinensis*. No species that affected the niche of *Sinocyclocheilus microphthalmus* by more than 10%, with which the biggest effect was 6% by *Hemibagrus guttatus*. An additional 31 species had less than a 10% effect on the rate of the niche variation of *Sinocyclocheilus microphthalmus*.

3.1.2.2.32 Sinocyclocheilus macrocephalus (Li, 1985)

The niche variation of *Sinocyclocheilus macrocephalus* (Li, 1985) ranged from 0% to 245% in the absence of different species (see figure 3.37). Among the 103 species of fish, 9 species were mutually beneficial to *Sinocyclocheilus macrocephalus*. There were 4 species that had more than a 10% effect on the niche of *Sinocyclocheilus macrocephalus*. Of these, in which the largest effect was 34% by *Ancherythroculter lini*. There were 94 species of fish in competitive relationships with *Sinocyclocheilus macrocephalus*. There were 79 species that affected the niche of *Lcucosoma chinensis* by more than 10%, with which the biggest effect was 23% by *Tachysurus argentivittatus*. An additional 39 species had less than a 10% effect on the rate of the niche variation of *Sinocyclocheilus macrocephalus*.

3.1.2.2.33 Mystacoleucus marginatus (Valenciennes, 1842)

The niche variation of *Mystacoleucus marginatus* (Valenciennes, 1842) ranged from 0% to 172% in the absence of different species (see figure 3.38). Among the 103

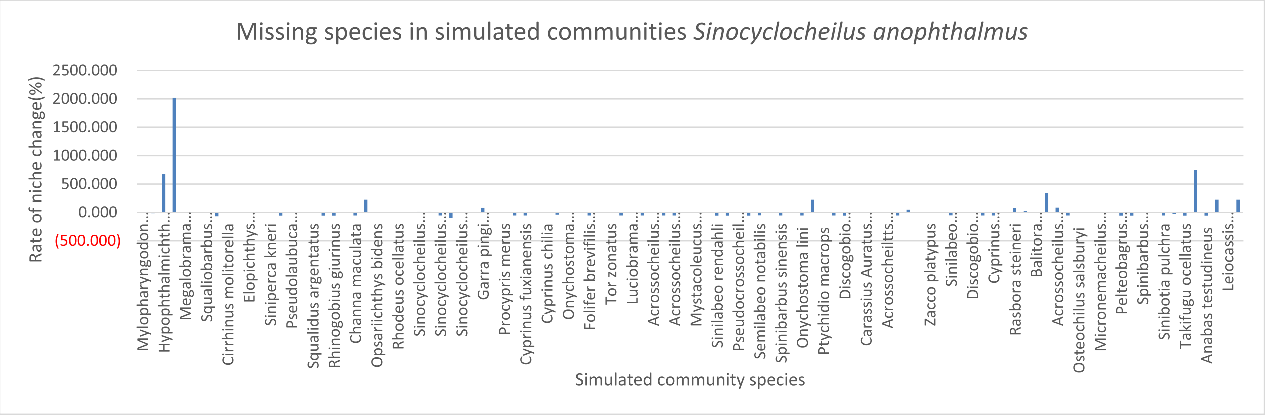

Fig. 3.35 – The responses of the niches of *Sinocyclocheilus anophthalmus* to various missing fish in the simulated community.

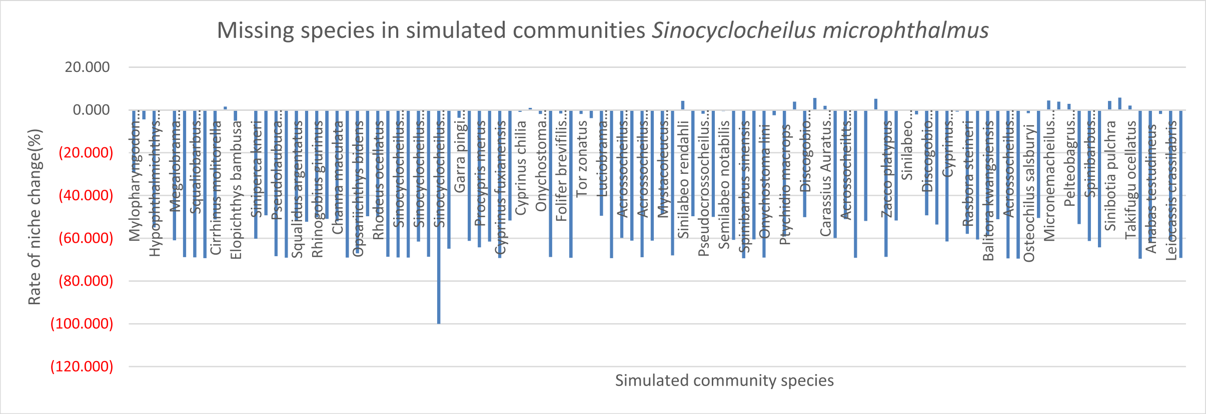

Fig. 3.36 – The responses of the niches of *Sinocyclocheilus microphthalmus* to various missing fish in the simulated community.

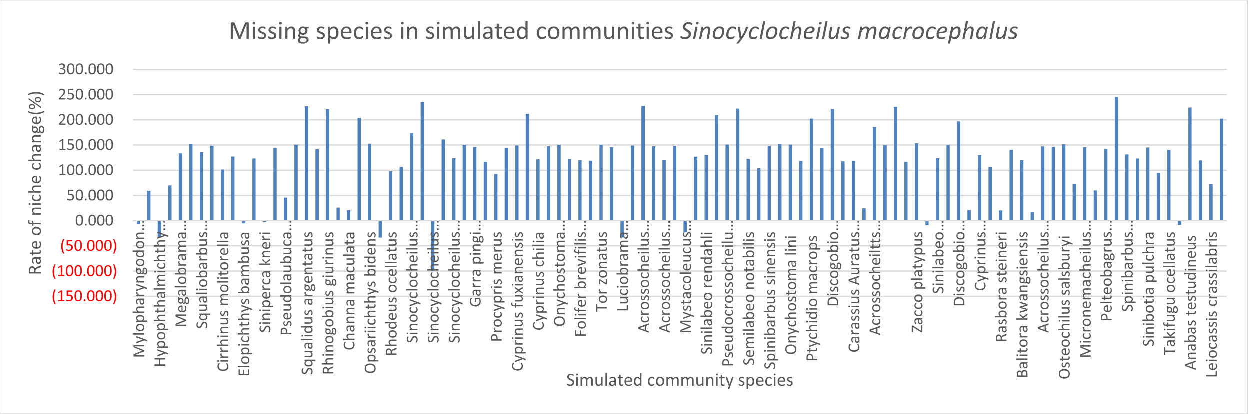

FIG. 3.37 – The responses of the niches of *Sinocyclocheilus macrocephalus* to various missing fish in the simulated community.

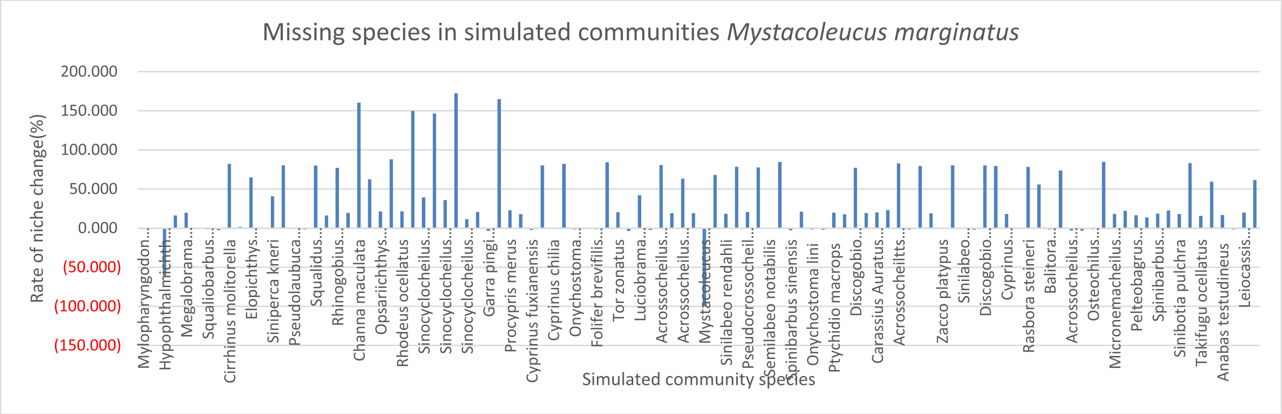

FIG. 3.38 – The responses of the niches of *Mystacoleucus marginatus* to various missing fish in the simulated community.

species of fish, 29 species were mutually beneficial to *Mystacoleucus marginatus*. Only one species had more than a 10% effect on the niche of *Mystacoleucus marginatus*. Of which was 61% by *Hypophthalmichthys molitrix*. There were 74 species of fish in competitive relationships with *Mystacoleucus marginatus*. There were 71 species that affected the niche of *Mystacoleucus marginatus* by more than 10%, with which the biggest effect was 172% by *Sinocyclocheilus anophthalmus*. An additional 31 species had less than a 10% effect on the rate of the niche variation of *Mystacoleucus marginatus*.

3.1.2.2.34 Luciocyprinus langsoni (Vaillant, 1904)

The niche variation of *Luciocyprinus langsoni* (Vaillant, 1904) ranged from 0% to 230% in the absence of different species (see figure 3.39). Among the 103 species of fish, 95 species were mutually beneficial to *Luciocyprinus langsoni*. There were 83 species that had more than a 10% effect on the niche of *Luciocyprinus langsoni*. Of these, in which the largest effect was 75% by *Elopichthys bambusa*. There were 8 species of fish in competitive relationships with *Luciocyprinus langsoni*. No species affected the niche of *Luciocyprinus langsoni* by more than 10%, with which the biggest effect was 5% by *Megalobrama skolkovii*. An additional 18 species had less than a 10% effect on the rate of the niche variation of *Luciocyprinus langsoni*.

3.1.2.2.35 Acrossocheiltts hemispinus hemispinus (Nichols, 1931)

The niche variation of *Acrossocheiltts hemispinus hemispinus* (Nichols, 1931) ranged from 0% to 221% in the absence of different species (see figure 3.40). Among the 103 species of fish, 49 species were mutually beneficial to *Acrossocheiltts hemispinus hemispinus*. There were 5 species that had more than a 10% effect on the niche of *Acrossocheiltts hemispinus hemispinus*. Of these, in which the largest effect was 40% by *Sinocyclocheilus macrocephalus*. There were 54 species of fish in competitive relationships with *Acrossocheiltts hemispinus hemispinus*. There were 28 species that affected the niche of *Acrossocheiltts hemispinus hemispinus* by more than 10%, in which the biggest effect was 221% by *Hypophthalmichthys nobilis*. An additional 70 species had less than a 10% effect on the rate of the niche variation of *Acrossocheiltts hemispinus hemispinus*.

3.1.2.2.36 Acrossocheilus beijiangensis (Wu and Lin, 1982)

The niche variation of *Acrossocheilus beijiangensis* (Wu and Lin, 1982) ranged from 0% to 1564% in the absence of different species (see figure 3.41). Among the 103 species of fish, 40 species were mutually beneficial to *Acrossocheilus beijiangensis*. There were 26 species that had more than a 10% effect on the niche of *Acrossocheilus beijiangensis*. Of these, in which the largest effect was 98% by *Acrossocheilus beijiangensis*. There were 63 species of fish in competitive relationships with *Lcucosoma chinensis*. There were 30 species that affected the niche of *Acrossocheilus beijiangensis* by more than 10%, in which the biggest effect was 1564% by *Hypophthalmichthys nobilis*. An additional 47 species had less than a 10% effect on the rate of the niche variation of *Acrossocheilus beijiangensis*.

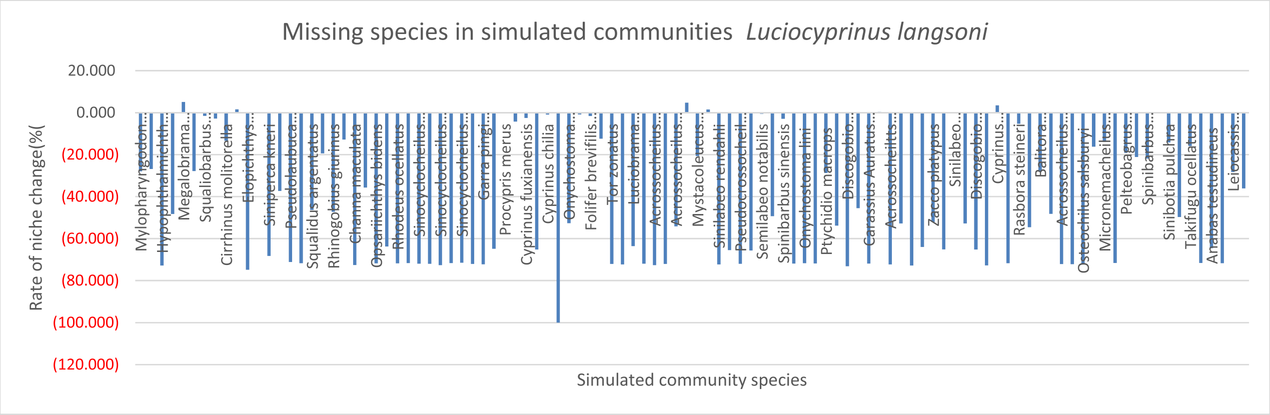

FIG. 3.39 – The responses of the niches of *Luciocyprinus langsoni* to various missing fish in the simulated community.

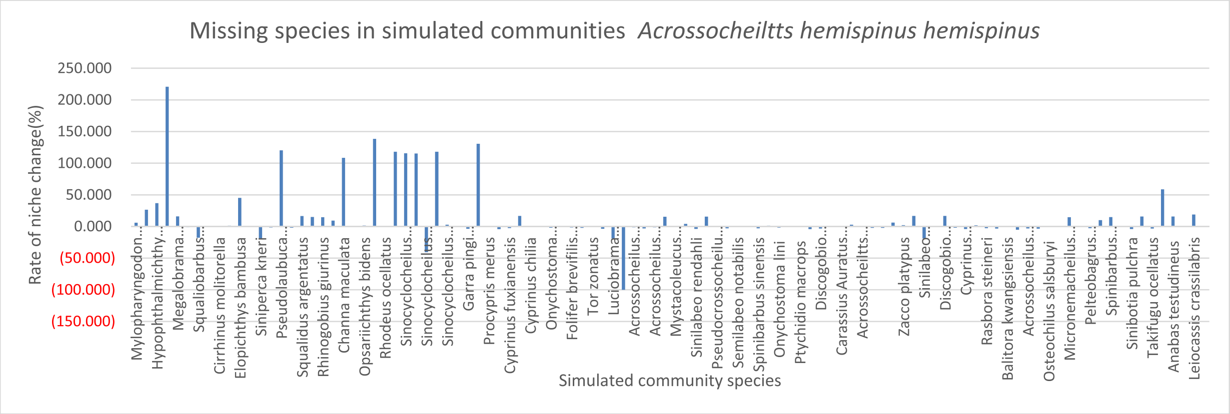

FIG. 3.40 – The responses of the niches of *Acrossocheiltts hemispinus hemispinus* to various missing fish in the simulated community.

3.1.2.2.37 Acrossocheilus paradoxus (Regan, 1908)

The niche variation of *Acrossocheilus paradoxus* (Regan, 1908) ranged from 0% to 69% in the absence of different species (see figure 3.42). Among the 103 species of fish, 67 species were mutually beneficial to *Acrossocheilus paradoxus.* There were 43 species that had more than a 10% effect on the niche of *Acrossocheilus paradoxus.* Of these, in which the largest effect was 63% by *Hemibagrus guttatus.* There were 36 species of fish in competitive relationships with *Acrossocheilus paradoxus.* There were 28 species that affected the niche of *Acrossocheilus paradoxus* by more than 10%, with which the biggest effect was 69% by *Ctenopharyngodon idella.* An additional 32 species had less than a 10% effect on the rate of the niche variation of *Acrossocheilus paradoxus.*

3.1.2.2.38 Acrossocheilus clivosius (Lin, 1935)

The niche variation of *Acrossocheilus clivosius* (Lin, 1935) ranged from 0% to 5774% in the absence of different species (see figure 3.43). Among the 103 species of fish, 15 species were mutually beneficial to *Acrossocheilus clivosius.* There were 2 species that had more than a 10% effect on the niche of *Acrossocheilus clivosius.* Of these, in which the largest effect was 57% by *Lcucosoma chinensis.* There were 88 species of fish in competitive relationships with *Acrossocheilus clivosius.* There were 76 species that affected the niche of *Acrossocheilus clivosius* by more than 10%, in which the biggest effect was 5774% by *Hypophthalmichthys molitrix.* An additional 25 species had less than a 10% effect on the rate of the niche variation of *Acrossocheilus clivosius.*

3.1.2.2.39 Acrossocheilus iridescens iridescens (Nichols and Pope, 1927)

The niche variation of *Acrossocheilus iridescens iridescens* (Nichols and Pope, 1927) ranged from 0% to 56% in the absence of different species (see figure 3.44). Among the 103 species of fish, 100 species were mutually beneficial to *Acrossocheilus iridescens iridescens.* There were 92 species that had more than a 10% effect on the niche of *Acrossocheilus iridescens iridescens.* Of these, in which the largest effect was 56% by *Takifugu ocellatus.* There were 3 species of fish in competitive relationships with *Acrossocheilus iridescens iridescens.* No species affected the niche of *Acrossocheilus iridescens iridescens* by more than 10%, with which the biggest effect was 2% by *Cyprinus carpio Linnaeus.* An additional 11 species had less than a 10% effect on the rate of the niche variation of *Acrossocheilus iridescens iridescens.*

3.1.2.2.40 Acrossocheilus fasciatus (Steindachner, 1892)

The niche variation of *Acrossocheilus fasciatus* (Steindachner, 1892) ranged from 0% to 96% in the absence of different species (see figure 3.45). Among the 103 species of fish, 81 species were mutually beneficial to *Acrossocheilus fasciatus.* All of those species had more than a 10% effect on the niche of *Acrossocheilus fasciatus.* Of these, in which the largest effect was 96% by *Carassius auratus auratus.* There were 22 species of fish in competitive relationships with *Acrossocheilus fasciatus.* There were 20 species that affected the niche of *Acrossocheilus fasciatus*

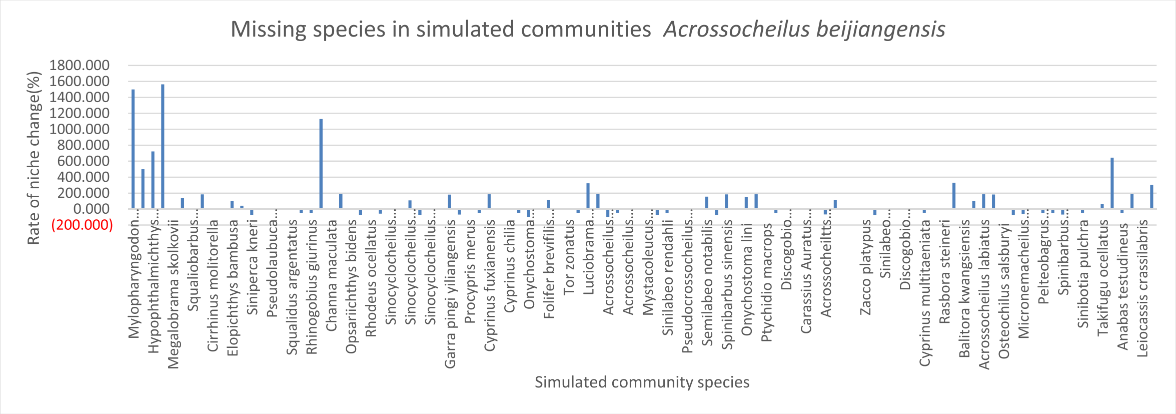

FIG. 3.41 – The responses of the niches of *Acrossocheilus beijiangensis* to various missing fish in the simulated community.

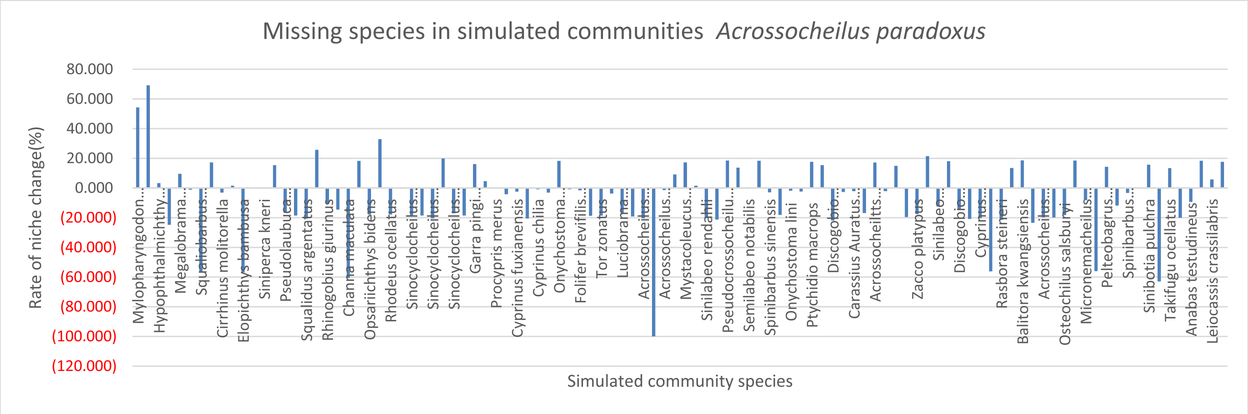

FIG. 3.42 – The responses of the niches of *Acrossocheilus paradoxus* to various missing fish in the simulated community.

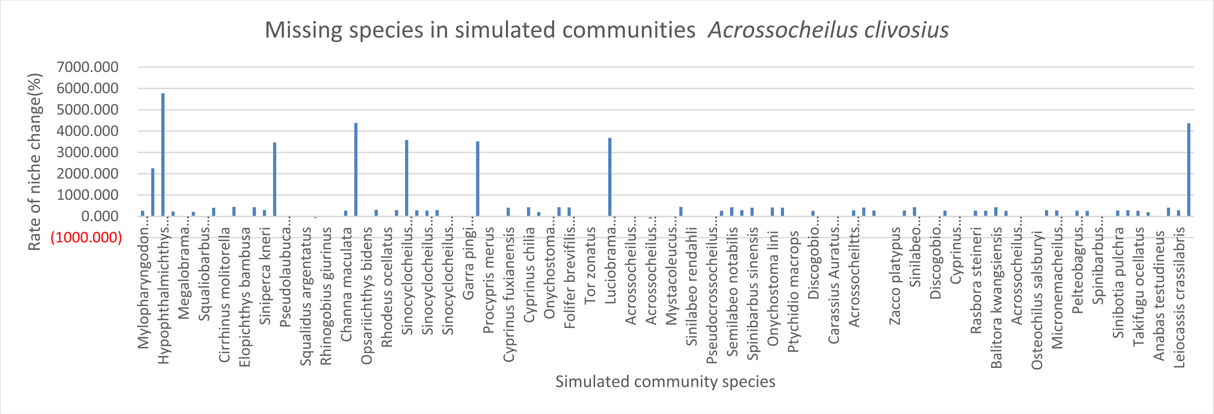

FIG. 3.43 – The responses of the niches of *Acrossocheilus clivosius* to various missing fish in the simulated community.

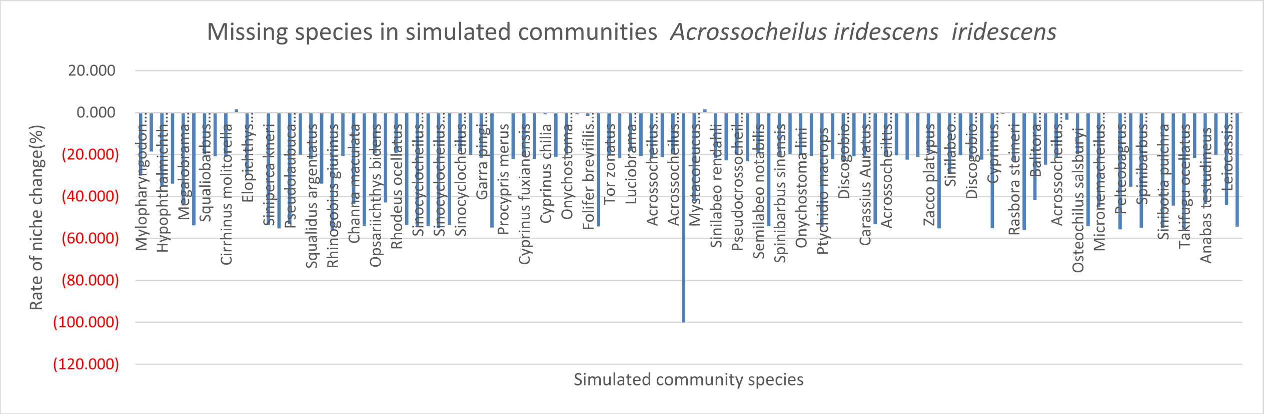

FIG. 3.44 – The responses of the niches of *Acrossocheilus iridescens indescens* to various missing fish in the simulated community.

by more than 10%, with which the biggest effect was 230% by *Lateolabrax japonicus*. An additional 3 species had less than a 10% effect on the rate of the niche variation of *Acrossocheilus fasciatus*.

3.1.2.2.41 Acrossocheiltts elongatus (Pellegrin and Chevey, 1934)

The niche variation of *Acrossocheiltts elongatus* (Pellegrin and Chevey, 1934) ranged from 0% to 579% in the absence of different species (see figure 3.46). Among the 103 species of fish, 54 species were mutually beneficial to *Acrossocheiltts elongatus*. There were 2 species that had more than a 10% effect on the niche of *Acrossocheiltts elongatus*. Of these, in which the largest effect was 63% by *Tachysurus argentivittatus*. There were 49 species of fish in competitive relationships with *Acrossocheiltts elongatus*. There were 27 species that affected the niche of *Acrossocheiltts elongatus* by more than 10%, in which the biggest effect was 579% by *Hypophthalmichthys molitrix*. An additional 74 species had less than a 10% effect on the rate of the niche variation of *Acrossocheiltts elongatus*.

3.1.2.2.42 Acrossocheilus labiatus (Regan, 1908)

The niche variation of *Acrossocheilus labiatus* (Regan, 1908) ranged from 0% to 284% in the absence of different species (see figure 3.47). Among the 103 species of fish, 40 species were mutually beneficial to *Acrossocheilus labiatus*. There were 22 species that had more than a 10% effect on the niche of *Acrossocheilus labiatus*. Of these, in which the largest effect was 49% by *Semilabeo notabilis*. There were 63 species of fish in competitive relationships with *Acrossocheilus labiatus*. There were 55 species that affected the niche of *Acrossocheilus labiatus* by more than 10%, with which the biggest effect was 284% by *Ctenopharyngodon idella*. An additional 26 species had less than a 10% effect on the rate of the niche variation of *Acrossocheilus labiatus*.

3.1.2.2.43 Onychostoma macrolepis (Bleeker, 1871)

The niche variation of *Onychostoma macrolepis* (Bleeker, 1871) ranged from 0% to 459% in the absence of different species (see figure 3.48). Among the 103 species of fish, 42 species were mutually beneficial to *Onychostoma macrolepis*. There were 24 species that had more than a 10% effect on the niche of *Onychostoma macrolepis*. Of these, in which the largest effect was 99% by *Lateolabrax japonicus*. There were 61 species of fish in competitive relationships with *Onychostoma macrolepis*. There were 52 species that affected the niche of *Onychostoma macrolepis* by more than 10%, with which the biggest effect was 459% by *Pelteobagrus fulvidraco*. An additional 27 species had less than a 10% effect on the rate of the niche variation of *Onychostoma macrolepis*.

3.1.2.2.44 Onychostoma sima (Sauvage and Dabry, 1874)

The niche variation of *Onychostoma sima* (Sauvage and Dabry, 1874) ranged from 0% to 970% in the absence of different species (see figure 3.49). Among the 103 species of fish, 92 species were mutually beneficial to *Onychostoma sima*. There were 14 species that had more than a 10% effect on the niche of *Onychostoma sima*. Of

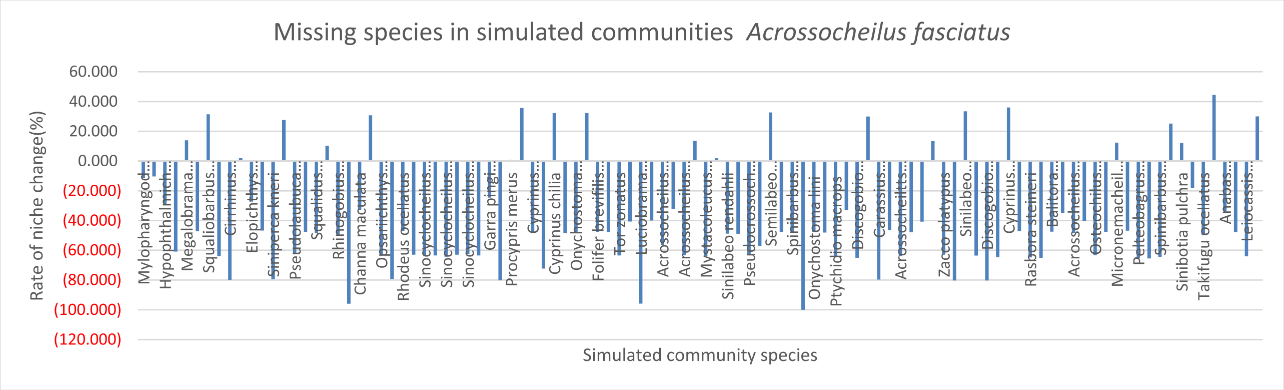

FIG. 3.45 – The responses of the niches of *Acrossocheilus fasciatus* to various missing fish in the simulated community.

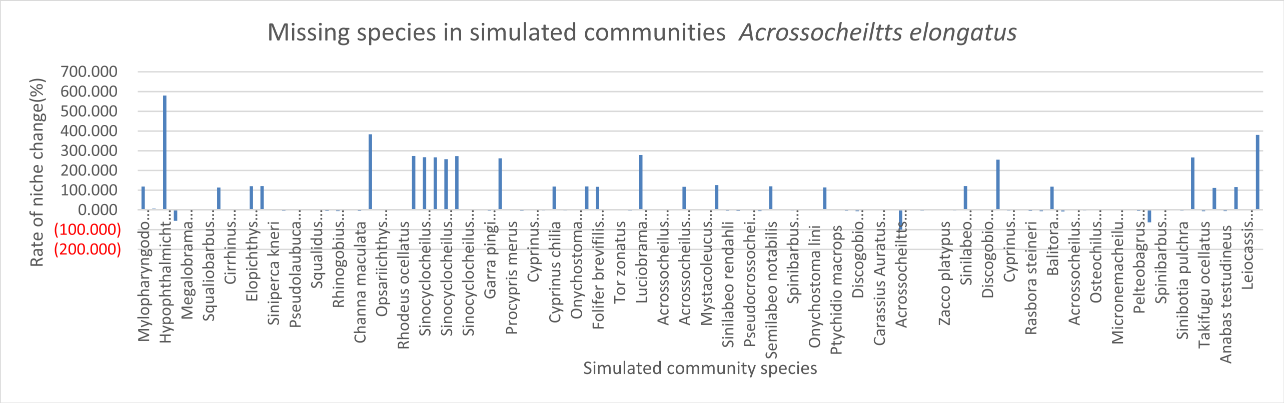

FIG. 3.46 – The responses of the niches of *Acrossocheiltts elongatus* to various missing fish in the simulated community.

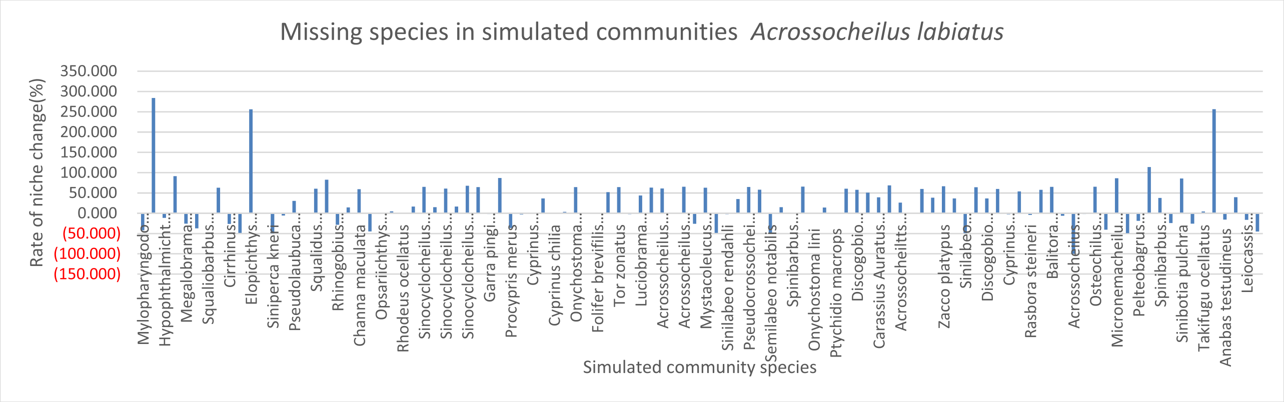

FIG. 3.47 – The responses of the niches of *Acrossocheilus labiatus* to various missing fish in the simulated community.

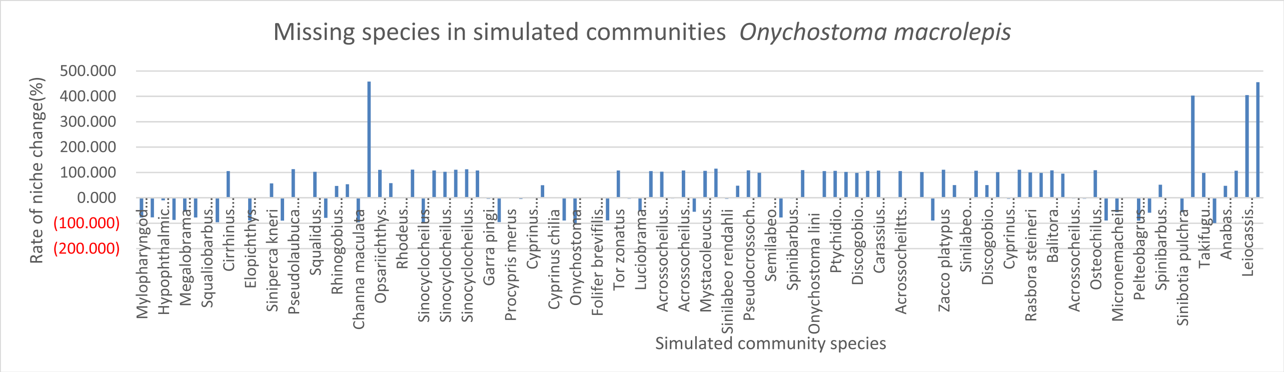

FIG. 3.48 – The responses of the niches of *Onychostoma macrolepis* to various missing fish in the simulated community.

these, in which the largest effect was 97% by *Luciobrama macrocephalus*. There were 11 species of fish in competitive relationships with *Onychostoma sima*. There were 2 species that affected the niche of *Onychostoma sima* by more than 10%, with which the biggest effect was 21% by *Sinilabeo discognathoides*. An additional 87 species had less than a 10% effect on the rate of the niche variation of *Onychostoma sima*.

3.1.2.2.45 Onychostoma lini (Wu, 1939)

The niche variation of *Onychostoma lini* (Wu, 1939) ranged from 0% to 1991% in the absence of different species (see figure 3.50). Among the 103 species of fish, 3 species were mutually beneficial to *Onychostoma lini*. There were 2 species that had more than a 10% effect on the niche of *Onychostoma lini*. Of these, in which the largest effect was 50% by *Leiocassis crassilabris*. There were 86 species of fish in competitive relationships with *Onychostoma lini*. There were 85 species that affected the niche of *Onychostoma lini* by more than 10%, in which the biggest effect was 1991% by *Hypophthalmichthys molitrix*. An additional 15 species had less than a 10% effect on the rate of the niche variation of *Onychostoma lini*.

3.1.2.2.46 Onychostoma barbatulum (Pellegrin, 1908)

The niche variation of *Onychostoma barbatulum* (Pellegrin, 1908) ranged from 0% to 2006% in the absence of different species (see figure 3.51). Among the 103 species of fish, 61 species were mutually beneficial to *Onychostoma barbatulum*. There were 34 species that had more than a 10% effect on the niche of *Onychostoma barbatulum*. Of these, in which the largest effect was 80% by *Sinilabeo rendahli*. There were 41 species of fish in competitive relationships with *Onychostoma barbatulum*. There were 30 species that affected the niche of *Onychostoma barbatulum* by more than 10%, in which the biggest effect was 2006% by *Hypophthalmichthys molitrix*. An additional 39 species had less than a 10% effect on the rate of the niche variation of *Onychostoma barbatulum*.

3.1.2.2.47 Onychostoma ovalis rhomboides (Tang, 1942)

The niche variation of *Onychostoma ovalis rhomboides* (Tang, 1942) ranged from 0% to 4618% in the absence of different species (see figure 3.52). Among the 103 species of fish, No species were mutually beneficial to *Onychostoma ovalis rhomboides*. All the species were competitive relationships with *Onychostoma ovalis rhomboides* by more than 200%, and 4618% with *Ctenopharyngodon idella*.

3.1.2.2.48 Folifer brevifilis brevifilis (Peters, 1881)

The niche variation of *Folifer brevifilis brevifilis* (Peters, 1881) ranged from 0% to 228% in the absence of different species (see figure 3.53). Among the 103 species of fish, 21 species were mutually beneficial to *Lcucosoma chinensis*. There were 7 species that had more than a 10% effect on the niche of *Lcucosoma chinensis*. Of these, in which the largest effect was 91% by *Hypophthalmichthys nobilis*. There were 82 species of fish in competitive relationships with *Lcucosoma chinensis*. There were 73 species that affected the niche of *Lcucosoma chinensis* by more than 10%, with which the biggest effect being 228% by *Hypophthalmichthys molitrix*. An additional

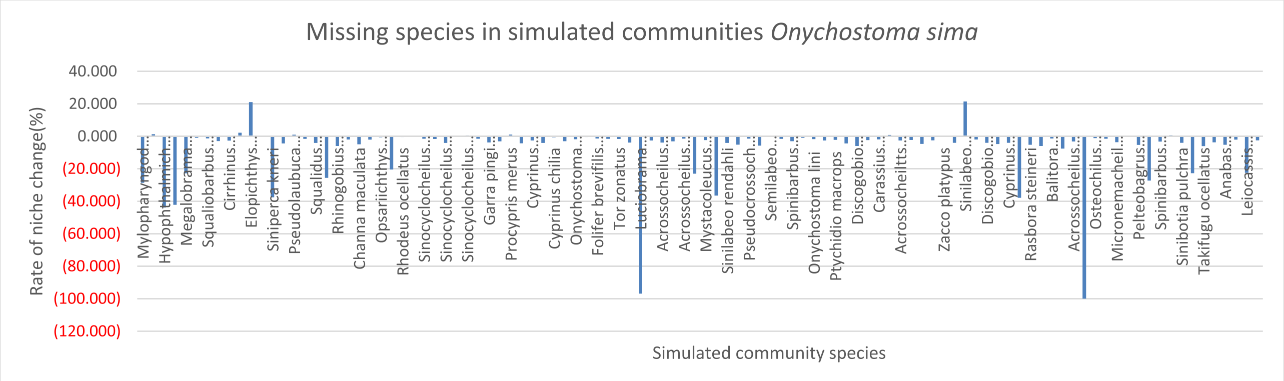

Fig. 3.49 – The responses of the niches of *Onychostoma sima* responses to various missing fish in the simulated community.

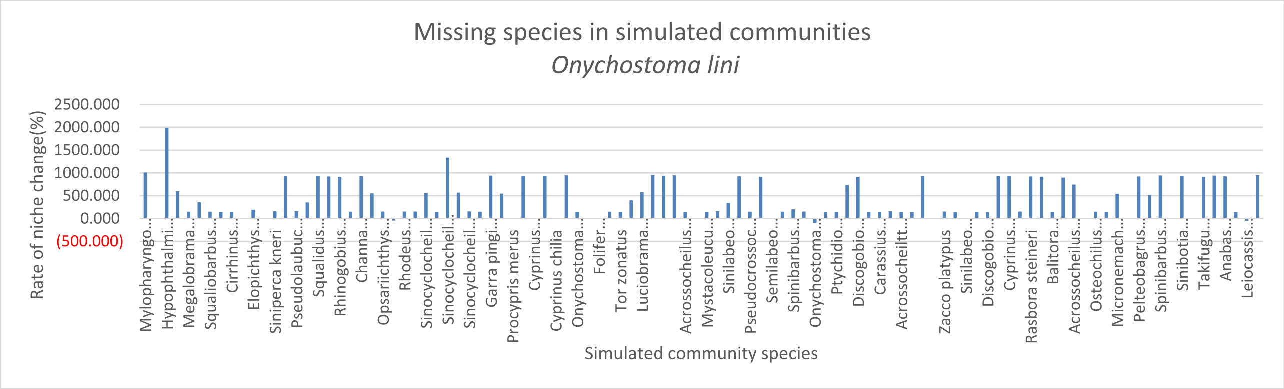

Fig. 3.50 – The responses of the niches of *Onychostoma lini* to various missing fish in the simulated community.

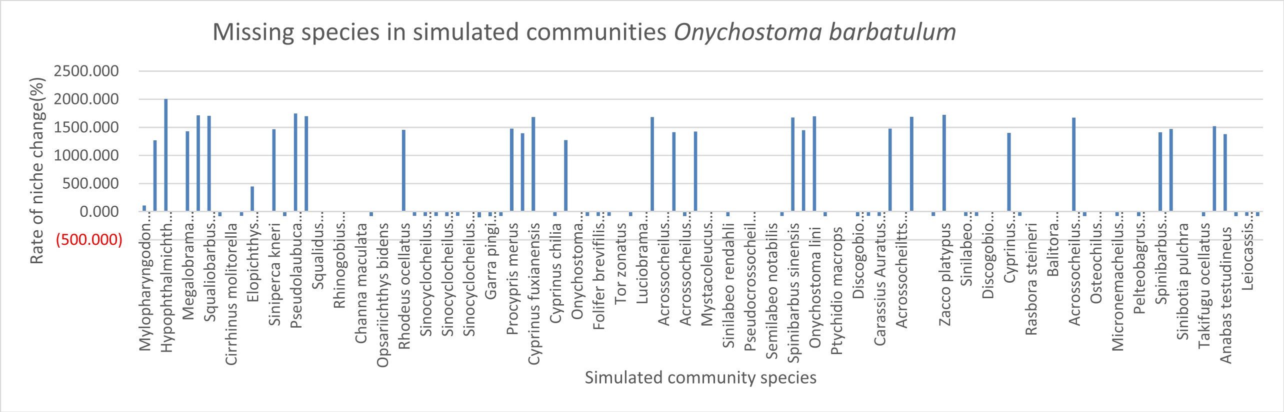

FIG. 3.51 – The responses of the niches of *Onychostoma barbatulum* to various missing fish in the simulated community.

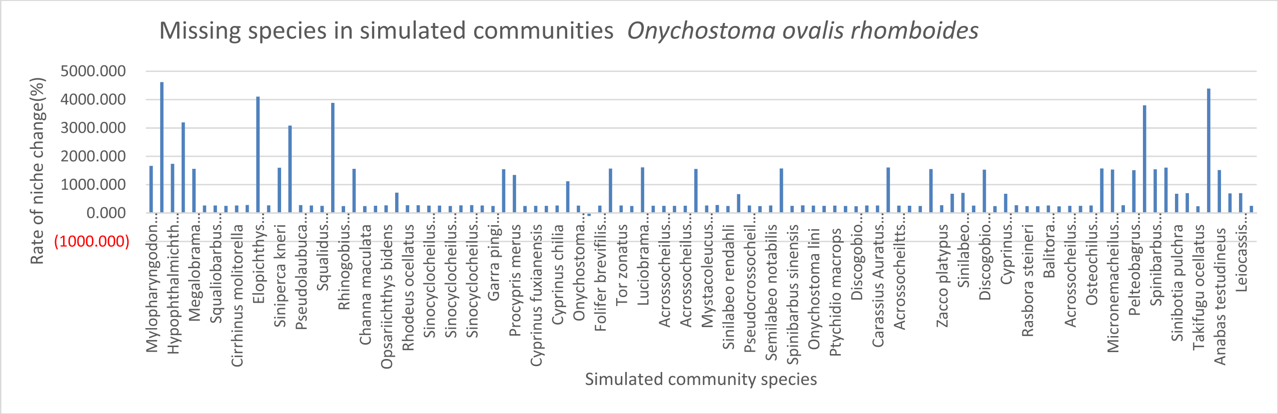

FIG. 3.52 – The responses of the niches of *Onychostoma ovalis rhomboides* to various missing fish in the simulated community.

23 species had less than a 10% effect on the rate of the niche variation of *Lcucosoma chinensis*.

3.1.2.2.49 Tor sinensis (Wu, 1977)

The niche variation of *Tor sinensis* (Wu, 1977) ranged from 0% to 65% in the absence of different species (see figure 3.54). Among the 103 species of fish, 63 species were mutually beneficial to *Tor sinensis*. There were 40 species that had more than a 10% effect on the niche of *Tor sinensis*. Of these, in which the largest effect was 65% by *Pelteobagrus vachellii*. There were 40 species of fish in competitive relationships with *Tor sinensis* by more than 10%, in which the biggest effect was 253% by *Hypophthalmichthys molitrix Tor sinensis* (Wu, 1977). An additional 62 species had less than a 10% effect on the rate of the niche variation of *Tor sinensis*.

3.1.2.2.50 Tor zonatus (Lin, 1935)

The niche variation of *Tor zonatus* (Lin, 1935) ranged from 0% to 3994% in the absence of different species (see figure 3.55). Among the 103 species of fish, 2 species were mutually beneficial to *Tor zonatus*. One of the species that had more than a 10% effect on the niche of *Tor zonatus*. In which the largest effect was 56% by *Tachysurus argentivittatus*. There were 101 species of fish in competitive relationships with *Tor zonatus*. There were 59 species that affected the niche of *Tor zonatus* by more than 10%, with which the biggest effect was 399% by *Hypophthalmichthys molitrix*. An additional 43 species had less than a 10% effect on the rate of the niche variation of *Tor zonatus*.

3.1.2.2.51 Bangana decora (Peters, 1881)

The niche variation of *Bangana decora* (Peters, 1881) ranged from 0% to 98% in the absence of different species (see figure 3.56). Among the 103 species of fish, 87 species were mutually beneficial to *Bangana decora*. There were 71 species that had more than a 10% effect on the niche of *Bangana decora*. Of these, in which the largest effect was 98% by *Sinocyclocheilus macrocephalus*. There were 16 species of fish in competitive relationships with *Bangana decora*. There were 11 species that affected the niche of *Bangana decora* by more than 10%, with which the biggest effect was 37% by *Cyprinus carpio*. An additional 21 species had less than a 10% effect on the rate of the niche variation of *Bangana decora*.

3.1.2.2.52 Sinilabeo rendahli (Kimura, 1934)

The niche variation of *Sinilabeo rendahli* (Kimura, 1934) ranged from 0% to 3930% in the absence of different species (see figure 3.57). Among the 103 species of fish, 7 species were mutually beneficial to *Sinilabeo rendahli*. There were 2 species that had more than a 10% effect on the niche of *Sinilabeo rendahli*. The largest effect was 91% by *Hypophthalmichthys nobilis*. There were 96 species of fish in competitive relationships with *Sinilabeo rendahli*. There were 66 species that affected the niche of *Sinilabeo rendahli* by more than 10%, with which the biggest effect was 3930% by *Elopichthys bambusa*. An additional 35 species had less than a 10% effect on the rate of the niche variation of *Sinilabeo rendahli*.

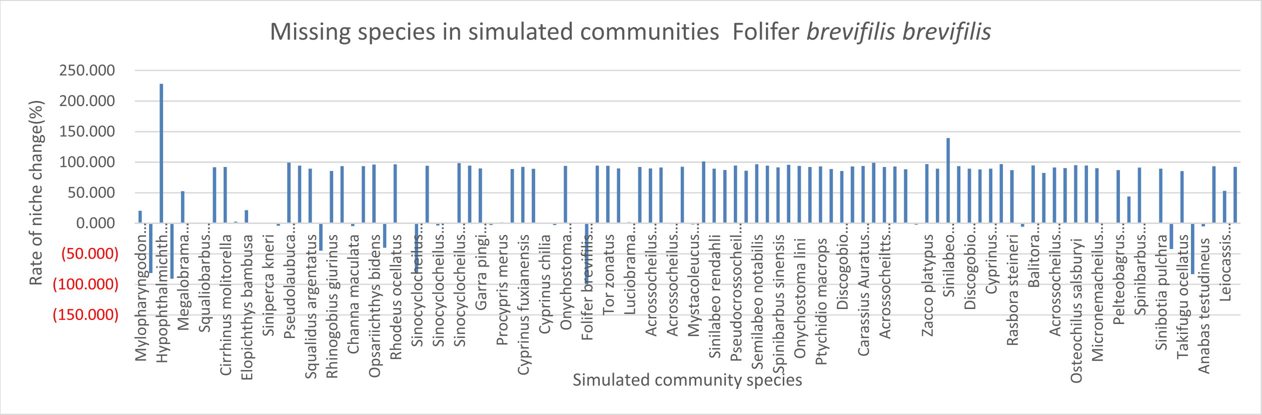

FIG. 3.53 – The responses of the niches of *Folifer brevifilis brevifilis* to various missing fish in the simulated community.

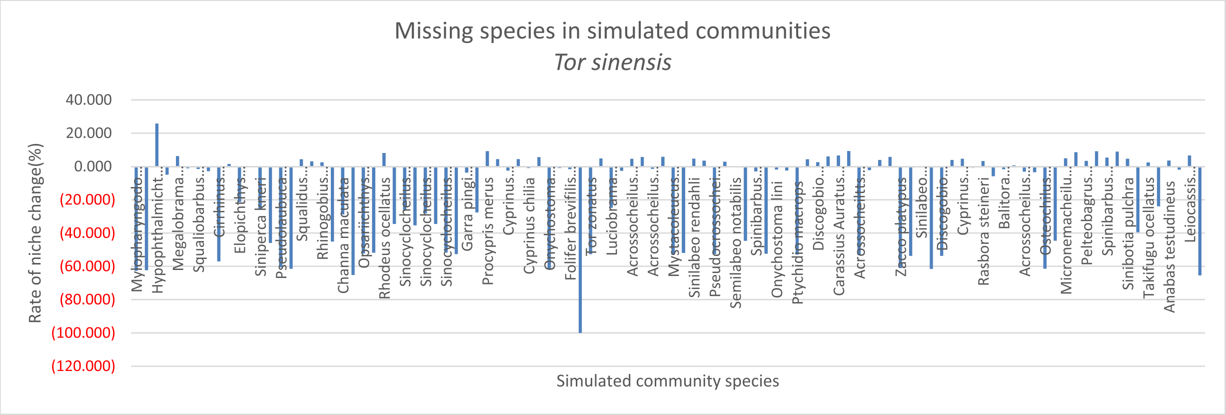

FIG. 3.54 – The responses of the niches of *Tor sinensis* to various missing fish in the simulated community.

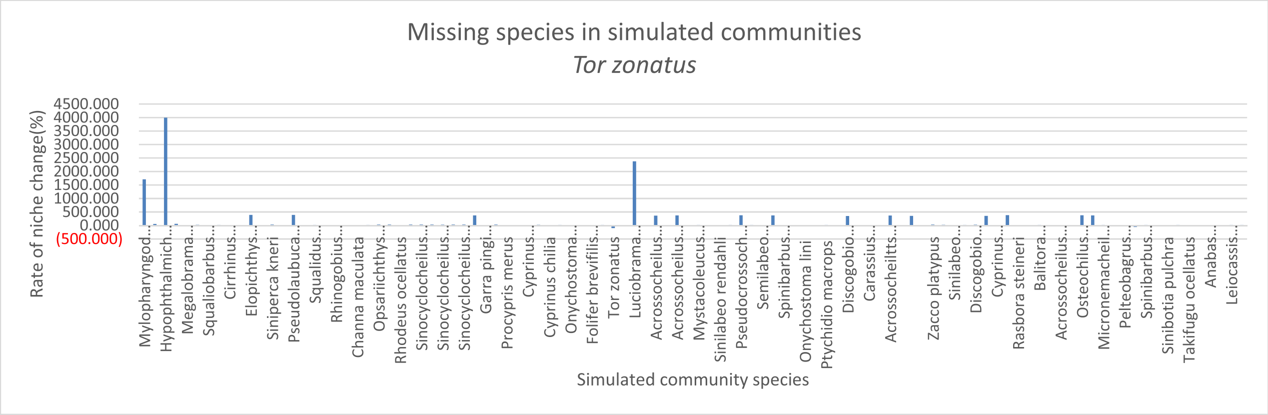

Fig. 3.55 – The responses of the niches of *Tor zonatus* to various missing fish in the simulated community.

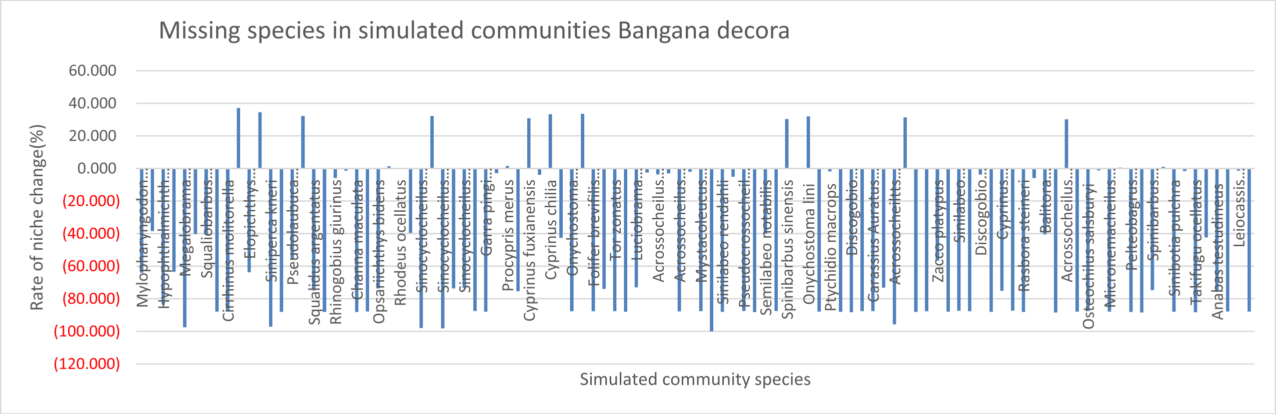

Fig. 3.56 – The responses of the niches of *Bangana decora* to various missing fish in the simulated community.

3.1.2.2.53 Parasinilabeo assimilis (Wu and Yao, 1982)

The niche variation of *Parasinilabeo assimilis* (Wu and Yao, 1982) ranged from 0% to 1049% in the absence of different species (see figure 3.58). Among the 103 species of fish, 65 species were mutually beneficial to *Parasinilabeo assimilis.* There were 34 species that had more than a 10% effect on the niche of *Parasinilabeo assimilis.* Of these, in which the largest effect was 34% by *Puntius semifasciolatus.* There were 38 species of fish in competitive relationships with *Parasinilabeo assimilis.* There were 19 species that affected the niche of *Parasinilabeo assimilis* by more than 10%, in which the biggest effect was 1049% by *Hypophthalmichthys molitrix.* An additional 50 species had less than a 10% effect on the rate of the niche variation of *Parasinilabeo assimilis.*

3.1.2.2.54 Sinilabeo discognathoides (Nichols and Pope, 1927)

The niche variation of *Sinilabeo discognathoides* (Nichols and Pope, 1927) ranged from 0% to 273% in the absence of different species (see figure 3.59). Among the 103 species of fish, 11 species were mutually beneficial to *Sinilabeo discognathoides.* No species had more than a 10% effect on the niche of *Sinilabeo discognathoides.* Of these, in which the largest effect was 4% by *Anabas testudineus.* There were 92 species of fish in competitive relationships with *Sinilabeo discognathoides.* There were 68 species that affected the niche of *Sinilabeo discognathoides* by more than 10%, with which the biggest effect was 273% by *Luciobrama macrocephalus.* An additional 35 species had less than a 10% effect on the rate of the niche variation of *Sinilabeo discognathoides.*

3.1.2.2.55 Sinilabeo discognathoides wui (Zheng and Chen, 1983)

The niche variation of *Sinilabeo discognathoides wui* (Zheng and Chen, 1983) ranged from 0% to 1097% in the absence of different species (see figure 3.60). Among the 103 species of fish, 32 species were mutually beneficial to *Sinilabeo discognathoides wui.* There were 13 species that had more than a 10% effect on the niche of *Sinilabeo discognathoides wui.* Of these, in which the largest effect was 88% by *Tachysurus argentivittatus.* There were 71 species of fish in competitive relationships with *Sinilabeo discognathoides wui.* There were 54 species that affected the niche of *Sinilabeo discognathoides wui* by more than 10%, in which the biggest effect was 1097% by *Bangana decora.* An additional 46 species had less than a 10% effect on the rate of the niche variation of *Sinilabeo discognathoides wui.*

3.1.2.2.56 Cirrhinus molitorella (Valenciennes, 1844)

The niche variation of *Cirrhinus molitorella* (Valenciennes, 1844) ranged from 0% to 369% in the absence of different species (see figure 3.61). Among the 103 species of fish, 70 species were mutually beneficial to *Cirrhinus molitorella.* There were 54 species that had more than a 10% effect on the niche of *Cirrhinus molitorella.* Of these, in which the largest effect was 79% by *Hypophthalmichthys nobilis.* There were 33 species of fish in competitive relationships with *Cirrhinus molitorella.* There were 19 species that affected the niche of *Cirrhinus molitorella* by more than 10%, with which the biggest effect being 369% by *Hypophthalmichthys molitrix.* An additional

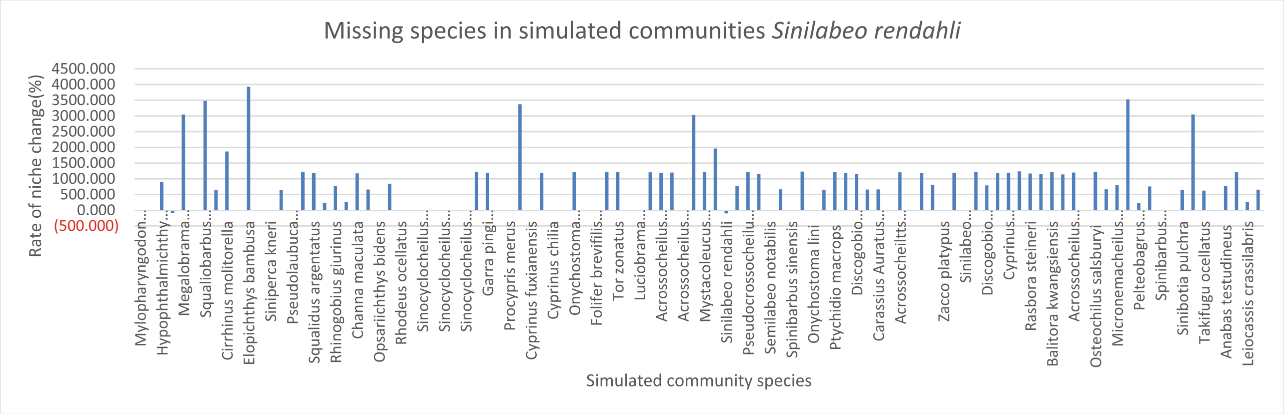

Fig. 3.57 – The responses of the niches of *Sinilabeo rendahli* to various missing fish in the simulated community.

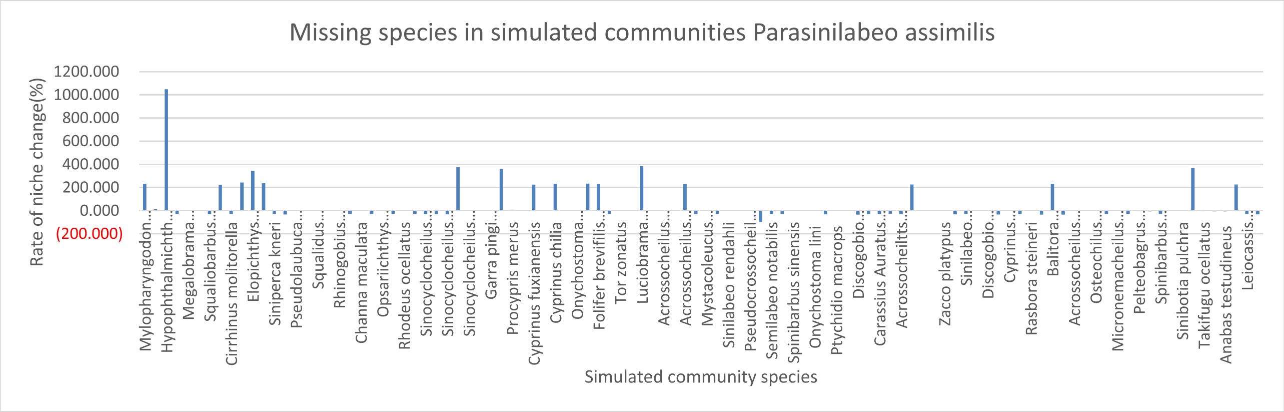

Fig. 3.58 – The responses of the niches of *Parasinilabeo assimilis* to various missing fish in the simulated community.

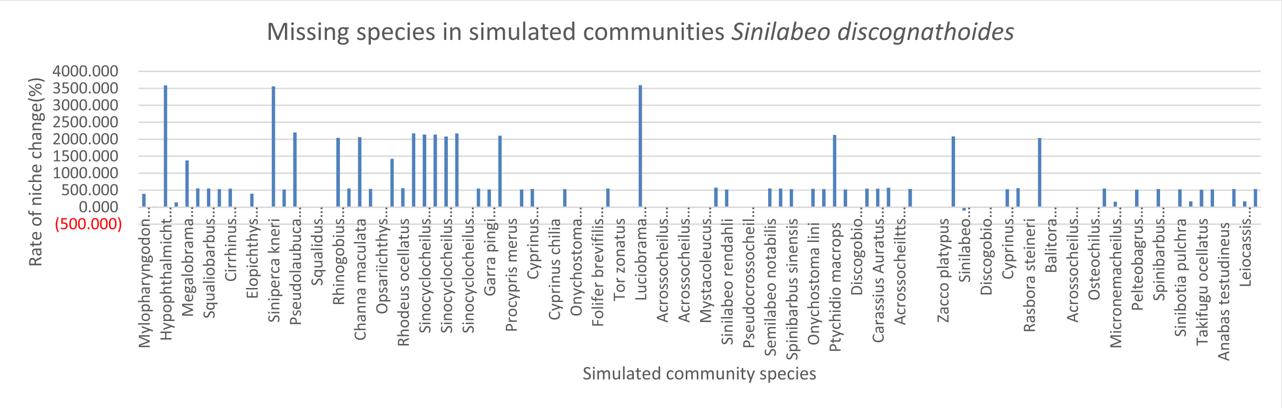

FIG. 3.59 – The responses of the niches of *Sinilabeo discognathoides* to various missing fish in the simulated community.

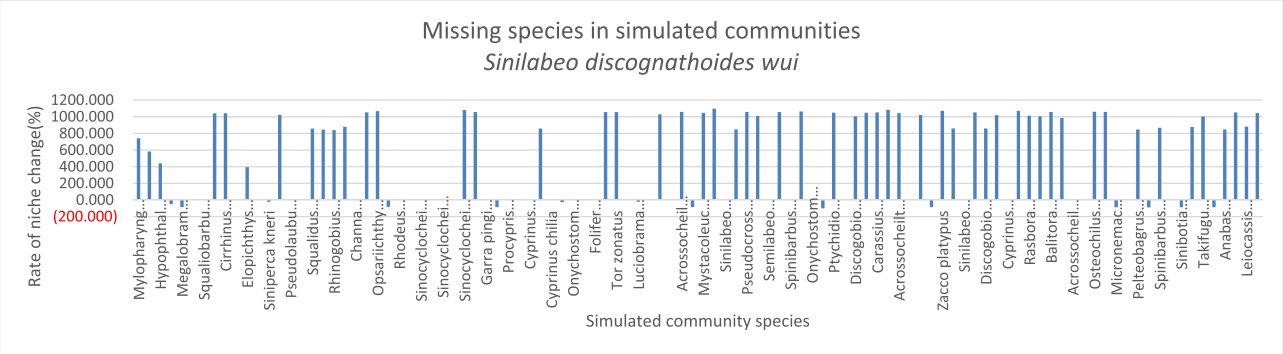

FIG. 3.60 – The responses of the niches of *Sinilabeo discognathoides wui* to various missing fish in the simulated community.

23 species had less than a 10% effect on the rate of the niche variation of *Cirrhinus molitorella*.

3.1.2.2.57 Rectoris posehensis (Lin, 1935)

The niche variation of *Rectoris posehensis* (Lin, 1935) ranged from 0% to 6097% in the absence of different species (see figure 3.62). Among the 103 species of fish, 33 species were mutually beneficial to *Rectoris posehensis*. There were 3 species that had more than a 10% effect on the niche of *Rectoris posehensis*. Of these, in which the largest effect was 49% by *Rectoris posehensis*. There were 70 species of fish in competitive relationships with *Rectoris posehensis*. There were 33 species that affected the niche of *Rectoris posehensis* by more than 10%, with which the biggest effect was 6097% by *Rectoris posehensis*. An additional 68 species had less than a 10% effect on the rate of the niche variation of *Rectoris posehensis*.

3.1.2.2.58 Semilabeo obscurus (Lin, 1981)

The niche variation of *Semilabeo obscurus* (Lin, 1981) ranged from 0% to 97% in the absence of different species (see figure 3.63). Among the 103 species of fish, 71 species were mutually beneficial to *Semilabeo obscurus*. There were 11 species that had more than a 10% effect on the niche of *Semilabeo obscurus*. Of these, in which the largest effect was 97% by *Sinilabeo rendahli*. There were 11 species of fish in competitive relationships with *Semilabeo obscurus*. There were 5 species that affected the niche of *Semilabeo obscurus* by more than 10%, with which the biggest effect was 95% by *Elopichthys bambusa*. An additional 27 species had less than a 10% effect on the rate of the niche variation of *Semilabeo obscurus*.

3.1.2.2.59 Semilabeo notabilis (Peters, 1881)

The niche variation of *Semilabeo notabilis* (Peters, 1881) ranged from 0% to 60% in the absence of different species (see figure 3.64). Among the 103 species of fish, 53 species were mutually beneficial to *Semilabeo notabilis*. There were 21 species that had more than a 10% effect on the niche of *Semilabeo notabilis*. Of these, in which the largest effect was 60% by *Elopichthys bambusa*. There were 50 species of fish in competitive relationships with *Semilabeo notabilis*. There were 3 species that affected the niche of *Semilabeo notabilis* by more than 10%, with which the biggest effect was 22% by *Ancherythroculter lini*. An additional 71 species had less than a 10% effect on the rate of the niche variation of *Semilabeo notabilis*.

3.1.2.2.60 Discocheilus wui (Chen en Lan, 1992)

The niche variation of *Discocheilus wui* (Chen en Lan, 1992) ranged from 0% to 1097% in the absence of different species (see figure 3.65). Among the 103 species of fish, 32 species were mutually beneficial to *Discocheilus wui*. There were 9 species that had more than a 10% effect on the niche of *Discocheilus wui*. Of these, in which the largest effect was 25% by *Ochetobius elongatus*. There were 92 species of fish in competitive relationships with *Discocheilus wui*. There were 65 species that affected the niche of *Discocheilus wui* by more than 10%, with which the biggest effect was

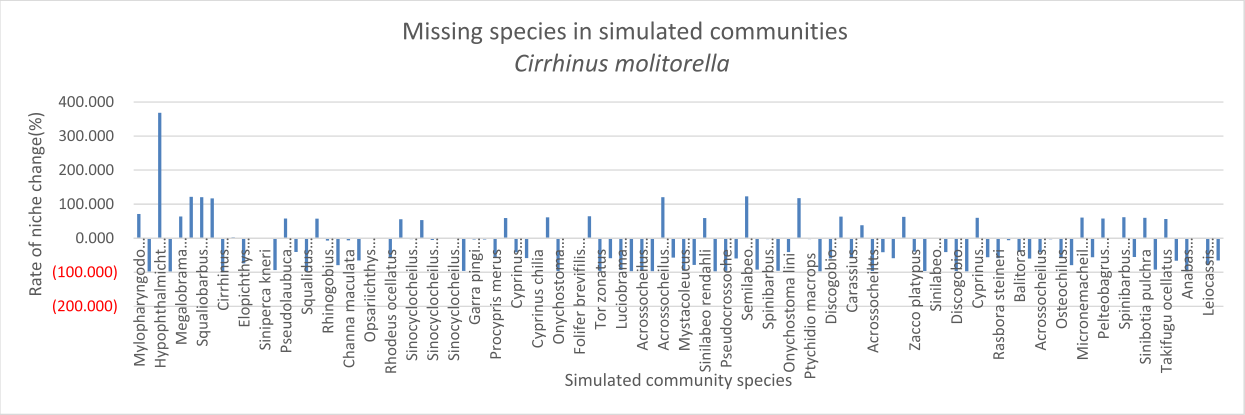

FIG. 3.61 – The responses of the niches of *Cirrhinus molitorella* to various missing fish in the simulated community.

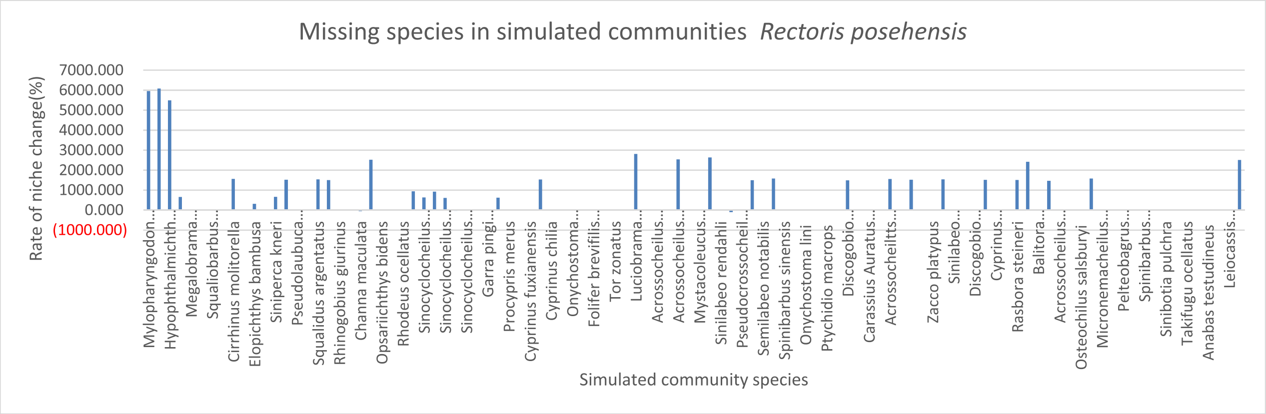

FIG. 3.62 – The responses of the niches of *Rectoris posehensis* to various missing fish in the simulated community.

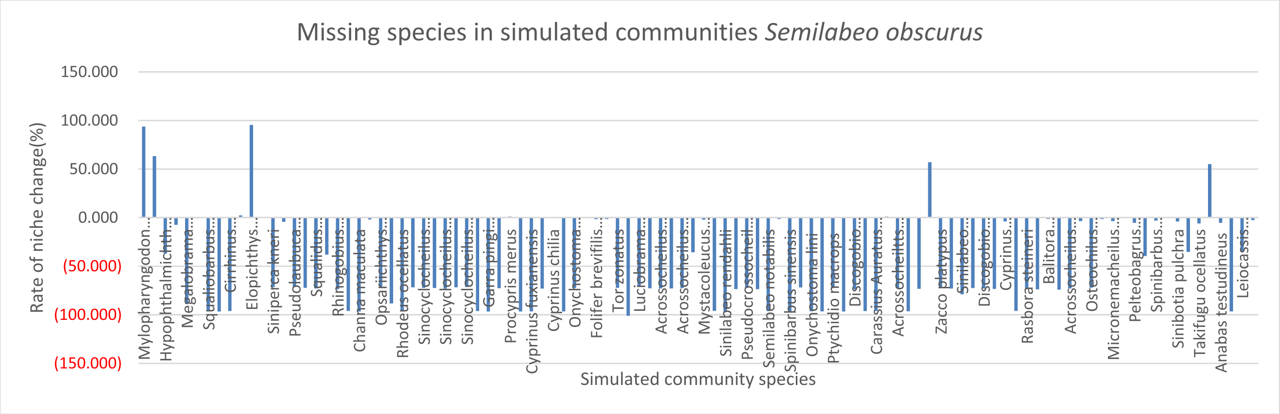

FIG. 3.63 – The responses of the niches of *Semilabeo obscurus* to various missing fish in the simulated community.

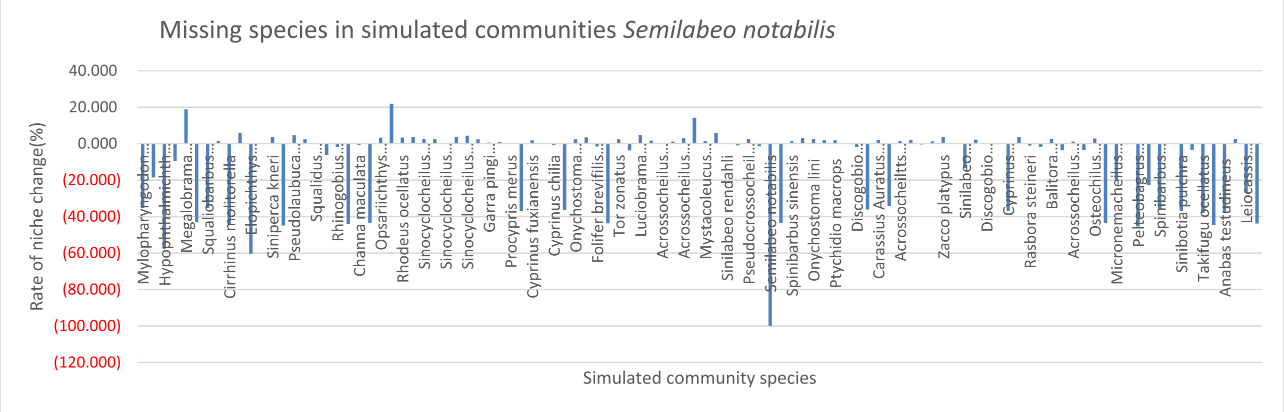

FIG. 3.64 – The responses of the niches of *Semilabeo notabilis* to various missing fish in the simulated community.

99% by *Leiocassis crassilabris*. An additional 46 species had less than a 10% effect on the rate of the niche variation of *Discocheilus wui*.

3.1.2.2.61 Osteochilus salsburyi (Nichols and Pope, 1927)

The niche variation of *Osteochilus salsburyi* (Nichols and Pope, 1927) ranged from 0% to 95% in the absence of different species (see figure 3.66). Among the 103 species of fish, 83 species were mutually beneficial to *Osteochilus salsburyi*. There were 50 species that had more than a 10% effect on the niche of *Osteochilus salsburyi*. Of these, in which the largest effect was 95% by *Elopichthys bambusa*. There were 20 species of fish in competitive relationships with *Osteochilus salsburyi*. There were 15 species that affected the niche of *Osteochilus salsburyi* by more than 10%, with which the biggest effect was 71% by *Luciocyprinus langsoni*. An additional 39 species had less than a 10% effect on the rate of the niche variation of *Osteochilus salsburyi*.

3.1.2.2.62 Pseudocrossocheilus bamaensis (Fang, 1981)

The niche variation of *Pseudocrossocheilus bamaensis* (Fang, 1981) ranged from 0% to 332% in the absence of different species (see figure 3.67). Among the 103 species of fish, 51 species were mutually beneficial to *Pseudocrossocheilus bamaensis*. There were 27 species that had more than a 10% effect on the niche of *Pseudocrossocheilus bamaensis*. Of these, in which the largest effect was 80% by *Hypophthalmichthys nobilis*. There were 52 species of fish in competitive relationships with *Pseudocrossocheilus bamaensis*. There were 46 species that affected the niche of *Pseudocrossocheilus bamaensis* by more than 10%, with which the biggest effect was 332% by *Bangana decora*. An additional 30 species had less than a 10% effect on the rate of the niche variation of *Pseudocrossocheilus bamaensis*.

3.1.2.2.63 Ptychidio macrops (Fang, 1981)

The niche variation of *Ptychidio macrops* (Fang, 1981) ranged from 0% to 243% in the absence of different species (see figure 3.68). Among the 103 species of fish, 42 species were mutually beneficial to *Ptychidio macrops*. There were 11 species that had more than a 10% effect on the niche of *Ptychidio macrops*. Of these, in which the largest effect was 40% by *Hypophthalmichthys nobilis*. There were 61 species of fish in competitive relationships with *Ptychidio macrops*. There were 51 species that affected the niche of *Ptychidio macrops* by more than 10%, with which the biggest effect was 243% by *Luciobrama macrocephalus*. An additional 41 species had less than a 10% effect on the rate of the niche variation of *Ptychidio macrops*.

3.1.2.2.64 Ptychidio jordani (Myers, 1930)

The niche variation of *Ptychidio jordani* (Myers, 1930) ranged from 0% to 86% in the absence of different species (see figure 3.69). Among the 103 species of fish, 31 species were mutually beneficial to *Ptychidio jordani*. There were 3 species that had more than a 10% effect on the niche of *Ptychidio jordani*. Of these, in which the

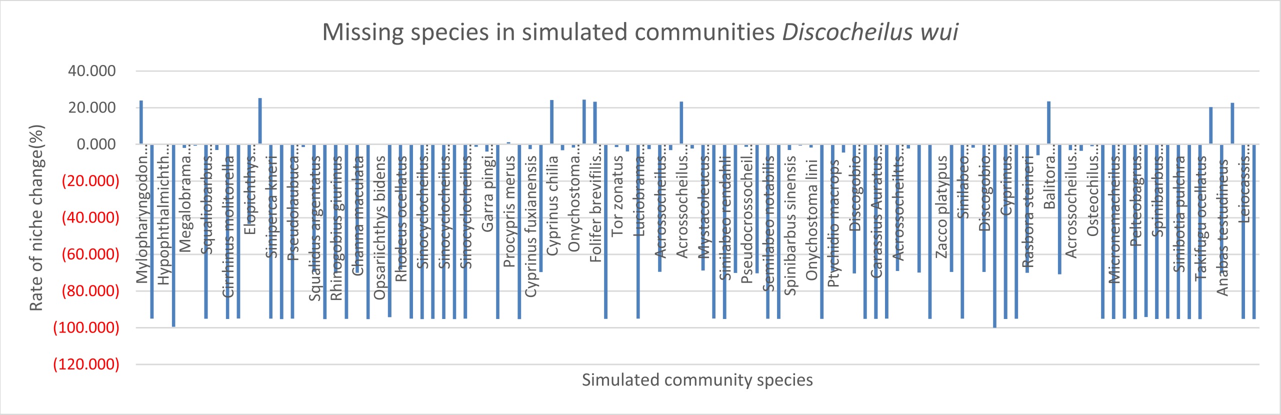

FIG. 3.65 – The responses of the niches of *Discocheilus wui* to various missing fish in the simulated community.

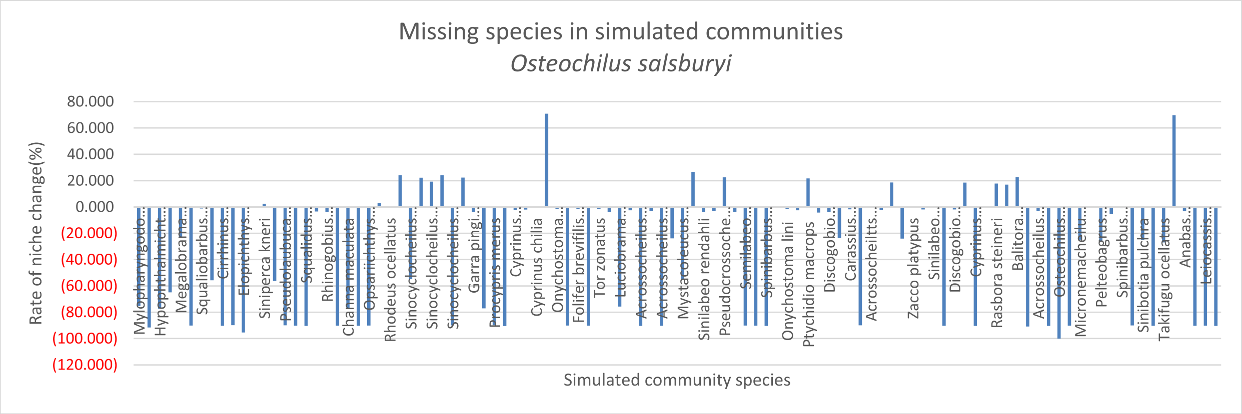

FIG. 3.66 – The responses of the niches of *Osteochilus salsburyi* to various missing fish in the simulated community.

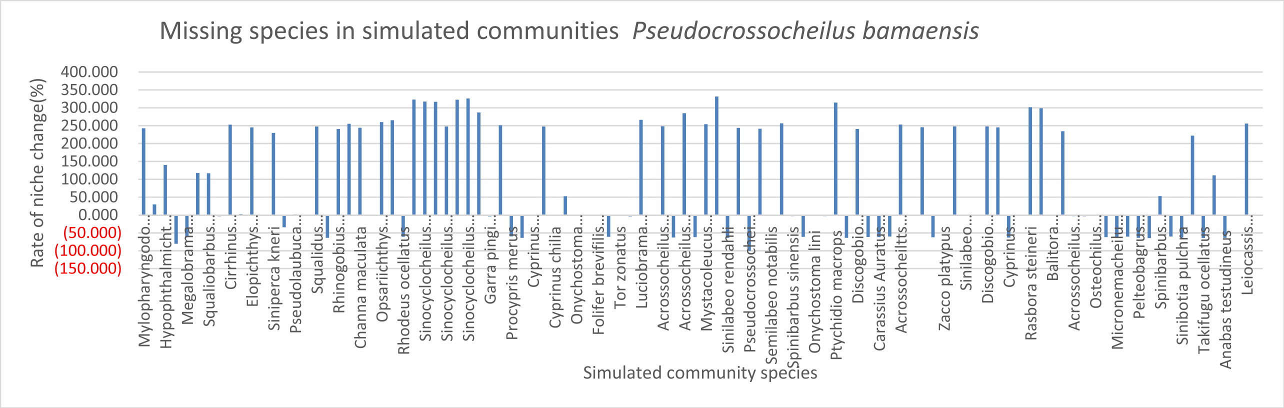

FIG. 3.67 – The responses of the niches of *Pseudocrossocheilus bamaensis* to various missing fish in the simulated community.

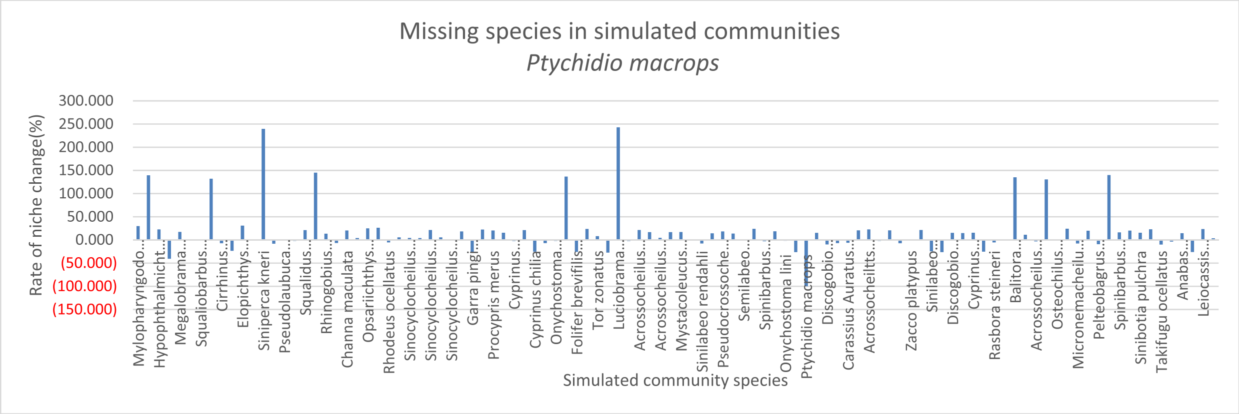

FIG. 3.68 – The responses of the niches of *Ptychidio macrops* to various missing fish in the simulated community.

largest effect was 36% by *Mylopharyngodon piceus*. There were 72 species of fish in competitive relationships with *Ptychidio jordani*. There were 67 species that affected the niche of *Ptychidio jordani* by more than 10%, with which the biggest effect was 86% by *Procypris merus*. An additional 33 species had less than a 10% effect on the rate of the niche variation of *Ptychidio jordani*.

3.1.2.2.65 Garra pingi yiliangensis (Wu and Chen, 1982)

The niche variation of *Garra pingi yiliangensis* (Wu and Chen, 1982) ranged from 0% to near 100% in the absence of different species (see figure 3.70). Among the 103 species of fish, 97 species were mutually beneficial to *Garra pingi yiliangensis*. There were 77 species that had more than a 10% effect on the niche of *Garra pingi yiliangensis*. Of these, in which the largest effect was nearly 100% by *Misgurnus anguillicaudatus*. There were 6 species of fish in competitive relationships with *Garra pingi yiliangensis*. No species affected the niche of *Garra pingi yiliangensis* by more than 10%, with which the biggest effect was 82% by *Cyprinus carpio*. An additional 61 species had less than a 10% effect on the rate of the niche variation of *Garra pingi yiliangensis*.

3.1.2.2.66 Garra pingi hainanensis (Chen and Zheng, 1983)

The niche variation of *Garra pingi hainanensis* (Chen and Zheng, 1983) ranged from 0% to 192% in the absence of different species (see figure 3.71). Among the 103 species of fish, 96 species were mutually beneficial to *Garra pingi hainanensis*. There were 88 species that had more than a 10% effect on the niche of *Garra pingi hainanensis*. Of these, in which the largest effect was 98% by *Anabas testudineus*. There were 7 species of fish in competitive relationships with *Garra pingi hainanensis*. There were 2 species that affected the niche of *Garra pingi hainanensis* by more than 10%, with which the biggest effect was 192% by *LMylopharyngodon piceus*. An additional 13 species had less than a 10% effect on the rate of the niche variation of *Garra pingi hainanensis*.

3.1.2.2.67 Garra pingi pingi (Tchang, 1929)

The niche variation of *Garra pingi pingi* (Tchang, 1929) ranged from 0% to 3207% in the absence of different species (see figure 3.72). Among the 103 species of fish, 57 species were mutually beneficial to *Garra pingi pingi*. There were 16 species that had more than a 10% effect on the niche of *Garra pingi pingi*. Of these, in which the largest effect was 76% by *Ctenopharyngodon idella*. There were 46 species of fish in competitive relationships with *Garra pingi pingi*. There were 32 species that affected the niche of *Garra pingi pingi* by more than 10%, in which the biggest effect was 3207% by *Hypophthalmichthys molitrix*. An additional 24 species had less than a 10% effect on the rate of the niche variation of *Garra pingi pingi*.

3.1.2.2.68 Garra orientalis (Nichols, 1925)

The niche variation of *Garra orientalis* (Nichols, 1925) ranged from 0% to 5216% in the absence of different species (see figure 3.73). Among the 103 species of fish, 14

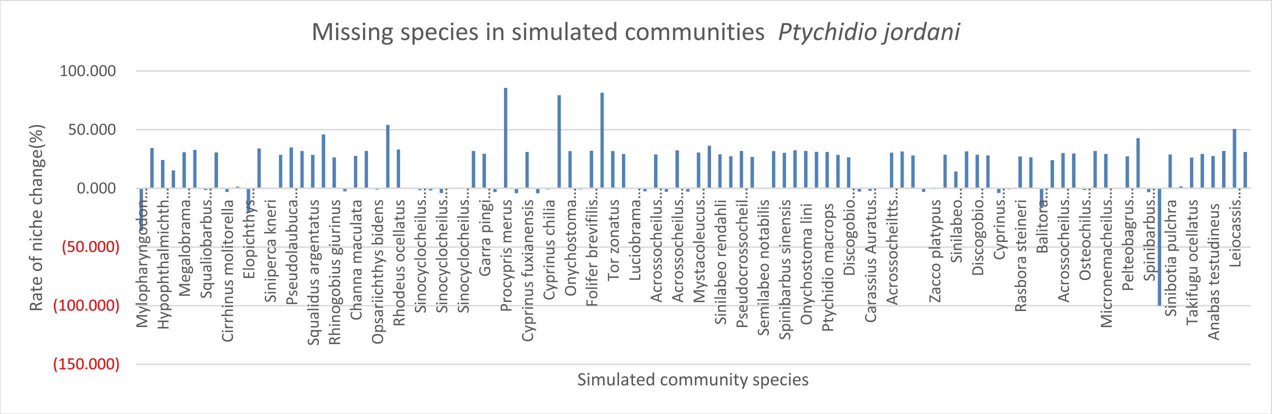

FIG. 3.69 – The responses of the niches of *Ptychidio jordani* to various missing fish in the simulated community.

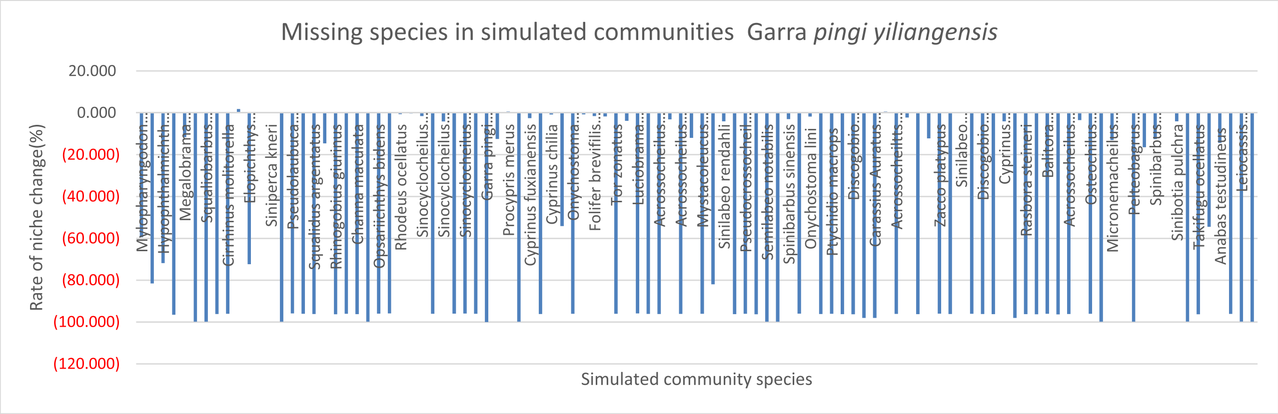

FIG. 3.70 – The responses of the niches of *Garra pingi yiliangensis* to various missing fish in the simulated community.

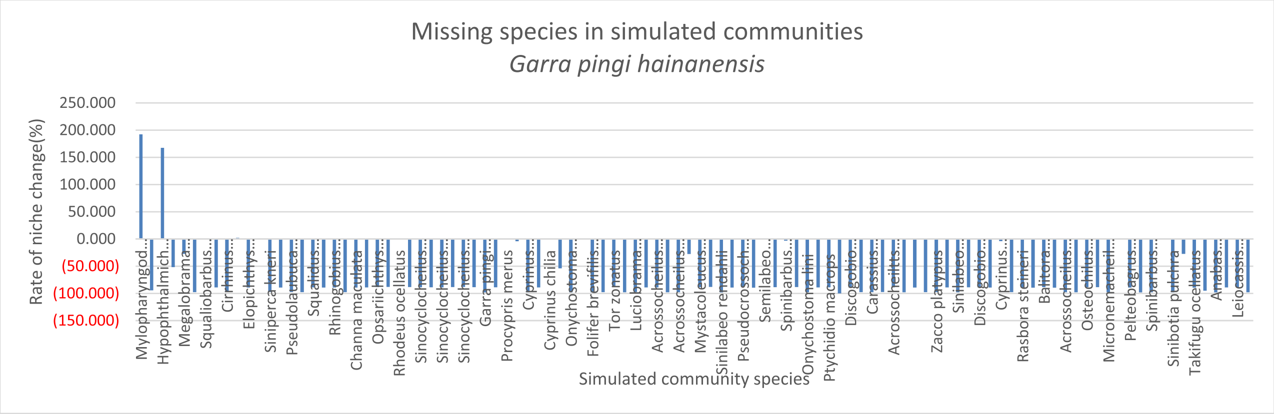

FIG. 3.71 – The responses of the niches of *Garra pingi hainanensis* to various missing fish in the simulated community.

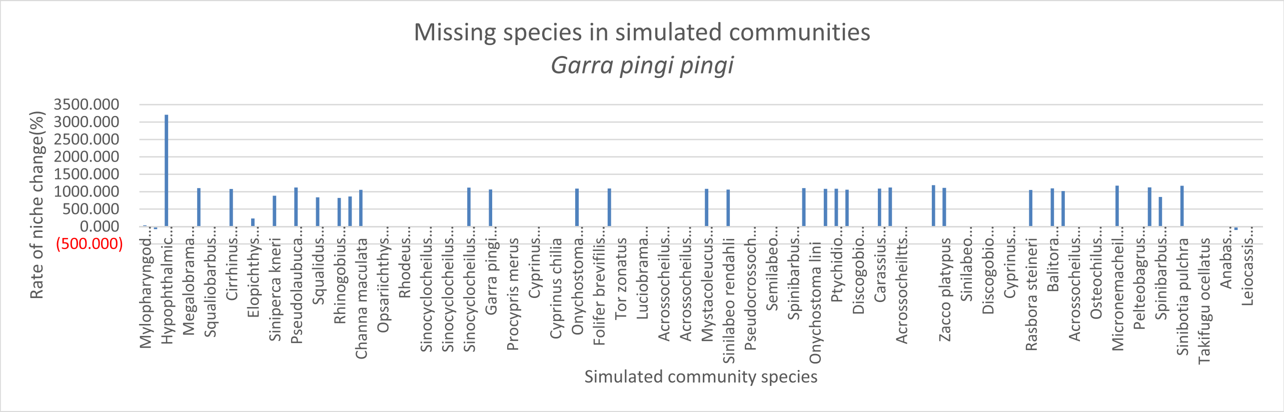

FIG. 3.72 – The responses of the niches of *Garra pingi pingi* to various missing fish in the simulated community.

species were mutually beneficial to *Garra orientalis*. All of the species had more than a 10% effect on the niche of *Garra orientalis*. Of these, in which the largest effect was 70% by *Anabas testudineus*. There were 89 species of fish in competitive relationships with *Garra orientalis*. There were 80 species that affected the niche of *Garra orientalis* by more than 10%, with which the biggest effect was 5216% by *Luciobrama macrocephalus*. An additional 46 species had less than a 10% effect on the rate of the niche variation of *Garra orientalis*.

3.1.2.2.69 Discogobio tetrabarbatus (Lin, 1931)

The niche variation of *Discogobio tetrabarbatus* (Lin, 1931) ranged from 0% to 213% in the absence of different species (see figure 3.74). Among the 103 species of fish, 76 species were mutually beneficial to *Discogobio tetrabarbatus*. There were 36 species that had more than a 10% effect on the niche of *Discogobio tetrabarbatus*. Of these, in which the largest effect was 98% by *Elopichthys bambusa*. There were 27 species of fish in competitive relationships with *Discogobio tetrabarbatus*. There were 17 species that affected the niche of *Discogobio tetrabarbatus* by more than 10%, with which the biggest effect was 213% by *Sinocyclocheilus yangzongensis*. An additional 50 species had less than a 10% effect on the rate of the niche variation of *Discogobio tetrabarbatus*.

3.1.2.2.70 Discogo biolongibarbatus (Wu, 1982)

The niche variation of *Discogo biolongibarbatus* (Wu, 1982) ranged from 0% to 99% in the absence of different species (see figure 3.75). Among the 103 species of fish, 58 species were mutually beneficial to *Discogo biolongibarbatus*. There were 45 species that had more than a 10% effect on the niche of *Discogo biolongibarbatus*. Of these, in which the largest effect was 99% by *Sinilabeo rendahlis*. There were 16 species of fish in competitive relationships with *Discogo biolongibarbatus*. There were 12 species that affected the niche of *Discogo biolongibarbatus* by more than 10%, with which the biggest effect was 36% by *Hypophthalmichthys molitrix*. An additional 45 species had less than a 10% effect on the rate of the niche variation of *Discogo biolongibarbatus*.

3.1.2.2.71 Discogobio brachyphysallidos (Huang, 1989)

The niche variation of *Discogobio brachyphysallidos* (Huang, 1989) ranged from 0% to 344% in the absence of different species (see figure 3.76). Among the 103 species of fish, 90 species were mutually beneficial to *Discogobio brachyphysallidos*. There were 66 species that had more than a 10% effect on the niche of *Discogobio brachyphysallidos*. Of these, in which the largest effect was 99% by *Misgurnus anguillicaudatus*. There were 13 species of fish in competitive relationships with *Discogobio brachyphysallidos*. There were 8 species that affected the niche of *Discogobio brachyphysallidos* by more than 10%, with which the biggest effect was 344% by *Ctenopharyngodon idella*. An additional 29 species had less than a 10% effect on the rate of the niche variation of *Discogobio brachyphysallidos*.

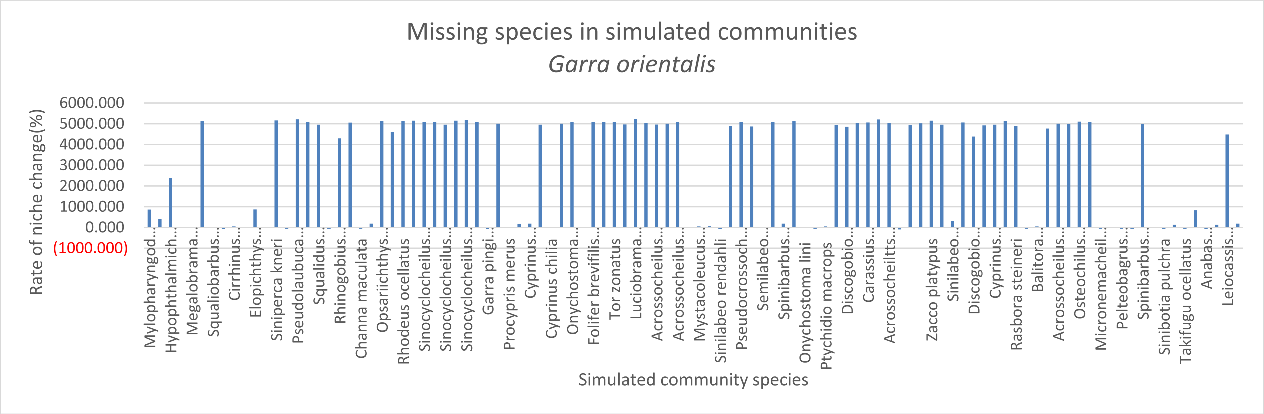

Fig. 3.73 – The responses of the niches of *Garra orientalis* to various missing fish in the simulated community.

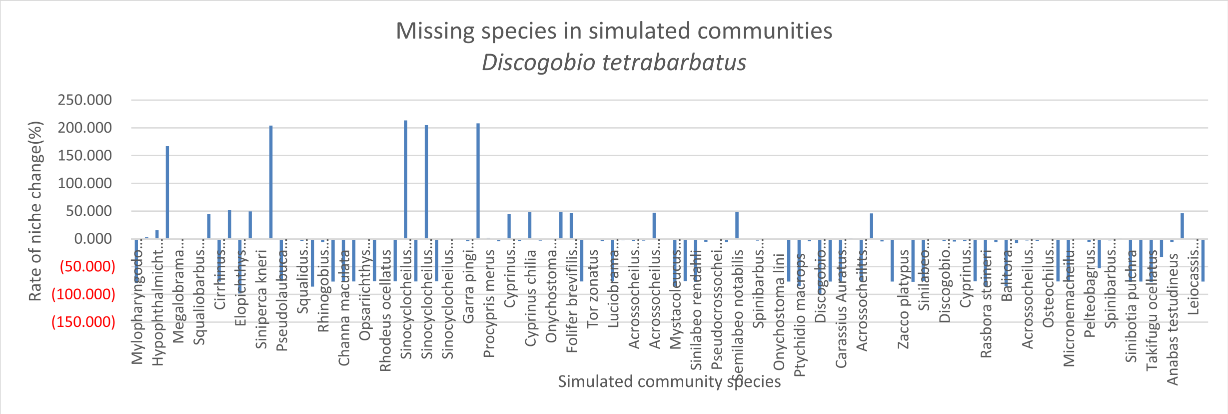

Fig. 3.74 – The responses of the niches of *Discogobio tetrabarbatus* to various missing fish in the simulated community.

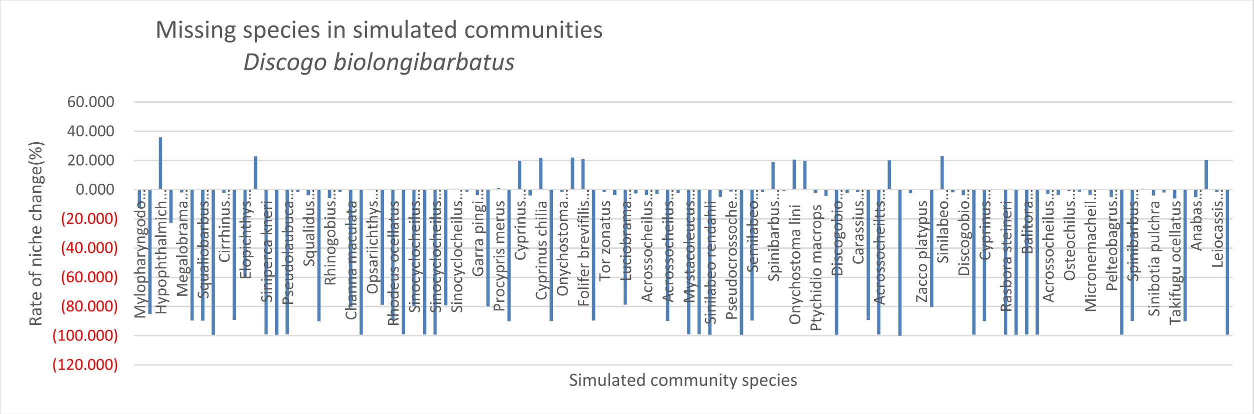

Fig. 3.75 – The responses of the niches of *Discogo biolongibarbatus* to various missing fish in the simulated community.

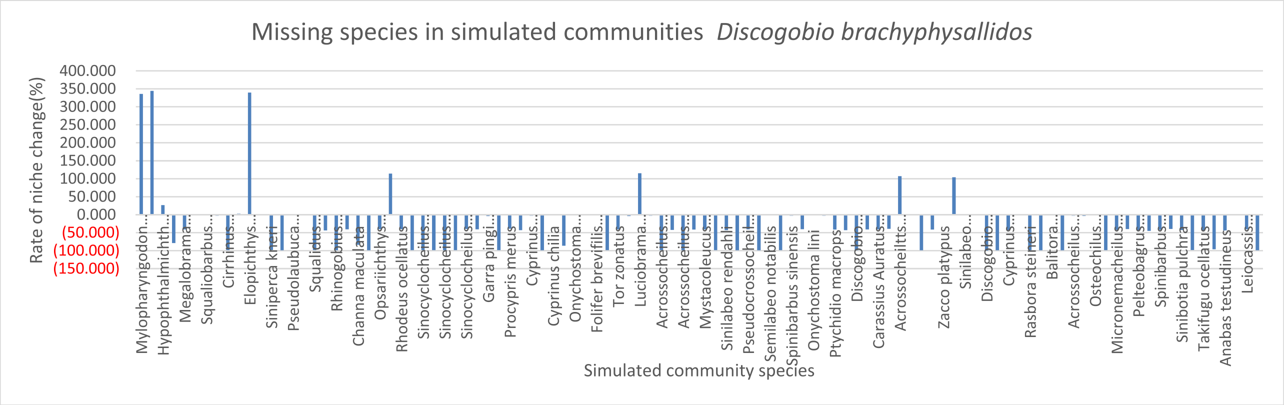

Fig. 3.76 – The responses of the niches of *Discogobio brachyphysallidos* to various missing fish in the simulated community.

3.1.2.2.72 Procypris merus (Lin, 1933)

The niche variation of *Procypris merus* (Lin, 1933) ranged from 0% to 1482% in the absence of different species (see figure 3.77). Among the 103 species of fish, 23 species were mutually beneficial to *Procypris merus.* There were 14 species that had more than a 10% effect on the niche of *Procypris merus.* Of these, in which the largest effect was 97% by *Schizothorax meridionalis.* There were 81 species of fish in competitive relationships with *Procypris merus.* There were 19 species that affected the niche of *Procypris merus* by more than 10%, in which the biggest effect was 1482% by *Onychostoma barbatulum.* An additional 46 species had less than a 10% effect on the rate of the niche variation of *Procypris merus.*

3.1.2.2.73 Cyprinus rabaudi (Tchang, 1930)

The niche variation of *Cyprinus rabaudi* (Tchang, 1930) ranged from 0% to 232% in the absence of different species (see figure 3.78). Among the 103 species of fish, 30 species were mutually beneficial to *Cyprinus rabaudi.* There were 3 species that had more than a 10% effect on the niche of *Cyprinus rabaudi.* Of these, in which the largest effect was 69% by *Hypophthalmichthys molitrix.* There were 73 species of fish in competitive relationships with *Cyprinus rabaudi.* There were 68 species that affected the niche of *Cyprinus rabaudi* by more than 10%, with which the biggest effect was 232% by *Hypophthalmichthys nobilis.* An additional 32 species had less than a 10% effect on the rate of the niche variation of *Cyprinus rabaudi.*

3.1.2.2.74 Cyprinus multitaeniatus (Pellegrin and Chevey, 1936)

The niche variation of *Cyprinus multitaeniatus* (Pellegrin and Chevey, 1936) ranged from 0% to 39% in the absence of different species (see figure 3.79). Among the 103 species of fish, 32 species were mutually beneficial to *Cyprinus carpio.* There were 25 species that had more than a 10% effect on the niche of *Cyprinus carpio.* Of these, in which the largest effect was 39% by *Takifugu ocellatus.* There were 71 species of fish in competitive relationships with *Cyprinus carpio.* There were 68 species that affected the niche of *Cyprinus carpio* by more than 10%, with which the biggest effect was 32% by *Ancherythroculter lini.* An additional 10 species had less than a 10% effect on the rate of the niche variation of *Cyprinus carpio.*

3.1.2.2.75 Cyprinus multitaeniata (Pellegrin and Chevey, 1936)

The niche variation of *Cyprinus multitaeniata* (Pellegrin and Chevey, 1936) ranged from 0% to 366% in the absence of different species (see figure 3.80). Among the 103 species of fish, 22 species were mutually beneficial to *Cyprinus multitaeniata.* Only *Hypophthalmichthys molitrix* had more than a 10% effect on the niche of *Cyprinus multitaeniata*, and the effect was 16%. There were 81 species of fish in competitive relationships with *Cyprinus multitaeniata.* There were 78 species that affected the niche of *Cyprinus multitaeniata* by more than 10%, with which the biggest effect was 366% by *Acheilognathus tonkinensis.* An additional 24 species had less than a 10% effect on the rate of the niche variation of *Cyprinus multitaeniata.*

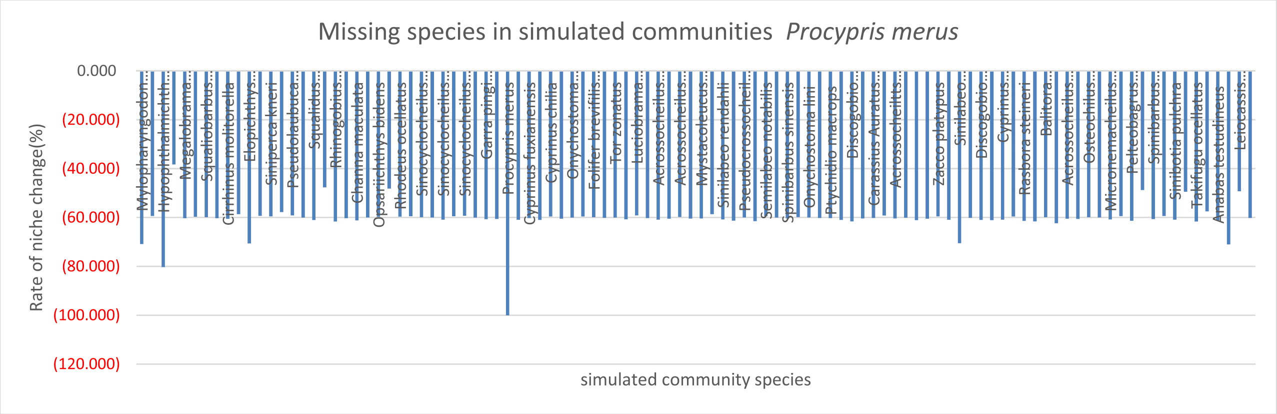

FIG. 3.77 – The responses of the niches of *Procypris merus* to various missing fish in the simulated community.

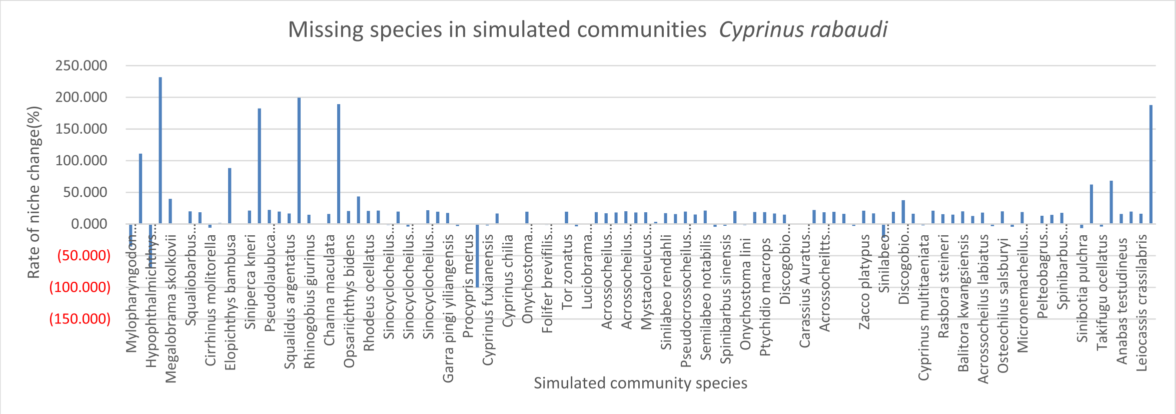

FIG. 3.78 – The responses of the niches of *Cyprinus rabaudi* to various missing fish in the simulated community.

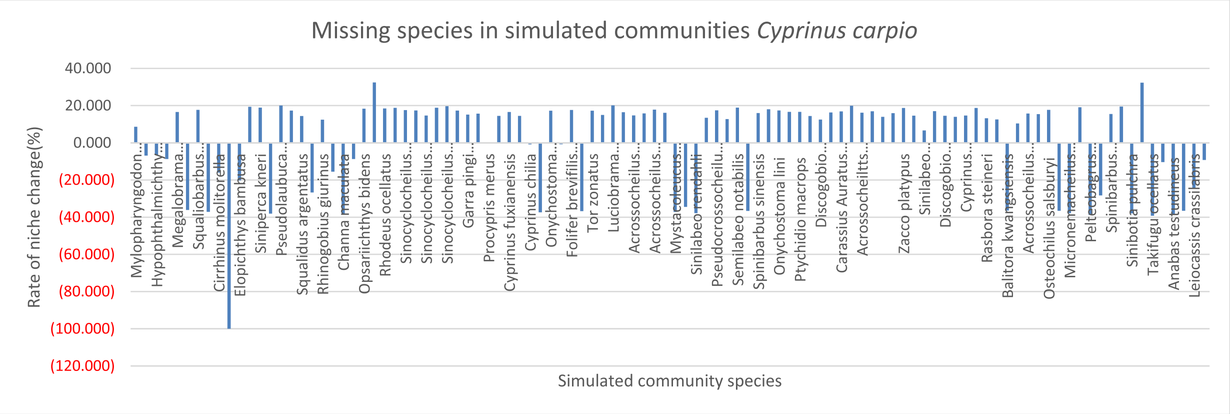

FIG. 3.79 – The responses of the niches of *Cyprinus carpio* to various missing fish in the simulated community.

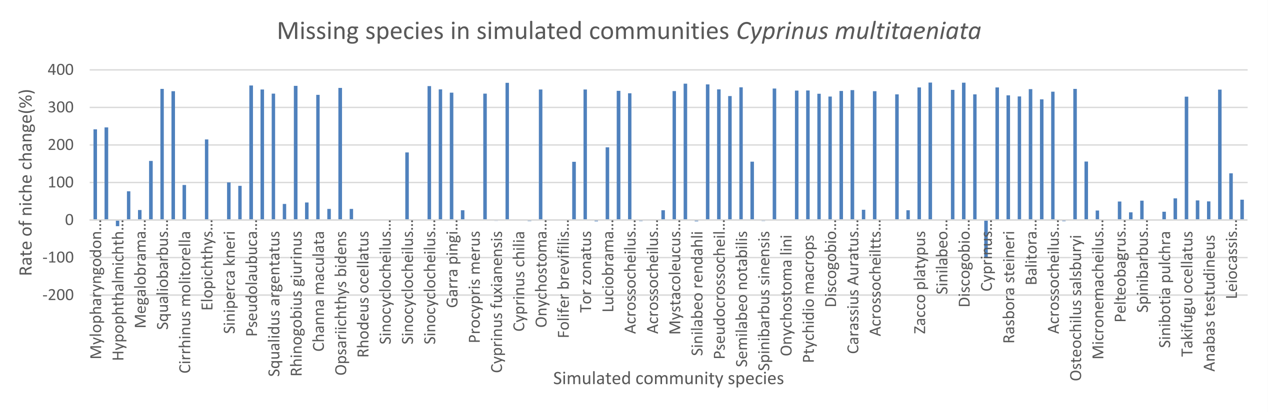

FIG. 3.80 – The responses of the niches of *Cyprinus multitaeniata* to various missing fish in the simulated community.

3.1.2.2.76 Cyprinus fuxianensis (Yang et al., 1982)

The niche variation of *Cyprinus fuxianensis* (Yang *et al.*, 1982) ranged from 0% to 2152% in the absence of different species (see figure 3.81). Among the 103 species of fish, only *Onychostoma sima* was mutually beneficial to *Cyprinus fuxianensis* with a 0.3% effect on the niche of *Cyprinus fuxianensis.* There were 102 species of fish in competitive relationships with *Cyprinus fuxianensis.* There were 87 species that affected the niche of *Cyprinus fuxianensis* by more than 10%, with which the biggest effect was 2152% by *Mylopharyngodon piceus.* An additional 15 species had less than a 10% effect on the rate of the niche variation of *Cyprinus fuxianensis.*

3.1.2.2.77 Cyprinus yilongensis (Yang et al., 1982)

The niche variation of *Cyprinus yilongensis* (Yang *et al.*, 1982) ranged from 0% to 742% in the absence of different species (see figure 3.82). Among the 103 species of fish, 69 species were mutually beneficial to *Cyprinus yilongensis.* There were 57 species that had more than a 10% effect on the niche of *Cyprinus yilongensis.* Of these, in which the largest effect was 97% by *Mylopharyngodon piceus.* There were 34 species of fish in competitive relationships with *Cyprinus yilongensis.* There were 31 species that affected the niche of *Cyprinus yilongensis* by more than 10%, with which the biggest effect was 742% by *Hypophthalmichthys molitrix.* An additional 5 species had less than a 10% effect on the rate of the niche variation of *Cyprinus yilongensis.*

3.1.2.2.78 Cyprinus chilia (Wu, 1963)

The niche variation of *Cyprinus chilia* (Wu, 1963) ranged from 0% to 4199% in the absence of different species (see figure 3.83). Among the 103 species of fish, no species were mutually beneficial to *Cyprinus chilia.* There were 100 species of fish in competitive relationships with *Cyprinus chilia* by more than 10%, in which the biggest effect was 4199% by *Leptobotia pellegrini.* An additional 3 species had less than a 10% effect on the rate of the niche variation of *Cyprinus chilia.*

3.1.2.2.79 Cyprinus pellegrini (Tchang, 1933)

The niche variation of *Cyprinus pellegrini* (Tchang, 1933) ranged from 0% to 937% in the absence of different species (see figure 3.84). Among the 103 species of fish, 86 species were mutually beneficial to *Cyprinus pellegrini.* There were 64 species that had more than a 10% effect on the niche of *Cyprinus pellegrini.* Of these, in which the largest effect was 90% by *Hypophthalmichthys nobilis.* There were 17 species of fish in competitive relationships with *Cyprinus pellegrini.* There were 5 species that affected the niche of *Cyprinus pellegrini* by more than 10%, with which the biggest effect was 937% by *Hypophthalmichthys molitrix.* An additional 46 species had less than a 10% effect on the rate of the niche variation of *Cyprinus pellegrini.*

3.1.2.2.80 Cyprinus longzhouensis (Yang and Hwang, 1982)

The niche variation of *Cyprinus longzhouensis* (Yang and Hwang, 1982) ranged from 0% to 80% in the absence of different species (see figure 3.85). Among the 103 species of fish, 100 species were mutually beneficial to *Cyprinus longzhouensis.* There were 79 species that had more than a 10% effect on the niche of *Cyprinus*

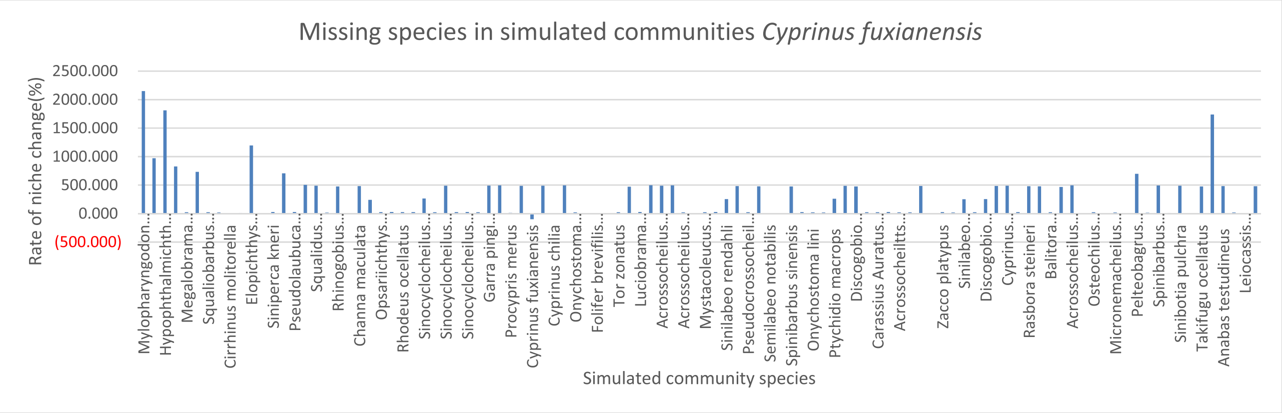

FIG. 3.81 – The responses of the niches of *Cyprinus fuxianensis* to various missing fish in the simulated community.

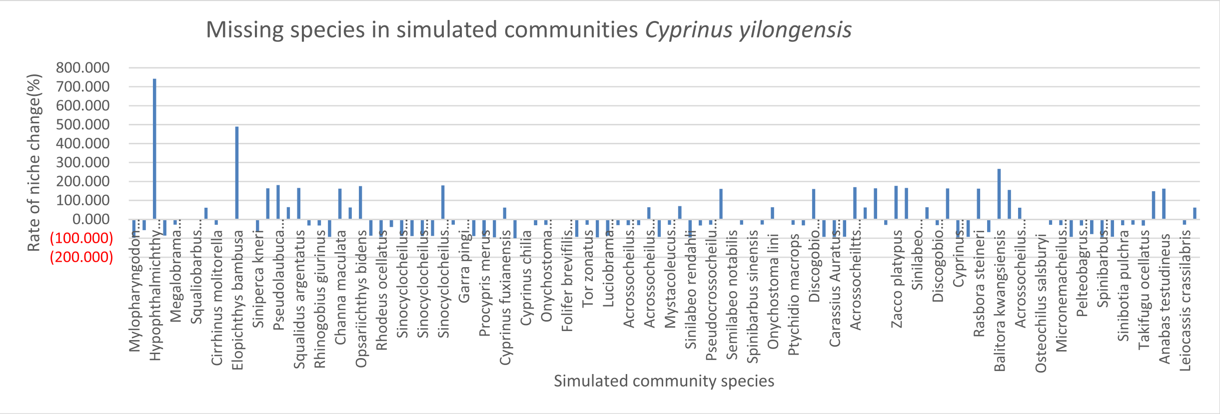

FIG. 3.82 – The responses of the niches of *Cyprinus yilongensis* to various missing fish in the simulated community.

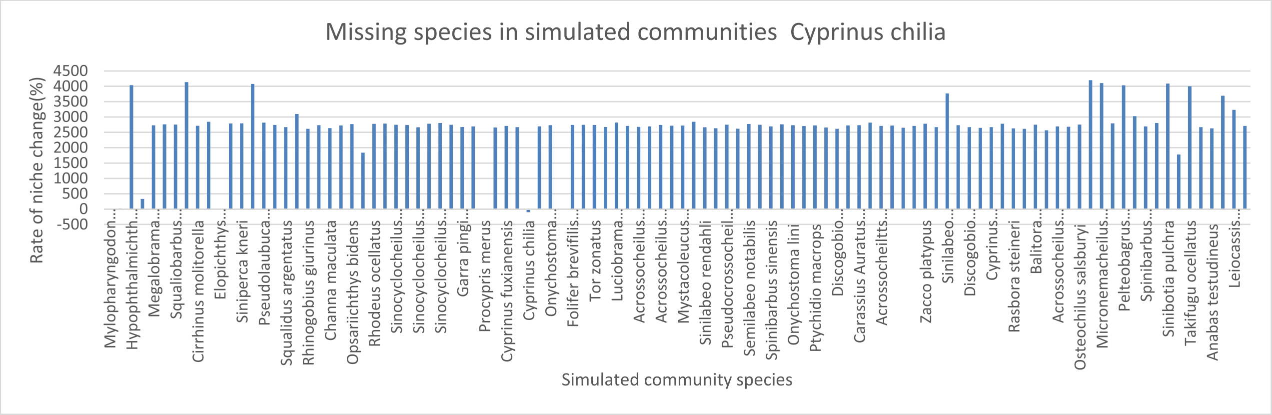

Fig. 3.83 – The responses of the niches of *Cyprinus chilia* to various missing fish in the simulated community.

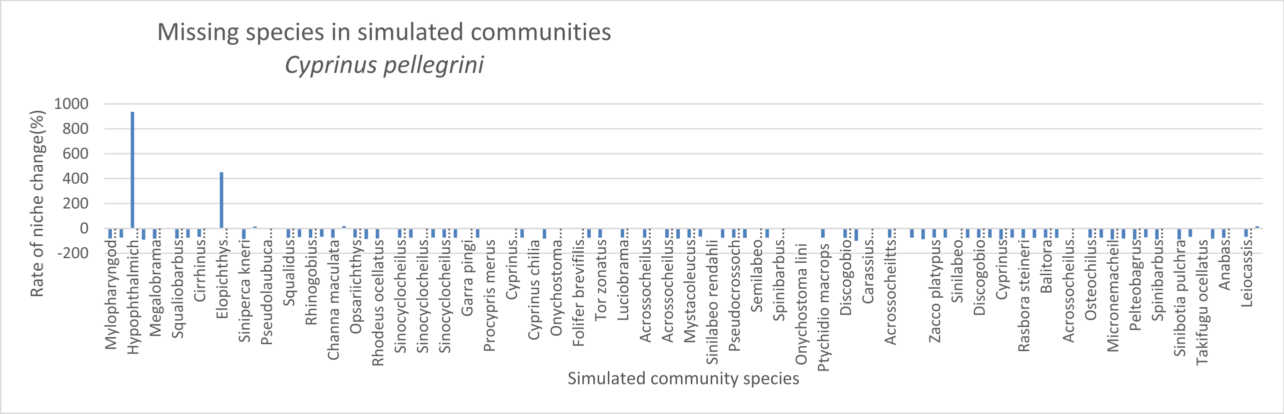

Fig. 3.84 – The responses of the niches of *Cyprinus pellegrini* to various missing fish in the simulated community.

longzhouensis. Of these, in which the largest effect was 80% by *Hypophthalmichthys molitrix*. There were 3 species of fish in competitive relationships with *Cyprinus longzhouensis*. No species that affected the niche of *Cyprinus longzhouensis* by more than 10%, with which the biggest effect was 1% by *Luciobrama macrocephalus*. An additional 24 species had less than a 10% effect on the rate of the niche variation of *Cyprinus longzhouensis*.

3.1.2.2.81 Carassius Auratus gibelio (Bloch, 1782)

The niche variation of *Carassius Auratus gibelio* (Bloch, 1782) ranged from 0% to 98% in the absence of different species (see figure 3.86). Among the 103 species of fish, 97 species were mutually beneficial to *Carassius Auratus gibelio*. There were 71 species that had more than a 10% effect on the niche of *Carassius Auratus gibelio*. Of these, in which the largest effect was 98% by *Hypophthalmichthys nobilis*. There were 6 species of fish in competitive relationships with *Carassius Auratus gibelio*. No species affected the niche of *Carassius Auratus gibelio* by more than 10%, with which the biggest effect was 2% by *Cyprinus carpio*. An additional 32 species had less than a 10% effect on the rate of the niche variation of *Carassius Auratus gibelio*.

3.1.2.2.82 Carassius auratus auratus (Linnaeus, 1758)

The niche variation of *Carassius auratus auratus* (Linnaeus, 1758) ranged from 0% to 300% in the absence of different species (see figure 3.87). Among the 103 species of fish, 57 species were mutually beneficial to *Carassius auratus auratus*. All of those species had more than a 10% effect on the niche of *Carassius auratus auratus*. Of these, in which the largest effect was 97% by *Misgurnus anguillicaudatus*. There were 46 species of fish in competitive relationships with *Carassius auratus auratus*. There were 44 species that affected the niche of *Carassius auratus auratus* by more than 10%, with which the biggest effect was 300% by *Ancherythroculter lini*. An additional 2 species had less than a 10% effect on the rate of the niche variation of *Carassius auratus auratus*.

3.1.2.2.83 Carassioides cantonensis (Heincke, 1892)

The niche variation of *Carassioides cantonensis* (Heincke, 1892) ranged from 0% to 2055% in the absence of different species (see figure 3.88). Among the 103 species of fish, 27 species were mutually beneficial to *Carassioides cantonensis*. There were 7 species that had near a 10% effect on the niche of *Carassioides cantonensis*. Of these, in which the largest effect was 10% by *Acrossocheiltts hemispinus hemispinus*. There were 76 species of fish in competitive relationships with *Carassioides cantonensis*. There were 61 species that affected the niche of *Carassioides cantonensis* by more than 10%, in which the biggest effect was 2055% by *Osteochilus salsburyi*. An additional 41 species had less than a 10% effect on the rate of the niche variation of *Carassioides cantonensis*.

3.1.2.2.84 Schizothorax meridionalis (Tsao, 1964)

The niche variation of *Schizothorax meridionalis* (Tsao, 1964) ranged from 0% to 2215% in the absence of different species (see figure 3.89). Among the 103 species of

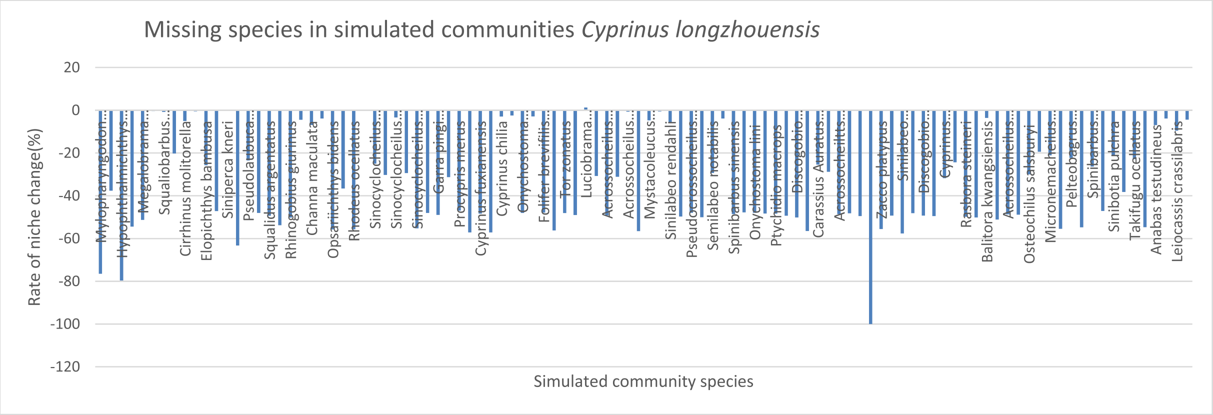

Fig. 3.85 – The responses of the niches of *Cyprinus longzhouensis* to various missing fish in the simulated community.

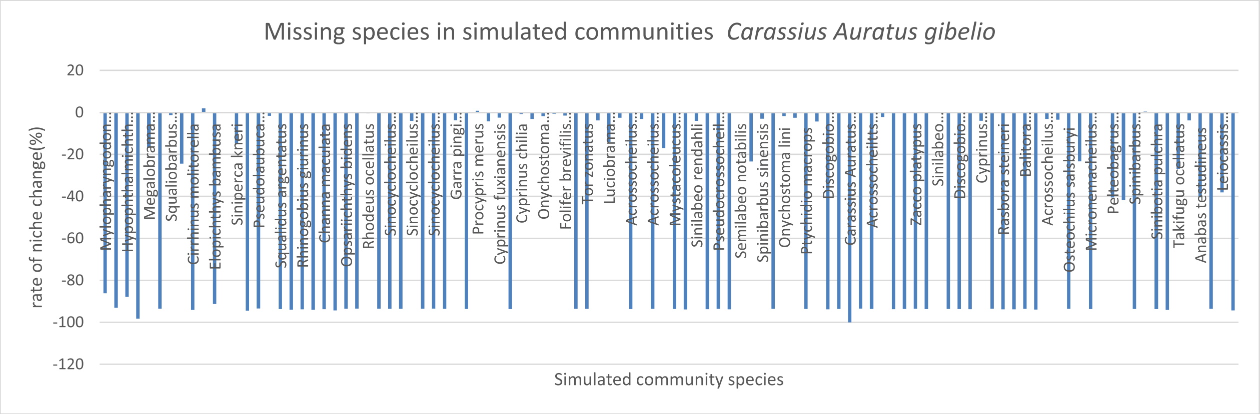

Fig. 3.86 – The responses of the niches of *Carassius Auratus gibelio* to various missing fish in the simulated community.

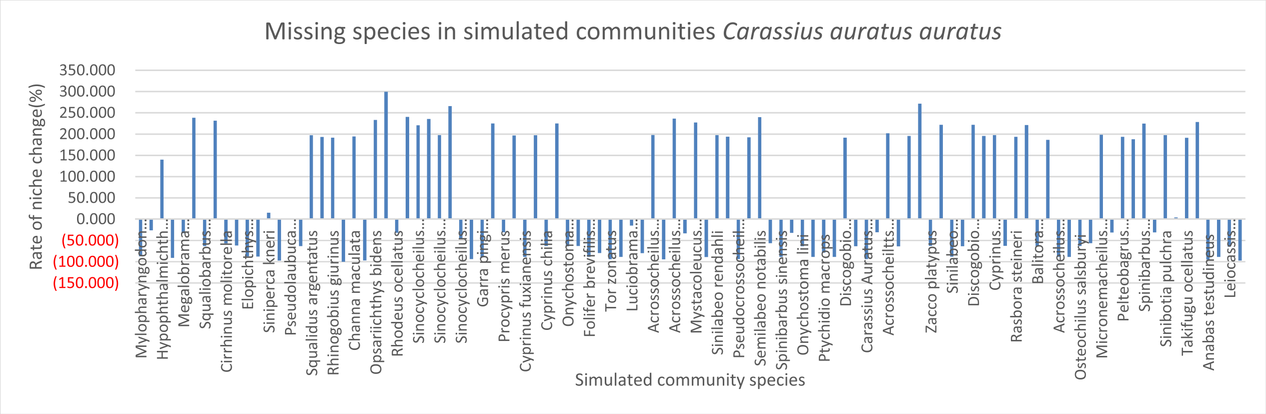

Fig. 3.87 – The responses of the niches of *Carassius auratus auratus* to various missing fish in the simulated community.

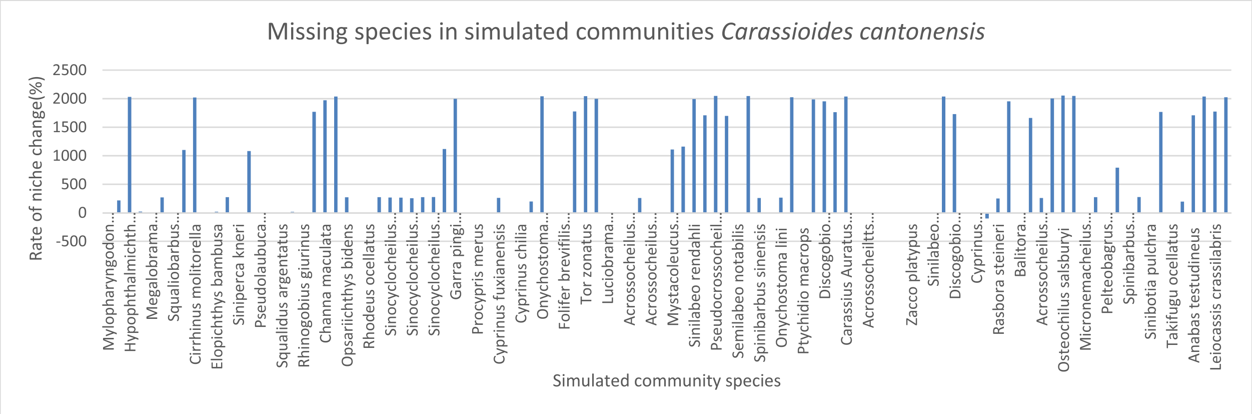

Fig. 3.88 – The responses of the niches of *Carassioides cantonensis* to various missing fish in the simulated community.

fish, 62 species were mutually beneficial to *Lcucosoma chinensis*. All those species had more than a 10% effect on the niche of *Lcucosoma chinensis*. Of these, in which the largest effect was 99% by *Mylopharyngodon piceus*. There were 41 species of fish in competitive relationships with *Lcucosoma chinensis*. There were 40 species that affected the niche of *Lcucosoma chinensis* by more than 10%, in which the biggest effect was 2215% by *Hypophthalmichthys nobilis*. An additional species had less than a 10% effect on the rate of the niche variation of *Lcucosoma chinensis*.

3.1.2.3 Balitora kwangsiensis (Fang, 1930)

The niche variation of *Balitora kwangsiensis* (Fang, 1930) ranged from 0% to 67% in the absence of different species (see figure 3.90). Among the 103 species of fish, 78 species were mutually beneficial to *Balitora kwangsiensis*. There were 49 species that had more than a 10% effect on the niche of *Balitora kwangsiensis*. Of these, in which the largest effect was 67% by *Ctenopharyngodon idella*. There were 25 species of fish in competitive relationships with *Balitora kwangsiensis*. All of those species affected the niche of *Balitora kwangsiensis* by less than 9%, and 9% by *Spinibarbus hollandi*. An additional 54 species had less than a 10% effect on the rate of the niche variation of *Balitora kwangsiensis*.

3.1.3 Siluriformes, Bagridae

3.1.3.1 Hemibagrus macropterus (Bleeker, 1870)

The niche variation of *Hemibagrus macropterus* (Bleeker, 1870) ranged from 0% to 105% in the absence of different species (see figure 3.91). Among the 103 species of fish, 64 species were mutually beneficial to *Hemibagrus macropterus*. There were 23 species that had more than a 10% effect on the niche of *Hemibagrus macropterus*. Of these, in which the largest effect was 20% by *Mylopharyngodon piceus*. There were 39 species of fish in competitive relationships with *Hemibagrus macropterus*. There were 30 species that affected the niche of *Hemibagrus macropterus* by more than 10%, with which the biggest effect was 105% by *Lateolabrax japonicus*. An additional 50 species had less than a 10% effect on the rate of the niche variation of *Hemibagrus macropterus*.

3.1.3.2 Hemibagrus guttatus (Lacepède, 1803)

The niche variation of *Hemibagrus guttatus* (Lacepède, 1803) ranged from 0% to 76% in the absence of different species (see figure 3.92). Among the 103 species of fish, 96 species were mutually beneficial to *Hemibagrus guttatus*. There were 9 species that had more than a 10% effect on the niche of *Hemibagrus guttatus*. Of these, in which the largest effect was 76% by *Hypophthalmichthys molitrix*. There were 7 species of fish in competitive relationships with *Hemibagrus guttatus*. All those species affected the niche of *Hemibagrus guttatus* by less than 10%, and *Hypophthalmichthys nobilis* was the biggest near 10% that affected *Hemibagrus*

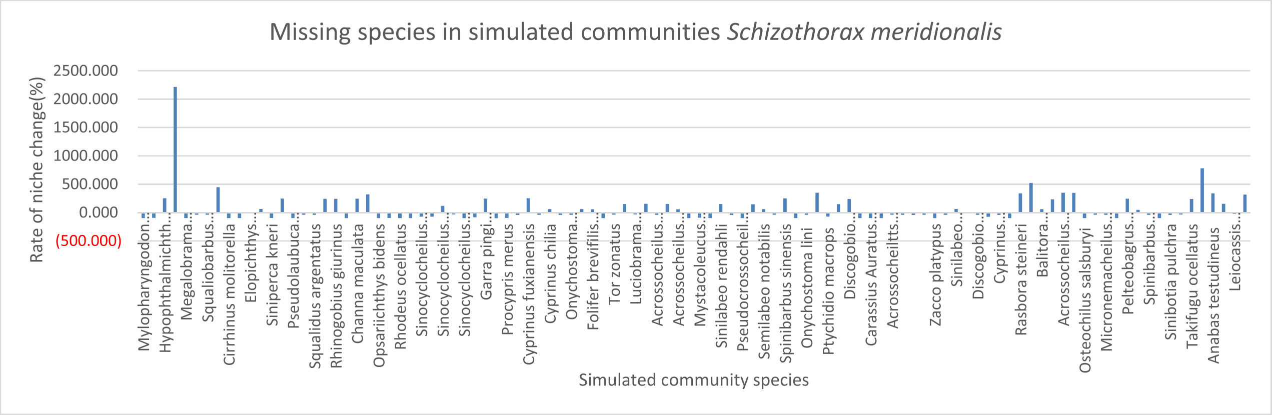

FIG. 3.89 – The responses of the niches of *Schizothorax meridionalis* to various missing fish in the simulated community.

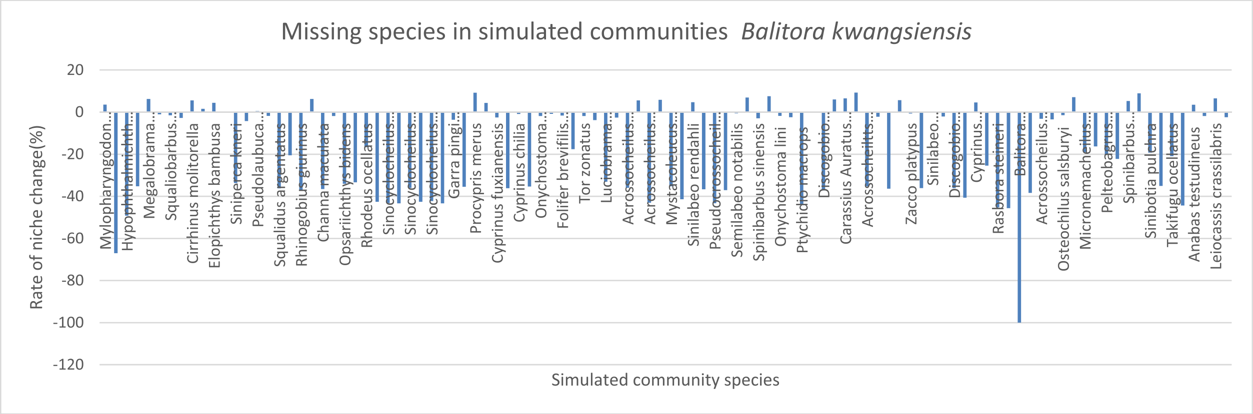

FIG. 3.90 – The responses of the niches of *Balitora kwangsiensis* to various missing fish in the simulated community.

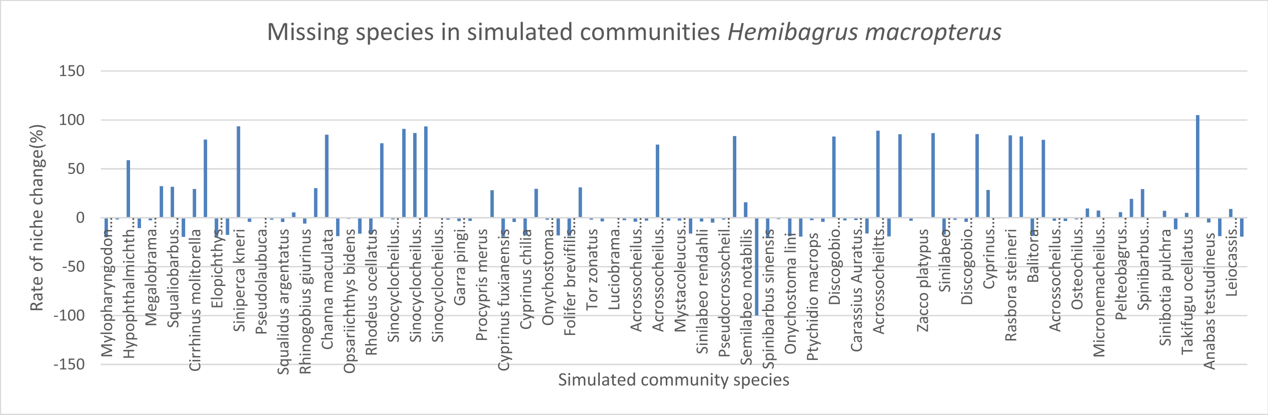

FIG. 3.91 – The responses of the niches of *Hemibagrus macropterus* to various missing fish in the simulated community.

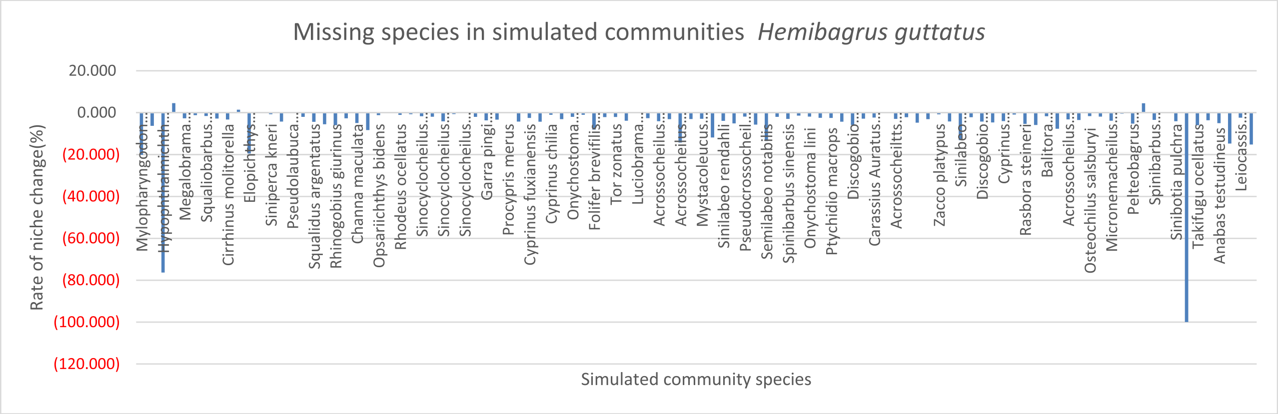

FIG. 3.92 – The responses of the niches of *Hemibagrus guttatus* to various missing fish in the simulated community.

guttatus. An additional 94 species had less than a 10% effect on the rate of the niche variation of *Hemibagrus guttatus*.

3.1.3.3 Tachysurus argentivittatus (Regan, 1905)

The niche variation of *Tachysurus argentivittatus* (Regan, 1905) ranged from 0% to 93% in the absence of different species (see figure 3.93). Among the 103 species of fish, 99 species were mutually beneficial to *Tachysurus argentivittatus*. There were 83 species that had more than a 10% effect on the niche of *Tachysurus argentivittatus*. Of these, in which the largest effect was 93% by *Hypophthalmichthys nobilis*. There were 4 species of fish in competitive relationships with *Tachysurus argentivittatus*. All those species that affected the niche of *Tachysurus argentivittatus* by less than 10%, and 2% of these were the biggest affected by *Cyprinus carpio*. An additional 20 species had less than a 10% effect on the rate of the niche variation of *Tachysurus argentivittatus*.

3.1.3.4 Leiocassis crassilabris (Günther, 1864)

The niche variation of *Leiocassis crassilabris* (Günther, 1864) ranged from 0% to 351% in the absence of different species (see figure 3.94). Among the 103 species of fish, 10 species were mutually beneficial to *Leiocassis crassilabris*. There were 2 species that had more than a 10% effect on the niche of *Leiocassis crassilabris*. Of these, in which the largest effect was 97% by *Hypophthalmichthys nobilis*. There were 93 species of fish in competitive relationships with *Leiocassis crassilabris*. There were 92 species that affected the niche of *Leiocassis crassilabris* by more than 10%, with which the biggest effect was 351% by *Acrossocheilus fasciatus*. An additional 9 species had less than a 10% effect on the rate of the niche variation of *Leiocassis crassilabris*.

3.1.3.5 Pelteobagrus vachellii (Richardson, 1846)

The niche variation of *Pelteobagrus vachellii* (Richardson, 1846) ranged from 0% to 44% in the absence of different species (see figure 3.95). Among the 103 species of fish, 96 species were mutually beneficial to *Pelteobagrus vachellii*. There were 14 species that had more than a 10% effect on the niche of *Pelteobagrus vachellii*. Of these, in which the largest effect was 33% by *Lateolabrax japonicus*. There were 7 species of fish in competitive relationships with *Pelteobagrus vachellii*. There were 4 species that affected the niche of *Pelteobagrus vachellii* by more than 10%, with which the biggest effect was 44% by *Hypophthalmichthys molitrix*. An additional 85 species had less than a 10% effect on the rate of the niche variation of *Pelteobagrus vachellii*.

3.1.3.6 Pelteobagrus intermedius (Nichols and Pope, 1927)

The niche variation of *Pelteobagrus intermedius* (Nichols and Pope, 1927) ranged from 0% to 103% in the absence of different species (see figure 3.96). Among the 103

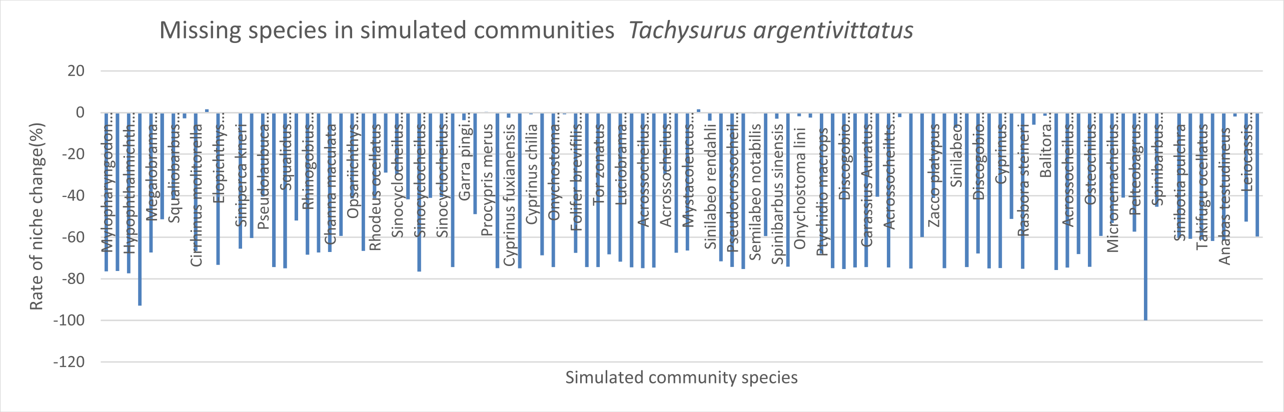

Fig. 3.93 – The responses of the niches of *Tachysurus argentivittatus* to various missing fish in the simulated community.

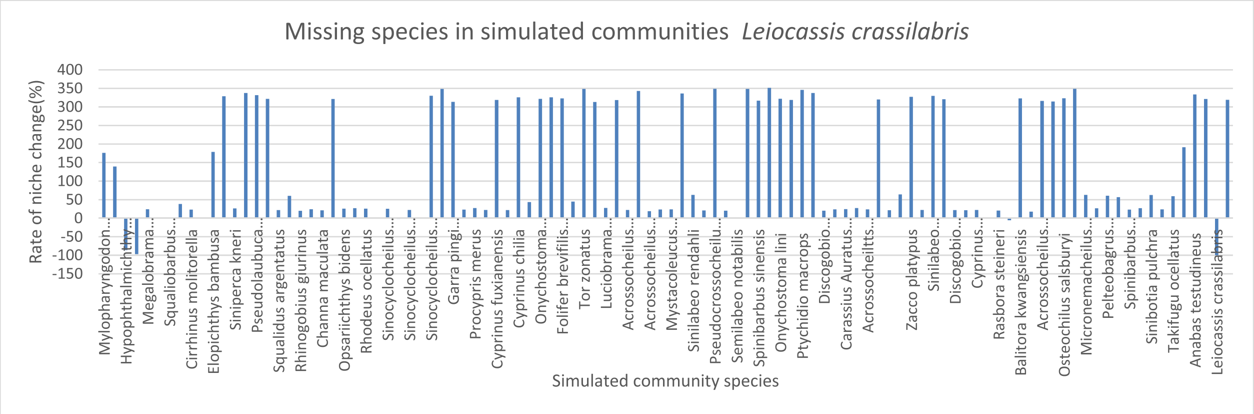

Fig. 3.94 – The responses of the niches of *Leiocassis crassilabris* to various missing fish in the simulated community.

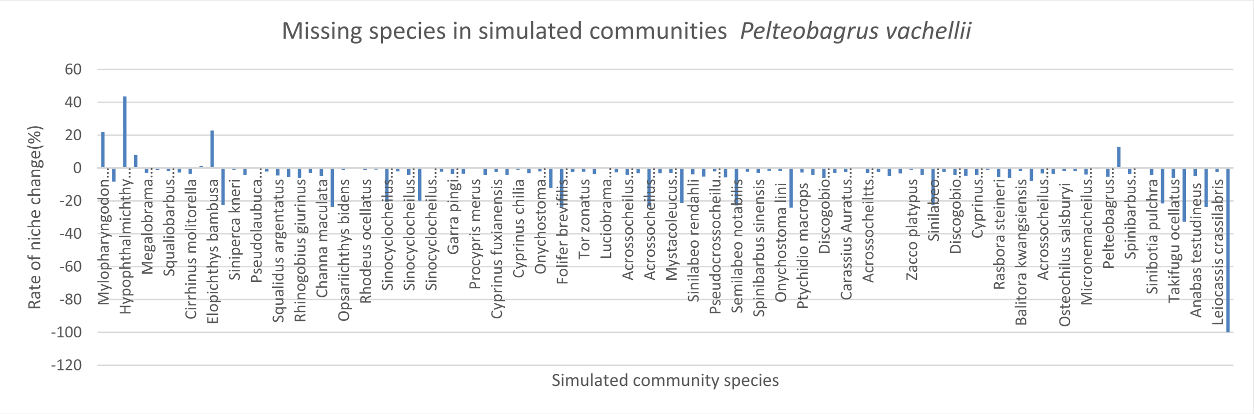

FIG. 3.95 – The responses of the niches of *Pelteobagrus vachellii* to various missing fish in the simulated community.

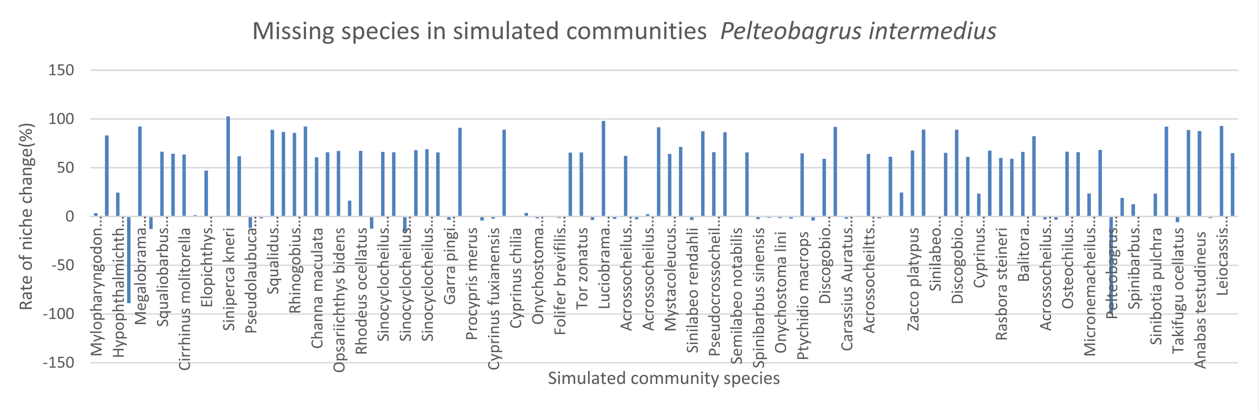

FIG. 3.96 – The responses of the niches of *Pelteobagrus intermedius* to various missing fish in the simulated community.

species of fish, 31 species were mutually beneficial to *Pelteobagrus intermedius*. There were 5 species that had more than a 10% effect on the niche of *Pelteobagrus intermedius*. Of these, in which the largest effect was 89% by *Hypophthalmichthys nobilis*. There were 72 species of fish in competitive relationships with *Pelteobagrus intermedius*. There were 65 species that affected the niche of *Pelteobagrus intermedius* by more than 10%, with which the biggest effect was 103% by *Siniperca kneri*. An additional 33 species had less than a 10% effect on the rate of the niche variation of *Pelteobagrus intermedius*.

3.1.3.7 Pelteobagrus fulvidraco (Richardson, 1846)

The niche variation of *Pelteobagrus fulvidraco* (Richardson, 1846) ranged from 0% to 35% in the absence of different species (see figure 3.97). Among the 103 species of fish, 95 species were mutually beneficial to *Pelteobagrus fulvidraco*. There were 15 species that had more than a 10% effect on the niche of *Pelteobagrus fulvidraco*. Of these, in which the largest effect was 35% by *Mylopharyngodon piceus*. There were 8 species of fish in competitive relationships with *Pelteobagrus fulvidraco*. There were 4 species that affected the niche of *Pelteobagrus fulvidraco* by more than 10%, with which the biggest effect was 22% by *Hypophthalmichthys nobilis*. An additional 80 species had less than a 10% effect on the rate of the niche variation of *Pelteobagrus fulvidraco*.

3.1.4 Perciformes

3.1.4.1 Lateolabrax japonicus (Cuvier, 1828)

The niche variation of *Lateolabrax japonicus* (Cuvier, 1828) ranged from 0% to 29% in the absence of different species (see figure 3.98). Among the 103 species of fish, 94 species were mutually beneficial to *Lateolabrax japonicus*. There were 8 species that had more than a 10% effect on the niche of *Lateolabrax japonicus*. Of these, in which the largest effect was 17% by *Pelteobagrus vachelli*. There were 9 species of fish in competitive relationships with *Lateolabrax japonicus*. There were 3 species that affected the niche of *Lateolabrax japonicus* by more than 10%, with which the biggest effect was 29% by *Hypophthalmichthys nobilis*. An additional 92 species had less than a 10% effect on the rate of the niche variation of *Lateolabrax japonicus*.

3.1.4.2 Anabas testudineus (Bloch, 1792)

The niche variation of *Anabas testudineus* (Bloch, 1792) ranged from 0% to 62% in the absence of different species (see figure 3.99). Among the 103 species of fish, 73 species were mutually beneficial to *Anabas testudineus*. There were 24 species that had more than a 10% effect on the niche of *Anabas testudineus*. Of these, in which the largest effect was 51% by *Hypophthalmichthys molitrix*. There were 30 species of fish in competitive relationships with *Anabas testudineus*. There were 25 species that affected the niche of *Anabas testudineus* by more than 10%, with which the biggest

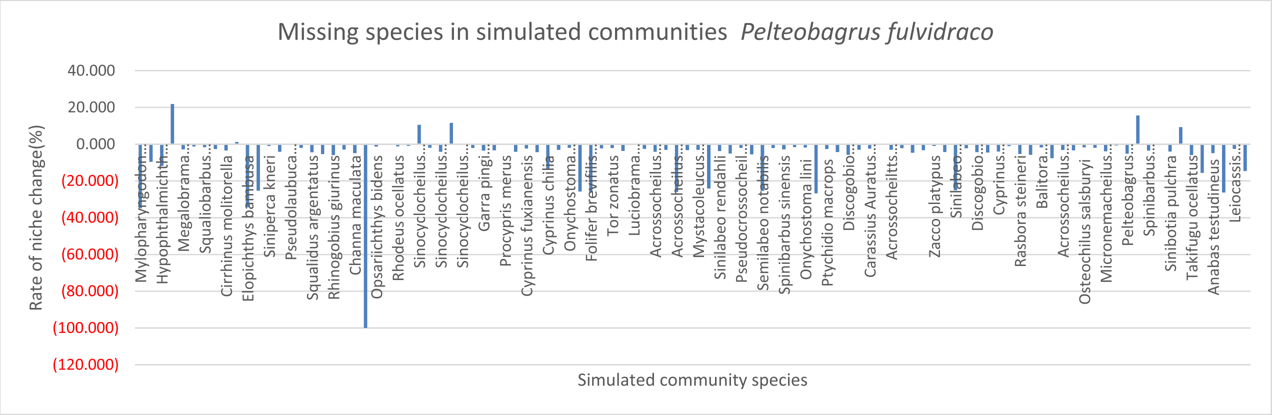

Fig. 3.97 – The responses of the niches of *Pelteobagrus fulvidraco* to various missing fish in the simulated community.

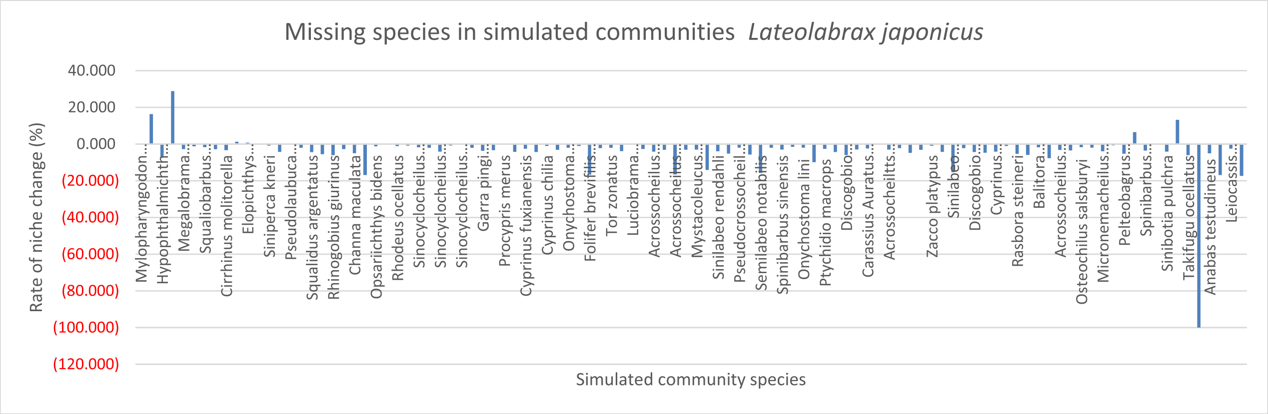

Fig. 3.98 – The responses of the niches of *Lateolabrax japonicus* to various missing fish in the simulated community.

effect was 62% by *Leiocassis crassilabris.* An additional 54 species had less than a 10% effect on the rate of the niche variation of *Anabas testudineus.*

3.1.4.3 Bostrichthys sinensis (Lacépède, 1801)

The niche variation of *Bostrichthys sinensis* (Lacépède, 1801) ranged from 0% to 186% in the absence of different species (see figure 3.100). Among the 103 species of fish, 76 species were mutually beneficial to *Bostrichthys sinensis.* There were 3 species that had more than a 10% effect on the niche of *Bostrichthys sinensis.* Of these, in which the largest effect was 90% by *Acrossocheilus clivosius.* There were 27 species of fish in competitive relationships with *Bostrichthys sinensis.* There were 17 species that affected the niche of *Bostrichthys sinensis* by more than 10%, with which the biggest effect was 186% by *Elopichthys bambusa.* An additional 23 species had less than a 10% effect on the rate of the niche variation of *Bostrichthys sinensis.*

3.1.4.4 Siniperca kneri (Garman, 1912)

The niche variation of *Siniperca kneri* (Garman, 1912) ranged from 0% to 109% in the absence of different species (see figure 3.101). Among the 103 species of fish, 65 species were mutually beneficial to *Siniperca kneri.* There were 19 species that had more than a 10% effect on the niche of *Siniperca kneri.* Of these, in which the largest effect was 35% by *Hypophthalmichthys molitrix.* There were 38 species of fish in competitive relationships with *Siniperca kneri.* There were 33 species that affected the niche of *Siniperca kneri* by more than 10%, in which the biggest effect was 109% by *Hypophthalmichthys nobilis.* An additional 51 species had less than a 10% effect on the rate of the niche variation of *Siniperca kneri.*

3.1.4.5 Channa maculata (Lacépède, 1801)

The niche variation of *Channa maculata* (Lacépède, 1801) ranged from 0% to 68% in the absence of different species (see figure 3.102). Among the 103 species of fish, 77 species were mutually beneficial to *Channa maculata.* There were 17 species that had more than a 10% effect on the niche of *Channa maculata.* Of these, in which the largest effect was 68% by *Hypophthalmichthys molitrix.* There were 26 species of fish in competitive relationships with *Channa maculata.* There were 23 species that affected the niche of *Channa maculata* by more than 10%, with which the biggest effect was 68% by *Sinocyclocheilus grahami tingi.* An additional 60 species had less than a 10% effect on the rate of the niche variation of *Channa maculata.*

3.1.4.6 Rhinogobius giurinus (Rutter, 1897)

The niche variation of *Rhinogobius giurinus* (Rutter, 1897) ranged from 0% to 178% in the absence of different species (see figure 3.103). Among the 103 species of fish, 25 species were mutually beneficial to *Rhinogobius giurinus.* There were 3 species that had more than a 10% effect on the niche of *Rhinogobius giurinus.* Of these, in which the largest effect was 17% by *Mylopharyngodon piceus.* There were 78 species

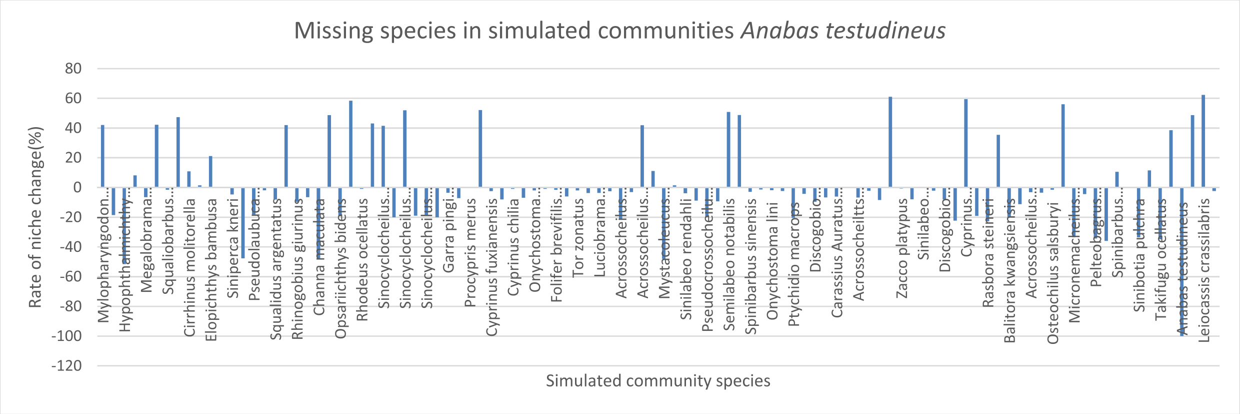

FIG. 3.99 – The responses of the niches of *Anabas testudineus* to various missing fish in the simulated community.

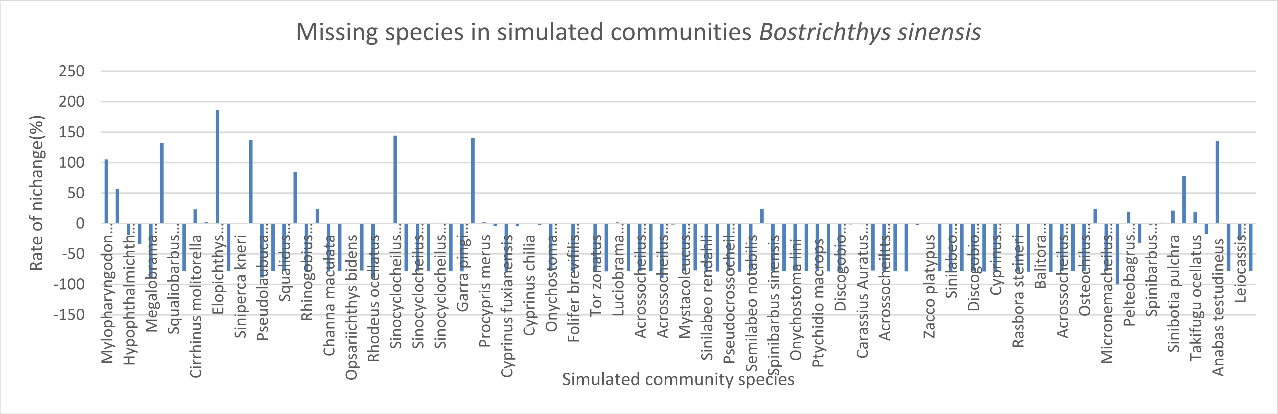

FIG. 3.100 – The responses of the niches of *Bostrichthys sinensis* to various missing fish in the simulated community.

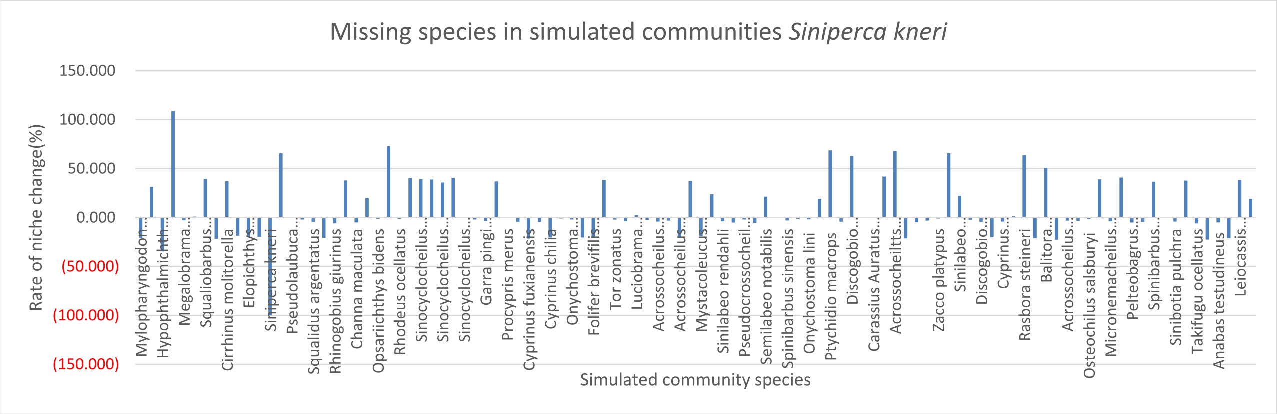

FIG. 3.101 – The responses of the niches of *Siniperca kneri* to various missing fish in the simulated community.

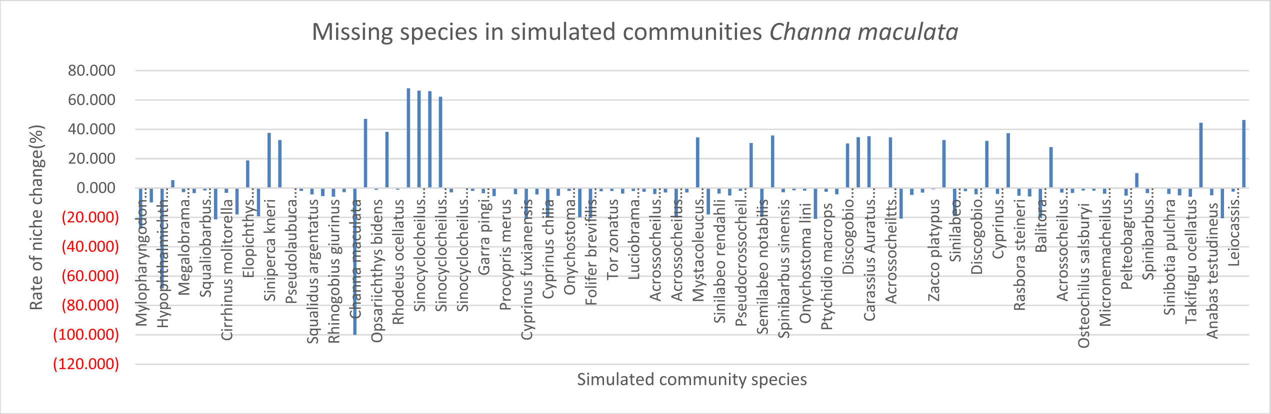

FIG. 3.102 – The responses of the niches of *Channa maculata* to various missing fish in the simulated community.

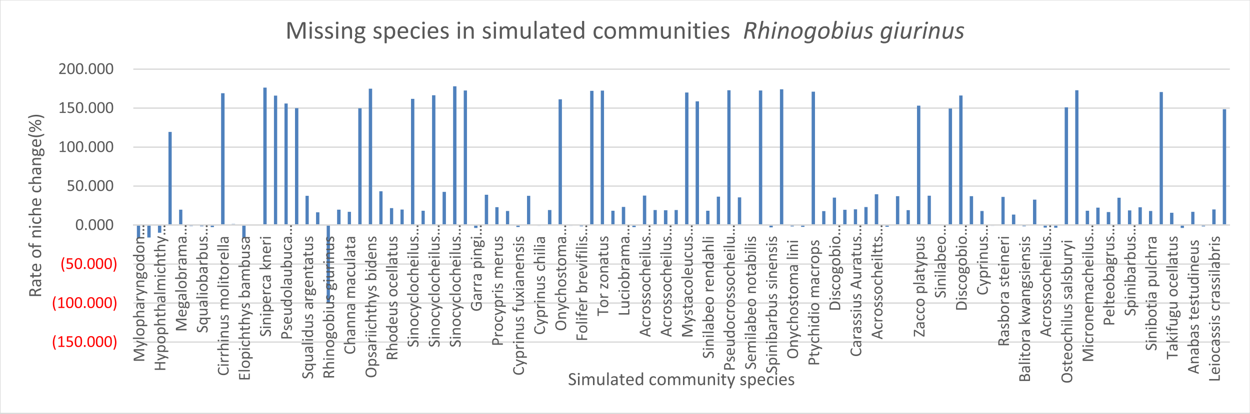

Fig. 3.103 – The responses of the niches of *Rhinogobius giurinus* to various missing fish in the simulated community.

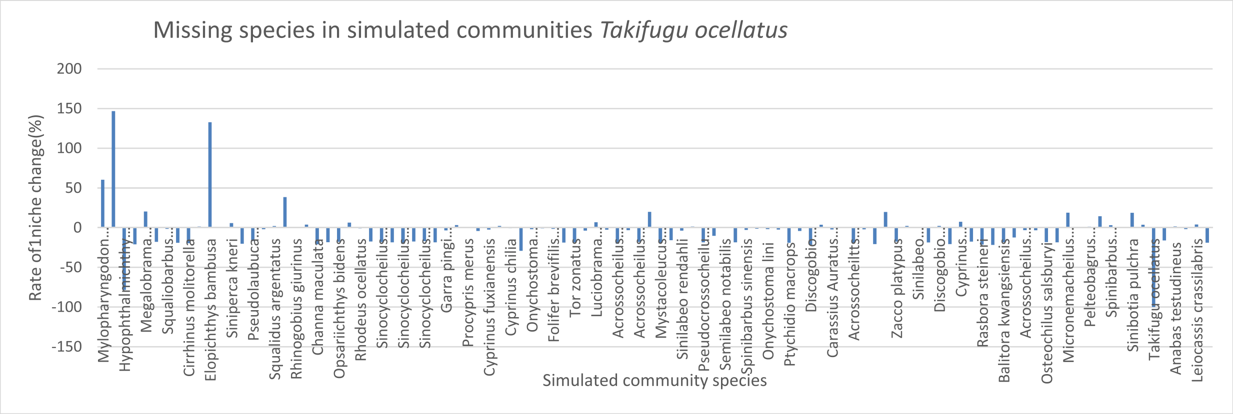

Fig. 3.104 – The responses of the niches of *Takifugu ocellatus* to various missing fish in the simulated community.

of fish in competitive relationships with *Rhinogobius giurinus*. There were 76 species that affected the niche of *Rhinogobius giurinus* by more than 10%, with which the biggest effect was 178% by *Sinocyclocheilus microphthalmus*. An additional 24 species had less than a 10% effect on the rate of the niche variation of *Rhinogobius giurinus*.

3.1.5 Tetraodontiformes

3.1.5.1 Takifugu ocellatus (Linnaeus, 1758)

The niche variation of *Takifugu ocellatus* (Linnaeus, 1758) ranged from 0% to 147% in the absence of different species (see figure 3.104). Among the 103 species of fish, 71 species were mutually beneficial to *Takifugu ocellatus*. There were 43 species that had more than a 10% effect on the niche of *Takifugu ocellatus*. Of these, in which the largest effect was 78% by *Hypophthalmichthys molitrix*. There were 60 species of fish in competitive relationships with *Takifugu ocellatus*. There were 10 species that affected the niche of *Takifugu ocellatus* by more than 10%, with which the biggest effect was 147% by *Ctenopharyngodon idella*. An additional 46 species had less than a 10% effect on the rate of the niche variation of *Takifugu ocellatus*.

3.2 Simulated Community

3.2.1 Niche Composition

The simulated community was composed of 104 species of fish that were distributed at 100% niche accumulation. The maximum niche was 10.647% for *Hypophthalmichthys molitrix*, while the minimum niche was 0.007% for *Sinocyclocheilus yangzongensis*. Across all fish, the numeric value of the middle bit of an ordered sort was 0.9615%. In total, 41 species were above the median, occupying 73.807% of the total niche, while 22 species occupied less than 10% of the median, accounting for 1.102% of the niche (see table 3.1).

Of the fish species occupying 74% of the niche, 33 (occupying 58% of the niche) are common species in the main stem and tributaries of the Pearl River, with the exception of *Luciocyprinus langsoni*, *Elopichthys bambusa*, *Sinocyclocheilus microphthalmus*, *Balitora kwangsiensis*, *Tor sinensis*, *Garra pingi yiliangensis*, *Cyprinus longzhouensis*, *Sinocyclocheilus grahami tingi*, and *Procypris merus*. Most of the remaining fish, accounting for 13.9% of the niche, were also common species, such as *Siniperca kneri*, *Ptychidio jordani*, *Ptychidio macrops*, *Rhodeus ocellatus*, *Onychostoma sima*, *Squaliobarbus curriculus*, *Osteochilus salsburyi*, *Pelteobagrus vachellii*, *Sinibotia pulchra*, *Rhinogobius giurinus*, *Ancherythroculter lini*, *Takifugu ocellatus*, *Hemiculter leucisculus*, *Pelteobagrus fulvidraco*, *Leiocassis crassilabris*, *Pelteobagrus intermedius*, *Carassius auratus auratus*, *Bostrichthys sinensis*, *Cirrhinus molitorella*, *Xenocypris argentea*, *Garra pingi pingi*, *Parasinilabeo*

Tab. 3.1 – The niches of the 104 fish species in the simulated community.

Niche greater than median		Niche less than the median			
		Niche less than median/greater than 10% of the median		Niche less than 10% of the median	
Fish	Niche (%)	Fish	Niche (%)	Fish	Niche (%)
Hypophthalmichthys molitrix	10.647	*Siniperca kneri*	0.954	*Schizothorax meridionalis*	0.093
Hypophthalmichthys nobilis	3.551	*Ptychidio jordani*	0.932	*Xenocypris argentea*	0.083
Opsariichthys bidens	2.664	*Ptychidio macrops*	0.912	*Garra pingi pingi*	0.080
Tachysurus argentivittatus	2.530	*Rhodeus ocellatus*	0.911	*Parasinilabeo assimilisParasinilabeo assimilis*	0.080
Luciocyprinus langsoni	2.381	*Onychostoma sima*	0.877	*Acrossocheilus beijiangensis*	0.078
Puntius semifasciolatus	2.232	*Squaliobarbus curriculus*	0.874	*Onychostoma barbatulum*	0.070
Sinocyclocheilus microphthalmus	2.178	*Cyprinus rabaudi*	0.858	*Carassioides cantonensis*	0.068
Balitora kwangsiensis	2.077	*Osteochilus salsburyi*	0.841	*Sinocyclocheilus anophthalmus*	0.065
Tor sinensis	2.061	*Pelteobagrus vachellii*	0.840	*Luciobrama macrocephalus*	0.062
Spinibarbus denticulatus denticulatus	1.943	*Mystacoleucus marginatus*	0.821	*Pseudogyrinocheilus prochilus*	0.062
Garra pingi yiliangensis	1.926	*Discogobiolongibarbatus*	0.821	*Tor zonatus*	0.053
Lcucosoma chinensis	1.844	*Sinibotia pulchra*	0.818	*Onychostoma lini*	0.045
Mylopharyngodon piceus	1.790	*Rhinogobius giurinus*	0.809	*Sinilabeo rendahli*	0.045
Acrossocheilus iridescens iridescens	1.773	*Ancherythroculter lini*	0.800	*Cyprinus fuxianensis*	0.038
Cyprinus longzhouensis	1.726	*Takifugu ocellatus*	0.789	*Sinocyclocheilus macrolepis*	0.037
Sinocyclocheilus grahami tingi	1.662	*Hemiculter leucisculus*	0.786	*Garra orientalis*	0.031
Procypris merus	1.656	*Pelteobagrus fulvidraco*	0.746	*Sinilabeo discognathoides*	0.024
Parabramis pekinensis	1.560	*Discocheilus wui*	0.741	*Acrossocheilus clivosius*	0.022
Elopichthys bambusa	1.513	*Rasborinus lineatus*	0.716	*Onychostoma ovalis rhomboides*	0.021

Tab. 3.1 – (continued).

Niche greater than median		Niche less than the median			
		Niche less than median/greater than 10% of the median		Niche less than 10% of the median	
Fish	Niche (%)	Fish	Niche (%)	Fish	Niche (%)
Acrossocheilus paradoxus	1.500	*Garra pingi hainanensis*	0.714	*Rectoris posehensis*	0.019
Cyprinus carpio	1.444	*Leiocassis crassilabris*	0.681	*Cyprinus chilia*	0.019
Rasbora steineri	1.439	*Pelteobagrus intermedius*	0.655	*Sinocyclocheilus yangzongensis*	0.007
Hemibagrus guttatus	1.430	*Cyprinus multitaeniata*	0.619		
Squalidus argentatus	1.406	*Carassius auratus auratus*	0.594		
Ctenopharyngodon idella	1.346	*Sinocyclocheilus macrocephalus*	0.589		
Anabas testudineus	1.282	*Semilabeo obscurus*	0.545		
Carassius Auratus gibelio	1.245	*Bangana decora*	0.544		
Micronemacheilus pulcher	1.244	*Discogobio brachyphysallidos*	0.460		
Lateolabrax japonicus	1.225	*Folifer brevifilis brevifilis*	0.445		
Zacco platypus	1.149	*Ochetobius elongatus*	0.415		
Acrossocheilus fasciatus	1.120	*Discogobio tetrabarbatus*	0.379		
Spinibarbus sinensis	1.098	*Acrossocheilus labiatus*	0.373		
Hemibagrus macropterus	1.075	*Bostrichthys sinensis*	0.354		
Misgurnus anguillicaudatus	1.060	*Onychostoma macrolepis*	0.338		
Semilabeo notabilis	1.053	*Cirrhinus molitorella*	0.327		
Megalobrama skolkovii	1.045	*Pseudocrossocheilus bamaensis*	0.302		
Pseudolaubuca sinensis	1.045	*Acheilognathus tonkinensis*	0.242		
Acrossocheiltts hemispinus hemispinus	0.977	*Cyprinus pellegrini*	0.209		

Tab. 3.1 – (continued).

Channa maculata	0.975	*Cyprinus yilongensis*	0.197		
Spinibarbus hollandi	0.969	*Acrossocheiltts elongatus*	0.155		
Leptobotia pellegrini	0.965	*Sinilabeo discognathoides wui*	0.106		
Niche subtotal%	73.807		25.090		1.1025

assimilis, and *Sinilabeo rendahli*. The linear river has a large geographical span, and the environmental difference among regions is great. We are puzzled by the fish species that were identified as the objects of the community study model, what ecological problems the results of the study represent, and the "boundary" problem of the model.

In total, 55 species are recorded as the main fishing targets (dominant species) in the Pearl River (Pearl River Fishery Resources Survey Commission, 1985). The total niche value of these fish was about 72%, and they also accounted for more than two-thirds of the ecological niche. Thus, to some extent, the model reflects the overall niche information for the dominant and non-dominant species in the community. Of the 104 species of fish in the simulated community, the main species of fish in the Pearl River were taken as the research object. The research results obtained from our model can be "mutually verified" with the fragmented data from historical records.

3.2.2 Niche Change

There are 104 species of fish in the community. In each analysis, one fish was removed, and the model analysis maintained 103 fish species. A total of 104 "communities" were analyzed, with one fish species missing from each "community." The median value of the average change rate in the niche of a given species during this cycle was 198%, and species with higher than median values accounted for 17.3%. The loss of these species caused a great change in community structure. Thus, in a sense, the niche of these types of fish in the simulated community was irreplaceable; that is, it was difficult for other fish to fill the niche of these particular species. Species below the median accounted for 83% of all species. Species with niches affected less than 50% by fish removal accounted for 61% of all species (see figure 3.105).

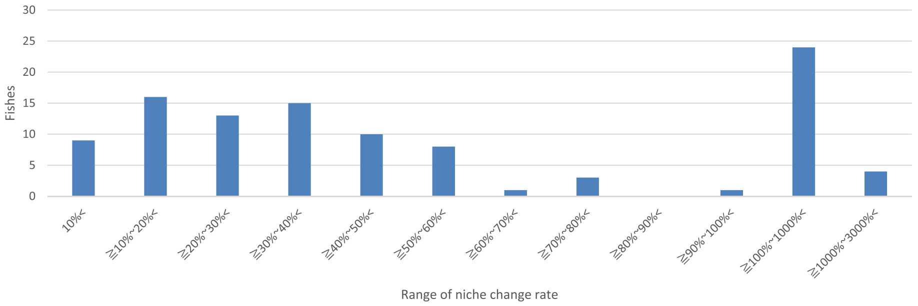

Fig. 3.105 – Distributions of species in the simulated community that affect niche change rate.

3.2.2.1 Niche Increase

A total of 26 fish species (see table 3.2) were included in the "primary community" of the 104 fish species, with each fish removed increasing the niche by more than 10%. Species 1–9 were mainly upriver species, which naturally became the "central community" of the upriver region in the model analysis. The species sensitive to niche increase (*i.e.*, an occurrence rate >5%) were *Leiocassis crassilabris* and *Cyprinus multitaeniata*. Species 10–26 were mainly distributed in the middle and lower river reaches and naturally became the "central community" of the middle and lower reaches in the model analysis. These niche-sensitive species included *Mylopharyngodon piceus*, *Ctenopharyngodon idella*, *Hypophthalmichthys nobilis*, *Squalidus argentatus*, *Hypophthalmichthys molitrix*, and *Rhinogobius giurinus* (table 3.1). The largest niche increase was in *Rhodeus ocellatus*, which increased by 51% due to *Ancherythroculter lini* removal; the next largest increase was in *Mylopharyngodon piceus*, which increased by 43% due to *Xenocypris argentea* removal.

Tab. 3.2 – Species with more than 10% niche increase.

No	Fish	Frequency of occurrence	Occurrence rate (%)
1	*Leiocassis crassilabris*	32	16.2
2	*Cyprinus multitaeniata*	30	15.2
3	*Sinocyclocheilus macrolepis*	8	4.0
4	*Sinocyclocheilus macrocephalus*	2	1.0
5	*Sinilabeo rendahli*	2	1.0
6	*Carassioides cantonensis*	2	1.0
7	*Onychostoma barbatulum*	1	0.5
8	*Rasborinus lineatus*	1	0.5
9	*Zacco platypus*	1	0.5
10	*Mylopharyngodon piceus*	24	12.1
11	*Ctenopharyngodon idella*	15	7.6
12	*Hypophthalmichthys nobilis*	14	7.1
13	*Squalidus argentatus*	12	6.1
14	*Hypophthalmichthys molitrix*	10	5.1
15	*Rhinogobius giurinus*	10	5.1
16	*Ochetobius elongatus*	9	4.5
17	*Carassius auratus auratus*	6	3.0
18	*Garra orientalis*	5	2.5
19	*Squaliobarbus curriculus*	4	2.0
20	*Xenocypris argentea*	2	1.0
21	*Elopichthys bambusa*	2	1.0
22	*Rhodeus ocellatus*	2	1.0
23	*Ptychidio jordani*	1	0.5
24	*Spinibarbus hollandi*	1	0.5
25	*Ptychidio macrops*	1	0.5
26	*Hemiculter leucisculus*	1	0.5
	Total	198	100

3.2.2.2 Niche Reduction

A total of 24 fish species were included in the "primary community" of the 104 fish species, with each fish removed reducing the niche by more than 10%. Among them, species 1–6 were mainly upstream species and naturally became the "central community" in the model analysis. The species sensitive to niche reduction (*i.e.*, with an occurrence rate is >5%) were *Garra pingi yiliangensis*, *Luciocyprinus langsoni*, *Elopichthys bambusa*, and *Sinocyclocheilus microphthalmus*. Species 7–24 were mainly distributed in the middle and lower reaches of the river and naturally became the "central community" in the middle and lower reaches of the river. These species included *Opsariichthys bidens*, *Tachysurus argentivittatus*, and *Carassius auratus auratus*. The largest decrease was in *Ancherythroculter lini*, which was an 87% decrease in response to the loss of *Squaliobarbus curriculus*. The next largest decrease (81%) was in *Siniperca kneri* due to *Carassius auratus auratus* loss (see table 3.3).

Tab. 3.3 – Species with greater than 10% niche reductions.

No	Fish	Frequency of occurrence	Occurrence rate (%)
1	*Garra pingi yiliangensis*	23	13.0
2	*Luciocyprinus langsoni*	14	7.9
3	*Sinocyclocheilus microphthalmus*	10	5.6
4	*Procypris merus*	6	3.4
5	*Cyprinus longzhouensis*	4	2.3
6	*Discocheilus wui*	1	0.6
7	*Opsariichthys bidens*	42	23.7
8	*Tachysurus argentivittatus*	21	11.9
9	*Carassius auratus auratus*	16	9.0
10	*Ochetobius elongatus*	8	4.5
11	*Ancherythroculter lini*	7	4.0
12	*Hypophthalmichthys molitrix*	4	2.3
13	*Osteochilus salsburyi*	3	1.7
14	*Hypophthalmichthys nobilis*	3	1.7
15	*Pseudolaubuca sinensis*	3	1.7
16	*Siniperca kneri Garman*	2	1.1
17	*Ctenopharyngodon idella*	2	1.1
18	*Cyprinus carpio*	2	1.1
19	*Rhinogobius giurinus*	1	0.6
20	*Xenocypris argentea*	1	0.6
21	*Channa maculata*	1	0.6
22	*Pelteobagrus fulvidraco*	1	0.6
23	*Misgurnus anguillicaudatus*	1	0.6
24	*Hemiculter leucisculus*	1	0.6
	Total	177	100

3.2.2.3 Niche Response Type

In a community consisting of species A, B, C, D, and E, the relationship between A and B is defined as competition if the absence of A results in the increase of B. If the absence of A results in the decrease of C, the relationship between A and C is defined as mutually beneficial. If the absence of A does not cause a change in D, then the relationship between A and D is defined as non-competitive. The responses of 103 fish species were analyzed in response to the absence of each of the 104 species of fish. If most of the other 103 species increased or decreased less than 10% in response to the absence of the removed species, the relationship between the removed species and the other species in the community was considered non-competitive. Across the 104 species, we identified 26 competitive species, 36 mutually beneficial species, and 42 intermediate species. Some fish in the same genus (*e.g.*, *Acrossocheilus* and *Cyprinus*) were grouped in the same category, reflecting the complex relationships among communities. Interspecific relationships among communities reflect the unity of competitive constraints and mutual benefits, and mutually beneficial fish may be better able to coexist with other fish.

Chapter 4

Relationship Between Community Niche and Succession

The stability of biodiversity and community structure results from the interaction between the environment and the organism, and the interactions between organisms and the environment, as well as among organisms, are balanced over large temporal scales. Therefore, changes in the environment of a region inevitably rebalance community composition and the environment. The time required to achieve equilibrium and reconstitute the community corresponds to the time required for certain species to die out or for populations to change, as well as that required for new species to emerge (Bertness and Leonard, 1997). River ecosystems are banded, with large geographic spans and large vertical environmental variability; due to the small range of cross-sectional observations, it is difficult both to characterize the full range of river features and to study biological communities (Kareiva and Washington, 1995). The biodiversity in a given community is influenced by the spatial scale, and larger spatial scales include greater levels of environmental heterogeneity (Cavender-Bares j *et al.*). Therefore, it is necessary to consider the boundaries of the biological community (Swenson *et al.*, 2006) in niche studies. The species chosen by the researchers can delineate the species boundaries of the community or can determine the geographical boundaries of species distributions. It is necessary to compare types of community composition at different geographic and taxonomic scales to reveal the mechanisms underlying the relationships between species and the environment in a heterogeneous habitat. Fausch *et al.* (2002) proposed the concept of an ovipositing field and a fattening field, but it was unclear how to determine the ovipositing field and fattening field as a research unit. We believe that the drift range from spawning ground to fattening ground as a spatial boundary is a solution to the problem. Because research goals differ, the data collection objects also vary. In this book, we generally continue to use the geographical names of simple habits to divide the geographic ranges of fish communities (some artificial river dams divide the areas), combining the distance between spawning grounds and the natural drift by an early fish resource at the river as an ecological unit for study. We also determined the “geographical boundary” using a “random” selection of species. Then, cross-analyses at different levels were performed to better understand the

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classifications and ecological characteristics of ecological communities, to study the mechanism of species coexistence and diversity, and to determine the common characteristics and mechanisms that maintain species diversity.

Species diversity and species richness are related to the niche, and the niche includes the competition and mutual benefits among species in the community. Niche is not a simple biological species structure, and community species composition is a product of the dynamic adaptation of species to environmental change (YosiakiItô *et al.*, 1981). The biome is the main body of the ecosystem and is in relative equilibrium among species and with the environment; the biome has stable characteristics and can maintain dynamic stability despite small disturbances (Yodzis, 1981). The biological community can resist disturbance and adapt to environmental change. Species composition, including interspecies relationships, is the basis of ecosystem stability.

Both species and biological traits are influenced by the environment, and habitat and niche differentiation together shape the patterns of species coexistence in the community (Kraft and Ackerly, 2010). Species distributions have geographical boundaries, and species composition has regional distribution characteristics, reflecting the constraints of environmental boundary factors (Convertino 2011; Glor and Warren, 2011). Environmental and spatial characteristics influence species distribution patterns (Henriques-Silva *et al.*, 2013), indicating that the characteristics of species communities can also reflect environmental characteristics. For example, fish with suckers on the abdomen must inhabit alpine and canyon rivers. The number of species in a community is related to the size of the geographical range, and there is a positive correlation between the size of the range and species abundance (Otso Ovaskainen *et al.*, 2016). At a regional scale, more species in the community imply higher biomass abundance and a larger adaptive space, while fewer species imply lower biomass abundance and a smaller adaptive space. With the exception of isolated island biotas, the persistent negative relationship found on Indo–Pacific islands represents a significant departure from the accepted positive relationship between range size and abundance (Reeve *et al.*, 2016). The mechanisms of community species construction are a focus of ecological research, and the ability to derive community characteristics from taxonomic characteristics is critical for an understanding of ecosystem evolution and community species construction. Morphological data are included in the process of community change (Erös *et al.*, 2012).

In this chapter, the relationships leading to species change described in the previous chapter were analyzed with respect to species succession. The niche formation of the "subunit community" was analyzed using the model, and the influences of interspecific morphological factors on the niche were explored. It should be noted that no specific data on the communities and ecological niche occupancy of the 104 species of fish from the Pearl River system, which represent 56 fish genera, are available due to a lack of historic data.

The "subunit community" mainly included the dominant species in the middle and lower reaches of the Pearl River. From 104 primitive communities to 25 fish "subunit communities," the total niche of four big fish reached more than 40%, and the catch of these four fish in the Pearl River System in the 1980s accounted for about 40% of the total catch, or about 50%–60% of the samples of the four major species collected (The fishery resources survey and compilation committee of the Pearl River System, 1985). It was thus difficult to use "standard" data to measure changes in community niches. The "fish community morphological model" can be used to calculate the "spatial niche" proportion of various species in the simulated community, and the data seem to reflect the data for certain historical periods (or specific spatiotemporal ranges). For example, the results for the four big fish seem to be close to the historical data (*i.e.*, "the four big fish represented about 40% of total catch or about 50%–60% of the early resource samples"). From 2016 to 2018, our laboratory estimated that the catch of the four big fish in the Pearl River at Guangdong and Guangxi was about 10%. As a "standard" measure, the results of the model showed that the actual fish community was disturbed. Interestingly, the model results might thus reflect a decline in the function of the Pearl River ecosystem from 50% to 10% in recent decades. This type of result exemplifies the goals of the model construction.

4.1 Characteristics of Community Stability

In communities, species coexistence depends on mechanisms of equilibrium and stability. Stability mechanisms are essential for species coexistence and include resource allocation, and predation, as well as other mechanisms that depend on spatial and temporal environmental factors that change with population density fluctuations. Equilibrium mechanisms reduce large disparities in fitness to stabilize species coexistence and diversity. One of the key aims of community research is to quantify niche relationships among species. Community construction methods must consider the ways in which species interconnect in localized communities, including the effects of species, populations, patchiness, and other ecological spatial relationships (Leibold *et al.*, 2004). The analysis of community succession using morphological models may provide insights into interspecific species associations based on specialized morphological information.

Based on the fish community morphological model, the fish niche succession model was used to simulate the "primitive community" composed of 56 genera and 104 species of fish in the Pearl River system. The modeling result showed that the niche loss of any one fish in the community led to the niche rearrangement of other species and that this rearrangement process was more complex: the niches of some fish species increased, those of others decreased, and still, others remained unchanged. The model analysis divided the interspecific relationship in the community into two main categories: competitive and mutual benefit.

Linear river ecosystems span a large geographic area. Upstream and downstream fish become "central communities." That is, closer relationships were formed within each group (upstream or downstream). In the analysis of niche rearrangement, some upstream (or downstream) fish were found to be absent, and these absences had little effect on the niches of the fish downstream (or upstream). Furthermore, the experimental communities were classified according to the distribution characteristics of fish in the upper, middle, and lower reaches of the Pearl River. The "large community" of fish was decomposed into several "small communities" more closely related with respect to morphology and function. The results helped to clarify some mechanisms of community stability.

The rates of change in the various niches in the simulated community in response to the absence of single fish species were weighted by the average rate of change, and the average rate of change in the community was calculated as the comprehensive rate of change across the community. The comprehensive rate of change reflected the roles of the species in community stability. In the community, the species with low comprehensive change rates had a little decisive effect on community stability, while the species with high comprehensive change rates had substantial decisive effects on the stability of the community. For example, *Hypophthalmichthys molitrix*, *Hypophthalmichthys nobilis*, *Puntius semifasciolatus*, *Misgurnus anguillicaudatus*, and *Luciobrama macrocephalus* (see table 4.1) are the five species that were most important for the stability of the simulated community, while *Cyprinus chilia*, *Procypris merus*, *Ochetobius elongatus*, *Cyprinus carpio*, and *Onychostoma ovalis rhomboides* were the five species with the least effect on the stability of the community. These results suggested that the relative stability effects of each species can be used to predict key species and their roles in community construction. Examination of the stability effects of species in the community sequentially may also provide methods and means for the optimization of community species composition.

TAB. 4.1 – Simulation of the effects of different community species on community stability.

Fish	Absolute value of the average change rate of the community species (%)
Hypophthalmichthys molitrix	592.5
Hypophthalmichthys nobilis	360.0
Puntius semifasciolatus	322.0
Misgurnus anguillicaudatus	316.5
Luciobrama macrocephalus	307.4
Discocheilus wui	307.2
Pelteobagrus vachellii	291.8
Rasbora steineri	289.4
Pelteobagrus fulvidraco	284.3
Lateolabrax japonicus	280.1
Rasborinus lineatus	275.6
Schizothorax meridionalis	273.3
Sinocyclocheilus macrocephalus	263.7
Ctenopharyngodon idella	255.3
Sinocyclocheilus yangzongensis	255.2
Elopichthys bambusa	253.1
Discogobio tetrabarbatus	244.8
Channa maculata	242.1
Acrossocheilus clivosius	241.0
Acheilognathus tonkinensis	240.7

Tab. 4.1 – (continued).

Fish	Absolute value of the average change rate of the community species (%)
Mylopharyngodon piceus	234.9
Sinocyclocheilus grahami tingi	234.6
Siniperca kneri	234.5
Xenocypris argentea	232.5
Leptobotia pellegrini	229.8
Pseudolaubuca sinensis	229.2
Acrossocheilus labiatus	228.3
Hemibagrus macropterus	228.2
Tor sinensis	224.5
Squalidus argentatus	224.0
Garra pingi pingi	223.7
Discogobiolongibarbatus	220.7
Parasinilabeo assimilis	219.4
Takifugu ocellatus	217.5
Cyprinus multitaeniata	215.5
Sinilabeo discognathoides wui	214.6
Rhinogobius giurinus	214.6
Acrossocheiltts elongatus	209.2
Spinibarbus denticulatus	208.5
Lcucosoma chinensis	207.5
Cyprinus rabaudi	205.8
Carassius auratus auratus	204.4
Acrossocheilus beijiangensis	204.3
Sinocyclocheilus anophthalmus	203.8
Cyprinus yilongensis	203.3
Sinocyclocheilus macrolepis	202.7
Carassioides cantonensis	202.6
Garra pingi hainanensis	198.4
Carassius Auratus gibelio	196.7
Pseudogyrinocheilus prochilus	196.2
Onychostoma sima	195.5
Garra pingi yiliangensis	193.7
Sinocyclocheilus microphthalmus	193.2
Rectoris posehensis	191.9
Tachysurus argentivittatus	191.2
Pelteobagrus intermedius	190.0
Tor zonatus	189.8
Anabas testudineus	189.7
Parabramis pekinensis	189.7
Acrossocheiltts hemispinus hemispinus	189.0
Osteochilus salsburyi	187.7
Hemiculter leucisculus	185.9

Tab. 4.1 – (continued).

Fish	Absolute value of the average change rate of the community species (%)
Onychostoma barbatulum	184.2
Cyprinus longzhouensis	184.2
Zacco platypus	183.4
Luciocyprinus langsoni	179.7
Cyprinus pellegrini	178.8
Onychostoma macrolepis	178.1
Sinibotia pulchra	176.8
Bangana decora	176.0
Leiocassis crassilabris	175.9
Pseudocrossocheilus bamaensis	175.2
Acrossocheilus fasciatus	173.8
Acrossocheilus paradoxus	173.3
Discogobio brachyphysallidos	173.3
Cirrhinus molitorella	173.1
Spinibarbus hollandi	171.6
Opsariichthys bidens	170.2
Semilabeo obscurus	164.8
Squaliobarbus curriculus	163.9
Ancherythroculter lini	160.0
Mystacoleucus marginatus	158.4
Ptychidio macrops	156.2
Sinilabeo rendahli	154.0
Hemibagrus guttatus	153.9
Cyprinus fuxianensis	151.3
Folifer brevifilis	151.3
Sinilabeo discognathoides N	149.9
Micronemacheilus pulcher	148.9
Spinibarbus sinensis	148.4
Semilabeo notabilis	146.9
Balitora kwangsiensis	141.3
Rhodeus ocellatus	132.6
Megalobrama skolkovii	128.0
Garra orientalis	114.5
Onychostoma lini	110.7
Acrossocheilus iridescens iridescens	109.3
Ptychidio jordani	101.9
Bostrichthys sinensis	85.7
Cyprinus carpio	76.8
Ochetobius elongatus	70.2
Onychostoma ovalis rhomboides	54.6
Procypris merus	49.2
Cyprinus chilia	40.5

4.1.1 Species Substitutability

In the simulated community of 104 species of fish, the niche of the community of 103 species (without species "X") changed after the removal of species "X." The species substitutability index of species "X" to the community was reflected by the average value of various niche change rates. In some cases, the average niche change rate of the "104-X" community was high, which shows that "X" is very important to community stability and is irreplaceable. In other cases, the average niche change rate of the "104-X" community was low after the removal of species "X", suggesting that the species in the community were not important ("X" substitutable). Based on the characteristics of the species composition of the simulated communities, the species substitutability indices for fish in the mainstream, middle reaches, and lower reaches were small, which indicates that species "X" is substitutable by other fish in the middle and lower reaches of the river ecosystem and that some species can fill in the niche vacated by species "X" after its removal. The high substitutability indices of fish species in the tributaries, middle reaches, and upper reaches showed that species "X" was not substitutable and that the fish in these communities do not complement one other. The results of this analysis were consistent with the general scientific principles of evolution in a riverine biological community: that is, from the ocean into rivers, fish first establish widely adaptive functional communities in estuaries and downstream, then expand upstream and into tributaries, which they evolve into functional-specific communities. From the perspective of systemic community function, the fish communities of the upstream areas and tributaries are simpler (function specialized to adapt to the specialized environment) and the species in the community are less replaceable as compared to the communities of downstream areas and the middle reaches.

In the analysis, the species loss of the community was reflected in the niche change rate of the community. The niche change rate varied from 3% to 2894.3% (see table 4.2), while the substitutability index of species "X" ranged from 1 to 964.8. The index value reflected the relationship between species "X" and other species in the community. Small index values indicated that the corresponding fish was more easily substituted. That is, other fish could fill the niche of species "X."

4.1.2 Community Cohesion

The niches of the simulated community of 104 fish changed after the removal of species "X." The average niche change rate of the observed species in each community (*i.e.*, the community of "104 species – species X") was used to represent the effects of each specific species on community stability. Without species "X," the average niche change rate of a given species in the n (103) "104-X" communities reflected the degree of association among species in the community. In highly cohesive communities, the contribution of a particular species to community formation is high, and *vice versa.*

TAB. 4.2 – Index of species substitutability in the simulated community.

Species ("X")	Alternative indicators
Hypophthalmichthys molitrix	1.0
Hypophthalmichthys nobilis	1.3
Ctenopharyngodon idella	1.3
Lateolabrax japonicus	1.5
Hemibagrus guttatus	1.6
Elopichthys bambusa	1.9
Pelteobagrus fulvidraco	2.2
Pelteobagrus vachellii	2.2
Onychostoma sima	2.5
Misgurnus anguillicaudatus	3.3
Sinocyclocheilus grahami tingi	3.5
Mylopharyngodon piceus	3.6
Squalidus argentatus	4.1
Semilabeo notabilis	4.3
Puntius semifasciolatus	4.6
Takifugu ocellatus	4.8
Channa maculata	4.9
Lcucosoma chinensis	5.4
Acrossocheilus paradoxus	5.6
Rasbora steineri	5.8
Acrossocheiltts hemispinus hemispinus	6.0
Anabas testudineus	6.2
Balitora kwangsiensis	6.3
Siniperca kneri	6.4
Cyprinus carpio	6.5
Tor sinensis	7.0
Squaliobarbus curriculus	7.3
Megalobrama skolkovii	7.5
Ptychidio jordani	7.6
Hemibagrus macropterus	8.0
Spinibarbus sinensis	8.3
Hemiculter leucisculus	8.4
Cyprinus rabaudi	8.6
Ptychidio macrops	8.9
Micronemacheilus pulcher	9.0
Spinibarbus denticulatus denticulatus	9.0
Leptobotia pellegrini	9.9
Acrossocheilus iridescens iridescens	9.9
Pseudolaubuca sinensis	11.1
Sinibotia pulchra	11.4
Cyprinus longzhouensis	11.7
Mystacoleucus marginatus	12.6
Osteochilus salsburyi	13.8

TAB. 4.2 – (continued).

Species ("X")	Alternative indicators
Zacco platypus	14.0
Sinocyclocheilus microphthalmus	14.2
Discogobio tetrabarbatus	14.4
Acrossocheilus labiatus	14.4
Discogobiolongibarbatus	14.4
Pelteobagrus intermedius	14.9
Luciocyprinus langsoni	14.9
Ancherythroculter lini	15.3
Spinibarbus hollandi	15.6
Acrossocheilus fasciatus	15.9
Tachysurus argentivittatus	17.3
Rasborinus lineatus	17.8
Acrossocheiltts elongatus	18.9
Rhinogobius giurinus	19.1
Semilabeo obscurus	19.1
Carassius Auratus gibelio	19.1
Discocheilus wui	19.3
Bangana decora	19.5
Bostrichthys sinensis	19.8
Discogobio brachyphysallidos	19.8
Procypris merus	20.0
Cirrhinus molitorella	20.2
Opsariichthys bidens	20.6
Cyprinus pellegrini	20.8
Garra pingi yiliangensis	21.2
Parasinilabeo assimilis	22.2
Sinocyclocheilus anophthalmus	22.5
Folifer brevifilis brevifilis	23.1
Rhodeus ocellatus	23.6
Onychostoma macrolepis	26.7
Garra pingi hainanensis	26.7
Cyprinus yilongensis	27.3
Parabramis pekinensis	30.7
Acrossocheilus beijiangensis	37.9
Acheilognathus tonkinensis	41.1
Pseudocrossocheilus bamaensis	41.1
Ochetobius elongatus	41.7
Sinocyclocheilus macrocephalus	42.1
Carassius auratus auratus	42.5
Tor zonatus	46.9
Leiocassis crassilabris	48.2
Schizothorax meridionalis	49.1
Cyprinus multitaeniata	60.8

Tab. 4.2 – (continued).

Species ("X")	Alternative indicators
Cyprinus fuxianensis	91.9
Garra pingi pingi	111.6
Onychostoma lini	142.6
Acrossocheilus clivosius	149.9
Onychostoma barbatulum	151.2
Sinilabeo discognathoides wui	171.5
Pseudogyrinocheilus prochilus	173.6
Xenocypris argentea	180.7
Sinilabeo discognathoides	194.1
Rectoris posehensis	199.7
Luciobrama macrocephalus	204.8
Carassioides cantonensis	237.8
Sinilabeo rendahli	266.7
Onychostoma ovalis rhomboides	268.8
Sinocyclocheilus yangzongensis	389.6
Sinocyclocheilus macrolepis	719.3
Cyprinus chilia	894.3
Garra orientalis	964.8

The treatment of common numbers in table 4.1 with an absolute value of 40.5%, showed that the cohesion of the simulated community was 1–15 (see table 4.3). The species-binding capacity reflects the effects of each species on niche composition and community stability. Higher species associations imply more stable community structures, suggesting that individual species make smaller contributions to the stability of the community structure.

4.1.3 Community Integration

The internal stability of the community structure is determined by species compatibility (or exclusion), and the compatibility between one fish species and other fish species can be determined using the model of morphological parameters established by us (see table 4.4). In the analysis of single species loss in the simulated community, qualitative increases and decreases in the niches of specific species were observed. If the niche of observed species (G) increased, this implied that G was in competition with the removed species. Next, the proportion of the competing species in the community of 103 simulated species (g) was calculated and treated according to the greatest common divisor in order to obtain the repulsion index of g in the simulated community. Species with large exclusion index values competed with the large inner niche of the community, whereas the species with small exclusion index values reflected the small mutual restrictions in the community to some extent.

TAB. 4.3 – Cohesion of the simulated community.

Specific species	Community cohesion
Hypophthalmichthys molitrix	14.8
Hypophthalmichthys nobilis	8.8
Puntius semifasciolatus	8.0
Misgurnus anguillicaudatus	7.9
Luciobrama macrocephalus	7.7
Discocheilus wui	7.6
Pelteobagrus vachellii	7.3
Rasbora steineri	7.2
Pelteobagrus fulvidraco	7.1
Lateolabrax japonicus	6.9
Schizothorax meridionalis	6.8
Rasborinus lineatus	6.8
Sinocyclocheilus macrocephalus	6.6
Sinocyclocheilus yangzongensis	6.4
Elopichthys bambusa	6.3
Ctenopharyngodon idella	6.3
Discogobio tetrabarbatus	6.1
Channa maculata	6.0
Acheilognathus tonkinensis	6.0
Acrossocheilus clivosius	6.0
Siniperca kneri	5.9
Mylopharyngodon piceus	5.9
Sinocyclocheilus grahami tingi	5.9
Leptobotia pellegrini	5.8
Pseudolaubuca sinensis	5.7
Hemibagrus macropterus	5.7
Xenocypris argentea	5.7
Acrossocheilus labiatus	5.7
Tor sinensis	5.6
Squalidus argentatus	5.6
Discogobiolongibarbatus	5.5
Garra pingi pingi	5.5
Parasinilabeo assimilis	5.5
Takifugu ocellatus	5.4
Cyprinus multitaeniata	5.4
Rhinogobius giurinus	5.4
Sinilabeo discognathoides wui	5.3
Acrossocheiltts elongatus	5.2
Spinibarbus denticulatus denticulatus	5.2
Lcucosoma chinensis	5.2
Cyprinus rabaudi	5.1
Carassius auratus auratus	5.1
Acrossocheilus beijiangensis	5.1

Tab. 4.3 – (continued).

Specific species	Community cohesion
Cyprinus yilongensis	5.1
Sinocyclocheilus anophthalmus	5.1
Carassioides cantonensis	5.1
Sinocyclocheilus macrolepis	5.1
Garra pingi hainanensis	5.0
Carassius Auratus gibelio	4.9
Pseudogyrinocheilus prochilus	4.9
Onychostoma sima	4.9
Sinocyclocheilus microphthalmus	4.8
Garra pingi yiliangensis	4.8
Rectoris posehensis	4.8
Pelteobagrus intermedius	4.8
Tachysurus argentivittatus	4.8
Parabramis pekinensis	4.7
Anabas testudineus	4.7
Tor zonatus	4.7
Acrossocheiltts hemispinus hemispinus	4.7
Osteochilus salsburyi	4.7
Hemiculter leucisculus	4.7
Cyprinus longzhouensis	4.6
Onychostoma barbatulum	4.6
Zacco platypus	4.6
Luciocyprinus langsoni	4.5
Cyprinus pellegrini	4.5
Onychostoma macrolepis	4.4
Bangana decora	4.4
Leiocassis crassilabris	4.4
Sinibotia pulchra	4.4
Pseudocrossocheilus bamaensis	4.4
Cirrhinus molitorella	4.3
Acrossocheilus paradoxus	4.3
Acrossocheilus fasciatus	4.3
Discogobio brachyphysallidos	4.3
Spinibarbus hollandi	4.3
Opsariichthys bidens	4.3
Squaliobarbus curriculus	4.1
Semilabeo obscurus	4.1
Ancherythroculter lini	4.0
Mystacoleucus marginatus	4.0
Ptychidio macrops	3.9
Sinilabeo rendahli	3.9
Hemibagrus guttatus	3.8
Folifer brevifilis brevifilis	3.8

Tab. 4.3 – (continued).

Specific species	Community cohesion
Sinilabeo discognathoides	3.8
Cyprinus fuxianensis	3.7
Micronemacheilus pulcher	3.7
Semilabeo notabilis	3.7
Balitora kwangsiensis	3.5
Rhodeus ocellatus	3.3
Megalobrama skolkovii	3.2
Garra orientalis	2.9
Onychostoma lini	2.8
Acrossocheilus iridescens iridescens	2.8
Ptychidio jordani	2.6
Cyprinus carpio	1.9
Ochetobius elongatus	1.7
Onychostoma ovalis rhomboides	1.4
Procypris merus	1.3
Cyprinus chilia	1.0

If the niche of the observed species (G) decreased after the removal of another species, then G and the removed species were in a mutually beneficial relationship. The proportion of mutually beneficial species out of the 103 remaining species was determined statistically and treated according to the greatest common divisor to obtain the compatibility index of G in the simulated community. Species with large compatibility index values reflected less competition in the inner niche of the community, whereas the species with small compatibility index values indicated a somewhat higher degree of competition in the community. The compatibility index may reflect the fusion degree of species in the community.

The stability of the community structure is determined by species compatibility, and the compatibility between one fish and all others can be obtained using the model of morphological parameters established by us. For example, *Sinocyclocheilus* sp. is closely related but highly morphologically differentiated, because each species inhabits limestone caves. Table 4.5 shows the results of the model analysis of six species of *Sinocyclocheilus*. In this table, "*" represents a mutual beneficial relationship, and "■" represents a competitive relationship. Using the percentage of mutually beneficial species as an index of compatibility, *Sinocyclocheilus microphthalmus* was the most compatible (86.4%) and *Sinocyclocheilus macrolepis* was the least compatible (1.9%). Although species in the genus *Sinocyclocheilus* are closely related to other species in same family, the compatibility results obtained by the model show that there are great differences among the species of *Sinocyclocheilus* within the community. The taxonomic properties of the morphological parameters, including the compatibility of species among communities, suggested that closely related fish might respond differently to the niche changes associated with the removal of a single species.

TAB. 4.4 – The indices of species exclusion and compatibility in the simulated communities.

Fish	Species exclusion index	Compatibility index
Cyprinus carpio	3.3	1.0
Procypris merus	3.0	1.3
Spinibarbus hollandi	2.7	1.8
Pseudolaubuca sinensis	2.6	1.9
Sinilabeo discognathoides	2.5	2.1
Luciobrama macrocephalus	2.3	2.3
Bangana decora	2.3	2.4
Tachysurus argentivittatus	2.2	2.5
Sinocyclocheilus microphthalmus	2.1	2.6
Mylopharyngodon piceus	2.1	2.6
Ptychidio jordani	2.1	2.6
Ancherythroculter lini	2.0	2.7
Bostrichthys sinensis	2.0	2.7
Hemibagrus guttatus	2.0	2.7
Ctenopharyngodon idella	2.0	2.7
Ochetobius elongatus	2.0	2.7
Acheilognathus tonkinensis	2.0	2.8
Hypophthalmichthys nobilis	1.9	2.8
Megalobrama skolkovii	1.9	2.8
Elopichthys bambusa	1.9	2.8
Siniperca kneri	1.9	2.8
Opsariichthys bidens	1.9	2.8
Sinocyclocheilus grahami tingi	1.9	2.8
Cyprinus longzhouensis	1.9	2.8
Puntius semifasciolatus	1.9	2.8
Hypophthalmichthys molitrix	1.9	2.9
Sinocyclocheilus macrolepis	1.9	2.9
Onychostoma barbatulum	1.9	2.9
Acrossocheilus clivosius	1.9	2.9
Pseudocrossocheilus bamaensis	1.9	2.9
Spinibarbus denticulatus denticulatus	1.9	2.9
Carassius auratus auratus	1.8	2.9
Pelteobagrus fulvidraco	1.8	2.9
Parasinilabeo assimilis	1.8	2.9
Discogobio tetrabarbatus	1.8	2.9
Acrossocheiltts elongatus	1.8	2.9
Discogobiolongibarbatus	1.8	2.9
Discocheilus wui	1.8	2.9
Rasbora steineri	1.8	2.9
Leiocassis crassilabris	1.8	2.9
Pelteobagrus vachellii	1.8	2.9
Squalidus argentatus	1.8	3.0
Schizothorax meridionalis	1.8	3.0

Tab. 4.4 – (continued).

Fish	Species exclusion index	Compatibility index
Acrossocheilus iridescens iridescens	1.8	3.0
Discogobio brachyphysallidos	1.8	3.0
Micronemacheilus pulcher	1.8	3.0
Sinibotia pulchra	1.8	3.0
Rhodeus ocellatus	1.8	3.1
Sinocyclocheilus macrocephalus	1.8	3.1
Sinocyclocheilus anophthalmus	1.8	3.1
Cyprinus yilongensis	1.8	3.1
Rectoris posehensis	1.8	3.1
Zacco platypus	1.8	3.1
Parabramis pekinensis	1.7	3.1
Rhinogobius giurinus	1.7	3.1
Sinocyclocheilus yangzongensis	1.7	3.1
Acrossocheilus fasciatus	1.7	3.1
Cyprinus pellegrini	1.7	3.1
Pelteobagrus intermedius	1.7	3.1
Takifugu ocellatus	1.7	3.1
Lateolabrax japonicus	1.7	3.1
Lcucosoma chinensis	1.7	3.2
Acrossocheilus beijiangensis	1.7	3.2
Ptychidio macrops	1.7	3.2
Rasborinus lineatus	1.7	3.2
Balitora kwangsiensis	1.7	3.2
Anabas testudineus	1.7	3.2
Channa maculata	1.7	3.2
Tor sinensis	1.7	3.2
Hemibagrus macropterus	1.7	3.2
Carassioides cantonensis	1.7	3.2
Leptobotia pellegrini	1.7	3.2
Cirrhinus molitorella	1.6	3.3
Tor zonatus	1.6	3.3
Mystacoleucus marginatus	1.6	3.3
Semilabeo notabilis	1.6	3.3
Carassius Auratus gibelio	1.6	3.3
Garra pingi pingi	1.6	3.3
Xenocypris argentea	1.6	3.3
Misgurnus anguillicaudatus	1.6	3.3
Luciocyprinus langsoni	1.6	3.3
Cyprinus multitaeniata	1.6	3.3
Pseudogyrinocheilus prochilus	1.5	3.4
Osteochilus salsburyi	1.5	3.4
Hemiculter leucisculus	1.5	3.4
Sinilabeo discognathoides wui	1.5	3.5

Tab. 4.4 – (continued).

Fish	Species exclusion index	Compatibility index
Sinilabeo rendahli	1.4	3.5
Garra pingi hainanensis	1.4	3.5
Squaliobarbus curriculus	1.4	3.6
Cyprinus rabaudi	1.4	3.6
Acrossocheilus paradoxus	1.4	3.6
Onychostoma macrolepis	1.3	3.6
Onychostoma ovalis rhomboides	1.3	3.6
Acrossocheilus labiatus	1.3	3.6
Cyprinus fuxianensis	1.3	3.7
Garra orientalis	1.3	3.7
Garra pingi yiliangensis	1.2	3.8
Cyprinus chilia	1.2	3.8
Folifer brevifilis brevifilis	1.2	3.8
Acrossocheiltts hemispinus hemispinus	1.2	3.8
Onychostoma lini	1.2	3.8
Spinibarbus sinensis	1.2	3.8
Semilabeo obscurus	1.1	4.0
Onychostoma sima	1.0	4.1

4.1.4 Characteristics of the Geographic Distribution of the Ecological Niche Response

The 104 fish species in the simulated community were divided into two groups: the mainstream species and the tributary stream species. There were 47 mainstream species and 57 tributary-stream species (see table 4.6). The average change rates of the tributary-stream fish were larger than those of the mainstream fish, suggesting that the niche variability and degree of disturbance of the tributary-stream species were higher, and community stability was lower. To some extent, variations in fish community niches were larger in small-scale streams than in large-scale streams. The results of this analysis were consistent with the characteristics of fish communities in tributaries.

During the analysis of the niche changes associated with the removal of species from the simulated community, each species' rates of niche change in the "104-X" community were calculated, and a weighted average of each species' niche change rates after missing "X" species was expressed as integrated niche change rates. The fish species with small integrated niche rates in the communities reflect high stability in the community; the fish species with large integrated niche rates in the communities reflect low stability in the community.

Although the "primitive community" constructed by the model had some factors of "random" selection, this community was also selected based on the fish species recorded in the real-world Pearl River system. The average niche variations in the "subunit community" fish species in the upper, middle, and lower reaches of the river were analyzed. When the average niche change was small, the community was highly

TAB. 4.5 – Compatibility differences among fish in the genus *Sinocyclocheilus* within the community. ("*" indicates a mutually beneficial relationship, and "■" indicates a competitive relationship).

Fish	*Sinocyclocheilus grahami tingi*	*Sinocyclocheilus microphthalmus*	*Sinocyclocheilus macrolepis*	*Sinocyclocheilus anophthalmus*	*Sinocyclocheilus macrocephalus*	*Sinocyclocheilus yangzongensis*
Sinocyclocheilus yangzongensis	*	*	■	■	■	*
Ptychidio macrops	■	*	■	*	■	*
Cirrhinus molitorella	■	*	■	*	■	*
Carassius auratus auratus	■	*	■	*	■	*
Cyprinus pellegrini	■	■	■	*	■	*
Acrossocheilus iridescens	■	*	*	*	■	*
Leiocassis crassilabris	■	*	■	*	■	*
Carassius Auratus	■	■	■	*	■	*
Hemibagrus macropterus	■	*	■	*	■	*
Megalobrama skolkovii	■	*	■	*	■	*
Tor sinensis	■	*	■	*	■	*
Mystacoleucus marginatus	■	*	■	*	*	*
Onychostoma barbatulum	■	*	■	*	■	■
Pseudocrossocheilus bamaensis	■	*	■	*	■	■
Osteochilus salsburyi	■	*	■	*	■	■
Carassioides cantonensis	■	*	■	*	■	■
Acrossocheilus fasciatus	■	*	■	*	■	■
Rhodeus ocellatus	■	*	■	*	■	■
Opsariichthys bidens	■	*	■	*	■	■
Bostrichthys sinensis	■	■	■	*	■	■
Zacco platypus	■	*	■	*	■	■
Siniperca kneri	*	*	■	*	*	■
Ptychidio jordani	■	*	■	■	■	■
Spinibarbus hollandi	■	*	■	■	■	■
Sinocyclocheilus microphthalmus	■	*	■	■	■	■
Procypris merus	■	*	■	■	■	■
Ancherythroculter lini	*	*	■	■	*	■
Pseudolaubuca sinensis	■	*	■	■	■	■
Luciobrama macrocephalus	*	*	■	■	*	■
Cyprinus carpio	■	■	■	■	■	■
Cyprinus longzhouensis	■	■	■	*	■	■
Tor zonatus	■	*	■	*	■	■
Acheilognathus tonkinensis	■	*	■	*	*	■

Tab. 4.5 – (continued).

Fish	*Sinocyclocheilus grahami tingi*	*Sinocyclocheilus microphthalmus*	*Sinocyclocheilus macrolepis*	*Sinocyclocheilus anophthalmus*	*Sinocyclocheilus macrocephalus*	*Sinocyclocheilus yangzongensis*
Tachysurus argentivittatus	■	*	■	*	■	■
Parasinilabeo assimilis	■	*	■	*	■	■
Rhinogobius giurinus	■	*	■	*	■	■
Pelteobagrus intermedius	■	■	■	*	■	■
Lcucosoma chinensis	■	*	■	*	■	■
Rectoris posehensis	■	*	■	*	■	■
Sinilabeo rendahli	■	■	■	*	■	■
Garra pingi hainanensis	■	■	■	*	■	■
Discogobiolongibarbatus	■	*	■	■	■	■
Semilabeo obscurus	■	*	■	*	■	■
Sinibotia pulchra	■	■	■	*	■	■
Sinocyclocheilus macrocephalus	*	*	■	*	*	■
Cyprinus multitaeniata	■	*	■	*	■	■
Cyprinus yilongensis	*	*	■	■	■	■
Luciocyprinus langsoni	■	■	■	*	■	■
Micronemacheilus pulcher	■	■	■	*	■	■
Acrossocheilus paradoxus	■	*	■	*	■	■
Acrossocheilus beijiangensis	■	*	■	*	■	■
Squalidus argentatus	■	*	■	*	■	■
Acrossocheiltts hemispinus hemispinus	■	*	■	*	■	■
Garra orientalis	■	*	■	*	■	■
Schizothorax meridionalis	*	*	■	*	■	■
Spinibarbus denticulatus denticulatus	■	*	■	*	■	■
Onychostoma lini	■	*	■	*	■	■
Acrossocheiltts elongatus	■	*	■	*	■	■
Onychostoma macrolepis	■	*	■	*	■	■
Pseudogyrinocheilus prochilus	■	*	■	*	■	■
Sinocyclocheilus macrolepis	*	*	*	■	■	■
Hemiculter leucisculus	■	*	■	*	■	■
Balitora kwangsiensis	*	*	■	*	■	■
Squaliobarbus curriculus	■	*	■	*	■	■
Cyprinus chilia	*	*	■	*	■	■
Parabramis pekinensis	■	*	■	*	■	■
Onychostoma ovalis rhomboides	*	*	■	*	■	■
Ochetobius elongatus	*	*	■	■	■	■

Tab. 4.5 – (continued).

Mylopharyngodon piceus	*	*	■	*	*	■
Elopichthys bambusa	*	*	■	*	*	■
Bangana decora	■	*	■	■	■	■
Discogobio brachyphysallidos	■	*	■	*	■	■
Hemibagrus guttatus	*	■	*	*	■	■
Sinocyclocheilus anophthalmus	*	*	■	*	■	■
Leptobotia pellegrini	■	*	■	*	■	■
Sinocyclocheilus grahami tingi	*	*	■	*	■	■
Discogobio tetrabarbatus	■	*	■	*	■	■
Anabas testudineus	■	*	■	*	■	■
Channa maculata	■	*	■	*	■	■
Cyprinus rabaudi	■	*	■	*	■	■
Spinibarbus sinensis	■	*	■	*	■	■
Folifer brevifilis brevifilis	*	*	■	*	■	■
Semilabeo notabilis	*	*	■	*	■	■
Sinilabeo discognathoides	*	■	■	*	■	■
Ctenopharyngodon idella	*	*	■	*	■	■
Takifugu ocellatus	■	■	■	*	■	■
Misgurnus anguillicaudatus	■	*	■	*	■	■
Garra pingi yiliangensis	■	*	■	■	■	■
Onychostoma sima	■	*	■	*	■	■
Cyprinus fuxianensis	■	*	■	*	■	■
Acrossocheilus clivosius	*	*	■	*	■	■
Rasbora steineri	■	*	■	■	■	■
Discocheilus wui	*	*	■	*	■	■
Acrossocheilus labiatus	■	*	■	■	■	■
Pelteobagrus vachellii	*	*	■	■	■	■
Sinilabeo discognathoides wui	*	*	■	■	■	■
Pelteobagrus fulvidraco	*	*	■	■	■	■
Puntius semifasciolatus	■	*	■	■	■	■
Lateolabrax japonicus	*	*	■	■	*	■
Garra pingi pingi	*	*	■	■	■	■
Hypophthalmichthys molitrix	*	*	■	■	*	■
Rasborinus lineatus Parabramis pekinensis	■	*	■	■	■	■
Xenocypris argentea	*	*	■	*	■	■
Hypophthalmichthys nobilis	*	*	■	■	■	■
Compatibility (%)	30	86	3	76	10	12

TAB. 4.6 – Mean differences in the of niche change rates of various fish in the simulated communities.

Fish	The average change rate of the niche of the mainstream type fish (%)	Fish	The average change rate of the niche of the tributary fish (%)
Hypophthalmichthys molitrix	3.0	*Onychostoma sima*	7.4
Hypophthalmichthys nobilis	3.8	*Sinocyclocheilus grahami tingi*	10.5
Ctenopharyngodon idella	4.0	*Semilabeo notabilis*	12.8
Lateolabrax japonicus	4.5	*Acrossocheilus paradoxus*	16.7
Hemibagrus guttatus	4.7	*Rasbora steineri*	17.5
Elopichthys bambusa	5.7	*Acrossocheiltts hemispinus hemispinus*	17.9
Pelteobagrus fulvidraco	6.6	*Balitora kwangsiensis*	18.8
Pelteobagrus vachellii	6.6	*Spinibarbus sinensis*	24.8
Misgurnus anguillicaudatus	10.0	*Cyprinus rabaudi*	25.8
Mylopharyngodon piceus	10.8	*Acrossocheilus iridescens iridescens*	29.7
Squalidus argentatus	12.3	*Cyprinus longzhouensis*	35.0
Puntius semifasciolatus	13.7	*Mystacoleucus marginatus*	37.8
Takifugu ocellatus	14.4	*Osteochilus salsburyi*	41.4
Channa maculata	14.6	*Discogobio tetrabarbatus*	43.1
Lcucosoma chinensis	16.2	*Acrossocheilus labiatus*	43.1
Anabas testudineus	18.6	*Discogobio longibarbatus*	43.3
Siniperca kneri	19.3	*Luciocyprinus langsoni*	44.8
Cyprinus carpio Linnaeus, 1758	19.6	*Sinocyclocheilus microphthalmus*	42.7
Tor sinensis	21.0	*Spinibarbus hollandi*	46.7
Squaliobarbus curriculus	22.0	*Acrossocheilus fasciatus*	47.7
Megalobrama skolkovii	22.4	*Acrossocheiltts elongatus*	56.7
Ptychidio jordani	22.8	*Semilabeo obscurus*	57.3
Hemibagrus macropterus	24.0	*Discocheilus wui*	57.8
Hemiculter leucisculus	25.3	*Bangana decora*	58.5
Ptychidio macrops	26.6	*Discogobio brachyphysallidos*	59.4

Tab. 4.6 – (continued).

Micronemacheilus pulcher	27.0	*Procypris merus*	60.1
Spinibarbus denticulatus denticulatus	27.1	*Opsariichthys bidens*	61.8
Leptobotia pellegrini	29.6	*Cyprinus pellegrini*	62.5
Pseudolaubuca sinensis	33.4	*Garra pingi yiliangensis*	63.7
Sinibotia pulchra	34.3	*Parasinilabeo assimilis*	66.6
Zacco platypus	42.1	*Sinocyclocheilus anophthalmus*	67.4
Pelteobagrus intermedius	44.6	*Folifer brevifilis brevifilis*	69.4
Ancherythroculter lini	45.9	*Onychostoma macrolepis*	80.0
Tachysurus argentivittatus	51.8	*Garra pingi hainanensis*	80.2
Rasborinus lineatus	53.4	*Cyprinus yilongensis*	81.9
Rhinogobius giurinus	57.2	*Acrossocheilus beijiangensis*	113.6
Carassius Auratus gibelio	57.4	*Acheilognathus tonkinensis*	123.3
Bostrichthys sinensis	59.3	*Pseudocrossocheilus bamaensis*	123.4
Cirrhinus molitorella	60.7	*Sinocyclocheilus macrocephalus*	126.2
Rhodeus ocellatus	70.9	*Tor zonatus*	140.6
Parabramis pekinensis	92.0	*Leiocassis crassilabris*	144.7
Ochetobius elongatus	125.2	*Schizothorax meridionalis*	147.2
Carassius auratus auratus	127.4	*Cyprinus multitaeniata*	182.5
Garra pingi pingi	334.7	*Cyprinus fuxianensis*	275.7
Xenocypris argentea	542.2	*Onychostoma lini*	427.9
Luciobrama macrocephalus	614.3	*Acrossocheilus clivosius*	449.7
Garra orientalis	2894.3	*Onychostoma barbatulum*	453.7
		Sinilabeo discognathoides wui	514.4
		Pseudogyrinocheilus prochilus	520.8
		Sinilabeo discognathoides	582.3
		Rectoris posehensis	599.0
		Carassioides cantonensis	713.4
		Sinilabeo rendahli	800.1

Tab. 4.6 – (continued).

Fish	The average change rate of the niche of the mainstream type fish (%)	Fish	The average change rate of the niche of the tributary fish (%)
		Onychostoma ovalis rhomboides	806.5
		Sinocyclocheilus yangzongensis	1168.7
		Sinocyclocheilus macrolepis	2157.8
		Cyprinus chilia	2682.9
Average rate of change (%)	122.9	Average rate of change (%)	260.4

stable and variability was low. Conversely, when the average niche change was large, community stability was low and variability was high.

4.1.5 Differences

4.1.5.1 Species Size Types

Species vary in size. It is generally believed that large species occupy more niches and have a greater impact on the community, while small species occupy fewer niches and have no impact on the community. The 104 species of fish were divided into four classes based on individual size. The results showed that the species with larger individuals had a substantial influence on the composition of the community niche. The average change rate of the community niche was greatest for large species but was greater for small species than for medium species (see table 4.7). This suggested that the composition of the community niche is related to the functional composition. Small fish are more sensitive to environmental changes. In a changing environment, fish are in a highly variable state. Because the species niche pattern is still adapting to the evolution of the ecosystem, the positional relationships among species "blending" into the community are more indispensable. This phenomenon was to some extent consistent with the results of the community deconstruction model.

Therefore, the effects of fish loss on community niche change are not entirely determined by the species size. Further analysis showed that, during ecological deletion and the rearrangement of species niches, niche allocation was not based on the size of the species in the community, and species of the same size had different niches. Similar results were obtained using both the "primitive communities" and the "104-X" communities. *Mylopharyngodon piceus, Ctenopharyngodon idella, Hypophthalmichthys molitrix, Hypophthalmichthys nobilis,* and *Elopichthys bambusa* are all the same size. The niches of these five fish exhibited "random" differences in response to fish removal from the simulated community, similar to *Megalobrama skolkovii* and *Parabramis pekinensis* (see table 4.8). This suggested that differences in the niche are not determined by species size, but by the implicit functional division of the community. This phenomenon was observed in large fish (see figure 4.1), medium fish (see figure 4.2), and small fish (see figure 4.3).

4.1.5.2 Affinities

The effects of fish with the same classification on the community niche differed. As shown in the graph below, the niche changes of different species of fish in the community were analyzed by selecting two closely related species of fish. In the model analysis of us, no similar niche effects were found among the cyprinids (seven species of *Cyprinus* and two species of *Procyprinus*; see figure 4.4) or the light-lipped fish (eight species; see figure 4.5). That is, fish with similar classification attributes differed with respect to the rate of niche change. Niche overlaps are common in multi-species communities, and the relationships among species in the food chain are a network. Close relatives of similar species or species with similar functional attributes exist simultaneously in the system, and different niche functions exist in

Tab. 4.7 – Average niche change rates and individual weight differences among community species.

Species ≥10 kg	Change rate (%)	Species ≥kg	Change rate (%)	Species ≥100 g	Change rate (%)	Species ≥g	Change rate (%)
Hypophthalmichthys molitrix	591	*Pelteobagrus vachellii*	291	*Pelteobagrus fulvidraco*	284	*Puntius semifasciolatus*	320
Hypophthalmichthys nobilis	353	*Channa maculata*	241	*Acrossocheilus clivosius*	238	*Misgurnus anguillicaudatus*	316
Elopichthys bambusa	251	*Lateolabrax japonicus*	275	*Acrossocheilus labiatus*	227	*Discocheilus wui*	305
Ctenopharyngodon idella	250	*Siniperca kneri*	236	*Tor sinensis*	225	*Rasbora steineri*	288
Mylopharyngodon piceus	235	*Hemibagrus macropterus*	228	*Takifugu ocellatus*	216	*Schizothorax meridionalis*	273
Luciobrama macrocephalus	307	*Xenocypris argentea*	228	*Cyprinus multitaeniata*	216	*Rasborinus lineatus*	271
		Spinibarbus denticulatus denticulatus	208	*Sinilabeo discognathoides wui*	212	*Sinocyclocheilus macrocephalus*	264
		Cyprinus rabaudi	205	*Acrossocheiltts elongatus*	209	*Sinocyclocheilus yangzongensis*	255
		Cyprinus yilongensis	203	*Carassius auratus auratus*	204	*Discogobio tetrabarbatus*	244
		Pelteobagrus intermedius	190	*Acrossocheilus beijiangensis*	204	*Acheilognathus tonkinensis*	240
		Tor zonatus	188	*Carassius Auratus gibelio*	197	*Sinocyclocheilus grahami tingi*	234
		Cyprinus longzhouensis	184	*Onychostoma sima*	194	*Leptobotia pellegrini*	231

TAB. 4.7 – (continued).

Luciocyprinus langsoni	180	*Parabramis pekinensis*	189	*Pseudolaubuca sinensis*	229
Cyprinus pellegrini	179	*Acrossocheiltts hemispinus hemispinus*	188	*Squalidus argentatus*	223
Cirrhinus molitorella	173	*Onychostoma barbatulum*	184	*Discogobiolongibarbatus*	220
Spinibarbus hollandi	171	*Onychostoma macrolepis*	177	*Garra pingi pingi*	220
Squaliobarbus curriculus	164	*Bangana decora*	177	*Parasinilabeo assimilis*	219
Semilabeo obscurus	163	*Leiocassis crassilabris*	176	*Rhinogobius giurinus*	216
Ancherythroculter lini	160	*Acrossocheilus paradoxus*	173	*Lcucosoma chinensis*	206
Ptychidio macrops	156	*Acrossocheilus fasciatus*	173	*Sinocyclocheilus anophthalmus*	203
Hemibagrus guttatus	153	*Semilabeo notabilis*	147	*Carassioides cantonensis*	202
Folifer brevifilis brevifilis	150	*Onychostoma lini*	110	*Sinocyclocheilus macrolepis*	202
Sinilabeo discognathoides	150	*Acrossocheilus iridescens iridescens*	110	*Garra pingi hainanensis*	198
Cyprinus fuxianensis	149	*Ptychidio jordani*	102	*Pseudogyrinocheilus prochilus*	196
Megalobrama skolkovii	128	*Onychostoma ovalis rhomboides*	54	*Sinocyclocheilus microphthalmus*	193

Tab. 4.7 – (continued).

Species ≥ 10 kg	Change rate (%)	Species ≥kg	Change rate (%)	Species ≥100 g	Change rate (%)	Species ≥g	Change rate (%)
		Procypris merus	50			*Garra pingi yiliangensis*	192
		Cyprinus chilia	40			*Rectoris posehensis*	192
		Cyprinus carpio	77			*Tachysurus argentivittatus*	190
		Ochetobius elongatus	69			*Anabas testudineus*	189
						Osteochilus salsburyi	187
						Hemiculter leucisculus	186
						Zacco platypus	183
						Sinibotia pulchra	176
						Pseudocrossocheilus bamaensis	175
						Discogobio brachyphysallidos	173
						Opsariichthys bidens	170
						Mystacoleucus marginatus	158
						Sinilabeo rendahli	154
						Micronemacheilus pulcher	148
						Balitora kwangsiensis	140
						Rhodeus ocellatus	132
						Garra orientalis	114
Community average niche change rate (%)	331		172		183		210

Tab. 4.8 – Community niches were not assigned proportional to species size (%).

Fish		*Mylopharyngodon piceus*	*Ctenopharyngodon idella*	*Hypophthalmichthys molitrix*	*Hypophthalmichthys nobilis*	*Elopichthys bambusa*	*Megalobrama skolkovii*	*Parabramis pekinensis*
Mylopharyngodon piceus	1.790		1.812	13.055	4.926	1.616	1.745	1.774
Ctenopharyngodon idella	1.346	1.508		1.538	1.885	1.174	1.311	1.335
Hypophthalmichthys molitrix	10.647	10.711	10.708		10.209	10.783	10.377	10.526
Hypophthalmichthys nobilis	3.551	3.737	3.594	0.070		3.742	3.468	3.515
Elopichthys bambusa	1.513	1.133	1.324	4.737	1.547		1.474	1.502
Megalobrama skolkovii	1.045	0.641	0.834	0.605	1.394	0.685		1.034
Parabramis pekinensis	1.560	0.954	0.911	0.331	1.537	0.684	1.979	

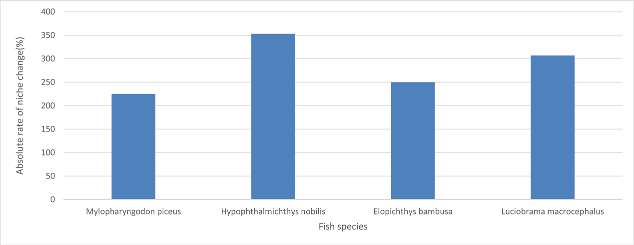

Fig. 4.1 – Variations in the ecological niches of the large fish in simulated communities.

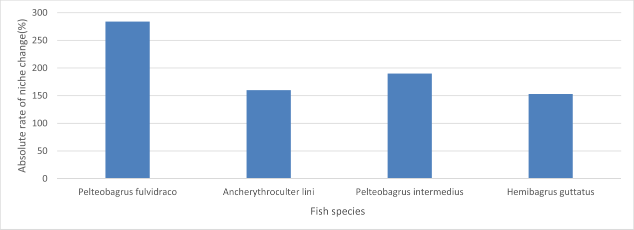

Fig. 4.2 – Variations in the ecological niches of the medium fish in simulated communities.

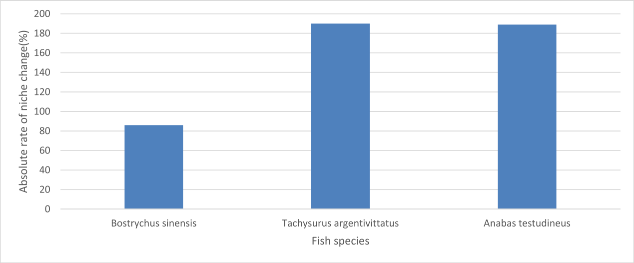

Fig. 4.3 – Variations in the ecological niches of the small fish in simulated communities.

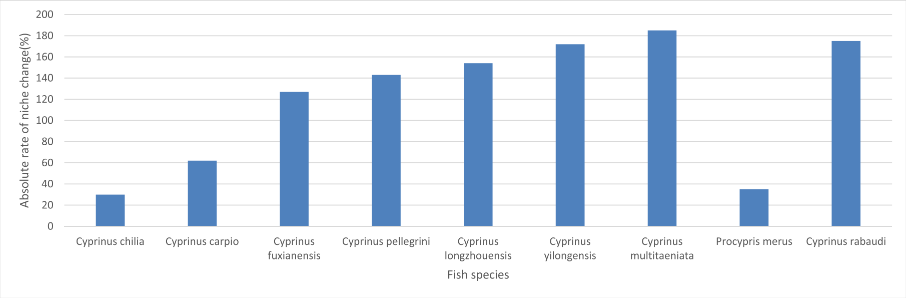

Fig. 4.4 – Variations in ecological niches of the fish similar to *Cyprinus* in simulated communities.

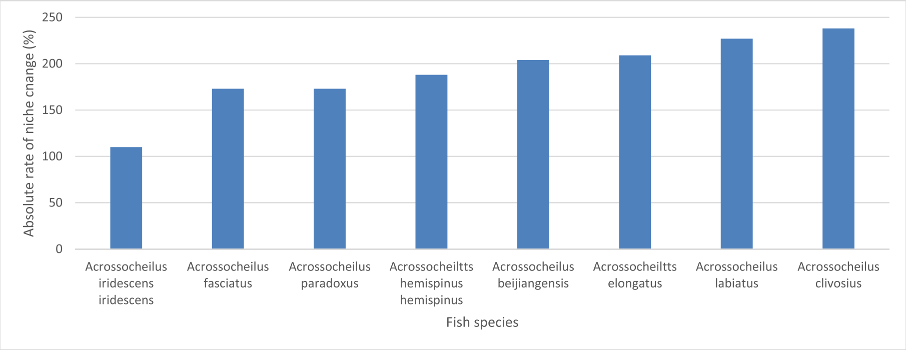

FIG. 4.5 – Variations in ecological niches of the *Acrossocheilus* in simulated communities.

different communities. The different functional division of species in different communities reflects their different effects on the communities. In real-world regional waters, fish of the same origin and function rarely appear together, and the differences identified by the model analysis also suggested that fish of the same origin and function inhabit different communities in the water and play a variety of distinct functional roles.

4.1.6 Feeding Habits

4.1.6.1 Carnivorous Fish

Community species compositions remain stable due to optimal acquired energy states. Under competitive pressure from other fish, the ecological niche of a species cannot be preserved. There are many competitive species in the community and great competitive pressure, so the proportion of competitive species to the greater community represents the competitive pressure. Competitive pressure can characterize the stability of a certain species in a community. In communities, predatory fish compete with one another. Thus, compatible community species are required for the maintenance of a stable niche. *Elopichthys bambusa, Lateolabrax japonicu, Mylopharyngodon piceus, Hypophthalmichthys nobilis, Ancherythroculter lin, Siniperca kneri,* and *Luciobrama macrocephalus* are all carnivorous fish. The model compatibility analysis showed that the species competing with *Luciobrama macrocephalus* reached 83%, while *Elopichthys bambusa* experienced only 8% of the competitive pressure (see table 4.9). High competitive pressure indicates a difficult niche in a community, or that niche maintenance may be greatly affected by community succession.

In the simulated community, carnivorous fish had various mutually beneficial relationships with other fish, including *Elopichthys bambusa,* 92%; *Lateolabrax japonicus*, 90%; *Mylopharyngodon piceus,* 88%; *Hypophthalmichthys nobilis,* 83%; *Ancherythroculter lini,* 66%; *Siniperca kneri,* 63%; and *Luciobrama macrocephalus,* only 17%. The visible niche of *Luciobrama macrocephalus* was least stable in the simulated community, suggesting that this species was more likely to be lost than the other six fish species. Figure 4.6 shows the response values of community niche

Tab. 4.9 – Differences in the responses of several carnivorous fish species responded to changes in removed niches.*

Fish	*Luciobrama macrocephalus*	*Elopichthys bambusa*	*Hypophthalmichthys nobilis*	*Ancherythroculter lini*	*Lateolabrax japonicus*	*Mylopharyngodon piceus*	*Siniperca kneri*
Siniperca kneri	39.2	−0.7	−0.2	−1.0	−0.8	−0.5	−100.0
Hypophthalmichthys molitrix	1583.5	213.0	−98.0	−51.9	−7.0	629.3	−34.5
Puntius semifasciolatus	1327.9	−7.8	−7.7	185.8	−7.7	−7.7	−22.5
Lateolabrax japonicus	1100.5	−3.0	−3.8	−26.1	−100.0	−3.1	−22.5
Xenocypris argentea	1258.3	−3.1	−2.9	−25.4	−2.8	−3.0	−21.7
Cyprinus fuxianensis	1408.3	−2.6	−2.6	−25.2	−2.5	−2.5	−21.5
Garra orientalis	824.2	−2.3	−2.2	−25.0	−2.2	−2.3	−21.3
Garra pingi pingi	1122.9	−14.3	3.2	−24.7	−16.8	−12.3	−21.0
Rasborinus lineatus Parabramis pekinensis	1356.2	−6.2	−3.1	59.0	−5.9	−6.0	−21.0
Folifer brevifilis brevifilis	1125.1	−1.8	−1.6	−24.6	−16.6	−1.7	−20.9
Lcucosoma chinensis	793.1	−4.5	−5.6	72.8	−5.5	−5.2	−20.7
Mylopharyngodon piceus	572.3	−25.1	5.2	54.4	−0.1	−100.0	−20.7
Acrossocheilus clivosius	979.9	−14.4	3.8	−24.4	−16.5	−12.1	−20.7
Onychostoma ovalis rhomboides	539.0	−1.0	−0.8	−24.1	−1.0	−1.0	−20.3
Cyprinus chilia	538.5	−1.1	−0.9	−24.1	−1.0	−1.0	−20.3
Elopichthys bambusa	−42.7	−100.0	5.4	−1.9	0.8	−9.7	−20.0
Discocheilus wui	1351.3	−5.0	−4.7	195.1	−4.7	−4.8	−20.0
Ochetobius elongatus	842.9	−0.3	−0.1	−23.6	−0.3	−0.2	−19.8
Mystacoleucus marginatus	1254.3	−2.8	−2.6	100.3	−2.9	−2.8	−18.7
Cyprinus carpio	−52.6	1.5	1.8	−22.3	1.3	1.5	−18.5
Rhinogobius giurinus	1071.3	−6.1	−6.0	−6.0	−6.0	−6.0	−6.0
Takifugu ocellatus	929.7	−5.4	−6.1	93.8	−6.0	−5.8	−6.0
Parasinilabeo assimilis	791.5	−5.9	−5.7	−5.6	−5.7	−5.8	−5.6
Pelteobagrus intermedius	795.5	−4.6	−2.5	−5.2	−5.2	−5.0	−5.2
Rectoris posehensis	511.0	−5.4	−5.2	−5.1	−5.1	−5.3	−5.1
Anabas testudineus	1369.9	−4.5	−5.2	−4.9	−5.0	−4.8	−4.9
Channa maculata	1227.1	−5.0	−5.0	96.0	−5.0	−4.9	−4.9
Discogobiolongibarbatus	370.8	−5.0	−4.7	−4.7	−4.7	−4.8	−4.7
Squalidus argentatus	229.9	−4.5	−4.2	−4.5	−4.4	−4.4	−4.4
Tachysurus argentivittatus	1608.1	4.3	−12.5	31.8	6.6	2.2	−4.3
Discogobio brachyphysallidos	230.0	−4.6	−4.1	−4.3	−4.3	−4.4	−4.3

Tab. 4.9 – (continued).

Garra pingi hainanensis	948.2	−4.6	−4.4	−4.3	−4.3	−4.5	−4.3
Cyprinus rabaudi	516.6	−4.0	−4.3	−4.2	−4.2	−4.1	−4.2
Acrossocheilus beijiangensis	230.5	−4.3	−4.0	−4.1	−4.1	−4.1	−4.1
Sinibotia pulchra	229.6	−3.6	−4.1	97.9	−4.1	−3.9	−4.0
Cyprinus multitaeniata	373.9	−3.8	−4.1	−4.0	−4.1	−3.9	−4.0
Micronemacheilus pulcher	520.0	−3.3	−3.8	98.3	−3.9	−3.7	−3.9
Sinilabeo rendahli	663.2	−4.2	−4.0	98.2	−3.9	−4.1	−3.8
Semilabeo obscurus	1243.4	−3.9	−3.9	−3.7	−3.8	−3.9	−3.8
Garra pingi yiliangensis	1391.1	−4.0	−3.8	−3.5	−3.6	−3.9	−3.6
Onychostoma sima	1248.1	−3.6	−3.5	−3.4	−3.5	−3.6	−3.4
Cyprinus longzhouensis	234.7	−2.9	−2.9	99.9	−3.1	−3.0	−3.2
Acrossocheilus labiatus	1251.5	−3.3	−3.2	−3.2	−3.2	−3.2	−3.2
Acrossocheilus paradoxus	524.0	−3.2	−3.2	−3.1	−3.1	−3.1	−3.1
Spinibarbus sinensis	1401.4	−2.9	−3.0	−2.9	−2.9	−2.9	−2.9
Megalobrama skolkovii	237.0	−2.6	−2.3	−2.8	−2.7	−2.5	−2.8
Acrossocheiltts hemispinus hemispinus	966.8	−2.7	−2.6	−2.6	−2.6	−2.6	−2.6
Pseudogyrinocheilus prochilus	677.8	−2.4	−2.0	−2.2	−2.2	−2.3	−2.2
Tor zonatus	238.3	−2.3	−1.8	−2.1	−2.0	−2.1	−2.1
Onychostoma barbatulum	238.7	−2.4	−1.7	−2.1	−2.0	−2.2	−2.0
Hemiculter leucisculus	532.6	−2.0	−1.8	−2.0	−2.0	−1.9	−2.0
Onychostoma macrolepis	237.5	−2.1	−1.9	−2.0	−2.0	−2.0	−2.0
Pseudocrossocheilus bamaensis	92.0	−2.2	1.2	−2.0	−1.9	−2.0	−1.9
Onychostoma lini	532.5	−1.9	−1.8	−13.3	−1.9	−1.9	−1.8
Osteochilus salsburyi	92.5	−2.1	−1.3	−13.2	−1.6	−1.8	−1.7
Acrossocheilus fasciatus	−54.0	−1.5	−1.1	−1.6	−1.5	−1.4	−1.5
Opsariichthys bidens	−53.9	−1.2	−0.8	−1.3	−1.2	−1.1	−1.3
Rhodeus ocellatus	−53.6	−1.4	−0.6	−1.2	−1.1	−1.1	−1.1
Luciocyprinus langsoni	232.4	−3.0	−3.2	−3.1	−3.2	−2.8	−0.9
Zacco platypus	−53.7	−0.8	−0.5	−1.0	−0.8	−0.7	−0.9
Cyprinus pellegrini	−54.6	−3.3	−2.4	100.5	−2.9	−3.1	−0.7

Tab. 4.9 – (continued).

Fish	*Luciobrama macrocephalus*	*Elopichthys bambusa*	*Hypophthalmichthys nobilis*	*Ancherythroculter lini*	*Lateolabrax japonicus*	*Mylopharyngodon piceus*	*Siniperca kneri*
Ptychidio jordani	−52.5	−0.2	0.2	−0.5	−0.3	−0.1	−0.4
Sinocyclocheilus microphthalmus	−53.1	−0.2	3.1	−0.2	−0.1	−0.0	−0.2
Carassius Auratus gibelio	91.1	−2.7	−2.0	101.5	−2.4	−2.5	−0.1
Procypris merus	−51.4	0.1	0.6	−0.2	−0.0	0.2	−0.1
Pseudolaubuca sinensis	−52.0	0.2	0.7	95.2	0.2	0.3	0.1
Hemibagrus macropterus	238.6	−1.2	−1.8	−2.1	−2.0	−1.6	0.2
Parabramis pekinensis	241.0	−0.8	−1.0	−24.3	−1.2	−0.9	1.0
Carassioides cantonensis	−53.7	−1.5	−0.4	104.5	−0.9	−1.2	1.3
Luciobrama macrocephalus	−100.0	0.7	0.7	210.9	0.2	0.6	2.4
Pelteobagrus vachellii	1972.4	−7.3	−2.6	179.1	−17.3	−2.0	19.1
Sinilabeo discognathoides wui	822.0	−2.8	−2.5	78.4	−9.9	−2.7	19.1
Pelteobagrus fulvidraco	1836.0	−0.7	−2.0	180.7	−16.8	−1.4	19.8
Semilabeo notabilis	541.0	−12.7	−0.5	−23.8	−15.7	−0.5	21.4
Sinilabeo discognathoides	544.4	−12.5	5.3	82.9	−15.3	−10.6	22.1
Bangana decora	554.6	−11.8	1.8	85.6	−14.1	0.9	23.8
Ctenopharyngodon idella	293.3	−12.5	1.2	18.7	16.3	1.2	31.3
Sinocyclocheilus macrocephalus	1504.2	−4.2	−4.1	−4.1	−4.1	−4.1	35.8
Spinibarbus denticulatus denticulatus	232.8	−3.1	−3.3	−3.5	−3.5	−3.2	36.8
Schizothorax meridionalis	233.1	−3.4	−3.2	−3.4	−3.3	−3.3	37.0
Cirrhinus molitorella	−54.6	−3.3	−2.8	99.6	−3.3	−3.3	37.1
Acrossocheilus iridescens iridescens	−54.8	−2.9	−2.7	−3.2	−3.1	−2.9	37.4
Hemibagrus guttatus	657.6	−1.4	−7.4	190.2	13.3	8.0	37.8
Carassius auratus auratus	237.7	−2.5	−2.2	100.8	−2.7	−2.6	37.9
Leiocassis crassilabris	238.2	−1.6	0.7	−2.6	−2.4	−2.1	38.3
Tor sinensis	238.8	−1.7	−1.8	101.9	−2.2	−1.9	38.6
Sinocyclocheilus macrolepis	1101.0	−2.1	−1.8	192.4	−1.9	−1.9	39.0

Tab. 4.9 – (continued).

Leptobotia pellegrini	238.8	−1.1	4.0	102.5	−1.9	−1.5	39.1
Sinocyclocheilus yangzongensis	1102.9	−1.8	−1.6	−1.7	−1.7	−1.7	39.3
Squaliobarbus curriculus	239.5	−1.4	−1.4	−13.1	−1.6	−1.4	39.4
Sinocyclocheilus grahami tingi	94.9	−0.8	−0.4	207.6	−0.8	−0.6	40.6
Sinocyclocheilus anophthalmus	522.3	−0.9	−0.4	207.7	−0.7	−0.7	40.7
Bostrichthys sinensis	−53.4	−0.6	−0.1	−0.7	−0.6	−0.5	40.9
Spinibarbus hollandi	−52.4	0.6	3.4	−0.1	0.1	0.4	41.9
Balitora kwangsiensis	976.9	−1.5	−1.5	−24.7	−1.7	−1.6	50.9
Discogobio tetrabarbatus	1214.0	−6.3	−6.0	−5.8	−5.9	−6.1	62.8
Rasbora steineri	1221.8	−5.3	−5.3	−5.3	−5.3	−5.3	63.8
Misgurnus anguillicaudatus	804.7	−3.2	−4.4	−4.2	−4.2	−3.8	65.6
Acheilognathus tonkinensis	229.9	−4.5	−4.1	196.6	−4.2	−4.3	65.7
Acrossocheiltts elongatus	234.9	−3.2	−2.7	200.7	−3.0	−3.0	68.0
Ptychidio macrops	382.7	−2.6	−2.3	−2.6	−2.6	−2.5	68.7
Ancherythroculter lini	−51.4	−0.5	0.4	−100.0	−0.2	−0.2	72.8
Hypophthalmichthys nobilis	1257.6	2.2	−100.0	−26.2	29.0	175.2	108.8
Cyprinus yilongensis	−12.4	−4.6	−4.4	20.6	247.8	1181.9	1911.6
Competitive fish species	85	8	18	35	10	12	39
Competitive pressure %	83	8	17	34	10	12	38

*Note: niche reduction %.

change rates after the loss of different carnivorous fish. Community species composition and diversity change are the basis of the formation of community functional diversity, which is a comprehensive embodiment of the ability to adapt to environmental changes.

4.1.6.2 Phytophagous Fish

In the simulated community, the mutually beneficial relationships between herbivorous fish and other fish differed. For example, *Ctenopharyngodon idella* was 91.3%, *Hypophthalmichthys molitrix* was 90.3%, *Megalobrama skolkovii* was 90.3%, and *Spinibarbus denticulatus denticulatus* was 85.4%, but *Parabramis pekinensis* was only 2.9%. Figure 4.7 shows that the community species relationships among the bream and the other four fish were not in the same dimension. Thus, the niche performance of *Parabramis pekinensis* was obviously restricted by other types of communities. If other species were removed (eliminated), the niche of *Parabramis pekinensis* would be increased greatly, and the other four phytophagous fish were highly compatible. Phytophagous fish use the primary productivity of the water system to obtain energy and had an overall lower rate of niche change in the simulated community than carnivorous fish. This might indicate that the energy competition pressure among these fish is lower than that among carnivorous fish. More precisely, phytophagous food sources are more widely available than carnivorous food sources. Figure 4.8 shows that five species of fish with the same phytophagic nature are missing the same fish, reflecting the difference in the rate of ecological niche change.

4.1.6.3 Omnivorous Fish

There are much omnivorous fish in rivers, such as *Procypris merus*, *Cyprinus longzhouensis*, *Cyprinus pellegrini*, *Cyprinus yilongensis*, *Cyprinus carpio*, *Cyprinus rabaudi*, *Cyprinus multitaeniata*, *Cyprinus fuxianensis,* and *Cyprinus chilia.* Community compatibility analysis showed that the niches of these species varied greatly in response to community change (see figure 4.9). *Cyprinus chilia* was completely incompatible with other species, while *Procypris merus* was 100% compatible with other community species (see table 4.10). Thus, one type of niche was relatively stable, containing fish such as *Cyprinus yilongensis, Cyprinus carpio,* and *Cyprinus rabaudi*, while the other type of niche was highly unstable, containing such fish as *Procypris merus*, *Cyprinus longzhouensis, Cyprinus pellegrini, Cyprinus multitaeniata, Cyprinus fuxianensis,* and *Cyprinus chilia.* Across these species, the niche of *Cyprinus carpio* was the most stable, and that of *Cyprinus chilia* was the most unstable.

4.2 "Subunit Community" Succession

Two species can be competitive or symbiotic depending on their mutual interests. Species relationships can be parasitic, partially symbiotic, or mutually beneficial. The longer a community evolves, the more favorable and stable its environment, and

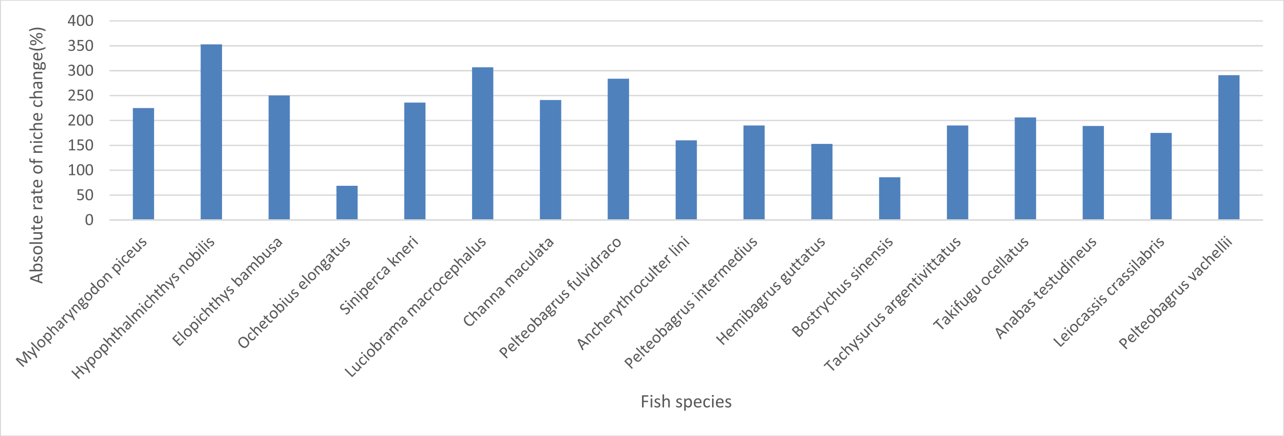

Fig. 4.6 – Variations in ecological niches of several carnivorous fish in simulated communities.

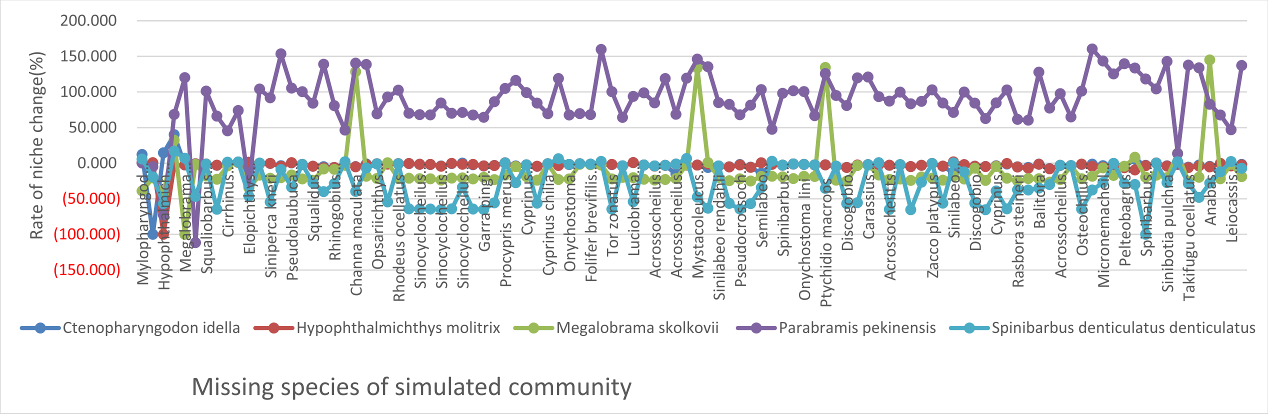

Fig. 4.7 – Differences in the responses of five phytophagous fish to the removal of various species from the community.

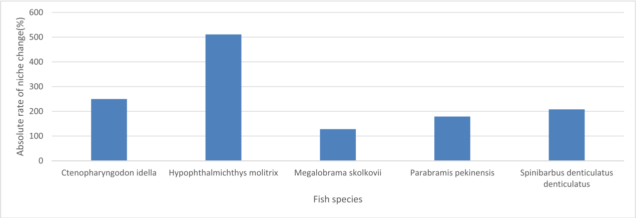

Fig. 4.8 – Variations in the ecological niches of several phytophagous fish in simulated communities.

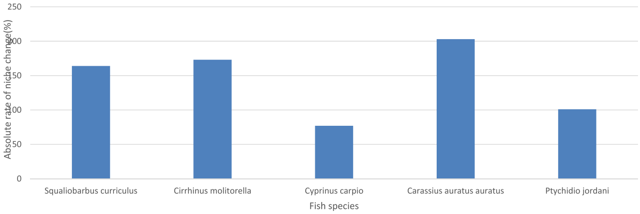

Fig. 4.9 – Variations in ecological niches of several omnivorous fish in simulated communities.

Tab. 4.10 – Niche differences among the *Cyprinus* in the community.

Fish	*Procypris merus*	*Cyprinus longzhouensis*	*Cyprinus pellegrini*	*Cyprinus yilongensis*	*Cyprinus carpio*	*Cyprinus rabaudi*	*Cyprinus multitaeniata*	*Cyprinus fuxianensis*	*Cyprinus chilia*
Consistency (%)	100.0	97.1	83.5	67.0	31.1	29.1	21.4	1.0	0
Niche average rate (%)	− 60.5	− 35.6	− 34.9	14.7	2.0	21.0	178.8	272.1	2656.1

the more species it contains. If two species utilize the same resources (niche overlap), they must compete and one species will be excluded. However, if the resource demands of one of the species change (niche differentiation), the two species may coexist. The trend in biological community development is toward niche differentiation and species increase. The study of the relationships among biological communities needs to go beyond the boundaries of specific taxa or taxon combinations (Bronstein, 1994). Morphological characters can reflect environmental characteristics and can be used to help understand the mechanisms underlying fish community composition in an ecosystem. By modeling community species, we can identify similar species types to better understand the diversity of species with the same functions, as well as the function-buffering ability of the ecosystem.

Although the "primitive community" constructed by the model had some factors of "random" selection, factors were also selected based on fish species recorded in the real-world Pearl River system. Because of the complexity of the river system and the diversity of the river habitats, the distributions of fish in the upper, middle, and lower reaches of the river differ noticeably. Such small communities correspond to small areas and may reflect characteristics that are more appropriate to a particular environment. In this section, we considered 25 dominant species in the middle and lower reaches of the Pearl River the "subunit community" in the simulated community of 104 species of fish (the "primitive community"; table 4.11, all fish) for the model analysis of niche succession by surplus species. The following table shows the species that have evolved into a "subunit community" (the italics in the table indicate hypothetical "subunit community" species).

The order in which the species were removed from the simulated community, was *Sinocyclocheilus macrolepis*, *Sinocyclocheilus macrocephalus, Sinocyclocheilus grahami tingi,* and *Pelteobagrus vachellii.* The niches of some species in the "subunit community" fluctuated up and down as the fish were eliminated one by one. If the niche value of the species in the "subunit community" was higher than that of the species before the loss, the removed fish is the competition object of the observed species in the "subunit community." From this, we concluded that the relationship between the "removed fish" and the "observed fish in the subunit community" was competitive. Alternatively, if the niche value species in the "subunit community" decreased in response to each removed fish as compared to the niche value before the removal, the relationship between the "removed fish" and the "observed fish in the subunit community" was judged to be mutually beneficial. If the niche value of the species in the "subunit community" did not change in response to simulated fish removal, the relationship between the "removed fish" and the "observed fish in the subunit community" was considered neutral.

4.2.1 Niche Changes in the "Subunit Community"

4.2.1.1 Mylopharyngodon piceus (Richardson, 1846)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Mylopharyngodon piceus* (Richardson, 1846) varied from 1.6227% and 12.8275%. The maximum extent of each deletion was 11.2049%, and the final niche

TAB. 4.11 – The “original community” (all fish in the table) and the “subunit community*” of the simulated communities.

Fish species						
*Mylopharyngodon piceus**	*Hemiculter leucisculus**	*Acrossocheilus labiatus*	*Tor zonatus*	*Discogobiolongibarbatus*	*Puntius semifasciolatus*	*Takifugu ocellatus*
*Ctenopharyngodon idella**	*Squalidus argentatus**	*Acrossocheiltts hemispinus hemispinus*	*Mystacoleucus marginatus*	*Discogobio brachyphysallidos*	*Spinibarbus hollandi*	*Lateolabrax japonicus*
*Hypophthalmichthys molitrix**	*Lcucosoma chinensis**	*Acrossocheilus beijiangensis*	*Sinilabeo rendahli*	*Discogobio tetrabarbatus*	*Spinibarbus sinensis*	*Balitora kwangsiensis*
*Hypophthalmichthys nobilis**	*Rhinogobius giurinus**	*Acrossocheiltts elongatus*	*Bangana decora*	*Discocheilus wui*	*Spinibarbus denticulatus denticulatus*	*Micronemacheilus pulcher*
*Megalobrama skolkovii **	*Carassius auratus auratus **	*Acrossocheilus paradoxus*	*Sinilabeo discognathoides*	*Schizothorax meridionalis*	*Sinocyclocheilus macrolepis*	*Anabas testudineus*
*Parabramis pekinensis**	*Channa maculata**	*Acrossocheilus fasciatus*	*Sinilabeo discognathoides wui*	*Procypris merus*	*Sinocyclocheilus macrocephalus*	*Pelteobagrus vachellii*
*Squaliobarbus curriculus**	*Pelteobagrus fulvidraco**	*Acrossocheilus clivosius*	*Osteochilus salsburyi*	*Cyprinus rabaudi*	*Sinocyclocheilus grahami tingi*	*Bostrichthys sinensis*
*Xenocypris argentea**	*Opsariichthys bidens**	*Acrossocheilus iridescens iridescens*	*Rectoris posehensis*	*Cyprinus fuxianensis*	*Sinocyclocheilus yangzongensis*	*Pelteobagrus intermedius*
*Cirrhinus molitorella**	*Ancherythroculter lini**	*Onychostoma macrolepis*	*Pseudocrossocheilus bamaensis*	*Cyprinus yilongensis*	*Sinocyclocheilus anophthalmus*	*Tachysurus argentivittatus*
*Cyprinus carpio**	*Rhodeus ocellatus*	*Onychostoma barbatulum*	*Parasinilabeo assimilis*	*Cyprinus longzhouensis*	*Sinocyclocheilus microphthalmus*	*Luciobrama macrocephalus*
*Elopichthys bambusa**	*Ptychidio jordani*	*Onychostoma sima*	*Semilabeo notabilis*	*Cyprinus chilia*	*Luciocyprinus langsoni*	*Rasbora steineri*
*Ochetobius elongatus**	*Ptychidio macrops*	*Onychostoma lini*	*Semilabeo obscurus*	*Cyprinus pellegrini*	*Hemibagrus guttatus*	*Zacco platypus*
*Siniperca kneri **	*Garra orientalis*	*Onychostoma ovalis rhomboides*	*Pseudogyrinocheilus prochilus*	*Carassioides cantonensis*	*Leptobotia pellegrini*	*Rasborinus lineatus*
*Misgurnus anguillicaudatus**	*Garra pingi pingi*	*Folifer brevifilis brevifilis*	*Garra pingi yiliangensis*	*Carassius Auratus gibelio*	*Leiocassis crassilabris*	*Acheilognathus tonkinensis*
*Pseudolaubuca sinensis Bleeker, 1865**	*Cyprinus multitaeniata*	*Tor sinensis*	*Garra pingi hainanensis*	*Sinibotia pulchra*	*Hemibagrus macropterus*	

was 12.5356%. As shown in figure 4.10, there were 48 corresponding competitive fish, 30 reciprocal fish, and one neutral fish. The maximum niche decrease of *Mylopharyngodon piceus* happens after the deletion of *Hemibagrus guttatus, and* the maximum niche increase of *Mylopharyngodon piceus* occurs after the deletion of *Anabas testudineus.*

4.2.1.2 Ctenopharyngodon idella (Valenciennes, 1844)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Ctenopharyngodon idella* (Valenciennes, 1844) varied from 1.1720% to 8.6426%. The maximum extent of each deletion was 7.4706%. As shown in figure 4.11, there were 51 corresponding competitive fish and 28 reciprocal fish. The maximum niche decrease of *Ctenopharyngodon idella* happens after the deletion of *Lateolabrax japonicus, and* the maximum niche increase of *Ctenopharyngodon idella* occurs after the deletion of *Takifugu ocellatus.*

4.2.1.3 Hypophthalmichthys molitrix (Valenciennes, 1844)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Hypophthalmichthys molitrix* (Valenciennes, 1844) varied from 10.4459% to 16.4285%. The maximum extent of each deletion was 5.9826%. As shown in figure 4.12, there were 45 corresponding competitive fish and 34 reciprocal fish. The maximum niche decrease of *Hypophthalmichthys molitrix* happens after the deletion of *Acrossocheilus fasciatus, and* the maximum niche increase of *Hypophthalmichthys molitrix* occurs after the deletion of *Spinibarbus sinensis.*

4.2.1.4 Hypophthalmichthys nobilis (Richardson, 1845)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Hypophthalmichthys nobilis* (Richardson, 1845) varied from 3.4881% to 10.9246%. The maximum extent of each deletion was 7.4365%. As shown in figure 4.13, there were 50 corresponding competitive fish, 29 reciprocal fish. The maximum niche decrease of *Hypophthalmichthys nobilis* happens after the deletion of *Discogo biolongibarbatus, and* the maximum niche increase of *Hypophthalmichthys nobilis* occurs after the deletion of *Zacco platypus.*

4.2.1.5 Megalobrama skolkovii (Dybowski, 1872)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Megalobrama skolkovii* (Dybowski, 1872) varied from 1.0454% to 3.9841%. The maximum extent of each deletion was 2.9387%. As shown in figure 4.14, there were 43 corresponding competitive fish and 36 reciprocal fish. The maximum niche decrease of *Megalobrama skolkovii* happens after the deletion of *Garra orientalis, and* the maximum niche increase of *Megalobrama skolkovii* occurs after the deletion of *Acrossocheiltts elongatus.*

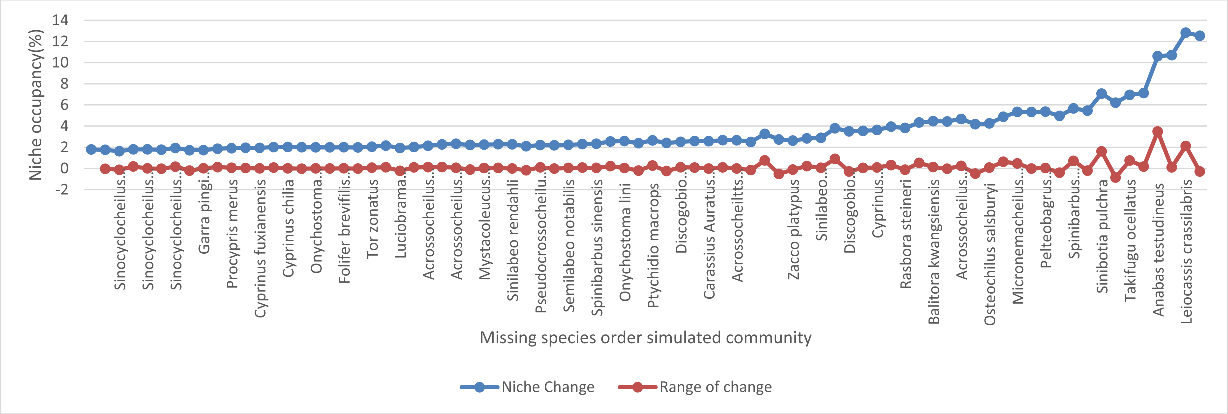

FIG. 4.10 – Amplitude of niche change for *Mylopharyngodon piceus* when species in the "primitive community" were removed one by one.

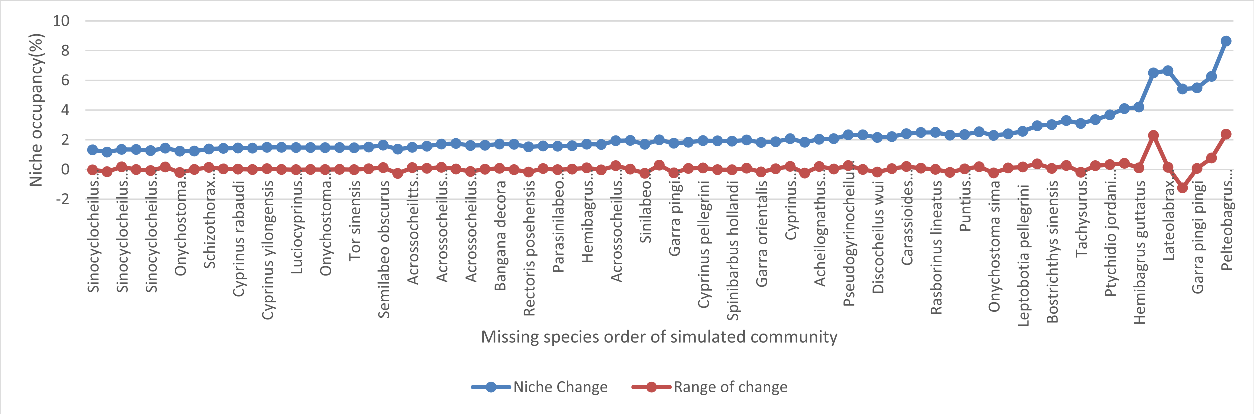

FIG. 4.11 – Amplitude of niche change for *Ctenopharyngodon idella* when species in the "primitive community" were removed one by one.

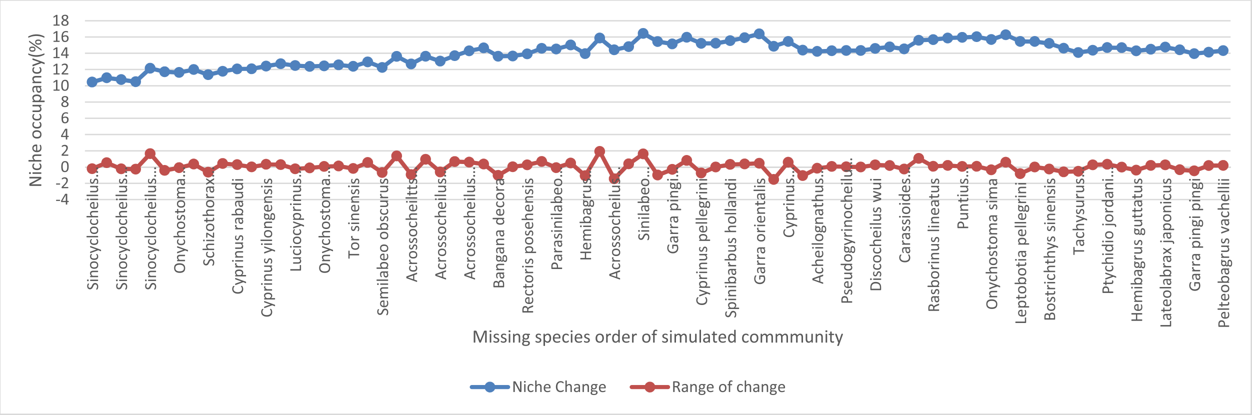

FIG. 4.12 – Amplitude of niche change for *Mhypophthalmichthys molitrix* when species in the “primitive community” were removed one by one.

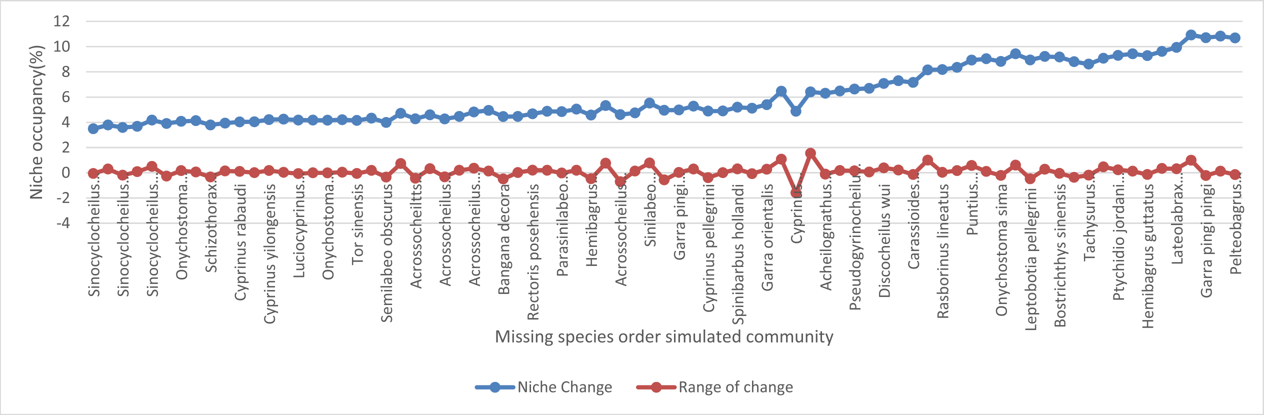

FIG. 4.13 – Amplitude of niche change for *Hypophthalmichthys nobilis* when species in the “primitive community” were removed one by one.

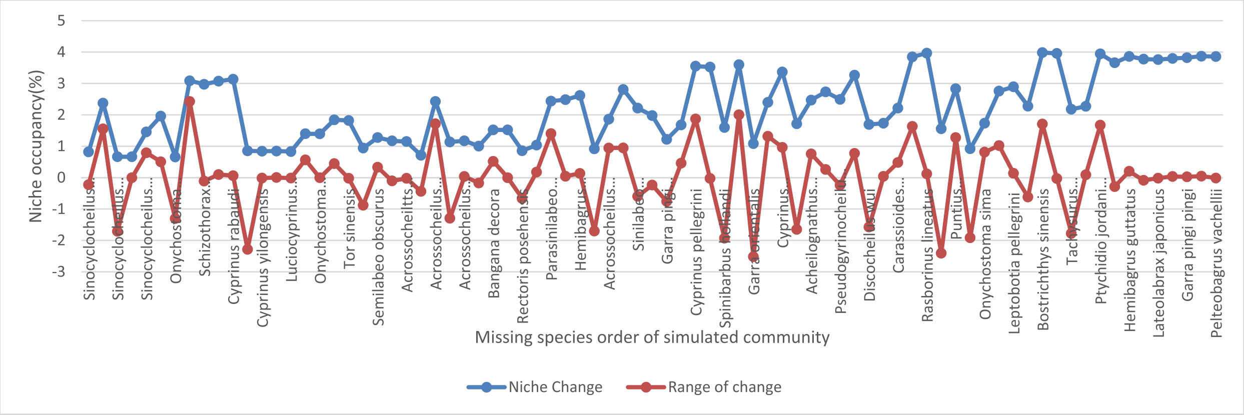

FIG. 4.14 – Amplitude of niche change for *Megalobrama skolkovii* when species in the “primitive community” were removed one by one.

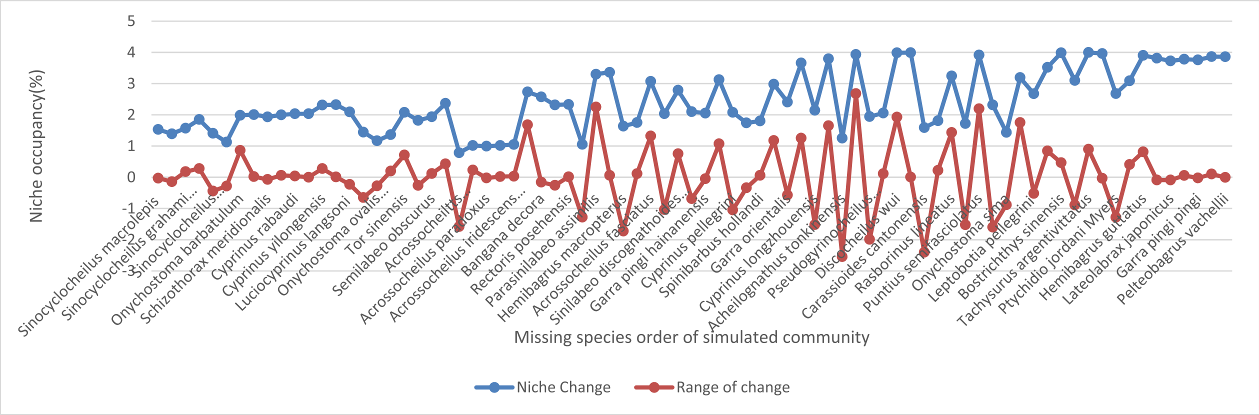

FIG. 4.15 – Amplitude of niche change for *Parabramis pekinensis* when species in the “primitive community” were removed one by one.

4.2.1.6 Parabramis pekinensis (Basilewsky, 1855)

When we deleted 79 species of fish from the “primitive community” one by one, the niche of *Parabramis pekinensis* (Basilewsky, 1855) varied from 0.7864% to 3.9975%. The maximum extent of each deletion was 3.211%. As shown in figure 4.15, there were 43 corresponding competitive fish, and 36 reciprocal fish. The maximum niche decrease of *Parabramis pekinensis* happens after the deletion of *Pseudogyrinocheilus prochilus, and* the maximum niche increase of *Parabramis pekinensis* occurs after the deletion of *Sinilabeo discognathoide.*

4.2.1.7 Squaliobarbus curriculus (Richardson, 1846)

When we deleted 79 species of fish from the “primitive community” one by one, the niche of *Squaliobarbus curriculus* (Richardson, 1846) varied from 0.5375% to 3.9975%. The maximum extent of each deletion was 3.4536%. As shown in figure 4.16, there were 43 corresponding competitive fish and 36 reciprocal fish. The maximum niche decrease of *Squaliobarbus curriculus* happens after the deletion of *Luciobrama macrocephalus, and* the maximum niche increase of *Squaliobarbus curriculus* occurs after the deletion of *Acrossocheiltts hemispinus hemispinus.*

4.2.1.8 Xenocypris argentea (Günther, 1868)

When we deleted 79 species of fish from the “primitive community” one by one, the niche of *Xenocypris argentea* (Günther, 1868) varied from 0.0029% to 2.569%. The maximum extent of each deletion was 2.5661%. As shown in figure 4.17, there were 45 corresponding competitive fish and 34 reciprocal fish. The maximum niche decrease of *Xenocypris argentea* happens after the deletion of *Discocheilus wui, and* the maximum niche increase of *Xenocypris argentea* occurs after the deletion of *Cyprinus multitaeniata.*

4.2.1.9 Cirrhinus molitorella (Valenciennes, 1844)

When we deleted 79 species of fish from the “primitive community” one by one, the niche of *Cirrhinus molitorella* (Valenciennes, 1844) varied from 0.0025% to 2.67%. The maximum extent of each deletion was 2.6675%. As shown in figure 4.18, there were 38 corresponding competitive fish and 41 reciprocal fish. The maximum niche decrease of *Cirrhinus molitorella* happens after the deletion of *Acrossocheilus beijiangensiss, and* the maximum niche increase of *Cirrhinus molitorella* occurs after the deletion of *Acrossocheilus paradoxus.*

4.2.1.10 Cyprinus carpio (Linnaeus, 1758)

When we deleted 79 species of fish from the “primitive community” one by one, the niche of *Cyprinus carpio* (Linnaeus, 1758) varied from 0.1598% to 3.9503%. The maximum extent of each deletion was 3.7905%. As shown in figure 4.19, there were 38 corresponding competitive fish and 41 reciprocal fish. The maximum niche decrease of *Cyprinus carpio* happens after the deletion of *Mystacoleucus marginatus,*

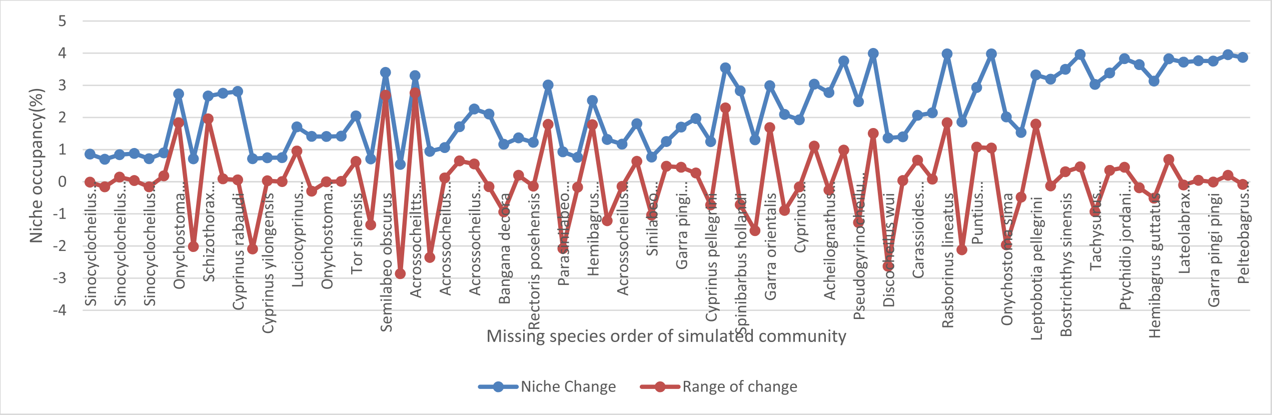

FIG. 4.16 – Amplitude of niche change for *Squaliobarbus curriculus* when species in the "primitive community" were removed one by one.

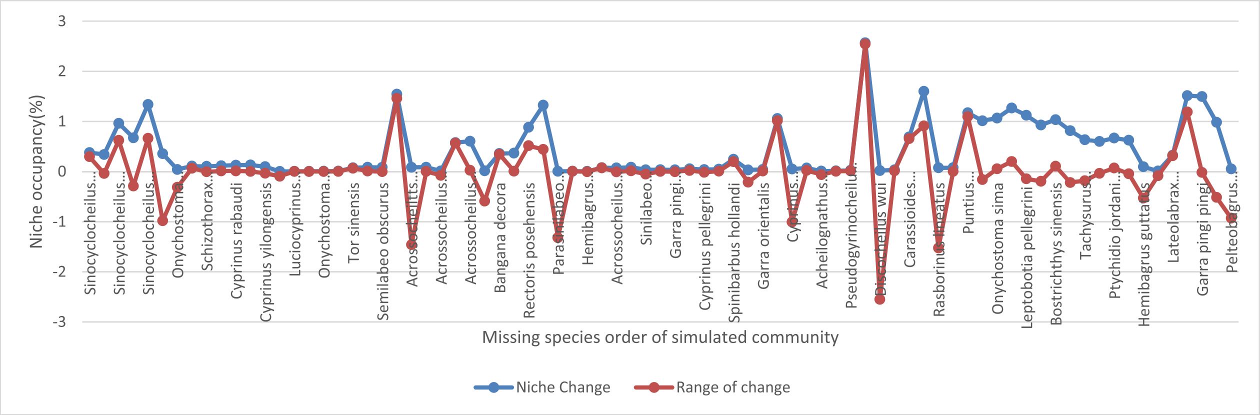

FIG. 4.17 – Amplitude of niche change for *Xenocypris argentea* when species in the "primitive community" were removed one by one.

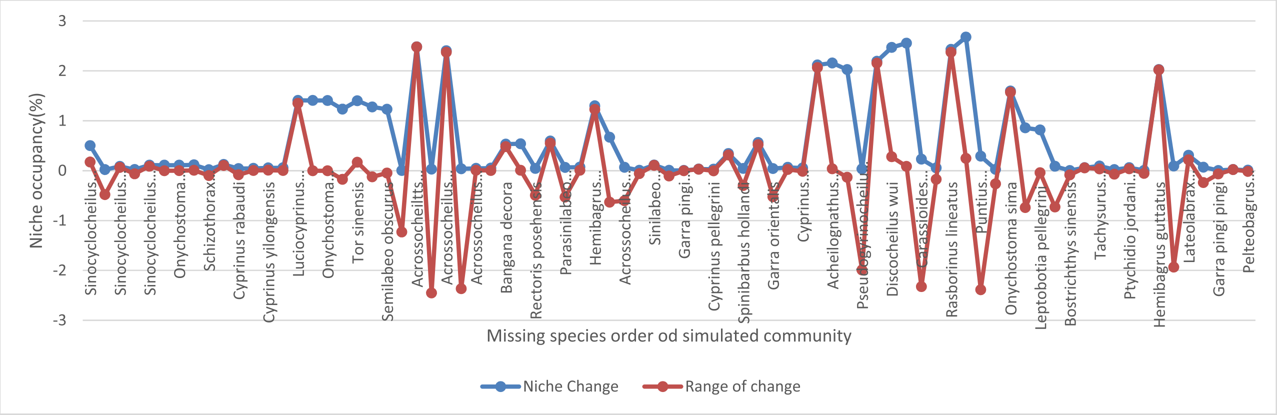

FIG. 4.18 – Amplitude of niche change for *Cirrhinus molitorella* when species in the “primitive community” were removed one by one.

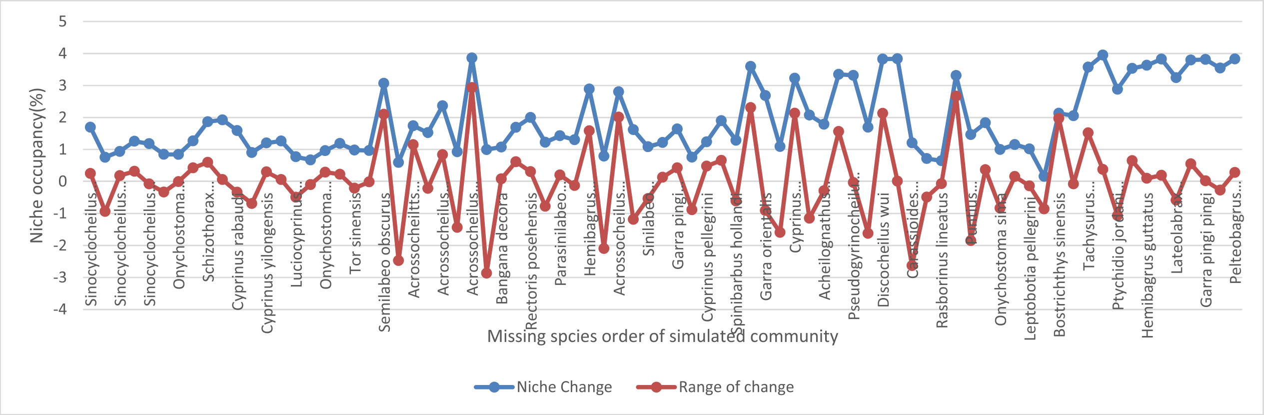

FIG. 4.19 – Amplitude of niche change for *Cyprinus carpio* when species in the “primitive community” were removed one by one.

and the maximum niche increase of *Cyprinus carpio* occurs after the deletion of *Acrossocheilus iridescens iridescens.*

4.2.1.11 Elopichthys bambusa (Richardson, 1845)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Elopichthys bambusa* (Richardson, 1845) varied from 1.3382% to 4.3429%. The maximum extent of each deletion was 3.0048%. As shown in figure 4.20, there were 46 corresponding competitive fish and 33 reciprocal fish. The maximum niche decrease of *Elopichthys bambusa* happens after the deletion of *Onychostoma sima, and* the maximum niche increase of *Elopichthys bambusa* occurs after the deletion of *Leptobotia pellegrini.*

4.2.1.12 Ochetobius elongatus (Kner, 1867)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Ochetobius elongatus* (Kner, 1867) varied from 0.0060% to 2.8333%. The maximum extent of each deletion was 2.8273%. As shown in figure 4.21, there were 46 corresponding competitive fish and 33 reciprocal fish. The maximum niche decrease of *Ochetobius elongatus* happens after the deletion of *Onychostoma sima, and* the maximum niche increase of *Ochetobius elongatus* occurs after the deletion of *Garra pingi pingi.*

4.2.1.13 Siniperca kneri (Garman, 1912)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Siniperca kneri* (Garman, 1912) varied from 0.0199 to 3.9541%. The maximum extent of each deletion was 3.9342%. As shown in figure 4.22, there were 46 corresponding competitive fish and 33 reciprocal fish. The maximum niche decrease of *Siniperca kneri* happens after the deletion of *Leptobotia pellegrini, and* the maximum niche increase of *Siniperca kneri* occurs after the deletion of *Leiocassis crassilabris.*

4.2.1.14 Misgurnus anguillicaudatus (Cantor, 1842)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Misgurnus anguillicaudatus* (Cantor, 1842) varied from 0.8690% to 3.9838%. The maximum extent of each deletion was 3.1148%. As shown in figure 4.23, there were 41 corresponding competitive fish and 38 reciprocal fish. The maximum niche decrease of *Misgurnus anguillicaudatus* happens after the deletion of *Puntius semifasciolatus, and* the maximum niche increase of *Misgurnus anguillicaudatus* occurs after the deletion of *Bostrichthys sinensis.*

4.2.1.15 Pseudolaubuca sinensis (Bleeker, 1865)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Pseudolaubuca sinensis* (Bleeker, 1865) varied from 0.7101% to 3.9933%.

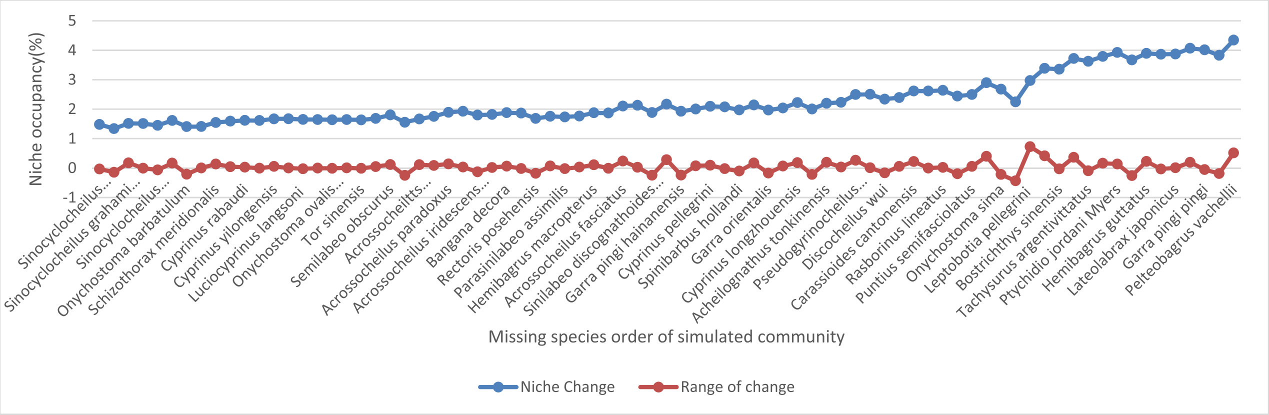

FIG. 4.20 – Amplitude of niche change for *Elopichthys bambusa* when species in the "primitive community" were removed one by one.

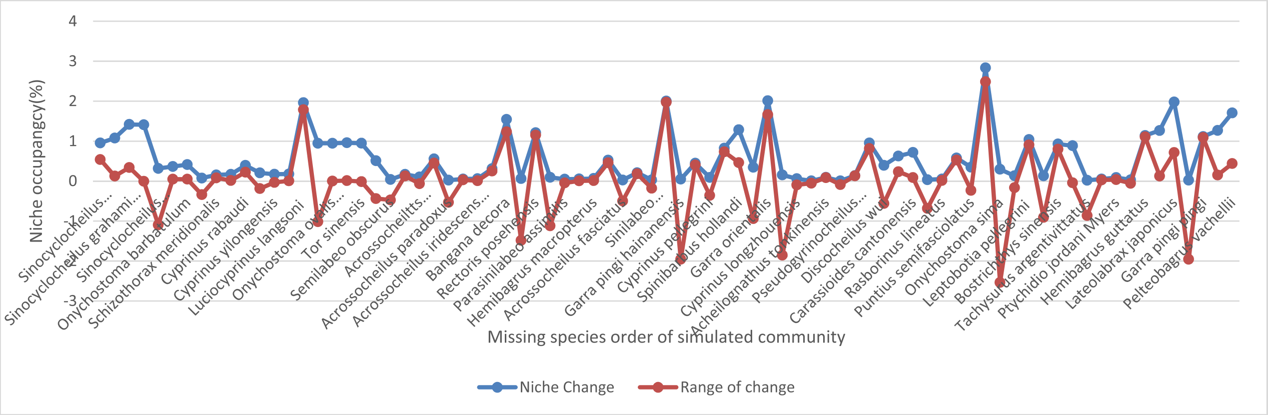

FIG. 4.21 – Amplitude of niche change for *Ochetobius elongatus* when species in the "primitive community" were removed one by one.

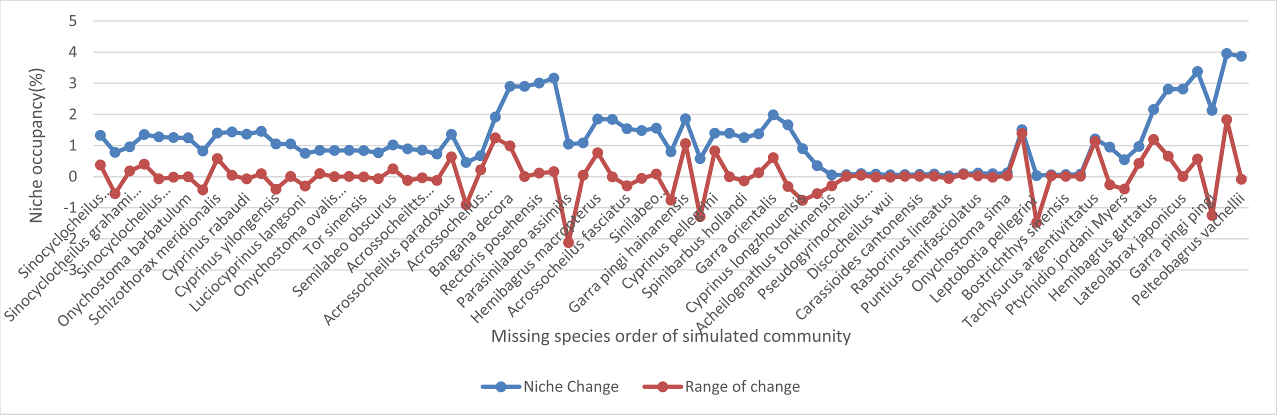

Fig. 4.22 – Amplitude of niche change for *Siniperca kneri* when species in the "primitive community" were removed one by one.

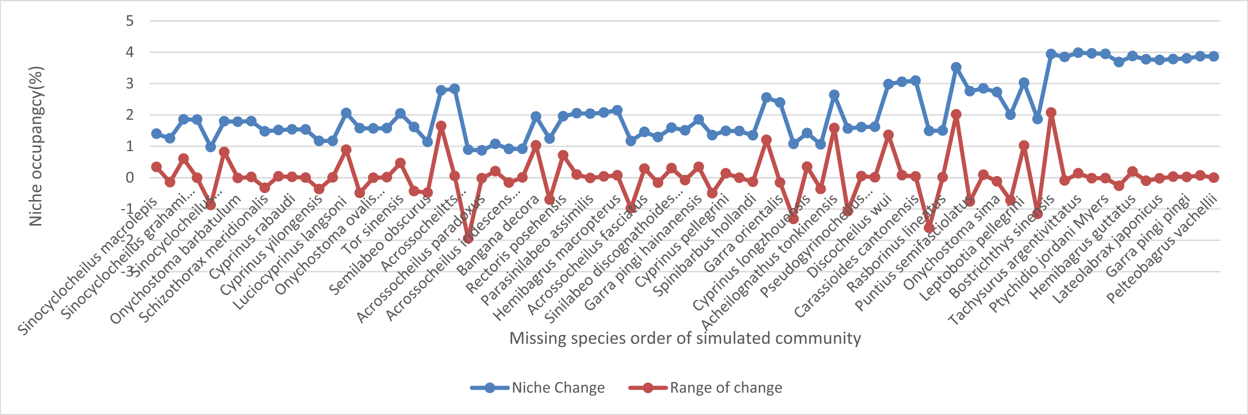

Fig. 4.23 – Amplitude of niche change for *Misgurnus anguillicaudatus* when species in the "primitive community" were removed one by one.

The maximum extent of each deletion was 3.2832%. As shown in figure 4.24, there were 44 corresponding competitive fish and 35 reciprocal fish. The maximum niche decrease of *Pseudolaubuca sinensis* happens after the deletion of *Acrossocheiltts hemispinus hemispinus, and* the maximum niche increase of *Pseudolaubuca sinensis* occurs after the deletion of *Luciobrama macrocephalus.*

4.2.1.16 Hemiculter leucisculus (Basilewsky, 1855)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Hemiculter leucisculus* (Basilewsky, 1855) varied from 0.0166% to 3.8568%. The maximum extent of each deletion was 3.8402%. As shown in figure 4.25, there were 36 corresponding competitive fish and 43 reciprocal fish. The maximum niche decresse of *Hemiculter leucisculus* happens after the deletion of *Puntius semifasciolatus, and* the maximum niche increase of *Hemiculter leucisculus* occurs after the deletion of *Anabas testudineus.*

4.2.1.17 Squalidus argentatus (Sauvage and Dabry De Thiersant, 1874)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Squalidus argentatus* (Sauvage and Dabry de Thiersant, 1874) varied from 0.0075% to 2.1739%. The maximum extent of each deletion was 2.1664%. As shown in figure 4.26, there were 47 corresponding competitive fish and 32 reciprocal fish. The maximum niche decrease of *Squalidus argentatus* happens after the deletion of *Rasbora steineri, and* the maximum niche increase of *Squalidus argentatus* occurs after the deletion of *Parasinilabeo assimilis.*

4.2.1.18 Lcucosoma chinensis (Osbeck, 1765)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Lcucosoma chinensis* (Osbeck, 1765) varied from 0.6837% to 3.9527%. The maximum extent of each deletion was 3.269%. As shown in figure 4.27, there were 39 corresponding competitive fish and 40 reciprocal fish. The maximum niche decrease of *Lcucosoma chinensis* happens after the deletion of *Balitora kwangsiensis, and* the maximum niche increase of *Lcucosoma chinensis* occurs after the deletion of *Rasborinus lineatus.*

4.2.1.19 Rhinogobius giurinus (Rutter, 1897)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Rhinogobius giurinus* (Rutter, 1897) varied from 0.0351% to 3.6267%. The maximum extent of each deletion was 3.5917%. As shown in figure 4.28 there were 48 corresponding competitive fish and 31 reciprocal fish. The maximum niche decrease of *Rhinogobius giurinus* happens after the deletion of *Rasborinus lineatus, and* the maximum niche increase of *Rhinogobius giurinus* occurs after the deletion of *Balitora kwangsiensis.*

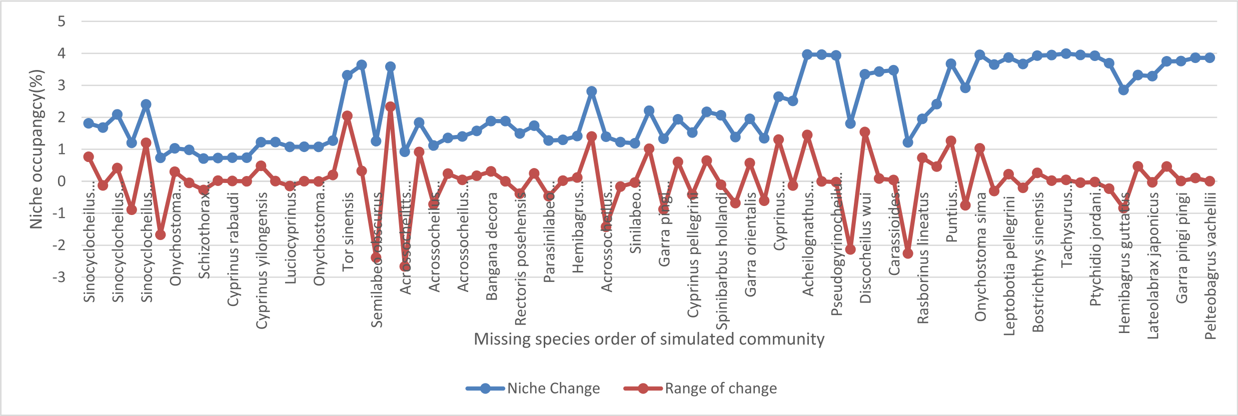

FIG. 4.24 – Amplitude of niche change for *Pseudolaubuca sinensis* when species in the “primitive community” were removed one by one.

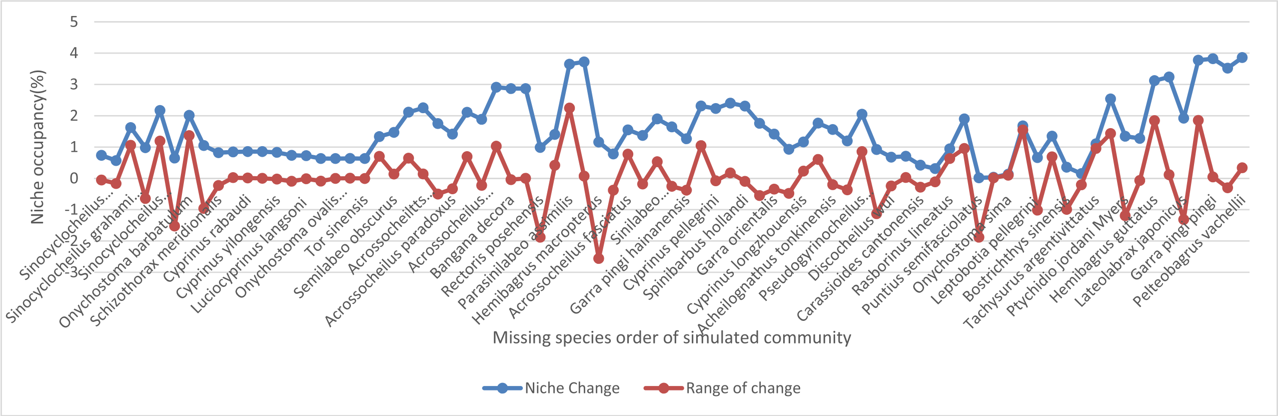

FIG. 4.25 – Amplitude of niche change for *Hemiculter leucisculus* when species in the “primitive community” were removed one by one.

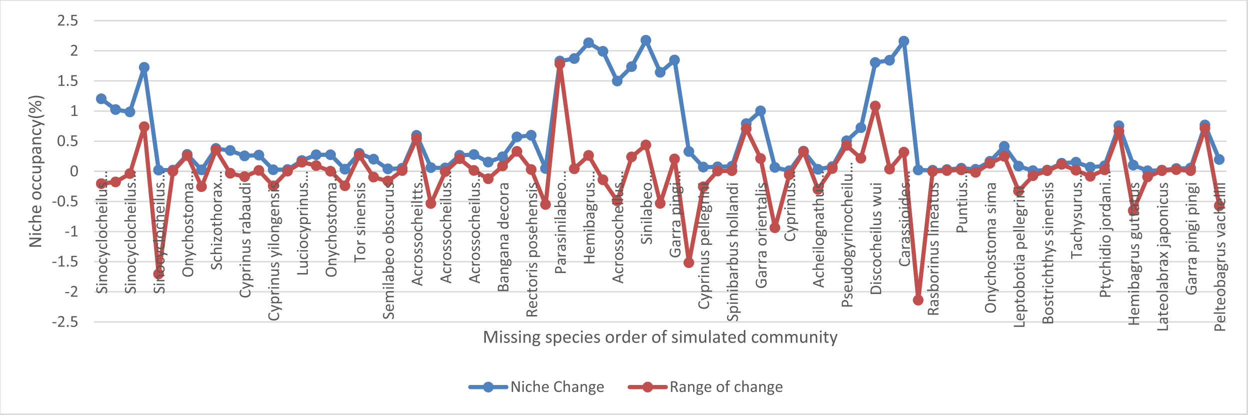

FIG. 4.26 – Amplitude of niche change for *Squalidus argentatus* when species in the "primitive community" were removed one by one.

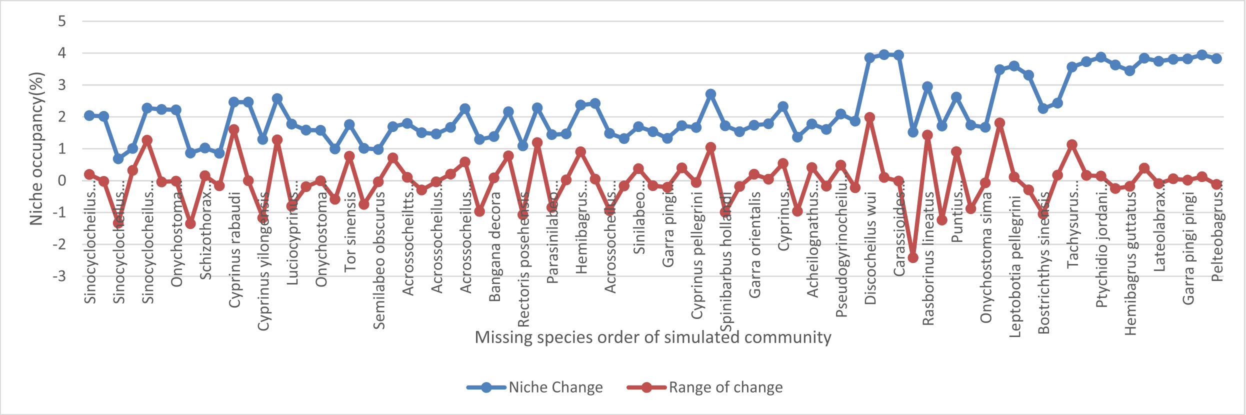

FIG. 4.27 – Amplitude of niche change for *Lcucosoma chinensis* when species in the "primitive community" were removed one by one.

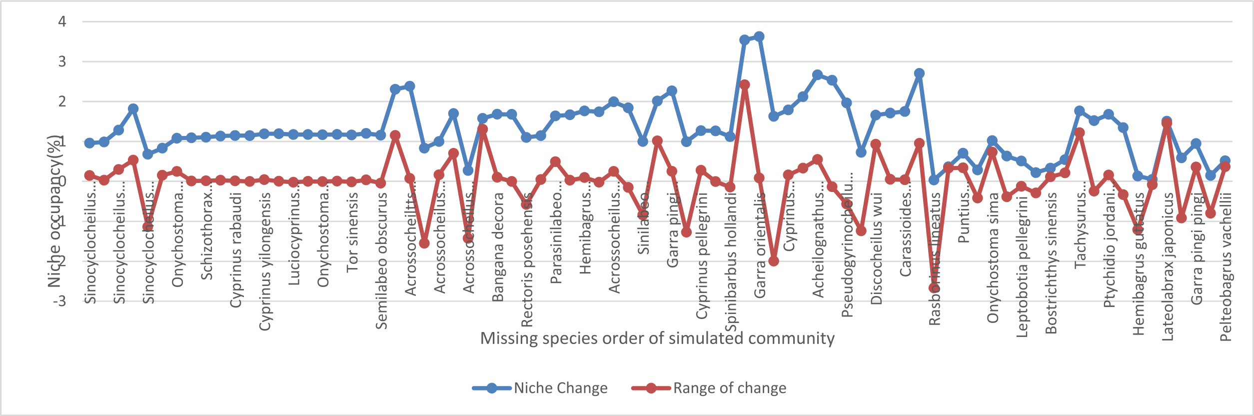

FIG. 4.28 – Amplitude of niche change for *Rhinogobius giurinus* when species in the "primitive community" were removed one by one.

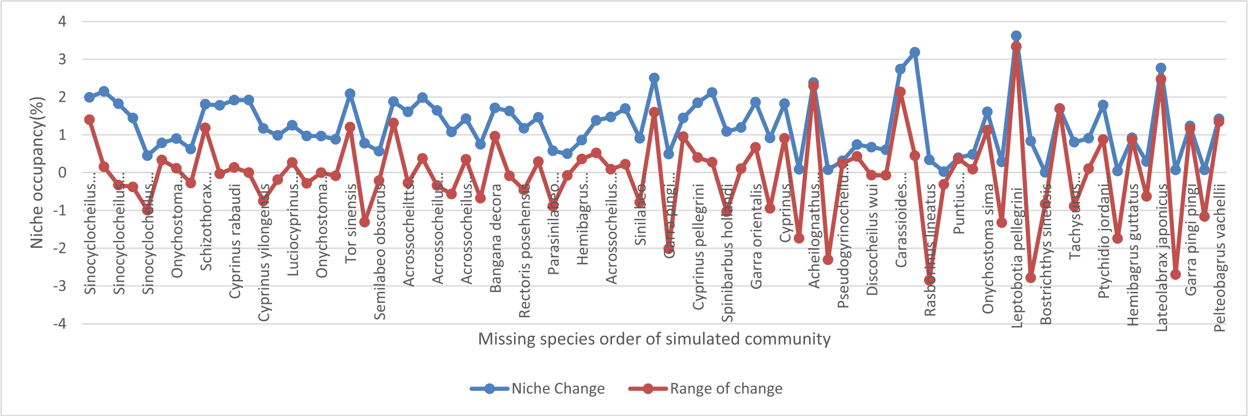

FIG. 4.29 – Amplitude of niche change for *Carassius auratus auratus* when species in the "primitive community" were removed one by one.

4.2.1.20 Carassius auratus auratus (Linnaeus, 1758)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Carassius auratus auratus* (Linnaeus, 1758) varied from 0.0068% ∼ 3.3347%. The maximum extent of each deletion was 3.6129%. As shown in figure 4.29, there were 41 corresponding competitive fish and 38 reciprocal fish. The maximum niche decrease of *Carassius auratus auratus* happens after the deletion of *Micronemacheilus pulcher, and* the maximum niche increase of *Carassius auratus auratus* occurs after the deletion of *Leptobotia pellegrini.*

4.2.1.21 Channa maculata (Lacépède, 1801)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Channa maculata* (Lacépède, 1801) varied from 0.4258% to 3.8833%. The maximum extent of each deletion was 3.4575%. As shown in figure 4.30, there were 49 corresponding competitive fish and 30 reciprocal fish. The maximum niche decrease of *Channa maculata* happens after the deletion of *Rectoris posehensis, and* the maximum niche increase of *Channa maculata* occurs after the deletion of *Onychostoma sima.*

4.2.1.22 Pelteobagrus fulvidraco (Richardson, 1846)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Pelteobagrus fulvidraco* (Richardson, 1846) varied from 0.565% to 3.998%. The maximum extent of each deletion was 3.433%. As shown in figure 4.31, there were 43 corresponding competitive fish, 35 reciprocal fish, and one neutral type. The maximum niche decrease of *Pelteobagrus fulvidraco* happens after the deletion of *Acheilognathus tonkinensis, and* the maximum niche increase of *Pelteobagrus fulvidraco* occurs after the deletion of *Sinibotia pulchra.*

4.2.1.23 Opsariichthys bidens (Günther, 1873)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Opsariichthys bidens* (Günther, 1873) varied from 0.0052% ∼ 2.6641%. The maximum extent of each deletion was 2.6589%. As shown in figure 4.32, there were 49 corresponding competitive fish and 30 reciprocal fish. The maximum niche decrease of *Opsariichthys bidens* happens after the deletion of *Cyprinus longzhouensis, and* the maximum niche increase of *Opsariichthys bidens* occurs after the deletion of *Discogobiolongibarbatus.*

4.2.1.24 Ancherythroculter lini (Luo, 1994)

When we deleted 79 species of fish from the "primitive community" one by one, the niche of *Ancherythroculter lini* (Luo, 1994) varied from 0.007% to 3.752%. The maximum extent of each deletion was 2.6589%. As shown in figure 4.33, there were

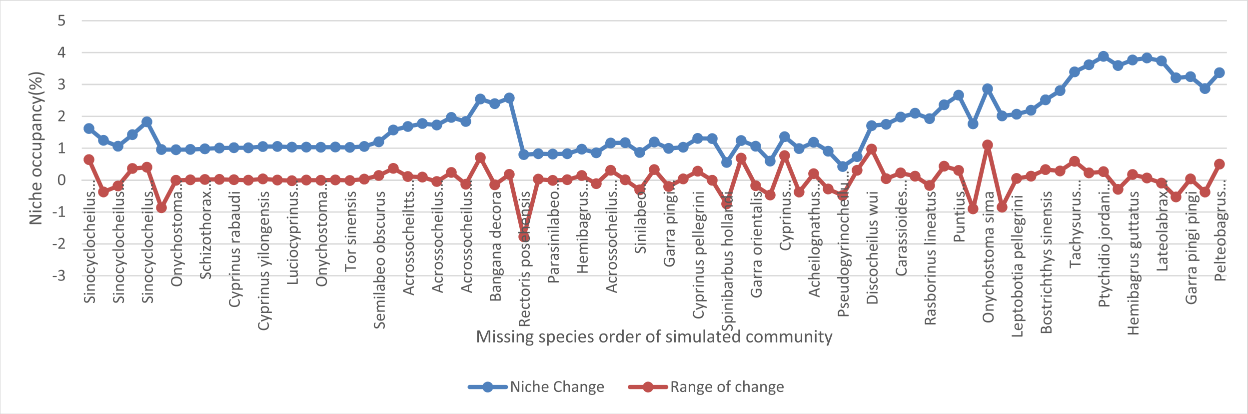

FIG. 4.30 – Amplitude of niche change for *Channa maculata* when species in the "primitive community" were removed one by one.

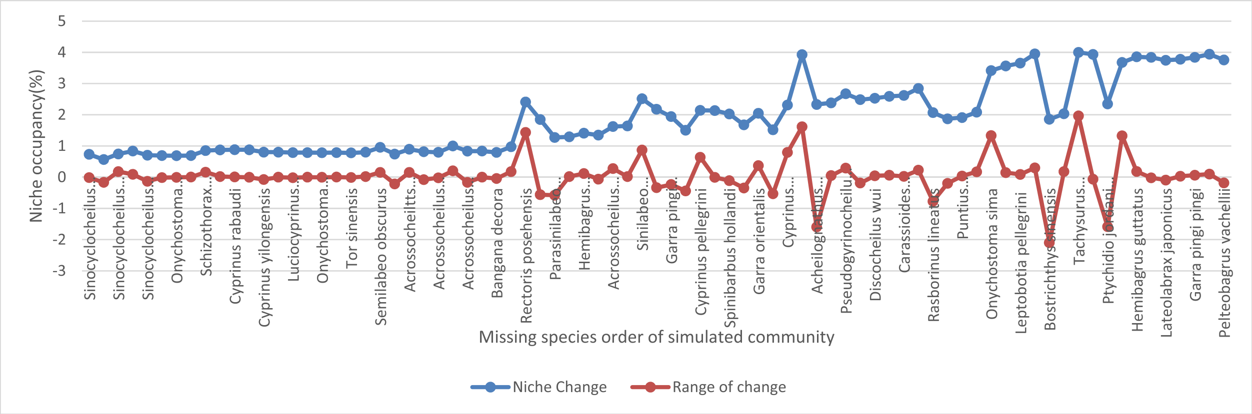

FIG. 4.31 – Amplitude of niche change for *Pelteobagrus fulvidraco* when species in the "primitive community" were removed one by one.

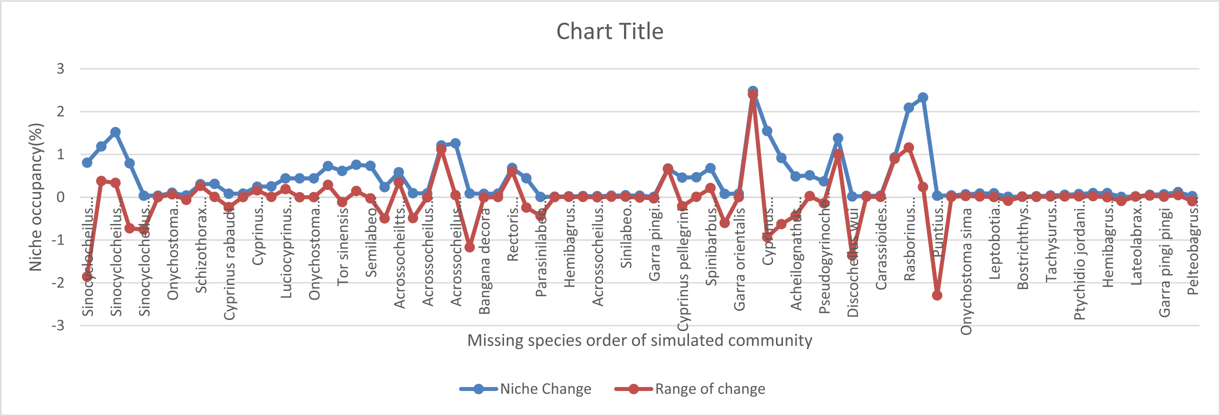

Fig. 4.32 – Amplitude of niche change for *Opsariichthys bidens* when species in the "primitive community" were removed one by one.

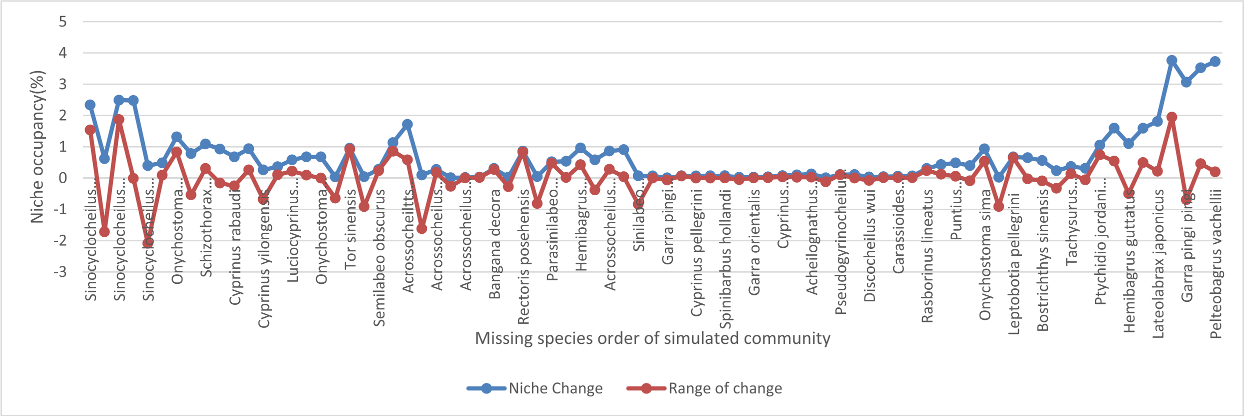

Fig. 4.33 – Amplitude of niche change for *Ancherythroculter lini* when species in the "primitive community" were removed one by one.

49 corresponding competitive fish and 30 reciprocal fish. The maximum niche decrease of *Ancherythroculter lini* happens after the deletion of *Sinocyclocheilus macrocephalus, and* the maximum niche increase of *Ancherythroculter lini* occurs after the deletion of *Sinocyclocheilus grahami tingi.*

4.2.1.25 Rhodeus ocellatus (Kner, 1867)

When we deleted 79 species of fish from the “primitive community” one by one, the niche of *Rhodeus ocellatus* (Kner, 1867) varied from 0.006% ~ 3.7226%. The maximum extent of each deletion was 3.7166%. As shown in figure 4.34, there were 46 corresponding competitive fish and 33 reciprocal fish. The maximum niche decrease of *Rhodeus ocellatus* happens after the deletion of *Cyprinus longzhouensis, and* the maximum niche increase of *Rhodeus ocellatus* occurs after the deletion of *Zacco platypus.*

4.2.2 Simulated Community Performance After Species Removal

Taking the initial niche occupation of the 104 species of fish as the reference standard, and assuming that some species disappear one by one, we compared increases and decreases in the niche occupation of each fish species after the removal of each other fish species to evaluate niche correlations between pairs of fish. If the niche occupation value decreased or increased, the removed fish was considered a “mutual benefit type” or “competitive type.” If the niche occupation value remained unchanged or changed very little, it was deemed a “non-competitive type.”

“Competitive,” “mutually beneficial,” and “non-competitive” are represented by “1,” “2,” and “3” in the model. The model analysis results for 74 fish and 25 fish in the “subunit community” were clustered. Figure 4.35 shows that most fish were “competitive” or “mutually beneficial.”

The 79 species of fish were roughly divided into four groups. The first group (the majority) was upstream fish. The second largest group was downstream fish, followed by the fish of the middle reaches, and, finally, highland or cavefish (see table 4.12).

The subcommunity had four clusters of relationships with the removed 79 species: category 1 included two species; category 2 included nine species; category 3 included eight species, and category 4 included six species. In total, 25 fish species exhibited different types of interspecies relationships (see table 4.13).

The classification of 104 fish based on relationships indicated that the model classifies the overall relationships among fish spatial distributions, consistent with the real-world spatial distribution patterns of such fish. The model analysis results also indicated that fish distributed in the upper, middle, and downstream river areas differ with respect to feeding composition, and the described niche relationships comply with the basic law of the food chain. This section describes the niche competition relationships among different types of fish.

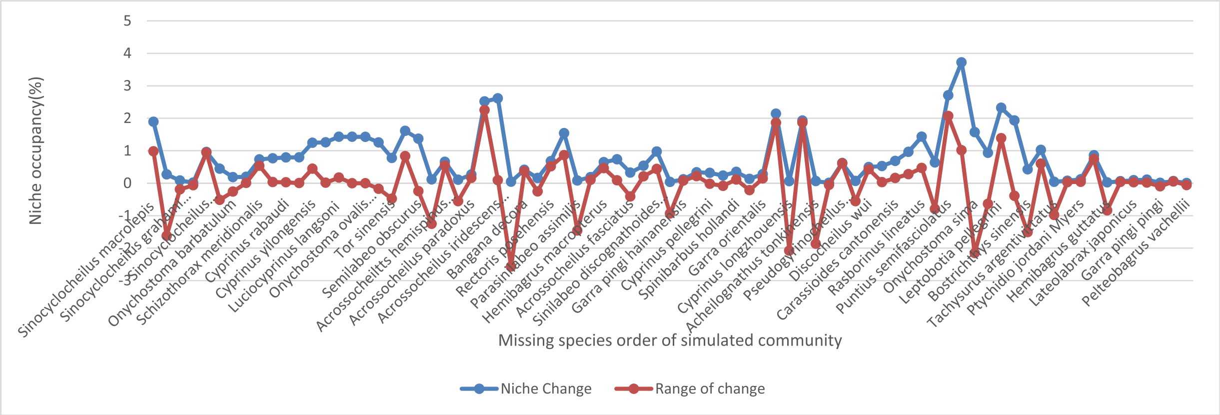

Fig. 4.34 – Amplitude of niche change for *Rhodeus ocellatus* when species in the “primitive community” were removed one by one.

Fig. 4.35 – The response of the “subunit community” to 79 species.

Tab. 4.12 – Cluster characteristics of the 79 fish species removed.

Cluster group	Fish species	Main geographical distribution characteristics
1	*Procypris merus*, *Cyprinus rabaudi*, *Cyprinus fuxianensis*, *Sinocyclocheilus macrocephalus*, *Sinocyclocheilus anophthalmus*, *Luciocyprinus langsoni*, *Folifer brevifilis brevifilis,Tor sinensis*, *Onychostoma sima*, *Onychostoma ovalis rhomboides*, *Onychostoma macrolepis*, *Sinilabeo rendahli*, *Parasinilabeo assimilis*, *Sinilabeo discognathoides*, *Sinilabeo discognathoides wui*, *Discocheilus wui*, *Rectoris posehensis*, *Discogobio brachyphysallidos*, *Mystacoleucus marginatus*, *Pseudocrossocheilus bamaensis*, *Zacco platypus*, *Luciobrama macrocephalus*, *Spinibarbus sinensis*, *Spinibarbus hollandi*, *Acrossocheilus iridescens iridescens*, *Acrossocheilus paradoxus*, *Acrossocheilus clivosius*, *Osteochilus salsburyi*, *Garra pingi hainanensis*, *Garra orientalis, Balitora kwangsiensis*, *Sinibotia pulchra*, *Tachysurus argentivittatus*, *Carassius Auratus gibelio*, *Bostrichthys sinensis*, *Anabas testudineus*	Mainly upstream
2	*Cyprinus pellegrini*, *Cyprinus longzhouensis*, *Semilabeo obscurus*, *Bangana decora*, *Discogobiolongibarbatus*, *Discogobio tetrabarbatus*, *Onychostoma lini*, *Onychostoma barbatulum*, *Acrossocheilus beijiangensis*, *Acrossocheilus fasciatus*, *Acrossocheilus fasciatus*, *Acrossocheiltts hemispinus hemispinus*, *Carassioides cantonensis*, *Rasborinus lineatus*, *Pseudogyrinocheilus prochilus*, *Micronemacheilus pulcher*, *Pelteobagrus intermedius*, *Spinibarbus denticulatus denticulatus*, *Ptychidio macrops*, *Lateolabrax japonicus*, *Garra pingi pingi*, *Pelteobagrus vachellii*, *Hemibagrus macropterus, Ptychidio jordani*, *Hemibagrus guttatus*, *Acrossocheilus labiatus*, *Leptobotia pellegrini*, *Leiocassis crassilabris*, *Acheilognathus tonkinensis*, *Takifugu ocellatus*	Midstream
3	*Semilabeo notabilis*, *Cyprinus multitaeniata*, *Ochetobius elongatus*, *Pseudolaubuca sinensis*, *Squalidus argentatus*, *Hemiculter leucisculus*, *Puntius semifasciolatus*, *Pelteobagrus fulvidraco*, *Siniperca kneri*, *Xenocypris argentea*, *Mylopharyngodon piceus*, *Ctenopharyngodon idella*, *Hypophthalmichthys molitrix*, *Hypophthalmichthys nobilis*, *Elopichthys bambusa*, *Ancherythroculter lini*, *Megalobrama terminalis*, *Parabramis pekinensis*, *Squaliobarbus curriculus*, *Misgurnus anguillicaudatus*, *Cirrhinus molitorella*, *Rasbora steineri, Opsariichthys bidens*, *Cyprinus carpio*, *Carassius auratus auratus*, *Channa maculata*, *Rhodeus ocellatus*, *Lcucosoma chinensis*, *Rhinogobius giurinus*	Downstream

Tab. 4.12 – (continued).

Cluster group	Fish species	Main geographical distribution characteristics
4	*Garra pingi yiliangensis*, *Cyprinus chilia*, *Sinocyclocheilus macrolepis*, *Sinocyclocheilus yangzongensis*, *Sinocyclocheilus microphthalmus*, *Sinocyclocheilus macrolepis*, *Cyprinus yilongensis*, *Sinocyclocheilus grahami tingi*, *Schizothorax meridionalis*	Primarily special habitats, such as plateaus or caves

Tab. 4.13 – Cluster characteristics of 25 fish species in the "subunit community."

Type	Fish species
1	*Hypophthalmichthys molitrix*, *Xenocypris argentea*
2	*Lcucosoma chinensis*, *Hemiculter leucisculus*, *Cyprinus carpio*, *Rhodeus ocellatus, Opsariichthys bidens*, *Squalidus argentatus*, *Ancherythroculter lini*, *Cirrhinus molitorella*, *Siniperca kneri*
3	*Squaliobarbus curriculus*, *Megalobrama terminalis*, *Carassius auratus auratus*, *Ochetobius elongatus*, *Rhinogobius giurinus*, *Pseudolaubuca sinensis*, *Channa maculata*, *Misgurnus anguillicaudatus*
4	*Elopichthys bambusa*, *Mylopharyngodon piceus*, *Ctenopharyngodon idella*, *Hypophthalmichthys nobilis*, *Pelteobagrus fulvidraco*, *Parabramis pekinensis*

4.2.3 The Evolutionary Characteristics of the "Subunit Communities"

4.2.3.1 The Changing Patterns of the "Subunit Community"

After 79 rounds of species removal, the niche after species removal (A'_1) minus the niche before species removal (A) was the niche change. Thus, the final niche of each species in the "subunit community" was $\sum (A'_1 - A_i)$, $i = 1, 2, 3, \ldots, 79$. This value was used as the final niche change for various fish in the "subunit community" to measure the status of the "subunit community" in the final subunit niche after succession. The analysis uncovers one species with an absolute niche change value ≥10%, two species with an absolute niche change value ≥5% and <10%, and six species with an absolute niche change value <0, corresponding to niche loss (see table 4.14). As the number of species in the community decreased, 80% of the fish species niches in the "subunit community" expanded to varying degrees, and the remaining 20% of the species niches were compressed. The niche gain for the community species during succession was not proportional to species body size. *Mylopharyngodon piceus*, grass carp, silver carp, bighead, and *Elopichthys bambusa* are all large fish. In the "original community" composed of 104 species of fish, the silver carp occupied more than 10% of the niches, and the other four species had similar niches. In comparison to the "original community," succession in the "subunit community" showed that although the *Elopichthys bambusa* niche increased, this increase was less than the niche increases in *Mylopharyngodon piceus*, grass carp, silver carp, and bighead. In the real-word data, *Elopichthys bambusa* niche increased by more than 5%. These results indicated that the parameters of fish form included niche information and were somewhat consistent with the real-world observations. The "subunit community" gradually evolved into a community dominated by *Mylopharyngodon piceus*, grass carp, silver carp, bighead, and *Elopichthys bambusa*, and the niche advantage of these five species was about 50%, indicating that the species diversity of the community decreased and the niches of the dominant species composed of large fish became prominent. Large fish, including *Mylopharyngodon piceus, Ctenopharyngodon idella, Hypophthalmichthys molitrix, Hypophthalmichthys nobilis,* and *Elopichthys bambusa*, also occupied large niches in the"primitive community."*Hypophthalmichthys molitrix* occupied more than 10% of the niche, and the other four fish had similar niches. When the "primitive community" acted as a "subunit community," the niche of *Elopichthys bambusa* increased greatly, but this increase was significantly less than niche increases of *Mylopharyngodon piceus, Ctenopharyngodon idella, Hypophthalmichthys molitrix,* and *Hypophthalmichthys nobilis.* The final result of the model agreed with the real-world data to some degree. The niche dominance of these five fish species was about 50% when the species diversity of the community declined. The dominant species are large fish that are prominent in the system.

4.2.3.2 Succession Trends

Analysis of the reaction of 25 species of fish to 79 species of fish indicated that these fish had little impact on changes in the four major fish (*Mylopharyngodon piceus,*

Tab. 4.14 – Absolute niche after the simulated community changes into "subunit community."

Fish	$\sum (A_1' - A_i)$ (%)	Subunit community (%)
Mylopharyngodon piceus	10.745428	12.53558
Ctenopharyngodon idella	7.296465	8.642592
Hypophthalmichthys nobilis	7.131931	10.68294
Hypophthalmichthys molitrix	3.6769	14.32392
Hemiculter leucisculus	3.07087	3.85675
Pelteobagrus fulvidraco	3.011	3.757
Squaliobarbus curriculus	2.99408	3.86841
Ancherythroculter lini	2.923	3.723
Siniperca kneri	2.91154	3.86522
Elopichthys bambusa	2.82953	4.3429
Pseudolaubuca sinensis	2.81752	3.86223
Megalobrama skolkovii	2.811249	3.856686
Misgurnus anguillicaudatus	2.80735	3.86688
Channa maculata	2.3955	3.3709
Cyprinus carpio	2.38339	3.82759
Parabramis pekinensis	2.299093	3.859293
Lcucosoma chinensisLcucosoma chinensis	1.98299	3.8274
Ochetobius elongatus	1.2908	1.70556
Carassius auratus auratus	0.82834	1.42218
Xenocypris argentea	−0.031	0.052
Rhinogobius giurinus	−0.29253	0.51655
Cirrhinus molitorella	−0.3175	0.0096
Rhodeus ocellatus	−0.9047	0.006
Squalidus argentatus	−1.21162	0.19488
Opsariichthys bidens	−2.6397	0.0244

Ctenopharyngodon idella, Hypophthalmichthys nobilis, and *Hypophthalmichthys molitrix*). This indicated that the fish community patterns in the Pearl River have formed over evolutionary time, and it is usually difficult for changes in other species to affect this pattern. According to Lu (1990), the fishing output of the middle and lower reaches of the Pearl River reached 40%–50% in the 1980s, and in this output, *Mylopharyngodon piceus, Ctenopharyngodon idella, Hypophthalmichthys nobilis,* and *Hypophthalmichthys molitrix* were primarily the dominant species. In recent decades, human activities have greatly changed the river ecosystem. These habitat changes have affected fish diversity and distribution patterns, especially those of dominant and rare species. Some of these fish have become endangered, while others have disappeared or gone extinct. It is meaningful to study changes in fish distribution patterns in order to understand species' roles and the impact of each fish on other fish. Such studies will help us to maintain and restore the structure and function of the ecosystem species community.

4.2.3.2.1 Negatively Correlated Variants

For the 25 fish species in the "subunit community," changes in the community niche were negatively correlated with increases in "primitive community" species, such as *Mylopharyngodon piceus, Ctenopharyngodon idella, Hypophthalmichthys molitrix, Hypophthalmichthys nobilis,* and *Elopichthys bambusa.* As the community species decreased, the ecological niche increased continuously; the initial niche of *Mylopharyngodon piceus* was 1.79%, and the niche increased to a maximum value of 12.83%, which corresponded to a niche elevation of 11.04% (see figure 4.36). In the figure, the dotted trend line indicates that the niche of *Mylopharyngodon piceus* was negatively correlated with species density.

The niche succession analysis suggested that the niches of species in the disturbed community were in a "disordered" state. The species in the "primitive community" were lost, and the niche change of 80% of the fish species in the "subunit community" did not exceed 5%. Moreover, the ecological niches of various fish were in a state of "alternating mutual complement" during community species change, maintaining the stable niche expansion of the dominant species in the system.

4.2.3.2.2 Positively Correlated Variants

The community niche changes of the "subunit community" species were positively associated with reductions in the "primitive community" species. The niche of *Opsariichthys bidens* decreased from 2.6641% to 0.0052% as the species were removed (see figure 4.37). Species of this type included *Rhodeus ocellatus, Rhinogobius giurinus, Opsariichthys bidens, Squalidus argentatus,* and *Carassius auratus auratus.*

Rhodeus ocellatus is a small fish in the simulated community that has a small niche in the original community. Overall, the niche of *Rhodeus ocellatus* diminished as species decreased. However, the disappearance of some fish species led to up to 4% increases in the niche of *Rhodeus ocellatus*, suggesting that these fish exist in a mutually beneficial relationship with *Rhodeus ocellatus.* Alternatively, another mechanism may adjust the balance of the community's ecological niche (see figure 4.38).

The analysis of the interspecific relationships within the simulated communities showed that the niches of some fish increased with the loss of the niches of other fish, and the niches of some fish decreased with the loss of the niches of other fish. These fish comprised the majority of the simulated communities.

4.2.3.2.3 Zigzag Patterns

The initial niche of *Megalobrama skolkovii* was 1.0454%, and the maximum niche value was 3.9841%, an increase of 2.9387% (see figure 4.39). *Megalobrama skolkovii* was a medium-sized fish in the simulated community that had a small niche in the original community. As the community species decreased, the niche of *Megalobrama skolkovii* fluctuated, with some fish removals decreasing the niche of *Megalobrama skolkovii* and some increasing this niche (up to a maximum of 4%). This alternation between competition and mutual benefit showed that *Megalobrama skolkovii* cannot adapt to environmental changes. Alternatively, some other mechanism may adjust the balance of community niches. Similar species included *Parabramis pekinensis,*

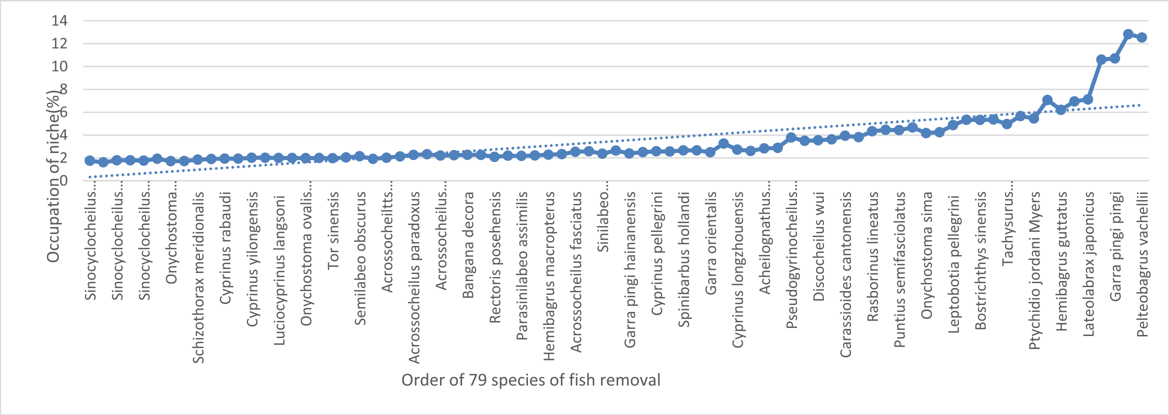

FIG. 4.36 – The niche of *Mylopharyngodon piceus* increased as 79 fish species were removed from the community.

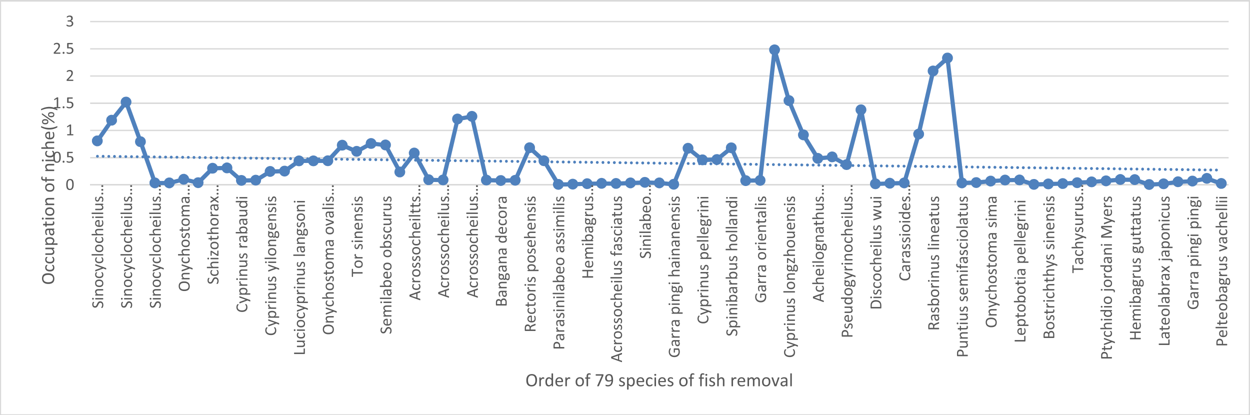

FIG. 4.37 – The niche of *Opsariichthys bidens* declined as 79 species were removed from the community.

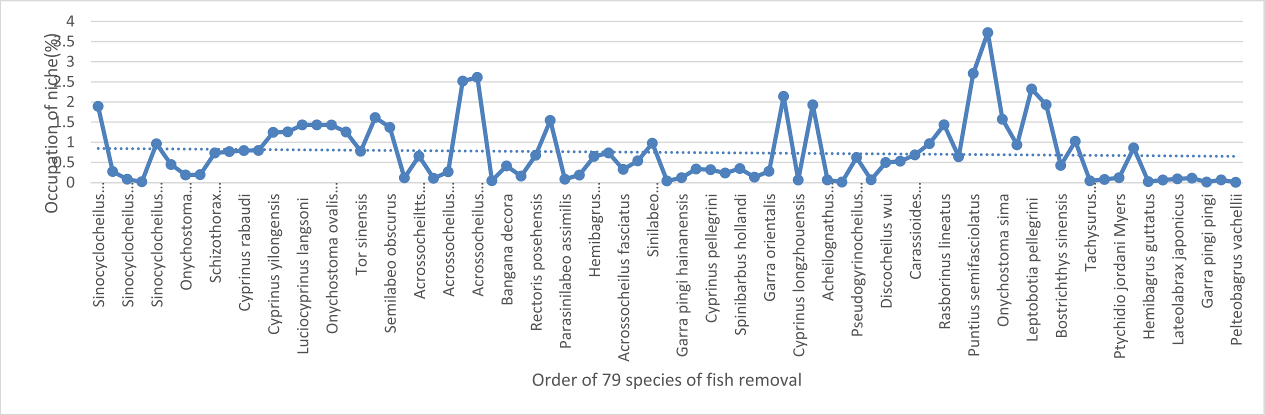

FIG. 4.38 – The niche of *Rhodeus ocellatus* decreased as 79 fish species were removed from the community.

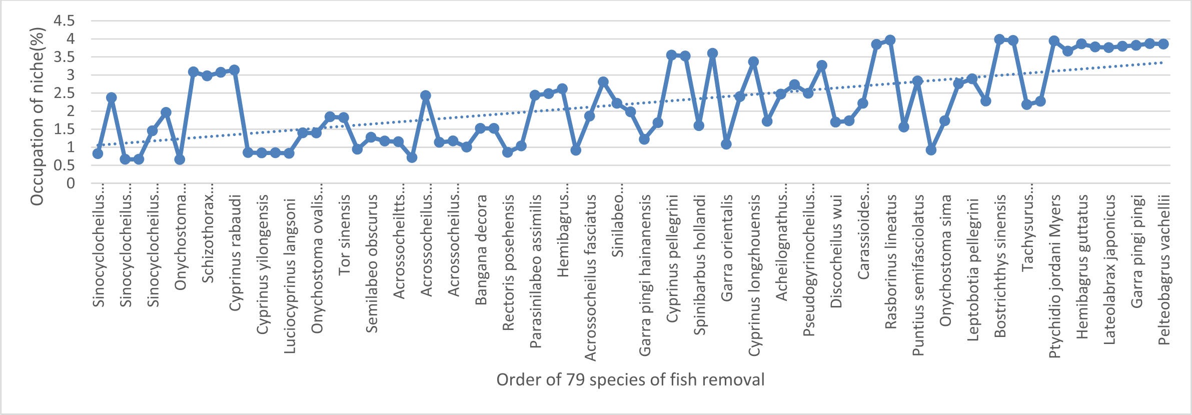

FIG. 4.39 – The niche of *Megalobrama skolkovii* changed in a zig-zag pattern as 79 fish species were removed from the community.

Megalobrama skolkovii Dybowski, *Squaliobarbus curriculus, Misgurnus anguillicaudatus, Pelteobagrus fulvidraco, Pseudolaubuca sinensis, Lcucosoma chinensis, Ochetobius elongatus, Siniperca kneri, Cirrhinus molitorella, Hemiculter leucisculus, Channa maculata, Cyprinus carpio, Ancherythroculter lini,* and *Xenocypris argentea.*

Chapter 5

Fish Community Reconstruction and Case Study

The basic characteristics of a biological community include species diversity, community growth form and structure (*i.e.*, spatial structure, temporal composition, and species structure), dominant species (*i.e.*, species whose size, number, or activity have decisive effects on community characteristics), relative abundance (*i.e.*, the relative proportions of different species in a community), and nutrition structure. From small organisms to large animals and plants, a community of species is not a collection of many separate species; it is instead a complex ecosystem formed due to interaction mechanisms that include resource competition, nutritional symbiosis, quorum sensing, and gene transfer (Chen *et al.*, 2021; Cao and He, 2015; Cai *et al.*, 2002). The community is in a dynamic succession pattern that is constantly changing, and ecological processes can be understood from changes in species distribution, abundance, and spatial patterns (Tanner *et al.*, 1995).

In natural ecosystems, species are interdependent and are characterized by many weak interactions in addition to a few strong interactions (*e.g.*, the likelihood that one species will be consumed by another). In the food web system, the types of interaction between weak and strong communities are important for the permanence and stability of community formation (McCann *et al.*, 1998). Interactions are the bonds of community stability (Stachowicz, 2001). Fish species co-exist by adjusting their abundance, body size, and age at sexual maturity (Jennings *et al.*, 1998). Community composition and distribution are adaptive characteristics, formed over species evolution, that reflect the state of resource utilization (Wang *et al.*, 2006; Hanskii, 1999). Because of the unprecedented loss of biodiversity due to human activities, current community research focuses on species succession and changes in dominant species, as well as the functional role and maintenance of species in the ecosystem food chain, in order to reveal the relationship between ecological function and community niche (de Mazancourt, 2001).

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5.1 River Ecosystems

Aquatic ecosystems can be divided into abiotic environments and biotic communities. The abiotic environment includes water bodies and their carriers, as well as sunlight, atmosphere, water, inorganic matter, and organic matter (*e.g.*, proteins, carbohydrates, lipids, and humus). The abiotic environment provides energy, nutrients, and space for living organisms. Every water body, including ponds, lakes, reservoirs, and rivers, is a water ecosystem.

Communities are classified according to their ecological functions into producers (*e.g.*, phytoplankton and aquatic vascular plants), consumers (*e.g.*, zooplankton, benthic animals, and fish), and decomposers (*e.g.*, bacteria and fungi); some bacteria also act as producers. Producers use the energy and nutrients of the abiotic environment to survive, while consumers and decomposers use producers in a food chain. According to the law of energy transfer, an ecological niche equilibrium can be realized among different biological levels. The distribution patterns of various organisms are the result of long-term adaptation and natural selection.

The number of water resources and terrestrial nutrients determines the state of river productivity. Environmental diversity affects the structure of basic organisms, while the structure of the food chain determines the function of the river ecosystem, the structure of the fish community, the distribution patterns of species diversity, and the construction mechanisms of the fish community. These factors contain many elements of the ecosystem as well as regional environmental characteristics. Understanding the mechanism of biological community construction from the perspective of the structural characteristics of species themselves is a new method in community ecology research. This study will provide different perspectives that may help to clarify ecosystem function, biodiversity maintenance, and functional community composition. The diverse patterns of species coexistence and the functional complementary mechanisms of niche overlap in fish communities are signs of mature communities and a stable systematic environment. Species attributes and environmental conditions together determine the niche allocation of the community (Mason *et al.*, 2008). In developing community systems, organismal dispersal capacity may determine the spatial extent of species distribution (Heino *et al.*, 2015), and ecosystems that are unstable are constantly disturbed at different frequencies and intensities. Therefore, natural communities are usually in a state of dynamic equilibrium. Community structure in river systems is determined by the spatiotemporal processes of species competition and niche allocation (Vanschoenwinkel *et al.*, 2010). An understanding of interspecific niche relationships is necessary in order to maintain ecosystem function and to ensure that ecosystem functions meet the needs of human development.

In addition to natural disasters, the factors that cause drastic changes in the river ecosystem include the obstruction of river connectivity, the smoothing of channels, the hardening of riverbeds, the crowding of the river space, water reductions, changes in hydrological characters, and water pollution. Changes in these factors are most likely to affect higher-order aquatic species, such as aquatic animals, as these organisms need spawning grounds for reproduction and aquatic plants.

Fish are particularly affected by these changes. As shown in the food analysis section, fish use primary phytoplankton, as well as high-grade plants, animals, humus, and almost all organic matter in aquatic ecosystems. Fish are the main biological group affecting the river ecosystem. The study of the functional mechanisms of fish community niche formation is of great significance to the construction and maintenance of fish communities. This work helps to ensure the optimal composition of river ecosystem functional groups and to achieve the goal of the functional guarantee of river ecosystems based on human needs.

5.1.1 River Structure

The total water reserves of the earth's hydrosphere are 1.386 billion cubic kilometers, most of which are held in oceans, rivers, lakes, reservoirs, marshes, and soils. Some of this water is in solid form in vast polar ice sheets, glaciers, snow packs, and frozen soils; a small amount of water exists as a vapor, primarily in the atmosphere. In total, 1.338 billion cubic kilometers of water are in the ocean, accounting for 96.5% of the total reserves, and only 2.53% of the total water reserves are freshwater. The water distributed on the continent is about half surface water and half groundwater. Surface water bodies are produced by rainfall, melting glaciers, and melting snow. During our planet's evolution, water flows have fluctuated from high to low, carving long, narrow concave channels in the earth's surface and forming a connected network. At the lower end of each channel is the mouth of a river. The water that eventually flows into the ocean is called the outflow river. Rivers that eventually flow into inland lakes or disappear into deserts are known as internal flow rivers.

The river is a complete continuum, consisting of upper and lower reaches as well as left and right banks. Most of the places of origin of rivers are springs, streams, glaciers, lakes, or marshes. In the middle reaches of a river, the slope is gradual and gentle, the river channel becomes wider, and there are often floodplains on both sides of the river. Changes in erosion and deposition are not obvious in the middle reaches, and the riverbed is relatively stable. The lower reaches of river channels are generally in plain areas. In this part of the river estuaries, the channel is broad, the riverbed slope and flow velocity are low, deposition is obvious, and shoals are abundant. Estuaries tend to form deltas due to the rapid deceleration of river flow and the associated sediment deposition. River width describes the transverse distance across a river and its adjacent vegetated area. The factors affecting river width include edge conditions, community composition, environmental gradients, and disturbances (including anthropogenic activities); these can affect adjacent ecosystems. Connectivity and width are important structural characteristics of the river ecosystem.

The structure of the river also includes the ecosystem. River morphological structure includes the biological species, the population sizes, spatial population patterns, temporal changes in the population, and the vertical and horizontal structure of the community. River nutritional structure, a functional unit that tightly links biotic and abiotic factors associated with nutrition, is composed of three major functional groups: producers, consumers, and decomposers. There is a closed cycle of matter and energy flow between these functional groups and the environment.

5.1.2 River Ecological Function

The longitudinal zonation, water carrier, and flow of a river determine its ability to carry materials, such as nutrients and water, into an ecosystem. This transport function is part of the earth's material and energy cycle.

The continuity of the upper and lower reaches of the river, the complete spatial system between the left and right banks, and the moist range of the water flow from the inner habitat and the marginal habitat, which together determine the habitat function of the river ecosystem. Habitat is an area where plants and animals (including humans) can live, grow, feed, reproduce, and perform other important parts of the life cycle. The inner habitat is the direct environment for aquatic life. Water is an essential element for living things, in conjunction with elements such as carbon (C), hydrogen (H), oxygen (O), nitrogen (N), phosphorus (P), sulfur (S), potassium (K), magnesium (Mg), calcium (Ca), silicon (Si), iron (Fe), manganese (Mn), zinc (Zn), copper (Cu), Boron (B), Molybdenum (Mo), chlorine (Cl), sodium (Na), and nickel (Ni). The aquatic communities interact with the aquatic environment to form a dynamic equilibrium with a certain structure and function *via* the circulation of materials and the flow of energy.

Aquatic organisms primarily include bacteria, fungi, phytoplankton, zooplankton, benthic organisms, aquatic plants, and fish. The basic components of aquatic life are carbon, hydrogen, oxygen, nitrogen, phosphorus, sulfur, iron, zinc, and other elements. Carbon, hydrogen, and oxygen together account for more than 90% of the dry weight of plants and are the main components of plants. These elements exist in the form of various carbohydrates, such as cellulose, hemicellulose, and pectin, which are components of the cell wall. Plant organisms use photosynthesis to synthesize sugars from water nutrients and solar energy during growth, as well as to form active substances, such as certain celluloses and plant hormones. Carbon, hydrogen, and oxygen are also components of sugars, fats, and acids. Plants are primary producers. In the food chain, plants provide energy and growth elements for animals and in this way participate in the material and energy cycle of the ecosystem.

Organisms form the structure of the food chain, participate in the energy and material cycle, and maintain the balance of aquatic ecosystems. Phytoplankton, as producers, is at the first trophic level of the food chain, while phytoplankton-consuming zooplankton is at the second trophic level. Zooplankton consumers, such as small fish and shrimp, are at the third trophic level, and large fish are at the next trophic level. Humans that consume fish are participating in the material and energy cycle of the river ecosystem. The size of the catch depends largely on plankton production. Fish biomass can control the food chain of the aquatic ecosystem, regulate the structure of the food chain under the energy system, and help balance the ecosystem.

The food chain and the food web are complex nutrient relationships among species. A trophic level is the sum of all the species at a particular link in the food chain. For example, producers in the Chloroplastida and all autotrophs form the first trophic level at the beginning of the food chain. All of the animals that feed on producers, primarily chloroplastids, fall into the second trophic level, which can also be considered the herbivore trophic level. The third trophic level includes all carnivores that feed on herbivores. Logic dictates that a further fourth and fifth trophic level may exist (*e.g.*, second and third carnivore trophic levels). In an ecosystem, only about 10% of the energy at each trophic level is transferred to the next trophic level. As a result of the food relationship, living things are mutually restricted as the energy and nutrients produced by photosynthesis are transferred along the food chain. Only about 10% of the material and energy is transferred to the next trophic level. The remaining 90% is dissipated into the environment as heat. This is known as Lindemann's 10th law, which states that the rate of energy conversion between organisms is influenced by environmental conditions.

The productivity of water bodies and the transformation of bait organisms also differ among regions. Table 5.1 shows the P/B coefficients of various bait organisms in lakes and reservoirs in different regions of China (in a given water area, P = annual bait production, and B = annual average biomass). These data indicate the impact of the environment on water productivity and the utilization of organisms (see table 5.2).

However, the relationships among food chains within communities or ecosystems are complex, and most organisms, with the exception of producers and herbivores, tend to belong to more than one trophic level. The trophic level of many organisms varies with age and conditions.

Tab. 5.1 – P/B coefficients of different bait organisms across regional lakes and reservoirs.*

Region	P/B ratio				
	Phytoplankton	Zooplankton	Zoobenthos	Periphyton	Small fish and shrimp
North China	40–90	15–30	2–6	40–80	1.5–2.0
Central and eastern regions of China	100–1150	25–40	3–6	80–120	2.2–2.5
China plateau area	40–120	20–35	2–5	40–100	1.5–2.5
Southern China	150–200	30–40	4–8	100–120	2.0–2.5

*See SC/T 1149-2020.

Tab. 5.2 – Maximum utilization rates and bait coefficient for different ecological nutrient types.**

Bait type	Maximum utilization rate allowed (%)	Bait coefficient
Organic detritus	50	200
Phytoplankton	40	80
Zooplankton	30	10
Aquatic vascular plant	25	100
Zoobenthos	25	6
Periphyton	20	100
Small bait fish	20	4

**See SC/T 1149–2020.

The trophic level reflects species composition, functional level, the mode of material and energy flow and transfer in the ecosystem, and the environmental state. Community niche is closely related to trophic level. To form a functional community, organisms first must determine their niche based on a trophic cascade effect. Community species support ecosystem functions. There are many species at the same trophic level, which is of great significance for the construction of functional ecosystem communities.

5.1.3 Composition of the Fish Diet

Fish species, as consumers in aquatic ecosystems, are differentiated into herbivores, carnivores, and omnivores. This demonstrates the ecological dominance of fish. The composition of the fish community is closely related to the bait organisms in the aquatic ecosystem, and the fish community must be constructed based on the characteristics of the food chain in the environment. There are many bait organisms in rivers, but it is difficult to identify bait species from the digestive tract because bait organisms are digested quickly and do not leave distinguishable remains. Figure 5.1 shows the dietary composition of 10 species of fish in the 1980s. The fish species included are *Tenualosa reevesii* (Richardson, 1846), *Clupanodon thrissa* (Linnaeus, 1758), *Coilia grayii* (Richardson, 1845), *Coilia mystus* (Linnaeus, 1758),

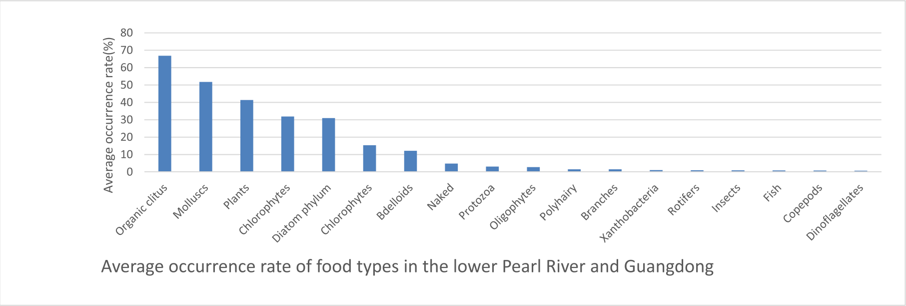

Fig. 5.1 – Components of the diets of 10 fish species in the Pearl River.

Mylopharyngodon piceus, Ctenopharyngodon idella, Squaliobarbus curriculus, Erythroculter pseudobrevicauda (Nichols, 1927), *Megalobrama terminalis* (Richardson, 1846), and *Parabramis pekinensis.* The diets of these fish include many species of zooplankton, benthic animals, aquatic plants, and other fish.

An analysis of gut contents of *Megalobrama terminalis* from the lower reaches of the Pearl River and the associated river network was performed. Although the identification of consumed food items was complicated by incomplete digestive residues and morphological ambiguity, diatoms, green algae, Cyanophyta, Gymnophyta, dinoflagellates, Xanthophyta, polychaetes, oligochaetes, protozoans, rotifers, Cladocera, Copepoda, insects, leeches, aquatic plants, and fish were detected in the gut samples. Figure 5.2 demonstrates that fish consume a wide range of foods, that fish are picky eaters, that the dietary composition of the same fish is different in different waters and that fish feed on different items based on environmental conditions. The results showed that the main foods of *Megalobrama terminalis* were organic detritus (about 60%–70%), mollusks (about 35%–70%), plants (about 14%–57%), and zooplankton (about 13%–55%) (Yuguo Xia *et al.*, 2017).

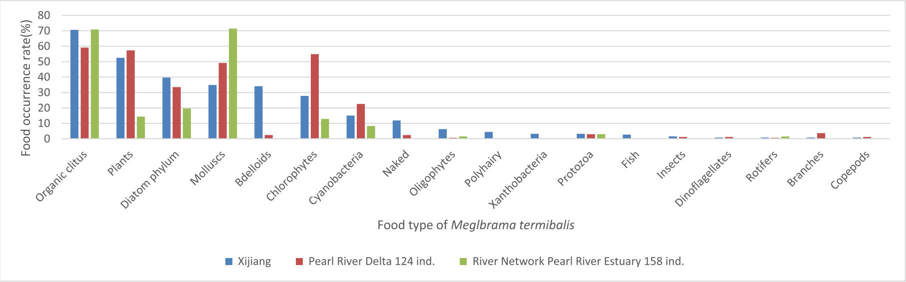

FIG. 5.2 – Frequency of food items detected in the intestines of *Megalobrama terminalis.*

Individual *Megalobrama terminalis,* including small juveniles, large juveniles, sub-adults, and adults, were collected from the middle and lower reaches of Pearl River for analysis of intestinal food samples. The weight percentage of residue (*i.e.*, a recognizable substance in the digestive tract) in the intestine with respect to average biomass was more than 84%. Many types of juvenile prey were consumed. In addition to the residues, the most commonly consumed taxa were the Chaetophorales (5.5% W, W = the weight percentage of residue), followed by the Cirsidiales (0.2% W) and crustaceans (0.2% W). Table 5.3 shows that there were no significant differences in the proportions of intestinal contents among groups and that the percentage of detritus consumed as the main food item changed little among groups. However, the percentage of prey items varied greatly among groups (see table 5.3; Yuguo Xia *et al.*, 2020).

The small juveniles fed mainly on prey in the Myrosiales, Chaetophorales, Chlorophyta, and Sarcoidoidea; these groups accounted for 87.1% of the total intestinal contents. Large juveniles fed mainly on residues, mussels, Chaetophorales,

Tab. 5.3 – Identifiable black amur bream prey in each size group sorted by taxa. Items with a percentage by weight over 0.1% and a percentage by number over 1% are listed. Percentage by number excludes detritus.

Food item	Small juvenile (N = 9)	Large juvenile (N = 6)	Sub-adult (N = 15)	Adult (N = 7)
Percent by weight % (%W, mean ± SD)				
Detritus	94.1 ± 16.4	84.5 ± 33.3	96.8 ± 7.0	92.7 ± 14.8
Chaetophorales	5.5 ± 16.4	1.4 ± 3.0	0	0
Mytiloida	0	13.8 ± 33.9	3.1 ± 7.1	7.2 ± 14.9
Coscinodiscales	0.2 ± 0.2	0.02 ± 0.04	0.08 ± 0.15	0.05 ± 0.08
Araphidiales	0.2 ± 0.5	0.05 ± 0.12	0.04 ± 0.08	0.01 ± 0.01
Ulvales	0	0.1 ± 0.3	0	0
Percent by number % (%N, mean ± SD)				
Coscinodiscales	53.6 ± 39.3	9.4 ± 22.6	45.0 ± 32.6	50.2 ± 36.7
Chaetophorales	12.5 ± 35.3	43.4 ± 49.1	0	0
Chlorococcales	11.7 ± 26.0	0.1 ± 0.3	16.0 ± 29.7	14.4 ± 21.1
Mytiloida	0	16.7 ± 40.8	0.02 ± 0.03	0.02 ± 0.04
Araphidiales	5.9 ± 12.6	2.4 ± 5.8	11.7 ± 11.2	6.7 ± 7.9
Chroococcales	0.1 ± 0.3	0	0	26.2 ± 38.7
Osillatoriales	1.0 ± 2.9	0	9.9 ± 17.5	0
Ulvales	0	6.1 ± 13.5	0	0
Biraphidinales	4.4 ± 6.5	21.8 ± 36.0	15.5 ± 30.3	1.1 ± 1.7
Aulonoraphidinales	9.3 ± 20.5	0	0.5 ± 1.5	0.4 ± 0.6

*(Yuguo Xia *et al.*, 2020).

and *Ulva*. The weight of intestinal residues and mussels in the adult population was 92.7% and 7.2%, respectively. In the large juveniles, the main items consumed were Chaetophorales, accounting for 43.4% of the total, while the subadults preyed mainly on Cirsidiales, accounting for 45.0% of the total, in addition to small amounts of Pycinidae and mussels. In the adult population, the main feeding targets were Coscinodiscales (50.2%). Also found were a few shell sutures, double shell sutures, tube shell sutures, and mussels.

In a water body, fish food sources are diverse. Analysis of the feeding habits of *Megalobrama terminalis* at different growth stages showed that the dietary composition of fish differs among growth stages. The results showed that fish trophic levels vary across developmental stages and productivity structures. This complexity must be carefully considered when constructing fish systems during ecosystem restoration. Fish use a certain range of food resources, and species communities with more fish can utilize diverse food sources efficiently.

The δ13C and δ15N contents in potential food source samples ranged from 31.00‰ to 13.07‰ and from 2.87‰ to 17.35‰, respectively. C4 plants on the riverbank had the highest δ13C levels and the lowest δ15N levels, with an average of 13.29 ± 0.21‰ and 4.06 ± 1.44‰, respectively. The lowest levels of δ13C and the highest levels of δ15N were found in *Corbicula fluminea* and *Macrobrachium nipponense*, respectively. The δ13C and δ15N levels in other potential food groups varied greatly, with some degree of overlap. The means and standard deviations of δ13C and δ15N for each group and a potential food source are shown in table 5.4. Among the potential food sources, c/n (% by weight, c = total carbon in food, n = total nitrogen in food) ranged from 3.17% to 77.32%, with the value of *Macrobrachium nipponense* being the lowest and the value of river bank C4 plants being the largest (0.02%–0.15%; see table 5.5). The contribution of 12 potential food species to the small-sized larvae ranged from 0.05% to 0.10%, the highest of which was *Corbicula fluminea*, and bank C4 plants were the lowest. Other contributions to juveniles were similar. In all groups, the contribution of the riparian C4 plants was low, while the contributions of zooplankton, *Macrobrachium nipponense*, and *Corbicula fluminea* were high. These taxa are very important to the *Megalobrama terminalis* population. The contributions of *Macrobrachium nipponense* and *Corbicula fluminea* to the growth of *Megalobrama terminalis* also increased between juveniles and adults; this was the result of dietary changes during fish growth (see table 5.4).

The total breadth of the nutrient niche was assessed using total niche width (TNW) to determine enteral nutrients and using corrected standard elliptic area (SEAC) to identify stable isotopes. Higher values corresponded to a greater niche width in a given group. The results of both analyses were similar and showed that the width of the nutrient niche increased with body length. The TNW and SEAC analyses found the highest values in the adult group, followed by the sub-adults, large juveniles, and small juveniles (see table 5.6).

During growth, juvenile fish have been observed to prefer zooplankton, while adult fish devour more animal prey. Many previous studies in the Pearl River Delta have shown that *Megalobrama terminalis* mainly feeds on detritus. Xia *et al.* (2017) used 18S rDNA sequencing to analyze the contents of the gut and found that juvenile *Megalobrama terminalis* had abundant plant ingredients, while adults had abundant benthic animals. Stable isotopes can be used to determine carbon sources and nutrients (Carreonmartinez and Heath, 2010), but it is preferable to detect specific nutrient interactions because the isotope values of potential prey often overlap (Hardy *et al.*, 2010). Stable isotope analysis showed that *Megalobrama terminalis* can use almost all food types (table 5.6); however, the different populations at different growth stages differ in specific bait utilization, and the results were consistent with the intestinal inclusion analysis. Isotopic analysis of gut inclusions identified far fewer species compared to microscopy and molecular identification (Xia *et al.*, 2017). Isotope approaches can support tracking the circulation of three foods *in vivo* (Peterson *et al.*, 1986), but they cannot yet address more than three foods (Post, 2002; Peterson and Howarth, 1985; Peterson *et al.*, 1985; tables 5.5 and 5.6).

Analysis of the dietary composition of fish species in Zhaoqing River showed that silver carp in this river section mainly feed on phytoplankton, and four groups of algae [*Melosira granulata* (Ehrenberg) Ralfs, 1861; *Melosira granulate* Her; *Melosira varians* (von Stosch, 1951); *Synedra ulna*] accounted for about 79% of the diet; detritus was not included. In the Zhaoqing river section in Guangdong, *Megalobrama terminalis* and *Cirrhinus molitorella* mainly fed on diatoms and benthic animals, while *Hypophthalmichthys nobilis* primarily consumed algae and benthic animals.

TAB. 5.4 – Summary statistics (mean ± SE) of δ^{13}C, δ^{15}N, and C/N in the different size groups of *Megalobrama terminalis* and potential prey sources in the sampling site. Values are mean ± SD.

Group/taxon	Code	N	δ^{13}C (‰)	δ^{15}N (‰)	C/N
Small juvenile	Small juvenile	11	−24.67 ± 1.75	11.60 ± 2.75	–
Large juvenile	Large juvenile	12	−25.53 ± 1.43	12.54 ± 2.44	–
Sub-adult	Sub-adult	15	−26.10 ± 1.52	13.53 ± 2.69	–
Adult	Adult	8	−25.58 ± 1.33	14.57 ± 3.09	–
Zooplankton	Zooplankton	2	−30.25 ± 1.07	9.95 ± 2.08	6.11 ± 0.66
Phytoplankton	Zooplankton	2	−27.94 ± 0.24	8.21 ± 1.13	8.40 ± 1.86
Riparian C_4 plants	C_4_P	4	−13.29 ± 0.21	4.06 ± 1.44	63.89 ± 10.35
Potamogeton sp.	Psp	6	−25.29 ± 3.26	7.45 ± 2.43	10.46 ± 1.26
Macrobrachium nipponense	Mni	9	−26.97 ± 0.66	15.95 ± 1.32	3.30 ± 0.07
Anodonta woodiana	Awo	2	−24.72 ± 0.65	6.46 ± 0.04	3.84 ± 0.06
Limnoperna fortunei	Lfo	1	−26.53	4.96	4.65
Semisulcospira cancellata	Sca	1	−24.16	9.51	3.91
Corbicula fluminea	Cfl	4	−30.27 ± 0.26	11.99 ± 0.31	4.65 ± 0.43
Bellamya sp.	Bsp	4	−22.28 ± 0.34	4.42 ± 1.02	4.14 ± 0.27
Benthic detritus	Bde	2	−26.11 ± 1.20	7.08 ± 1.50	12.57 ± 4.50
Sediment	Sediment	3	−25.23 ± 0.39	5.85 ± 0.23	10.47 ± 1.23

[*] (Yuguo Xia *et al.*, 2020).

TAB. 5.5 – Contributions of different potential prey taxa to different size groups of *Megalobrama terminalis*, according to stable isotope Bayesian mixed models. CI95%, lower – higher confidence intervals.

Prey	Small juvenile		Large juvenile		Sub-adult		Adult	
	Mean	CI95%	Mean	CI95%	Mean	CI95%	Mean	CI95%
Zooplankton	0.09	0−0.18	0.11	0−0.21	0.13	0−0.25	0.11	0−0.21
Phytoplankton	0.08	0−0.17	0.09	0−0.19	0.09	0−0.20	0.09	0−0.19
C_4_P	0.05	0−0.11	0.03	0−0.07	0.02	0−0.06	0.03	0−0.08
Psp	0.09	0−0.17	0.08	0.01−0.18	0.07	0−0.18	0.08	0−0.19
Mni	0.09	0−0.17	0.11	0−0.20	0.14	0.03−0.25	0.15	0.02−0.27
Awo	0.08	0−0.17	0.07	0−0.17	0.05	0−0.14	0.06	0−0.15
Lfo	0.09	0−0.17	0.08	0−0.17	0.06	0−0.15	0.06	0−0.16
Sca	0.08	0−0.17	0.07	0−0.17	0.06	0−0.15	0.07	0−0.16
Cfl	0.10	0−0.18	0.13	0.01−0.23	0.15	0.01−0.29	0.12	0.01−0.23
Bsp	0.08	0−0.16	0.06	0−0.14	0.04	0−0.10	0.05	0−0.13
Bde	0.08	0−0.17	0.08	0−0.18	0.09	0−0.20	0.09	0−0.19
Sediment	0.08	0−0.17	0.08	0−0.18	0.09	0−0.20	0.09	0−0.19

*(Yuguo Xia *et al.*, 2020).

Tab. 5.6 – Metrics quantifying trophic niche and individual specialization in *Megalobrama terminalis*. Same superscript letters indicate no significant differences (Kruskal–Wallis test, $p > 0.05$).

	Small juvenile	Large juvenile	Sub-adult	Adult
Taxonomic richness per gut (mean ± SD)	5.5 ± 3.0^{a}	2.8 ± 1.5^{a}	4.8 ± 2.2^{a}	4.8 ± 1.6^{a}
TNW	0.058	0.699	0.862	0.938
WIC/TNW	0.250	0.951	0.637	0.610
Diet similarity	0.339	0.185	0.375	0.386
NR (‰)	9.49	7.77	10.07	9.56
CR (‰)	5.54	4.80	6.13	3.48
CD (‰)	2.61	2.40	2.47	2.55
MNND ± SD (‰)	1.04 ± 1.07	1.37 ± 0.62	1.15 ± 1.10	1.69 ± 2.05
TA	19.22	21.74	30.87	17.52
SEA (‰)	9.446	10.041	11.240	12.957
SEA_c (‰)	10.496	11.045	12.104	15.116

[*](Yuguo Xia *et al.*, 2020).

The energy stored in organic matter in an ecosystem is carried through the food chain layer by layer. The food chain can be subdivided into the predator food chain, scavenger food chain, and parasitic food chain based on the relationships among organisms. The structure of the food web is related to species diversity, and the loss or extinction of key species greatly affects the structure of the food web (Dunne *et al.*, 2002). Intensive exploitation of fish communities often results in a significant reduction in the abundance of targeted species, affecting the structure and stability of the entire ecosystem. Intensive exploitation of fish communities often results in a significant reduction in the abundance of key species, affecting the structure and stability of the entire ecosystem. This reduction of key species is also reflected in changes in the average nutrient levels of fish communities. Declines in average nutrient levels are due to decreases in the number of large fish-eating species and increases in the number of smaller pelagic species foraging at lower nutrient levels. The decline in spawning stock biomass of traditional target species is associated with intensive fishing and long-term climate variability. In general, a decrease in the average trophic level of the entire fish community may enable the system to maintain a high fishery yield (Pinnegar *et al.*, 2002).

5.1.4 Fish Trophic Levels

The earth's biosphere is a large ecosystem. The species, abundance, biomass, life history, and spatial distributions of organisms in the system must follow the laws of energy flow and material circulation. Biotic communities are not only adapting to the environment in the ecosystem but also changing the appearance of the surrounding environment in the ecosystem. Various growth factor materials closely link biological communities together. There are more than 15 000 species of freshwater fish worldwide (Fishbase, 2021; https://www.fishbase.de/2021,0810). The composition of the fish community differs among river ecosystems. The trophic level of the fish community reflects the state of the river ecosystem. In the food chain of the ecosystem, fish species with common functional attributes at the same level can be classified into a single niche type, such as predatory niche-type fish. This classification can simplify the complicated relationships among the species in the food web and help to guide studies of the mechanisms of fish community construction and the reconstruction of fish communities in the aquatic ecosystem. The food web is also implicated in a number of other processes related to community structure, including the regulation of habitat heterogeneity, changes in community function over time with respect to the environment, productivity gradients, the direct and indirect cascade effects of predation, intra-row predation, indirect reciprocity, species competition, ecosystem stability, and nutrient dynamics. Food web analyses cannot be reduced to a few linear "trophic levels" and thus must also consider trophic cascades, as well as top-down/bottom-up mechanisms of community regulation (Polis *et al.*, 1996a; Winemiller and Polis, 1996).

The mass of existing organic matter in a community is its biomass, and the biomass and biomass accumulation rates of different types of communities differ noticeably. The biological composition of the community includes the food chain, which progresses from plants to herbivores to carnivores. Due to various types of energy consumption, the productive forces gradually decrease. Primary productivity only accounts for 0.1%–1% of solar energy, while secondary productivity represented by animals only accounts for 10% of the former.

Each kind of living creature obtains the energy needed for survival, growth, and reproduction in a unique way. There are complex food relationships among the organisms in an ecosystem; fish can be divided into herbivores and carnivores according to their feeding habits. There may be two to five trophic levels. In one system, with the exception of fish at high trophic levels (more than 4.5), the trophic levels of other species were not obviously regular. This may be partially due to variability in the fish diet; that is, the fish diet may change independently according to environmental conditions to most efficiently obtain energy. Alternatively, it may be that the fish themselves have the ability to access different food sources, and the artificial trophic level classification results in a lack of comprehensive understanding of the ways in which fish obtain energy in the ecosystem.

Two species may be competitive or symbiotic, depending on their mutual interests. Relationships may be parasitic, partially symbiotic, or mutually beneficial. If two species use the same resource (niche overlap), they will compete and one species will be excluded. However, if the resource demands of one species change (niche differentiation), the two species may coexist. The longer a community has evolved, the more favorable the environment is and the more stable the species are. As more species are included in the community, the trend of community development is toward niche differentiation and species increase. The diversity of community species structures indicates that the complexity of community structure increases with the resources used in the ecosystem. Complex communities have more ecological niches, the competition among the various organisms in the community is relatively weak, and the community structure is relatively stable. Therefore, the species structure of the community reflects the environmental characteristics of the ecosystem, and the organisms in a community are in constant interaction.

When the total primary productivity of a community is greater than the total community respiration, and the net primary productivity is greater than ingestion by animals and decomposition by microorganisms, organic matter accumulates. The community then grows until it reaches a mature stage, where accumulation ceases and production and respiratory consumption are balanced. This process is called succession, and the final stage of succession is called a climax community. The productivity of the climax community is not equivalent to maximum productivity, but the biomass is maximized and the net ecosystem production is very low or even zero. In a climax community, species diversity may decrease, but the community is maximally complex and stable. Communities do not have the same processes of genetic regulation and humoral integration as individuals, and the path of succession is entirely determined by interspecies interactions and the balance of material and energy flow. Therefore, the characteristics of climax communities depend on both the environmental conditions and the species.

The trophic level depends on species composition, functional level, mode of material and energy flow and transfer in the ecosystem, and environmental state. Community niche is closely related to trophic level. To form a functional community, the organism niche must first be determined based on the trophic cascade effect. As shown in table 5.7 (Fishbase, 2021; https://www.fishbase.de/2021,0810), freshwater fish generally have a tropic level of approximately 2–4.7. The data from some regions suggest that the average trophic level of fish communities in freshwater ecosystems maybe 3.0–3.8. The average trophic level can reflect the trends in changing group compositions and trophic levels in the ecosystem.

Tab. 5.7 – Average trophic level of fish in some inland waters (Fishbase, 2021; https://www.fishbase.de/2021,0810).

	Average nutritional level
Azores	3.7991
New Zealand	3.2985
Australia	3.2714
France	3.263
USA (North America)	3.1875
Philippines	3.1838
South Africa	3.1827
Cambodia	3.1669
Zimbabwe	3.1633
Thailand	3.1524
Malaysia	3.139
Vietnam	3.1061
Angola	3.0611
Hawaii (USA)	3.0537
China	3.0374

For example, the fish are shown in table 5.8 (Fishbase, 2021; https://www.fishbase.de/2021,0810) were classified in increments of 0.5. Analysis of the proportion of freshwater fish at each trophic level in the community showed that the functions of species in different regions were plastic. The trophic level composition provides insight into the function of species diversity within the ecosystem.

Tab. 5.8 – The nutritional grade composition (%) of some fish in inland waters.

%	4.51–	4.0–4.5	3.5–3.99	3.0–3.49	2.5–2.99	2–2.49
China		2.3	7.0	49.9	27.6	13.3
Australia		7.1	18.8	46.8	22.1	5.0
Cambodia		4.7	25.2	37.3	17.3	15.6
France		13.3	9.2	49.0	21.4	7.1
Angola		3.7	10.0	46.8	24.4	15.1
Azores	57.1	14.3	28.6			
Hawaii (USA)	1.7	5.0	21.7	25.0	20.0	26.7
Malaysia		3.8	18.6	44.2	19.7	13.8
New Zealand		12.9	9.7	64.5	6.5	6.5
Philippines		6.0	22.2	39.5	19.8	12.6
South Africa	0.6	3.4	22.7	42.0	20.5	10.8
Thailand		4.1	18.5	46.3	18.6	12.5
Vietnam		2.6	17.1	43.9	22.0	14.3
Zimbabwe		6.6	19.2	38.4	22.5	13.2
USA (North America)	0.1	5.2	8.5	56.6	24.8	4.8

Of the 1581 freshwater fish recorded in China, about 1225 species (accounting for 78% of the total) have trophic levels ranging from 2.5 to 3.49 (see table 5.9), with omnivorous fish being the most common.

Tab. 5.9 – Nutritional grade distributions of major fish species in China.

Nutritional level range	Species	%
4.0–4.5	36	2
3.5–3.99	110	7
3.0–3.49	789	50
2.5–2.99	436	28
2–2.49	210	13

Xiong *et al.* (2015) found that the trophic levels of fish in Yangtze Plain floodplain lakes were 2.0–4.2, with a mean trophic level of about 3. Nearly 40% of the fish in the Yangtze Plain assemblage were omnivorous fish, which is common in aquatic food webs, especially in fish communities (Zhang *et al.*, 2013; Vanni *et al.*, 2005; Drenner *et al.*, 1996; Diehl, 1992). The results of GAM analysis showed that only fish at high and low trophic levels had relatively stable morphological characteristics; at medium trophic levels, there was not sufficient evidence of speciation. Ba *et al.* (2015) found that the trophic levels of the main biological resources in the middle reaches of the Yangtze River were between 2.42 and 4.88, but that the trophic levels of most resources were 2.83–3.61. The average trophic level of fish was 3.28, and 80.85% of all species had trophic levels greater than 2.83. This indicated that the fish community structure differed in different environments within the same river.

Ye *et al.* (2021) analyzed the trophic level of Yangcheng Lake and found that the fish community's level was 2.12–3.75 in the summer. The fish with the lowest trophic level was *Xenocypris microlepis*, while the fish with the highest trophic level was *Taenioides cirratus* (Blyth, 1860). The trophic level range was 2.56–3.71 in the autumn, with *Hypophthalmichthys nobilis* and *Culter dabryi* having the lowest and highest trophic levels, respectively. The range of fish trophic levels in the spring was 2.03–3.98, with *Ctenopharyngodon idella* and *Cultrichthys erythropterus* having the lowest and highest trophic levels, respectively. These results suggest that trophic levels also differ among water bodies. Xu *et al.* (2020) analyzed the nutritional structure of the aquatic animal food network in the Yangtze estuary and found that trophic levels ranged from 2.0 to 4.0; the trophic levels of the 12 dominant fish were lower than was previously calculated in the 1990s, with decreases from 3.80 to 2.87. In addition, the number of species and the abundance of fish at high trophic levels decreased. For example, the trophic levels of *Lateolabrax japonicus* decreased by 1.28. Finally, the proportion of low-grade carnivorous fish decreased from 20.0% to 18.6%. The results indicated that the trophic levels of a single species might change depending on the food source during environmental change.

The trophic levels of Pearl River fish ranged from 2 to 4.5, with an average trophic level of 3.40 (see table 5.10). The average trophic level of estuarine and migratory species was 3.54, and that of exotic species was 2.94. The trophic level of estuarine fish was the highest, followed by the average trophic level of native freshwater fish. The trophic level of exotic species was relatively low. This suggested that the niche of fish at low trophic levels in Chinese rivers may be vacant and that there is an opportunity for alien species to fill this niche.

Historical records indicate that the 16 fish species with trophic levels between 2 and 2.5 in the Pearl River have not changed. Table 5.10 showed that there were 10 species at the same trophic level that were invasive alien species in the community. We speculate that there are two explanations for this finding: First, the biomass of indigenous fish on the same trophic level may be insufficient, resulting in a loss of niche space and allowing the alien species to enter the niche. Thus, the invasive species coexist with the indigenous fish in the same region. Alternatively, fish in the same niche in local areas of linear rivers may have been lost, similarly giving alien species the opportunity to fill the niche. The trophic level of *Ctenopharyngodon idella* and *Hypophthalmichthys molitrix* was 2.00, and the catch output of the "four big fish" in the middle and lower reaches of the Pearl River was more than 40%

greater than historical catches, mainly due to catches of *Ctenopharyngodon idella* and *Hypophthalmichthys molitrix*. In aquatic ecosystems, productivity and nutrients cannot be exported through the food chain, and the system requires fish at lower trophic levels.

Some scholars argue that conservation efforts can be strongly complementary to all types of diversity and that systematic conservation planning is an important means of allocating limited resources (Strecker *et al.*, 2011). It has been suggested that in restoring or reconstructing ecosystem species comminutes, it is possible to optimize the energy output for species collocation.

Material and energy in river ecosystems are transmitted step by step from autotrophic groups to heterotrophs and eventually to fish; the quality of nutrients brought in by the water cycle determines the basic biomass of the system. Over evolutionary time, organisms adapt to the environment and form fixed types of communities; community types can be identified based on the species composition of the biological system. Currently, the average daily output of fish in the Guangdong section of the Pearl River system is 189.2 tons, including 30 species (classes) of fish, with an average nutritional level of about 3.1 (see table 5.11). Fish with biomass ≥1% include *Pseudolaubuca sinensis, Hemiculter leucisculus, Megalobrama terminalis, Tilapia* spp., *Cyprinus carpio*, *Hypophthalmichthys molitrix*, *Cirrhinus molitorella, Ctenopharyngodon idella*, *Hypophthalmichthys nobilis, Squaliobarbus curriculus*, *Pelteobagrus fulvidraco,* and *Culter alburnus.* About 66.3% of all fish species have relative biomass values between 1% and 20%, with an average nutritional level of 2.73. Analysis of the nutrient levels of exported fish products indicates that the proportion of the low-nutrient-level fish in the waters where the aquatic products were produced was relatively small, and it was inferred that the utilization of the primary productivity of the water body was insufficient. The annual runoff volume of the Pearl River is about 330 billion cubic meters, and the annual runoff volume of 330 billion cubic meters can export about 165 000 tons of fish products per year; the water body (runoff) was calculated to export 0.5 g/cubic meter. From 2016 to 2018, only about 40 000–60 000 tons of fish were caught from the river system every year, suggesting the lack of fish in river ecosystems. The food chain system should be restored and ecosystem function should be repaired by recovery starting with the fish with low trophic levels.

The average daily output of fish over three years in Guangxi was 222.0 tons and included 29 species (classes) of fish, with an average nutritional level of about 3.1. The fish with biomass values ≥1% included *Tilapia* spp., *Cyprinus carpio*, *Hemiculter leucisculus, Hypophthalmichthys nobilis, Ctenopharyngodon idella, Hypophthalmichthys molitrix, Squaliobarbus curriculus, Pelteobagrus fulvidraco, Lcucosoma chinensis, Carassius auratus auratus,* and *Cirrhinus molitorella.* Species comprising about 79.2% of the total fish biomass contributed 1.3% and 22% to the total biomass and had an average nutritional level of 2.55 (see table 5.12).

Tab. 5.10 – Trophic level distributions of fish in the Pearl River.

Nutritional level range	$2 < x \leq 2.5$	$2.5 < x \leq 3$	$3 < x \leq 3.5$	$3.5 < x \leq 4$	$4 < x \leq 4.5$	Mean trophic level/species
Species number	33	20	176	90	35	3.40/354
No. alien species	23	20	173	86	33	3.42/335
Native species	16	6	83	20	6	3.24/131
Estuary and migration type	7	13	90	66	27	3.54/204
Exotic species	10		3	4	2	2.94/19

Tab. 5.11 – Sample river fish varieties captured using ships in Guangdong Province from 2016 to 2018.

Species	Trophic level	Total output over three years	Proportion of total fish %
Siniperca kneri	4.5	393.9	0.190121097
Silurus asotus (Linnaeus, 1758)	4.4	754	0.36
Clarias gariepinus (Burchell, 1822)	4.4	1	0.00
Ictalurus punctatus (Rafinesque, 1818)	4.4	17	0.01
Siniperca scherzeri (Steindachner, 1892)	3.9	7	0.00
Hemibagrus guttatus	3.7	62.84	0.03
Monopterus albus (Zuiew, 1793)	3.6	22	0.01
Cranoglanis bouderius (Richardson, 1846)	3.5	154.6	0.07
Pelteobagrus fulvidraco	3.5	2742.75	1.32
Elopichthys bambusa	3.5	41.8	0.02
Culter alburnus	3.4	2259.4	1.09
Culter recurviceps	3.3	13.95	0.01
Megalobrama terminalis	3.3	12618.45	6.09
Lcucosoma chinensis	3.2	1439	0.69
Pseudolaubuca sinensis	3.2	43361.5	20.93
Mylopharyngodon piceus	3.2	214.05	0.10
Pseudohemiculter dispar	3.2	563.5	0.27
Cyprinus carpio	3.1	8776.2	4.24

Tab. 5.11 – (continued).

Channa maculata	3	85.5	0.04
Hypophthalmichthys nobilis	2.8	5991.5	2.89
Mastacembelus armatus (Lacepede, 1800)	2.8	43.55	0.02
Hemiculter leucisculus	2.8	21767	10.51
Squaliobarbus curriculus	2.7	3700.05	1.79
Tilapia	2	11396.5	5.50
Cirrhinus molitorella	2	8385.5	4.05
Hypophthalmichthys molitrix	2	8732.45	4.21
Carassius auratus auratus	2	651.7	0.31
Ctenopharyngodon idella	2	7581.1	3.66
Parabramis pekinensis	2	1226	0.59
Trash fish	3.1	64179.95	30.98
			100.00

TAB. 5.12 – Sample river fish varieties captured using ships in Guangxi from 2016 to 2018.

Species	Trophic level	Average of species (%)
Siniperca kneri	4.5	0.8
Silurus asotus (Linnaeus, 1758)	4.4	0.6
Clarias gariepinus (Burchell, 1822)	4.4	0
Plecoglossus altivelis (Temminck & Schlegel, 1846)	4.2	0
Siniperca scherzeri (Steindachner, 1892)	3.9	0.1
Hemibagrus guttatus	3.7	0.7
Pelteobagrus fulvidraco	3.5	3.5
Elopichthys bambusa	3.5	0
Culter alburnus	3.4	0.2
Megalobrama terminalis	3.3	0.4
Culter recurviceps	3.3	0
Lcucosoma chinensis	3.2	2.5
Mylopharyngodon piceus	3.2	0.9
Cyprinus carpio	3.1	13
Hemiculter leucisculus	2.8	10.2
Hypophthalmichthys nobilis	2.8	7.3
Mastacembelus armatus	2.8	0.6
Squaliobarbus curriculus	2.7	5.2
Xenocypris argentea	2.6	0
Cirrhinus mrigala (Hamiltom, 1822)	2.2	0.7
Labeo rohita (Hamiltom, 1822)	2.2	0.3
Tilapia	2	21.7
Ctenopharyngodon idella	2	7
Hypophthalmichthys molitrix	2	6.1
Carassius auratus auratus	2	1.4
Cirrhinus molitorella	2	1.3
Trash fish	3.057	15.2

5.2 Molecular Mechanisms of Energy Utilization and Ecological Niche

Niche is a reflection of the interspecific relationships within communities and the food chain established by certain basic organisms, such as fish and invertebrates in aquatic ecosystems; niche also indicates habitat characteristics (Green, 1971). Living things and the environment comprise the river ecosystem. Freshwater ecosystems comprise only about 1% of the earth's surface but provide rich biodiversity and irreplaceable ecosystem services, such as drinking water and aquatic products. However, due to population growth, the rapid development of the social economy, and the unreasonable exploitation and utilization of biological resources, the ecological environment has been seriously damaged. The degradation of ecosystem function is manifested by changes in biodiversity and damage to species communities. Major causes of the rapid decline in freshwater ecosystem function include dam constructions that block fish movement, loss of fish spawning grounds due to reservoir formation, overfishing, deterioration of water quality, eutrophication, and the invasion of alien species (Shuai *et al.*, 2017a, 2017b).

The molecular mechanisms of energy utilization are those processes of community niche differentiation, species development, evolution, and functional community construction that aim to obtain energy. Solar radiation is the basic energy source on the surface of the earth and is the main energy source influencing changes in ecosystems and biological communities. Biological organisms convert solar energy into biological energy, which can be transferred to other organisms through the food chain, supporting growth. Algae and plants produce energy from the sun using photosynthesis, while bacteria convert chemical energy into biological energy. Biological energy is fixed at about 1.55×10^{11} tons of carbon per year (Zhou Liangjun, 1986), or about 4.5×10^{21} j. Species aim to obtain energy. Since the emergence of unicellular organisms hundreds of millions of years ago, energy competition has been a factor in interspecies relationships. For example, plant organisms differentiated into trees, shrubs, and herbs to better compete for and utilize energy in "three-dimensions."

The energy that supports the activities of animal life comes from the food chain, which is based on the energy of plant origin. Animals differentiate into species with different feeding habits and form biological communities containing diverse species, rich food chain levels, and perfect energy circulation. Each species establishes its niche with the goal of maximizing energy. Thus, the mechanisms used in the establishment of community relationships function along the energy axis. The law of energy transfer through the food chain and food web means that community species must use different methods of energy acquisition, which corresponds to dietary differentiation in the fish community. River fish can be divided into carnivorous, herbivorous, filter-feeding, and omnivorous species according to their feeding habits. Starch is the basis of energy in the food chain, and amylase is involved in the hydrolysis of starch and glycogen. Amylase is widely found in animals, plants, and microorganisms. Salivary amylase and pancreatic amylase are predominant in mammals (Takahiro *et al.*, 1986). As an important digestive enzyme, pancreatic amylase plays an important role in obtaining energy for fish.

5.2.1 Fish Amylase

Amylase (AMY/AMS) generally acts on enzymes that hydrolyze α-1,4-glycosidic bonds, such as soluble starch, amylose, and glycogen. Enzyme hydrolysates can be classified into alpha-amylase (EC3.2.1.1.) and β-amylase (EC3.2.1.2.) based on the isomerization type of the hydrolysates. Alpha-amylases are found in animals (*e.g.*, in saliva and the pancreas), plants (*e.g.*, malt and arugula), and microorganisms. Alpha-amylases break down internal A-1-4-glycosidic bonds (M.J. Darias *et al.*, 2006). From archaea to mammals, alpha-amylase plays a role in providing energy to living organisms (A. Pandey *et al.*, 2000; M. Machius *et al.*, 1995). Most organisms initially store energy as carbohydrates, including starch and glucose polymers. More than 50% of the body's energy comes from the breakdown of carbohydrates, which begins with the enzyme amylase in saliva in the mouth and travels through the digestive system to the small intestine (W.F. Caspary, 1992). Amylase has various tissue-specific characteristics, including composition, copy number, and expression pattern. Salivary amylase is encoded by the *amy1* gene and pancreatic amylase is encoded by the genes *amy2a* and *amy2b*. The copy number of the salivary amylase gene varies greatly among species and even within the same population; *amy1* is more widely distributed than *amy2a* and *amy2b*. Changes in the *amy1* copy number are closely related to the levels of amylase in the saliva and serum. The changes in the *amy1* copy number in humans are related to the starch content of the diet. Unlike salivary amylase, pancreatic amylase is mainly derived from the pancreas and parotid gland. The mRNA expression levels of amylases in the AR42J cells of the pancreas are related to the activity of the amylases. The glucose/carbohydrate contents in the AR42J cells of the pancreas regulate the expression of amylases at the transcription level (C.D. Logsdon *et al.*, 1987). Glucocorticoid regulates the expression of pancreatic amylase and binds to the glucocorticoid receptor binding site on the amylase promoter, mediating hormonal responses (E.P. Slater *et al.*, 1993). The glucocorticoid response element (GR) in fish stimulates amylase gene expression using cortisol (glucocorticoid) (P. Ma *et al.*, 2004a; P. Ma *et al.*, 2004b). Transcription factor NF-Y plays an important role in glucose metabolism (Goel *et al.,* 2003) and can be positively regulated (Kawata *et al.*, 2003). ARNTL/BMAL1 is a transcriptional activator that controls various physiological processes by regulating the circadian rhythm of gene expression for about 24 h, thus affecting the metabolism and behavioral rhythms.

As an important digestive enzyme, amylase plays a critical role in the energy gain of fish. Amylase is found in all fish. The organs that secrete amylase differ among fish. In some fish, amylase is mainly secreted by the pancreas, while, in other fish, the intestine is an important organ of amylase secretion. Fish amylase is associated with feeding habits, and amylase activity levels are higher in herbivorous fish than in omnivorous fish (Douglas *et al.*, 2000; Akira *et al.*, 1987). Agrawal *et al.* (1975) compared amylase activity levels among carnivorous, omnivorous, and herbivorous fish and found that the amylase activity of herbivorous fish was greater than that of carnivorous fish. Hidalgo *et al.* (1999) showed that the amylase activity of *Anguilla japonica* was higher than that of *Oncorhynchus mykiss* and that the amylase activity levels of herbivorous and omnivorous fish were higher than those of carnivorous fish. It is necessary to characterize the mechanisms of fish community construction in the river ecosystem in order to understand the relationships between fish dietary differentiation and energy pathways.

The alpha-amylase gene in fish is similar to the *amy2a* gene in humans. The cDNA sequences of alpha-amylase genes have been published for many fish, such as *Siniperca kneri, Latescal cadfer*, *Brachydani orerio*, *Salmo salar*, *Tetraodon nigroviridis*, *Anguilla japonica*, *Myxocyprinus asiaticus*, *Pleuronectes americanus,* and *Epinephelus coioides*. The cDNA sequences of alpha-amylase genes are highly similar across fish species. For example, the saddle tail grouper amylase gene was 91.8% similar to the amylase genes of various other fish (Hu and Gallo, 2010, Chen *et al.*, 2009). The homology of the coding region of the amylase gene was 79.7% between zebrafish and *Siniperca kneri*. The coding region of the amylase gene is highly conserved across fish taxa. Chen (2007) cloned the cDNA sequence of *Myxocyprinus asiaticus* alpha-amylase and studied the expression patterns of alpha-amylase in different tissues of *Myxocyprinus asiaticus*. Qin Bangyong *et al.* (2013) cloned the alpha-amylase gene of *Cynoglossus semilaevis* and studied the effect of feed additives on alpha-amylase gene expression.

5.2.2 Gene Sequence and Niche

The regulatory region at the 5′-terminal of the pancreatic alpha-amylase gene in various fish with different diets contains different gene sequences. The 5′-terminal region has many important regulatory factors, such as promoter and transcription factor binding sites, regulating the alpha-amylase gene expression. Alpha-amylase mRNA expression levels are correlated with enzyme activity, and alpha-amylase genes are transcriptionally regulated (Moal *et al.*, 2000). Multiple regulatory elements were found in the 5′-terminal regulatory region of the alpha-amylase gene of *Siniperca kneri* (Chen *et al.*, 2009). Ma *et al.* (2004a, 2004b) found that the transcription factor GR regulated amylase gene expression in *Latescal cadfer*. The tissue-specific regulation of the pancreatic amylase gene may be related to the presence of transcription factor 1 (PTF1) in the pancreas (S.L. Weinrich *et al.*, 1991; M. Cockell *et al.*, 1989). Gene transcription sites related to salinity and food quantity, including GATA-1, AP-1, and SP1, were identified in the structural gene of the amylase by Huang *et al.* (2016), suggesting a close relationship between amylase gene expression and food source.

The nucleotide sequences at the 5′-terminals differ, but functionally regulated sequences are more evolutionarily conserved (Ludwig M Z *et al.*, 2000). The evolution of gene transcriptional regulation is driven by changing gene expression, rather than by changing the amino acid sequence (German *et al.*, 2016; Shapiro M D *et al.*, 2004). Fish amylase genes were highly similar within species lineages from the start codon to 167 bp upstream; beyond 167 bp upstream, many fragments were missing.

We performed a phylogenetic analysis of the amylase genes from 32 fish belonging to 12 orders and 19 families. In the resulting tree, some species clustered into recognized classes and families such as the Perciformes and Cyprinidae. Omnivorous fish in the same lineage were not clustered into a specific category, and a variety of omnivorous fish was identified in a single lineage, suggesting that the fish-amylase gene promoter sequence was conserved at the order level (Zhu *et al.*, 2020). More closely related families and species did not appear in the same lineage, suggesting the existence of a community niche differentiation mechanism with the energy system as the axis. The functional system of the animal energy axis includes the amylase system, which is related to hydrolyzed carbohydrates (feeding); the decomposing system, which includes lipases and proteases (carnivorous); and the mixed hydrolyzed carbohydrate and lipoprotein enzyme system (omnivorous). There are three types of functional enzyme systems in animal bodies. However, the transcriptional regulation of the gene region that encodes the functional enzymes of the energy system varies according to community functional differentiation.

5.2.3 Amylase Gene Transcription and Animal Feeding Habits

Plants differentiate into high- and low-order community species in order to compete for solar energy. Animals can be divided into herbivores, omnivores, and carnivores. In order to compete for energy, different animals have different feeding habits. Although all three groups of animals have characteristic amylase genes, the expression levels of the amylase genes differ among animals. Feeding preference may influence the expression of the amylase gene, and differences in the regulatory sequence of the amylase gene (tf, transcription factor) may correlate with niche differentiation in animal communities. In addition to the single transcriptional mechanisms regulating pancreatic amylase gene expression, there are also multi-transcriptional co-mediated regulation mechanisms. Upregulation of the pancreatic amylase gene is associated with the binding of hepatocyte nuclear factor 3(HNF3) β or 3 γ and Ptf1 to the promoter, and these cytokines act synergistically to strongly express the pancreatic amylase gene (M. Cockell *et al.*, 1995). The co-regulation of the pancreatic amylase gene *via* multiple transcriptions increased gene specificity and flexibility for the control of development, differentiation, and growth (Z. Tan *et al.*, 2018; Z. Wang *et al.*, 2018; P.D. Radler *et al.*, 2017; D.T. Odom *et al.*, 2006; M.I. Arnone and Davidson, 1997). Transcriptional functional recognition methods (Z. Hu *et al.*, 2007, 2010) were used to analyze and evaluate the transcription factors that might be involved in regulating the pancreatic amylase *2A* gene in herbivores, omnivores, and carnivores. It was found that GR, NFAT, and PR were the common hubs of the tf–tf interaction network across the different feeding groups. GR was the only tf regulatory network in herbivores and SPZ1 was the only tf regulating carnivore genes. Sequence analysis showed that tfs were highly similar within animal populations.

Amylase gene expression in omnivorous animals is also regulated by a variety of transcription factors (tfs). The interactions among transcription factors that regulate the pancreatic amylase gene in three different feeding habit groups were analyzed. The selected subjects included 77 herbivores, 25 omnivores, and 118 carnivores. Computer simulations of tf regulatory networks indicate that known pancreatic-specific tfs (such as GR, NFAT, and PR) may have non-pancreatic-specific tf mechanisms in the tf–tf interaction network. This may provide flexibility for the control of pancreatic amylase gene expression in different feeding habit groups. The results of this study suggested that combinatorial transcriptional regulation may be a key component in controlling the expression of the pancreatic amylase gene. The results suggested that the differential expression of energy-producing genes, including amylase, may be the key to the formation of herbivores, omnivores, and carnivores. Although amylase genes are present in all animal communities, their expression patterns in each community are controlled by different mechanisms, and tf regulation is probably related to food differentiation (Xinhui Li *et al.*, 2020). Wang *et al.* (2015) found that, during herbivore transformation, the expression pattern of circadian rhythm-related genes in the gut was reset, and that *Ctenopharyngodon idella* might obtain enough available nutrients to sustain its rapid growth through continuous high-intensity food intake.

Transcription factor Pax-2 performs the transcriptional activation of glucagon gene expression (Hoffmeister *et al.*, 2002). Glucocorticoid plays a major role in carbohydrate and protein metabolism. Any process which changes cellular state or activity (including movement, secretion, enzyme production, and gene expression) can be induced by glucocorticoid stimulation. MyoD is involved in the cellular response to glucocorticoids and regulates cellular metabolic processes.

We analyzed the upstream sequences of 32 pancreatic alpha-amylase genes from fish, including the promoters (Zhu Shuli *et al.*, 2020), to identify the major transcription factors that influence differences in fish feeding habits. Potential transcriptional factors that contributed more than 3.5% to differences in fish feeding habits were identified. It was found that E47, C/EBPalpha, NF-Y, and Pax-2 were the main transcription factors to identify fish as herbivorous or carnivorous, while deltaEF1, MyoD, NF-Y, AREB6, and Pax-2 were the main transcription factors to identify fish as herbivorous or omnivorous. The transcription factors that differ between omnivores and carnivores were GATA-1, SRY, MyoD, HFH-8, AREB6, Pax-2, STAT5A, and AP-1 (Li Xinhui *et al.*, 2020). This suggested that the differences in the transcription factors associated with the 5'-terminal region of the pancreatic alpha-amylase gene were related to dietary differentiation in fish. Transcription factors E47 and C/EBPalpha contribute 3.57% to the difference between herbivorous and carnivorous fish, and these are potential transcription factors that distinguish herbivorous and carnivorous fish. E47 plays a more important role in the expression of the alpha-amylase genes in herbivorous fish. PAX-2 also differed significantly between herbivorous-omnivorous and carnivorous fish; the difference contribution of NF-Y was 3.77% and that of PAX-2 was 4.67%. The MyoD and alpha-amylase genes differed significantly between omnivorous-herbivorous and carnivorous fish, and these genes were less likely to occur in carnivorous fish (Zhu *et al.*, 2020). When food resources are restricted, the differentiation among transcription factors led to niche differentiation in species communities. This mechanism of community construction focused on energy has theoretical significance for species management, conservation, and restoration, as well as the preservation of ecosystem communities.

5.3 Species Selection for Community Construction

River aquatic ecosystems are facing pressure due to global climate change, environmental changes caused by economic development, and the over-exploitation of water resources. These factors affect the sustainable development of the social economy. Fish biomass is an important factor for water system stability and water quality security. As a result of human activities and natural changes, river ecology has changed substantially. For example, the food chain system cannot fully utilize nutrients from the water body. In addition, deteriorated water quality cannot be used by people, which restricts the sustainable development of society. Against a background of the increasing pressure of environmental pollution, functional guarantees of the river ecosystem, which are demanded by human beings, have become a target of social concern. Fish play the role of "scavenger" in the functional guarantee of water quality in the river ecosystem, and growing fish continuously transfer materials out of the water body and purify the water. The ecological management of rivers is developing toward the goal of guaranteed water quality, and the biological reconstruction of river fish is developing to meet the needs of energy circulation in the river ecosystem. It is important to control fish communities and biomass according to the needs of the river water-quality guarantee. The nutrients in the river enter the food chain through the absorption and growth of autotrophs, and these nutrients are transported from primary productivity to secondary productivity to the fish output. If fish are lacking, the transport chain will become blocked, surplus organisms will decay, and the quality of the ecosystem will deteriorate. This will become a vicious cycle.

The environmental characteristics of the river basin are formed during natural evolution and the biomass of the river ecosystem is subject to the number of mineral nutrients entering the system. At present, many aspects of the fish living environment are under stress, especially with respect to insufficient biomass. The food chain is responsible for material transport in the aquatic ecosystem. In addition to community types, biomass is also required to meet the needs of the ecosystem. Observation of the nutrients in river water, the productivity of the water ecosystem, fish food availability, and product availability will help evaluate the functional quality of river ecosystems, help evaluate the management objectives, and help establish a river ecosystem management scheme with fish biomass as the target. The increase of fish resources in the water space can greatly enhance the nutrient output of the aquatic ecosystem and reduce the pressure of nitrogen and other nutrients on water quality in the river ecosystem. Wang *et al.* (2020) suggested that the reciprocal relationships between species have a significant top-down influence on predators and consumers and that these reciprocal relationships have a greater influence on predators than on consumers. Low trophic-level biomass has a significant bottom-up effect on consumers and predators, and this effect decreases with the increase in nutrient level. High-trophic-level organisms are influenced from bottom to top by low-trophic-level biodiversity, and carnivores are mainly influenced by mutually beneficial organisms from top to bottom. Food webs with reciprocal relationships are highly complex, and the interactions between trophic levels are significant. A food web can be functionally assessed by measuring the "total input–output interaction intensity" (Xu *et al.*, 2020).

The functional connections between biological communities and ecosystems have received substantial research attention. However, it is now common practice to equate biodiversity with species diversity (Díaz and Cabido, 2001), ignoring the role of interspecies relationships in ecosystem processes. Ecosystem function depends not only on the number of species but also on the functional traits of the species (Lepš *et al.*, 2001). Two communities with the same number of species are likely to exhibit significant differences in functional diversity due to the differences in species traits and characteristics between the communities (Leps *et al.*, 2006). Therefore, it has been increasingly commonly proposed that community studies should consider the diversity of functional traits instead of species diversity (Jiang and Zhang, 2010). The functional diversity represented by the traits is closely related to the function of the ecosystem, which more clearly reflects the interactions among species in the community (Hooper *et al.*, 2002; Díaz and Cabido 2001). That is, functional diversity is defined as the overall differences in or diversity of functional characteristics among species within a community (Petchey and Gaston, 2006). In comparison to ecosystems with low functional diversity, ecosystems with high functional diversity tend to have more differentiated niches, to maximally use resources, to be more stable, to have higher productivity (Tilman *et al.*, 1997), to be more resilient (Nyströ and Folke, 2001), and to have a higher resistance to invasion (Dukes, 2001; Prieur-Richard and Lavorel, 2000). Community functional ecology has become an important present-day approach to the treatment of ecological problems (Cameron, 2002; Loreau *et al.*, 2001).

The spatial differences among fish communities are closely related to the environment (Shuai *et al.*, 2017b, 2020; Zhang *et al.*, 2020). In each specific environment, fish communities show common functional characteristics, such as the long narrow bodies favorable for fast swimming in fish adapted to rapids' habitats. Thus, fish develop special functional structures to adapt to the niche (Shuai *et al.*, 2016, 2017b, 2018a, 2018b). In a study of the niches and functions of fish in ecosystems, Mason *et al.* (2008) proposed three independent functional diversity indices: functional richness (FRic), functional evenness (FEve), and functional divergence (FDvar). The niche space occupied by a species, the distribution of species characters in the space occupied, and the degree of niche complementarity among species in a community were characterized. The functional divergence (FDvar) index was proposed to quantify the distribution and multiplicity of species in the functional space (Sébastien Villéger *et al.*, 2008). Fish community ecological process should be based on indices of functional specialization (FSpe), functional dispersion (FDis), and functional entropy (FEnt). These are the factors to be considered in the construction of fish groups. Hoeinghaus *et al.* (2007) collated species abundance data from 157 streams in Texas, USA, and classified fish into functional groups based on trophic level and life history features. Taxonomic analysis showed that the fish communities were determined by the size of the river and the classification of the biogeography patterns. Functional group analysis showed that the characteristics of the fish community were not related to river scale and geographical region but were instead related to habitat type. It was concluded that the structures of the fish assemblages in local rivers were ultimately determined by factors at multiple scales, and the relative importance of each scale depended on the biological unit (species or functional group) used (Hoeinghaus *et al.*, 2007). The river ecosystem is linear, with a large environmental span, and high heterogeneity. Thus, differences among fish communities are correspondingly great, and fish community construction studies need to consider the indigenous biology priority program. Fish community construction must be guided by community niche theory. Although the same species of fish occur in different communities, the occupied niche may differ. Thus, it is necessary to consider various river environments when building different fish communities.

Some species have a wider geographical range in nature than others, and such widespread species are well adapted to the environment, independent of their size (Lester *et al.*, 2007). These species are of concern for the formation of diverse communities. Biological interactions shape the spatial distributions of species at local spatial scales, but the role of these interactions beyond the local scale (10 km to global) is generally considered unimportant. Contemporary and palaeoecological analyses show that biological interactions shape species distributions, including individual species ranges, functional groups, and species richness patterns, beyond local scales. This suggests that biological interactions leave clear marks on species distributions and influence species assemblages across all spatial scales (Wisz *et al.*, 2013). One long-standing concept of community research is that closely related species compete more fiercely than do distant relatives. Ecologists invoke this "restricted similarity hypothesis" to explain patterns in community structure and function and to provide information for conservation, restoration, and the management of invasive species. However, Fritschie *et al.* (2014) found evidence that interspecies interactions are independent of phylogenetic distance. Thus, interactions between any pair of species (including alien species) may be random. The potential free association of species may be supported by the food differentiation theories discussed above.

River fish communities have unique patterns and are affected by non-random processes (Ostrand and Wilde, 2002; Jackson *et al.*, 2001). Environmental factors (*e.g.*, water flow velocity, dissolved oxygen concentration, water temperature, and dissolved organic matter) affect the fish composition and distribution (Sharma *et al.*, 2011; Mason *et al.*, 2007; Mouillot *et al.*, 2007; Peres-Neto *et al.*, 2006; Grenouillet *et al.*, 2004) and affect strategies for fish resource use (Pof NL and Allan, 1995). Ecosystems have changed dramatically since humans have come to dominate the environment, and conservation action is urgently needed (Banse, 2007). During the process of ecological protection, the reconstruction of biological communities must be guided by the theory of continuous development. Importantly, the key to stable community reconstruction is a detailed understanding of the relationships between organisms and habitats and of the interactions among species. The processes of ecosystem evolution and community succession should be considered during ecosystem reconstruction. The mechanisms of energy output by primitive communities and the evolution of species from low trophic levels to higher trophic levels may act as a reference. That is, the efficiency of energy output should be considered first in the process of reconstruction, and low trophic-level organisms should be given priority in community construction.

The reconstruction of a biological community should be performed with the goal of ecosystem function. The reconstruction of biological communities in the river ecosystem can be divided into two aspects according to functional needs. The first aspect is biodiversity reconstruction, which includes the maintenance of harmonious relationships among target species and community reconstruction (aquatic) species; the problem of regional biodiversity collapse must be solved through community reconstruction. The second aspect is ecosystem restoration, which must serve human needs and consider special functions, such as the functional impairment of energy delivery systems due to the loss of species or biomass in river ecosystems disturbed by human activities. Ecosystem communities that need rebuilding are usually located in eutrophic waters and waters with high primary productivity, and functional communities need to be constructed using fish communities that can utilize primary productivity and the available biomass.

Niches are linked in a community by the food chain, and species niches are often manipulated by superior predators from above (Grange and Duncan, 2006). Urban (2004) postulated that community species diversity, abundance, and nutrient structure were determined at the time of ecosystem formation and by local environmental changes. Heterogeneous perturbations determine community structural properties, barriers restrict many taxa to localization, species cannot adapt to the disturbance, and a normal biological interaction relationship could not be established. Blocking may also affect local dynamics through mass effects. Many species have "abandoned their adaptation to dam disturbance" and "abandoned their adaptation to biological interactions" due to the formation of "artificial freshwater lakes" in rivers due to cascade dams. Changes in the fish community lead to deficiencies in the food chain system, which is reflected in changes in the composition of fish trophic levels. The relationship between phylogenetic distance and ecological similarity is the key to an understanding of community mechanisms. Phylogenetic information can be used to infer the mechanisms of community construction, niche conservation (habitat filtration), and species interaction (competition or promotion). These factors affect community composition, and phylogenetic relationships affect species interaction intensity (Jean H. Burns and Strauss, 2011). Alien species can alter resource availability and trophic level structure at the ecosystem level, thus affecting ecosystem function and even ecosystem stability (Cucherousset *et al.*, 2012; Britton *et al.*, 2010).

Space, time, and trophic niche are three typical dimensions considered in the construction of a species niche, as these variables independently describe the ecological location and animal resource use. When multiple species coexist in the same community, they inevitably interact within various dimensions of the niche (Sæbø, 2016). Spatial, temporal, and trophic niches provide three variable coordinate dimensions for predators, and animals can adjust their ecological breadth and range in each dimension through adaptation or behavior changes in interspecies competition to maximize returns (Bruno *et al.*, 2003; Schoener, 1974). Spatial, temporal, and trophic niches also reduce the intensity of competition among species, including interference competition (direct encounter and killing) and exploitation competition (Kronfeld-Schor and Dayan, 2003). The plasticity and adaptation of predators in space, time, and trophic niches is an evolutionary consequence that retards competition and promotes the coexistence of different species (Sæbø, 2016). The spatial niche is fundamental for an understanding of the regional coexistence and interactions of carnivores. Species can potentially interact in niche dimensions such as time and nutrition only if they co-exist within certain spatial scales (Farris *et al.*, 2020). Differences in spatial use can effectively promote species coexistence, but species with similar ecological characteristics do not enforce complete spatial competitive exclusion on a global scale; instead, species chose spaces with similar resources to promote coexistence (Davis *et al.*, 2018).

The trophic niche, which is an important attribute of the wildlife niche, can affect the functions of animals in the ecosystem and the food web. Comparison of the food habits of sympatric species can reveal the extent of trophic niche overlap among different species and serve as a measure of potential competition among species (de Satgé *et al.*, 2017). The trophic niche overlap among carnivores tended to decrease in a non-linear manner as body weight difference increased; at the minimum body weight difference (about 0.01 kg), the predicted trophic niche overlap was 62%. The predicted trophic niche overlap was 12% at the maximum weight difference (160 kg) (Lanszki *et al.*, 2019). Large and small carnivores distributed in the same domain generally do not have a high degree of food overlap (Gómez-Ortiz *et al.*, 2015), and similar-sized predators are more likely to engage in intense interspecies competition and even slaughter one another as they hunt similar prey (Donadio and Buskirk, 2006). Coordinated and complementary spatial, temporal, and trophic niches promote the regional coexistence of species, and it is important to consider differences in habitat preference among species.

Li *et al.* (2021) devised an indexing system to evaluate the functional state of the river ecosystem and to provide a reference for the biomass demand of the river fish community. The eutrophication of the river water ecosystem must be reversed by eliminating nutrient input and establishing a biological output system. It has become commonly understood in society that it is necessary to reduce the point and non-point flow of nutrients into water bodies, but methods to establish biological community systems and to enhance the export of water substances still remain to be developed. By determining the biomass demand of fish, the fish community morphological model can be used to analyze the relationships between fish and the community and may provide an analytical method for niche construction for community species.

5.3.1 Multispecies Model

It is difficult to measure the impact of biodiversity on ecosystem function because it is difficult to design and analyze the impact of a species loss on ecosystems in nature. Changes in the consumption patterns of large vertebrates, such as humans, are highly disruptive to ecosystems, and the main effects of biodiversity changes on ecosystem functioning appear to be in the form of nutrient-mediated processes (Duffy, 2003), particularly energy processes. In ecosystems disturbed by anthropogenic activities, the special ecological functions of human beings should be considered during the reconstruction of the biological community. The effects of humans on the energy transmission functions of the ecosystem are greater than those of high-level carnivores. Usually, the energy output (removal) of the system depends on the realization of high-level carnivore function, and the reduction in carnivore numbers will thus affect the material transfer functions of the system. Because human beings are unusual animals in the biological community due to their broad-spectrum diet, wide feeding abilities, and creativity, humans do not replace the carnivores in the original system. Instead, humans act as the terminal energy output of various natural ecosystems, changing the structure and function of the ecosystem. Therefore, with human effort, the ecosystem's energy output can finally become balanced.

During adaptation, large and small organisms form a pattern of coexistence, and the relationships among species niches in the community are not exclusive. These mechanisms should be related to the maximum utilization of energy in the ecosystem. Aarssen *et al.* (2006) indicated that the ecological niche of large, tall trees was dominant. However, the gaps among the trees provided space for the survival of small species and promoted the coexistence of large and small species. In the animal system, energy circulation requires the predator-prey relationship in the food chain. If the predator has the exclusive behavior in the niche, there is no basis for its existence. Therefore, the "linking" of the niche is the rational distribution of energy in the system, which provides the basic condition for the coexistence of large and small species. It is not only when competition is weak that positive intraspecific interactions, such as cooperative defense against predation or enhanced foraging success, occur. Thus, interactions can be positive only if the benefits outweigh the costs, but competition is not necessarily weak and interactions can have a net positive outcome. Strong benefits, such as improved survival, can outpace the negative competitive effects of growth, and net positive interactions are costly for co-existing species. The overall biota may also be more resilient to physiological stress than isolated individuals. In stressful environments, bioclusters can cushion the environment. On coasts with higher plant and animal densities, shade from some species compensates for extreme variability of air temperatures, reducing evaporation.

The evolutionary relationships and phylogenic positions of coexisting species can be studied in a community. In a balanced system, biological heterogeneity (*e.g.*, due to alien species) can lead to imbalance. The coexistence of species with spatial differences in resource supply must balance at a regional scale along the environmental gradient. Environmental heterogeneity may lead to the exclusion of the dominant competitors of a given species within certain ranges (Shurin *et al.*, 2004). There is no single explanation for the patterns of species richness found in coexistence studies of plant species. A more general interpretation of species coexistence makes use of the idealized concept of an empty community, defined as an undisturbed community within a stable band of vegetation that includes an entire pool of potential species. The number of potential species will then depend largely on evolutionary factors (*e.g.*, speciation). For historical reasons, most "real" communities have small species pools, and migration has not yet taken place. In this local pool of species, asymmetrical interspecific competition is a major force in reducing species richness. The competition takes place at the ecological level (within ecological time scales), but the outcome is governed by the characteristics determined by individual evolution. Ecological factors affect the number of coexisting species in two cases: First, when habitat conditions change and one species pool replaces another; second when certain external factors (such as grazing or mowing) that change the character of an individual also change the outcome of the competition (Zobel, 1992). Methods of systematic species construction, reconstruction, community niche modeling, and development need to be devised (Webb *et al.*, 2002).

The structure of the food web is related to species diversity, and the loss and extinction of key species greatly affect the structure of the food web (Dunne J A *et al.*, 2002). Interspecific and intraspecific interactions have a significant impact on the structure and function of ecosystems, as does the avoidance of physical stress. The idea that changes in the habitat of one species might benefit another species was submitted by early plant ecologists decades ago as an important mechanism for community succession. Understanding how biological communities form has been a central issue in ecological research. The traditional concept, with set rules, reflects the idea that species do not co-occur at random, but are restricted by interspecies competition, and that the co-occurrence of species is the product of opportunity. Thus, historical patterns of speciation and migration, diffusion, abiotic environmental factors, and biological interactions are not mutually exclusive (Gtzenberger *et al.*, 2012).

Trade-offs between mutually beneficial actors (Wang *et al.*, 2008), namely the prevention of competition (conflict) between the recipient and the cooperating actor in a cooperative system, remain one of the biggest problems in evolutionary biology. Self-restraint, fragmentation, or spatial restraint can prevent direct competition for local resources or any other common resource, thus maintaining stable cooperative interactions, but these restrictions do not sufficiently prevent the symbiote from using more local resources at the expense of the recipient. The conflict may disrupt cooperative interactions, which occur when local resources are saturated by symbiotes. Increased repression of symbionts, which in turn inhibits the use of local resources during the conflict, is essential for sustaining and developing cooperation.

There are significant differences among types of predator-prey interactions; these interactions may be stable, competitive, and fluctuating. The probability of the stability of the predator-prey network is reduced by the presence of a large number of weak interactions in the food network structure. As long as the predator–prey pair is tightly coupled, a stable predator-prey network can be arbitrarily complex (Allesina and Tang, 2012).

Food chain systems are associated with species coexistence, and increasing ecosystem size can also promote coexistence, increasing the length of the food chain by changing the predator or increasing the number of prey (Takimoto *et al.*, 2012). There are many alternatives to consider when rebuilding biological communities in a given environment, but maintaining multiple species at multiple trophic levels is challenging, and in measuring the stability of multispecies coexistence, differences in the mean fitness and stability of species are key (Chesson, 2018). Community research needs to focus on mutualism and coevolution, as well as on quantifying species richness in communities. An improved understanding of these forces will improve our understanding of mutualism (coevolution), including the identification of coevolutionary units and coevolutionary interactions (Hall *et al.*, 2020).

5.3.2 The Food Chain is Fully Functional

The community of the aquatic ecosystem is influenced by environmental factors, such as global warming. Due to global warming, the tropical community has expanded toward the subtropical and temperate zone; such an expansion has been observed globally in tilapia. Human introduction hastened the expansion of tilapia. Human-induced cascade development accelerated the loss of habitat for indigenous low-trophic fish, giving tilapia the opportunity to expand and occupy the vacant niche. In the future, it remains possible to further develop the river ecosystem from the current environment. The main body of the fish community in the aquatic ecosystem must be low trophic-level or omnivorous fish, as these provide the environmental conditions necessary for low trophic-level fish like tilapia to enter the food chain system of the river ecosystem in China. As an invasive species, tilapia (*Oreochromis niloticus*) has attracted much international attention in studies of community structure and ecosystem function (Shuai *et al.*, 2018a, 2018b, 2019; Yuguo Xia *et al.*, 2019; Tan *et al.*, 2012), as well as in analyses of biological invasion using geo-material information for niche modeling, of invasion pressure using niche conservation models (showing stagnation and maintaining niche parameters over time), and of niche evolution (adapting to changes in niche parameters) (Dudei and Stigall, 2010). To model biological modification, environmental regulation, and species distribution (Linder *et al.*, 2012), the biological modification environment can be expressed as additional variables in the SDMS. Exotic species have altered the body sizes of freshwater fish worldwide (Blanchet *et al.*, 2010) to varying degrees, thereby affecting the functional diversity of freshwater fish (Matsuzaki *et al.*, 2013). The impacts of alien species can be analyzed and predicted by establishing models based on population expansion data (Shuai *et al.*, 2015). However, it is difficult to predict the distribution trends of invasive species by using species distribution models when data are limited. At present, the differences in a niche location, size, and structure between local and large scales are quantified using multivariate similarity data and climate prediction factors (annual minimum and maximum temperatures). The niche change of the target species was realized by repeating the niche study using simulated species (Larson and Olden, 2012). Tilapia, which grows in natural waters, is not easily utilized by humans and is, at present, the lowest trophic-level fish that is gradually expanding in the southern Chinese rivers. From the point of view of ecosystem function, tilapia replenish the niche space of low trophic-level fish, and this species has a strong ability to adapt to the environment.

We analyzed the community structure of native fish. Data from resource supplements and the literature indicated that the entire Chinese river ecosystem was short of fish, especially low trophic-level fish such as *Ctenopharyngodon idella* and *Hypophthalmichthys molitrix*. We suggest that tilapia may be environmentally suitable for entrance into the food chain system in Chinese rivers, as tilapia, which are low tropic-level fish, fill the ecological gap left by native fish. It is necessary to comprehensively study the impacts of exotic species on the functions of the river ecosystem in China. Niche models can be used to study the mechanisms of invasion and niche expansion of a species in a community (Ebeling *et al.*, 2008). The analysis of fossil data can reveal the processes and forms of niche evolution (Malizia and Stigall, 2011). In general, the functional differences in the resource requirements of alien aquatic organisms have a significant impact on aquatic ecosystem processes (Azzurro *et al.*, 2014; Zhao *et al.*, 2014).

5.3.3 Species Compatibility

Community construction must solve the problems of species coexistence and species diversity maintenance, but the mechanisms of local community construction remain controversial. Maron *et al.* (2004) argued that phenotypic plasticity is the main mechanism by which alien plants adapt to rapidly evolving environments.

Phenotypic change processes reflect the niche change process of the species. Species with different traits (especially those that determine their impact on the environment) coexist differently depending on evolutionary history or the interactions among resources, predation, and prey. In near-equilibrium local communities, species coexistence is compatible, not random, with strong interaction mechanisms (Leibold, 1998). Chai and Yue (2016) holds that it is possible for theoretical ecologists to study the mechanisms of community construction based on functional traits and community genealogical structure; in addition, spatiotemporal scale, environmental factors and vegetation type, species and numbers of selective traits, intraspecific trait variation, and human disturbance should also be considered. Meng *et al.* (2020) studied the construction of microbial communities and concluded that microbial survival, growth, and reproductive traits can reflect microbial responses to environmental changes. Subsequently, microbial species distribution patterns, community construction mechanisms, and corresponding ecosystem functions are affected. In community construction research, it is also important to study the relationship between characters and species distribution patterns, biodiversity, ecosystem function, and response to environmental change. During community restoration and reconstruction, species, functional, and phylogenetic diversity can recover rapidly given small- and large-scale surrounding natural vegetation (Sun *et al.*, 2018). This edge effect requires that the physical environment of the system not be fragmented.

When transforming nature, it is important to consider the law of material metabolism. That is, we should only exploit biological resources at a reasonable level in the process of production, and we should not exhaust fishing resources. Biological evolution is a product of the interactions between living things and the environment. Living things continuously import and export materials from the environment, and the material environment that is changed by living things in turn influences or selects living things. This process is commonly known as normal natural succession. The environmental characteristics of the watershed are formed over the course of natural evolution, and the biomass of the system is related to the mineral nutrition of the water body. Similarly, the biological capacity of a river ecosystem is limited by the number of nutrients entering the system. Currently, many aspects of the fish habitat are under stress, especially with respect to insufficient biomass, although the food chain performs material transport in the aquatic ecosystem. River ecosystems need more reasonable community diversity, and biomass is also required to meet the needs of the ecosystem. The increase in fish resources in the water space can greatly enhance the nutrient output of the aquatic ecosystem and reduce the pressure of nitrogen and other nutrients on water quality in the river ecosystem (Li *et al.*, 2021a, 2021b).

In the study of species relationships within a community, the species relationship model can be used as a dynamic ecological model with which to study the coexistence and competitive exclusion of species in the community. Community construction is mainly driven by deterministic and stochastic processes, and one of the key issues in community construction is the quantification of the relative contributions of deterministic and stochastic processes to community construction (Luo *et al.*, 2021). Deterministic processes are controlled by the inherent properties of the species in the community, and the stochastic processes reflect the results produced by the environment. Xu Y. *et al.* (2019) suggested that the decomposition and quantification of environmental impact factors should be considered in community construction, in addition to the impact of spatiotemporal dynamic changes. An improved understanding of the shared and unique traits of construction mechanisms among communities will emphasize integration with other ecological processes and the mechanisms of community construction. The regional coexistence of terrestrial animals is a relatively stable state that has been formed over evolutionary time; animals coexist through niche separation, and co-adaptation plays an important role in their regional coexistence (Li Zhilin *et al.*, 2021). In community construction, the degree of contribution of each species is usually determined by niche relationship or population number. Yang *et al.* (2020) analyzed the construction mechanisms of fish communities at different spatial scales in the middle reaches of the Yangtze River and found that the competitive effects of small-scale environmental filtration become those of large-scale environmental filtration. Lou *et al.* (2020) used phylogenetic community structure analysis to study the characteristics of fish communities in rivers filtered by the environment. These studies indicated that the important roles of competition and coexistence in maintaining the stability of the fish community should be fully considered in the process of community reconstruction. Zhou *et al.* (2021) used feeding habits and trophic levels to rank the 30 most common fish species based on the dominance of resources, biomass, and catch rate in the Wanshan area of the Pearl River estuary. Based on the trophic level of the food chain, seven key functional groups of fishery resources in marine ranches, which were composed of the top economic species, were identified, and the proportion of each trophic level in the food chain was determined. The functional groups included the Silver Pomfret Functional Group, the Sea Bass Functional Group, the Spiny Pomfret Functional Group, the Grey Mullet Functional Group, the *Penaeus monodon* Functional Group, and the Green Crab Functional Group. In aquatic ecosystems, microorganisms and plants convert inorganic and chemical energy into biological energy and enter the food chain. As the end group of energy output in the food chain of the aquatic ecosystem, fish species are rich in diversity and have different feeding habits, including filter-feeding on phytoplankton and zooplankton, omnivory, saprophagy, and carnivory. These groups play different roles in the chemical and energy cycles within the system. Lin *et al.* (2020) postulated that predation is the most important interspecific interaction in the Pearl River Delta fish community because predation is the most direct means by which the whole community and ecosystem can achieve energy flow and express ecological functions. Predation is also a direct factor that fish community construction efforts need to consider. Fish are the most important carriers of material circulation and energy flow in river ecosystems. The structure and stability of the fish community determine the function of the river ecosystem. Interspecific relationships are particularly important in fish community restructuring.

In the river ecosystem, fish depend on the environment and have different reproduction requirements. Therefore, it is necessary to consider whether there is a suitable condition for fish reproduction and to build fish communities that enable reproduction. The distribution patterns of fish species differ in different areas due to the differences in climate and environment between the north and south. Fish species require different water temperatures for breeding. For example, the breeding water temperature of *Lota lota* (Linnaeus, 1758) in Heilongjiang is about 0 °C; the breeding water temperature of *Cyprinus carpio* and *Carassius auratus* is about 15 °C; the breeding water temperature of *Ctenopharyngodon idella, Hypophthalmichthys molitrix,* and *Hypophthalmichthys nobilis* is above 18 °C; and the optimum water temperature for tilapia reproduction is 25–28 °C. The spawning behaviors of broodstock are mainly determined by water temperature, and spawning behaviors are inhibited if the water temperature is too high or too low (Wang and Li, 2010; Mu Yunlei, 1999; Yu Zhitang *et al.*, 1985). The characteristics of the fish community are controlled by temperature, and the suitability of the species for the temperature environment should be considered in the construction of fish communities. Some fish require suitable conditions for the development of floating eggs. After the eggs are laid, they swell to form a large periovale, which is a little lighter than water. The fertilized eggs are suspended in the water column in running water and sink to the bottom in still water. Fish that produce floating eggs include *Ctenopharyngodon idella, Mylopharyngodon piceus, Hypophthalmichthys molitrix*, *Hypophthalmichthys nobilis, Squaliobarbus curriculus*, *Sinibotia pulchra, Luciobrama macrocephalus*, *Ochetobius elongatus,* and *Elopichthys bambusa.* Some fish spawn and sink to the bottom or adhere to the pebbles, gravel, or developing reefs. The viscous spawning fish, such as *Acipenser sinensis* (Gray, 1834), *Megalobrama terminalis, Zacco platypus, Oreonectes furcocaudalis, Spinibarbus denticulatus denticulatus, Spinibarbus denticulatus denticulatus, Onychostoma sima, Onychostoma meridionale, Onychostoma meridionale, Onychostoma gerlachi, Discogobio tetrabarbatus, Glyptothorax fukiensis*, and species in the Tetraodontidae, have eggs that sink to the bottom or adhere to pebbles, gravel, or reefs. Some eggs are lighter than water and float. There are a few species of river fish that produce floating eggs, including *Coilia* spp., *Monopterus albus, Channa argus, Siniperca kneri, Maropodus* spp., and *Tenualosa reevesii.* The eggs are generally small and contain oil globules. Fish eggs are typically colorless, transparent, and free-floating in the upper water layers. The presence, color, number, size, and distribution of the oil globules in the egg are important classification characteristics for fish eggs. Some fish eggs have only a single oil globule, such as those of *Clupanodon punctatus.* Some fish eggs, such as those of *Tenualosa reevesii*, contain several different sizes of oil globules, and they are known as multi-oil-globule eggs. During embryonic development, the oil globules of single-oil-globule eggs are located at the plant pole of the ovum, while the oil globules of multiple-oil-globule eggs are scattered around the yolk. The oil globules collect before and after hatching, forming an oil lump at one end of the yolk sac that is eventually absorbed or removed. Some fish produce eggs after adhering to the stems and leaves of aquatic plants (these fish include *Cyprinus carpio* and *Carassius* *auratus*). Other fish, such as *Acheilognathus macropterus*, *Acheilognathus barbatulus* (Günther, 1873), and *Acheilognathus tonkinensis* (Vaillant, 1892), lay their eggs in mussels. During the construction of fish communities, fish breeding habits should be considered to ensure that species can reproduce in the system environment.

Habitat restoration projects, especially the estimation of the habitat requirements of a spawning ground, should consider the niche of the fish community. Li xinhui *et al.* (2020a, 2020b, 2020c, 2020d, 2020e, 2021a, 2021b) established a theoretical system of ovipositing field function, which involves several functional concepts including unit, hydrodynamics, and flux.

5.4 Examples of Model Application

The river environment changes dramatically under the influence of non-natural factors. Thus, species whose life history processes depend on a certain habitat and cannot adapt to environmental change will go extinct. The surviving species are fixed in the community relationship formed by ecosystem evolution and cannot adapt to the niche vacancy caused by species loss in a short time. The food chain breaks, the energy cycle is disrupted, and the ecosystem falls into disarray. The function of the river ecosystem deviates from human needs, and the river ecosystem needs to be rebuilt. For this effort, species compatibility, including the compatibility among species within the community and between species and environmental factors, is important. An understanding of the biological characteristics of the species, combined with a model to predict the structure of the proposed community, will help to clarify the need for ecosystem reconstruction.

5.4.1 Relationship Between Model "Potential" and Community Abundance

Data from field observations are affected and restricted by many factors. Particularly due to data mutations and discontinuity, it is not easy to obtain satisfactory quantitative results. Analysis of the species richness of the community formed by the early fish resources in the Pearl River showed that seasonal spawning times, spawning rate, and spawning frequency differed among the 19 species of fish. However, for certain species, it is only possible to use traditional methods of studying fish biomass; due to larval size gaps and data discontinuity at different times (some fish may be present as larvae for only 10–20 days per year), a valid quantitative model cannot be obtained. During the establishment of the niche model of community species based on morphological parameters, the spatial relationships among community species were determined within the framework of species morphological parameters. Then, the niche "site-abundance" relationship was calculated based on the measured biomass indices (*i.e.*, the abundance of supplementary resources). Specifically, the number of species (species richness) was added to the morphological parameter matrix of the species, and the corresponding analysis was performed in the model to obtain the two-dimensional graph of community relationships. In this graph, the ecological niches of all fish were shown along the two principal axes (*i.e.*, the *x*- and *y*-coordinates).

Because there is not a simple linear relationship between the biomass abundance of a given species and its morphology-derived community niche, screening and comparison must be performed to establish a regression model using powers of 1–2 or 1–3. Thus, the relationship between the abundance of each fish and its biomass can be calculated as follows:

Ci (The abundance of a certain fish in a community) = F($\mathbf{X}_{A1}$ (x coordinates of the first fish),... $\mathbf{X}_{A19}$ (x coordinates of the 19th fish), $\mathbf{Y}_{A1}$ (Y coordinates of the first fish),... $\mathbf{Y}_{A19}$ (y coordinates of the 19th fish). The x, x^2, x^3 and y, y^2, y^3 in the functional equation are the different powers of the *x* and *y* coordinate values of fish, respectively. For example, in the equation of *Mylopharyngodon piceus*, CA1 indicates the abundance value (%) in the community, CA1 function:

$$C_{A1} = \mathbf{12.74 + 247.15 \times X_{A1} - 2150.9 \times X_{A1}^{2} - 27023.41 \times X_{A1}^{3} + 401.68 \times X_{A2} + 740.17 \times X_{A2}^{2} - 21797.43 \times X_{A2}^{3} - 41.25 \times X_{A3} - 6629.48 \times X_{A3}^{2} - 42345.35 \times X_{A3}^{3} + 740.52 \times X_{A4} + 2389.03 \times X_{A4}^{2} - 7406.19 \times X_{A4}^{3} + 245.65 \times X_{A5} + 96.31 \times X_{A5}^{2} + 45.63 \times X_{A5}^{3} + 197.55 \times X_{A6} - 3905.47 \times X_{A6}^{2} - 69146.59 \times X_{A6}^{3} + 247.17 \times X_{A7} + 44.18 \times X_{A7}^{2} + 228.1 \times X_{A7}^{3} + 249.05 \times X_{A8} - 10.79 \times X_{A8}^{2} + 92.41 \times X_{A8}^{3} + 202.98 \times X_{A9} + 389.08 \times X_{A9}^{2} - 2285.08 \times X_{A9}^{3} + 226.82 \times X_{A10} - 2615.18 \times X_{A10}^{2} + 76161.11 \times X_{A10}^{3} + 4342.93 \times X_{A11} + 97153.81 \times X_{A11}^{2} + 751580.81 \times X_{A11}^{3} - 1302.99 \times X_{A12} - 56317.97 \times X_{A12}^{2} - 769106.03 \times X_{A12}^{3} - 3810.92 \times X_{A13} - 89458.46 \times X_{A13}^{2} - 640143.54 \times X_{A13}^{3} + 313.24 \times X_{A14} - 290.36 \times X_{A14}^{2} - 5112.97 \times X_{A14}^{3} + 245.59 \times X_{A15} + 218.4 \times X_{A15}^{2} - 375.99 \times X_{A15}^{3} + 216.01 \times X_{A16} - 578.24 \times X_{A16}^{2} + 3150.88 \times X_{A16}^{3} + 257.13 \times X_{A17} + 350.13 \times X_{A17}^{2} - 2579.95 \times X_{A17}^{3} + 130.23 \times X_{A18} - 460.38 \times X_{A18}^{2} + 928.24 \times X_{A18}^{3} + 184.09 \times X_{A19} + 71.55 \times X_{A19}^{2} + 50.98 \times X_{A19}^{3} - 65.08 \times Y_{A1} - 7691.46 \times Y_{A1}^{2} + 46708.18 \times Y_{A1}^{3} + 180.01 \times Y_{A2} + 5441.13 \times Y_{A2}^{2} + 103436.12 \times Y_{A2}^{3} + 514.6 \times Y_{A3} + 2628.08 \times Y_{A3}^{2} - 3297.11 \times Y_{A3}^{3} + 214.22 \times Y_{A4} - 1990.7 \times Y_{A4}^{2} + 37700.16 \times Y_{A4}^{3} + 346.43 \times Y_{A5} - 172.25 \times Y_{A5}^{2} + 485.56 \times Y_{A6} - 284.79 \times Y_{A6}^{2} - 32269.7 \times Y_{A6}^{3} + 350.65 \times Y_{A7} - 121.46 \times Y_{A7}^{2} + 200.29 \times Y_{A7}^{3} + 312.95 \times Y_{A8} - 122.38 \times Y_{A8}^{2} + 282.14 \times Y_{A9} + 124.56 \times Y_{A9}^{2} + 213.07 \times Y_{A10} + 2051.29 \times Y_{A10}^{2} + 478.6 \times Y_{A11} + 994.49 \times Y_{A11}^{2} + 302.75 \times Y_{A12} - 1675.17 \times Y_{A12}^{2} + 524.59 \times Y_{A13} + 3987.59 \times Y_{A13}^{2} + 493.71 \times Y_{A14} + 127.88 \times Y_{A14}^{2} + 327.07 \times Y_{A15} - 335.11 \times Y_{A15}^{2} + 250.3 \times Y_{A16} + 98.87 \times Y_{A16}^{2} + 250.95 \times Y_{A17} + 2653.54 \times Y_{A17}^{2} + 255.89 \times Y_{A18} - 517.99 \times Y_{A18}^{2} + 254.84 \times Y_{A19} - 216.44 \times Y_{A19}^{2}}$$

Comment: A1 (*Mylopharyngodon piceus*), A2 (*Ctenopharyngodon idella*), A3 (*Hypophthalmichthys molitrix*), A4 (*Hypophthalmichthys nobilis*), A5 (*Megalobrama terminalis*), A6 (*Parabramis pekinensis*), A7 (*Xenocypris argentea*), A8 (*Squaliobarbus curriculus*), A9 (*Cirrhinus molitorella*), A10 (*Cyprinus carpio*), A11 (*Elopichthys bambusa*), A12 (*Ochetobius elongatus*), A13 (*Siniperca kneri*), A14 (*Sinibotia pulchra*), A15 (*Hemiculter leucisculus*), A16 (*Squalidus argentatus*), A17 (*Pseudolaubuca sinensis*), A18 (*Lcucosoma chinensis*), A19 (*Rhinogobius giurinus*)

The equation for *Mylopharyngodon piceus* biomass abundance has a mean relative error of 0.50% and an average relative error of 2.91% across the 103 samples (table 5.13).

TAB. 5.13 – Factors and statistical errors of biomass abundance and the spatial coordinates of community species with the model of fish morphological parameters.

Fish	The power of x- and y-coordinates (the independent variables) in the fitting function	The rejudgment error of fitted samples (%)	The relative error of assessment sample (%)
Mylopharyngodon piceus	All six species of fish XY contained one or two or three power, such as. **A1, A2, A3, A4, A7, A6**. Thirteen species of fish X contain two or two powers,such as **A5, A8, A9, A10, A11, A12, A13, A14, A16, A17, A15, A18, A19** *Rhinogobius giurinus.*	0.50	2.91
Ctenopharyngodon idella	Like *Mylopharyngodon piceus*	1.06	2.21
Hypophthalmichthys molitrix	Like *Mylopharyngodon piceus*	0.18	6.03
Hypophthalmichthys nobilis	Like *Mylopharyngodon piceus*	0.25	2.12
Megalobrama terminalis	Like *Mylopharyngodon piceus*	0.06	5.04
Parabramis pekinensis	Like *Cirrhinus molitorella*	0.48	9.64
Xenocypris argentea	Like *Mylopharyngodon piceus*	2.3	7.63
Squaliobarbus curriculus	XY all contains one, two, and three powers such as **A8, A16, A19**. X contains one, two powers, and Y contains one, two, and cubic powers such as **A1, A2, A3, A4, A5, A6, A7, A9, A10, A11, A12, A13, A14, A15**. XY all contains one, two, and three powers such as **A17, A18**.	8.4	5.49

Tab. 5.13 – (continued).

Fish	The power of x- and y-coordinates (the independent variables) in the fitting function	The rejudgment error of fitted samples (%)	The relative error of assessment sample (%)
Cirrhinus molitorella	XY all contains one, two, and three powers such as **A5, A7, A8, A9, A18, A19**. Thirteen species of fish X contain one or three powers, The y contains a quadratic power such as **A1, A2, A3, A4, A6, A10, A11, A12, A13, A14, A16, A17, A15**.	0.27	9.21
	Mean relative error	1.23	6.40

The average return error across the 19 fish models was ≤23% (*i.e.*, the accuracy was 98.7%; table 5.13). The regression model for all fish was 2.3%, with the exception of *Squaliobarbus curriculus* and *Squalidus argentatus*, which were >4%; *Xenocypris argentea* was >2%. Assessment with nine real-time samples from different years returned an average relative error of 6.4% across the 19 fish species, which better illustrated the validity of the model. This analysis demonstrated that ecological niches could be used to characterize the relationships among fish biomass abundance. Notably, the main reason for the larger error with the predictive sample is that relative error increased with smaller sample sizes. Alternatively, the percentage of outlier data may have increased. The error for several fish, such as *Parabramis pekinensis*, *Cirrhinus molitorella*, *Squalidus argentatus*, *Pseudolaubuca sinensis*, *Lcucosoma chinensis,* and *Rhinogobius giurinus,* was 9%–11%. However, this error is within acceptable limits for an ecological study.

In this section, a method to determine the biomass niche based on spatial relationships was established by using multivariate statistical correspondence analysis to convert between biomass abundance and model data. Thus, the biomass abundance of community species at any spatial location can be deduced to evaluate the niche assignments of the model.

5.4.2 Environmental Impact Analysis Reference Frame

Based on the data for the early fish resources in the Zhaoqing section of the Pearl River, the number of various types of replenishments of the early fish resources is constantly changing due to environmental fluctuations. According to monitoring and analysis data, 19 species (taxa) were found among the early drifting resources in the Zhaoqing section of the Pearl River, accounting for about 70% of the biomass of the fishing resources in the study area (Li Xinhui *et al.*, 2021b). It is thus important to study the niche relationships among fish communities in the regional ecological units containing these species. The impacts of annual environmental changes on a fish niche can be characterized by using biomass to reflect abundance or niche occupation. These results are shown in table 5.14. The model values provide a common frame of reference for the impact of annual environmental changes.

Because of the rapid changes in the aquatic ecological environment, fish living conditions and competition parameters have changed greatly. The overall trajectory of community change (the state of deviation from the center of the coordinates; see figure 5.3) can be understood by using the coordinate values of the "integrated impact factors" (*i.e.*, the integrated factors reflecting the changes in various abundance values; see table 5.15). Table 5.15 shows that variations in the abundance of *Squaliobarbus curriculus* are increasing, which is consistent with the trend of the "comprehensive impact factor" away from the origin of the coordinates. This trend may reflect a tendency toward niche expansion in this dominant species. In contrast, the niches of *Mylopharyngodon piceus, Ctenopharyngodon idella, Hypophthalmichthys molitrix, Hypophthalmichthys nobilis,* and other fish were decreasing. Thus, the community niche was in an unbalanced state.

TAB. 5.14 – Abundance of the early floating resources of the main species (classes) in Xi River in the Pearl River system*.

Fish/Time	Model value	2006	2007	2008	2009	2010	2011	2012	2013
Mylopharyngodon piceus	8.07	0.072	0.591	0.205	0.54	0.419	0.071	0.1	0.22
Ctenopharyngodon idella	9.1	2.148	0.29	1.138	1.275	1.194	1.02	1.1	1.3
Hypophthalmichthys molitrix	12.31	2.86	1.078	4.512	2.971	2.205	1.755	2.7	2.9
Hypophthalmichthys nobilis	11.39	1.136	0.124	0.513	0.778	0.572	0.296	1.12	0.99
Megalobrama terminalis	5.715	29.592	29.951	12.132	15.104	11.914	20.337	21.8	4.1
Parabramis pekinensis	4.04	1.208	1.389	1.569	0.573	0.735	0.673	0.55	0.43
Xenocypris argentea	7.019	22.024	19.318	10.44	8.913	26.534	5.878	9.11	5.9
Squaliobarbus curriculus	7.666	26.113	24.842	45.226	46.208	32.506	43.969	49.35	54
Cirrhinus molitorella	7.159	4.584	14.064	8.789	11.549	10.434	10.704	4.49	7.8
Cyprinus carpio	1.312	0.145	0.021	0.103	0.022	0.01	0.01	0.002	0.008
Elopichthys bambusa	4.75	0.32	0.249	0.615	0.4	0.419	0.847	0.66	0.32
Ochetobius elongatus	2.07	0.052	0.052	0.072	0.324	0.316	0.306	0.3	0.123
Siniperca kneri	3.782	0.341	0.093	0.369	0.227	0.204	0.092	0.15	0.15
Sinibotia pulchra	2.79	0.227	0.404	4.451	3.771	2.246	1.184	1.36	2.1
Hemiculter leucisculus	1.834	4.605	5.161	4	2.895	4.033	8.041	3.36	1.1
Squalidus argentatus	6.792	1.105	0.363	2.718	2.409	5.431	3.245	0.9	18
Pseudolaubuca sinensis	1.904	1.642	1.005	1.979	0.951	0.47	0.571	0.39	0.35
Lcucosoma chinensis	0.94	1.198	0.591	0.656	0.14	0.092	0.378	0.13	0.077
Rhinogobius giurinus	1.35	0.63	0.415	0.513	0.951	0.265	0.622	0.19	0.134

*of total annual output (%).

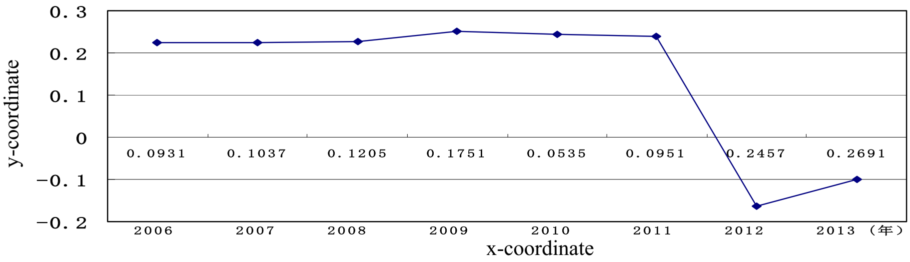

Fig. 5.3 – The X and Y coordinates of the "abundance factor" of 19 fish species of Xijiang River changed from 2006 to 2013.

Tab. 5.15 – The x- and y-coordinates of the "composition factors" of 19 fish species in the Xijiang River from 2006 to 2013.

Time	2006	2007	2008	2009	2010	2011	2012	2013
x	0.0931	0.1037	0.1205	0.1751	0.0535	0.0951	0.2457	0.2691
y	0.2252	0.2244	0.2268	0.251	0.2439	0.2399	-0.164	−0.1

5.4.3 Analysis of the Niche of the Artificial Community

Changes in the niche of a specific species will lead to various niche changes across the community. In reality, river biodiversity and resource recovery conservation efforts usually target specific species, such as the silver carp and bighead carp, in lakes with high primary productivity. However, due to the serious declines in river fishery resources, it is necessary to evaluate the niche structure and environmental capacity of certain species in the community by investing in black carp, grass carp, silver carp, and bighead carp. There are also random releases of species, which require systematic evaluation. In an ecosystem, an increase in the biomass of one species will affect the niches of other species in the community. If a given increase is not suitable for the food chain, new imbalances in the ecosystem may arise.

The species community niche structure is different from the concept of the environmental capacity of a given species. The species community niche structure is based on the composition of the food chain system and the niche value of each species, and this concept emphasizes the biological match between the niche and the energy cycle. The environmental capacity of a species refers to the environmental matching between the ecological niche and the energy cycle based on the total energy requirement.

Using the model, we can analyze and calculate the preset target amounts of biodiversity conservation and resource restoration for one species (or several species) while observing the niche changes of other species (species matching and biomass matching). This provides an analytical tool for community management. Using different fish as targets, the resulting niche composition of the remaining fish in the community was calculated to reflect the function of the model, as shown in table 5.16.

Tab. 5.16 – Simulated community niches targeting different fish (%).

Fish/sample name	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8	Model 9
Mylopharyngodon piceus	1.19	7.03	8.8	14.6	8.89	15.15	13	13.5	13.9
Ctenopharyngodon idella	1.4	10.03	12	11	12.5	17.9	16	16.5	15.28
Hypophthalmichthys molitrix	12.95	9.18	8.5	10.3	16	11.5	10	11.5	16.76
Hypophthalmichthys nobilis	11.87	10.88	9.3	11.3	12	9.2	15	15.5	16.66
Total target ecological niche of *Mylopharyngodon piceus, Ctenopharyngodon idella, Hypophthalmichthys molitrix, Hypophthalmichthys nobilis*	27.41	37.12	38.6	47.2	49.39	53.75	54	57	62.6
Megalobrama terminalis	6.47	5.14	5.14	3.6	4.27	3.9	4.99	3.99	3.39
Parabramis pekinensis	4.64	1.03	2.03	1.4	3	3.2	1.02	1.02	1.7
Xenocypris argentea	9.94	8.45	7	7.6	5.5	3.7	5.5	4.5	2.14
Squaliobarbus curriculus	9.93	9.25	8	4.2	4	2.8	5.99	4.99	3.71
Cirrhinus molitorella	9.6	2.85	3.63	3.1	4.72	2.75	4.7	3.7	5.52
Cyprinus carpio	1.62	0.71	1.5	0.58	0.28	0.28	1.1	1.1	1.38
Elopichthys bambusa	4.02	4.44	3.8	4.91	1.5	6.4	2.6	2.6	1.08
Ochetobius elongatus	0.54	4.57	3.7	2.6	3	4.3	1.18	1.68	2.65
Siniperca kneri	5.69	4.57	5	4.4	2	5.5	2.04	2.04	2.42
Sinibotia pulchra	4.62	2.4	3.2	3.6	1.9	4.3	1.39	1.89	1.36
Hemiculter leucisculus	2.16	2.68	1.6	3.7	5.2	2.2	4.64	4.14	1.91
Squalidus argentatus	8.3	7.65	6.2	4.6	5.2	3.05	4.63	4.13	6.32
Pseudolaubuca sinensis	2.16	3.85	4.1	5.4	4	1.85	3.53	3.53	1.7
Lcucosoma chinensis	1.65	3.63	4	0.77	3.04	1.45	1.63	2.13	1.59
Rhinogobius giurinus	1.29	1.66	2.5	2.34	3	0.21	1.06	1.56	0.53

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