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 leuciscul us	■	*	■	*	■	■
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	

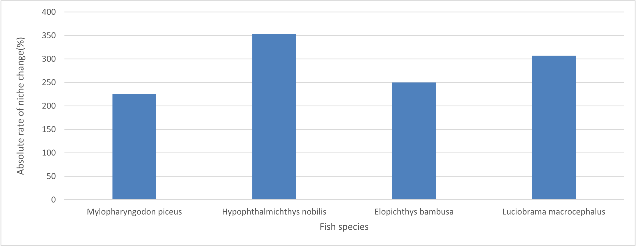

FIG. 4.1 – Variations in the ecological niches of the large fish in simulated communities.

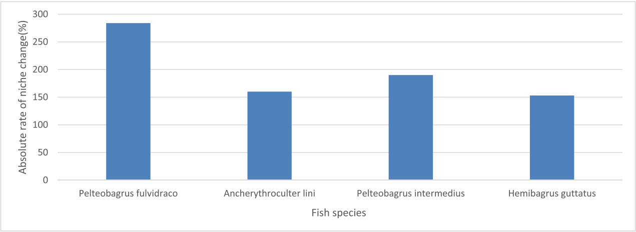

FIG. 4.2 – Variations in the ecological niches of the medium fish in simulated communities.

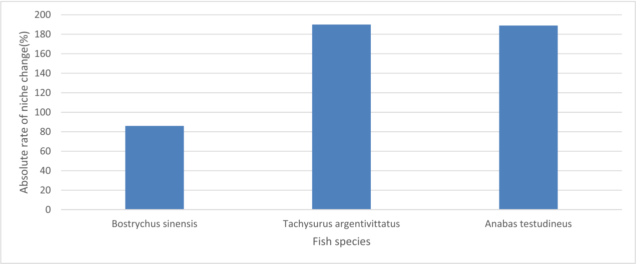

FIG. 4.3 – Variations in the ecological niches of the small fish in simulated communities.

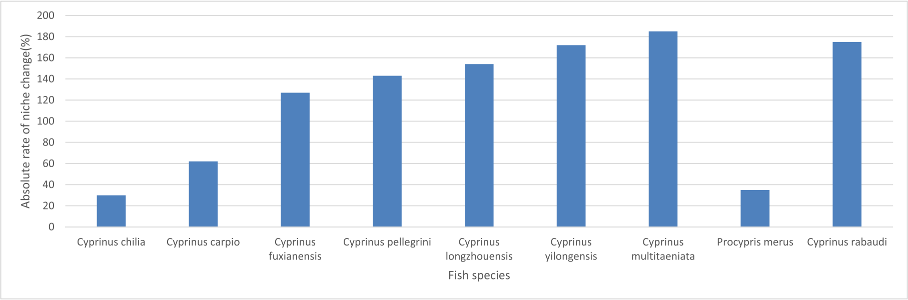

FIG. 4.4 – Variations in ecological niches of the fish similar to *Cyprinus* in simulated communities.

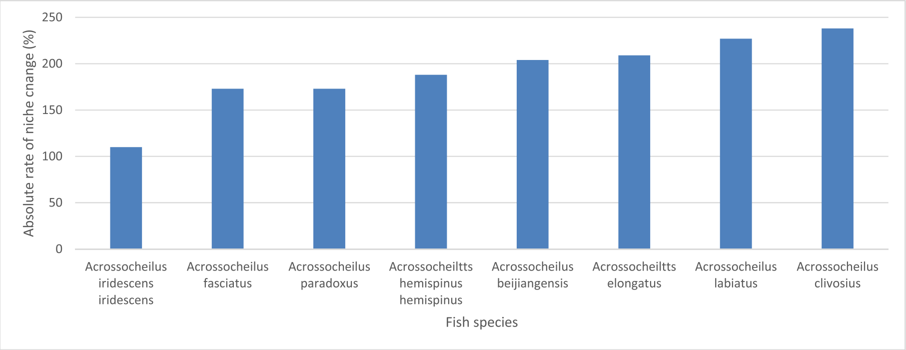

FIG. 4.5 – Variations in ecological niches of the *Acrossocheilus* in simulated communities.

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

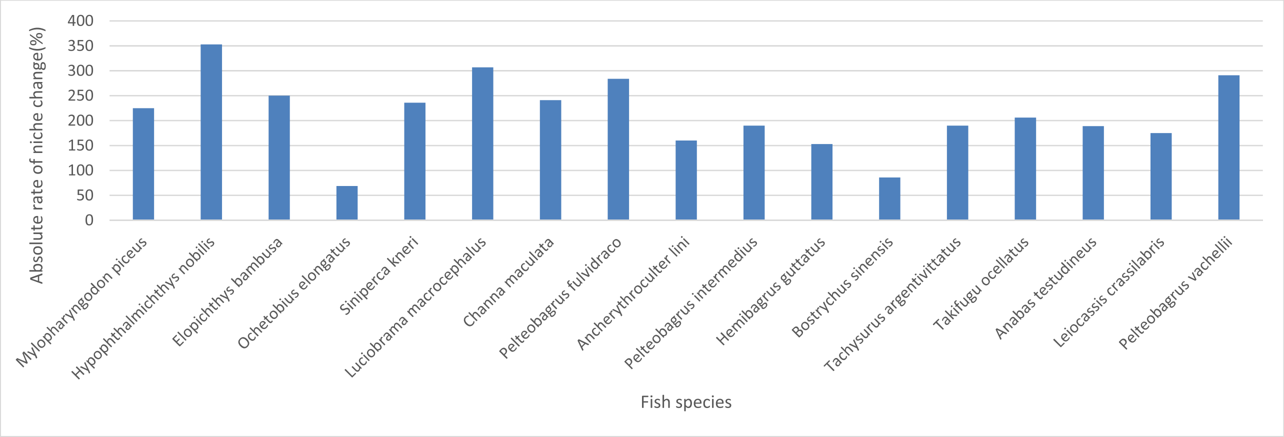

FIG. 4.6 – Variations in ecological niches of several carnivorous fish in simulated communities.

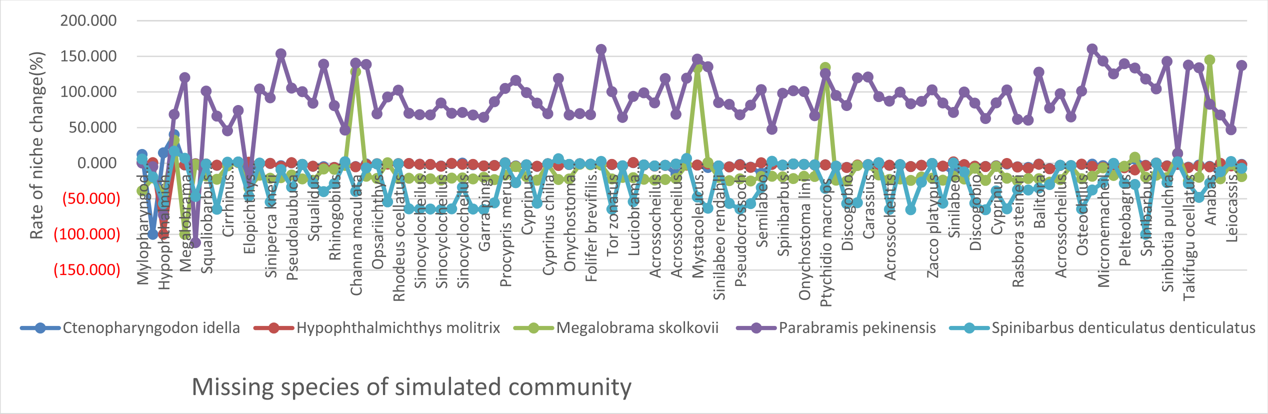

FIG. 4.7 – Differences in the responses of five phytophagous fish to the removal of various species from the community.

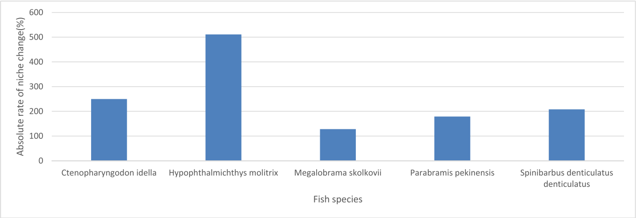

Fig. 4.8 – Variations in the ecological niches of several phytophagous fish in simulated communities.

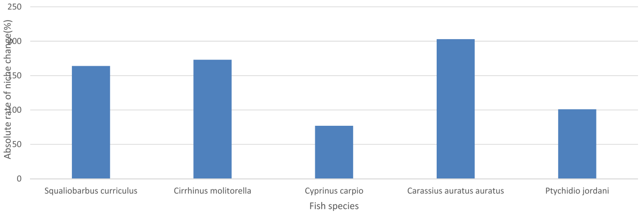

Fig. 4.9 – Variations in ecological niches of several omnivorous fish in simulated communities.

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.*

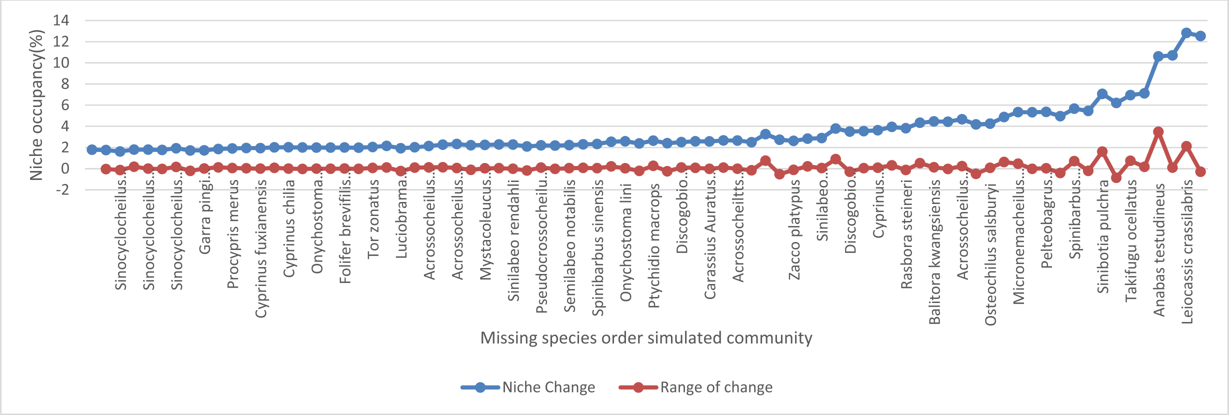

FIG. 4.10 – Amplitude of niche change for *Mylopharyngodon piceus* when species in the "primitive community" were removed one by one.

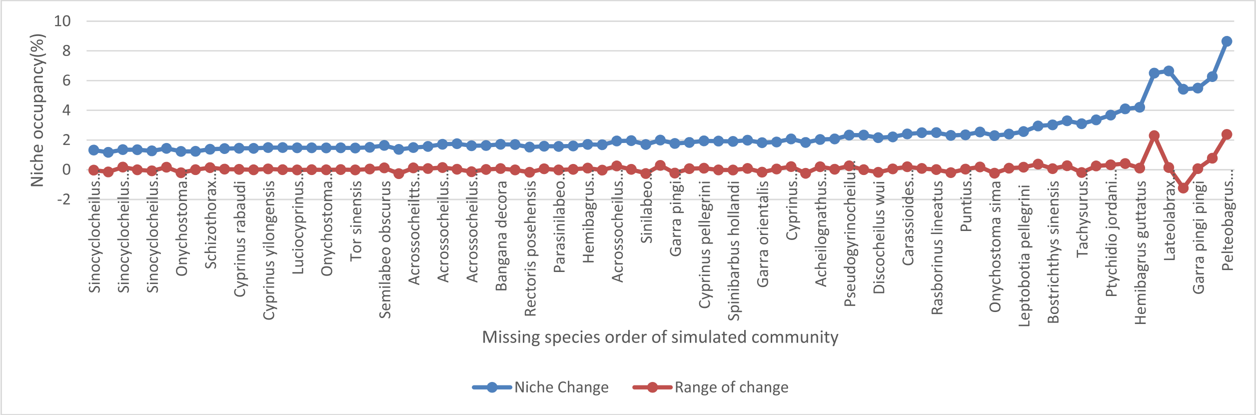

FIG. 4.11 – Amplitude of niche change for *Ctenopharyngodon idella* when species in the "primitive community" were removed one by one.

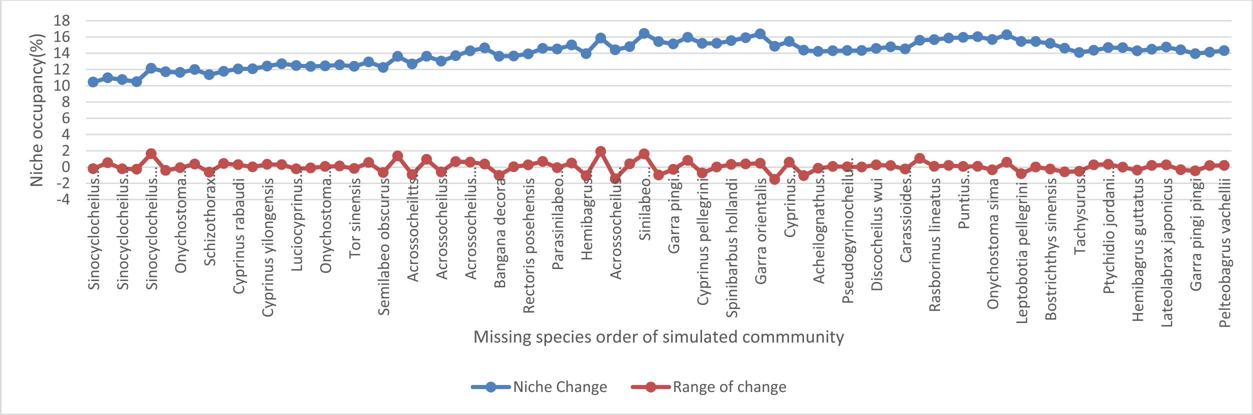

FIG. 4.12 – Amplitude of niche change for *Mhypophthalmichthys molitrix* when species in the "primitive community" were removed one by one.

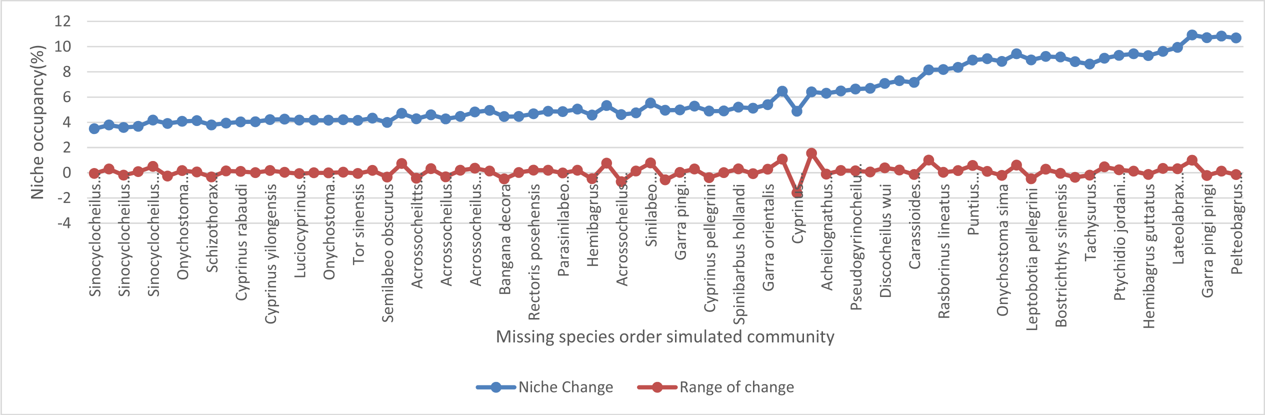

FIG. 4.13 – Amplitude of niche change for *Hypophthalmichthys nobilis* when species in the "primitive community" were removed one by one.

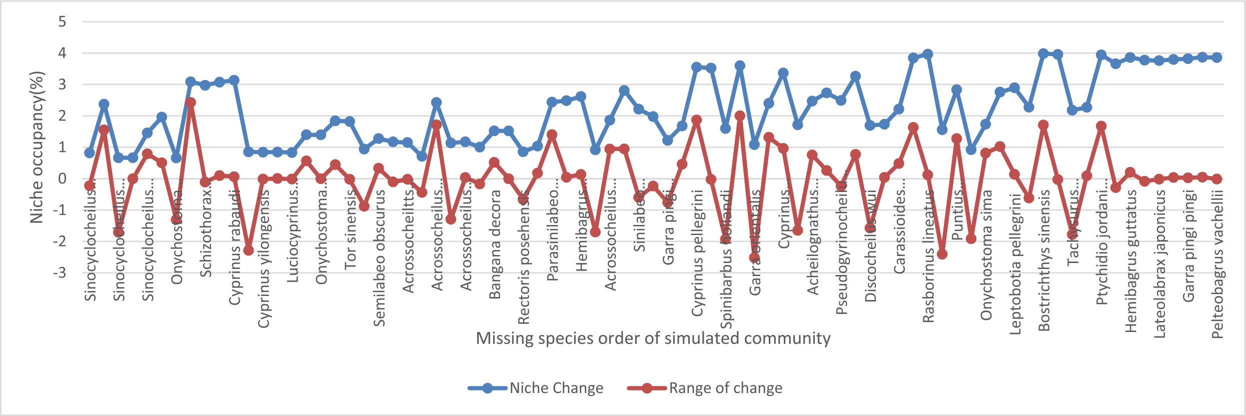

Fig. 4.14 – Amplitude of niche change for *Megalobrama skolkovii* when species in the "primitive community" were removed one by one.

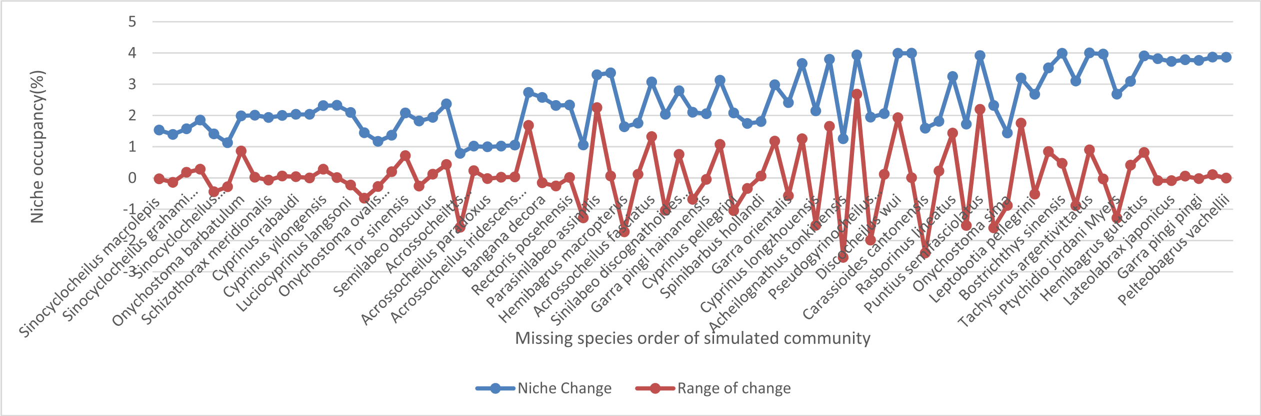

Fig. 4.15 – Amplitude of niche change for *Parabramis pekinensis* when species in the "primitive community" were removed one by one.

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,*

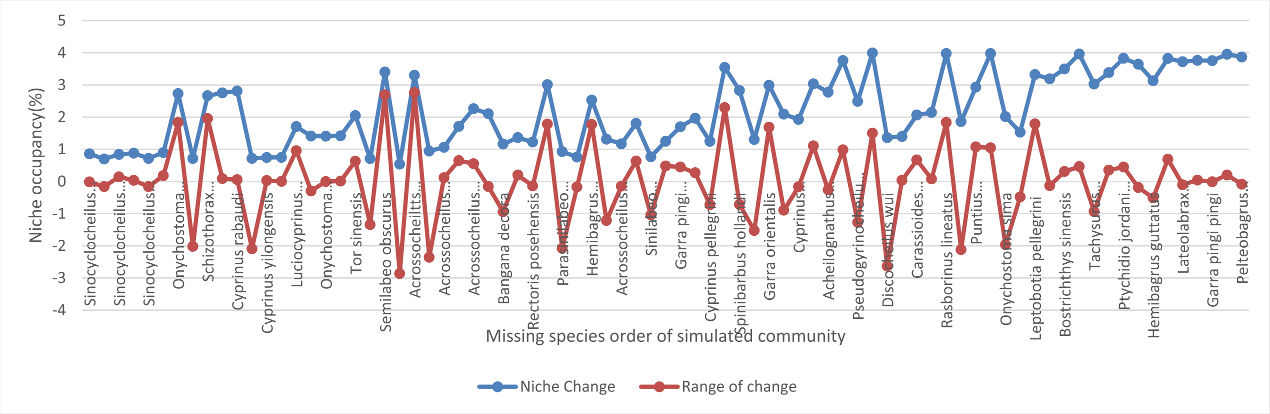

FIG. 4.16 – Amplitude of niche change for *Squaliobarbus curriculus* when species in the “primitive community” were removed one by one.

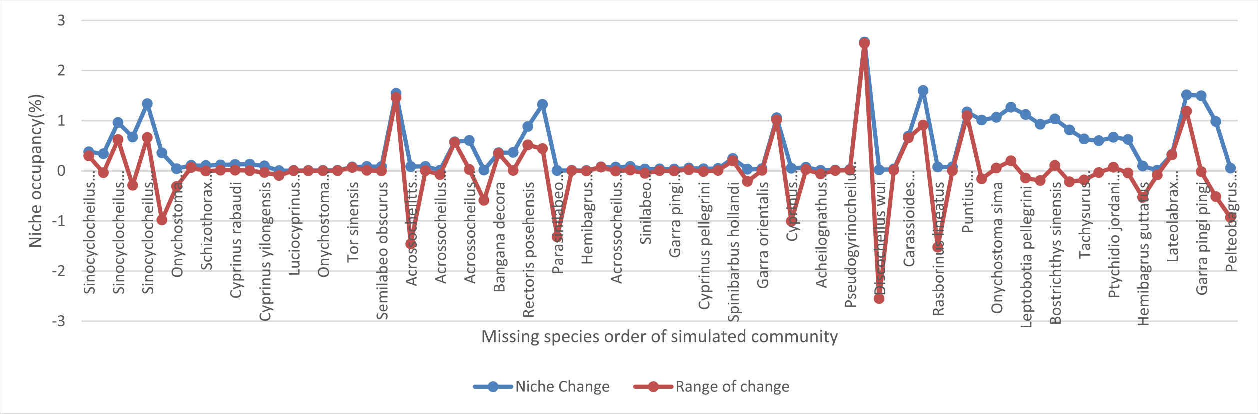

FIG. 4.17 – Amplitude of niche change for *Xenocypris argentea* when species in the “primitive community” were removed one by one.

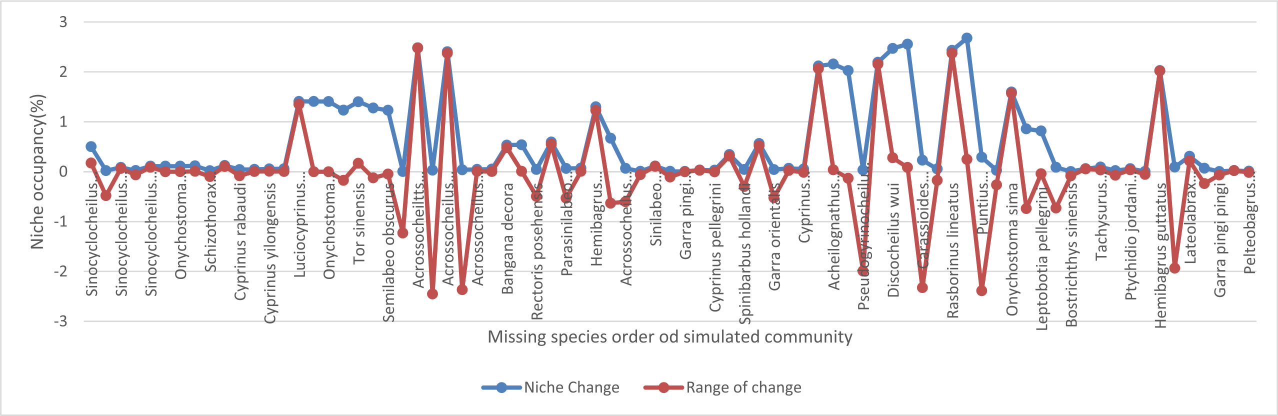

Fig. 4.18 – Amplitude of niche change for *Cirrhinus molitorella* when species in the “primitive community” were removed one by one.

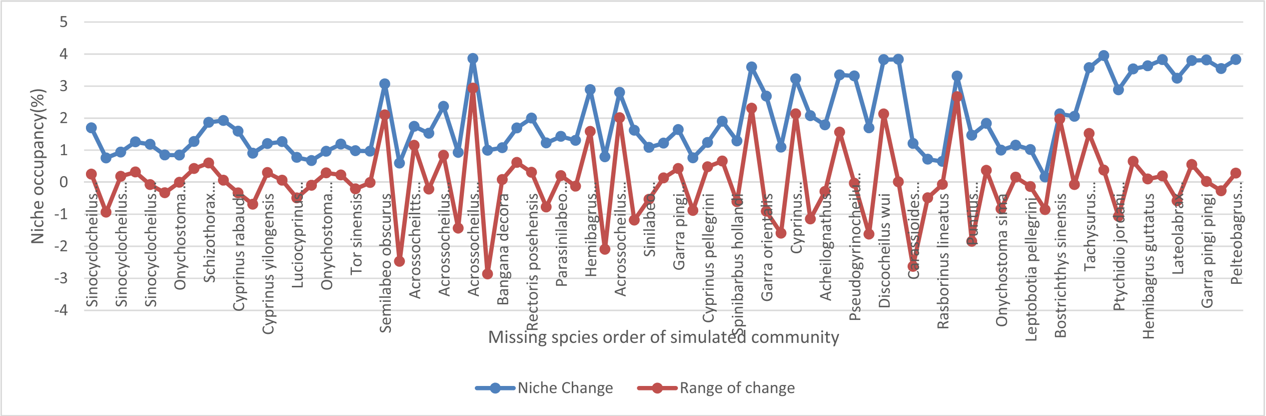

Fig. 4.19 – Amplitude of niche change for *Cyprinus carpio* when species in the “primitive community” were removed one by one.

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%.

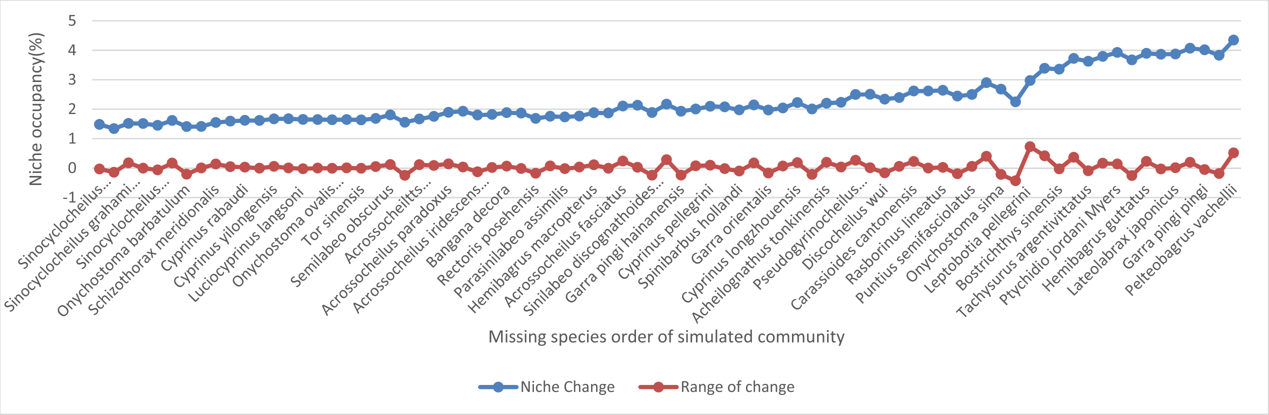

FIG. 4.20 – Amplitude of niche change for *Elopichthys bambusa* when species in the "primitive community" were removed one by one.

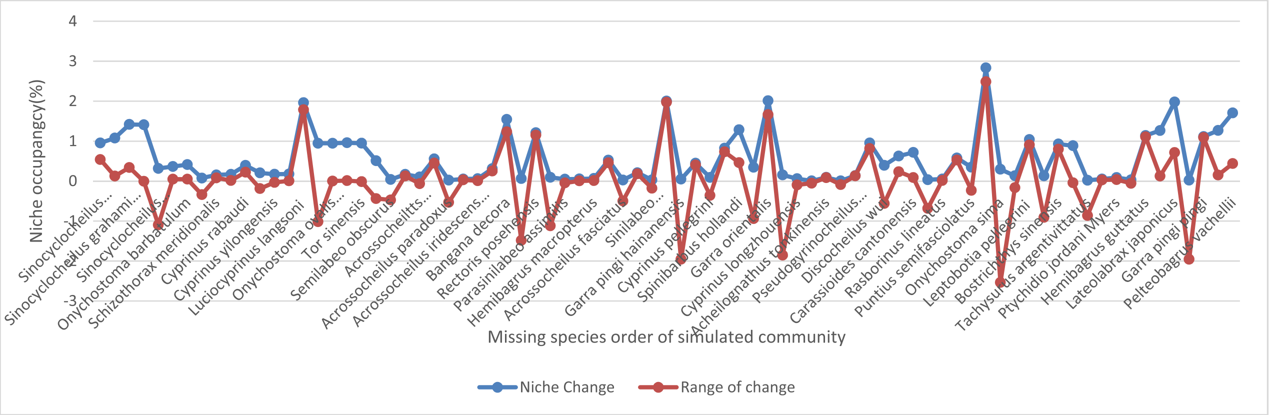

FIG. 4.21 – Amplitude of niche change for *Ochetobius elongatus* when species in the "primitive community" were removed one by one.

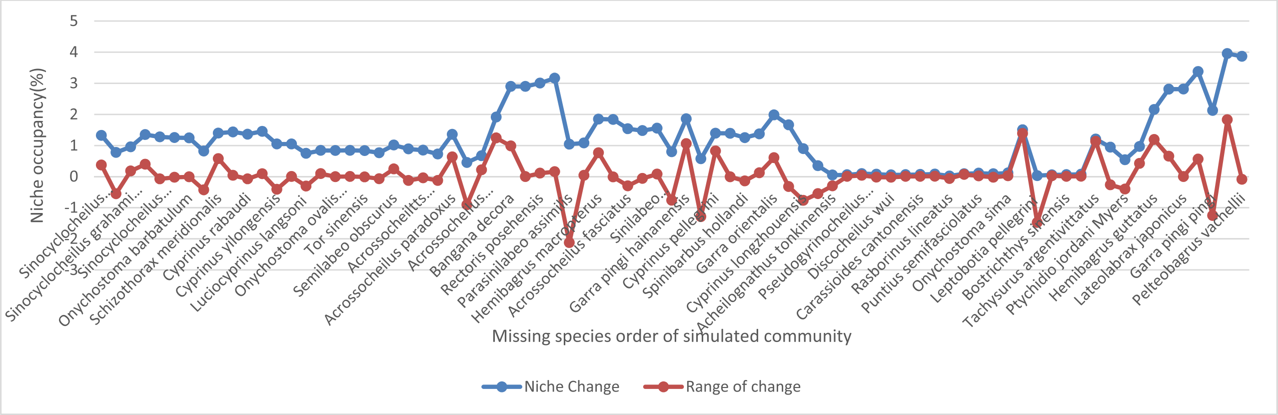

Fig. 4.22 – Amplitude of niche change for *Siniperca kneri* when species in the "primitive community" were removed one by one.

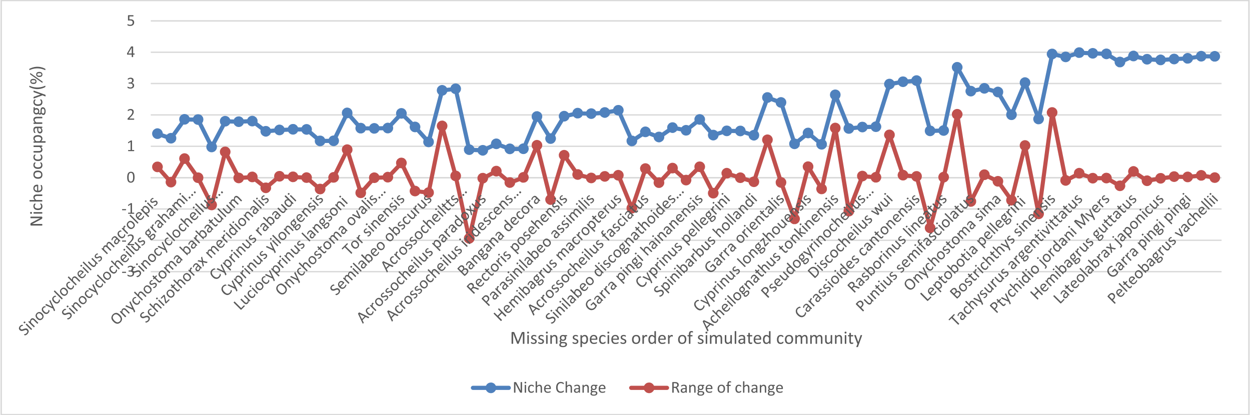

Fig. 4.23 – Amplitude of niche change for *Misgurnus anguillicaudatus* when species in the "primitive community" were removed one by one.

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.*

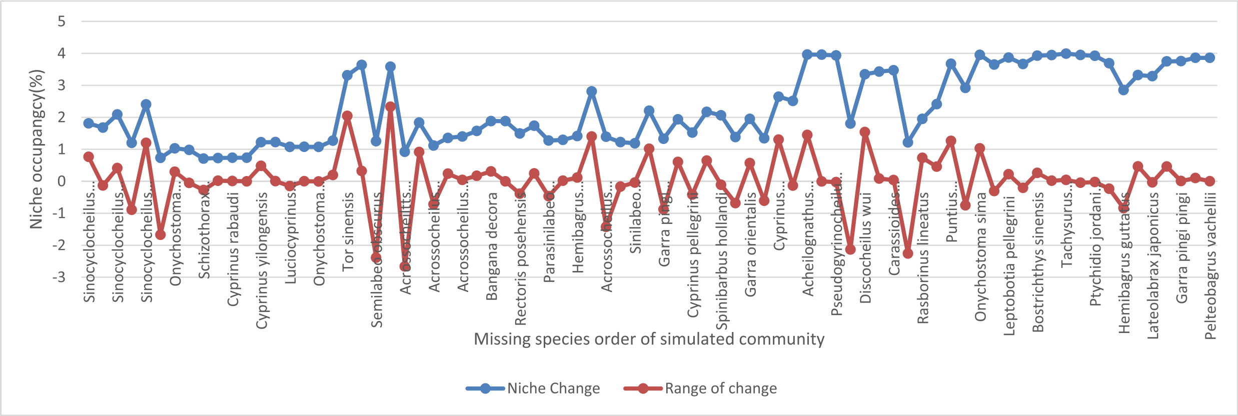

FIG. 4.24 – Amplitude of niche change for *Pseudolaubuca sinensis* when species in the "primitive community" were removed one by one.

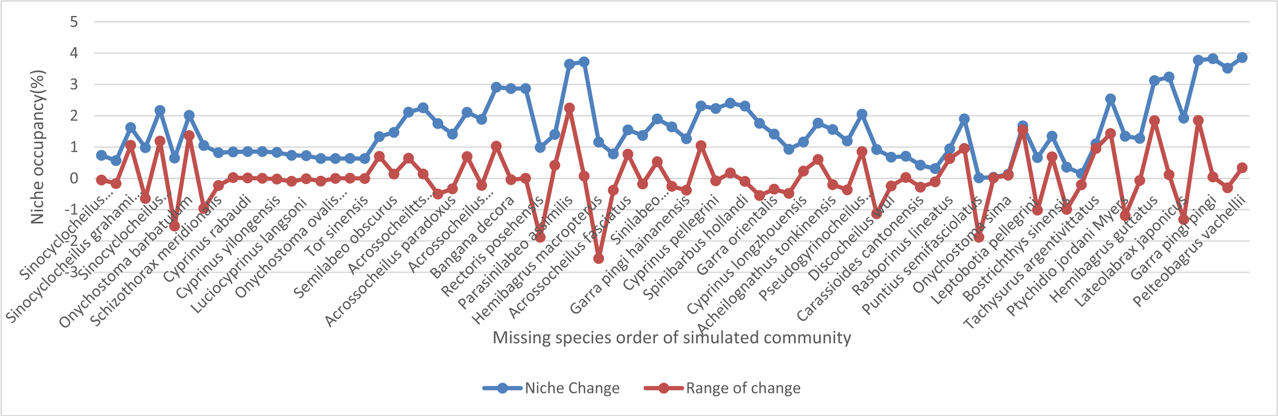

FIG. 4.25 – Amplitude of niche change for *Hemiculter leucisculus* when species in the "primitive community" were removed one by one.

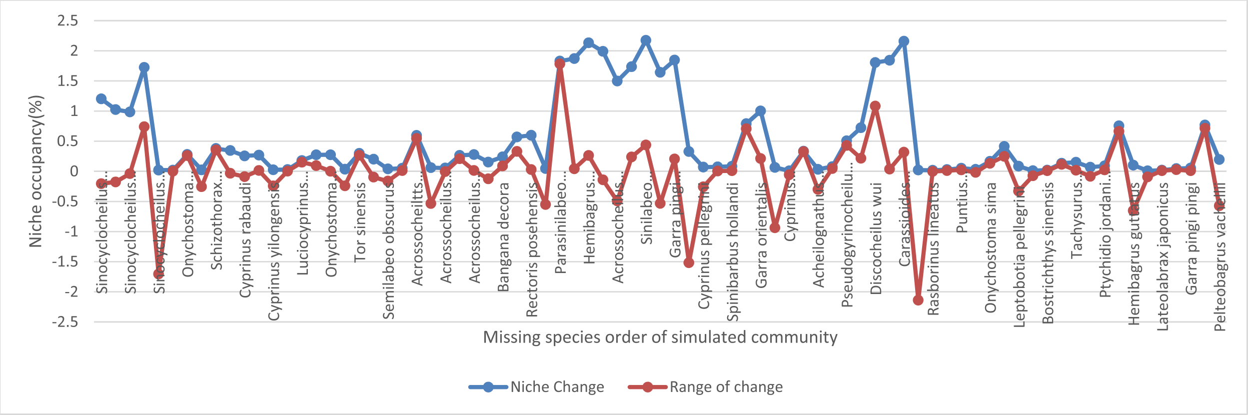

FIG. 4.26 – Amplitude of niche change for *Squalidus argentatus* when species in the "primitive community" were removed one by one.

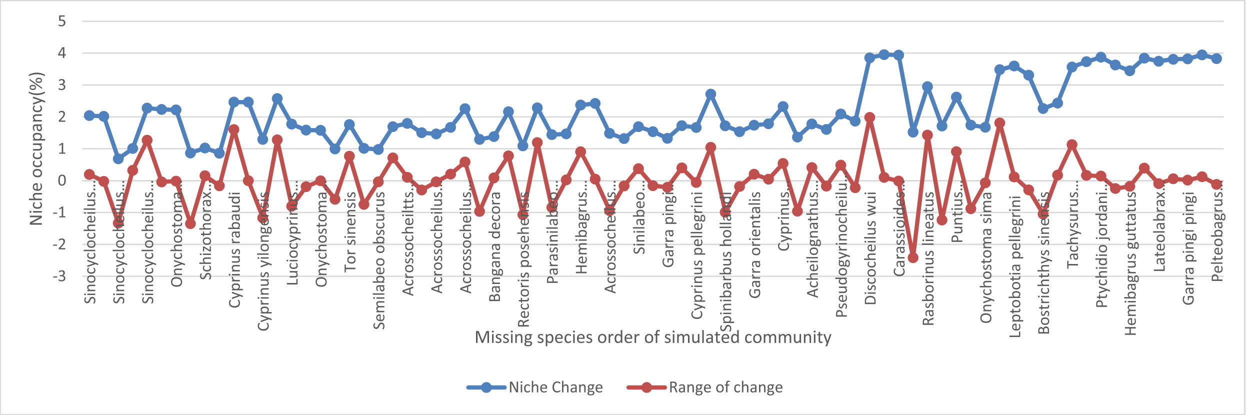

FIG. 4.27 – Amplitude of niche change for *Lcucosoma chinensis* when species in the "primitive community" were removed one by one.

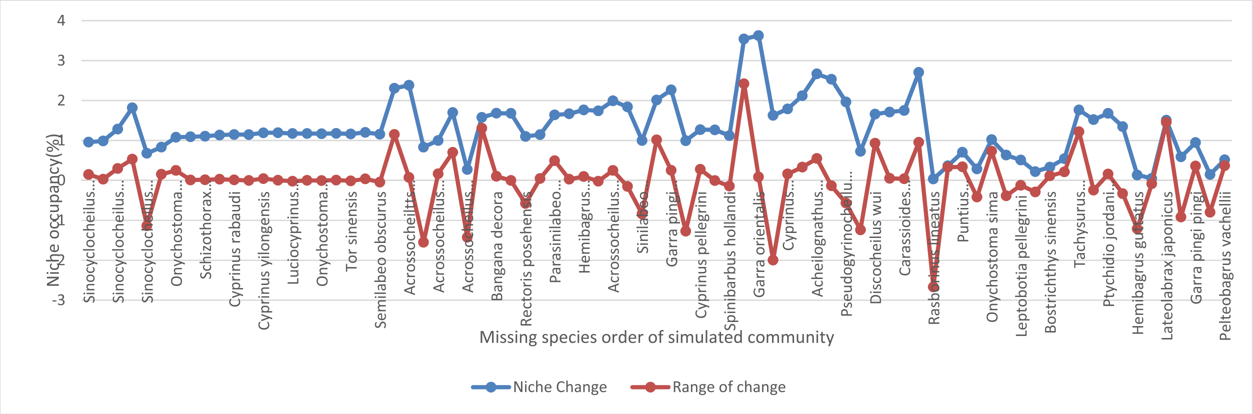

FIG. 4.28 – Amplitude of niche change for *Rhinogobius giurinus* when species in the “primitive community” were removed one by one.

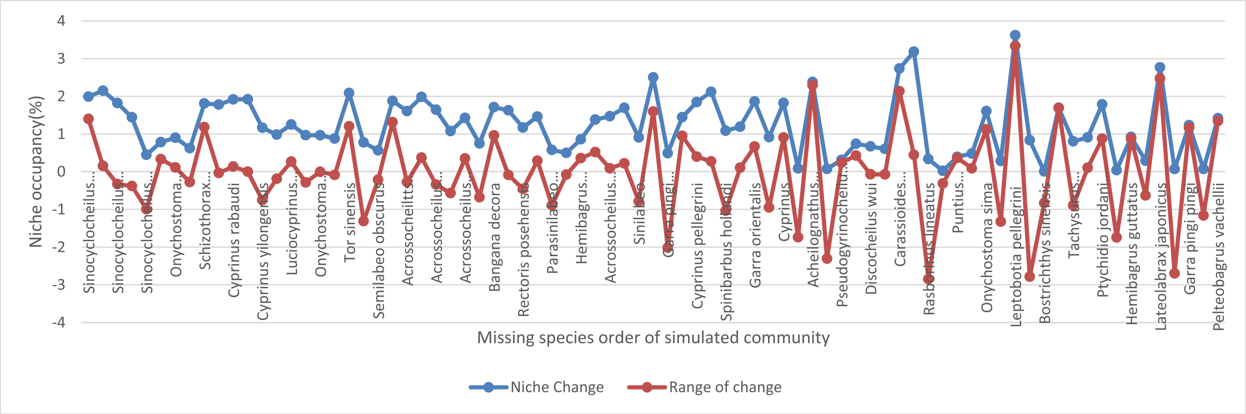

FIG. 4.29 – Amplitude of niche change for *Carassius auratus auratus* when species in the “primitive community” were removed one by one.

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

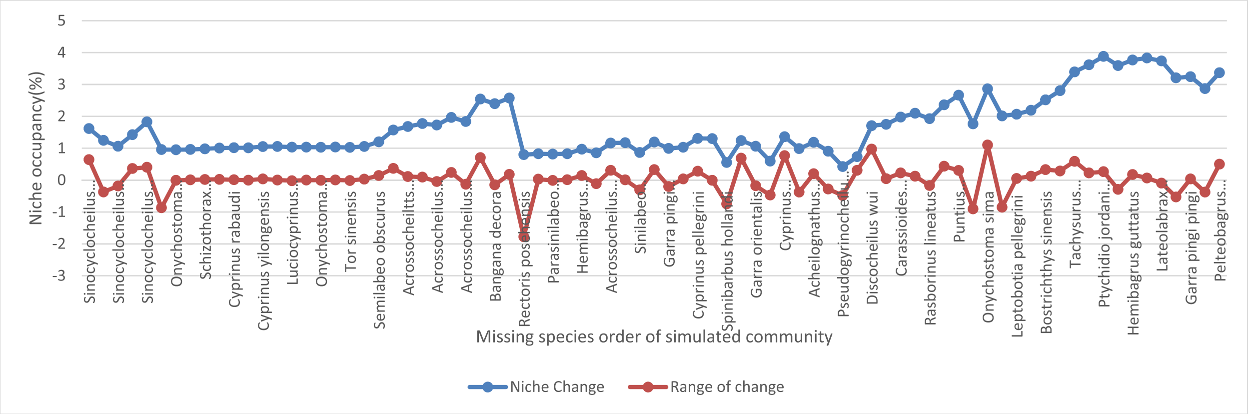

Fig. 4.30 – Amplitude of niche change for *Channa maculata* when species in the “primitive community” were removed one by one.

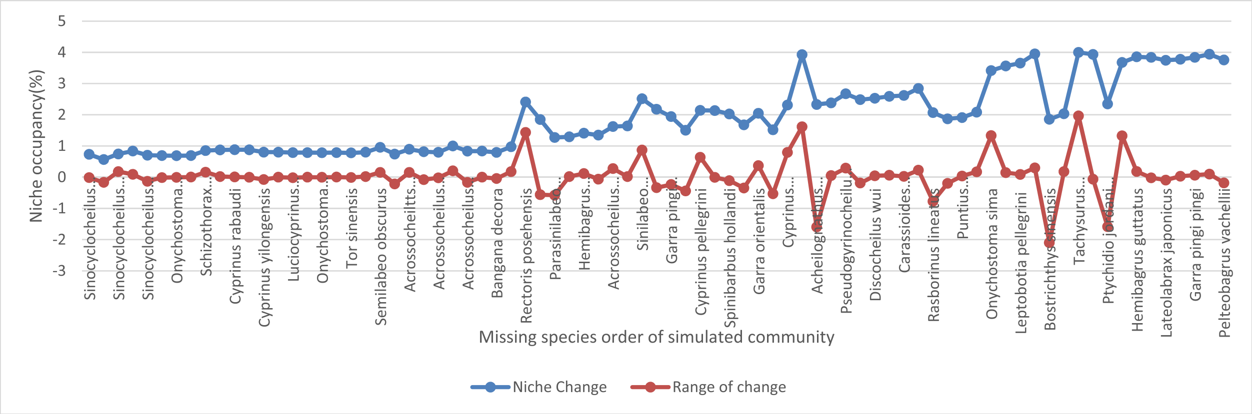

Fig. 4.31 – Amplitude of niche change for *Pelteobagrus fulvidraco* when species in the “primitive community” were removed one by one.

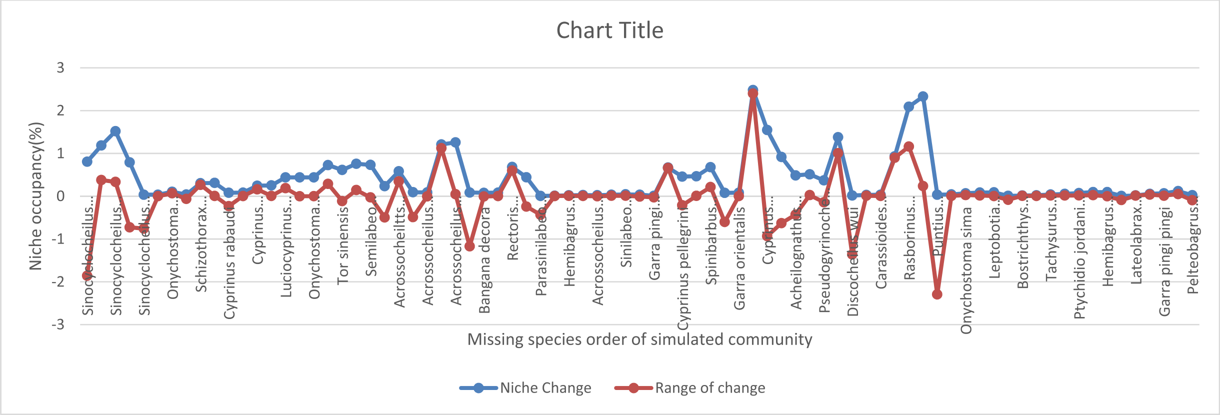

FIG. 4.32 – Amplitude of niche change for *Opsariichthys bidens* when species in the “primitive community” were removed one by one.

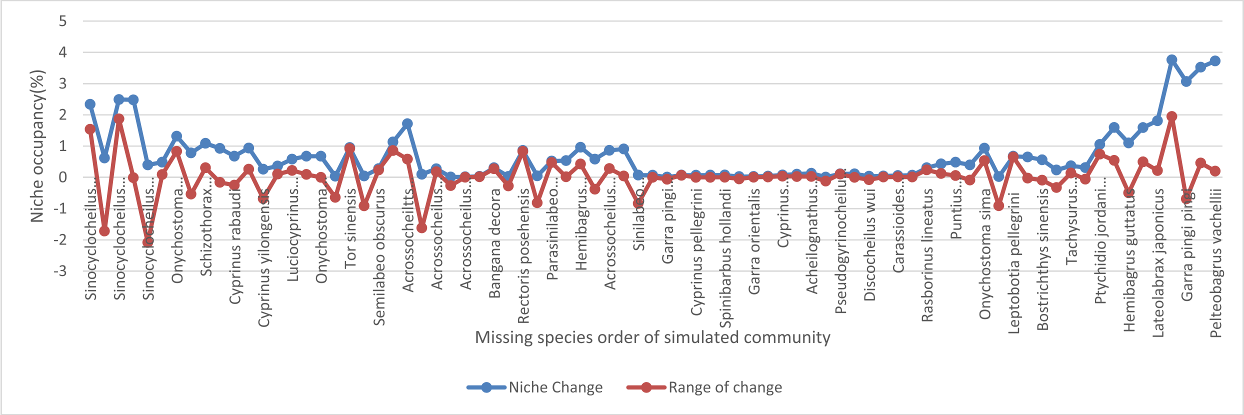

FIG. 4.33 – Amplitude of niche change for *Ancherythroculter lini* when species in the “primitive community” were removed one by one.

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.

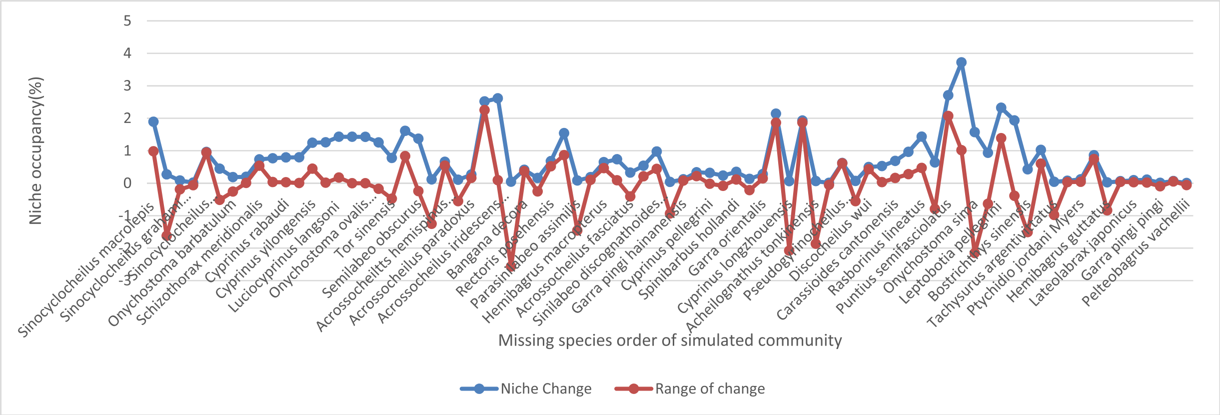

FIG. 4.34 – Amplitude of niche change for *Rhodeus ocellatus* when species in the “primitive community” were removed one by one.

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,*

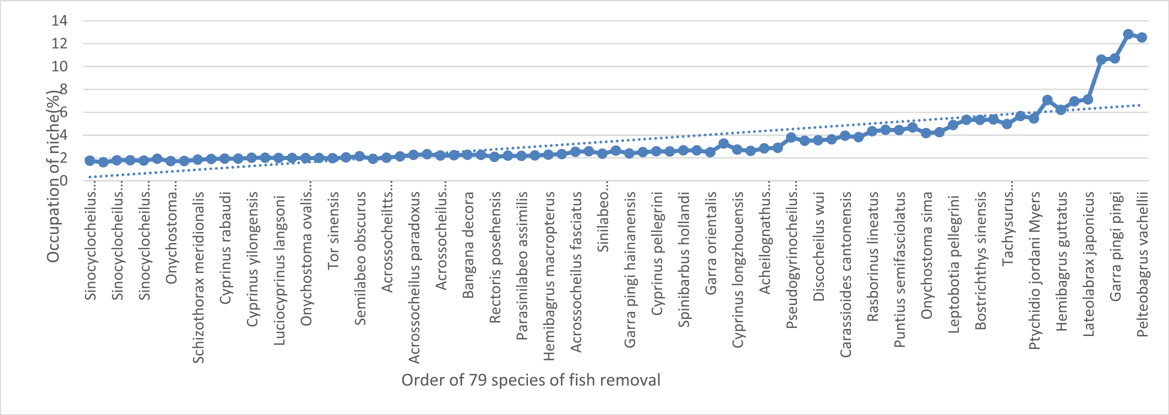

FIG. 4.36 – The niche of *Mylopharyngodon piceus* increased as 79 fish species were removed from the community.

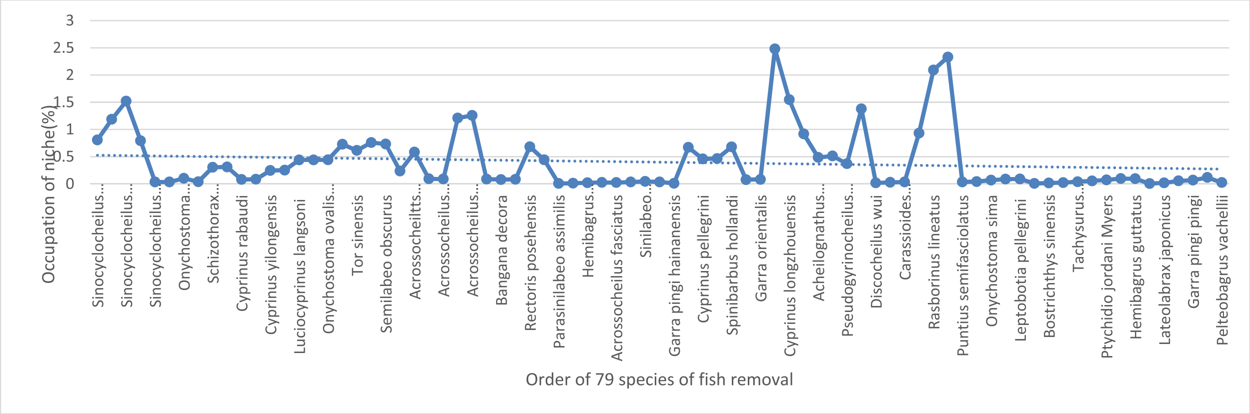

FIG. 4.37 – The niche of *Opsariichthys bidens* declined as 79 species were removed from the community.

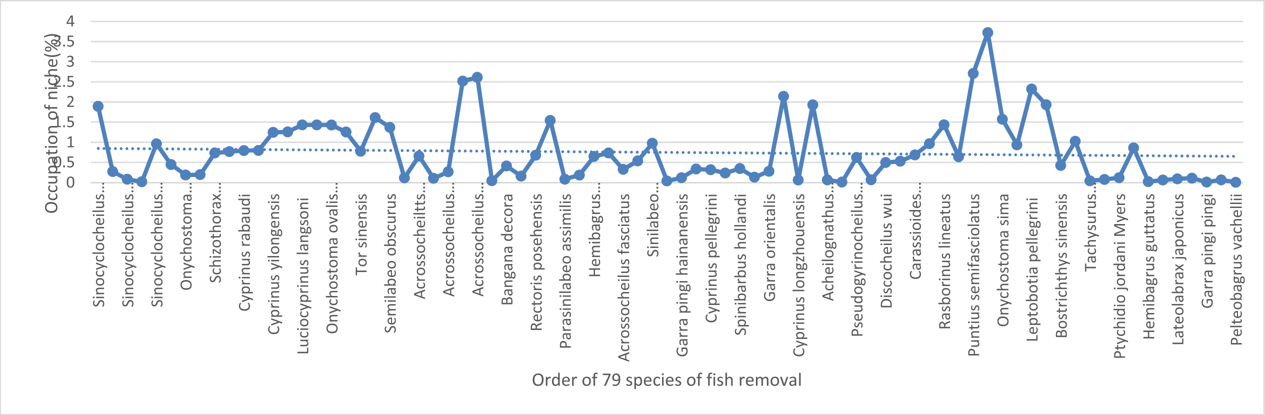

FIG. 4.38 – The niche of *Rhodeus ocellatus* decreased as 79 fish species were removed from the community.

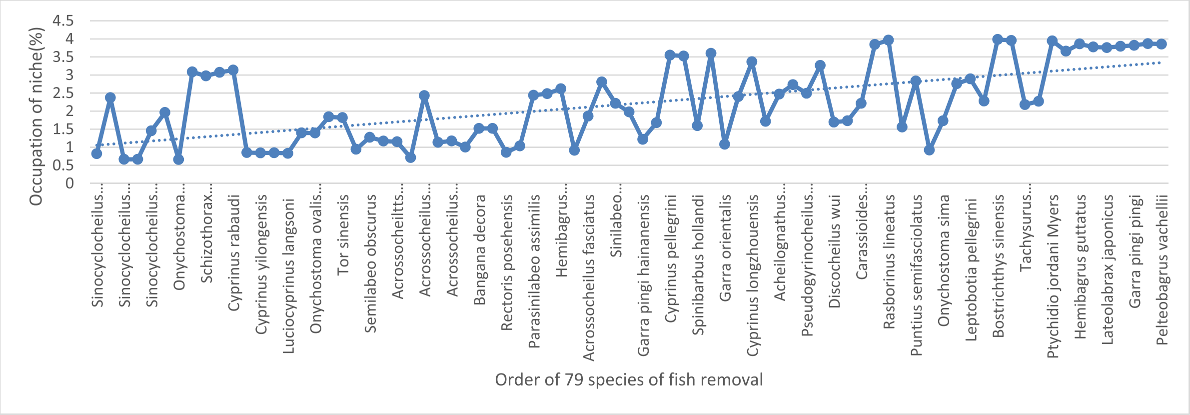

FIG. 4.39 – The niche of *Megalobrama skolkovii* changed in a zig-zag pattern as 79 fish species were removed from the community.

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),

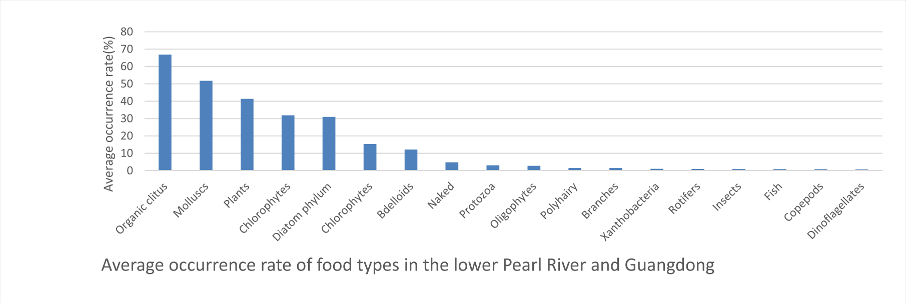

Fig. 5.1 – Components of the diets of 10 fish species in the Pearl River.
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Mylopharyngodon piceus, Ctenopharyngodon idella, Squaliobarbus curriculus, Erythroculter pseudobrevicauda (Nichols, 1927), *Megalobrama terminalis* (Richardson, 1846), and *Parabramis 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).

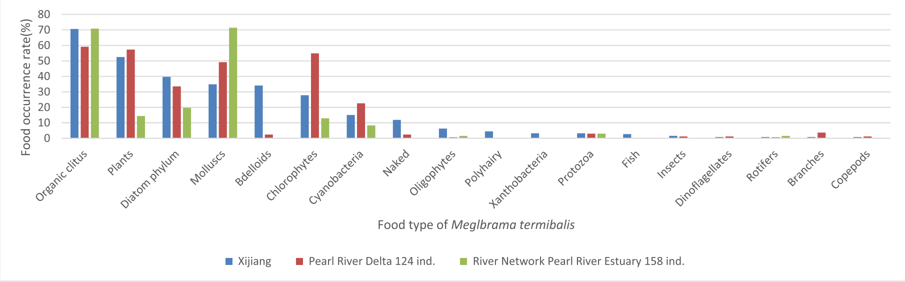

Fig. 5.2 – Frequency of food items detected in the intestines of *Megalobrama terminalis.*

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 (%).

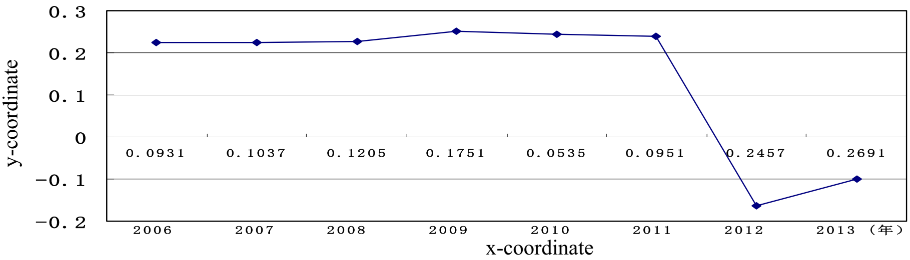

Fig. 5.3 – The X and Y coordinates of the “abundance factor” of 19 fish species of Xijiang River changed from 2006 to 2013.

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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