Article

Some topological properties of arthropod food webs in paddy fields of South China

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Abstract

To explore the topological properties of paddy arthropod food webs is of significance for understanding natural equilibrium of rice pests. In present study, we used Pajek software to analyze the topological properties of four full arthropod food webs in South China. The results showed that predators were significantly abundant than preys, and the proportion of predators to preys (3.07) was significantly higher than previously reported by Cohen in 1977 (1.33). In the food webs, the number of top species was the largest, accounted for about 50% of the total. The number of intermediate-intermediate links was far greater than the other three links. The average degree of paddy arthropod food webs is 6.0, 6.04, 5.74 and 7.75, respectively. Average degree and link density did not change significantly with the change of the number of species, but the connectance reduced significantly. In the paddy ecosystems, the increase of species diversity does not lead to an increase proportionally to the links among species. The link density and connectance of food webs of early season rice field were less than that from late season rice field. Cycles of all food webs cycles were 0. The maximum chain length of the basal species was 3, and the largest chain length of the top species was typically 2 or 3. Neutral insects were found to play a very important role in the paddy ecosystem. *Nilaparvata lugens* and *Sogatella furcifera* were found to be the dominant species of rice pests. *Pardosa pseudoannulata, Tetragnatha maxillosa, Pirata subparaticus, Arctosa stigmosa* and *Clubiona corrugate* were identified as the important predatory species that may effectively control the pest population. The keystone species calculated from keystone index and network analysis are analogous, indicating either keystone index or network analysis can be used in the analysis of keystone species.

Keywords food webs; topological properties; paddy ecosystems; arthropods; natural enemies.

1 Introduction

Arthropod food webs in paddy ecosystems are complex ecological networks, which primarily describe the relationship between natural enemies and rice pests. A food web can explicitly express between-species trophic relationship. Studies on food webs can provide new ideas for rice pest control and management (Valladares et al., 1999). Arthropods are one of the most important organisms in paddy ecosystems (Zhang, 2011). The changes of a paddy arthropod community may indicate the occurrence situation and development trends of rice pests. Therefore the research on paddy arthropod food webs is one of the fundamental works to optimize the biological or natural control of rice pests (You et al., 1993).

Trophic relationship between species within a biome are expressed as the directional links between species in the food web, which depicts the intrinsic attributes of interdependence, mutual restrain and co-evolutionary relationship between the various organisms. Food webs are important part of the studies of biological communities (Price, 1981; Crichlow et al., 1982; DeAngelis et al., 1989; Zhang, 2007, 2011, 2012a, 2012b, 2012c). In recent years, a lot of studies have been done on food webs, including arthropod food webs (Guo et al., 1995; Crook et al., 1984; Prabhakar et al., 2012). For example, Jiang et al. (2006) recorded the dynamics of arthropod communities in paddy fields of Anhui Province.Yuan et al. (2010) studied the community structure of organic rice fields in Yangtze River farms and evaluated the effects of natural enemies on the control of rice insect pests. Wang et al. (2013) compared the community structure of arthropods between ecological and conventional rice fields. Furthermore, studies have indicated that climatic conditions (Zhang et al., 1997), pesticides, pest-resistance varieties of rice, and water-saving irrigation (Fuet al., 2013) would affect paddy arthropod communities. Overall most studies have focused on the effects of changes in ecosystems in different habitats, such as environmental changes, invasive species, species extinction, etc., on the structural components and dynamics of arthropod food webs. For example, Oraze (1988) studied the changes of spider community in the flooded rice fields. Gratton and Denno (2006) restored an arthropod food web following removal of an invasive plant. The concept of neutral insects was first put forward by Wu (1994). Neutral insects are defined as the insects neither natural enemies nor insect pests in rice ecosystems, such as chironomids, mosquitoes, flies and springtails, etc (Guo et al., 1995; Liu, 2000; Liu et al., 2002). Meanwhile, many researchers used different methods, such as serological method (Crook et al., 1984), population dynamics investigation method, ELISA method (Zhang et al., 1996; Liu et al., 2002), and the isotope method (Schmidt SN et al., 2007)to study the relationship between natural enemies and neutral insects and insect pests,, in order to guide utilization and protection of natural enemies and neutral insects.

The topological properties of food webs have been a hot topic since the presentation of food web concept (MacArther, 1955; Sprules and Bowerman, 1988; Hall and Raffaelli, 1991; Lafferty et al., 2006; Rzanny and Voigt, 2012).Some basic properties of food webs, including the number of species, the number of links, connectance, link density and the relationship among them were studied (Sugihara et al., 1989; Dunne et al., 2002; Navia et al., 2010). These properties stressed the importance of species in maintaining the stability of food webs. Nevertheless, so far the research on the topological properties of paddy arthropod food webs is fewer. In present study, we analyzed some topological properties of paddy arthropod food webs, aiming to provide a theoretical basis for improving the structure of arthropod food webs and for protecting natural enemies of insect pests.

2 Materials and Methods

2.1 Materials

2.1.1 Data sources

The data sources are listed as follows:

Name	Matrix (S×S)	District	Period	Data sources
FW1	26×26	Dasha Guangdong	The overall pattern	Liu et al. (2002)
FW2	57×57	Hunan	The overall pattern	Liu (2009)
FW3a	23×23	Wengyuan, Guangdong	The overall pattern of early season rice	Gu et al.(2006)
FW3b	24×24	Wengyuan, Guangdong	The overall pattern of late season rice	Gu et al.(2006)

2.1.2 Data description

Paddy arthropod food webs are composed of natural enemies, pests, neutral insects and plants. The food webs in present study primarily describe the relationship between the natural enemies and rice pests. The arthropod food web FW1 contains 24 species of arthropods, including 19 species of predators and 5species of preys which contain 4 rice insect pest species and 1 neutral insect species (Table 1). There are 55 arthropod species in FW2, including 36 predator species, and 19 prey species which contain 13 rice insect pest species and 6 neutral insect species (Table 2). FW3a has 21 arthropod species, including 16 species of predators, and 5 prey species which contain 4 rice insect pest species and 1 neutral insect species (Table 3). FW3b contains 22 arthropod species, including 17 predator species and 5 prey species in which there are 4 rice insect pest species and 1 neutral insect species (Table 4).

Table 1 Species and their roles in FW1.

ID	Species	Category	ID	Species	Category
1	*Araneus inustus*	predator	14	*Marpissa magister*	predator
2	*Dyschiriognatha quadrimaculata*	predator	15	*Microvelia horvathi*	predator
3	*Tetragnatha nitens*	predator	16	*Cyrtorrhinus livdipennis Reuter*	predator
4	*Coleosoma octomaculatum*	predator	17	*Casnoidea indica*	predator
5	*Hylyphantes graminicola*	predator	18	*Paederus fuscipesCurti*	predator
6	*Ummeliata insecticeps*	predator	19	*Micraspis discolor*	predator
7	*Pirata subparaticus*	predator	20	*Cnaphalocrocis medinalis Guenee*	prey
8	*Pardosa pseudoannulata*	predator	21	*Sogatella furcifera*	prey
9	*Pardosa tschekiangensis*	predator	22	*Nilaparvata lugens*	prey
10	*Clubiona corrugata*	predator	23	*Oxya chinensis*	prey
11	*Clubiona corrugata*	predator	24	*Chironomus sp*	prey
12	*Oxyopes sertatus*	predator	25	*Rice*	
13	*Bianor hotingchiechi*	predator	26	*Humus*	

Table 2 Species and their roles in FW2.

ID	Species	Category	ID	Species	Category
1	*Pirata japonious*	predator	29	*Paederus fuscipes Curti*	predator
2	*Pirata subparaticus*	predator	30	*Micraspis discolor*	predator
3	*Pardosa pseudoannulata*	predator	31	*Casnoidea indica*	predator
4	*Pardosa tschekiangensis*	predator	32	*Ophionea indica*	predator
5	*Tetragnatha nitens*	predator	33	*Colliuris chaudoiri Bohem*	predator
6	*Neoscona nautica*	predator	34	*Carabiade*	predator
7	*Neoscona theisi*	predator	35	*Coccinella septempunctata*	predator
8	*Neoscona griseomaculata*	predator	36	*Harmonia axyridis*	predator
9	*Acusilas coccneus*	predator	37	*Culex triaeniorhynchus*	prey
10	*Araneidae*	predator	38	*Chironomus sp*	prey
11	*Araneus inustus*	predator	39	*Salina sp*	prey
12	*Argiope aemula*	predator	40	*Entomobrya griseoolivata*	prey
13	*Dyschiriognatha quadrimaculata*	predator	41	*Hypogastramatura*	prey
14	*Coleosoma octomaculatum*	predator	42	*Bourletiella christianseni*	prey
15	*Clubiona corrugata*	predator	43	*Sogatella furcifera*	prey
16	*Bianor hotingchiechi*	predator	44	*Nilaparvata lugens*	prey
17	*Salticidae*	predator	45	*Oxya chinensis*	prey
18	*Ummeliata insecticeps*	predator	46	*Naranga aenesc*	prey
19	*Hylyphantes graminicola*	predator	47	*Cnaphalocrocis medinalis Guenee*	prey
20	*Oxyopes sertatus*	predator	48	*Tryporyza incertulas*	prey
21	*Ebrechtella tricuspidata*	predator	49	*Nephotettix bipunctatus*	prey
22	*Marpissa magister*	predator	50	*Empoasea subrufa*	prey
23	*Clubiona corrugata*	predator	51	*Tettigoniella spectra*	prey
24	*Tetragnatha maxillasa*	predator	52	*Mythimna separata*	prey
25	*Dolomedes sp*	predator	53	*Tettigoniidae*	prey
26	*Plecippussetipe sp*	predator	54	*Oxya chinensis*	prey
27	*Cyrtorrhinus livdipennis Reuter*	predator	55	*Nephotettix cincticeps*	prey
28	*Microvelia horvathi*	predator	56	*Rice*	
			57	*Humus*	

Table 3 Species and their roles in FW3a.

ID	Specifies	Category	ID	Species	Category
1	*Pirata piratoides*	predator	13	*Ummeliata insecticeps*	predator
2	*Tetragnatha maxillosa*	predator	14	*Pardosa pseudoannulata*	predator
3	*Neoscona nautica*	predator	15	*Pirata subparaticus*	predator
4	*Tetragnatha nitens*	predator	16	*Bianor aurocinctus*	predator
5	*Tetragnatha mandibulata*	predator	17	*Sogatella furcifera*	prey
6	*Thalassius affinis*	predator	18	*Nilaparvata lugens*	prey
7	*Micraspis discolor*	predator	19	*Cnaphalocrocis medinalis Guenee*	prey
8	*Staphylinidae*	predator	20	*Oxya chinensis*	prey

9	*Cyrtorrhinus livdipennis Reuter*	predator	21	*Chironomus sp*	prey
10	*Oxyopes lineatipes*	predator	22	*Rice*	
11	*Bianor hotingchiehi Schenke*	predator	23	*Humus*	
12	*Pardosa laura*	predator			

Table 4 Species and their roles in FW3b.

ID	Species	Category	ID	Species	Category
1	*Arctosa stigmosa*	predator	13	*Ummeliata insecticeps*	predator
2	*Tetragnatha maxillosa*	predator	14	*Pardosa pseudoannulata*	predator
3	*Neoscona nautica*	predator	15	*Pirata subparaticus*	predator
4	*Tetragnatha nitens*	predator	16	*Pardosa laura*	predator
5	*Tetragnatha mandibulata*	predator	17	*Bianor aurocinctus*	predator
6	*Tetragnatha caudicula*	predator	18	*Sogatella furcifera*	prey
7	*Micraspis discolor*	predator	19	*Nilaparvata lugens*	prey
8	*Staphylinidae*	predator	20	*Cnaphalocrocis medinalis Guenee*	prey
9	*Cyrtorrhinus livdipennis Reuter*	predator	21	*Oxya chinensis*	prey
10	*Oxyopes lineatipes*	predator	22	*Chironomus sp*	prey
11	*Leucauge blanda*	predator	23	*Rice*	
12	*Coleosoma octomaculatum*	predator	24	*Humus*	

2.1.3 Data conversion

Species were labeled with ID codes (see Tables 1, 2, 3 and 4). In the Pajek environment, choose the directory and execute the command as follows: Open data →Data editors →Matrix editor, in the UCINET software, and save them as the files in ".##h" format. Finally, choose the directory and execute the command: File→Open→Ucinet dataset→network, in Netdraw software; choose and open the ".##h" file, and then save it to the file in ".net" format by the command: File→Save data as→Pajek→Net file.The resultant four".net" files formed the basis for topological analysis.

2.2 Methods

2.2.1 Pajek software (Network analysis)

Pajek is a software platform for the network analysis of the large and complex networks with up to millions of nodes. It is a fast visualized tool for program operation. Pajek contains various methods/algorithms on analysis of topological properties.

2.2.2 Topological properties and measures

2.2.2.1 Classification of species

Species in a food web can be divided into three categories, top species T, intermediate species I, and basal species B (Pimm et al., 1991). Atop species is a species not eaten by any species in the web. An intermediate species is a species that has both at least one predator and at least one prey. A basal species is a species that eats no species.

2.2.2.2 Link analysis

Links in a food web can be divided into four categories, the basal-intermediate links, the basal-top links, the intermediate-intermediate links, and the intermediate-the top links (Cohen and Newman, 1985). For example, a

basal-intermediate link is a link from a basal species to an intermediate species.

2.2.2.3 Degree analysis

Degree is a basic property for a network. The degree of a node is defined as the number of its connected nodes. In general, the greater the degree of a node, the more important the node is in the food web (Zhang, 2012d). We obtained the degree of nodes by performing the command: Net→Parations→Degree→In/Out/All in Pajek software, where All is the sum of outgoing degree and incoming degree.

2.2.2.4 Connectance and link density

Connectance is defined as the number of observed trophic interactions divided by the number of possible interactions (Zhang, 2012a, 2012d). The number of possible interactions may be S^2 if cannibalistic interactions are counted, and $S(S\text{-}1)$ if only interspecific interactions are counted. Link density is equal to the ratio of total number of links to the total number of species.

2.2.2.5 Chain cycle analysis

A chain cycle refers to a closed loop in the food chain. For example, cannibalism is a cycle where one species feeds upon itself. In Pajek, chain cycles can be obtained by using command: Net→Count→4-rings→directed→cyclic.

2.2.2.6 Chain length analysis

Chain length is defined as the number of links connected to each other through two adjacent species between the basal species and the top species. We obtained chain length by the command: Net → K-neigbours→input/output.

2.2.3 Keystone index

Keystone index is a two-way trapezoidal index, and proposed by Jordán et al. (1999) based on the food web. It includes top-down and bottom-up control of material flow and information flow in food webs, namely K_b for botton-up, K_t for top-down and K for bidirectional processes ($K = K_b + K_t$). The specific formula is as follows:

$$K_b(i) = \frac{1 + K_b(j)}{m(i)(j)}$$

$$K_t(i) = \frac{1 + K_t(j)}{n(i)(j)}$$

$$K(i) = K_b(i) + K_t(i)$$

where $K_b(j)$ is the bottom-up keystone index of the jth predator, $m(i)(j)$ is the number of its direct preys. $K_t(j)$ is the top-down keystone index of the jth prey, and $n(i)(j)$ is the number of its direct predators. Keystone index is a measure on the basis of topological structure of food web. Thus it is theoretically similar to some measures in network analysis.

3 Results

3.1 Species analysis

As indicated in Tables 1, 2, 3 and 4, the numbers of predators/preys in the four arthropod food webs are 19/5, 36/19, 16/5 and 17/5, respectively. The average number of each predator feeds on prey species is 3.8, 1.9, 3.2 and 3.4, respectively. This is basically different from that of Cohen (1977) (4:3, i.e., 1.33). It is found that the more species in the food web, the less average number of each predator feeds on prey.

Briand and Cohen (1984) proposed that top species, intermediate species and basal species were all approximately proportional to the number of total species, and the proportion was 0.29, 0.53 and 0.19, respectively. Table 5 exhibits that in paddy arthropod food webs, the number of predators is significantly greater than that of preys. The proportion of top species is the largest, with about half of the total species, and the proportion of basal species is the least.

Table 5 Species analysis of food webs.

Food web	Trophic level	Number of species	Total number of species	Proportion	Species ID
FW1	T	13	26	50%	1-6, 8-11, 13-15
	I	11		42.3%	7, 12, 16-24
	B	2		7.7%	25,26
FW2	T	31	57	54.4%	1, 3-19, 21-26, 28, 31-36
	I	24		42.11%	2, 20, 27, 29, 30, 37-55
	B	2		3.49%	56, 57
FW3a	T	11	23	47.83%	1-6, 11-13, 15, 16
	I	10		43.48%	7-10, 14, 17-21
	B	2		8.69%	22,23
FW3b	T	12	24	50%	1-6, 11-14, 16, 17
	I	10		41.67%	7-10, 15, 18-22
	B	2		8.33%	23, 24

Table 6 Link analysis of food webs.

Food web	Trophic level	Number of links	Total number of links	Proportion
FW1	B-I	5	78	6.41%
	B-T	0		0
	I-I	21		26.92%
	I-T	52		66.67%
FW2	B-I	19	172	11.04%
	B-T	0		0
	I-I	32		18.61%
	I-T	121		70.35%
FW3a	B-I	5	66	7.57%
	B-T	0		0
	I-I	11		16.67%
	I-T	50		75.76%
FW3b	B-I	5	93	5.38%
	B-T	0		0
	I-I	14		15.05%
	I-T	74		79.57%

3.2 Link analysis

Briand and Cohen (1984) proposed that the proportion T: I: B of food webs is a constant. Similarly, the proportions of the basal-intermediate links, the basal-top links, the intermediate-intermediate links, and the intermediate-top links are also constants (0.27, 0.08, 0.30 and 0.35, respectively). However, the link analyses of paddy arthropod food webs showed that the number of the intermediate-intermediate links is far greater than the number of the other three types of links, and the number of the basal-top links in all food webs is 0.

Therefore, the link density and connectance of FW1 are3 and 0.12, respectively; for FW2 they are 3.02 and 0.05, respectively; for FW3a they are 2.87 and 0.13, respectively, and for FW3b they are 3.88 and 0.17, respectively. Obviously, the link density of all food webs is similar to each other. But FW2, which harbors the richest species, has the smallest connectance. It means that in the paddy ecosystems, the increase of species diversity does not lead to an increase proportionally to the links among species. In addition, the link density and connectance of early season rice field are less than that of late season rice field. This demonstrates that the number of links in late season rice fieldis richer than that in the early rich field, i.e., the interactions between predators and preys in the late season rice field are more active than that in the early season rice field.

3.3 Analysis of chain cycle and chain length

Cycles of all paddy arthropod food webs are zeros, which is in consistent with the conclusion that the cycles are rare in the food webs (Pimm et al., 1991).

Chain length analysis of species No. 25 and 26 in FW1 indicates that the chain length of rice and humus is 3 (Fig. 1). Similarly, chain length of FW2, FW3a and FW3b is 3.
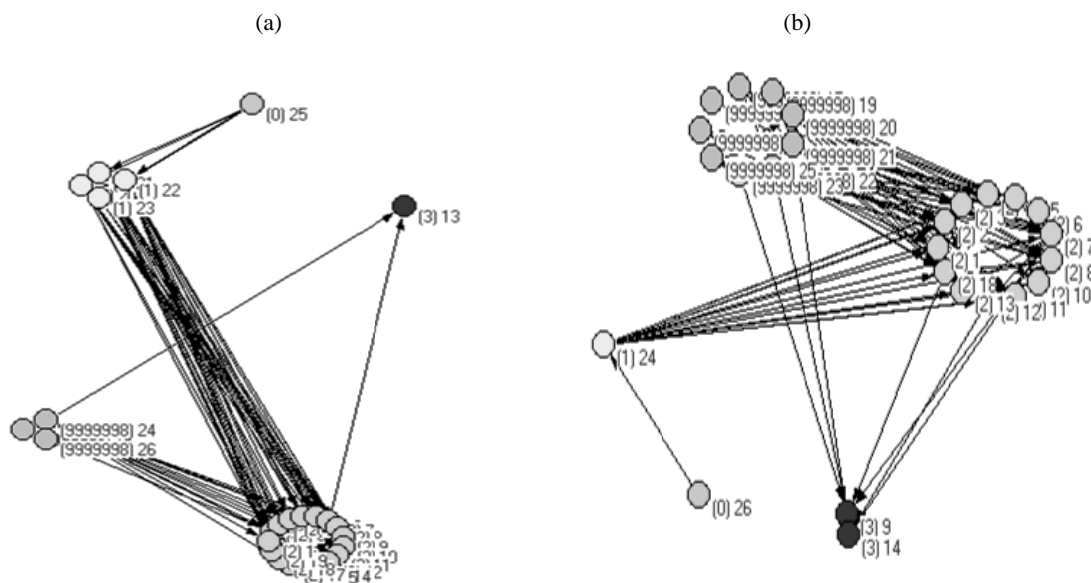

Fig. 1 Chain length analysis of species No. 25 (a) and 26 (b) in FW1. For each species, the number in parenthesis is chain length and the number outside parenthesis is species ID code. The species No. 9,999,998 means that it is not reachable to the current node.

Chain length analysis of top species demonstrates that the maximum chain length from the basal species to the top species is typically 2 or 3; chain length 1 is rarely found, and the chain length larger than 3 occurs seldom (Table 7), which are in consistent with the conclusions of Pimm et al. (1991).

Table 7 Chain length analysis of top species in food webs.

Top species (ID) in FW1	1	2	3	4	5	6	8	9	10	11	13	14	15			
Maximum chain length	2	3	2	2	2	2	2	3	2	2	3	2	2			
Top species (ID) in FW2	1	3	4	5-12	13	14	15	16	17	18	19	21	22	23-26	28	31-36
Maximum chain length	2	2	3	2	3	2	2	4	2	2	2	2	2	2	2	2
Top species (ID) in FW3a	1	2	3	4	5	6	11	12	13	15	16					
Maximum chain length	3	2	2	2	2	2	3	2	2	2	1					
Top species (ID) in FW3b	1	2	3	4	5	6	11	12	13	14	16	17				
Maximum chain length	2	2	2	2	2	3	2	2	2	2	1	3				

3.4 identification analysis of keystone species

By Pajek analysis, the average degrees of paddy arthropod food webs are 6.0, 6.04, 5.74 and 7.75, respectively. As indicated in Fig.2, in FW1 and FW2, the species with the largest incoming degree is *Pardosa pseudoannulata*, followed by *Pirata subparaticus* and *Clubiona corrugate*; namely *Pardosa pseudoannulata* has the widercontrol spectrum on the rice pests. In FW3a, both *Pardosa pseudoannulata* and *Tetragnatha maxillosa*are the most significant. The most significant species are *Pardosa pseudoannulata*, *Tetragnatha maxillosa* and *Arctosa stigmosa*in FW3b.
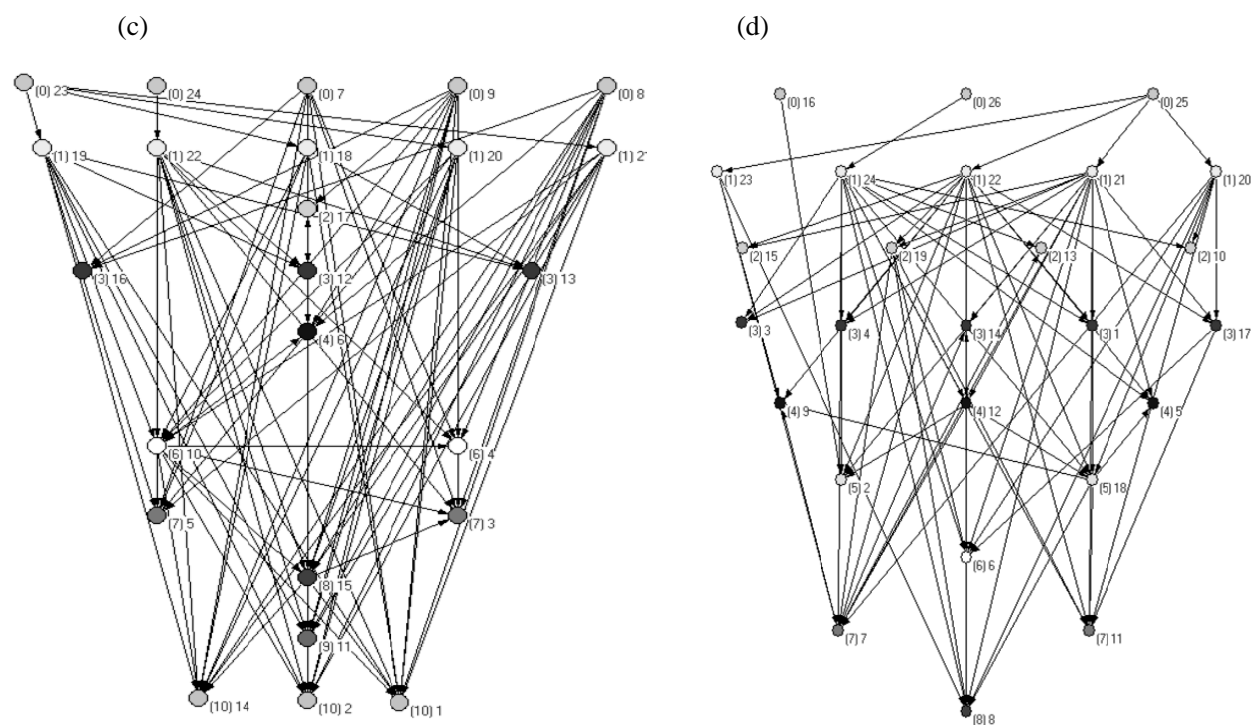
(a)   (b)
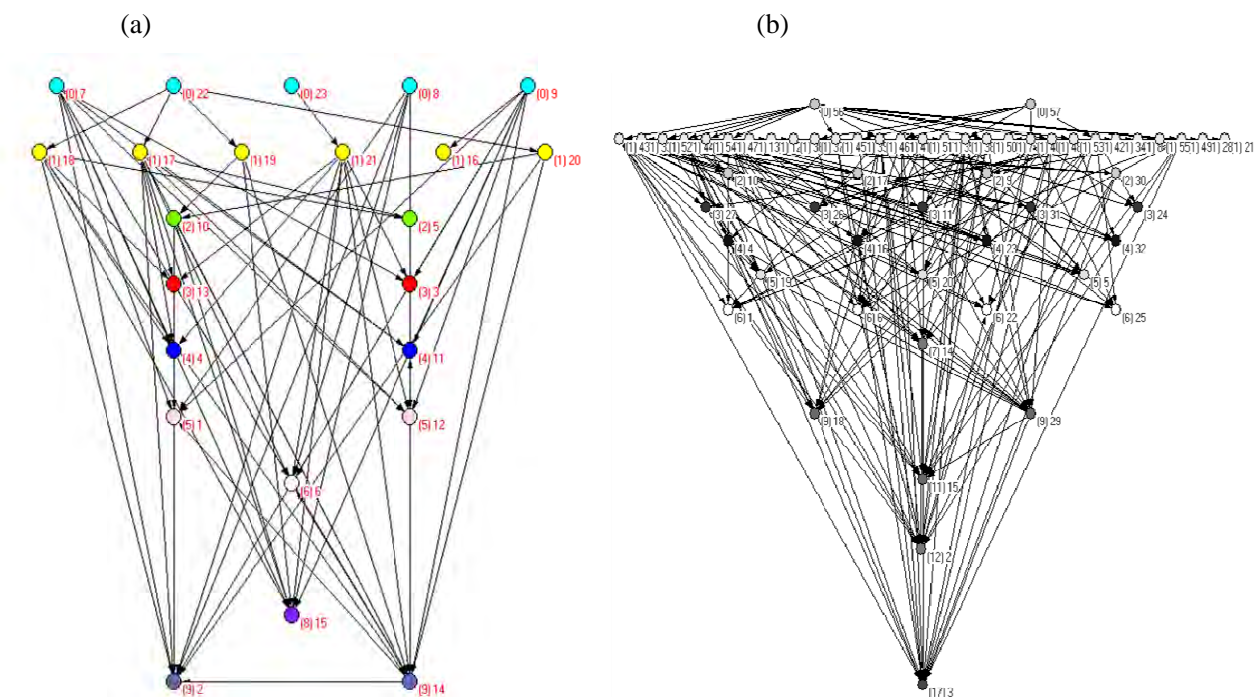
Fig. 2 Food web links of incoming degree analysis onfood webs FW1 (a), FW2 (b), FW3a(c) and FW3b (d), respectively. For each species, the number in parenthesis is incoming degree and the number outside parenthesis is species ID code.

Gu et al. (2006) argued that the arthropod species *Pardosa pseudoannulata, Ummeliata insecticeps, Pirata subparaticus* and *Tetragnatha maxillosa* would play an important role in controlling insect pests in paddy ecosystems, among which *Pardosa pseudoannulata* and *Ummeliata insecticeps* were the dominant species. In present network study, we further confirmed that *Pardosa pseudoannulata* held an absolutely important position in paddy arthropod food webs. However, *Ummeliata insecticeps* did not show its importance in food webs. This may be attributed to that *Ummeliata insecticeps* doesn't feed on other predators and not be preyed by other predators;it only feeds on pests and neutral insects, leading to its lower incoming degree than other predators.The dominant speciesinFW3a and FW3b are similar to each other, but *Arctosa stigmosa*did not proposed as a dominant species in Gu et al. (2006). In summary, *Pardosa pseudoannulata, Tetragnatha maxillosa, Pirata subparaticus*, *Clubiona corrugate* and *Arctosa stigmosa* are important species in paddy arthropod food webs.

From species composition of different food webs, we conclude that the important species in the paddy arthropod communities would not be relevant to the number of prey species.

However, the results as shown in Table 8 through the top-down keystone index, K_t, the species with the largest K_t value in FW1 is *Pardosa pseudoannulata*, followed by *Clubiona corrugate* and *Pardosa tschekiangensis*; The species has the widest control spectrum on the rice pests in FW2 is *Pardosa pseudoannulata,* followed by *Clubiona corrugate* and *Pirata subparaticus*; In FW3a, *Tetragnatha maxillosa* is the most significant species, followed by *Pardosa pseudoannulata* and *Pirata subparaticus*; In FW3b, The most significant species are *Arctosa stigmosa*, *Tetragnatha maxillosa*, *Pardosa pseudoannulata*. Compared with network analysis, the key species obtained by ecological analysis did not produce much difference. The key species in FW1 and FW2 is *Pardosa pseudoannulata*, but *Pirata subparaticus* in FW1 did not show the

critical importance in keystone species analysis, but *Pardosa tschekiangensis*. Furthermore, the keystone index results of FW3a and FW3b were consistent with the results of network analysis, but there were differences in their values, shown that the arrangement of the importance of species was different. Similarly, the most significant species *Ummeliata insecticeps* in Gu et al. (2006) did not show a larger K_t value.

Table 8 Species with higher K_t value and their ID codes in the four paddy arthropod food webs.

|	FW1			FW2			FW3a			FW3b	
ID	K_t value	species	ID	K_t value	species	ID	K_t value	species	ID	K_t value	species
8	1.91	*Pardosa pseudoannulata*	3	4.71	*Pardosa pseudoannulata*	2	2.68	*Tetragnatha maxillosa*	1	1.7	*Arctosa stigmosa*
11	1.91	*Clubiona corrugata*	15	3.17	*Clubionacorrugata*	14	2.28	*Pardosa pseudoannulata*	2	1.7	*Tetragnatha maxillosa*
9	1.76	*Pardosa tschekiangensis*	2	3.13	*Pirata subparaticus*	15	1.86	*Pirata subparaticus*	14	1.7	*Pardosa pseudoannulata*
2	1.58	*Dyschiriognatha quadrimaculata*	4	2.37	*Pardosa tschekiangensis*	1	1.67	*Pirata piratoides*	11	1.46	*Leucauge blanda*
6	1.47	*Ummeliata insecticeps*	22	2.22	*Marpissa magister*	6	1.6	*Thalassius affinis*	3	1.22	*Neoscona nautica*
7	1.47	*Pirata subparaticus*	18	2.09	*Ummeliata insecticeps*	11	1.18	*Bianor hotingchiehi Schenke*	15	1.18	*Pirata subparaticus*
14	1.17	*Marpissa magister*	16	1.73	*Bianor hotingchiechi*	21	1	*Chironomus sp*	5	1.14	*Tetragnatha mandibulata*
24	1	*Chironomus sp*	29	1.29	*Paederus fuscipes Curti*	12	0.78	*Pardosa laura*	22	1	*Chironomus sp*

(a)
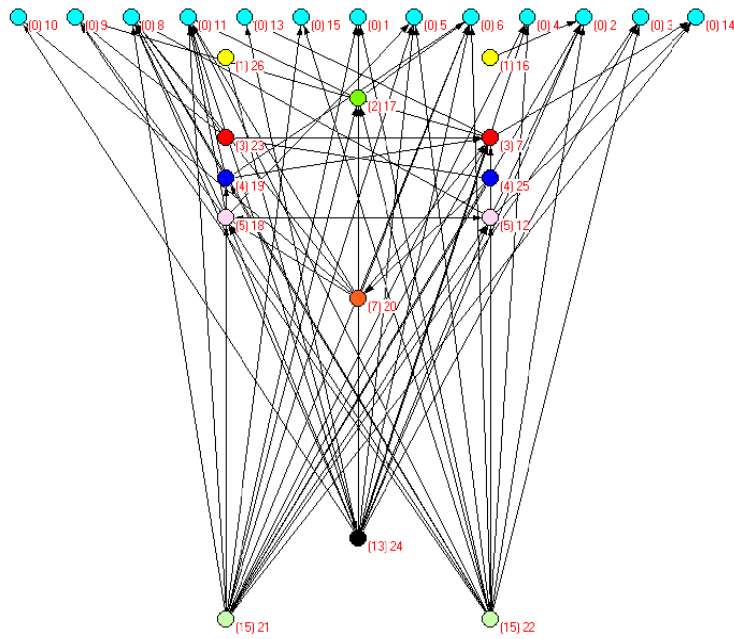
(b)
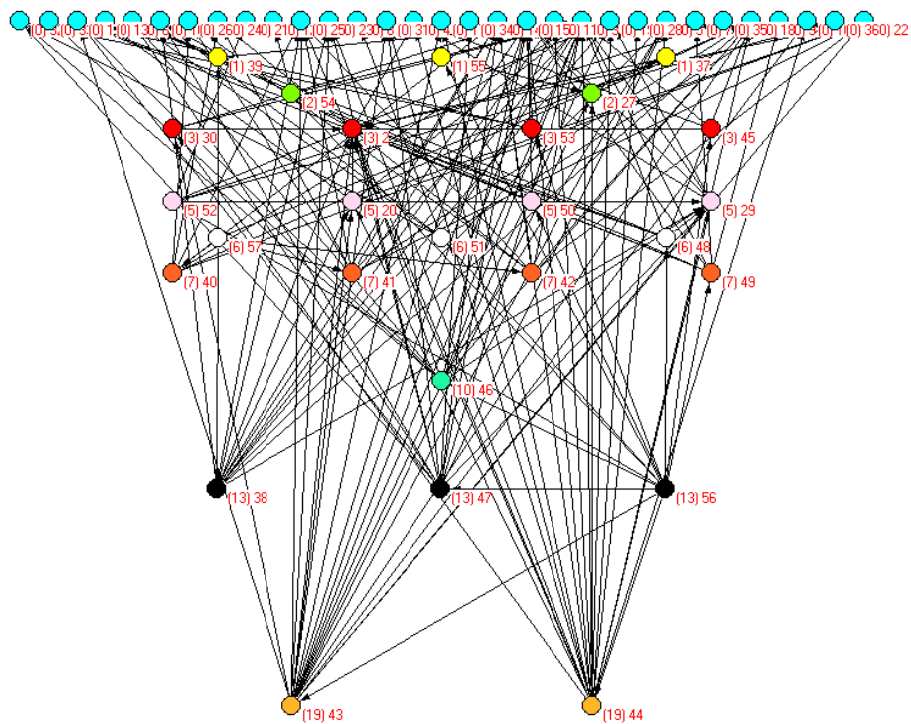
(c)
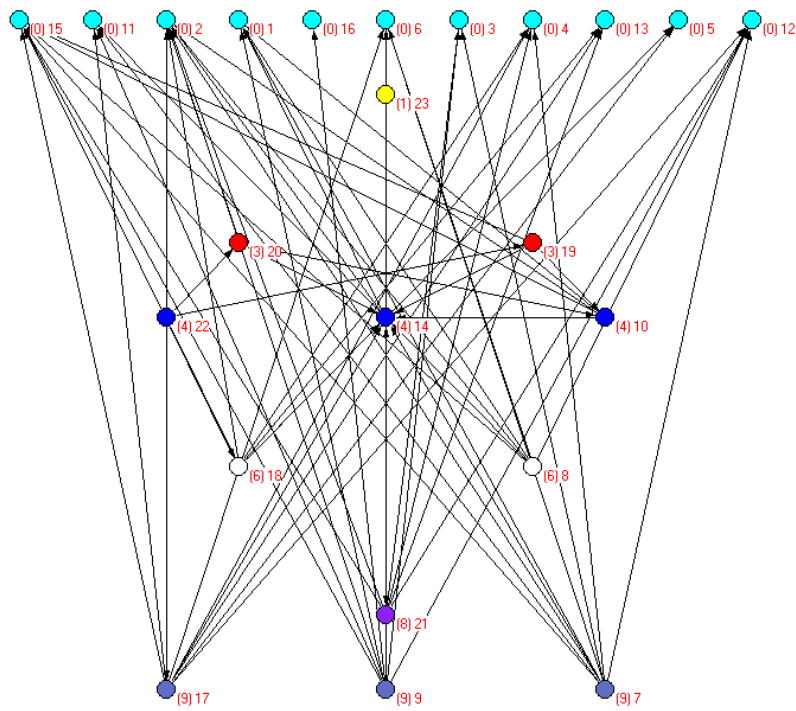
(d)
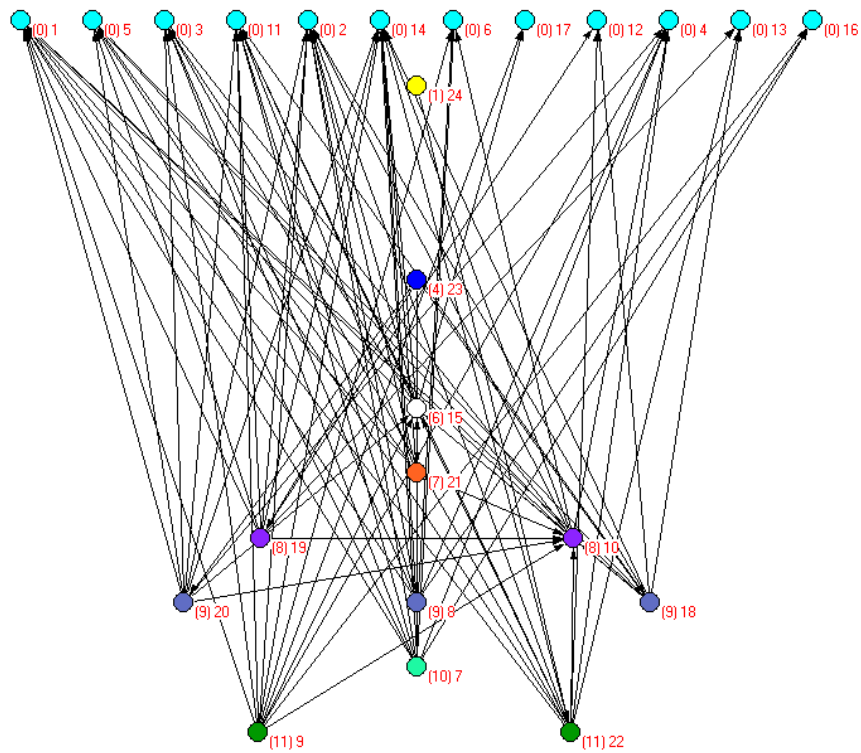
Fig. 3 Food web links of outgoing degree analysis of FW1 (a), FW2 (b), FW3a(c) and FW3b (d), respectively. For each species, the number in parenthesis is outgoing degree and the number outside parenthesis is species ID code.

It can be found from Fig. 3, that the outgoing degree of *Chironomus sp* is just less than *Nilaparvata lugens* and *Sogatella furcifera*, two rice pests in the FW1 and FW2.The outgoing degree of *Chironomussp* in FW3a is less than *Micraspis discolor, Cyrtorrhinus livdipennis Reuter* and *Sogatella furcifera.* In FW3b, *Chironomus sp* and *Cyrtorrhinus livdipennis Reuter* have the largest outgoing degree. In addition, the bottom-up keystone index, K_b, has shown in Table 9. In FW1 and FW2, both *Sogatella furcifera* and *Nilaparvata lugens* have the largest K_b values, and species with the largest K_b value in FW3a and FW3b is *Cyrtorrhinus livdipennis Reuter*. These results mean that *Nilaparvata lugens* and *Sogatella furcifera*are the dominant pest species, and their natural enemies are abundant also. *Cyrtorrhinus livdipennis Reuter* is the most significant predator. The outgoing degree of neutral insect, e.g., *Chironomussp*, further verifies its role as a complementary food in the arthropod food webs; it can be used as supplementary prey source of natural enemies.

Table 9 Species with higher K_b value and their ID codes in the four paddy arthropod food webs.

	FW1			FW2			FW3a			FW3b	
ID	K_b value	species	ID	K_b value	Species	ID	K_b value	species	ID	K_b value	species
21	5.43	*Sogatella furcifera*	44	6.01	*Nilaparvata lugens*	9	2.58	*Cyrtorrhinusli vdipennis Reuter*	9	2.44	*Cyrtorrhinus livdipennis Reuter*
22	5.35	*Nilaparvata lugens*	43	5.09	*Sogatella furcifera*	17	2.13	*Sogatella furcifera*	22	2.16	*Chironomus sp*
24	4.31	*Chironomus sp*	52	3.38	*Mythimnase parata*	7	1.83	*Micraspis discolor*	18	1.85	*Sogatella furcifera*
20	2	*Cnaphalocrocis medinalis Guenee*	47	3.23	*Cnaphalocrocis medinalis Guenee*	21	1.71	*Chironomus sp*	7	1.7	*Micraspis discolor*
12	1.31	*Oxyopes sertatus*	38	2.63	*Chironomus sp*	18	1.51	*Nilaparvata lugens*	19	1.6	*Nilaparvata lugens*

Comprehensive analysis of the bottom-up and top-down keystone index have shown in Table 10. *K* is sum of K_b and K_t. *Nilaparvata lugens* and *Sogatella furcifera*as rice pests in FW1 and FW2 have the largest *K* value, and the main keystone species in FW1 and FW2 is *Pardosa pseudoannulata*, *Pirata subparaticus*, *Clubiona corrugate*and *Pardosa tschekiangensis. Pardosa pseudoannulata*, *Tetragnatha maxillosa*, *Cyrtorrhinus livdipennis Reuter* and *Pirata subparaticus* in FW3a are the keystone species, and in FW3b, *Arctosa stigmosa* and *Oxyopes lineatipes* are also the keystone species. Spiders, as the major arthropod species, have significant control effect on the rice insect pests. Therefore, in order to achieve sustainable integrated pest prevention, it should strengthen the ecological protection of paddy field spiders.

Table 10 Species with higher *K* value and their ID codes in the four paddy arthropod food webs.

	FW1			FW2			FW3a			FW3b	
ID	*K* value	species	ID	*K* value	species	ID	*K* value	species	ID	*K* value	species
21	5.68	*Sogatella furcifera*	44	6.09	*Nilaparvata lugens*	14	3.01	*Pardosa pseudoannulata*	22	3.16	*Chironomus sp*
22	5.6	*Nilaparvata lugens*	43	5.17	*Sogatella furcifera*	21	2.71	*Chironomus sp*	9	2.44	*Cyrtorrhinus livdipennis Reuter*
24	5.31	*Chironomussp*	3	4.71	*Pardosa pseudoannulata*	2	2.68	*Tetragnatha maxillosa*	15	2.23	*Pirata subparaticus*
7	2.55	*Pirata subparaticus*	2	3.8	*Pirata subparaticus*	9	2.58	*Cyrtorrhinus livdipennis Reuter*	10	2.15	*Oxyopes lineatipes*
20	2.25	*Cnaphalocrocis medinalis Guenee*	52	3.46	*Mythimnase parata*	17	2.38	*Sogatella furcifera*	18	2.1	*Sogatella furcifera*
8	1.91	*Pardosa pseudoannulata*	47	3.31	*Cnaphalocrocis medinalis Guenee*	15	2.86	*Pirata subparaticus*	19	1.85	*Nilaparvata lugens*
11	1.91	*Clubiona corrugata*	15	3.17	*Clubiona corrugata*	7	1.83	*Micraspis discolor*	20	1.75	*Cnaphalocrocis medinalis Guenee*
9	1.76	*Pardosatschekiang ensis*	38	2.8	*Chironomus sp*	18	1.76	*Nilaparvata lugens*	1	1.7	*Arctosa stigmosa*
12	1.63	*Oxyopessertatus*	46	2.44	*Naranga aenesc*	1	1.67	*Pirata piratoides*	2	1.7	*Tetragnatha maxillosa*
2	1.58	*Dyschiriognathaqu adrimaculata*	4	2.37	*Pardosa tschekiangensis*	6	1.6	*Thalassius affinis*	7	1.7	*Pardosa pseudoannulata*

4 Conclusions and Discussion

Paddy arthropod food webs are generally complex ecosystems. Various ecological interactions can be found, including parasitism, predation, etc., which closely relate to biological control of rice insect pests. Therefore, the topological properties analysis of paddy arthropod food webs is a fundamental work for the biological control of insect pests. From analysis above, we draw some major conclusions as follows:

(1) Overall the ratios of predators to preys in the arthropod food webs are quite different from the results of Cohen (1977). The reason of the ratio for FW2 being close to the proposed by Cohen (1977) may be attributed to that the data of FW1, FW3a andFW3b were collected in the empirical fields, and the food web data of

Cohen and FW2weremostly qualitative collated. Under certain conditions, the number of species in a qualitative summary of food webs is significantly larger than the actual number of species found in the empirical fields. Therefore, a systematic review and analysis of paddy arthropod food webs should focus on practical (observed) communities.

(2)   Proportions of different trophic levels and the ratios of link types are different from Briand and Cohen (1984). In present study, the number of top species is about half of the total number of species, and the number of intermediate species is slightly little than the number of top species. The number of intermediate-intermediate links is far greater than the number of the other three kinds of links, and the basal-top links are all absent. These may be due to the absence of predators fed on predatory spiders.

(3)   Average degree and link density of arthropod food webs do not change much with the change of the number of species, but the connectance significantly reduces. Link density and connectance of the early season rice field and late season rice field show certain difference. Therefore, food webs should not be constructed through qualitative summary.

(4)   There are not cycles in arthropod food webs. The maximum chain length of the basal species is 3, and the largest chain length of the top species is typically 2 or 3, which are in consistent with Pimm et al (1991). Thus the topological properties of paddy arthropod food webs are in coincident with the cascade model, which can be further validated in future studies.

(5)   In the paddy ecosystems studied, *Pardosa pseudoannulata*is the dominant natural enemy species. The natural enemies *Tetragnatha maxillosa, Pirata subparaticus, Arctosa stigmosa* and *Clubiona corrugate* have stronger control effects on pests also. Furthermore, the outgoing degree and K value of *Chironomus sp* indicates that neutral insects play an important role in the paddy ecosystems (Guo, 1995).

(6)   The keystone species calculated from keystone index and network analysis are analogous, indicating either keystone index or network analysis can be used in the analysis of keystone species.

In present study, paddy arthropod food webs were constructed based on the matrixes representing relationship between pests, predators and neutral insects. Parasites, predatory birds and other predators were not included in the food webs. In future studies, we suggest that: (1) Complete food webs should further include parasites and predatory birds, etc. (2) In food web analysis, some models, such as the cascade model (Cohen and Newman, 1985), the niche model (Williams and Martinez, 2000) and nested model (Cattin et al., 2004) may be fitted and analyzed. (3) Both temporal and spatial aspects of food webs should be considered in order to provide a better theoretical basis for biological control and ecosystem maintenance in paddy fields.

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