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# Arthropod Abundance and Diversity in *Bt* and Non-*Bt* Rice Fields

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**ABSTRACT** In a field experiment, possible effects of transgenic *Bt* rice on arthropod communities under paddy field conditions were assessed for 3 yr in terms of arthropod guild dominance, family composition, dominance distribution of each guild, individuals of each guild, and community indices (including Shannon-Weaver diversity index and dominant concentration index). Our results overall suggested no significant differences between the *Bt* and control rice plots in these arthropod community-specific parameters. The similarity of arthropod communities in the *Bt* and control rice plots was apparently high. Based on our findings, we conclude that *Bt* rice generally exerts no marked negative effects on the arthropod community in paddy fields.

**KEY WORDS** transgenic, *Bt* rice, biodiversity, species richness, Shannon-Weaver diversity index

With the global population steadily growing, the amount of arable land is steadily decreasing. Thus, it is essential that sustainable strategies be implemented to use agricultural resources more efficiently to yield an abundant healthy diet. Experience to date with genetically engineered crops has shown that this technology can make substantial contributions toward this goal. Among the first transgenic crops approved for release were *Bt* maize and *Bt* cotton, which contain genes encoding insecticidal proteins from the bacterium *Bacillus thuringiensis* Berliner. These crops have been readily adopted by farmers, have resulted in increased yields and reductions in insecticide applications, and have been sustainable when used with resistance management programs (Shelton et al. 2002). However, emerging controversies surrounding the risks and benefits of this novel technology have limited its benefits in many parts of the world (Obrycki et al. 2001, Schuler et al. 2001, Groot and Dicke 2002, Conner et al. 2003, Carrière et al. 2004).

Rice is the target crop for many improvement programs because it is the staple diet for nearly two billion people worldwide and the major food for over one half of those living in Asia (Khush 1997). In 2002, rice production in China reached 177 million tons, of which 3.1 million tons was exported, producing revenues of U.S. \$578 million (<http://www.irri.org/science/ricestat/index.asp>). These numbers represent only a fraction of what might be available if rice plants were not subject to insect attack. Many rice varieties have been genetically transformed with genes encoding various *Bt* crystal (Cry) proteins and have been shown to be resistant to

one or more lepidopteran pests, the most important of which are the yellow stem borer [*Scirpophaga incertulas* (Walker)], the striped stem borer [*Chilo suppressalis* (Walker)], and several species of leaf-folders [*Marasmia* spp. and *Cnaphalocrocis medinalis* (Guenée)] (Shu et al. 2000, Tu et al. 2000, Ye et al. 2001a, 2001b, 2003). Field trials of *Bt* rice started in China in 1998, but no *Bt* rice or other transgenic rice varieties have yet been released for commercialization.

The toxins produced by *Bt* plants kill only a narrow range of insect species. Many rice varieties have been transformed with genes encoding various *Bt* crystal (Cry) proteins and are resistant to one or more lepidopteran pests of rice. Thus, one might expect decreased abundance of susceptible lepidopterans and their specialist natural enemies. However, the potential for broader effects exists. Many herbivores may consume the toxin and survive. Predators that consume such herbivores may be adversely affected. For example, *Chrysoperla carnea* (Stephens) that consumed *Spodoptera littoralis* (Boisduval) reared on a diet with *Bt* toxin had lower survival rate than *C. carnea* that fed on *S. littoralis* reared on a diet without *Bt* toxin (Hillbeck et al. 1999). Such interactions are likely to be complex, because neither all herbivores that feed on *Bt* plants uptake the toxin nor are natural enemies always affected by consuming prey that have taken up the toxin (Dutton et al. 2002).

Many studies related to the impact of *Bt* crops on nontarget organisms have examined the interaction of one or a few species in the laboratory (Sims 1995, Hillbeck et al. 1998a, 1998b, 1999, Zwahlen et al. 2000, Dutton et al. 2002). Some results indicated no significant effects on the nontarget organisms, whereas some found there were negative effects on the natural enemies. However, translating laboratory results to

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the field may be problematic because the concentration of toxin doses used in the laboratory may be higher than the doses that the arthropods encounter in the field, and highly mobile species may spend only a fraction of their life in *Bt* fields. Despite these limitations, laboratory studies can provide valuable insights into potential effects and the causal mechanisms of patterns in field data.

Most field studies assessing potential impacts of *Bt* crops have focused on a limited numbers of species (Wilson et al. 1992, Hardee and Bryan 1997, Orr and Landis 1997, Pilcher et al. 1997, Pilcher 1999, Wold et al. 2001, Jasinski et al. 2003, Liu et al. 2003, Men et al. 2003, Schoenly et al. 2003). Here, we surveyed all of the arthropods on *Bt* and non-*Bt* rice at three field sites in Zhejiang Province of China: two in 3 yr and one in 2 yr. Our primary goal was to determine whether major differences occur between the plant-dwelling arthropod community on transgenic *Bt* and non-*Bt* rice.

### Materials and Methods

**Transgenic *Bt* Rice Lines and Their Parental Cultivars.** Two lines of transgenic *indica* rice with the *cry1Ab* gene, namely B1 and B6, were tested along with their corresponding untransformed parental cultivar Jiaza935. Two homogenous lines of transgenic *indica* rice containing the *cry1Ab/cry1Ac* genes, i.e., TT9-3 and TT9-4, were tested along with their corresponding untransformed parental cultivar IR72. One line of transgenic *japonica* rice containing the *cry1Ab* gene, KMD1, was tested along with its corresponding untransformed parental cultivar Xiushui11.

**Field Experiments.** The experiments were conducted in 2003, 2004, and 2005 at three different sites where field trials of *Bt* rice are permitted in Zhejiang province in China.

The first set of experiments was conducted at the Experimental Farm of Zhejiang University at Hangzhou (120.19 E, 30.26 N), consisting of three plots each of B1, B6, and the control line (Jiaza935). Plot sizes were 20 by 25 m.

The second set was planted at a local experimental field in the suburbs of Jiande (119.27 E, 29.49 N), consisting of three plots each of TT9-3, TT9-4, and the control line IR72. Plot sizes were 20 by 35 m.

The third set was carried out at the Experimental Farm of the China Rice Research Institute at Fuyang (119.95 E, 30.07 N), with three plots each of KMD1 and the Xiushui11 control. Plot sizes were 20 by 35 m.

All experiments were designed as randomized complete block with three replications for each treatment. For each experiment of every year at each test site, seedlings were manually transplanted with one seedling per plant or hill spaced 16.5 by 16.5 cm apart. Each experimental plot was bordered on all sides by an unplanted walkway 50 cm wide, and the entire experimental field of each location was planted with five border rows of the nontransgenic rice plants.

**Table 1.** Diversity indices of arthropod communities in *Bt* (B1, B6, TT9-3, TT9-4, and KMD1) and non-*Bt* rice lines

Site	Year	Line	H'	C
Hangzhou	2003	B1	3.156 ± 0.389a	0.132 ± 0.055a
		B6	3.069 ± 0.376a	0.161 ± 0.037a
		935	3.070 ± 0.374a	0.172 ± 0.046a
	2004	B1	3.465 ± 0.291a	0.107 ± 0.03a
		B6	3.286 ± 0.273a	0.121 ± 0.033a
		935	3.277 ± 0.250a	0.125 ± 0.028a
	2005	B1	3.266 ± 0.442a	0.132 ± 0.061a
		B6	3.099 ± 0.449a	0.167 ± 0.084a
		935	3.142 ± 0.434a	0.174 ± 0.074a
Jiande	2003	TT9-3	1.479 ± 0.558a	0.515 ± 0.170a
		TT9-4	1.536 ± 0.563a	0.474 ± 0.167a
		IR72	1.668 ± 0.504a	0.431 ± 0.179a
	2004	TT9-3	2.518 ± 0.407a	0.225 ± 0.063a
		TT9-4	2.140 ± 0.263a	0.322 ± 0.092a
		IR72	2.905 ± 0.175a	0.182 ± 0.074a
	2005	TT9-3	2.451 ± 0.409a	0.227 ± 0.072a
		TT9-4	2.161 ± 0.311a	0.333 ± 0.112a
		IR72	2.358 ± 0.150a	0.291 ± 0.041a
Fuyang	2004	KMD1	2.436 ± 0.152a	0.224 ± 0.036a
		Xiushui11	1.645 ± 0.608a	0.429 ± 0.207a
	2005	KMD1	1.469 ± 0.891a	0.535 ± 0.299a
		Xiushui11	1.352 ± 0.728a	0.566 ± 0.246a

Means ± SE within a column per site and year followed by the same letter are not significantly different based on ANOVA (LSD test,  $P \leq 0.05$ ). H' and C stand for Shannon-Weaver diversity index and dominance concn index, respectively.

Agronomic practices such as fertilization and irrigation for growing rice were the same as followed by local farmers.

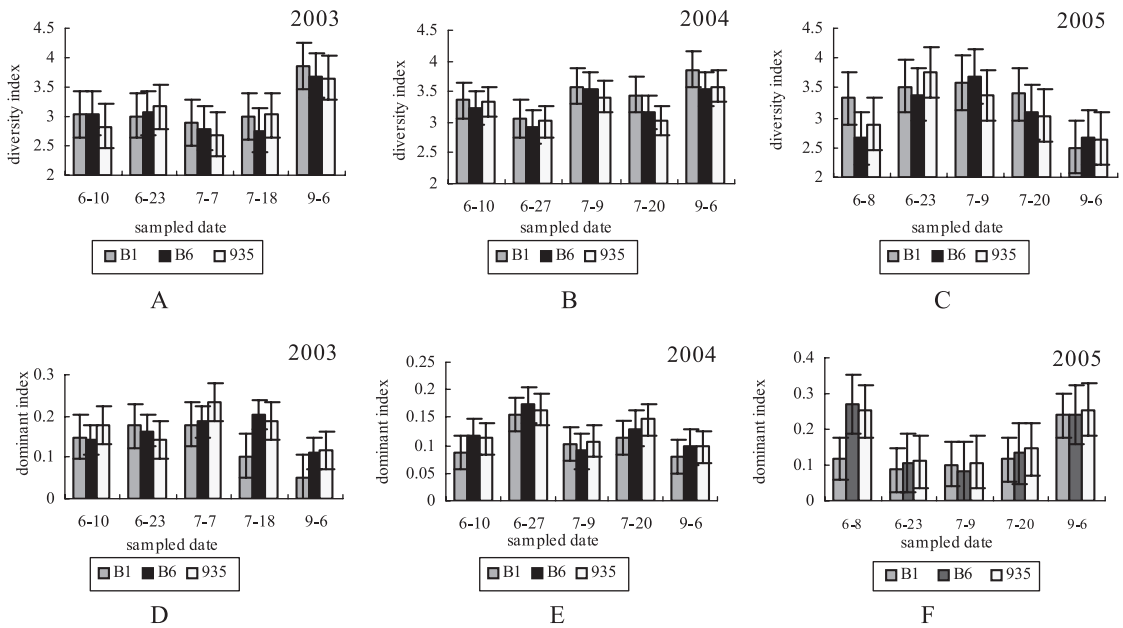
**Sampling.** Numbers of arthropods were sampled randomly at each site every 15 d during the rice growing season each year. Arthropods on the plants were collected by vacuum-suction machine, modified according to Carino et al. (1979), and were taken to the laboratory, stored in 95% ethanol, identified to species, and counted.

**Data Analysis.** Most of the arthropods sampled were identified to species. The Shannon-Weaver diversity index H' and dominance concentration index C were calculated. The Shannon-Weaver diversity index H' (Shannon and Weaver 1949),

$$H' = - \sum p_i \log_e p_i$$

where  $p_i$  is the proportion of the  $i$ th species in the total sample and was calculated as a measure of the arthropod community diversity (all species of insects) and pest and natural enemy subcommunities in the treatment plots. The dominance concentration index was calculated as  $C = \sum (p_i)^2$ .

The arthropods were split into five guilds: phytophages, parasitoids, predators, detritivores, and others. The dominance distribution is the percentage of each subcommunity among the total communities. All data on population densities of insects from different treatments in the field were analyzed using analysis of variance (ANOVA), and means were compared with the least significant difference (LSD) as calculated by SAS software (SAS Institute 2001).



**Fig. 1.** Temporal dynamics of main indices of arthropod community diversity in plots containing different lines of rice at Hangzhou, China, in 2003, 2004, and 2005. (A–C) Diversity indices. (D–F) Dominant concentration indices. Bars are 95% CIs.

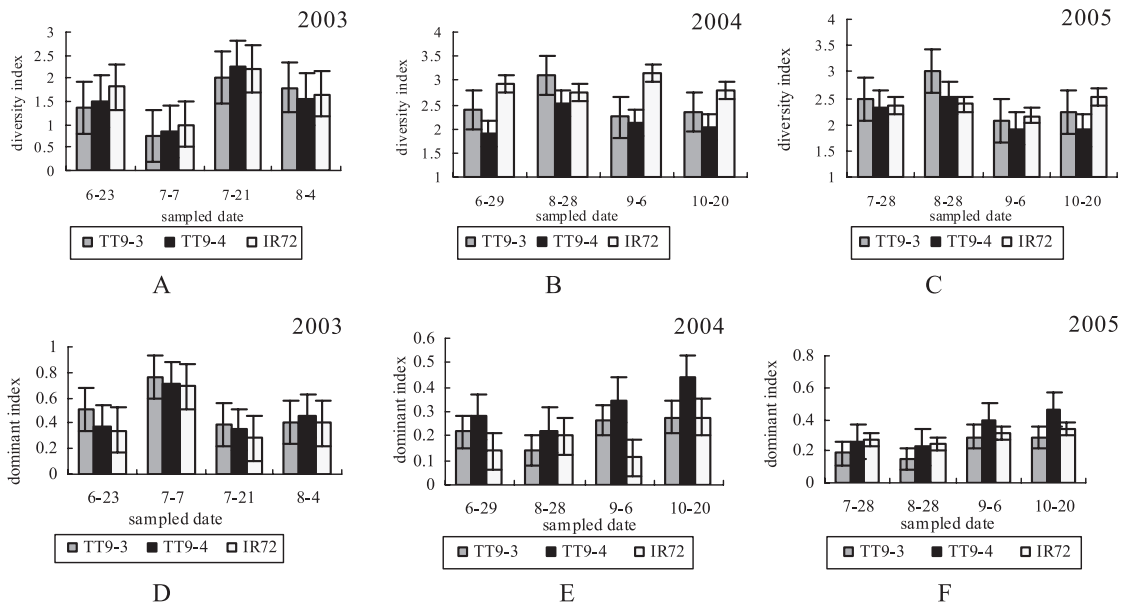
### Results

**Abundance of Arthropods in Rice Fields.** Overall, 17,706 individual insects and spiders were recorded in 3 yr in both *Bt* and non-*Bt* rice fields.

In Hangzhou, a total 62 species of insects and some spiders in 53 families were observed in the experi-

mental plots during the 3 yr of study. The total number of arthropod individuals in 3 yr at Hangzhou was 4,014 (766, 1,239, and 2,009 in 2003, 2004, and 2005, respectively).

In Jiande, 40 species insects and some spiders in 37 families were observed in the experimental plots dur-



**Fig. 2.** Temporal dynamics of main indices of arthropod community diversity in plots containing different lines of rice at Jiande, China, in 2003, 2004, and 2005. (A–C) Diversity indices. (D–F) Dominant concentration indices. Bars are 95% CIs.

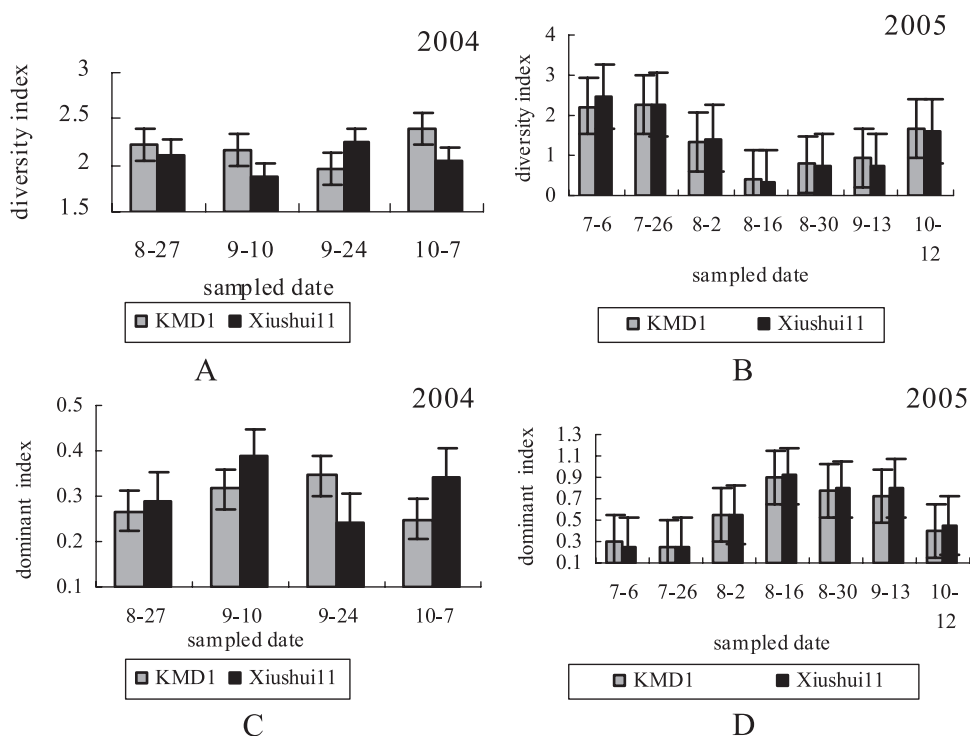


Fig. 3. Temporal dynamics of main indices of arthropod community diversity in plots containing different lines of rice at Fuyang, China, in 2004 and 2005. (A and B) Diversity indices. (C and D) Dominant concentration indices. Bars are 95% CIs.

ing the 3 yr of study. The total number of arthropods in 3 yr at Jiande was 3,800 (1,694, 1,006, and 1,100 in 2003, 2004, and 2005, respectively).

We conducted studies in Fuyang for only 2 yr. A total 46 species of insects and some spiders in 41 families were observed in the experimental plots during the 2 yr of study. The total number of arthropods in 2 yr at Fuyang was 9,892 (1,798 and 8,094 in 2004 and 2005, respectively).

For 3 yr, the total number of arthropods in *Bt* and non-*Bt* rice at the three sites were not significantly different. At Hangzhou, the abundance of arthropods in *Bt* rice was a little lower than in non-*Bt* rice. In 2003, the number of arthropods in B1 rice was 231, in B6 rice was 186, and in the control (Jiazao935) was 347. In 2004, there were 369 individuals in B1, 429 in B6, and 391 in the control. In 2005, there were 423 individuals in B1, 620 in B6, and 915 in the control.

At Jiande, the abundance of arthropods in *Bt* rice was a little higher than in non-*Bt* rice. In 2003, the number of arthropods in TT9-3 rice was 675, in TT9-4 rice was 588, and in the control (IR72) was 431. In 2004, there were 431 in TT9-3, 342 in TT9-4, and 233 in the control. In 2005, there were 449 in TT9-3, 337 in TT9-4, and 314 in the control.

At Fuyang, the same trend was observed as in Hangzhou. The number of arthropods in *Bt* rice did not differ significantly from that in non-*Bt* rice. In 2004, the number of arthropods in KMD rice was 948,

whereas in the control (Xiushui 11) was 850. In 2005, there were 4,137 in KMD and 3,957 in the control.

**Species Richness and Diversity.** Some common community indices (including Shannon-Weaver diversity index  $H'$  and dominance concentration index C) calculated for different plots during the 3 yr are shown in Table 1. Analysis of these indices revealed no significant differences between *Bt* and non-*Bt* plants within paddy fields (Table 3).

The temporal dynamics of these main indices of arthropod community diversity revealed the differences between the *Bt* and non-*Bt* rice. At Hangzhou, the dominant index of the non-*Bt* rice was a little higher than those of *Bt* rice (least significant difference [LSD] test:  $P \leq 0.05$  each comparison). The diversity index did not differ significantly between these two plots (Fig. 1). However, the diversity index of the non-*Bt* rice arthropods in Jiande was a little higher than those of *Bt* rice (LSD test:  $P \leq 0.05$  each comparison), with no significant difference in the dominant index (Fig. 2). At Fuyang, the results of the study revealed no significant differences between non-*Bt* and *Bt* rice (LSD test:  $P \leq 0.05$  each comparison; Fig. 3).

**Dominance Distribution.** The arthropods were separated into five guilds: phytophages, parasitoids, predators, detritivores, and others. The Phytophagous subcommunity includes Cicadellidae, Delphacidae, Aphididae, Thripidae, Itonididae, Trypetidae, Agromyzidae, Drosophilidae, Ephyridae, Chloropidae, Pyrali-

**Table 2. Dominance distribution of arthropod subcommunities in *Bt* (B1, B6, TT9-3, TT9-4, and KMD1) and non-*Bt* rice lines**

Sites	Year	Line	Phytophagous	Parasitoids	Predators	Detritivores	Others
Hangzhou	2003	B1	0.153 ± 0.126A	0.244 ± 0.086A	0.049 ± 0.038A	0.313 ± 0.081a	0.240 ± 0.155a
		B6	0.180 ± 0.143A	0.149 ± 0.073A	0.028 ± 0.005A	0.396 ± 0.150a	0.247 ± 0.181a
		935	0.171 ± 0.135A	0.228 ± 0.082A	0.019 ± 0.009A	0.312 ± 0.178a	0.270 ± 0.256a
	2004	B1	0.370 ± 0.122a	0.049 ± 0.018a	0.128 ± 0.103a	0.182 ± 0.070a	0.270 ± 0.187a
		B6	0.403 ± 0.122a	0.028 ± 0.019a	0.075 ± 0.053a	0.185 ± 0.059a	0.310 ± 0.104a
		935	0.465 ± 0.089a	0.052 ± 0.037a	0.043 ± 0.035a	0.124 ± 0.079a	0.316 ± 0.131a
	2005	B1	0.432 ± 0.149a	0.042 ± 0.022a	0.079 ± 0.065a	0.133 ± 0.090a	0.314 ± 0.175a
		B6	0.494 ± 0.214a	0.032 ± 0.019a	0.046 ± 0.033a	0.079 ± 0.093a	0.348 ± 0.234a
		935	0.391 ± 0.110a	0.055 ± 0.046a	0.024 ± 0.023a	0.126 ± 0.076a	0.405 ± 0.191a
	2003	TT9-3	0.817 ± 0.101a	0.016 ± 0.009a	0.137 ± 0.069a	0.010 ± 0.011a	0.019 ± 0.023a
		TT9-4	0.758 ± 0.152a	0.021 ± 0.019a	0.178 ± 0.092a	0.022 ± 0.034a	0.020 ± 0.013a
		IR72	0.803 ± 0.086a	0.021 ± 0.016a	0.121 ± 0.088a	0.018 ± 0.010a	0.037 ± 0.059a
Jiande	2004	TT9-3	0.672 ± 0.253a	0.022 ± 0.013a	0.225 ± 0.220a	0.036 ± 0.032a	0.045 ± 0.006a
		TT9-4	0.559 ± 0.279a	0.037 ± 0.023a	0.227 ± 0.266a	0.025 ± 0.019a	0.152 ± 0.192a
		IR72	0.572 ± 0.217a	0.034 ± 0.019a	0.101 ± 0.062a	0.098 ± 0.151a	0.203 ± 0.063a
	2005	TT9-3	0.609 ± 0.261a	0.059 ± 0.091a	0.216 ± 0.146a	0.048 ± 0.043a	0.068 ± 0.058a
		TT9-4	0.646 ± 0.319a	0.036 ± 0.018a	0.199 ± 0.232a	0.022 ± 0.008a	0.096 ± 0.094a
		IR72	0.483 ± 0.234a	0.022 ± 0.010a	0.394 ± 0.238a	0.044 ± 0.033a	0.058 ± 0.034a
	2004	KMD1	0.485 ± 0.388a	0.031 ± 0.027a	0.039 ± 0.027a	0.023 ± 0.012a	0.422 ± 0.386a
		Xiushui11	0.412 ± 0.321a	0.024 ± 0.016a	0.063 ± 0.046a	0.042 ± 0.014a	0.459 ± 0.347a
		KMD1	0.852 ± 0.113a	0.003 ± 0.002a	0.055 ± 0.049a	0.017 ± 0.012a	0.073 ± 0.069a
	2005	KMD1	0.859 ± 0.112a	0.005 ± 0.006a	0.043 ± 0.030a	0.010 ± 0.013a	0.083 ± 0.084a

Means (± SE) within column followed by the same letter are not significantly different based on ANOVA (Least significant difference test,  $P \leq 0.05$ ).

dae, Noctuidae, Chrysomelidae, Elateridae, Curculionidae, Miridae, Coreidae, Pentatomidae, Saldidae, and Psocidae. The Parasitoid subcommunity includes Ichneumonidae, Braconidae, Eulophidae, Pteromalidae, Mymaridae, Diapriidae, Scelionidae, Figitidae, Formicidae, Conopidae, Pipunculidae, and Tachinidae. The predators include Coenagrionidae, Dolichopodidae, Xylomyidae, Therevidae, Dolichopodidae, Empididae, Anthocoridae, and Veliidae. The Detritivore subcommunity includes Thichoceridae, Tipulidae, Stratiomyidae, Phoridae, Calliphoridae, Scathophagidae, Muscidae, and Melolonthidae.

There was almost significant dominance of phytophagous subcommunities at each site during the 3 yr, except 2003 at Hangzhou. Parasitoids and detritivores displayed the second highest level of dominance among the subcommunities. There was no significant difference in subcommunity composi-

**Table 4. Statistics for repeated-measure analyses of dominance distribution of subcommunities**

Sites	Year	Treatment	F	df	p
Hangzhou	2003	Phytophagous	0.05	2,12	0.9520
		Parasitoids	2.00		0.1778
		Predators	2.39		0.1341
		Detritivores	0.58		0.5750
		Others	0.03		0.9702
	2004	Phytophagous	0.92	2,12	0.4240
		Parasitoids	1.30		0.3088
		Predators	1.91		0.1904
		Detritivores	1.21		0.3314
		Others	0.14		0.8669
	2005	Phytophagous	0.51	2,12	0.6155
		Parasitoids	0.68		0.5271
		Predators	2.01		0.1767
		Detritivores	0.56		0.5857
		Others	0.26		0.7769
Jiande	2003	Phytophagous	0.28	2,9	0.7640
		Parasitoids	0.13		0.8771
		Predators	0.49		0.6282
		Detritivores	0.32		0.7373
		Others	0.29		0.7535
	2004	Phytophagous	0.24	2,9	0.7883
		Parasitoids	0.73		0.5105
		Predators	0.51		0.6165
		Detritivores	0.76		0.4970
		Others	1.92		0.2027
	2005	Phytophagous	0.39	2,9	0.6866
		Parasitoids	0.50		0.6231
		Predators	1.06		0.3864
		Detritivores	0.72		0.5121
		Others	0.35		0.7137
Fuyang	2004	Phytophagous	0.08	1,6	0.7827
		Parasitoids	0.2		0.6698
		Predators	0.79		0.4088
		Detritivores	4.13		0.0883
		Others	0.02		0.8908
	2005	Phytophagous	0.01	1,12	0.9085
		Parasitoids	0.89		0.3631
		Predators	0.31		0.5877
		Detritivores	0.97		0.3434
		Others	0.05		0.8235

**Table 3. Statistics for repeated-measure analyses of diversity indices**

Site	Year	Index	F	df	p
Hangzhou	2003	H'	0.09	2,12	0.9180
		C	1.01		0.3919
	2004	H'	0.76	2,12	0.4889
		C	0.47		0.6380
	2005	H'	0.19	2,12	0.8259
		C	0.47		0.6354
Jiande	2003	H'	0.13	2,9	0.8811
		C	0.24		0.7914
	2004	H'	6.62	2,9	0.0171
		C	3.45		0.0773
	2005	H'	0.92	2,9	0.4336
		C	1.76		0.2263
Fuyang	2004	H'	0.07	1,6	0.7939
		C	0.05		0.8333
	2005	H'	6.38	1,12	0.0449
		C	3.82		0.0985



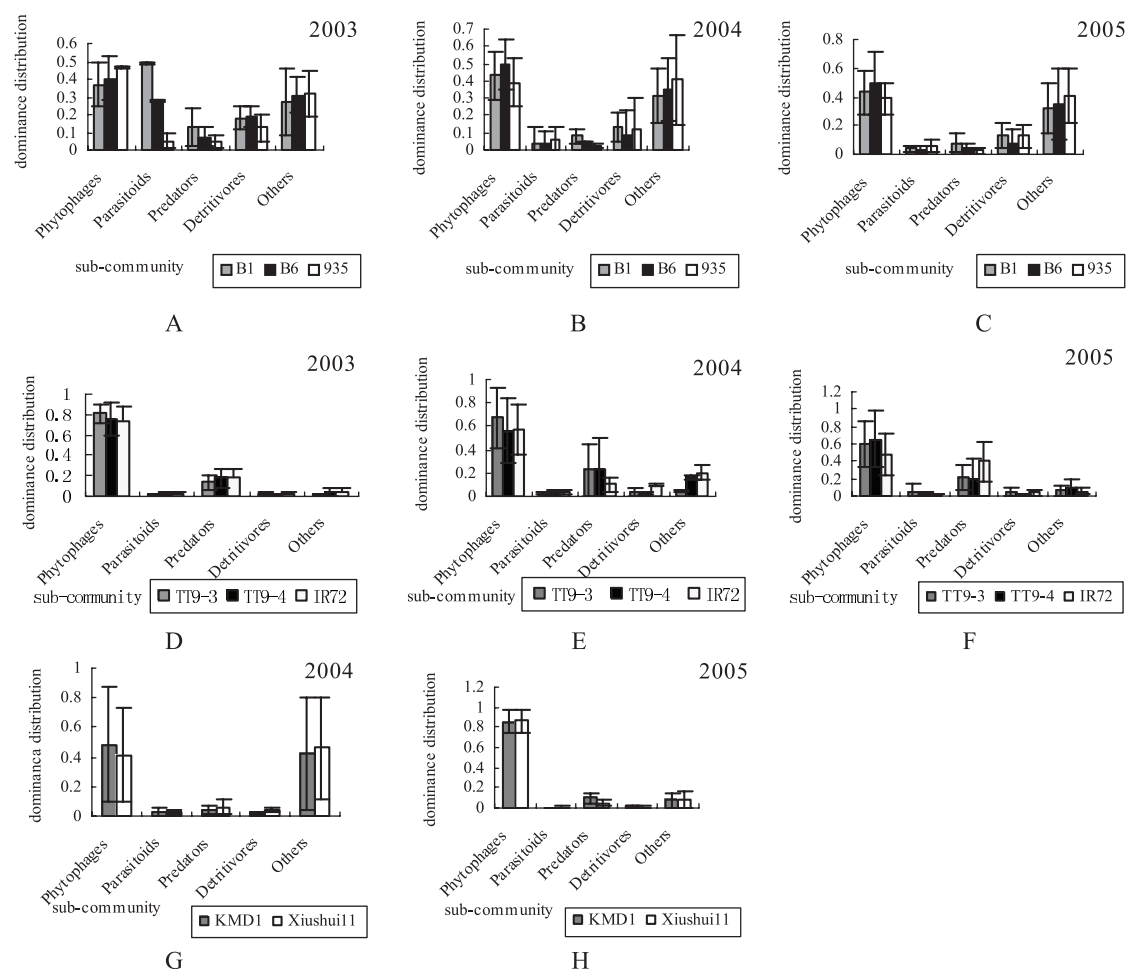


Fig. 4. Dominance distribution of sub-communities of arthropods in plots containing different lines of rice. (A–C) Hangzhou. (D–F) Jiande. (G–H) Fuyang. Bars are 95% CIs.

tion between the *Bt* rice and non-*Bt* rice (Tables 2 and 4; Fig. 4).

### Discussion

The number of arthropod species found in this study was obviously lower than those of other studies from tropical area (Settle et al. 1996, Schoenly et al. 1998). This was probably caused by the different study locations and differences in sampling strategies. Our study area was located near the northern border of the subtropics where species biodiversity is believed much less than that in the tropics.

We found that plots of *Bt* rice and non-*Bt* rice did not differ significantly in diversity or dominance distribution of arthropods. Thus, the similarity of arthropod communities in *Bt* and control rice plots was apparently high. It was quite clear that *Bt* rice generally had no marked negative effects on the arthropod community in the paddy fields, a result similar to that of Liu et al. (2003) for *cry1Ab/cry1Ac*-carrying transgenic *Bt* rice and non-*Bt* rice.

Laboratory studies suggest that the effects of *Bt* crops on natural enemies may depend on whether the prey or host takes up the toxin or is affected by the toxin (Romeis et al. 2006). Accordingly, no impact is expected for natural enemies attacking phloem-feeding herbivores (Dutton et al. 2002, Obrycki et al. 2003). If the natural enemy is a specialist on an herbivore that has high susceptibility to the toxin, the natural enemy's numbers are likely to decline in the field because of the absence of the host (Schuler et al. 2001, Andow and Hilbeck 2004). In our results, we did not find a difference in the abundance of parasitoids and predators among treatments (Table 2). This might be because of the target lepidopteran pests having a significantly lower dominance distribution among all arthropod phytophages, whereas nontarget pests like Cicadellidae and Delphacidae were more dominant. It has been suggested that *Bt* rice does not adversely affect nontarget planthopper and leafhopper populations and poses no potential risk of increasing their occurrence or damage (Chen et al. 2003, 2006). Therefore, the effects of *Bt* rice on the target pests and their

natural enemies may have been masked by the dominant nontarget pests.

The effect of transgenic plants on arthropod communities has been examined in other crops. Men et al. (2003) indicated that *Bt*-cotton increased the diversity of arthropod communities and pest subcommunities; however, it decreased the diversities of natural enemy subcommunities. Sisterson et al. (2004) showed minor differences in the arthropod community between *Bt* and non-*Bt* cotton. A long-term study showed essentially no effects of *Bt* cotton on natural enemy function in Arizona cotton, and in a companion study, minor reductions in density of several predator taxa in *Bt* cotton were observed (Naranjo 2005). The abundance of canopy- and ground-dwelling predators across 3 yr in cotton fields was not negatively impacted by *Bt* cotton (Torres and Ruberson 2005). A slight difference was shown between the total community in unsprayed conventional and *Bt* cotton in Australia (Whitehouse et al. 2005). In China, the diversity of arthropod communities in transgenic cotton plots was similar to that in conventional cotton fields without spraying (Li et al. 2004). In corn, numbers of soil mites, Collembola, and nematodes were similar in soil planted with *Bt* corn and soil planted with its isoline (Al-deeb et al. 2003). Candolfi et al. (2004) observed no effects of *Bt* corn on the communities of soil-dwelling and nontarget plant-dwelling arthropods. Dively (2005) found that densities of most nontarget taxa exposed to the *Bt* corn showed no differences compared with the isogenic control. Bitzer et al. (2005) observed few differences in the abundance of individual Collembola species in *Bt* and isoline corn, nor did the estimated species richness or the Shannon or Simpson diversity indices differ significantly between *Bt* and isoline corn at two locations over 3 yr, indicating no effect of *Bt* corn on springtail diversity. Furthermore, the use of insecticide to control the same pests more strongly impacts springtails and their predators than did the transgenic crop (Bitzer et al. 2005).

In conclusion, our findings suggest that the *Bt* rice generally has no marked negative effects on the arthropod community in paddy fields. We acknowledge several limitations to our study, in that we did not study arthropods living on the ground or in the soil and water, and our sample sizes were not large enough to enable rigorous comparisons between *Bt* and non-*Bt* rice for rare families of arthropods. The generality of our results can be enhanced by experimentally addressing these issues.

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