Field Response of Aboveground Nontarget Arthropod Community to Transgenic Bt-*Cry1Ab* Rice Plant Residues in Postharvest Seasons

ENTOMOLOGY 2011
ESA 59TH ANNUAL MEETING
NOVEMBER 13-16, RENO, NV

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ABSTRACT:

During 2006-08, two field trials were conducted in Chongqing, China to investigate the effects of transgenic rice expressing *Bacillus thuringiensis* (Bt) Cry1Ab protein on arthropod communities. Pitfall traps were used to sample arthropods in non-Bt and Bt rice fields. Aboveground arthropods during the postharvest seasons were abundant, while community densities varied significantly between the two trials. A total of 52,386 individual insects and spiders, representing 93 families, were captured during two postharvest seasons. Predominant captures were detritivores, which accounted for 91.9% of the total captures. Other arthropods sampled included predators (4.2%), herbivores (3.2%), and parasitoids (0.7%). In general, there were no significant differences among non-Bt and Bt rice plots in all arthropod community-specific parameters for both trials, suggesting no adverse impact of the Bt rice residues on the aboveground non-target arthropod communities during the postharvest season. The results of this study provide additional evidence that Bt rice is safe to non-target arthropod communities in the Chinese rice ecosystems.

INTRODUCTION

- Transgenic Bt rice is effective for managing major lepidopteran rice pests and can significantly reduce the use of chemical insecticides in China (Shu et al. 2000).
- High expression and long-term persistence of Cry proteins in Bt rice plant residues may cause possible risks on non-target arthropods.
- The abundance and diversity of arthropods in rice fields during postharvest season are of critical importance for natural control of rice arthropod pests.
- To date, limited studies have addressed the risk assessments of Cry1Ab rice plant residues to aboveground arthropod communities in postharvest seasons.

OBJECTIVE

To determine if there were any potential impacts of Bt rice on abundance and diversity of arthropod communities in postharvest season.

MATERIALS AND METHODS

Rice lines: Two Bt-*Cry1Ab* rice lines KMD1 (Bt-1) and KMD2 (Bt-2) and one non-Bt rice parental line XS11 (non-Bt) were used in two field trials.

Site and field experimental design: Two independent field trials were conducted in Agricultural Farm of Southwest University, Chongqing,China. One trial was conducted in 2006/07postharvest season and another trial was performed during 2007/08. After harvest, Bt rice plant residues were scattered uniformly on the soil surface of the corresponding plots (Fig. 1).

Field sampling of arthropods: The sampling method of pitfall trap used in the current study was the same as described in Bai et al. (2010) (Fig. 1).

Data analysis: Arthropods sampled were identified to the family level. Arthropods sampled were separated into four guilds: detritivores, predators, parasitoids, and phytophages (Fig. 2). The total arthropod abundance, Shannon-Weaver diversity index H, and dominance concentration index C were analyzed using a one way ANOVA.

Fig. 1 Pitfall trap in postharvest fallow fields

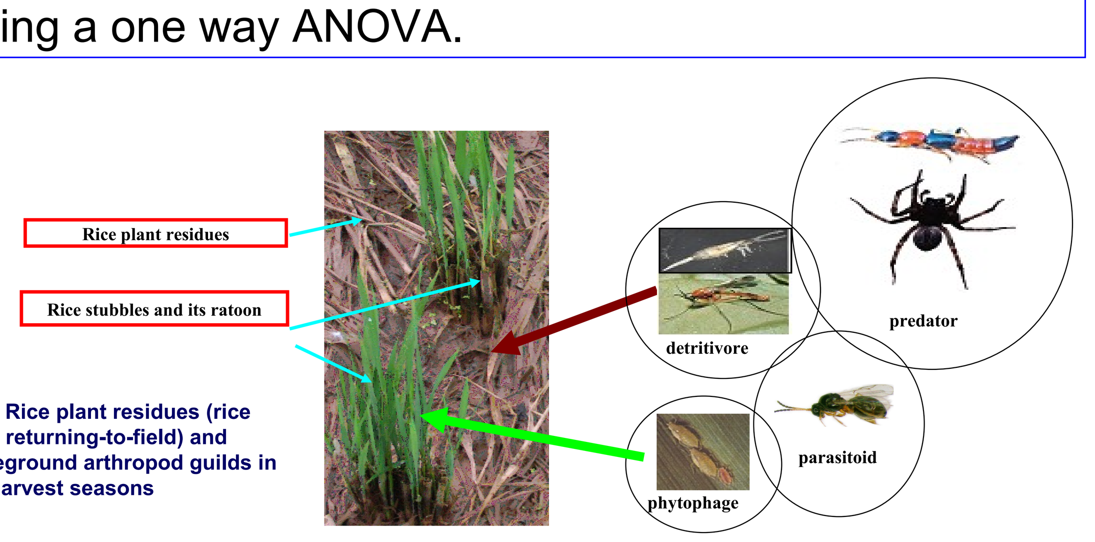

Fig. 2 Rice plant residues (rice straw returning-to-field) and aboveground arthropod guilds in postharvest seasons

Table 2 Total captures of arthropod subcommunities in non-Bt and Bt rice plots in two postharvest seasons.

Postharvest seasons/Sites	Sub-communities	Treatments			ANOVA	
		non-Bt	Bt-1	Bt-2	F2,8	P
2006/07 Xiaomotan	Detritivores	565.3 ± 32.7	836.0 ± 25.4	1016.0 ± 81.2	18.58	<0.01
	Predators	78.0 ± 5.0	79.0 ± 6.3	88.0 ± 4.0	1.13	0.38
	Parasitoids	25.7 ± 2.0	29.3 ± 1.7	21.7 ± 3.5	2.32	0.18
	Phytophages	78.0 ± 14.7	100.3 ± 9.9	59.3 ± 3.8	3.82	0.09
2007/08 Pingqiao	Detritivores	4607.0 ± 570.2	4217.3 ± 465.9	4800.7 ± 203.4	0.45	0.66
	Predators	145.7 ± 22.5	176.3 ± 28.3	161.0 ± 25.5	0.36	0.71
	Parasitoids	13.7 ± 3.2	13.3 ± 0.3	12.3 ± 1.5	0.12	0.89
	Phytophages	116.3 ± 15.0	95.3 ± 13.7	109.7 ± 20.9	0.41	0.68

RESULTS

Table 1 Abundance, Shannon diversity index H' and dominance concentration index C of arthropods sampled in rice plots of non-Bt and Bt in two postharvest seasons

Postharvest seasons/ Sites	Treatments			ANOVA	
	non-Bt	Bt-1	Bt-2	F2,8	P
Abundance					
2006/07 Xiaomotan	972.3 ± 142.8	1028.6 ± 53.4	1169.7 ± 3.7	1.33	0.33
2007/08 Pingqiao	4883.7 ± 606.9	4503.0 ± 500.1	5084.0 ± 237.4	0.39	0.70
Diversity indices H'					
2006/07 Xiaomotan	2.24 ± 0.09	2.05 ± 0.09	1.87 ± 0.10	4.22	0.07
2007/08 Pingqiao	1.42 ± 0.09	1.38 ± 0.06	1.23 ± 0.06	1.88	0.23
Dominance concentration indices C					
2006/07 Xiaomotan	0.19 ± 0.03	0.23 ± 0.03	0.29 ± 0.04	2.76	0.14
2007/08 Pingqiao	0.39 ± 0.05	0.41 ± 0.05	0.46 ± 0.05	0.63	0.57

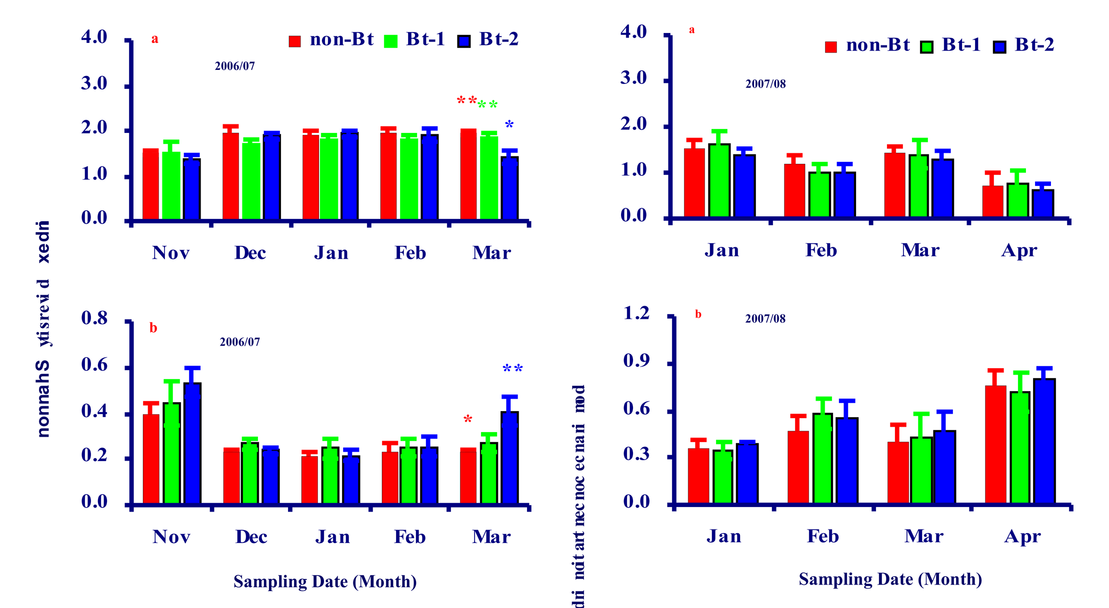

Fig. 3 Monthly comparison of arthropod community diversity indices among rice plots of non-Bt and Bt (Bt-1 and Bt-2) in two postharvest seasons in Chongqing, China. (a) and (b) Shannon diversity index H', (c) and (d) dominance concentration index C. A asterisk of "*" or "**" above bars indicates significant treatment differences in mean (LSD tests, P < 0.05).

- A total of 52,386 individual insects and spiders were captured in the two trials. The total number of insects and spiders captured in Xiaomotan during 2006/07 postharvest season was 8,974, which represented 10 orders and 73 families. A total number of 43,412 insects and spiders were sampled in Pingqiao during the postharvest season, which represented 10 orders and 70 families. There were no significant differences ($P > 0.05$) in the total captures among the three rice plots for both trials (Table 1).
- No significant differences ($P > 0.05$) were observed in the Shannon-Weaver diversity index H' and the dominance concentration index C among the three rice plots for the two trials (Table 1). The month-long comparison of the two indices revealed few differences between the non-Bt and Bt rice plots (Fig.3).
- In both trials, the detritivore subcommunity was the overwhelmingly dominant guild, which accounted for > 90 % of total arthropods captured. Predators and phytophages displayed the second highest level of dominance, accounting for 3-5 % of total captures. Parasitoids were rare, < 1 %. There were generally no significant differences among the Bt and no-Bt rice plots in the total monthly captures of arthropods (Fig. 4) and in each individual group of the four subcommunities (Table 2) for both trials

CONCLUSION

- The overall results of the two independent trials were very consistent. Although there were considerable differences in the total captures of non-target arthropods between the two trials, there was a high similarity in the abundance and diversity of arthropod communities among non-Bt and Bt rice plots for both trials.
- The results suggested that exposure to the Cry1Ab protein in rice plant residues had no adverse impact on the arthropod communities during postharvest season.

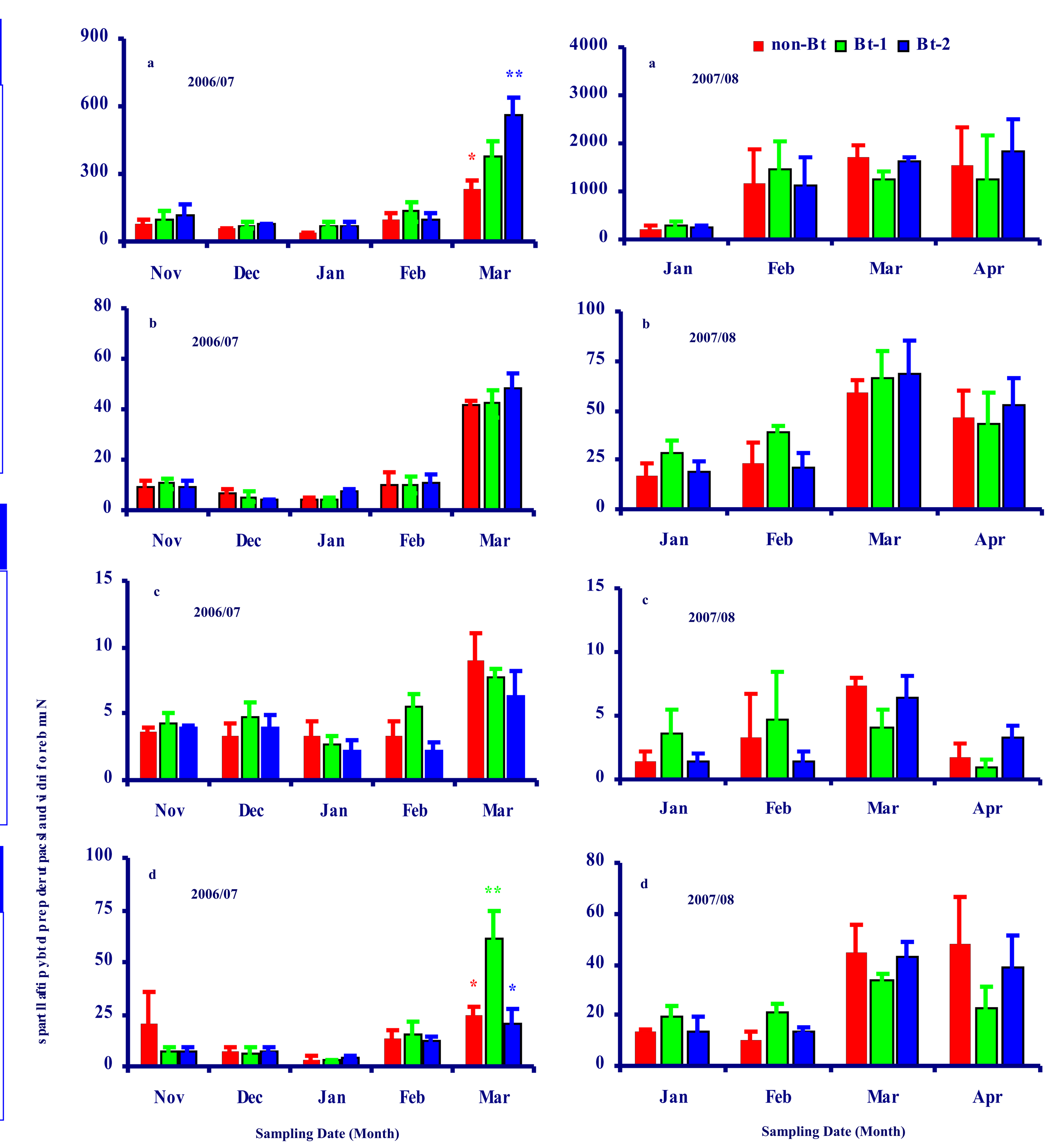

Fig. 4 Monthly comparison of the abundance of arthropod subcommunities among rice plots of non-Bt and Bt (Bt-1 and Bt-2) in Chongqing, China, in two postharvest seasons. (a) detritivores, (b) predators, (c) parasitoids, (d) phytophages. A asterisk of "*" or "**" above bars indicates significant treatment differences in mean (LSD tests, $P < 0.05$)

ACKNOWLEDGMENTS

This project represents work supported by the China National Program on Key Basic Research Projects (973 Program, 2007CB109202), the National Natural Science Foundation of China (30671411), and the Postdoctoral Science Foundation of China.

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