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Rove beetle (Coleoptera: Staphylinidae) communities in transgenic Bt (MON810) and near isogenic maize

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ABSTRACT

Field experiments were conducted to investigate the mechanism of the underlying patterns (abundance, species richness, diversity and similarity) of rove beetles in transgenic Bt (MON810) and in near isogenic maize stands in Hungary. During the three-year (2001–2003) survey, 1538 individuals and 21 species were sampled with pitfall traps. The *Cry1Ab* protein expressed by the MON810 maize hybrid did not influence the overall community structure. After grouping staphylinids into guilds we found no significant differences for non-aphidophagous predators and parasitoids, whereas there were significantly and marginally significantly higher abundances for predators with aphids in their diet in isogenic maize stands in 2002 and 2003 respectively. The abundance of the prey *Rhopalosiphum padi* (L.) showed a high fluctuation between stands and years and was numerically higher only in isogenic stands in the second half of the maize-growing season. The abundance of predatory guilds including aphids in their diet did not correlate with the total annual number of *R. padi* in the same year, but there was a linear correlation in successive years.

1. Introduction

The adoption of genetically modified insect-resistant plants in agriculture has become a powerful tool for controlling key pests (Farinós et al., 2008). The planting of transgenic maize MON810 with the *Cry1Ab* gene from *Bacillus thuringiensis* Berliner var. *kurstaki* expressing *Cry1Ab* insecticidal protein, specific to certain lepidopteran species, was first approved for cultivation in Europe in 1998 to control the European corn borer (*Ostrinia nubilalis* Hübner) (Kiss et al., 2003). In 2009, transgenic varieties of cotton and maize that express Bt proteins were grown on 32.1 million hectares worldwide. Numerous crops expressing novel insecticidal proteins are also under development, and these are expected to soon be commercialised (Romeis et al., 2008). In spite of a broad range of available scientific information on the impact of Bt maize on non-target arthropods, certain relevant taxa have not been studied in detail in Europe (Pons et al., 2005; Eizaguirre et al., 2006). This issue is crucial to the soil biodiversity considerations of insect-resistant GM crops (Saxena et al., 2004). Representative non-target insects that have been tested include Diptera, Neuroptera, Odonata, Trichoptera, Hymenoptera and Coleoptera. These groups include such species as the major predators and parasitoids that attack insect pests as well as the disease vectors that are the targets of Bt applications (Kiss et al., 2003; Metz, 2003; Farinós et al., 2008).

Staphylinidae is one of the largest beetle families with more than 47,000 species and is distributed worldwide in almost all types of ecosystems (Bohac, 1999; Markgraf and Basedow, 2002). However, rove beetles have rarely been used in integrated pest management largely because of taxonomic constraints and a lack of information on species ecology and prey preferences (Balog et al., 2008a,b,c; Balog and Markó, 2008). Studies in maize have demonstrated that natural enemies consist primarily of ants, spiders, rove beetles, predaceous mites and ground beetles. These predator groups comprise 24% of total individuals, staphylinids being the most abundant coleopteran group, averaging 13.6 beetles per trap per week (Rose and Dively, 2007). The variability in activity–density patterns of the rove beetle fauna in maize is mainly influenced by the year, but no detrimental effects have been attributed to its management (Farinós et al., 2008). In Spanish studies, the transgenic variety MON810 had more rove beetles at Lleida in

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2001, whereas the non-transgenic one exhibited a significantly higher abundance in the Madrid region in 2000 (Poza et al., 2005). Wolfenbarger collaborators (2008) found that Bt crops showed no significant effects on the detritivores on any of the five collembolan families and their carabid and staphylinid predators, or on the non-collembolan detritivore families Lathridiidae and Japygidae.

Rove beetles are rarely tested under laboratory conditions (with *Cry* proteins and *in planta* tests) because of difficulties in rearing and maintenance (Stacey et al., 2006; Raybould et al., 2007). Moreover, there is a lack of field data on arthropod communities in Bt crops from Europe, especially on rove beetles. Although the exposure of rove beetles to *Cry* proteins is likely to be low, the additive and unanticipated effects on the transgene can only be assessed in field trials. In this study, we evaluated the activity–density of non-target rove beetles in Bt MON810 and near isogenic maize. We estimated the effect of the prey *Rhopalosiphum padi* on rove beetle populations.

2. Materials and methods

A three-year (2001, 2002 and 2003) field experiment was carried out in an experimental maize stand surrounded by large peach and apricot orchards west of Budapest (47° 25′ N, 18° 47′ E) in Hungary. Plots (30 m × 30 m each) with Bt maize (DK 440 BTY) transformation event MON810 and its near isogenic line (DK 440) were established on Chernozem soil and arranged alternatively, with six replications each. An alley distance of 3 m was used between plots. A maize hybrid of similar maturity to the test hybrid was planted in the retention zone (a pollen capture crop surrounded the entire test field) in accordance with the requirements of the release permit. Maize was planted between late April and early May at a seed rate of 65,000 seeds/ha, which was reduced to 50,000 plants/ha after emergence, and harvested between mid-October and early November, depending on the year. No insecticides were applied during the experiment.

Rove beetles were collected using pitfall traps (300 cm^3 in size, 8 cm in diameter, half-filled with 4% formaldehyde solution as killing and preservative). Two pitfall traps were placed in the central part (15th row) of each plot, 10 m from each other and the left and right borders of the plot. Sampling lasted from late July in 2001 and from late May in 2002 and 2003 until harvest. Samples were collected weekly. Rove beetles were sorted and identified into species using the works of Freude et al. (1964, 1974). The abundance of the most common and almost exclusively occurring aphid species *R. padi* was assessed in each block weekly by the washing off method using leaves from 10 randomly selected maize plants (Jenser et al., 2010). The aphids were collected in plastic bags and counted in the laboratory.

Analyses of variance were performed and similarities were compared using the O'Brien and Levene tests to determine the differences in abundance, species richness and diversity of rove beetles in Bt and isogenic crops. Values of *F* and *p* were computed using SPSS software and confidence limits of $p \leq 95\%$ were considered significant. To avoid pseudoreplication analyses of variance were performed using the means of abundance and species richness of the cumulative data of each treatment. The Fisher alpha diversity index was calculated as a measure of biodiversity for each treatment. Metric ordination, principal coordinate analysis (PCoA) and the Horn index were all computed to study the similarities of rove beetle communities in maize stands. Because of the low abundances in 2001 and 2002 the cumulative data from the three years of collection were pooled for PCoA analysis.

Rove beetle species were classified into three guilds according to their prey preference: parasitoids; predatory guilds with aphids in their diet (PredAph+); and predatory guilds without aphids in their

Table 1
The classification on the guilds of the rove beetle species. Significantly high activity–density was observed for PredAph+ guild ($df = 2$, $F = 5.2$, $p < 0.001$).

Guilds	Species	Individuals
PredAph+ guild (Vickerman et al., 1986; Good and Giller, 1986)	*Anotylus inustus* (Gravenhorst)	44
	Philonthus cognatus (Stephens)	5
	Platystethus spinosus Erichson	1143
	Tachyporus chrysomelinus (L.)	6
	Tachyporus hypnorum (F.)	68
	Tachinus signatus Gravenhorst	14
	Total PredAph+ guild	**1280*****
Parasitoids guild (Good and Giller, 1986)	*Aleochara bilineata* Gyllenhal	65
	Aleochara bipustulata (L.)	47
	Total parasitoids	**112**
PredAph– guild (Good and Giller, 1986)	*Amisha analis* (Gravenhorst)	2
	Aloconota gregaria (Erichson)	12
	Drusilla canaliculata (Fabricius)	25
	Heterothops dissimilis (Gravenhorst)	13
	Lordithon trinotatus (Erichson)	1
	Ocypus olens Müller	2
	Omalium caesum Gravenhorst	18
	Quedius cinctus (Paykull)	2
	Paederus litoralis Gravenhorst	2
	Platydracus stercorarius (Olivier)	1
	Stenus sp.	4
	Xantholinus linearis (Olivier)	51
	Xantholinus longiventris (Heer)	13
	Total PredAph– guild	**136**

Notation: ***: $p < 0.001$.

Table 2
Species of rove beetles, their distribution by year and relative abundance (*R*) in Bt MON810 and near isogenic line.

	Species/year	2001		2002		2003		R (%)
		Bt	Iso	Bt	Iso	Bt	Iso	
1	***Aleochara bilineata***	**2**	**2**	**21**	**12**	**25**	**3**	**6.9**
2	***Aleochara bipustulata***	**2**		**7**	**14**	**13**	**11**	**4.5**
3	*Aloconota gregaria*	1		4	5	1	1	2.1
4	*Amisha analis*						2	0.1
5	*Anotylus inustus*	6	4	7	7	12	8	2.6
6	*Drusilla canaliculata*			7	4	7	7	1.6
7	*Heterothops dissimilis*			3	2	1	7	1.3
8	*Lordithon trinotatus*					1		0.1
9	*Ocypus olens*				1	1		0.6
10	*Omalium caesum*	1	1	1	6	6	3	2.3
11	*Paederus litoralis*	1		1				0.1
12	*Philonthus cognatus*				1	1	3	0.3
13	*Platydracus stercorarius*						1	0.1
14	***Platystethus spinosus***	**24**	**12**	**1**	**4**	**456**	**646**	**65.6**
15	*Quedius cinctus*						2	0.1
16	*Stenus* sp.			3			1	0.2
17	*Tachinus signatus*	4		2	7		1	1.2
18	*Tachyporus chrysomelinus*			1	4		1	0.3
19	***Tachyporus hypnorum***	**1**	**11**	**17**	**29**	**5**	**5**	**5.4**
20	***Xantholinus linearis***			**14**	**6**	**13**	**18**	**3.1**
21	*Xantholinus longiventris*			2	1	6	4	0.8
	No. of individuals	**42**	**30**	**91**	**103**	**548**	**724**	**1538**
	No. of species	**9**	**5**	**15**	**15**	**14**	**18**	**21**