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SOIL ECOLOGICAL AND ECONOMIC EVALUATION OF GENETICALLY MODIFIED CROPS — ECOGEN

Microbial and microfaunal community structure in cropping systems with genetically modified plants

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Summary

Soils from field sites at Foulum (DK), Narbons (FR) and Varois (FR) planted with genetically modified maize expressing either the insecticidal *Bacillus thuringiensis* protein (*Bt*) or herbicide tolerance (HT), as described elsewhere in this volume, were analysed for nematodes, protozoa and microbial community structure. These analyses were mirrored in single-species testing and in mesocosm experiments, and were coordinated with field samples taken for microarthropods, enchytraeids and earthworms so allowing for cross-comparison and a better understanding of the results observed in the field. Over the first 2 years of the field experiments (in 2002 and 2003), the effect of *Bt*-maize was within the normal variation expected in these agricultural systems. Sampling in 2004 and 2005 was expanded to include the effects of tillage (i.e. reduced tillage versus conventional tillage) and also the use of HT-maize. Tillage had major effects regardless of soil type (Varois or Foulum), with reduced-tillage plots having a greater abundance of microfauna and a different microbial community structure (measured both by phospholipid fatty-acid analysis (PLFA) and by community-level physiological profiling (CLPP)) from conventionally tilled plots. Grass, as a contrasting cropping system to maize, also had an effect regardless of soil type and resulted in greater microfaunal abundance and an altered microbial community structure. Differences in crop management, which for the *Bt*-maize was removal of the insecticide used to control European corn borer and for HT-maize was a change in herbicide formulation, were only tested at single sites. There were differences in microbial community structure (CLPP but not PLFA) and

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sporadic increases in protozoan abundance under the *Bt*-crop management. The HT-maize cropping system, which covered a shorter period and only one site, showed little change from the conventional system other than an altered microbial community structure (as measured by PLFA only) at the final harvest. The *Bt*-trait had a minimal impact, with fewer amoebae at Foulum in May 2003, fewer nematodes at Foulum in May 2004 but more protozoa at Varois in October 2002 and an altered microbial community structure (PLFA) at Foulum in August 2005. These were not persistent effects and could not be distinguished from varietal effects. Based on the field evaluations of microfauna and microorganisms, we conclude that there were no soil ecological consequences for these communities associated with the use of *Bt*- or HT-maize in place of conventional varieties. Other land management options, such as tillage, crop type and pest management regime, had significantly larger effects on the biology of the soil than the type of maize grown.
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Introduction

Despite the large area of *Bt*-maize (i.e. genetically modified (GM) maize expressing an insecticidal protein from *Bacillus thuringiensis*) and other *Bt* crops planted, there are still scientifically interesting questions to be addressed with regard to the little-known soil compartment (see, for example, reviews by Groot and Dicke, 2002; Bruinsma et al., 2003; Dunfield and Germida, 2004; Motavalli et al., 2004; Stotzky, 2004; O'Callaghan et al., 2005). The same is true of herbicide-tolerant (HT) crops, with few studies related to soil ecological effects. A practical consequence of the introduction of these (i.e. *Bt* and HT) GM crops is the likely modification of the cropping system to maximize the benefits associated with the technology. Thus, for GM plants expressing the *Bt* protein this includes the reduced application of insecticide and for HT-crops the likely conversion to reduced-tillage operations. In a study of the impacts of GM plants on soil populations and processes, it is relevant, therefore, to compare not only the GM and conventional cultivars but also the likely cropping systems in which these GM plants would be grown. To address these issues the European Commission-funded ECOGEN project (www.ecogen.dk) was initiated. Initial results from the ECOGEN project revealed minimal differences between *Bt* and conventional cultivars. Results after the first 2 years of field trials with Cry1Ab-expressing maize showed that changes to microbial and microfaunal (protozoan and nematode) communities due to the *Bt* trait were small and less than changes due to different (non-*Bt*) maize cultivars and different crops (Griffiths et al., 2005). Decomposition of wheat straw in the same field trials was unaffected by *Bt*-maize (Cortet et al., 2005). A similar conclusion was drawn from a pot experiment, that although there are effects of the *Bt* trait on soil microbial and faunal communities, they are relatively small compared with effects of soil type (field site) and maybe confounded by natural variation between different maize lines (Griffiths et al., 2006, 2007). To expand these findings into a comparison of cropping systems including GM cultivars, the field trials (described elsewhere in this volume, Andersen et al., 2007) were modified to include the likely cropping-system changes associated with the production of GM maize, namely, reduced tillage and no insecticide application to control European corn borer (*Ostrinia nubilalis* Hübner). These different management practices had the additional benefit of providing a set of internal positive controls against which to compare differences due to the cultivars planted (either conventional or GM). As the same field plots were used as previously reported on (Griffiths et al., 2005), the data presented here also represent the final 2 years of 4-year continuous *Bt*-maize production at the Foulum site.

Materials and methods

Field sites

The field sites at Foulum (Northern Jutland, Denmark), Varois (Bourgogne, France) and Narbons (Midi-Pyrenées, France) are described in detail by Andersen et al. (2007, this volume) and were sampled during 2004 and 2005. Briefly, at Foulum different maize varieties were grown in a four-block, split-plot design, with each plot divided into a conventionally tilled part and a reduced-tillage part. The maize varieties were MEB307 (a MON810 *Bt*-variety, from Monsanto); Monumental (the conventional variety isogenic to MEB307 but without

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