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Crop genetic diversity benefits farmland biodiversity in cultivated fields

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ABSTRACT

This study tested whether increasing crop genetic diversity benefited farmland biodiversity in bread wheat (*Triticum aestivum*) fields, using an experimental approach in which arthropod and wild plant diversity were compared in a genetically homogeneous wheat variety vs. a variety mixture. The diversity of wild plant species was not affected by crop genetic diversity. However, we showed for the first time a positive impact of crop genetic diversity on below (collembola) and aboveground arthropod (spiders and predatory carabids) diversity at field scale in agroecosystems, which may be caused by a wider variety of food resources or more complex crop architecture. Increasing crop genetic diversity could therefore be an easy-to-implement scheme benefiting farmland biodiversity.

1. Introduction

Crop genetic diversity has been decreasing steadily in the agricultural landscapes of developed countries since the early 20th century (FAO, 1997; Secretariat of the Convention on Biological Diversity, 2006). This is mostly due the widespread replacement of genetically diverse traditional varieties or landraces by homogeneous modern varieties (Hoisington et al., 1999), leading to decreased genetic diversity in the fields, both within and between varieties. Hence, in spite of an increasing number of registered crop varieties since the sixties, the majority of agricultural land in developed countries is now covered with a few "winning" productive varieties, with generally a single crop per field, so that the actual cultivated diversity is in fact low (e.g. FranceAgriMer and ARVALIS Institut du Végétal, 2009 in France). The resulting crop genetic homogenization is postulated to threaten the sustainability of production systems, and several studies now emphasize the importance of both inter- (e.g. Altieri, 1999; Lin, 2011) and intra-specific (e.g. Hajjar et al., 2008; Macfadyen and Bohan, 2010) crop diversity to increase and stabilize crop yield, via e.g. improved pest control (see e.g. Tooker and Frank, 2012 for a review).

Another potential consequence of decreased crop genetic diversity that has received little attention so far is erosion of wild biodiversity in agroecosystems. Previous studies in natural systems (e.g. Whitham et al., 2006) have shown that the phenotype (hence the genotype) of some plant species may affect the composition of the dependent community. These particular species, referred to as foundation species, are abundant in the ecosystem (often, but not always, tree species, Whitham et al., 2006). Because they represent a large fraction of the biomass of an ecosystem, they structure a community by creating locally stable conditions for other species (e.g. habitats and food sources) and by modulating and stabilizing fundamental ecosystem processes (see Ellison et al., 2005 for definitions). The impact of the genotype of a single species on a community is known as a "community phenotype", i.e. an effect of genes at the community level ("Community genetics", Whitham et al., 2003). High genetic and phenotypic diversity in foundation

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species can result in a diversity of local environments, thereby benefiting species diversity in the dependent community and affecting ecosystem processes (Bangert et al., 2005; Whitham et al., 2006; Wimp et al., 2004). Although well documented in natural ecosystems, the influence of genetic diversity on community diversity has never been investigated in agroecosystems. Several lines of evidence nonetheless suggest that crop genetic diversity can greatly affect wild species diversity. First, crops are dominant in terms of biomass in a field and can be considered foundation species. Second, crops are known to be involved in numerous (though altered, Macfadyen and Bohan, 2010) interactions with non-crop species, which may create community phenotypes similar to wild foundation species. These interactions include exploitation and interference competition with weed species (e.g. allelopathy, demonstrated for several cereals: Belz, 2007; Bertholdsson, 2010), trophic interactions with phytophages (e.g. species that feed on root and leaf secretions or excreta), or mutualistic interactions via the creation of microhabitats for predators by below and aboveground vegetative architecture (e.g. Johnson, 2008). As a result, decreased crop genetic diversity should alter farmland biodiversity within and among fields, via a reduction in the diversity of available ecological niches or food sources (Bangert et al., 2005).

The present study assessed the relationship between in-field crop genetic diversity and the species diversity of several taxonomic groups (springtails, ground-dwelling macroarthropods and plants), using an experimental approach in the field. We worked with winter wheat (*Triticum aestivum*), the main crop in the study region, which also exhibits large phenotypic variation among varieties. Species diversity was compared between plots sown with a pure line variety and plots sown with a combination of several varieties. The following predictions were tested: (1) local (α) diversity at each sampling point should be higher in the variety mixture than in the pure line variety, due to the diversity of genotypes (and therefore phenotypes) surrounding each sampling point; (2) β-diversity (between sampling points) should be low within the pure variety because one wheat genotype should be preferentially associated with one community phenotype, whereas β-diversity in the variety mixture should be higher due to high spatial heterogeneity of wheat genotype associations in the field; (3) consequently, γ-diversity, the sum of α- and β-diversity, should be higher in the variety mixture than the pure line variety. We discuss the most likely underlying mechanisms, as well as possible consequences for ecosystem services and opportunities for agricultural sustainability.

2. Methods

The experiment took place in an organic farm in northern France. In winter 2007–2008 ten contiguous square plots (60 m wide) were sown with either a “pure line” bread wheat variety (*T. aestivum* “Renan”, INRA, five plots) or a genetically diverse seed mixture including 30 landraces and several pure line varieties, among which the “Renan” variety. Pure line varieties are obtained by successive (usually 6–10) self-fertilizations of a few selected plants so that all plants are eventually highly homozygous and genetically identical. These two crop diversity treatments were distributed in a checkerboard-like pattern (see Appendix A). This limited confounding spatial effects but did not fully discard them, owing to the partly unbalanced experimental design that was constrained by field shape. However, these confounding effects appeared to be minor: for example, the only plot not bordered by the surrounding matrix (plot R2, Appendix A) did not exhibit extreme ecological diversities compared to other plots in the same treatment. No mechanical or chemical treatment was applied between sowing and harvest, as is often the case in organic farming; plots were surrounded by a wheat variety not used in the experiment itself.

2.1. Community sampling

Springtails (collembola) were sampled at the beginning of May 2008, using five soil cores (5 cm diameter, 12 cm deep) per plot (one in the center of the plot, the other four at the center of each quarter). After ten days of extraction with the Berlese method (Edwards and Fletcher, 1971), individuals were counted and identified to species level. Water content (dry weight/wet weight) and pH (method NF ISO 10390) were also measured in each soil core.

Ground-dwelling macroarthropods were sampled twice in May and June 2008, during two-week trapping sessions separated by a two-week interruption. To this end, five pitfall traps (9.5 cm diameter, 11.4 cm deep, filled with ethylene glycol) were located at the corners and center of a 10 m × 10 m square centered in each plot. This distribution reduced the capture of individuals from neighboring plots, while maintaining enough distance between the five pitfall traps of a same plot to consider them as relatively independent replicates. The two most abundant groups, carabids and spiders, were identified to species level. All individuals of small carabid species ($\leq$4 mm) without identification were grouped (190 individuals, 6.8% of total carabids) and six larger individuals could be identified to genus level only. All spider juveniles that could not be identified to species level were discarded (1674 individuals, 20% of total spiders); the number of discarded individuals was however not significantly different across crop diversity treatments ($F_{1,8} = 4.41$, $P = 0.07$). For aboveground and belowground invertebrates, other taxonomic groups were observed in the samples (including flies, ants, non-carabid Coleoptera and slugs above ground; mites and earthworms below ground), but these represented a small fraction of total abundance (1–5%) and a small number of species.

Finally, all wild plants growing in the experimental area were sampled twice, at the beginning of May and June 2008. At each sampling date, all plant species were recorded in 25 1 m^2 quadrats evenly distributed within each plot, i.e. a total of 500 quadrats. All individual plants were identified to species level. The quadrats were divided into 25 20 cm × 20 cm squares to estimate abundance as the number of squares where a species was present.

2.2. Wheat individual measurements

Morphological and phenological characters that are classically used to describe phenotypes in wheat (e.g. IBPGR Secretariat, 1985; Murphy et al., 2008; UPOV, 1996) were measured to assess wheat phenotypic diversity within each crop diversity treatment: tiller number (five quadrats per plot, 1068 individuals), flowering date (eight quadrats per plot, 2205 individuals), total height at maturity, length, width and position along the stalk of the first leaf, and spike number (four samples of ten individuals per plot). Although these traits were not chosen on the basis of involvement in interspecific interactions, but to provide a general index of phenotypic diversity, some are nonetheless known to influence plant–plant interactions (e.g. plant height and competition for light) or plant–invertebrate interactions (e.g. plant architecture creating microhabitats, Langellotto and Denno, 2004).

For each measured character, we checked that wheat diversity was actually different between the two crop diversity treatments with a non-parametric Fligner test for homogeneity of variance. Wheat phenotypic diversity was then summarized within each plot by normalizing and combining the five morphological characters describing vegetation structure (total height, length, width and position of the first leaf, spike number) to calculate Rao’s diversity coefficient (Rao, 1982) with the Mahalanobis distance,