
Genetic Diversity of Oilseed Rape Fields and Feral Populations in the Context of Coexistence with GM crops

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Abstract

Despite growing concern about transgenes escaping from fields, few studies have analysed the genetic diversity of crops in an agroecosystem over several years. Accurate information about the dynamics and relationship of the genetic diversity of crops in an agroecosystem is essential for risk assessment and policies concerning the containment of genetically modified crops and their coexistence with crops grown by conventional practices.

We analysed the genetic diversity of oilseed rape plants from fields and feral populations over 4 years in an agricultural landscape of 41 km². We used exact compatibility and maximum likelihood assignment methods to assign these plants to cultivars.

Even pure lines and hybrids cultivar seed lots contained several genotypes. The cultivar diversity in fields reflected the conventional view of agroecosystems quite well. Three types of field emerged: fields sown with a single cultivar, fields sown with two cultivars, and unassigned fields. Field plant diversity was higher than expected, indicating the persistence of cultivars that were grown for only one year. The cultivar composition of feral populations was similar to that of field plants, with an increasing number of cultivars each year. By using genetic tools, we found a link between the cultivars of field plants in a particular year and the cultivars of feral population plants in the following year. Feral populations on road verges were more diverse than those on path verges.

All of these findings have consequences in the context of coexistence with genetically modified crops.

Keywords: Brassica napus L., population genetics, cultivar, feral population

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