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

Diane Bailleul∗1,2, Sébastien Ollier2, and Jane Lecomte†2

1MARine Biodiversity, Exploitation and Conservation (MARBEC) – UMR 9190, Institut Français de Recherche pour l’Exploitation de la Mer (IFREMER) – Avenue Jean Monnet, CS 30171, 34203 Sete Cedex, France, France
2Ecologie, Systématique et Evolution (ESE) – AgroParisTech, Université Paris XI - Paris Sud, CNRS – UMR8079 – bat. 362 91405 ORSAY CEDEX, France

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 26 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 unsigned 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

∗Speaker
†Corresponding author: jane.lecomte@u-psud.fr