

# Science for Environment Policy

## Oilseed rape genes transfer from inside to outside of crop fields: study could aid GM risk assessment

**This study is one of few to assess the genetic diversity of crops in an agroecosystem over several years.** Researchers analysed the genetic makeup of oilseed rape plants within and outside crop fields over four years. They found similarity between cultivars of field plants in one year and those of feral plants (unplanted) in the following year. They also found persistence of the cultivars within the feral plants, which suggests that feral populations with genetically modified (GM) traits might result from persistent GM traits within field seed banks. The researchers say their findings could aid impact assessments of GM crops.

The **diversity** of genes in crop plants is important for food security, as a greater variety of genes give plants a better chance of adapting to environmental change. Information on the genetic diversity of crops is also important for understanding agroecosystem function, and has recently garnered attention in the context of GM crops. Understanding the dynamics and relationships of gene flow in agroecosystems can help to assess the **impacts** of growing GM crops alongside conventional crops.

This study focused on genetic diversity in oilseed rape. Oilseed rape is an economically important crop across Europe (although GM versions are not currently authorised for cultivation). It is also useful in studying the large-scale movement of genetic material (gene flow).

Natural diversity among oilseed rape is generated by several processes, including pod shattering – a common phenomenon that causes seeds to be lost during harvest, which can then establish long-lived seed banks in the soil. Originating from these seed banks, oilseed rape volunteers (plants that grow on their own, without being planted) are common in fields. Volunteers, although grown from the seeds of particular cultivars (a group of plants with similar characteristics), can be different to the parent plant. Feral populations of oilseed rape, those that grow outside fields, are common along roadsides and railways (due to seed spillage from trucks, for example).

A consequence of the ability of oilseed rape to establish feral and volunteer populations and exchange genetic material through cross pollination is the appearance of plants with multiple GM traits, that are not found in grown cultivars (due to exchange of GM traits through pollen). Recent studies have shown that after GM crops have been grown in a field, it is not possible to meet the EU threshold for 'no GM' labelling for crops grown in the field in the years after.

To better understand how genes move between oilseed rape fields and populations, this study used sophisticated molecular techniques. The study was based on a four-year survey of oilseed rape plants (both field and feral) in a typical open-field **agricultural** landscape, a 41 km<sup>2</sup> field in central France, where local farmers take their harvested grain for storage. The researchers carried out a survey twice a year, from 2002 to 2005, once during oilseed rape flowering and once before harvesting. Field and feral populations were recorded and mapped, and plants were analysed using genetic markers to assign them to a cultivar.

*Continued on next page.*



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The results showed a succession of cultivars, some of which were grown for longer periods because of good traits, some that were used only for a year, and others that were gradually adopted (e.g. numbers of the cultivar gradually increased over time). As a result, the authors identified three field types:

- fields sown with a single cultivar;
- fields sown with two cultivars;
- unassigned fields (fields with many cultivars or unassigned plants).

Plant diversity in fields was higher than the researchers expected, which suggests that even cultivars grown purposely for only a year persisted in the fields for longer periods. They also found that feral populations have a similar level of cultivar diversity to those in fields and that their diversity increases over time. This is because they persist (due to survival in seed banks created by seed losses during harvest or truck spillage for example). Feral populations on the sides of roads were also more diverse than those on the side of paths. The researchers suggest this is due to truck traffic, which is linked to seed spilling.

This study shows that agroecosystems are complex, and that the plants within them are strongly affected by human activities. Specifically, it shows that oilseed rape fields are not uniform — not the products of sowing seeds from a single cultivar. Instead, fields display a 'cultivar footprint', which includes plants previously grown in the area.

The most important outcome of this study is the demonstration of a link between the diversity of feral populations in one year and that of field plants in the previous — demonstrating gene flow from the field. This is the first time such a link between feral and field plants has been demonstrated in an agroecosystem using genetic tools.

The researchers suggest that feral populations containing GM traits could be due not only to the 'one-off' escape of GM material, but also due to GM *persistence* among field plants. They propose that persistent feral populations could act as a 'relay' to contaminate crop fields with GM traits. They further suggest that these findings could improve assessments of agricultural landscape function, as well as the impacts of GM organisms.

