

Outcrossing among crops and feral descendents - geneflow

G R Squire

Scottish Crop Research Institute, Invergowrie, Dundee DD2 5DA

g.squire@scri.sari.ac.uk

Rationale

Crops and wild plants have always lived side by side and exchanged genes. Crops have become weeds and weeds have become crops. Oilseed rape typifies these exchanges, having arisen from two wild species and being now a crop and a weed at the same time. Oilseed rape is also an outcrossing species: its crop and weed (or feral) forms exchange genes freely. The fields and feral populations form a shifting patchwork that changes spatially over time as crops are sown and harvested and as feral populations arise and die. The crop and ferals provide an interesting case study of evolution in fragmented and dynamic populations, but they have also brought to wider attention the issues of crop purity and integrity of habitat, specially following applications by seed companies to grow GM oilseed rape and other GM crops in Europe. Debate has intensified during the present Farm Scale Evaluations of herbicide-resistant GM crops. Particular issues are -

- outcrossing between nearby fields might lead to impurities in yield
- feral populations left by an earlier crop might cause impurities within a subsequent crop
- feral populations might become more competitive than species in the existing arable seedbank, and so change the composition of the seedbank assemblage, specially if they acquire GM traits such as herbicide resistance.

Various authorities have set, or are considering, thresholds for GM impurities should GM crops be commercially grown. Quantitative and predictive approaches to geneflow and population dynamics are therefore sought.

Methods of study

Research on geneflow and GM impact assessment is well networked internationally. Major projects are underway in North America, Australia, France, Germany and the UK, among other countries. Within this subject of study, the Scottish Crop Research Institute and its collaborators have developed a major capability in geneflow research with an emphasis on regional processes. Facilities and expertise include -

- a study area of around 600 km² in Tayside and Angus in which the configurations of fields and ferals are used to examine regional dynamics
- a range of molecular diagnostic techniques for detecting and estimating geneflow and paternity
- techniques using male sterile 'bait' plants for estimating distance and frequency of geneflow from fields into the surrounding region (1 to 10 km)
- the study of physiological traits (e.g. induced dormancy) that differentiate crop varieties and encourage persistence

- an extensive network of sites in the UK for tracking the population dynamics of feral weeds in the seedbank and their effect on the arable plant community,
- predictive models of gene flow and persistence of crop-derived feral seed (relevant to management of GM residues)
- advanced diagnostic and statistical sampling techniques for estimating whole-field average cross-pollination between fields, including GM crop fields

The principles developed in this work are applicable to other crops, as defined variously by the mating system, persistence, dispersal, etc.

NB. Results from the Farm Scale Evaluations of GM crops will not be discussed until the results have been peer reviewed and published.

Gene flow between and from crops

Research in the early 1990s at SCRI found that gene flow in oilseed rape was more extensive than was previously believed. Subsequent models of regional gene flow over several kilometers suggested cross-pollination at a receptor field or population should depend on the arrangement of donor fields in the landscape; moreover, the proportion of crossing from a particular type or variety of crop should depend on the proportion of this type among all donor fields.

A regional scale experiment was therefore put in place to test this hypothesis. A combination of male sterile bait plants (which are only fertilised by pollen from external sources), male fertile plants and molecular diagnostic techniques was used by Gavin Ramsay, Caroline Thompson and colleagues at SCRI to measure gene flow from normal commercial fields and a field that had unique markers. This experiment demonstrated that insects were important vectors - the previous model has incorporated only wind-borne pollen; that after declining very steeply over 50 m from a field-edge, gene flow continued at low frequency for several kilometres; and that cross-pollination from different types of donor field was indeed in proportion to their area and configuration. From this research, and complementary studies by Jeremy Sweet and colleagues at the National Institute of Agricultural Botany (NIAB), workers in France and more recently in Australia, whole field cross-pollination was estimated to be less than 0.1%, i.e. 1 seed in one thousand set on the plants in a field would be from a pollen source outside the field. These estimates were highly uncertain, however.

Work is now in progress to measure outcrossing from fields in Scotland which are sown with the GM herbicide-tolerant crops of oilseed rape used in the Farm Scale Evaluations. The easily detectable markers in these crops should allow more accurate estimates of cross-pollination at low frequency than had been possible before. For wider applications, a consortium led by SCRI is developing advanced, high throughput diagnostic techniques for measuring gene flow at low frequency among non-GM fields. Together these studies will also quantify the pollination efficiency of insects, such as bumble bees, hive bees and pollen beetles that contribute to crossing, quantify the spatial patterns of crossing in fields, and develop the sampling protocols necessary to estimate whole-field crossing accurately.

Persistence and role of ferals

Feral populations are established when seed from a crop drops to the soil during harvest or is moved around by farm machinery and vehicles. The populations decline rapidly during their first two years, but then persist as a residual in many fields at a typical density of 100 m⁻². Oilseed rape is one of very few species to have entered the arable seedbank community in the 20th century. It is now a widespread weed of middle to low rank in abundance. Factors that have caused its appearance are seed shatter at or before harvest, then inducible dormancy if conditions at the soil surface do not promote germination. Commercial varieties differ greatly in the fraction of seed that can be induced into dormancy by factors such as low temperature or dryness. The trait is largely unobserved in conditions used for standard testing of uniformity in crop varieties.

Given that ferals commonly persist for more than five years, and that oilseed rape appears as a 'break' crop in a cereal rotation every two to four years, oilseed rape fields commonly consist of the sown crop and an assortment of ferals of different origin. This has caused little concern when the sown crop and ferals are of the same general oil type (e.g. both are food-quality varieties). If the ferals were of GM origin, and the sown crop not, then GM seed would be present in the harvested seed, though no GM-derived protein would be in the oil processed from the seed. Our understanding of the evidence on biosafety is that GM traits such as herbicide tolerance are neither more harmful nor beneficial to human or animal health than non-GM varieties. However, the presence or degree of GM impurity in harvested yield is an issue for many people. As a guide to management, therefore, mathematical models of GM feral persistence in the seedbank and in harvested yield have been constructed, based on research by SCRI and other groups, notably Peter Lutman and colleagues at Rothamsted Research. The models will be used to define forms of field management that would keep impurities below specified thresholds.

Impact on habitat integrity

At present, feral oilseed rape is less abundant than the main cruciferous weeds such as charlock (*Sinapis arvensis*) but more frequent than most of the wild and feral relatives with which it might potentially cross (albeit at very low frequency). Very substantial records now exist on the 'position' of feral oilseed rape in the arable plant community. It has not risen to dominance in weed populations despite the high seed drop that occurs at each harvest, nor has it invaded semi-natural habitats around farmland. Even in field management regimes that allowed many other species to increase in population, feral oilseed rape has remained a small component of the seedbank. Whether it will increase, die out or stay as it is is uncertain. If it did adapt to become a more abundant weed, then its presence might alter field practice and possibly the profile of herbicides used on the farm, and it might diminish other weed species, including non-target weeds that stabilise soil processes and diversify the food web. Other weed species have risen or declined over time, but the weed community has remained a dynamic assemblage. It is very unlikely therefore that a single weed species could cause major disruption to the habitat. Concerns

that feral oilseed rape possessing GM herbicide-tolerance traits would increase in abundance to the point of having major effects on the habitat are therefore probably unfounded, but are being considered and quantified. At present, many other options exist to control such GM feral plants.

Conclusions

- geneflow in oilseed rape occurs at low frequency over several km, mediated by a range of insect vectors and wind-borne pollen.
- geneflow is a regional process depending on the configuration of fields in a locality
- best current estimates indicate cross pollination between nearby fields is 1 in 1000 or less; the values might be much higher to fields of partial male fertility (as in some modern varieties) or from fields to small feral populations
- ferals persist in the arable seedbank and can contribute more (i.e. 1 in a 100) to impurities in crops than does geneflow by pollen movement from other crops
- impurities cannot be prevented in the harvested yield of outcrossing crops or crops that give rise to feral populations, but could be reduced by rigorous field management and regional segregation of crop types
- herbicide-tolerant feral populations should have no selective advantage except where the specific herbicide is used
- geneflow and feral persistence in oilseed rape makes an interesting 'model' for studying the links between physiological process and regional meta-population, but the ecological risk of ferals, herbicide tolerant or otherwise, is presently small.

Present work -

- Definitive estimates of crop to crop and crop to feral geneflow from realistic GM crop sites.
- Further measures of persistence in feral populations in the arable seedbank over a wide range of sites in the UK, and their role in the seedbank assemblage
- Advanced diagnostic and sampling methodologies for estimating whole-field average cross-pollination
- The contribution of geneflow to the dynamics of small populations

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