Field to field geneflow in oilseed rape

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An important topic in European agriculture is the coexistence of conventional, organic and GM farming. For coexistence to be feasible, transfer of genetic material between crops would have to be kept below stated thresholds. If gene movement between fields happens only at low frequency and over very short distances, then different types of farming should be possible within small areas of land (e.g. 10 km^2). However, if gene flow occurs above, say, 0.3% and over several km, then coexistence may only be possible by segregating types of farming into different regions. Progress is limited by a lack of sensitive detection techniques for measuring pollination at low frequency in the very large samples that are required to estimate out-crossing between whole fields in the landscape. To remedy this, the UK government has funded a four-year project to measure gene movement between fields, to determine how the type of receiving crop affects the result and to explore ways to minimize gene movement. The project is run by six organizations – SCRI, Rothamsted Research, CEH, CSL, NIAB and ADAS – who between them have the necessary range of disciplines, laboratories and field sites.

The major challenges in the first two years are to devise sensitive techniques for detecting very low pollination-frequencies and to characterize the spatial variation of pollination over fields. The first task was to select donor and receptor varieties for developing the detailed methodologies. For preliminary analysis, a high erucic acid (HEAR) type was chosen as the donor and a low erucic (LEAR) type as the receptor. The key enzyme in erucic acid biosynthesis in *Brassica* species is the product of the Fatty Acid Elongation 1 (*FAE*1) genes, β-keto-acyl-CoA synthase (KCS). The trait is controlled by two highly homologous genes BN-FAE1.1 and BN-FAE1.2, corresponding to the parental species *B. rapa* and *B. oleracea FAE*1 genes. Mutations in these genes are responsible for the low erucic trait of LEAR types. To explore the variation in these genes, DNA was extracted and analysed for >90 varieties of *B. napus* and other *Brassica* species. Small differences between donor and receptor sequences were found in the form of a 2-base and a 4-base deletion in the BN-FAE1.2 gene sequence of the receptor. The differences were considered sufficient to be able to detect pollination from HEAR to LEAR types and a real-time PCR assay has been developed using these deletions as markers.

Plot experiments were set up in 2002/03 to test insect-capture techniques at Rothamsted and to estimate low frequency pollination in an isolated plot at SCRI (Fig. 1). Donor and receptor fields were then sown at both sites for measuring gene movement over short and moderate (1 km) distance in 2004. Subsequent objectives are to confirm the most suitable donor and receptor types for large-scale studies and to develop assays based on real-time (TaqMan) quantitative PCR for high-throughput screening of samples. The project scales up in 2005 and 2006 to examine low-frequency geneflow over several kilometers in arable regions throughout the UK. The final outcome of the work will be recommendations to policy-makers and growers on what is needed to achieve economic coexistence of conventional, organic and GM farming where oilseed rape is used as a break crop. The preliminary results are already informing several EU member states who are defining or implementing their own policies on coexistence. The project is funded by Defra/SEERAD and coordinated at SCRI.

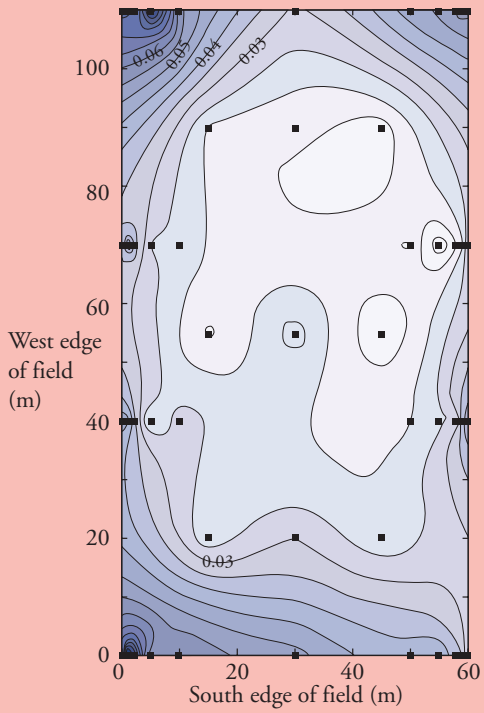

Figure 1 Contour diagram of low-level gene flow into an isolated plot of male sterile oilseed rape, showing greater pollination at the corners and edges.