

QUANTIFYING GENE FLOW FROM OILSEED RAPE TO ITS WILD RELATIVES USING REMOTE SENSING (LANDSAT TM)

Luisa J. Elliott*, Dave C. Mason
NERC-Environmental Systems Science Centre
Harry-Pitt Building
3 Earley Gate
The University of Reading, Whiteknights
PO Box 238, Reading, RG6 6AL, UK
* Email: lje@mail.nerc-essc.ac.uk

Mike J. Wilkinson, Joel Allainguillaume
Department of Agricultural Botany
School of Plant Sciences
The University of Reading, Whiteknights
PO Box 221, Reading, RG6 6AS, UK

EXTENDED ABSTRACT

Gene flow is defined as the movement of genes between populations and is a naturally occurring phenomenon among sexually compatible individuals. Crops have exchanged genes with their wild and weedy relatives for centuries, however this process has recently caused concern. The rapid advances in genetic engineering have hit an immense wall of opposition and gene flow is now seen as a possible escape route for transgenes. The safety of genetically modified (GM) crops has been fervently debated and the possible risks, to both the consumers of the crops and to the environment, have prevented their commercialisation in Britain and many other countries. Concern has arisen that if detrimental effects were to be detected post release of any GM crop, withdrawal may be difficult, or impossible, if gene flow has already occurred. Other potential, undesirable consequences of gene flow are the evolution of increased weediness and the extinction of wild relatives. It is thought that crop to wild gene flow has caused increased weediness in seven wild relatives of the world's thirteen most important crops and extinction in two (Ellstrand *et al.* 1999).

Gene flow can only prove a substantive risk if suitable recipients grow sympatric to the GM crop (i.e. in the same geographic location), if the transgene combines stably within the recipient to form a fertile hybrid and if the fitness of the hybrids is not reduced to a deleterious extent. In the UK more than ten crops have been found to spontaneously hybridise with one or more elements of the local flora (Raybould & Gray, 1993). Oilseed rape provides an example of one of these crops and is a useful species for modelling gene flow. Within Britain the species of rape that is grown commercially for oilseed is *Brassica napus*, a hybrid between *Brassica rapa* and *Brassica oleracea*. Both of these parent species grow wild throughout Britain, with *B.rapa* growing exclusively on riverbanks and *B.oleracea* at a few known coastal sites (Rich, 1991; Mitchell & Richards, 1979). There are two planting times for oilseed rape in Britain, winter and spring and it has been found that the winter-sown variety flowers concurrent to *B.rapa* whereas the spring-sown variety flowers later. However, due to the long flowering period of the wild species there can be some overlap with the flowering of spring-sown rape and low rates of hybridisation may be possible (Jorgensen & Anderson, 1994).

It is widely believed that patterns of gene flow on a commercial scale cannot be extrapolated from small-scale investigations. Remote sensing provides a useful tool whereby crops can be located and hybridisation quantified on a large scale. A preliminary study was carried out in the southeast of England using remote sensing to identify possible areas where gene flow was likely by searching for oilseed rape fields adjacent to rivers and cliff tops, since it is these areas that provide suitable habitats for the parent species (Wilkinson *et al.*, 2000; Davenport *et al.*, 2000). These sites were visited in the subsequent growing season and screened for hybrids. It was found that gene flow was more likely between oilseed rape and *B.rapa* than with *B.oleracea* and one naturally occurring *B.napus/B.rapa* hybrid was located. This rate of hybridisation was lower than expected.

The aim of the current study is to investigate the distribution of *B.rapa* in the whole of Britain and estimate the extent of sympatry with oilseed rape and hybridisation rates. Using agricultural statistics, a map of oilseed rape area was constructed and this showed that the majority of oilseed rape was grown in central and eastern England. Digital

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rivers data (1:50,000 scale) were acquired which showed that there were over 260,000km of river in Britain, giving a large number of possible habitats for *B.rapa*. Several Landsat TM satellite images were acquired for areas of Britain that fitted the selection criteria of having a large area of oilseed rape combined with a dense river network. Thus, images taken in May (the peak of oilseed rape growing season) in a variety of years over Lincolnshire, Oxfordshire and Kent were classified to detect oilseed rape and the rivers data were overlaid. The oilseed rape fields falling within a set buffer zone around the river were then selected. The proceeding stage was to estimate the distribution of *B.rapa* by combining the data from several river surveys with the present knowledge of *B.rapa* habitats. *B.rapa* proved to be absent from a significant area of Britain and was only present in a small proportion of the preliminary study area in southeast England, which explains the unexpectedly low hybridisation rates in this preliminary study. The predicted distribution of *B.rapa* was combined with the information on oilseed rape fields growing sympatric to a river to highlight the areas where gene flow was possible. The remote sensing data proved to be enormously useful at this stage in guiding the search for hybrids, as fieldworkers could be directed to specific stretches of river that had oilseed rape growing sympatric in the previous year and were predicted to have *B.rapa* along their banks. On the basis of these results the number of hybrids formed across the whole of Britain each year was estimated, together with the error rate of this prediction.

This research provides a method for predicting gene flow on a commercial, countrywide scale and thus serves as an important precursor to the introduction of a GM crop into a country. The results show that gene flow will occur from oilseed rape to *B.rapa* and hybrids will form. This highlights the necessity for careful assessments on the safety of GM oilseed rape and vigilant post release monitoring.

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