Risks from transgenic crops

SIR — Debate continues over the possible risks posed by transgene movement via pollen following the commercial release of genetically modified oilseed rape[1,2]. We have investigated the likelihood of glufosinate-tolerant transgenes first moving into and then influencing the survival of feral populations of the crop.

We monitored airborne pollen densities at 0 m, 100 m, 360 m and 1.5–2.5 km from isolated oilseed rape fields (3–10 ha) for three years. Densities at 360 m were 10–12% of those at the field margin; we consistently observed low densities at 1.5–2.5 km. It has been reported[3] that the decay in pollen concentration, C, with distance, r, from a source could be approximated by an exponential function $C\alpha e^{-r/\alpha}$, where α is the characteristic dispersal distance. The value of α for oilseed rape has been calculated[3] to lie between 2.3 and 8.8 m. The same function fitted to our data, however, suggests that α lies between 128 and 172 m, with 95% confidence. The use of an exponential rather than a power-law model[4], and the subtraction of pollen levels at 2 km as a background correction, makes this a conservative estimate of long-range dispersal. We suggest the increased value of α presented here can be explained at least partly by our use of commercial-sized fields, 24-hour monitoring and widely spaced sampling sites. Our results show that significant quantities of pollen travel over large distances; this has implications for transgene recruitment by feral populations, provided pollen viability and competitiveness are unaffected by dispersal.

The proportion of potential seeds on stands of emasculated plants showed the same dependence on distance from an isolated field as the pollen profile, suggesting that pollen viability is unaffected by dispersal. We also exposed emasculated and subsequently self-pollinated plants (cv. Comet) to airborne pollen from an isolated field (cv. Libravo). We identified intercultivar hybrids at 0 m (6.3%, 8/126), 100 m (0.5%, 1/195) and 360 m (3.7%, 5/135) by simple-sequence repeat PCR (polymerase chain reaction) and RAPD (randomly amplified polymorphic DNA) analyses (Fig. 1). The significance of these results for the levels of gene flow expected in the natural environment depends on the proximity of fields and feral populations. In our three-year survey (1993–95) of a 480-km^2 area of Angus, Scotland, for example, we found that between 31% (28/89) and 42% (35/83) of feral populations were sited within 360 m of an oilseed rape field .

It follows that attention should now focus on the probable effects of any introduced transgenes. In the case of a glufosinate-tolerant cultivar, it is important to establish whether the transgene would confer direct selective advantage in the feral environment, as might be expected if the herbicide is widely applied (Fig. 2). Our survey of feral populations in 1995 revealed that 44% had been subjected to control measures. The most widely used method, mowing, was applied to 39% of populations. Herbicides were used on only 5.7% of populations; we found no evidence of glufosinate application using any of the commercial formulations available. Close examination of five populations sprayed with herbicides revealed that all contained survivors which set seed. Thus, although tolerant individuals would have clear selective advantage if sprayed, our results suggest that few populations are likely to receive such treatment, and that even in these, not all plants would be affected.

We infer that, in the area surveyed, the possession of glufosinate-tolerance is unlikely to affect the survival of feral populations significantly. This assertion takes no account of future changes in glufosinate application in non-agricultural situations, of pleiotropic effects of the transgene, or of effects on agricultural volunteers. Our work demonstrates the need for a careful, case-by-case approach to the risk assessment of genetically modified organisms.

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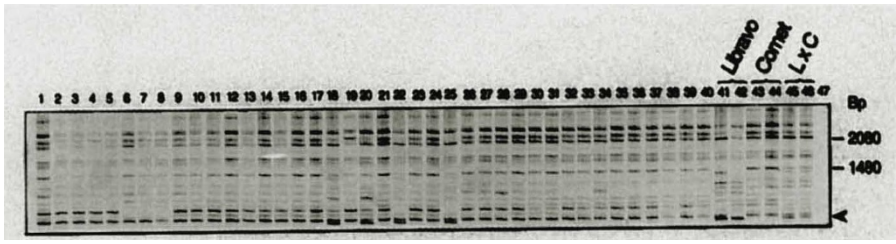

FIG. 1 Identification of hybrids between cultivars Libravo and Comet using the 5′ anchored simple-sequence repeat primer 1425 and PCR according to ref. 5. Lanes 1–40, offspring of emasculated plants (cv. Comet) sited 360 m from the field (cv. Libravo); lanes 41, 42, cv. Libravo; lanes 43, 44, cv. Comet; lanes 44–46, F_1 hybrids (cv. Libravo × cv. Comet); lane 47, control. Intercultivar hybrids can be identified in lanes 18, 20, 22 and 25 by the presence of a Libravo-specific fragment (arrowed). Hybrid status was checked using a 900-base-pair Libravo-specific fragment obtained after RAPD analysis using primer 5′-CCACCGCCAG-3′. Band homology was confirmed by Southern analysis.

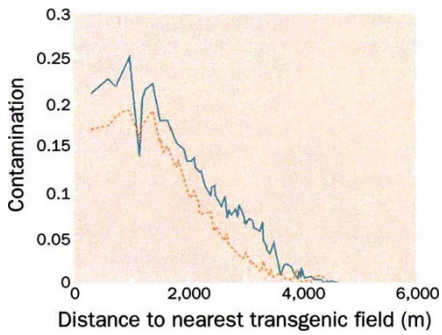

FIG. 2 Simulated average proportion of transgenic seed set in wild-type feral populations as a function of distance from the nearest genetically modified field in a region where 10% of oilseed rape fields are transgenic. Feral population sizes were assumed to follow the frequency distribution observed in the survey. The proportion of genetically modified to nongenetically modified seed set in a feral population was assumed to be proportional to the relative concentration of airborne pollen originating from each type of pollen source. The curves result from a numerical solution of the equation $\delta C/\delta t = D\nabla^2 C - v\nabla C - kC$, where C is airborne pollen concentration, D is the dispersal coefficient, v is the prevailing wind velocity and k is a first-order deposition constant. Values of k and D are derived from our pollen-trap data. Solid line, the case where fields are less clustered (fractal dimension of 1.26); dotted line, fields which are more clustered (dimension of 1). The number of feral sites, non-genetically modified and genetically modified fields is identical in both cases, and each point represents the average of three (more clustered) or five (less clustered) random realizations of the spatial distribution of field and feral sites.

1. Coghlan, A. *New Scient.* **145** (1967), 5 (1995).
2. Mikkelsen, T. R., Andersen, B. & Jorgensen, R. B. *Nature* **380**, 31 (1996).
3. McCartney, H. A. & Lacey, M. E. *J. agric. Sci., Camb.* **107**, 299–305 (1991).
4. Shaw, M. W. *Proc. R. Soc. Lond.* **259**, 243–248 (1995).
5. Charters, Y. M., Robertson, A., Wilkinson, M. J. & Ramsay, G. *Theor. appl. Genet.* (in the press).

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