The Use Of Genomics Technologies In Contemporary
Rubus And Ribes Breeding Programmes

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Introduction

Cultivars from the SCRI Ribes and Rubus programmes have for many years been among the most popular in Europe, eg. raspberry cultivar ‘Glen Ample’ (Fig. 1) and the ‘Ben’ series of blackcurrants. Further cultivar releases are planned, through the Fruit Product Innovation Centre at SCRI eg. ‘Loch Tay blackcurrants. Further cultivar releases have been among the most popular in Europe, eg. raspberry cultivar ‘Glen Moy and the North American cultivar Latham (Graham et al., 2003). The map, which forms seven linkage groups (group 2 is shown in Fig. 3), is based on AFLP and SSR markers (both genomic and cDNA-derived) (Graham et al. 2002) from Glen Moy. In addition, a range of phenotypic data is being collected from the Moy x Latham population and linked to mapped markers using MapQTL. The data includes morphological data based on commercially important phenotypes segregating within the population, eg. cane spines and spawn density, pest and disease resistance traits and more complex fruit quality components.

The production of a linkage map in Ribes is advancing along similar lines, using a mapping population between two SCRI breeding lines segregating for a range of agronomic and quality traits.  To date, genomic SSRs (Brennan et al., 2002) and AFLPs have been mapped on this population.  In addition, we have sequenced cDNA-clones derived from fruit at an early opening stage (Woodhead et al., 1998) (Fig. 4), to identify SSRs linked to genes of functional relevance to fruit quality in Ribes (Table 1).

Mapping of resistance to Phytophthora root rot

The Rubus linkage map provides an unrivalled resource for mapping both single gene and multigenic traits and developing diagnostic markers for those of greatest value. Recent work at SCRI is focused on resistance to Phytophthora root rot. (Phytophthora fragariae var. rubi), which causes damage to UK raspberry crops estimated at over £1.5 million annually (Fig. 5) (Graham and Smith 2002). Using replicated mapping progenies of cv. Glen Moy (susceptible) x cv. Latham (resistant) (Fig. 6), identification of markers linked to resistant phenotypes is in progress.  This will lead to the development of a diagnostic system for the rapid identification of root rot-resistant germplasm within the SCRI breeding programmes and reduce the time taken to produce resistant cultivars by up to 4 years.

Future Research in Rubus at SCRI

Raspberry is a model species for the Rosaceae in genomics research, since it is diploid with a very small genome (275Mbp), making it highly amenable to genetic and physical mapping. A nebulised small insert genomic library is currently being sequenced to allow us to estimate gene density. Large insert genomic libraries (BACs) are being constructed to serve as a source of genomic DNA for physical mapping, positional cloning and as a scaffold for whole genome sequencing.  Anchoring the physical map to the genetic map will enable alignment of the maps and facilitate the identification of genomic harbouring genes controlling important phenotypes.  An integrated physical/genetic map will also allow the extent of synteny and colinearity of the Rubus genome with other members of the Rosaceae to be determined.

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References