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

Scottish Crop Research Institute

Julie Graham, Ingo Hein, Joanne Russell, Rex Brennan, Kay Smith, Linzi Jorgensen Mary Woodhead and Wayne Powell.

Genome Dynamics Programme, Scottish Crop Research Institute, Invergowrie, Dundee, Scotland DD2 5DA, UK.

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' blackberry (Fig. 2), and in order to ensure the continuing success of the SCRI programmes, the breeding work is becoming more closely integrated with underpinning genomics research.

Fig. 1 SCRI Raspberry Cv. Glen Ample
Fig. 2   SCRI Blackberry Cv. Loch Tay (flower and fruit)

Linkage Mapping in *Rubus* & *Ribes*

The first reported genetic linkage map of the red raspberry *R. idaeus* has been constructed from a cross between the phenotypically diverse European red 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 ripening stage (Woodhead *et al.*, 1998) (Fig. 4), to identify SSRs linked to genes of functional relevance to fruit quality in *Ribes* (Table 1).
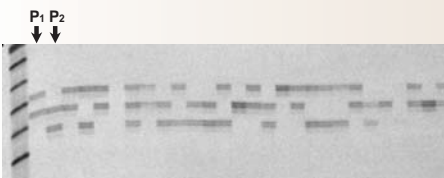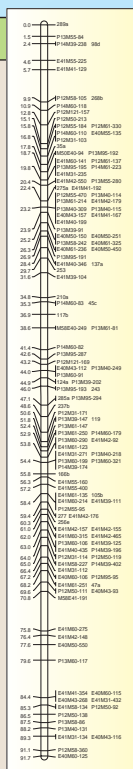

P₁ P₂

Fig. 3 Linkage Group 2 from map of *Rubus idaeus* cv. Glen Moy

Fig. 4 EST-derived SSR showing polymorphism in segregating mapping population of *Ribes nigrum*. P₁ and P₂ indicate parental genotypes

Table 1

Clone Name	Homology
Erb01-01	Fragaria x ananassa expansin (Exp1) mRNA,
Erb01-118	*Vitis vinifera* putative transcription factor mRNA, complete cds
Erb01-322	Peach developing fruit mesocarp *Prunus persica* cDNA clone
Erb01-400	Almond developing seed *Prunus dulcis* cDNA clone PA__Ea0006M15f
Erb01-448	Ripening Grape berries Lambda Zap II Library *Vitis vinifera* cDNA clone
Erb01-569	thiamin biosynthesis protein thi1 - sweet orange [*Citrus sinensis*]
Erb01-578	An expressed sequence tag database for abiotic stressed leaves of *Vitis vinifera* var. Chardonnay *Vitis vinifera* cDNA clone
Erb01-706	Almond developing seed *Prunus dulcis* cDNA clone PA__Ea0006M15f
Erb01-721	Peach developing fruit mesocarp *Prunus persica* cDNA clone PP_LEa0030M03f
Erb01-732	*Malus x domestica* MdCHS mRNA for chalcone synthase, complete cds
Erb01-745	40S ribosomal protein S8 [*Prunus armeniaca*]
Erb01-799	Peach developing fruit mesocarp *Prunus persica* cDNA clone PP_LEa0024F01f,
Erb01-801	Peach developing fruit mesocarp *Prunus persica* cDNA clone PP_LEa0020C14f,
Erb01-806	An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay *Vitis vinifera* cDNA clone VVB023B09 5.
Erb01-811	*Ribes nigrum* mRNA for hypothetical protein
Erb01-822	thiamin biosynthesis protein thi1 - sweet orange [*Citrus sinensis*]
Erb01-891	Peach developing fruit mesocarp *Prunus persica* cDNA clone PP_LEa0007I11f.
Erb01-903	*Vitis vinifera* putative transcription factor mRNA, complete cds
Erb01-908	An expressed sequence tag database for abiotic stressed leaves of *Vitis vinifera* var. Chardonnay
Erb01-922	Ribes nigrum mRNA for mitochondrial carrier protein
Erb01-951	Ripening Grape berries *Vitis vinifera* cDNA clone

Mapping of resistance to *Phytophthora* root rot

The *Rubus* linkage map provides an unrivalled resource for mapping both single gene and polygenic traits and developing diagnostic markers for those of greatest value. Recent work at SCRI is focused on resistance to raspberry 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.

Fig. 5 Damage caused by *Phytophthora fragariae* var. *rubi*

Fig. 6 Replicated plots of Glen Moy x Latham population segregating for root rot resistance

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 regions harbouring genes controlling important phenotypes. An integrated physical/genetic map will also allow the extent of synteny or colinearity of the *Rubus* genome with other members of the *Rosaceae* to be determined.

Acknowledgements

References

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