



# A genetic linkage map of blackcurrant (*Ribes nigrum* L.)

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Breeding of new blackcurrant cultivars is generally protracted, partly due to the heterozygous nature of the germplasm involved and also to the fact that effective screening of breeding germplasm for many of the most important traits, such as gall mite resistance, can take several years to complete. As a consequence, there is considerable potential utility for marker-assisted breeding and earlier identification of desirable phenotypes in *Ribes*. There are also breeding objectives of increasing the levels of both ascorbic acid and anthocyanins within the breeding germplasm and ultimately in new cultivars for the industry, in order to enhance the nutritional value of the fruit. Developmental traits, such as time of budbreak, are also important, as the effects of increasingly mild winters on dormancy break of blackcurrant are already a matter of concern (Atkinson *et al.*, 2005).

The development and potential use of molecular markers in *Ribes* has been previously reported (e.g. Brennan *et al.*, 2002), and now the first genetic linkage map of blackcurrant (*Ribes nigrum* L.) has been constructed using Amplified Fragment Length Polymorphism (AFLP), Simple Sequence Repeat (SSR), both genomic and expressed sequence tag (EST)-derived, and single nucleotide polymorphism (SNP) markers. The population used, designated 9328, comprises a  $F_1$  full-sib progeny from a cross between two diverse breeding lines from SCRI. The parental types were selected for their diversity across a range of agronomic, developmental and fruit quality traits; these included resistance to gall mite, berry size, time of budbreak and flowering, anthocyanin content and ascorbic acid level, all of which are key traits in the SCRI blackcurrant breeding programme. The offspring were

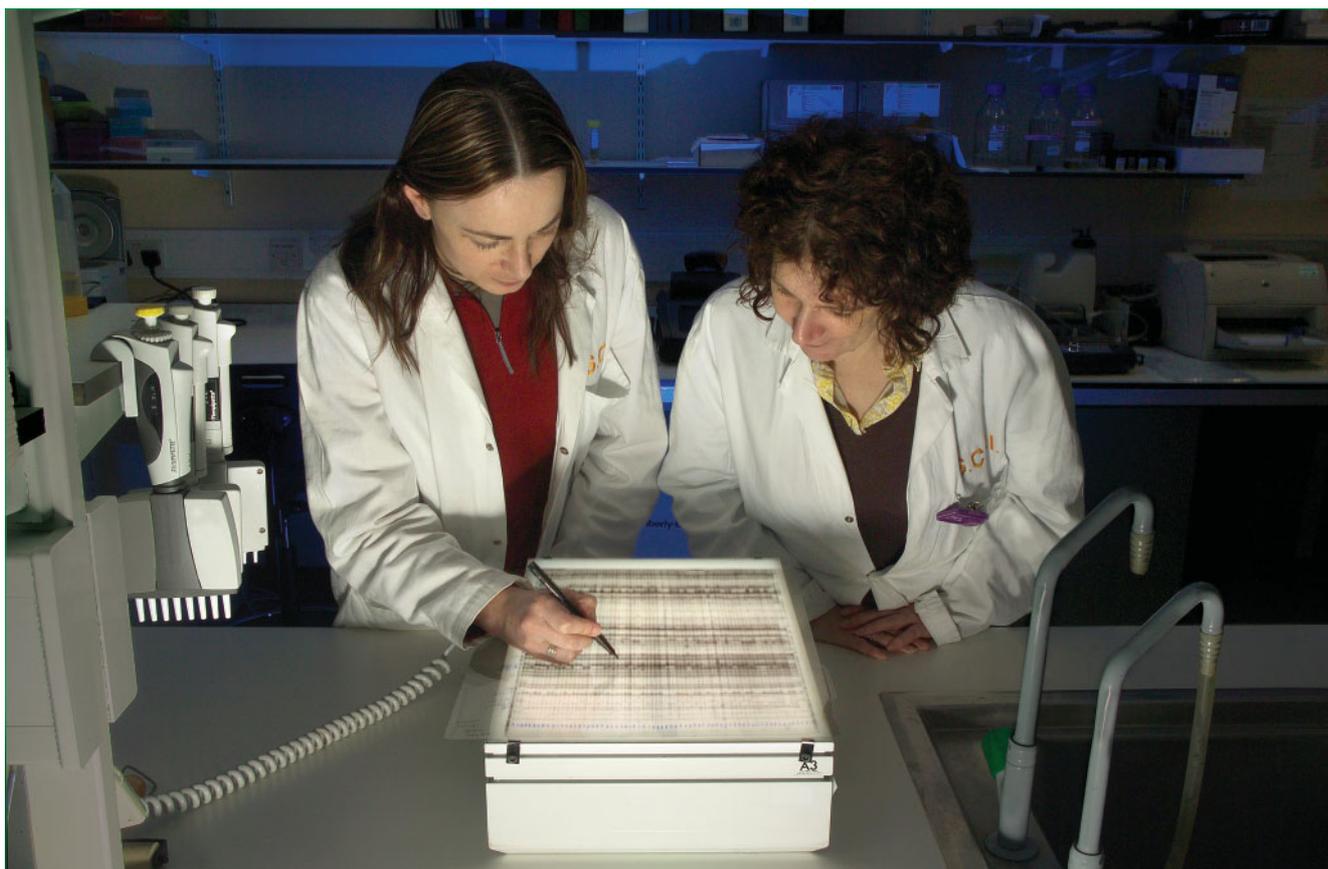


SCRI-bred blackcurrant cv. 'Ben Starav'

scored for these traits in a three-year field trial.

Cluster analysis of the marker data from this population revealed that the individuals formed two distinct sub-populations, with segregation ratios consistent with one sub-population having the two intended parents, and the other being selfed segregants. The latter sub-population provided useful additional information that improved the construction of the genetic linkage map: it provided a more informative estimate of recombination frequency than the crossed sub-population for some marker configurations, and also revealed the presence of two unlinked loci affecting viability, whose positions could be mapped approximately.

Quantitative trait locus (QTL) interval mapping was used to identify locations on the marker map that are associated with variation in the trait data. A single gene for gall mite resistance was mapped to linkage group 2. A total of five QTLs for developmental traits (bud break, first leaf, first flower and full flower) were identified. Three QTLs for pH were found, and two for ascorbic acid, one



Analysing mapping data

of which was close to the gene for gall mite resistance. Three QTLs for berry size were also found, two of which were close to the loci affecting viability in the selfed segregants.

This analysis provides a framework for the development of marker-assisted breeding strategies for blackcurrant, to improve breeding efficiency and time to cultivar. Further analysis, particularly of the quantitative traits, will require a larger mapping population, and this is currently in progress at SCRI with an extension of the 9328 population to 300 individuals. Additionally,

markers located close to the map position for gall mite resistance are currently undergoing validation across a range of diverse germplasm, with initial indications very promising in terms of a robust marker with utility within the SCRI blackcurrant breeding programme.

#### References

- Atkinson, C., Sunley, R., Jones, H.G., Brennan, R.M. & Darby, P. 2005. Defra desk study on winter chill in fruit. *Defra Report No. CTC 0206*.
- Brennan, R.M., Jorgensen, L., Woodhead, M. & Russell, J. 2002. Development and characterisation of SSR markers in *Ribes* sp. *Molecular Ecology Notes* **2**, 327-330.