

Developing molecular markers for quality traits in red raspberry



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Raspberry is a high value horticultural crop, interest in which is expanding due to benefits associated with human health¹. The production of red raspberries for fresh consumption has been revitalized by new horticultural strategies, specifically protected cultivation, and new cultivars adapted to their environment are essential for future expansion of the raspberry industry.

Commercial success in conjunction with environmental sustainability will ultimately depend on an understanding of the resources available in terms of genes controlling traits and the ability to combine desirable phenotypes in the same plant. The speed and precision of breeding can be improved by the utilization of genetic linkage maps which provide the basis to locate and manipulate quantitative traits in breeding programmes.

Marker assisted breeding is the attractive future for plant breeding and projects linking phenotype to genotype will greatly contribute to our understanding of the genetic control of commercially important traits and therefore our ability to combine desirable traits in the same cultivar.

The main quality traits of interest to producers and buyers alike are the overall appearance of the raspberry which includes not only size and colour but overall drupelet cohesion and shape. Second to that is the sweetness and sourness of fruit as well as the balance and intensity of the two combined. Fruit colour not only affects appearance, desirability and associated freshness but is also important for flavour perception.

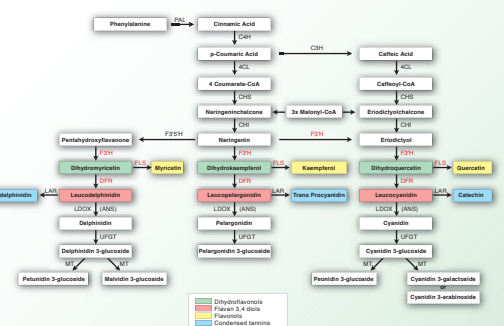
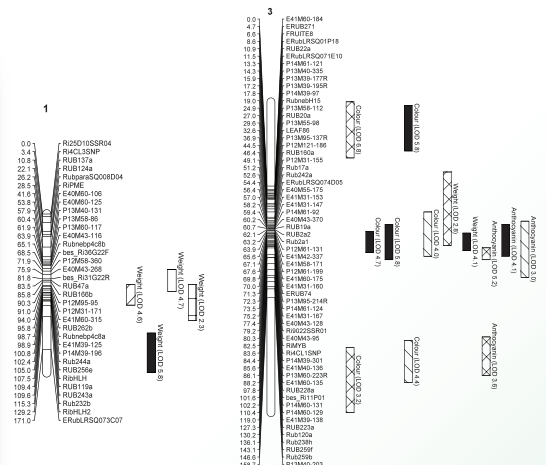
Results

Linking the phenotype of individual seedlings from a Glen Moy (large, pale red, moderately sweet) and Latham (small, sweet, dark red) cross to the actual genotype, was done to determine the genetic and environmental controls of flavonoid synthesis and ten berry weight across three fruiting seasons and three environmental locations (one open field and two protected sites).

Potential candidate genes related to the structural and functional synthesis of flavonoid components, including flavonol synthase (FLS), flavonoid 3'-hydroxylase (F3'H), glutathione S-transferase (GST), dihydroflavonol 4-reductase (DFR), O-methyl-transferase (OMT), anthocyanin reductase (ANR) and basic helix loop helix (bHLH), were mapped onto the *Rubus idaeus* linkage map^{2,3}. Several of these genes were found to underlie quantitative trait loci for quantitative and qualitative anthocyanin composition which is a major factor contributing to variations in fruit colour. No candidate genes were identified relating to ten berry weight measures but several SSR markers were identified which underlie QTLs contributing to variations in fruit size.



Glen Moy pictured from SCRi polytunnel site (left) and SCRi field site (right).



Conclusion

These studies can lead to the development of markers which can be screened for as part of a molecular assisted breeding strategy by identifying molecular markers linked to the quality traits of interest through phenotypic analysis as well as using a candidate gene approach.

References

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