

Understanding and then utilising the genetic basis of important traits including sensory quality and pest and disease resistance is a major challenge in a rapidly evolving market. With the increasing demand for high-quality fruit grown in low input/Integrated Crop Management (ICM) production systems, rather than the repeated pesticide/fungicide regimes that have been the norm for most producers, the main obstacle is a lack of cultivars resistant to some of the most damaging pests and pathogens, notably to raspberry root rot caused by *Phytophthora fragariae* var. *rubi*. In this case, no commercially viable resistant cultivars are available.

With the development of the raspberry genetic linkage map, the next stage is to define and delineate genetic traits relevant to pest and disease resistance, berry and fruiting quality and commercially acceptable plant architecture by the identification of trait-linked DNA markers. This will give breeders a tool kit for marker-assisted breeding technologies leading to the more rapid production of premium quality varieties with resistance to raspberry root rot and other pests and diseases of importance, thus enhancing the success of new varieties. For example, raspberry root rot has a devastating effect on many growers, rendering their plantations uneconomic and ultimately unsuitable for

raspberry production. The control measures for root rot involve the use of significant quantities of fungicide coupled with modified growing regimes. However, by mapping the genetic basis of resistance in the Latham Glen Moy cross, an understanding of the genetics of the resistance in Latham coupled with the development of diagnostic markers linked to disease resistance can be incorporated into future breeding programmes. The use of markers to detect disease resistance will greatly reduce the breeding time of new cultivars by eliminating the need for 3-4 years of glasshouse and field screening currently required per cross to identify resistant progeny. The linkage map developed here will provide an excellent genetic framework for qualitative and quantitative trait analysis for the Rosaceae. A major future thrust will be to move from anonymous markers to functional polymorphisms based on expressed sequence tagged simple sequence repeats (EST-SSRs) and single nucleotide polymorphisms (SNPs). Access to mapped markers will allow new approaches to breeding of complex traits that are difficult to manipulate in breeding programmes.

References

- ¹Graham, J., Smith, K., MacKenzie, K., Jorgenson, L., Hackett, C. & Powell, W. (2004) *Theoretical and Applied Genetics* **109**, 740-749