Raspberry mapping and marker-assisted breeding

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The raspberry industry in the UK is currently **L** worth £52 million, making it the third most valuable fruit crop after strawberries and dessert apples. With the move towards high-value fresh fruit produced under protected cultivation, there is great potential for a significant increase in production and, therefore, consumption of fresh raspberries, through the development of new premium fruit cultivars that are suitable for growth under low input regimes. Current estimates suggest only 6% of the UK population consume fresh

raspberries each season. For future expansion, new cultivars producing high quality fruit over a longer growing season and with genetically based durable pest and disease resistance must be developed. Breeding in raspberry, however, is time-consuming due to its highly heterozygous nature and relatively long period of juvenility.



Figure 1 Raspberry genetic linkage groups 1-3.

Understanding the genetic control of commercially and nutritionally important traits such as fruit quality and disease resistance and the linkage of these characteristics to molecular markers on chro-

mosomes is the future of plant breeding. This is now achievable in raspberry (Rubus idaeus), which is diploid (2 n = 2 x = 14)with a small genome (270 Mb). Over the last three years, we have produced genetic linkage map which is the key component of this strategy. The speed and precision of raspberry breeding will be improved by utilising this

genetic linkage map¹, to develop diagnostic markers for polygenic traits and the identification of genes controlling complex phenotypes. The raspberry genetic linkage map has been constructed from a fullsib family generated from a cross between two phenotypically different cultivars: the recent European cultivar, Glen Moy, released from SCRI in the 1980s and the older North American cultivar, Latham, estimated to be around 60% similar at the genetic level. Latham was one of the first cultivars produced through controlled breeding in the 1930s, and is an exceedingly hardy, extremely spiny, brown-caned, small, round, glossy-fruited plant with very sweet aromatic darkish fruit and, importantly, with resistance to raspberry root rot, yellow rust and cane spot. Glen Moy, released in 1981, in contrast, is a large conicalfruited cultivar with good, slightly sweet flavour, good sensory characteristics, susceptible to low temperature damage, spine-free and green-caned with other disease resistance including cane botrytis and spur blight. The map of the seven raspberry chromosomes, and incorporation of ever greater numbers of co-dominant molecular markers that enhance resolution, can be translatable into targeted breeding for traits that meet grower, retailer and ultimately consumer requirements.

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 markerassisted 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