Molecular breeding for root rot resistant raspberries suitable for low input growing systems

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BioSS

The UK raspberry industry is faced with new challenges in a rapidly-evolving market; with the shift of production to low input systems, under cover, and with the use of fewer pesticides. However, there is a lack of cultivars resistant to some of the most damaging pathogens, notably to raspberry root rot caused by *Phytophthora fragariae* var. *rubi*, which is one of the most devastating diseases of raspberry.

Breeders have limited resources and breeding can be more precise and rapid with the use of a genetic linkage map and the development and utilisation of diagnostic markers associated with genes that control complex QTLs. Marker-assisted selection offers the ability to select plants with the desired trait(s) accurately and at an early stage of growth. Rather than screening for a particular phenotype, a breeder can screen for a marker tightly linked to the gene of interest that is identified through the construction of a linkage map in a population segregating for that trait.

The key areas of this project are;

- Development of raspberry cultivars resistant to raspberry root rot (caused by *Phytophthora fragariae* var *rubi*) providing a source of high quality red raspberry fruit

- Development and application of molecular breeding protocols, identifying genetic markers linked to disease resistance loci

- Utilization of markers in breeding programmes for early selection of resistant cultivars

Glasshouse screening

Replicates of the Moy x Latham mapping population were inoculated with two types of *Phytophthora fragariae var. rubi*. Plant data such as root density and damage on a scale of 0 to 5 (figure 1) were collected and analysed for significant differences.

Figure 1: The roots of Glen Moy and Latham, where Glen Moy there is evidence of root rot; scale 5, and Latham roots are healthy and disease free; scale 0.

Field screening

The parents and the segregating population were planted and maintained at two environmental sites based at SCRI, one uninfected field (figure 2), and the other is heavily infested with *Phytophthora fragariae var rubi* (figure 3). Data was collected on plant health, growth, & viability and analyses of data for significant differences in all plant growth factors carried out.

Figure 2: Moy x Latham population at uninfected site

Figure 3: Moy x Latham Population at Infected site

To assist with accurate mapping of root rot resistance identified in glasshouse and field experiments, SSR's and EST-SSR's were developed and mapped

Results

Glasshouse
Significant differences were found between means for inoculated & control plants.

Latham has lower damage scores than Moy, with both treated and untreated plants.

Field results
Significant differences were found in plant growth between the two sites - highlighting the effect of the fungal disease on the plants.

Data on disease symptoms were analysed by BIOSS & placed in JoinMap

Two map regions were identified on linkage group I and VI. Interestingly results of root density and diameter parameters were also located on linkage group VI.
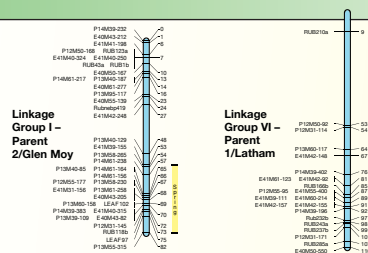

Linkage Group I – Parent 2/Glen Moy

Linkage Group VI – Parent 1/Latham

Figure 4: Latham (resistant) at infected site

Glen Moy (susceptible) at infected site

Summary & Next Phase

- Field results – map to areas where resistance and susceptibility are known, therefore need to further saturate with SSR's & AFLP's, including another 96 progeny to enhance map

- Further Data correlation from field and continue with glasshouse assessment

- New root rot site has been established at SCRI (figure 5) to verify results of the field trial in 2006

In summary, it has been noted that the areas on the linkage groups where the field results map to areas where resistance/susceptibility are known, need to be further saturated with SSR and AFLP markers, including another 96 progeny to enhance the map and reduce the confidence gap in these results, and investigate a whole range of germplasm to explore allele diversity. It is also interesting that early data on an earlier population, markers were also found to lie on Linkage Group I.

Figure 5: The new root rot trial established at SCRI