

Statistical contribution by BioSS to soft fruit research at SCRI

Christine Hackett, Katrin MacKenzie, Jim McNicol

State-of-the-art statistical analyses are an essential component of the soft fruit research at SCRI.

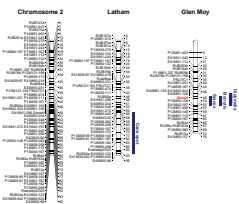
These analyses are undertaken in collaboration with Biomathematics and Statistics Scotland, BioSS, whose primary remit is "to support the research programme of the Scottish Executive through specialist advice and training, and to provide research in statistics and biomathematics."

This poster illustrates some of BioSS's recent inputs to the SCRI soft fruit programme.

Consultancy

Linkage analysis and disease mapping in raspberry

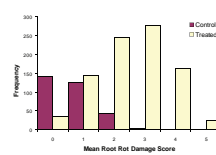
Raspberry linkage analysis has been carried out on a cross between the American cultivar Latham and the European Glen Moy. Glen Moy has hairy canes, controlled by a single gene, gene H. Linkage analysis mapped gene H to chromosome 2. QTL analysis showed that this region was associated with spines and increased resistance to botrytis and spur blight (*Didymella*). Latham has a QTL for resistance to cane spot on the same chromosome.



Raspberry Root Rot Glasshouse Trial

A glasshouse trial was set up to determine the susceptibility to raspberry root rot of 323 raspberry plants from a cross between Glen Moy (susceptible) and Latham (resistant).

The population was too large to test in a single batch, so 5 batches were formed. Latham, Glen Moy and a few offspring were repeated in more than one batch. A mixed model was used to combine root damage scores over batches.



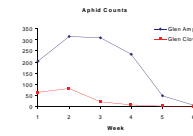
This data will be used in combination with field trial data to investigate whether glasshouse trials are equivalent to field trials for root rot infection.

Aphid Resistance in Raspberry

The aim of this experiment was to investigate factors affecting aphid numbers in raspberry plants. Aphid count data were collected from leaves on different cultivars, canes, positions on the cane eg top, middle, bottom. Data were collected weekly over 9 weeks in two years.



A generalised linear mixed model showed differences in aphid counts between cultivars and positions.



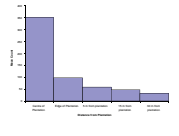
Controlling Raspberry Beetle

This project looked at the efficacy of sticky traps in catching Raspberry Beetle. Traps were set up in and around a raspberry plantation. Vials containing a chemical that attracts raspberry beetle were located beside each trap.



Analysis of variance shows that traps in the plantation collected significantly higher numbers of raspberry beetle than those outside with numbers falling off with distance from the plantation.

This experiment has led on to further experiments with different types of trap and different attractants.

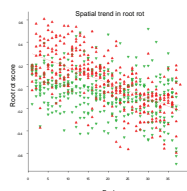


Research

Spatial analysis of raspberry root rot field trials

In large field trials, diseases may not occur uniformly. On a sloping field, moisture levels will vary and raspberry plants in the moister parts may have a higher pressure of root rot. A spatial analysis checks for trends in disease levels across the field trial and adjusts for it if present. This gives more precise comparisons among raspberry lines.

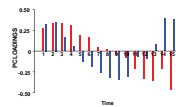
In this two-replicate trial, root rot scores were highest in the low numbered beds, especially in replicate one (red points). Disease levels decreased with increasing bed number. A linear model removed this spatial variation.



Gene expression during dormancy release in raspberry buds

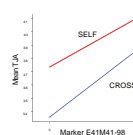
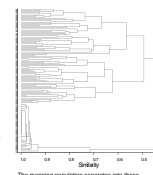
To help understand bud break in raspberry (*Rubus idaeus* L.) a microarray experiment was designed to follow changes in gene expression during dormancy transition. The 5300 probes were obtained from endodormant and paradormant raspberry bud cDNA libraries. RNA was extracted from buds (cv. Glen Ample) of canes immediately after removal from cold rooms at 15 consecutive time points, representing different degrees of chilling.

Principal component (PC) analysis of the 15-point expression profiles showed 96% (PC1) of the variation to be unrelated to chilling time, 2% (PC2) to be the contrast between early (prior to endodormancy) and later (paradormant buds) time points and 1% (PC3) to be the contrast between mid-time (dormancy transition) and all other times.



The first linkage map of blackcurrant

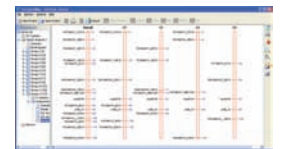
QTL analysis can be used to study the inheritance of juice quality and disease resistance traits in blackcurrant. This was complicated when some of the mapping population proved to come from self-fertilisation of the female parent. In effect, there were two related sub-populations. However estimates of distance between the markers were more accurate using the related subpopulations.



The two subpopulations also confirm the relationship between trait and markers. Here the presence of marker E41M41-98 on chromosome 3 increases titratable juice acidity in both the selfed and crossed populations.

Forward look: genetics of blueberry, an autotetraploid species

Methods for genetic linkage analysis and QTL mapping are well-established in diploid crops such as raspberry and blackcurrant. Autotetraploid crops require a specialised analysis. BioSS and SCRI have developed a programme, TetraploidMap, to analyse autotetraploid potato populations. In future we plan to adapt this to study blueberry genetics and to locate important blueberry genes for breeding programmes.



TetraploidMap shows potato chromosome IV

Training

SCRI's soft fruit researchers have taken part in the following training courses developed by BioSS:

- Basic Statistics
- Experimental Design and Analysis of Variance
- Graphical Methods for Multivariate Data
- Statistical Methods for Repeated Measures Data
- An Introduction to Sequence Analysis
- Phylogenetic Trees from Molecular Sequences
- Statistical Design and Analysis of Microarray Experiments
- Linkage analysis and QTL mapping in plants

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