

Advances in Rubus Genomics

Mary Woodhead, Julie Graham, Kay Smith, Ailsa Weir, Christine Hackett & Nikki Jennings
SCRI, Invergowrie, Dundee DD2 5DA.

Introduction

A cross between Glen Moy and Latham forms the basis of the Rubus genetic linkage map and a framework to begin linking genotype to phenotype for traits e.g. fruit ripening¹ and quality², cane characters and disease resistance³. Linkage groups 2, 3 and 6 are important for many traits. Work is underway to populate these regions with new markers and to begin identifying Rubus BAC clones to allow the regions to be sequenced.



Figure 1: Cane hairs



Materials & Methods

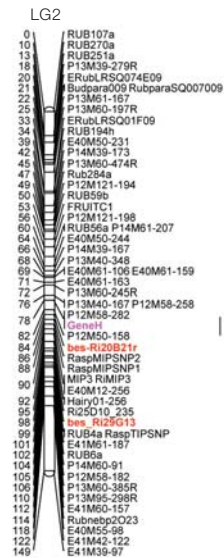
Candidate genes identified from Rubus ESTs⁴ and from other Rosaceae are being mapped. Markers close to traits of interest have been used to screen the Rubus BAC library. BAC clones are being mapped and sequenced.

Results

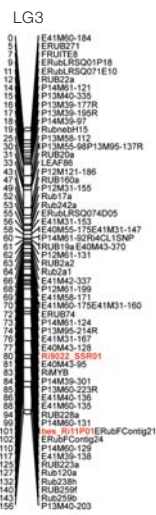
Linkage group 2 – QTLs for cane diseases, fruit quality & time to ripening are located on linkage group 2. The Gene H region is particularly important for several traits e.g. cane hairs (Fig. 1), disease resistance and ripening. BAC_20B21 (~130kb) is ~6 cM from Gene H and is being sequenced. To date a PROTODERMAL FACTOR2 like gene, (involved in epidermal cell differentiation) and several SSRs have been identified and are being mapped.

Linkage group 3 – QTLs for root rot, cane splitting and fruit quality and ripening are located on linkage group 3. Sequencing of BAC9O22 (~140kb) at ~80 cM is underway. So far a MYB 11 like gene and an AP2 aintegumenta-like transcription factor, (controls plant growth and development in response to developmental or environmental signals) have been identified.

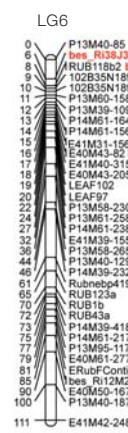
Linkage group 6 – QTL for many traits are located at the top of this group, most notably root rot, fruit volatiles and cane splitting. BAC38J03 (~150kb) spans ~2 cM and is being sequenced. New markers derived from the BAC are being assessed for mapping purposes.



Spines & Borlysis
Ripening
Colour



Fruit set/ripening
Spines
Cane Splitting
Root Rot



Fruit Colour
Fruit Volatiles
Root Rot
Cane Splitting
Fruit Ripening

Discussion & Future Work

- Using the Rubus genetic linkage map and QTL data we are targeting regions of importance and using the BAC library to begin to develop physical maps.
- BAC sequencing of key regions will continue.
- More markers and new traits will be added to the map - aiming for marker assisted breeding.
- Preparing for 454 sequencing of Moy & Latham cDNAs for SNP identification and mapping.
- Longer term, sequencing of the raspberry genome (275 Mbp) is being considered.

References

- Graham *et al.* TAG, accepted (2008)
- Kassim *et al.*, Mol. Nut. Food Res., In Press (2008)
- Graham *et al.*, TAG, 112, 818-831 (2006)
- Woodhead *et al.*, Mol. Breeding, 22, 555-563 (2008)