



Blackcurrant breeding at the James Hutton Institute: present and future prospects

Rex Brennan,
Fruit Breeding Group, JHI

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Future-proofing berryfruit
CLIMAFRUIT

Ribes Breeding

- *Ribes* – member of Saxifragaceae (no related crop members)
- All spp. diploid
- Blackcurrant world production *ca.* 137k tonnes
- Added value through processing
- Breeding at SCRI for juice processing since 1970
- Also breeding for fresh market since 2006
- SCRI cultivars commercially successful globally



Recent SCRI Blackcurrant Cultivars



Ben Avon



Big Ben*



Ben Dorain



Ben Gairn



Ben Vane



Ben Hope



Ben Klibreck



Ben Maia*



Ben Starav



Ben Finlay

* Fresh market cv.

Breeding Objectives

Fruit quality

- Brix/acid ratio
- Low total acidity
- Anthocyanin levels (dephinidins preferred)
- Vitamin C (AsA)
- Sensory traits

Agronomic

- Environmental resilience
- Pest resistance for low-input growing
- Acceptable yield

Trial seedlings from GSK/JHI breeding programme



JHI 9265-6

Late mid season cv.

Tall vigorous growth

Good yields at Ben Hope/Alder levels



JHI 92127-1

Early mid season

Yields good in trials in 2009 & 2010

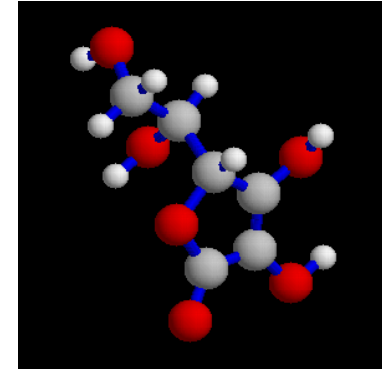
Very stocky upright growth, with dense foliage
High anthocyanins, medium AsA

Good 'hangability' (only 10% drop after 14 days)

Marker targets

■ *Ribes*-specific traits

- Single gene traits, eg. pest resistance
- Quantitative traits, eg. nutritional components in fruit (AsA, Acy)

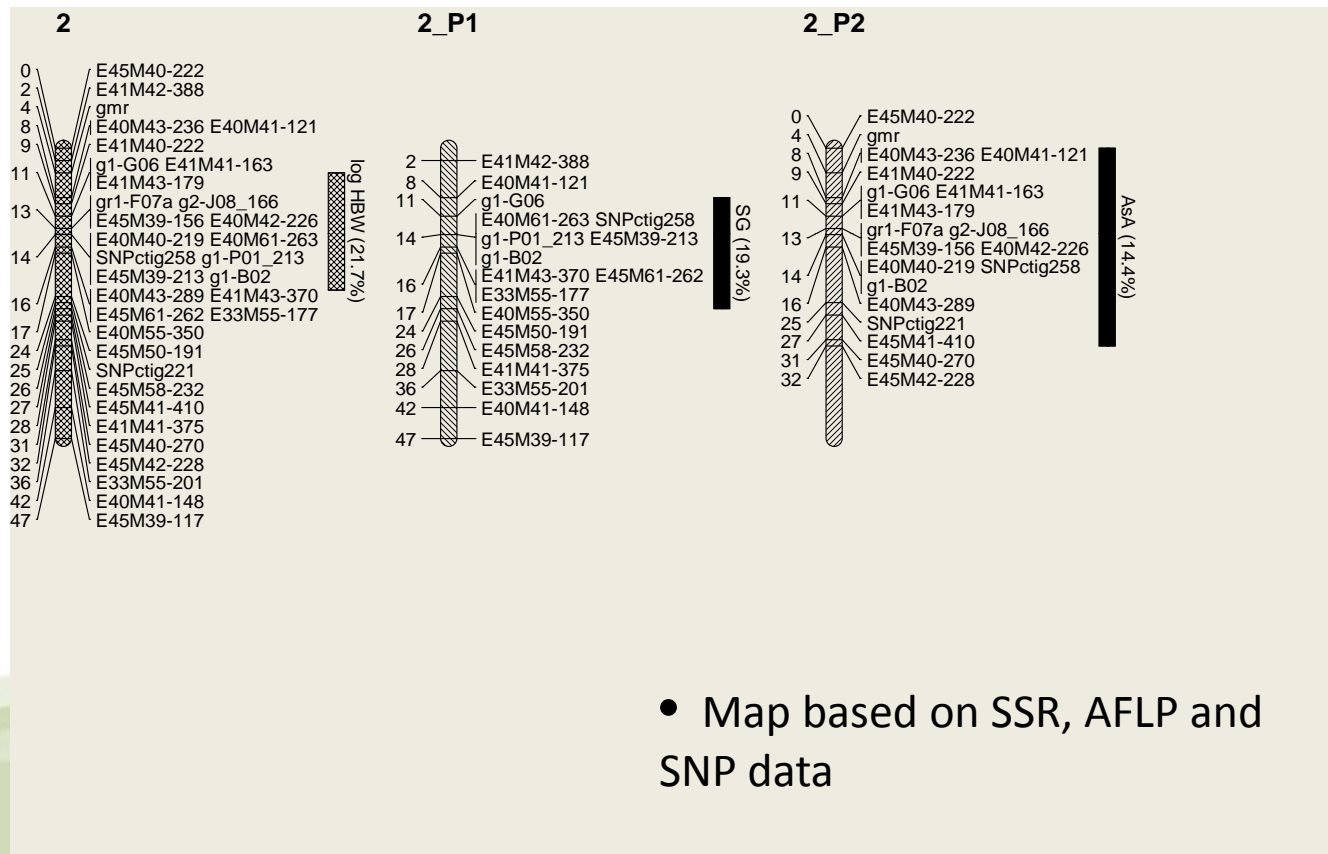


■ Generic

- Quantitative traits, eg. dormancy



Linkage Map Development



- Map based on SSR, AFLP and SNP data

Blackcurrant Gall Mite (*Cecidophyopsis ribis* Westw.)

- Highly host-specific eriophyid mite, producing galling of buds ('big bud')
- Sole vector of Blackcurrant Reversion Virus (BRV)
- Difficult to control
 - Until 1990 – Endosulfan
 - 1990-2005 – Fenpropathrin
 - 2005 – present – sulphur
- Resistance derived from gooseberry (*R. grossularia*), controlled by single gene *Ce*
- Introgressed into blackcurrant (*R. nigrum*) in 1970s at East Malling
- Extensive backcrossing to restore key fruit quality traits
- Now at BC₀ - commercial releases now emerging ('Ben Finlay', 2009)
- Identification of resistant plants – field infestation plot for 4 years



Section through
mite-infested bud



'Big bud' symptoms



Mite infestation
plot, Dundee 2006

Gall mite marker

- Maps to within 4-5 cM of phenotype resistance on linkage map

- Accuracy in test genotypes *ca.* 95%

- Mapping population
- Cultivars
- Trial lines

- **Marker now routinely deployed in SCRI breeding programmes as a breeding tool**

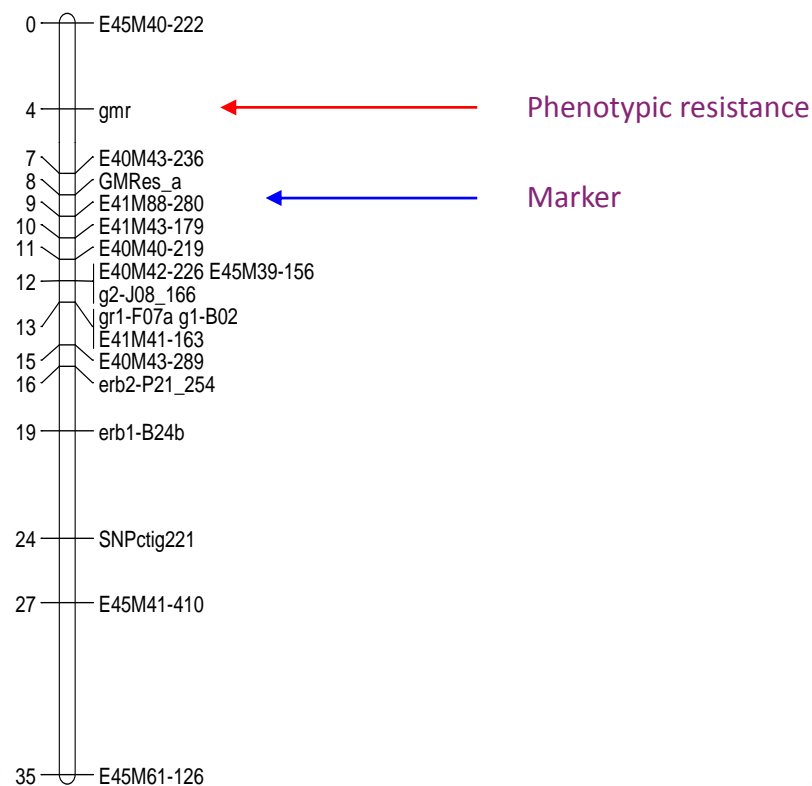
- **2009** First trial lines selected using marker, seedling progenies tested during year

- Field infestation plot removed

- **2011 Separate plots of exclusively resistant material initiated**

- Material tested for other programmes, eg. ISK, Poland

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Resistant Lines in Trial

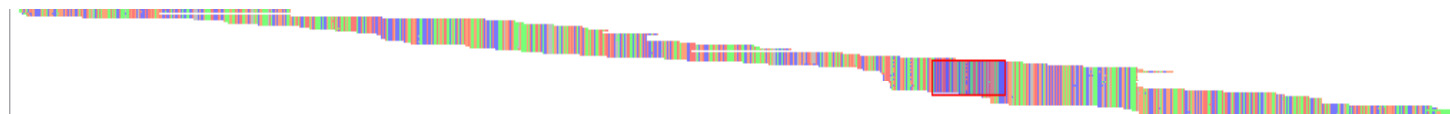


Mite-resistant cv. :
Ben Finlay
(released 2010)

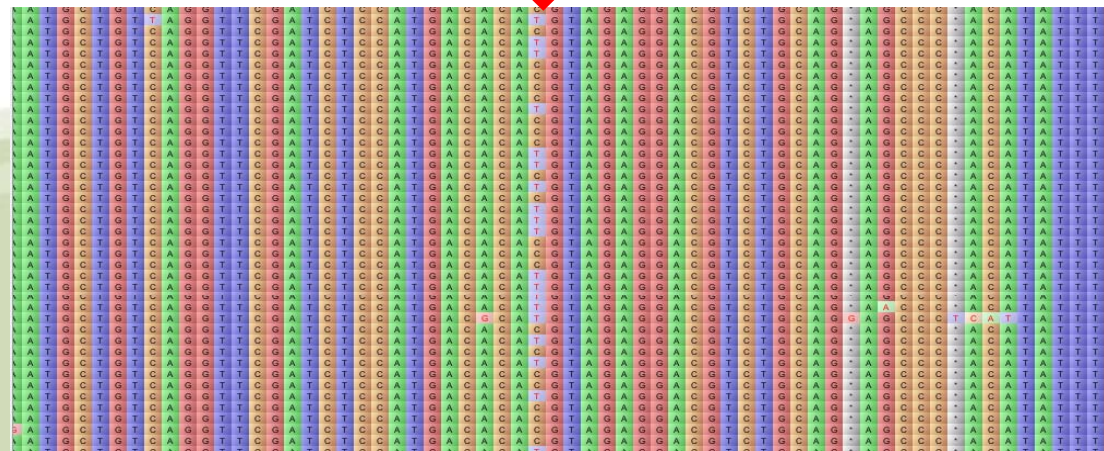


Next Generation Sequencing in *Ribes*

- Large scale 454 transcriptomic sequencing of two *Ribes* genotypes (9328 reference mapping parents)
- 526293 reads (117.9 Mbp of blackcurrant transcriptome)
- Reads assembled into 46411 contigs
- 7245 SNPs and 3179 SSRs discovered
- Set of 384 SNPs representing heterozygous categories for one or both parents selected using 'Tablet' programme for validation on Illumina BeadXpress platform
- New SNP-based linkage map developed, markers and trait associations in progress *



SNP



* Russell *et al.* (2011)
Identification, utilisation and
mapping of novel
transcriptome-based markers
from blackcurrant (*Ribes
nigrum*) **BMC Plant Biology**
(in press)

Trait associations

● Fruit quality traits

Metabolomic analysis for sugars, organic acids and phenolics

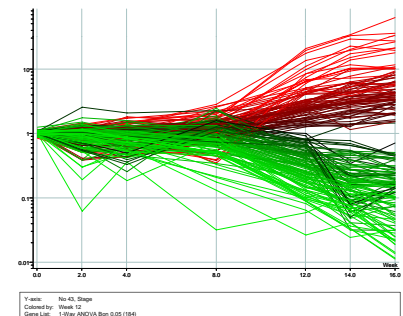
Putative QTL developed on SNP map, validation in progress

● Dormancy-related traits

Differentially-regulated genes identified using microarrays mapped to LG3 on original linkage map in area where QTL for budbreak and flowering is located

Ongoing analysis using SNP map and diverse germplasm including population segregating for chilling requirement with Plant and Food (NZ)

Significance for future sustainability of blackcurrant production



Summary

- Marker-assisted breeding strategies are now being used in blackcurrant
- Screening using PCR-based marker linked to gall mite resistance is now a routine part of the breeding programme at JHI, and new resistant lines are in commercial trials
- SNP platform developed from NGS in *Ribes* offers real opportunities for developing marker-based selection for key quality and developmental traits in a minor fruit crop
- Longer-term aim is to move breeding towards genomic selection approaches – genotyping by sequencing is now being investigated in blackcurrant



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BioSS

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