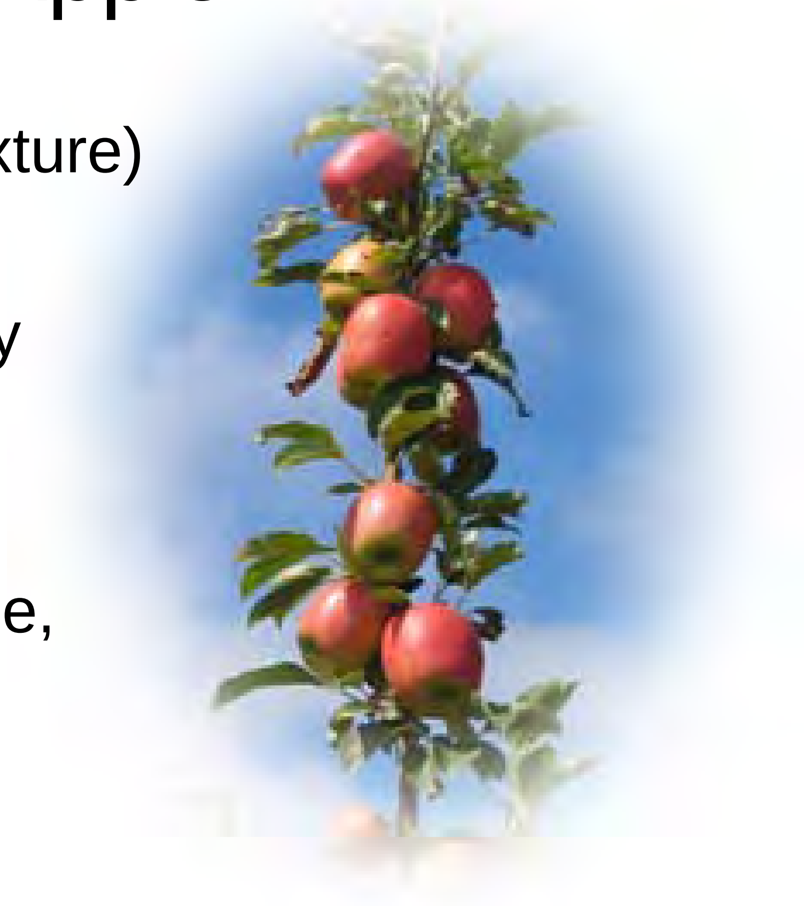
Fruit and Nut Trees
Genomics and Quantitative Genetics

Jasper Rees
Department of Biotechnology
University of the Western Cape
South Africa
jrees@uwc.ac.za

The Challenges of Tree Breeding

- Long breeding cycles – long juvenile periods
- Heterozygous germplasm – lots of variation
- Self-incompatibility – no backcrossing
- Many breeding objectives
  - Fruit quality
  - Post harvest issues
  - Disease resistance
  - Climatic adaptation
  - Horticultural characters

The Perfect Apple



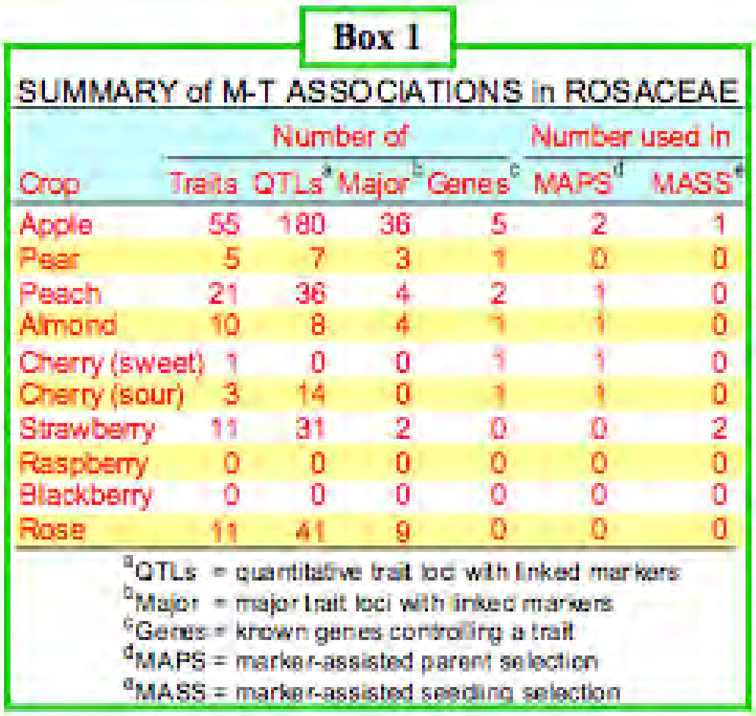
- Fruit quality (colour, flavour, texture)
- Disease resistance
- Chilling requirements/dormancy
- Flowering/fruiting time
- Precocious flowering
- Post harvest properties (disease, maturation)
- Plant development/structure

Current Apple Genetic Maps

- Mostly SSR based (200-600 markers)
- Easily portable markers
- Wide range of mapping populations
- Integrated mapping with FlexQTL
- DArT marker maps giving up to 800 markers
- SNP maps currently being developed, will give from 1000-100 000 markers depending on design.

QTL Mapping in Fruit

- Many QTLs mapped
- In some cases in large linked populations
- Population sizes vary from 40-600 progeny
- Synteny analysis provides important additional information



Box 1

SUMMARY of M-T ASSOCIATIONS in ROSACEAE

	Number of				Number used in	
Crop	Traits	QTLs[a]	Major[b]	Genes[c]	MAPS[d]	MASS[e]
Apple	55	180	36	5	2	1
Pear	5	7	3	1	0	0
Peach	21	36	4	2	1	0
Almond	10	8	4	1	1	0
Cherry (sweet)	1	0	0	1	1	0
Cherry (sour)	3	14	0	1	1	0
Strawberry	11	31	2	0	0	2
Raspberry	0	0	0	0	0	0
Blackberry	0	0	0	0	0	0
Rose	11	41	9	0	0	0

[a] QTLs = quantitative trait loci with linked markers

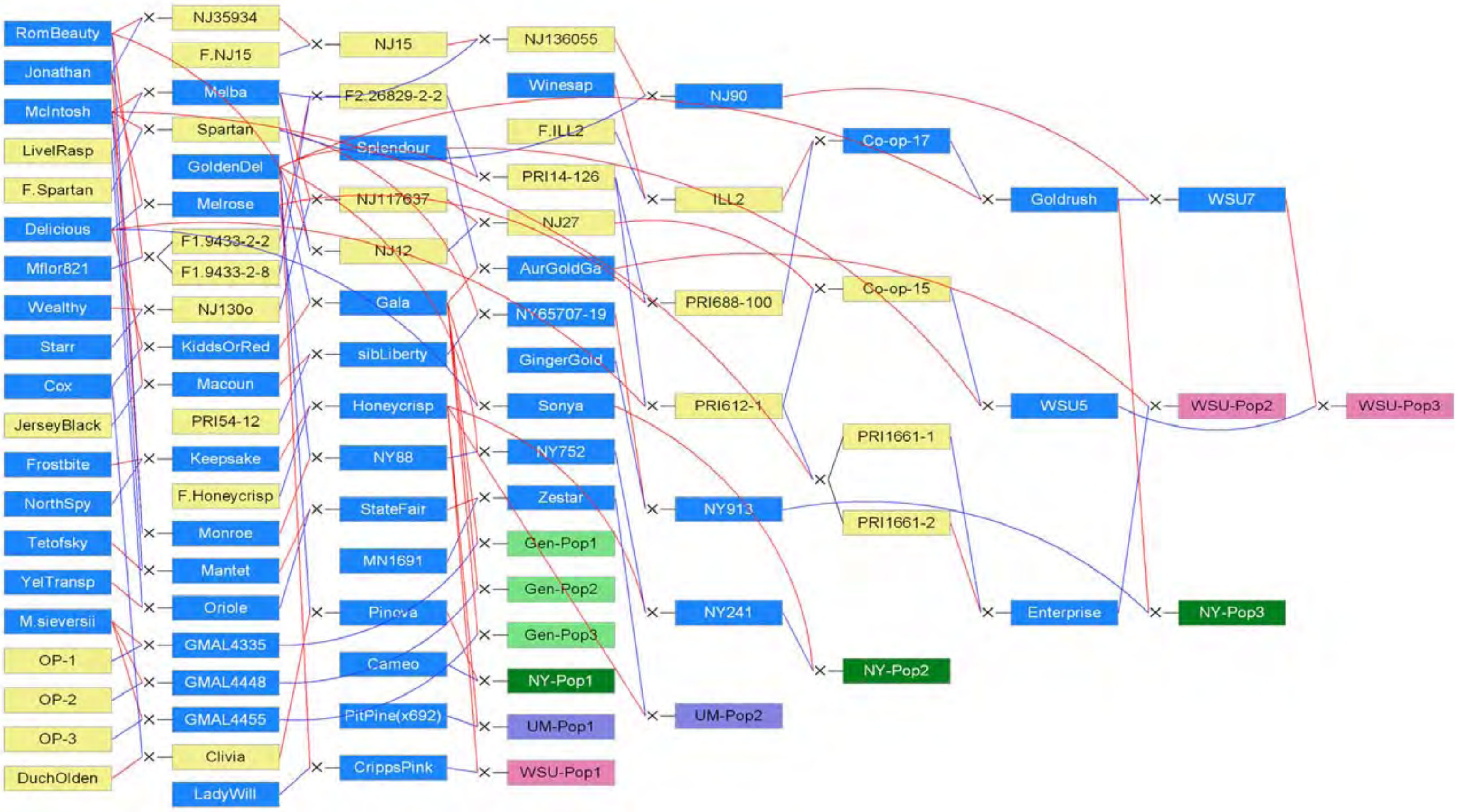
[b] Major = major trait loci with linked markers

[c] Genes = known genes controlling a trait

[d] MAPS = marker-assisted parent selection

[d] MASS = marker-assisted seedling selection

Pedigree Mapping – for Linkage by Descent and integrated QTL maps



Fruit and Nut Tree Genomics Ongoing genome sequencing

- Published
  - Grape (2 variants, more in progress)
- First drafts about to be published
  - Apple – diploid Golden Delicious
  - Peach – doubled haploid Lovell
  - (Strawberry – diploid *F. vesca*)
- Projects in progress or planned
  - Citrus, Mango, Banana, etc
  - Hazelnut, walnut, chestnut, cacao, coffee
- Lots or other species in need of genomics and genetics

Genome resequencing

- Apple: 30 founders and selections being resequenced at 5-10x coverage
- Peach: up to 20 genotypes being resequenced
- SNP development will depend on the level of use expected from SNP chips and the number of SNPs required for analysis
- Rosaceae SNP chip towards the end of 2010

Next Generation Transcriptomics

- *de novo* sequencing and assembly work well to give representative transcriptomes
- Quantitative re-sequencing generates data that is better than micro-arrays
- Sample multiplexing increases throughput
- Increases in throughput mean that costs are rapidly becoming affordable

Pathogen and virus genomics

- Fungal, bacterial and viral genome and transcriptome studies just starting
- NGS producing exciting data from all systems
- Opens the way to understanding biology and developing control strategies

de novo genome sequencing

- Current NGS technologies provide a good basis for draft genomes
- Critical issue is length of paired end inserts used
- Computation issues rapidly becoming less important
- Need to link back to genetic maps: SNP-Seq
- Maybe no need for traditional physical maps
- Will soon be possible to generate *de novo* sequences without physical or genetic maps

Whole Genome Resequencing

- Whole genome sequencing
- Reduced Representation Re-Sequencing
- How deep to cover?
  - 1 X from many genotypes
  - 5 from fewer genotypes
  - 30x from 10% coverage?
- Depends on the application
- Soon becomes irrelevant because of increased throughput, decreased costs
- Expect to sequence whole genomes of mapping populations by 2012

3rd Generation Sequencing

- Hugely increased throughput
- Ultra-long reads
- Problems with heterozygosity will be avoided
- *de novo* assemblies will become simpler, allowing all crop genomes to be accessible
- Will derive extensive haplotype information from sequence data

Next Generation Tree Breeding

- Need early flowering transgenics (flower in first year) – already available for citrus, apple and plum
- High throughput genotyping tools
- Whole genome resequencing
- Association genetics and quantitative genetics
- eQTLs and mQTL studies
- Highly standardised phenotyping

Phenotyping

- Absolute requirement for application of genomics to breeding
- Must be high quality, and quantitative
- Needs good statistical designs
- Technical and biological replication
- Lots and lots and lots of data!

Are these technologies for the developing world?

- YES!
- Through collaboration, investment and capacity development
- Using integrated pipelines that link breeding to genomics across country boundaries
- With Biotech platforms and hubs
- And simplified point-of-use genomics technology

UWC Life Sciences
Opened 2010