Queensland Government

Mango in Queensland

- Valued at >$A60M annually
- Kensington Pride has over 60% of the market
- Out of the breeding program
  - R2E2
    - Selected in 1982
    - Released into production in 1991
  - Calypso
    - Released in 2007
  - Three new varieties released in 2014

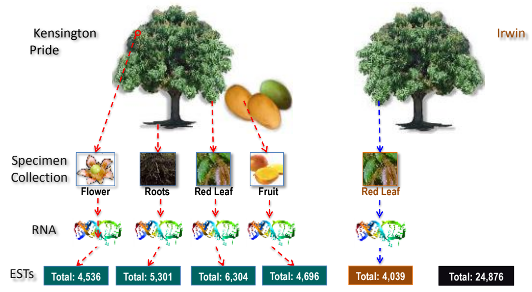
Mango Genomics Initiative

- Starting in 2005 with a view to:
  - Indentify genes and markers for traits of interest
    - Fruit colour and flavour
    - Novel bioactives
    - Production traits – small tree, high productivity initiative
  - Toolkit for mango breeders
  - Improved breeding efficiency / targeted breeding
- Multidisciplinary project
  - Breeding
  - Physiology
  - Pathology
  - Molecular biology
  - Sensory
  - Consumer

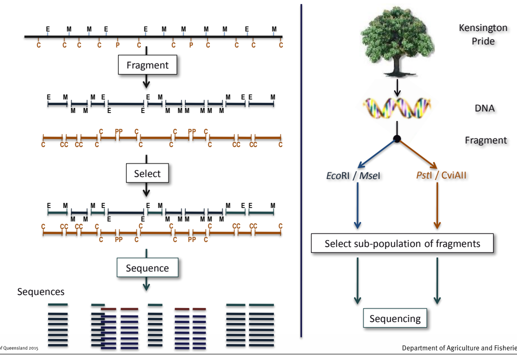
Mango Genomics Initiative

- Resources
  - A long history of successful mango breeding
  - Global collection of over 300 mango accessions
    - All with molecular fingerprints
      - SSRs (Dillon et al, 2013)
      - SNPs being done in collaboration with Dr David Kuhn
  - Four (4) Hybrid mapping populations
    - All share Kensington pride as male parent

Mango Genes



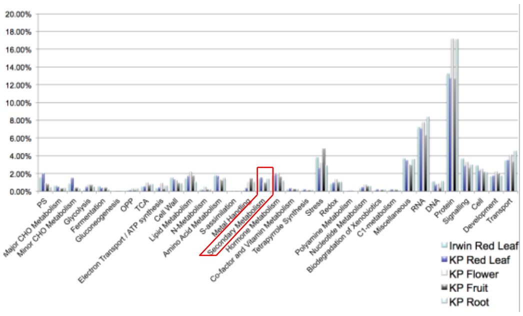
Genome Complexity Reduction



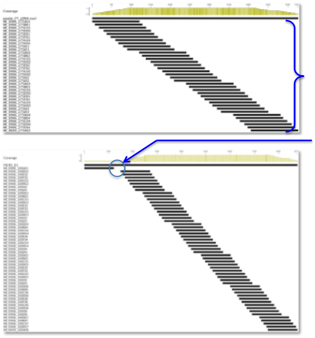
Sequence Data

Library	Type	Annotated Sequences	No Annotation	Number of Sequences	Average Seq Length
KP Red Leaf	cDNA	5,290	1,014	6,304	473
KP fruit skin	cDNA	4,518	177	4,695	623
KP Flower	cDNA	4,215	285	4,500	550
KP Root	cDNA	5,242	60	5,302	704
Ir Red Leaf	cDNA	3,463	576	4,039	564
Total	cDNA	22,728	2,112	24,480	579
EM Library	Genomic	4,909	77,132	82,041	111
PC Library	Genomic	12,819	56,942	69,761	141
Total	Genomic	17,728	134,074	151,802	124
Total	**All**	**40,456**	**136,186**	**176,282**	

Fishing for Sequences



Preparing the Bait

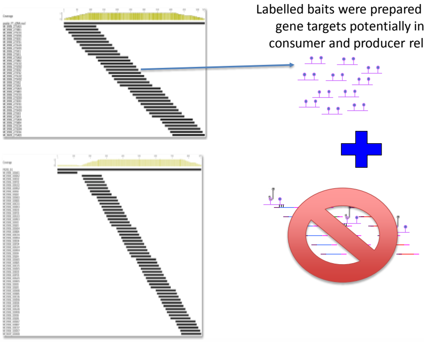


cDNA sequence

Tiled 120 base oligo arrays

Remove probes that
- Contain regions of low complexity
- Contain repetitive DNA
- Are complementary to other probes in the set
- Target more that one sequence

Preparing the Bait



Labelled baits were prepared for over 250 gene targets potentially involved in consumer and producer related traits

Labelled baits

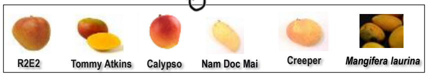
Fragmented Genomic DNA

Going Fishing

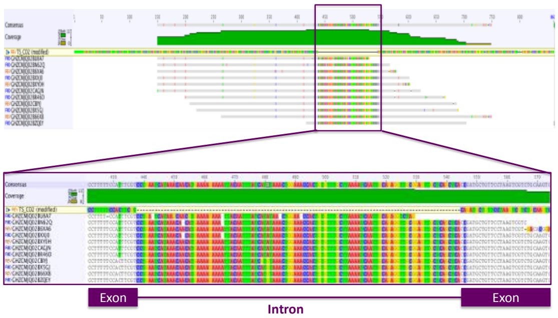

Irwin

Baits designed based on KP (mostly) sequences were used to fish out sequences from 15 mango accessions


KP

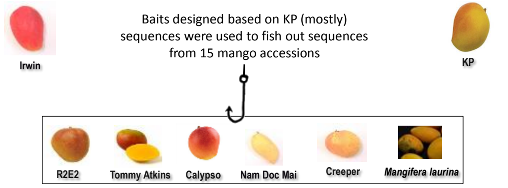


Sequencing Results



Targeted Sequencing

Going Fishing



Baits designed based on KP (mostly)
sequences were used to fish out sequences
from 15 mango accessions

144 SNPs contributed to the generation of a mango linkage map (Dr David Kuhn USDA)
80 genes potentially involved in plant structure / flowering were used to design 45 SNP assays of which 21 were applied to the Creeper x KP population

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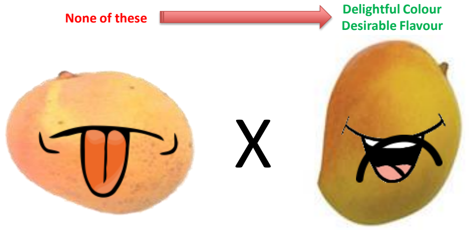
Sequencing the Kensington Pride Genome

- In July 2015, a joint initiative lead by Horticulture Innovation Australia Ltd and
  - Department of Agriculture and Fisheries (Qld)
  - International Crop Research Institute for the Semi-Arid Tropics (ICRISAT)
  - Beijing Genomics Institute (BGI)
- Strategy
  - Libraries insert sizes: 170, 200, 500, 800, 2000 and 5000 bp
  - 87 Gb of cleaned reads
  - SOAP de novo assembly
- Very preliminary results
  - N50: Contig - 16 kb; Scaffold - 129 kb
  - Genome size 407 Mbb
  - Depth: 210X
  - Highly heterozygous

The King of Kings*

Creeper | **Kensington Pride (KP)**



None of these

Delightful Colour
Desirable Flavour

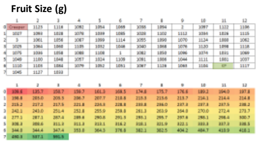
Small tree architecture

Excessive vigour
Irregular bearing

* At least it is in Australia

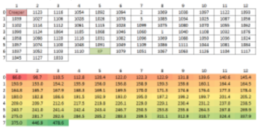
Creeper x KP

Fruit Size (g)

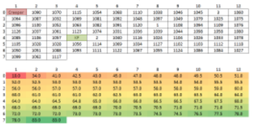


Pulp Colour

Flesh Weight (g, No seed)



Trunk Diameter (mm, above graft)

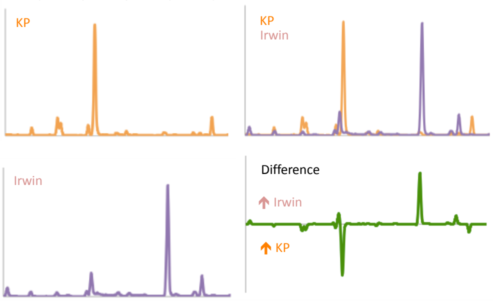


Aroma, Flavour and Colour

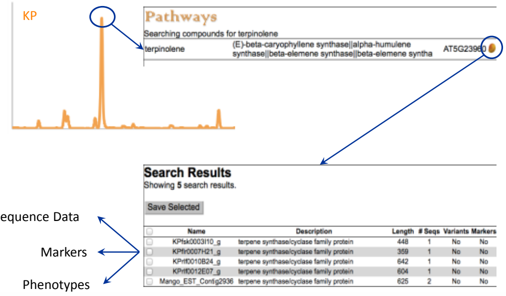
Zoom (15 – 20 mins)

Overlay

Difference



Pulling It All Together



Pathways

Searching compounds for terpinolene

terpinolene (E)-beta-caryophyllene synthase||alpha-humulene synthase||beta-elemene synthase||beta-elemene syntha AT5G23960

Search Results

Showing **5** search results.

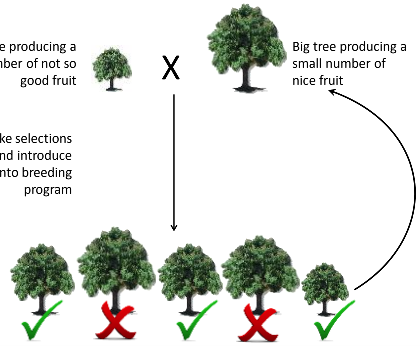
☐	Name	Description	Length	# Seqs	Variants	Markers
☐	KPfsk0003I10_g	terpene synthase/cyclase family protein	448	1	No	No
☐	KPflr0007H21_g	terpene synthase/cyclase family protein	359	1	No	No
☐	KPrlf0010B24_g	terpene synthase/cyclase family protein	642	1	No	No
☐	KPrlf0012E07_g	terpene synthase/cyclase family protein	604	1	No	No
☐	Mango_EST_Contig2936	terpene synthase/cyclase family protein	625	2	No	No

Sequence Data

Markers

Phenotypes

Conventional Breeding



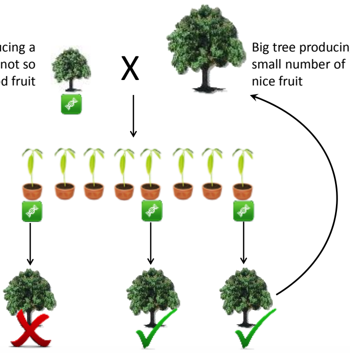
Small tree producing a large number of not so good fruit

X

Big tree producing a small number of nice fruit

Make selections and introduce into breeding program

Marker Assisted Selection



Small tree producing a large number of not so good fruit

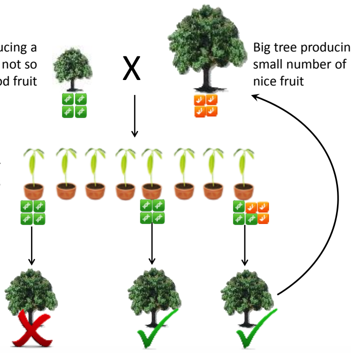
X

Big tree producing a small number of nice fruit

Check for marker In seedlings

Make selections and introduce into breeding program

Marker Assisted Selection



Small tree producing a large number of not so good fruit

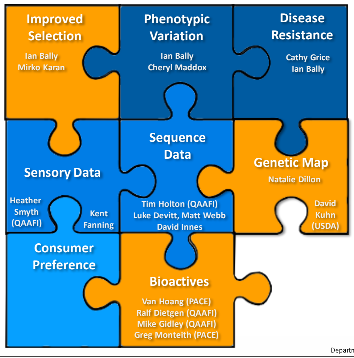
X

Big tree producing a small number of nice fruit

Check for marker In seedlings

Make selections and introduce into breeding program

All Together In One Place



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