

Gwen Progeny Mapping Population

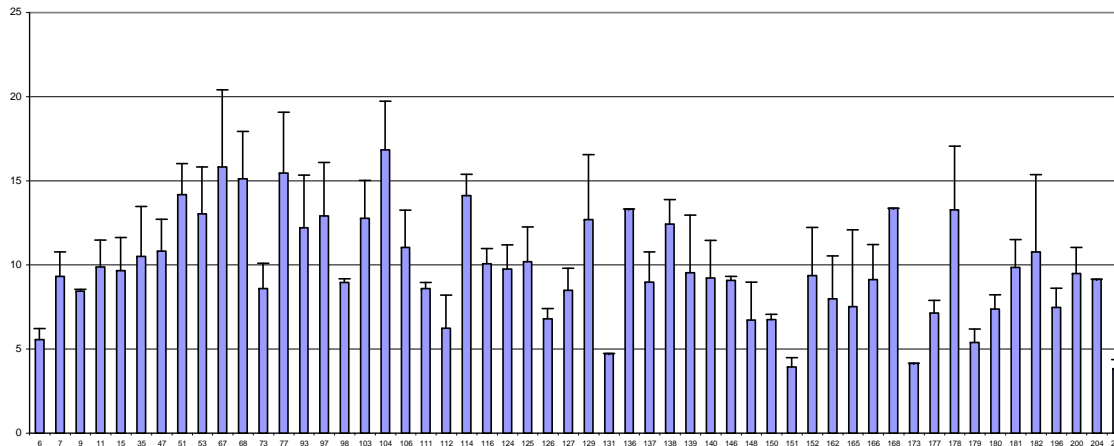
Avocado Genetics and
Plant Improvement Meeting
11–13 January 2012, UCR

Harley Smith, Mary Lu Arpaia; Michael Clegg

*Carlos Calderón, Mary Durbin, Livia Tommasini,
Haofeng Chen, Vanessa Ashworth*

Our work to date:

- Since 1999
- establishment of experimental population
- phenotypic measurements (clonal replication)
- markers developed: SNPs, SSRs
- linkage map developed
- implementation of MAS in progress



Experimental Population

- Progeny of 'Gwen'
- 204 distinct genotypes
- Duke 7 rootstock
- 4 clonal replicates
- Two locations (Riverside, Irvine)
- Two randomized blocks per location
- Planted out 2001-2003



Irvine



Riverside



Pollen Sources of Mapping Population

- 54 Fuerte
- 49 Bacon
- 44 Zutano
- 56 miscellaneous
- 1 self (!)



Mean effect of different pollen donors

	Height (cm/mo)	Canopy Diameter (cm/mo)	Trunk Diameter (cm/mo)	Flower Abundance	Fruit Set
Bacon	5.931(A,B)	6.045(B)	0.226(A)	1.965(A)	1.410(B)
Fuerte	5.002(C)	6.482(A)	0.213(A)	1.418(C)	1.385(B)
Zutano	5.774(B)	5.241(C)	0.197(B)	1.846(A)	1.614(A)
Mixed donor	6.289(A)	6.484(A)	0.223(A)	1.604(B)	1.446(B)

*A, B and C: significantly different ($p < 0.05$); measured 2002-2005
(Chen et al. 2007)

Initial SNP development:

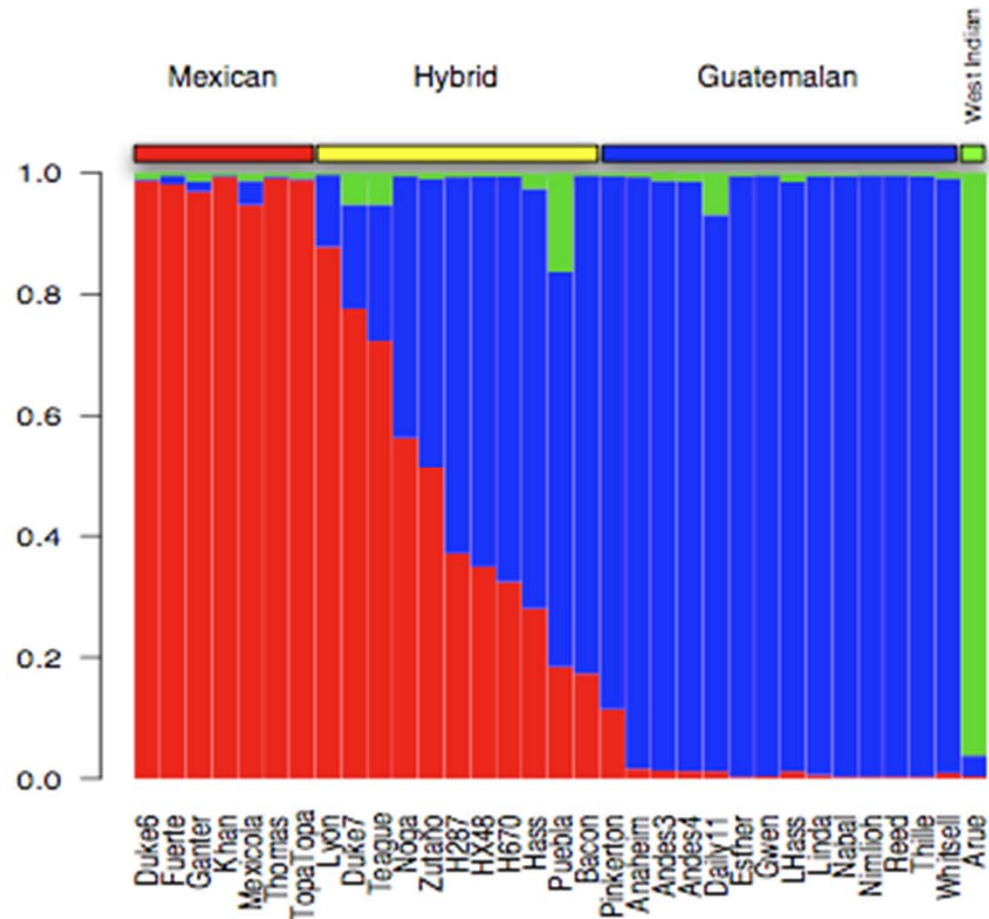
213 SNPs in 4 genes (5690 bp of DNA)

sequenced in 33 cultivars and 21 wild accessions

(Chen et al. 2009)

- Cellulase
- Chalcone synthase
- Flavonol-3-hydroxylase
- Serine-threonine kinase

Population structure analysis (Structure software)



SNP development:

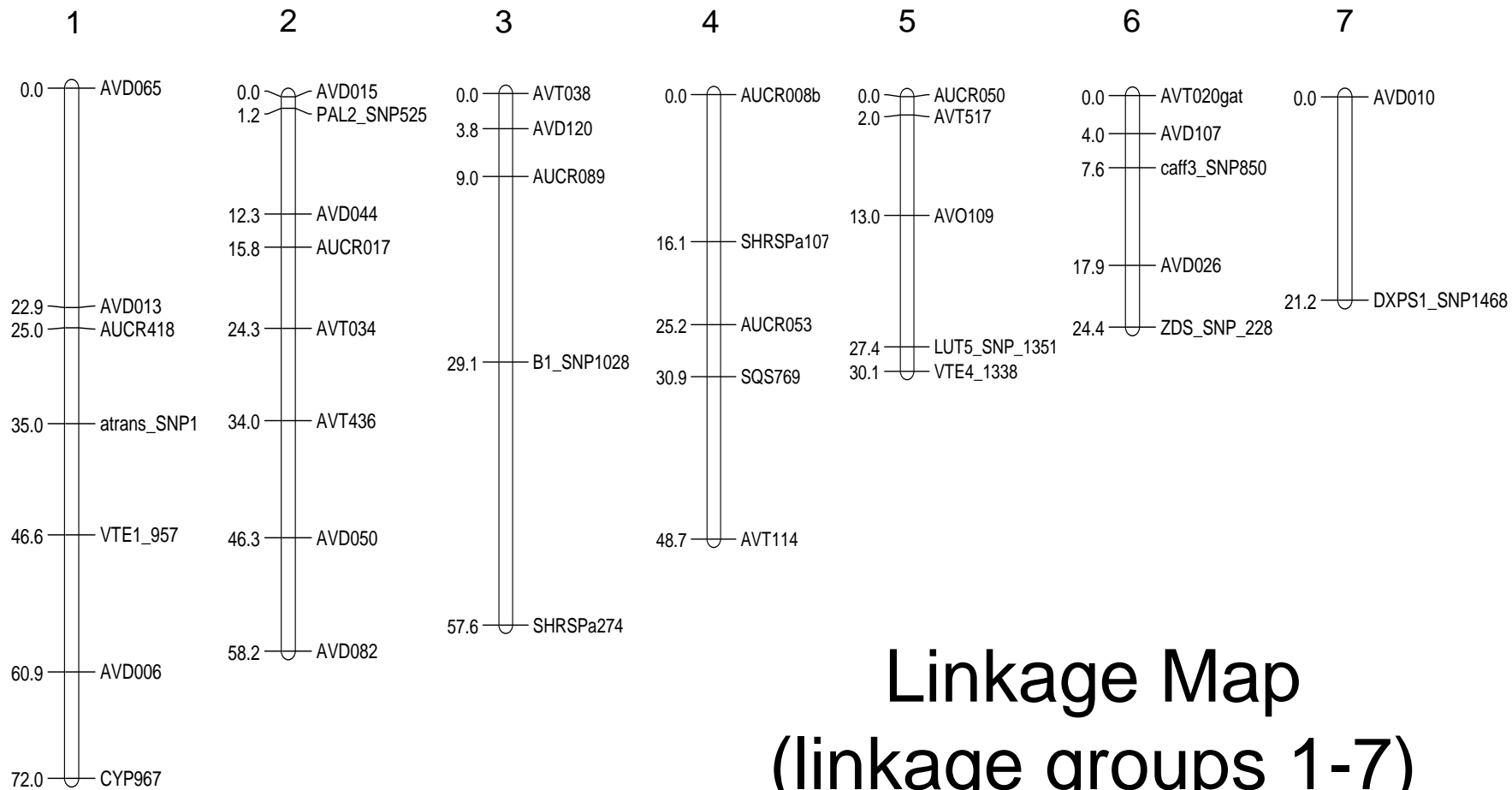
- Candidate gene approach
- Fruit nutritional composition
- Carotenoids, Vitamin B complex, Vitamin E, Vitamin C, fatty acids, flavonoid/anthocyanin/phenyl-propanoids, isoprenoid/beta-sitosterol biosynthesis pathways
- Avocado EST/cDNA sequences (Floral Genome project; HortResearch (NZ), CINVESTAV (Mexico); cDNA library of ripe fruit of Hass
- SNPs developed by screening 10 Gwen progeny genotypes

Markers used for linkage map:

- Microsatellites (47 + 18 = 65)
- SNPs (83 from 28 candidate genes in 8 pathways)
- 148 markers; 91 markers used for linkage map (JoinMap, OneMap)

In progress: microarray study (CINVESTAV)

- Transcription factors
- metabolism-related genes



Linkage Map
(linkage groups 1-7)
91 markers

Trait	Heritability
Carotenoids	47% (69%, 61%) 2009-2010
Sitosterols	65% (80%, 62%) 2009-2010
Vitamin E	68% (2009 only)
Proanthocyanidins	31% (2009 only)
Fruit weight (FW)	49% (2009 only)
Fruit dry weight	35% (2009 only)
Fruit pulp weight	35% (2009 only)
Pulp wt/fruit wt	63% (2009 only)
Tree height	34% (2002-2005)
Canopy diameter	30% (2002-2005)
Stem girth	29% (2002-2005)
Flowering	32% (2002-2005)
Fruit yield/tree	23% (2002-2005)

Marker-assisted selection

- ca. 200 fruit from 8 genotypes was germinated

- seedling DNA extracted (ca. 1600 samples)

Association analyses revealed two markers showing an association with nutritional phenotype:

- AVD103 with carotenoids

- SNPs in MCR gene (24-dehydrocholesterol reductase)
with beta-sitosterol

TaqMan assay can be run on a BIO-RAD CFX96 real-time PCR instrument

