Genome-wide association study to identify loci controlling fruit quality traits in sweet cherry

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UMR BFP- Sweet cherry adaptation to climate change (A3C) team

Overview on the sweet cherry production

- World production: 2.2 Million t/year
- Dominated by Turkey, USA, Chile, Italy, Spain and soon China
- France: 4th producer in Europe – production declining since the last 40 years

  112,000t 1980 -> 30-40,000t
- Delicate culture, affected by the climate change

The objectives of our team is to identify the genetic control of

- Flowering phenology in response to global warming
- Fruit quality (fruit cracking, fruit firmness and size)

create sweet cherry varieties adapted to future climatic conditions producing high quality fruits

QTLs and candidate genes for fruit traits in cherry

QTL fruit color LG3- CG MYB10	Sooriyapathirana *et al*. 2010
QTL fruit size LG1, 2	Zhang *et al*. 2010
QTL fruit size LG1, 2, 3, 6	Rosyara *et al*. 2013
CG CNR for fruit size	De Franceschi *et al*. 2013
QTL - CG fruit weight (LG2,3,5,6), firmness (LG2,5,6)	Campoy *et al.* 2015
QTL LG2 hotspot	Cai *et al.* 2017
QTL Fruit firmness LG4 - domestication	Cai *et al*. 2019
QTL fruit firmness LG1	Balas *et al*. 2019, Calle *et al*. 2020
QTL LG4 hotspot (firmness-SSC-TA-maturity date)-CG NAC	Calle & Wunsch 2020
QTL fruit cracking LG5 PE, 4 SE, 2 FS	Quero-Garcia *et al*. submitted

All from biparental populations….

Goal

Identify genomic regions that control fruit quality traits from a sweet cherry germplasm core collection

Task

1- Phenotype 25 fruit traits during 2 to 6 years

2- Genotyping by sequencing (GBS)

3- GWAS

✓ compare 3 genomes used as reference: Sweet cherry ‘Regina’, ‘Satonishiki’ and Peach

✓ compare two statistic models

MLMM: Multiple Loci Linear Mixe Model

FamCPU:Fixed and Random Model Circulating Probability Unification

✓ compare GWAS and QTL

4- investigate putative functions of the CGs associated with the SNPs

Sweet cherry germplasm collection

210 accessions

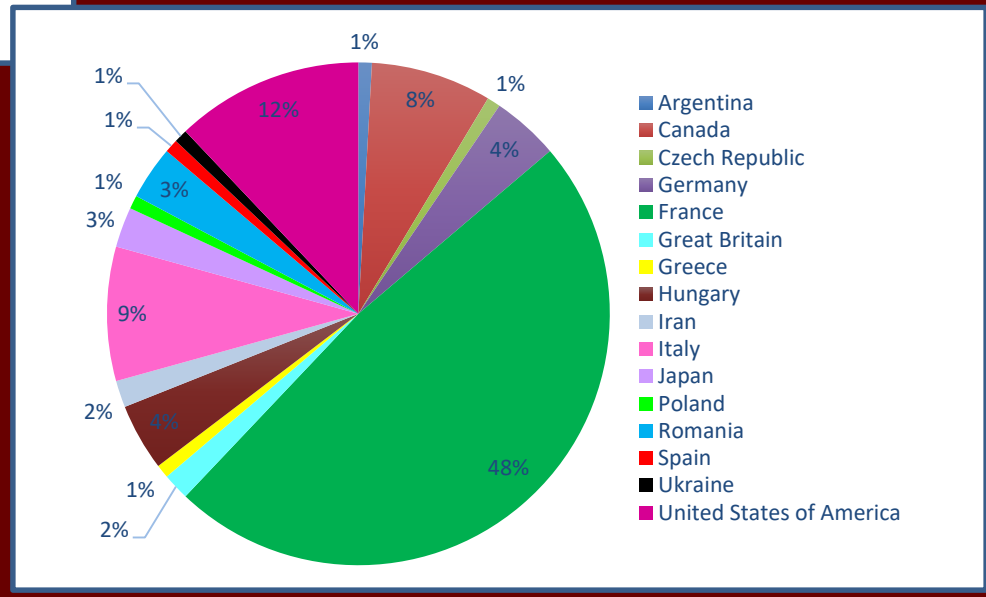
111 improved (84 modern varieties)

99 old varieties

- 50% of French origin, and 16 countries
- genotyped with the 6K SNP
- structured in 9 clusters

(Campoy *et al.* 2016)

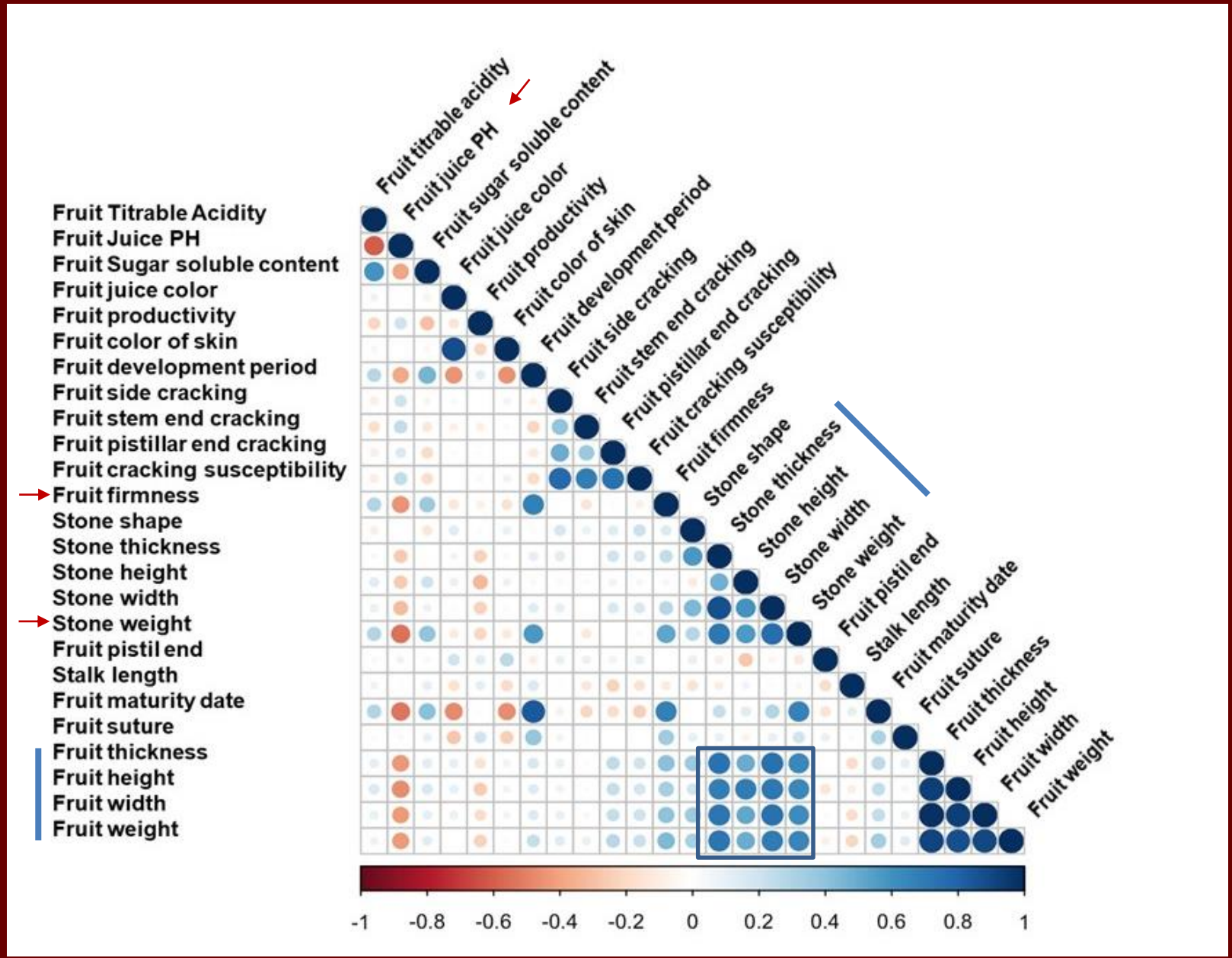
core collection
116 accessions



1- Phenotyping

25 fruit traits
- Organoleptic quality
- Fruit cracking
- Fruit firmness
- Fruit weight –size
- Stone traits

25 fruits / genotype



GBS ApeKI, 96 plex CIRAD genotyping platform (Montpellier)

389 682 215 fragments

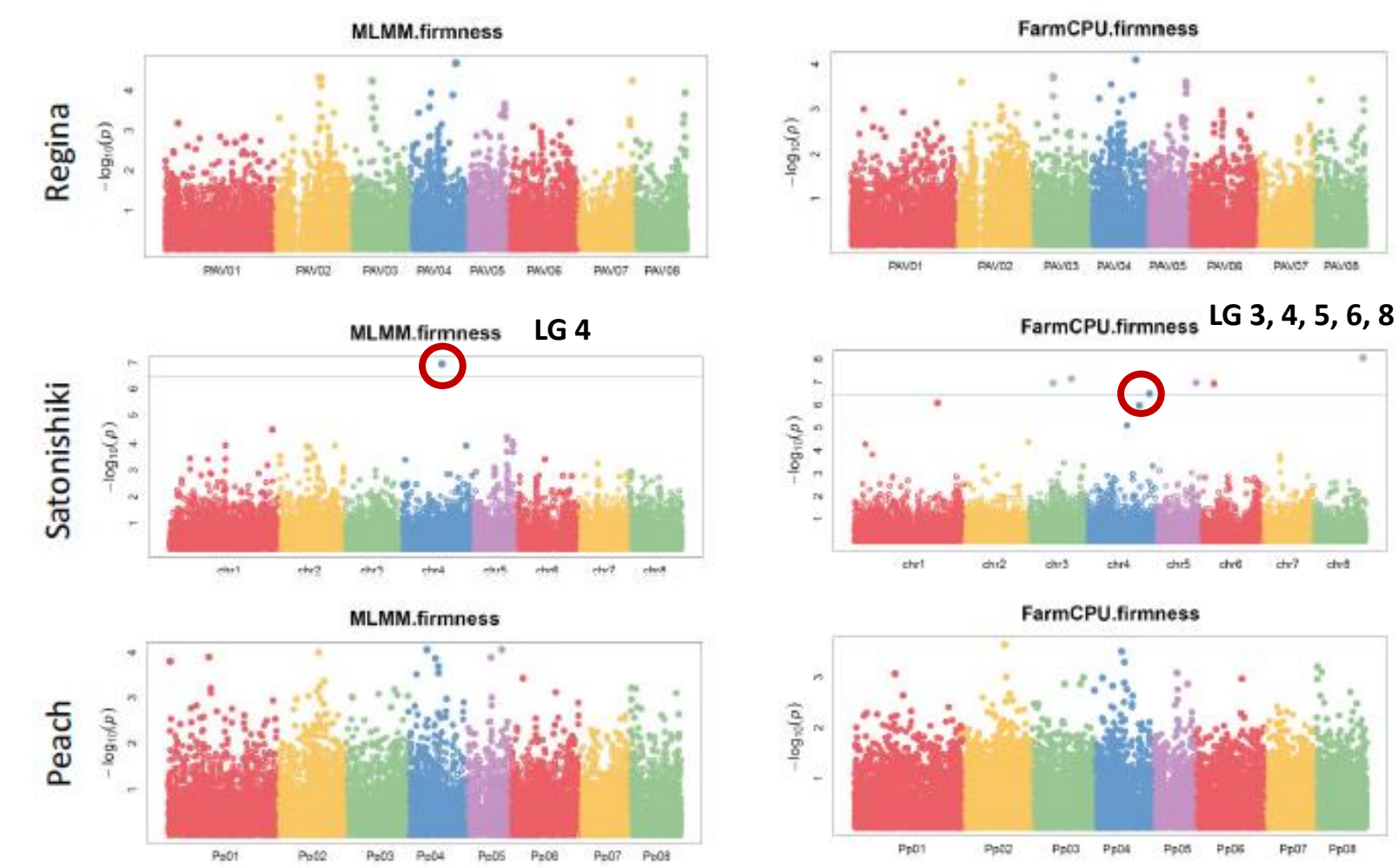
7 914 593 fragments on average / accession

SNPs selection: several filters to minimize the numer of false positives SNPs

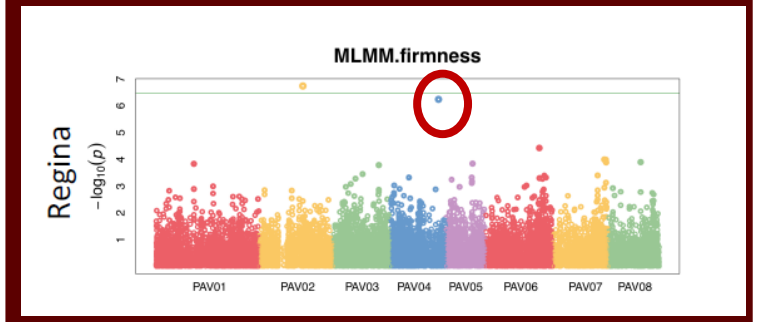
	Cherry Regina v1 (Le Dantec *et al. In prep*)	Cherry Satonishiki v1 (Shirasawa *et al.* 2017)	Peach v2 (Verde *et al.* 2017)
➢ Trimmed sequences aligment on 3 genomes			
➢ Filtering SNPs (minQ, depth, 20% NA)	75 916 SNPs	72 649 SNPs	165 442 SNPs
➢ 5% of MAF filtered	28 198 SNPs	34 864 SNPs	33 760 SNPs

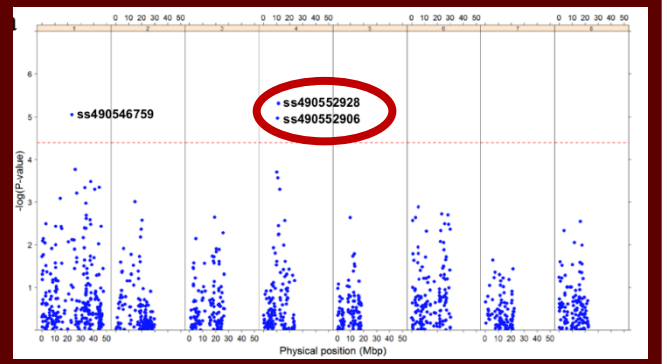
Results

Fruit firmness (H^2 = 0.90)



LG 4

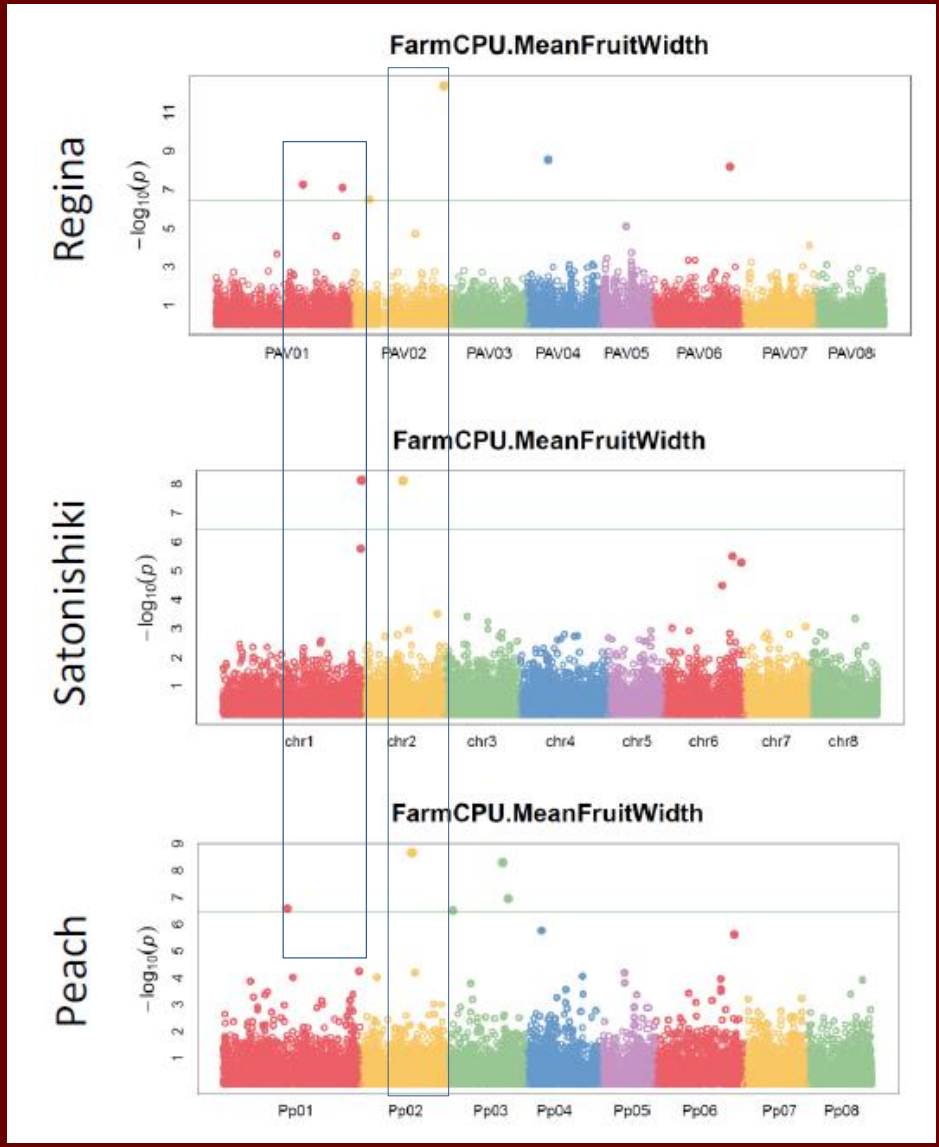




Cai *et al*. 2019

Results

Fruit width (H^2 = 0.81)

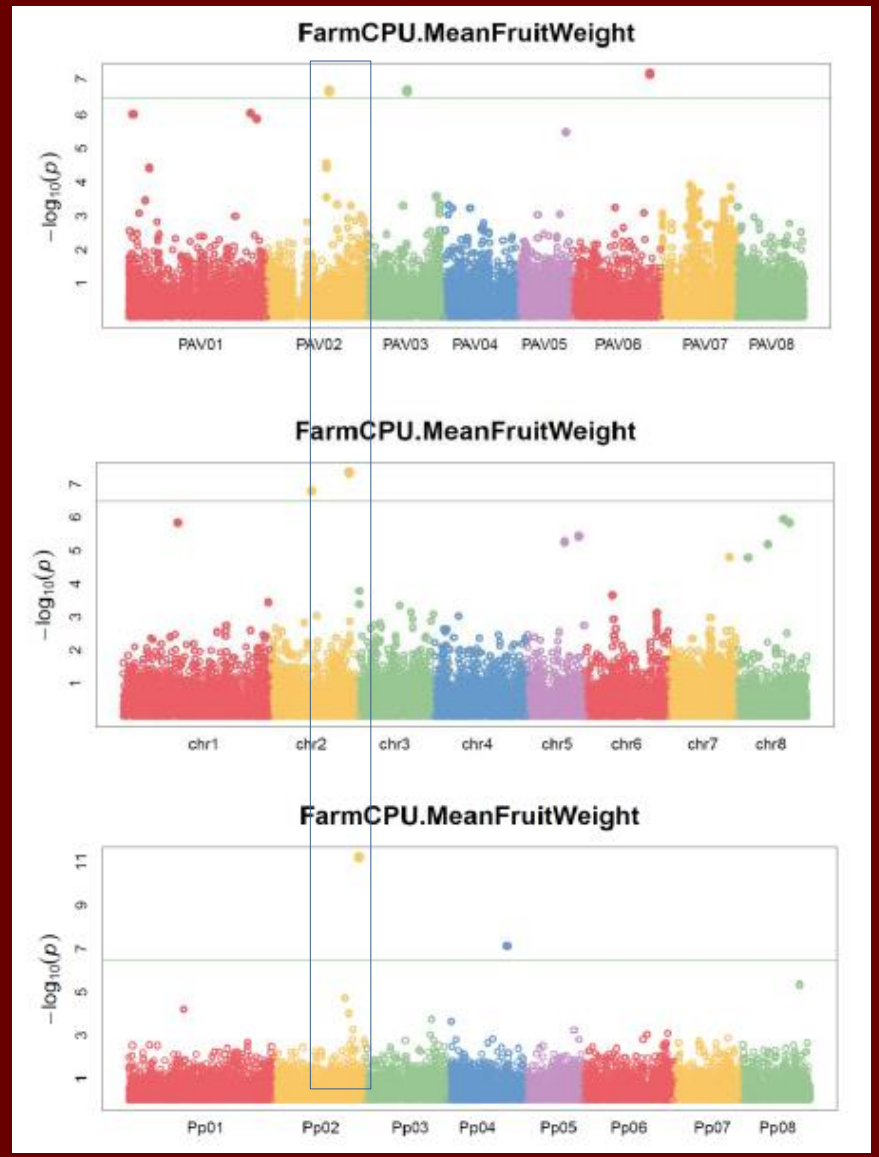


QTLs
Fruit size

LG **1, 2**
Zhang *et al*.
2010

LG **1, 2**, 3, 6
Rosyara *et al*.
2013

Fruit weight (H^2 = 0.92)



QTLs
LG **2**,3,5,6

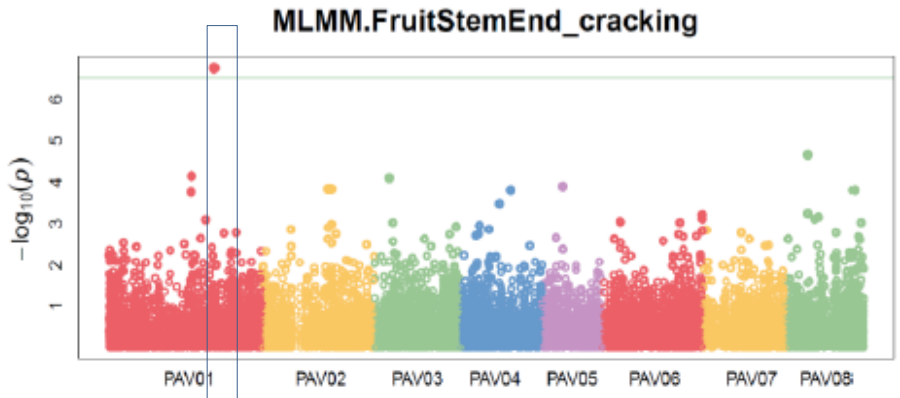
Campoy *et al* 2015

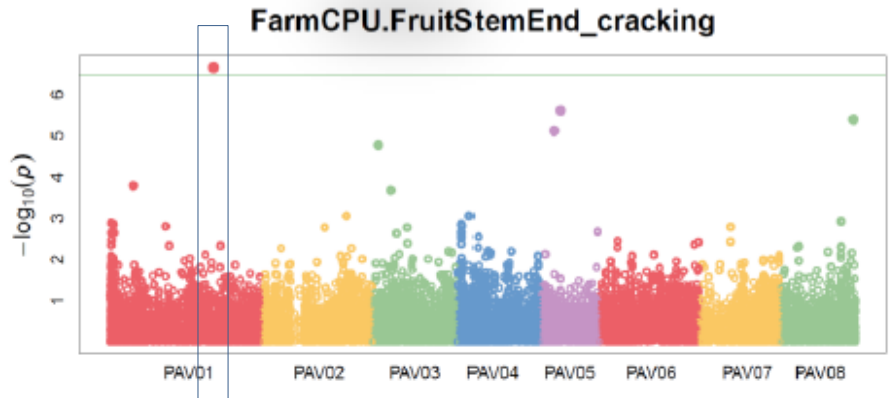
Results: Fruit cracking (Stem end, Pistilar end, Fruit side)

Stem end cracking (H^2 = 0,58)

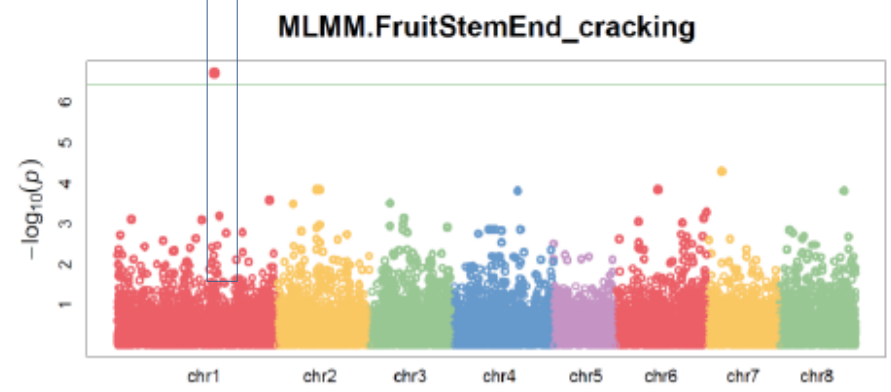
LG 1

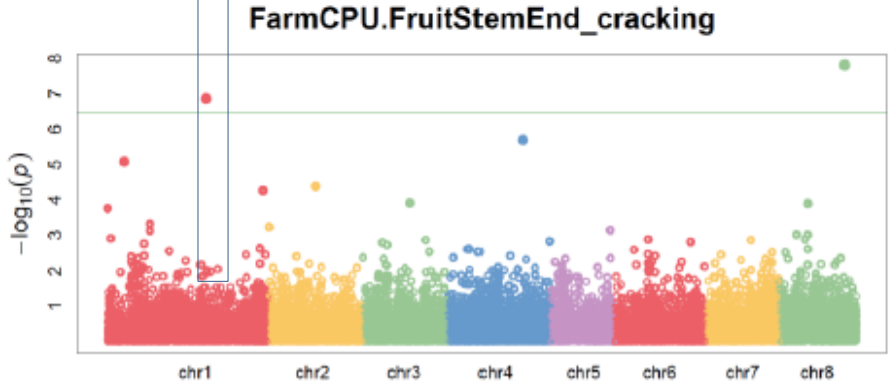
Regina





Satonishiki

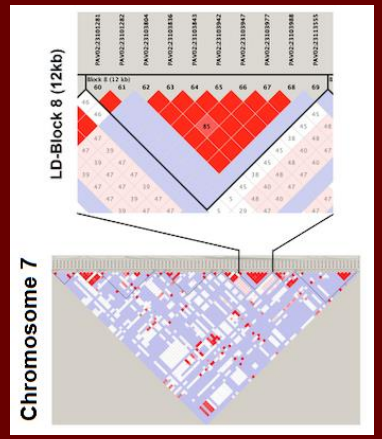




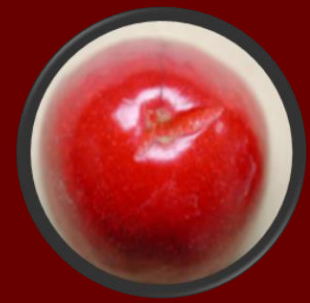
However, main QTLs were detected on LG 4 and 6 (Quero-Garcia *et al submitted)*

Results

Main QTLs LG4, LG5
Quero-Garcia *et al.* submitted



Pistillar end cracking (H^2 = 0,64)

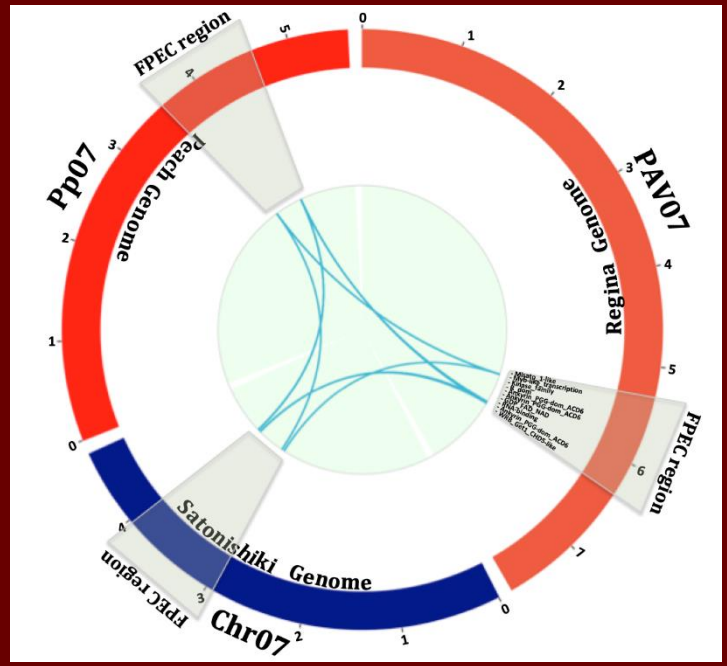


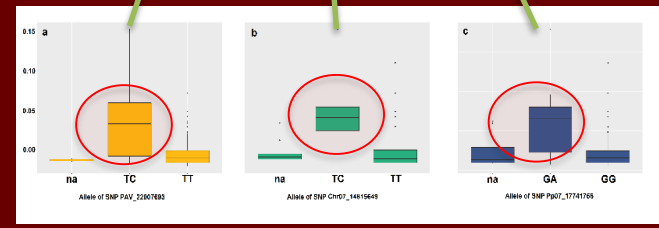
10 CGs in the LD blocks

ACD6 (*ACCELERATED CELL DEATH6)*

salicylic acid-mediated defense signaling networks

SNP in the coding sequence





- SNP with significative alleles effect
- Improvement of breeding programs

- Associated SNPs
  - May vary according to the reference genome used for mapping the GBS fragments but most of them are in the same region
  - May be significant or not according to the GWAS models
- Associations in agreement with QTLs but not always…
- **Associations must be confirmed on additional genotypes to be validated**
- **GWAS is powerful as the SNPs can be transformed into KASP markers easily usable for MAS**

Thanks!

- CRB *Prunus* (INRAE Fruit Tree Experimental Unit, Bourran)

- Team A3C/BFP

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