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Combining genome-wide association analyses and QTL detection to identify loci controlling phenology-related and fruit quality traits in sweet cherry

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INTRODUCTION

In perennial fruit species, phenology and fruit quality traits are highly dependent on environmental conditions. In the context of climate change, a rise of fall and winter temperatures leads to a slowing down of the dormancy release which may result in a dramatic decrease of the production. Also, a rise of spring temperatures induces a significant advance of blooming date, increasing risks of damages by the frost. Moreover, the higher frequency of spring rainy periods has serious consequences for fruit quality, particularly on fruit cracking (Fig 1).

The objective of our study is to identify the genetic determinism of the cherry tree response to the climate change. Several F₁ sweet cherry progenies and a germplasm collection were evaluated for phenological traits and fruit quality. One of the mapping progenies, Regina × Lapins, was evaluated in five sites in order to study the genotype × environment interactions (Fig 2). The progenies were genotyped with the SNP RosBREED arrays and the collection using a genotyping-by-sequencing (GBS) approach. QTLs detection and GWAS were performed allowing the identification of the genomic regions associated with the phenological and the fruit quality traits.

Fig 1. Impacts of climate change

Rise in temperature in Winter



Early blooming date and increasing risks of frost damages

Higher frequency of spring rainy periods



Increasing fruit cracking damage

Fig 2. Genotype x environment interactions based on multi-site trials

Regina x Lapins (RxL): 122 hybrids x 2 (clonal copies)

Toulonne, France (2011-2012)



Forli, Italy (2013-2014)



Maribor, Slovenia (2009-2010 / 2011-2012)



Nîmes, France (2012-2013)



Murcia, Spain (2012-2013)



Phenotyped for

- Blooming date
- Floribondity
- Fruit quality

Fruit firmness, weight and cracking, maturity date

GWAS methods & results

The 38,283 filtered SNPs (provided from "Regina" cherry genome) datasets discovered from the 116 core collection of sweet cherry population were used to perform GWAS for the several traits studied. GWAS was carried out by applying two different models (such as MLMM and FarmCPU). Both the kinship matrix (Fig 3) and principal components were included to correct for familial relatedness and population structure (Fig 4). SNPs associated with phenology and fruit quality traits were detected (Fig 5).

Fig 3. Kinship matrix

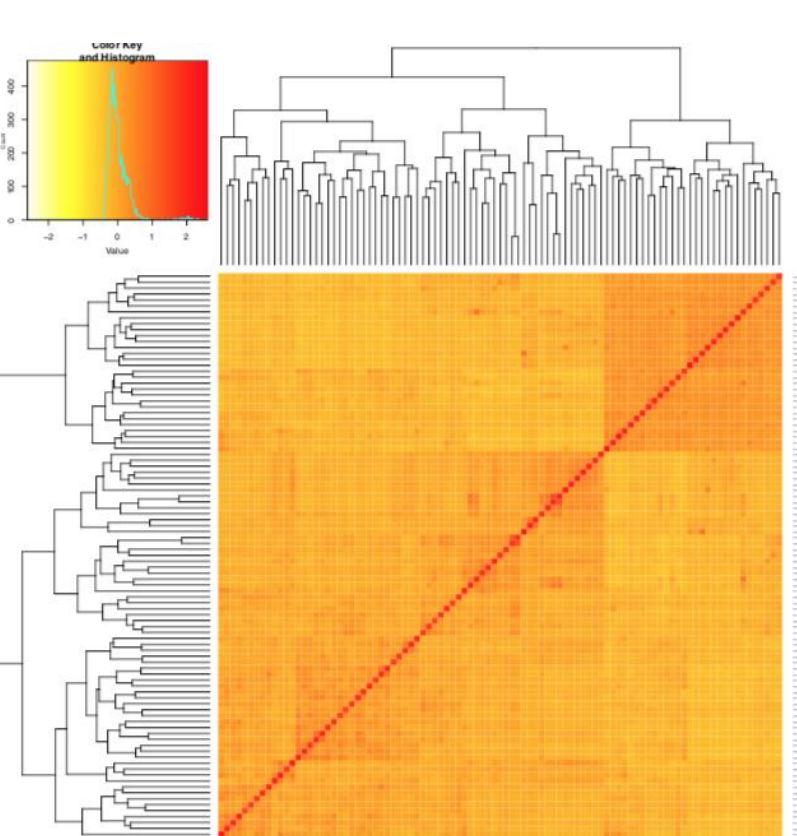


Fig 4. Population structure of 116 accessions used for GWAS (K=6)

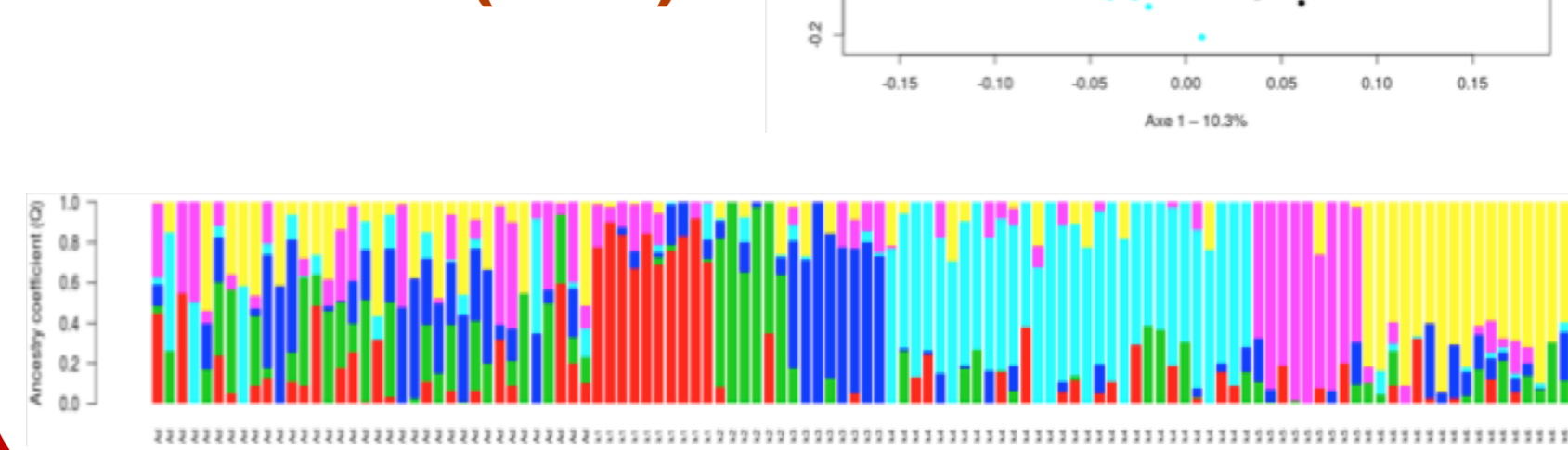


Fig 5. GWAS : GBS/ phenology – Fruit quality

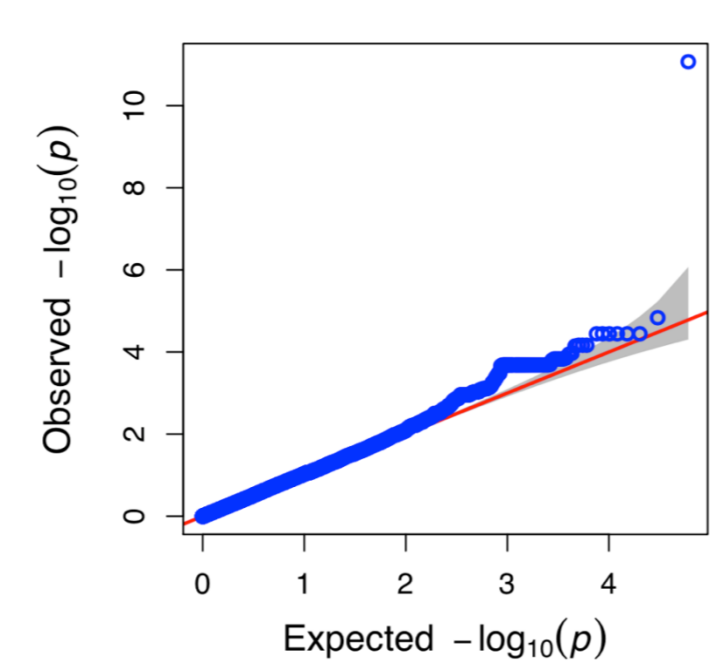
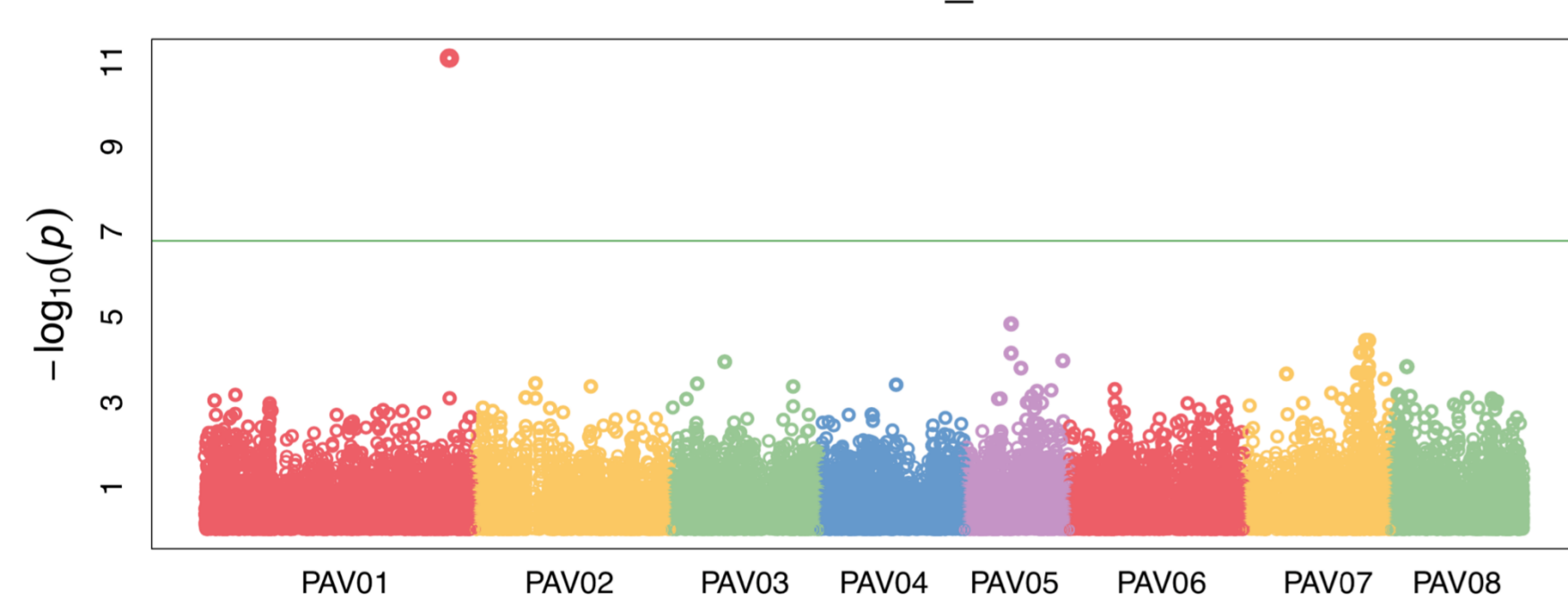
Collection of genetic resources (116 accessions)

Blooming date

Chilling requirement

MLMM.CU_50

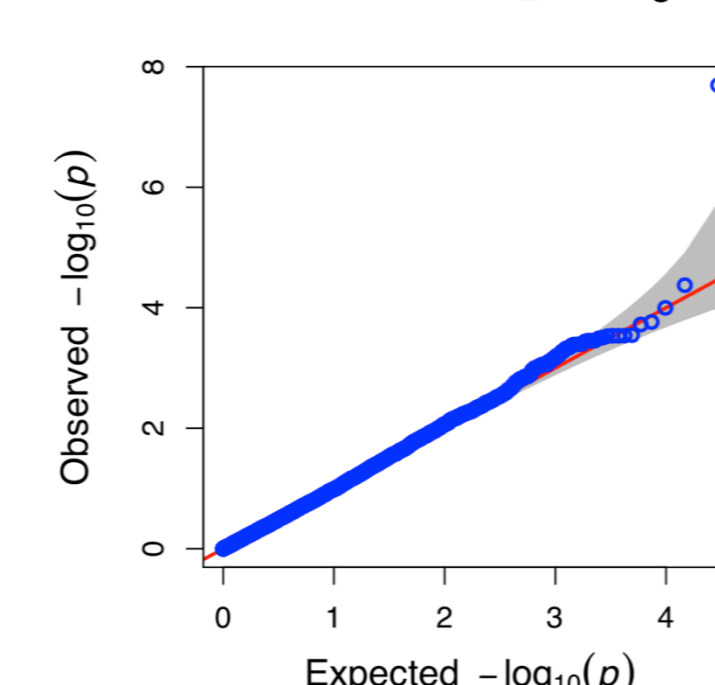
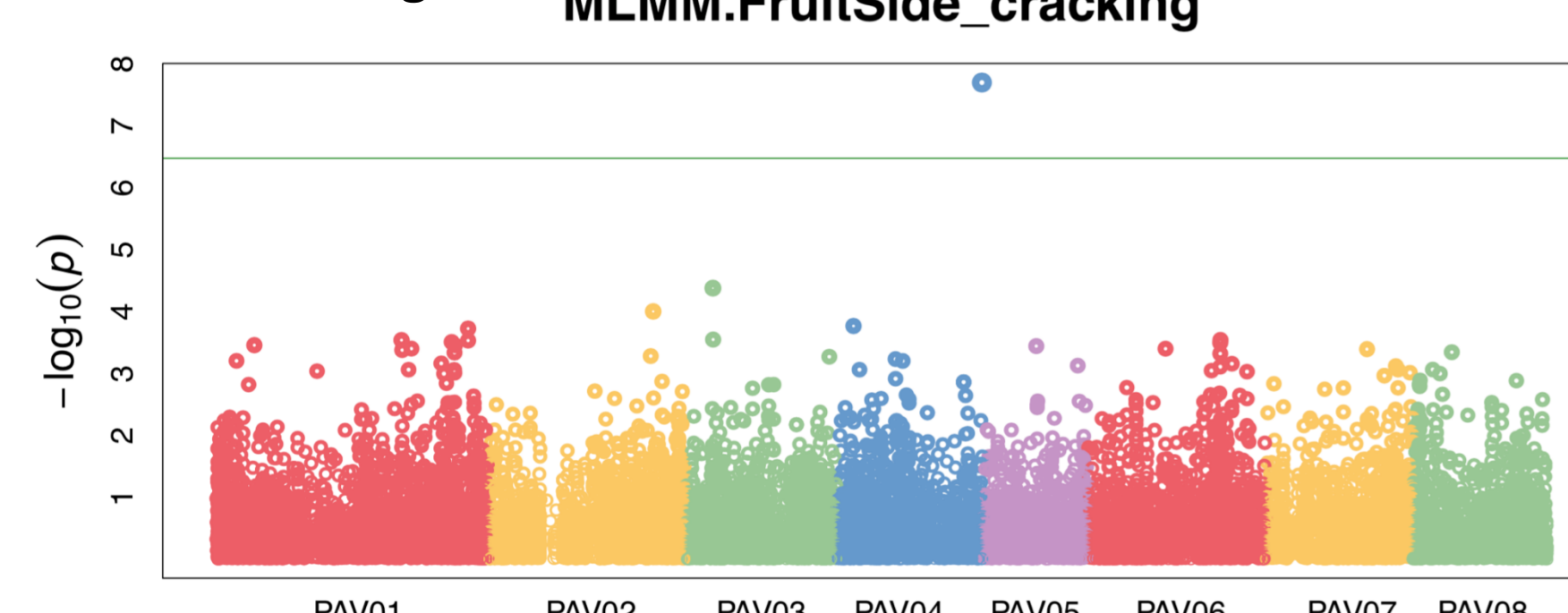
MLMM.CU_50



Fruit Side cracking

MLMM.FruitSide_cracking

MLMM.FruitSide_cracking



QTLs methods & results

QTLs detection using genetic maps obtained with the RosBREED cherry 6K SNP array allowed us to confirm the presence of a major QTL on linkage group 4 (LG4), explaining up to 40% of the phenotypic variation for the flowering time (Table 1). This QTL is highly significant in all environments but Murcia, the only site characterized by a mild winter. Another region was identified at the end of LG1 and is the major one in this location. Indeed, this loci presents a PEV equal to up to 25,6% in Murcia, whereas it explains only between 2 and 12,6% of the variation of the blooming date in the other environments.

Table 1. QTLs for blooming date according to the location and the year (multi-location and multi-year analysis in MultiQTL)

Linkage group	LOD	Toulonne			Nîmes			Forli		Maribor		Murcia			
		2016	2017	2018	2017	2018	2019	2018	2019	2017	2018	2019			
R: Regina, L: Lapins															
R1	15,38	1,9	6,3	2,7	5,3	3,3	2,7	5,7	3,1	2,1	2,0	0,8	2,2	18,1	2,8
R4	87,44	20,2	18,4	19,6	24,5	21,3	22,7	17,4	24,1	15,9	38,9	39,4	1,8	8,8	1,3
R5	20,78	2,5	4,5	2,3	1,0	6,5	4,9	5,6	2,3	4,0	5,1	6,0	2,2	11,1	7,3
L1	21,13	6,3	4,5	4,3	2,9	2,0	2,3	4,4	4,0	12,5	3,1	4,2	20,6	25,6	4,3
L5	14,6	2,0	5,9	3,5	5,3	5,6	6,2	2,3	0,9	2,2	1,3	1,6	4,4	10,1	1,2
L6	29,56	13,6	14,4	16,4	9,9	11,5	10,7	5,8	5,3	3,8	4,6	1,8	1,9	13,7	1,4

CONCLUSIONS

For both datasets, we revealed that a genomic region at the end of Chromosome 1 controls both flowering and chilling requirements in sweet cherry (Fig 5, Table 1), consistent with the observed strong phenotypical correlation between these traits. In the collection, the SNP in GL1 associated to blooming date is very much linked to the presence of two 'low chilling' varieties and therefore capable of lifting their dormancy in mild winter conditions (just like in Murcia). For the first time, marker-trait associations on several chromosomes were found for traits related to sweet cherry fruit quality (example of the SNP linked to fruit side cracking on Chromosome 4, Fig 5).

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