



HAL
open science

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

Camille Branchereau, Armel Donkpegan, Teresa Barreneche, Loïck Le Dantec, Anton Ivancic, Daniela Giovannini, Gregorio López-Ortega, Federico García-Montiel, José Quero-García, Elisabeth Dirlewanger

► To cite this version:

Camille Branchereau, Armel Donkpegan, Teresa Barreneche, Loïck Le Dantec, Anton Ivancic, et al.. Combining genome-wide association analyses and QTL detection to identify loci controlling phenology-related and fruit quality traits in sweet cherry. International Plant & Animal Genome XXVIII, Jan 2020, San Diego, United States. hal-03318844

HAL Id: hal-03318844

<https://hal.science/hal-03318844v1>

Submitted on 11 Aug 2021

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

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

Camille Branchereau¹, Armel Donkpegan¹, Teresa Barreneche¹, Loïck le Dantec¹, Anton Ivancic², Daniela Giovannini³, Gregorio López-Ortega⁴, Federico García-Montiel⁴, José Quero-García¹, Elisabeth Dirlewanger¹

¹INRAE, Univ. Bordeaux, BFP, Villenave d'Ornon, France, ²Faculty of Agriculture and Life Sciences, University of Maribor, Hoče, Slovenia, ³CREA, Research Centre for Olive, Citrus and Tree fruit, Forlì, Italy, ⁴IMIDA, Instituto Murciano de Investigación y Desarrollo Agrario y Alimentario, Murcia, Spain

INTRODUCTION

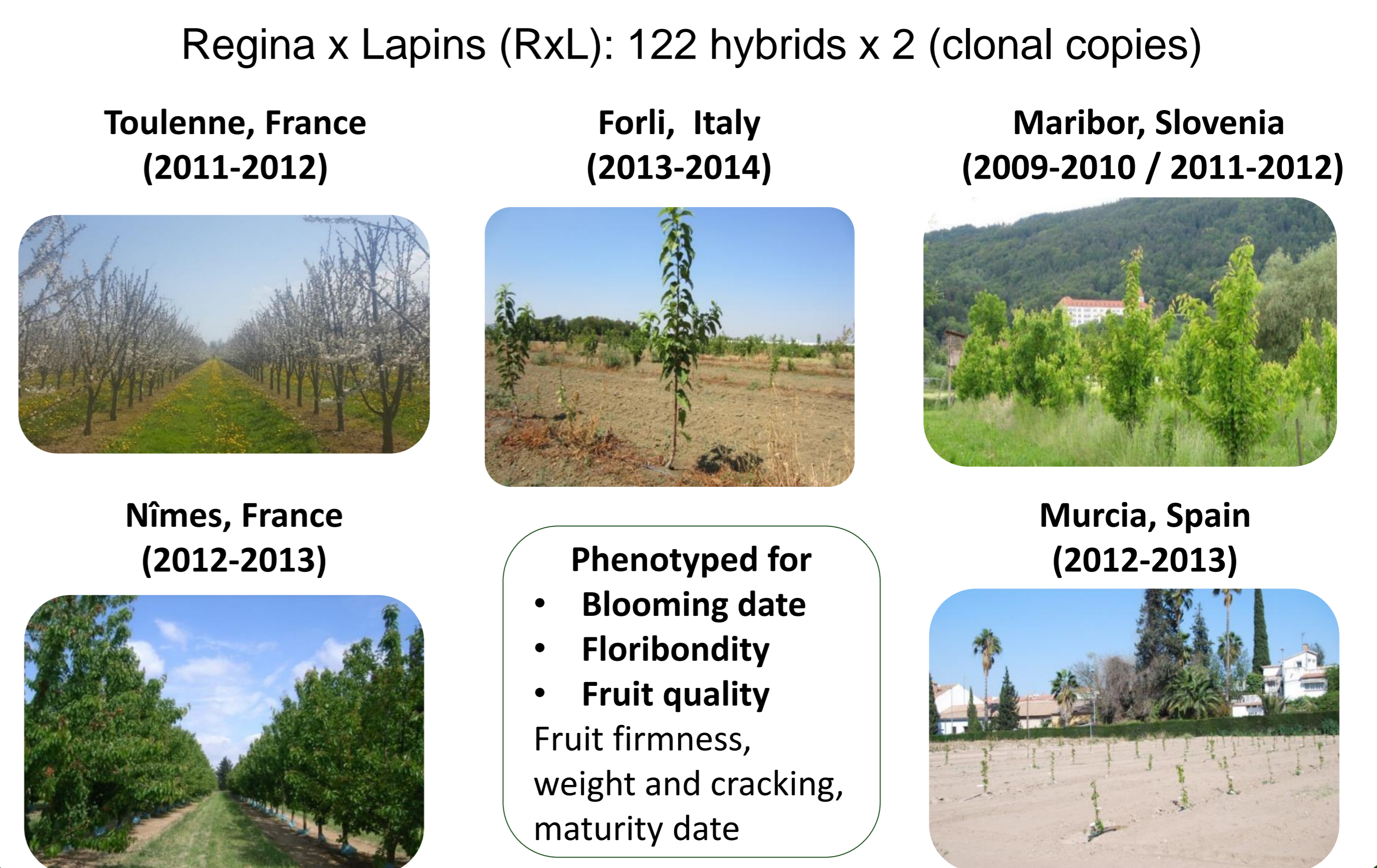
In perennial fruit species, phenology and fruit quality traits are highly dependent on environmental conditions. In the context of climate change, a rise of fall and winter temperatures leads to a slowing down of the dormancy release which may result in a dramatic decrease of the production. Also, a 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



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



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

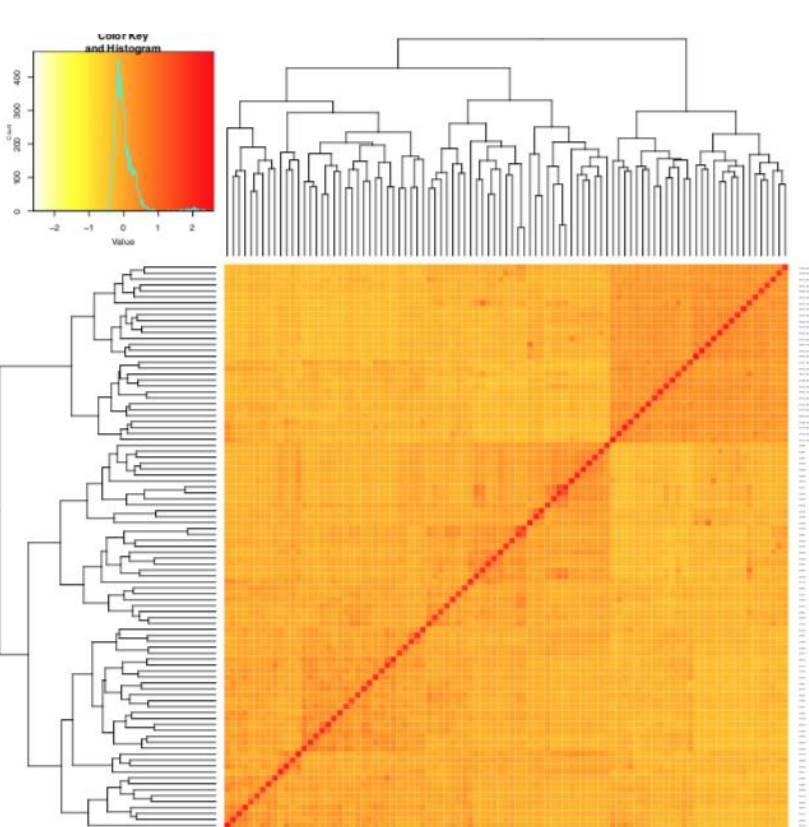


Fig 4. Population structure of 116 accessions used for GWAS (K=6)

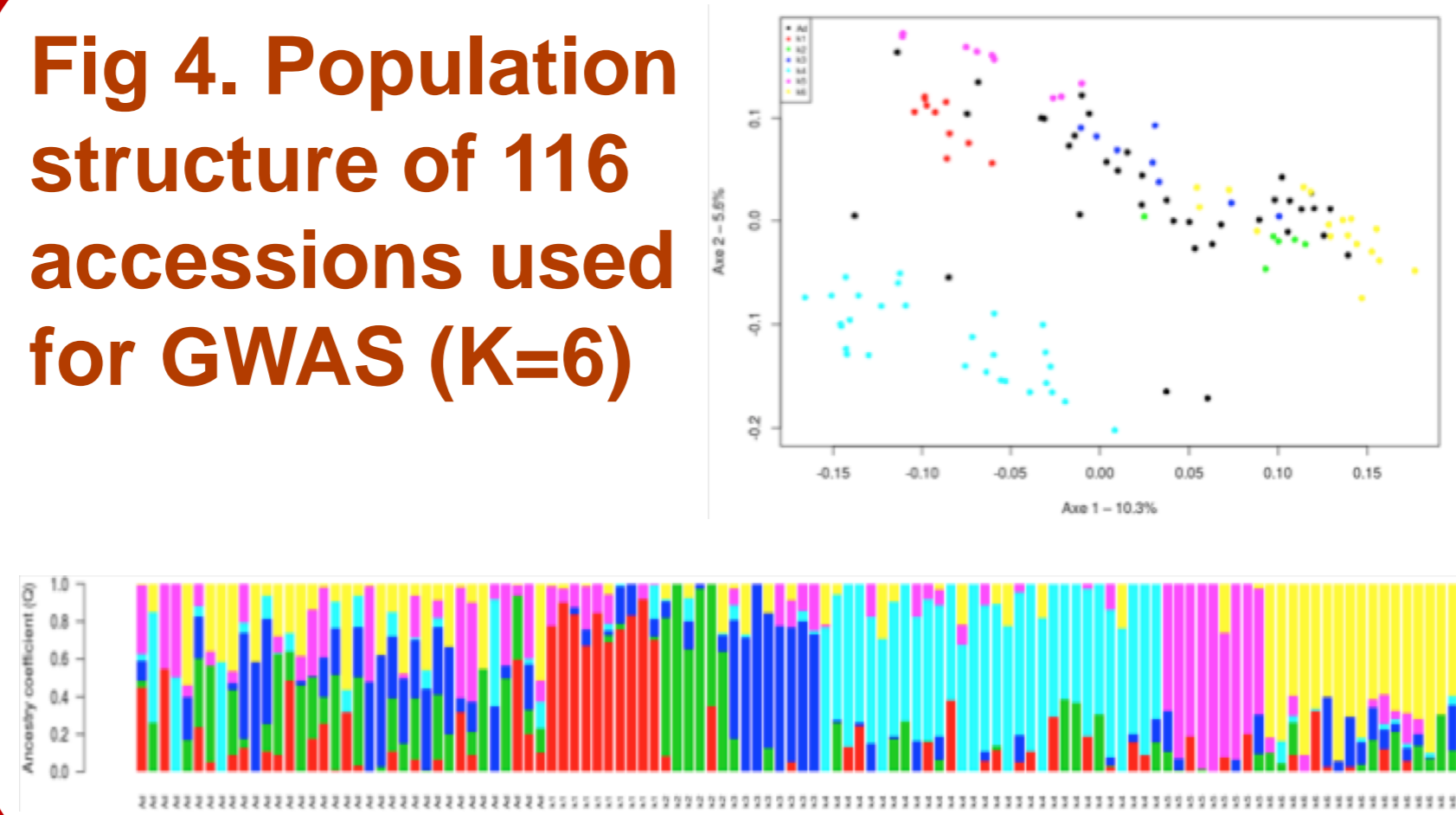
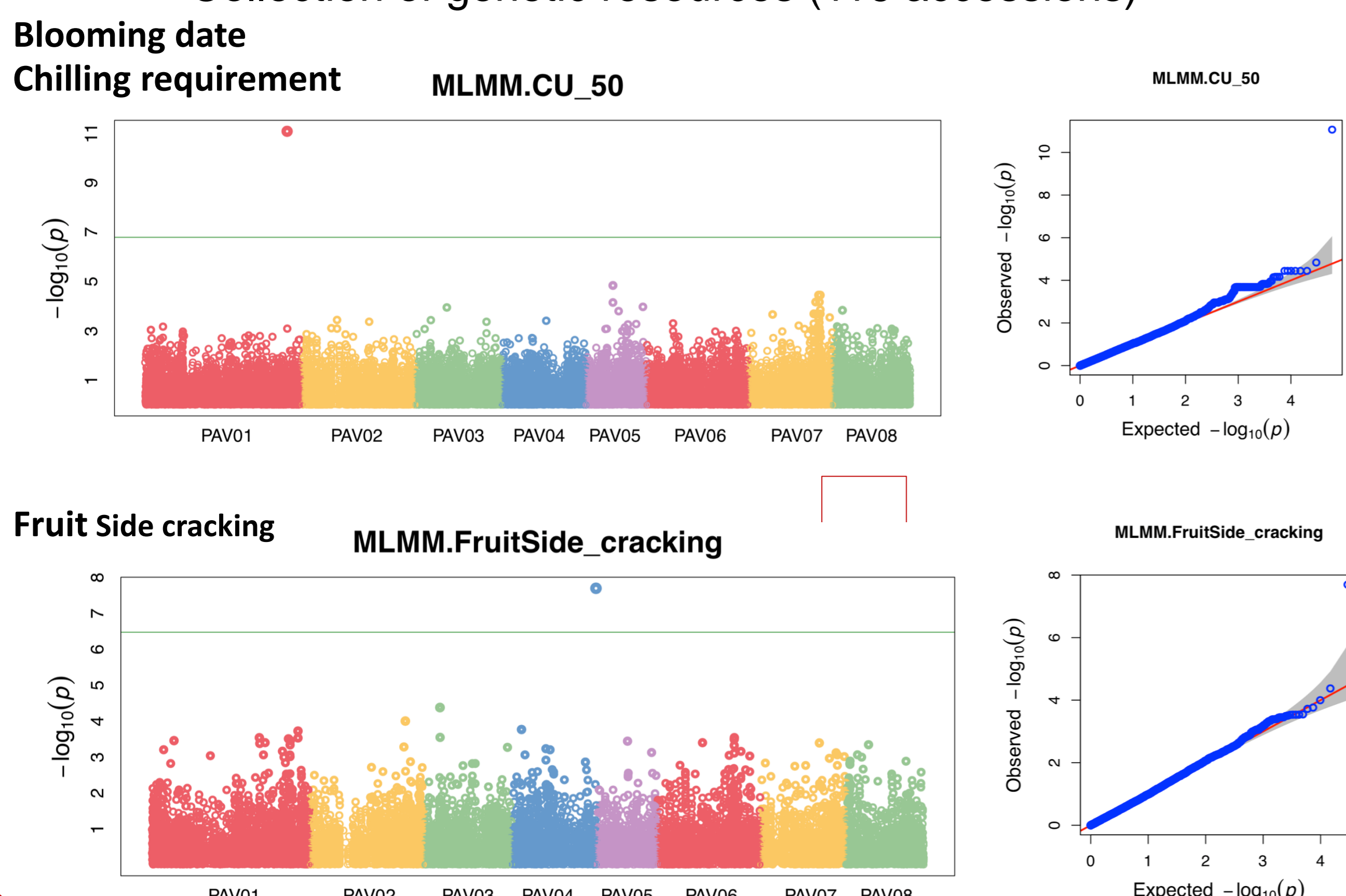


Fig 5. GWAS : GBS/ phenology – Fruit quality



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).

Acknowledgements: This work was supported by INRA BAP Division and the Nouvelle-Aquitaine Region. We thank the Fruit Experimental Unit (INRA) for orchard management.