



FINAL WORKSHOP

April 2-3, 2025

Pre-breeding strategies for obtaining new resilient and added value berries

Objective

- Offer to breeders an opportunity to **screen and select** their genotypes of interest against a suite of markers
- **MAS** identify molecular markers which can be useful to breeders across all raspberry breeding programmes
- **GWAS** find location in the genome that are important for different traits



Our Experience

Genotypes provided by G-Berries

FIELD SELECTION: 14 genotypes

ADVANCED SELECTION: 15 genotypes

VARIETIES: 19 genotypes

SEEDLINGS: 338 came from two crosses
(MO.LA.21-004 - MO.LA.21-005)



Our Experience

Traits of interest and phenotypic data

VEGETATIVE PARAMETERS

- Leaf bud break
- Leafing out
- Flower bud swell
- Open flower
- 1° pick
- Senescence beginnig
- Senescence end



Leaf bud break
03/03 – 01/04



Leafing out
24/03 – 24/04



Flower bud swell
04/04 – 05/05



Open flower
15/04 – 25/05

Our Experience

Traits of interest and phenotypic data

PEST AND DISEASES

- Aphids
- Red Spider Mite
- Chrysodeixis Chalcites
- Rust
- Spur Blight
- Powdery Mildew
- Root rot



Spur Blight



Red Spider Mite

Our Experience

Traits of interest and phenotypic data

FRUIT QUALITY TRAITS

- Size
- Color (1-5 scale)
- Firmness (1-3 scale)
- Brix



Our Experience

Suitable leaf samples

In May 2022, 4-6 leaf disc from each genotypes were collected following the instructions provide by the coordinator and sent to a dedicated lab for the DNA extraction

	A	B	C	D	E	F	G	H	I
1									
2	1. Accepted submission format: 96-well plates					96-well plates			
3									
4	2. Enter all samples included in the shipment in the list below; use the reformatter sheets to convert data from other sorting formats.								
5	No special characters are allowed in sample names								
6	When pasting, use the "paste values only" option								
7	Final results from us will typically use the "sample identifier"								
8	For replicated samples, use identical "Sample name" and tick the "Contains a replicated sample" column								
9	Do not re-sort the rows of this sheet! You may use the reformatter sheets to convert data from other sorting formats.								
10									
11	3. Check that the number of identified samples is correct:					384			
12	4. If you have ordered specific bioinformatic analysis, proceed to the service-specific sheet to finalise the form. Always applicable to SeqSNP / SeqSNP HT!								
13	Please note that invalid or inconsistent data will delay the processing of your samples.								
14	OPTIONAL			MANDATORY			OPTIONAL	OPTIONAL	OPTIONAL
	#	Plate	Well	Plate name	Sample name	Sample identifier	Blank / Negative control sample	Contains a replicated sample	Concentration
15									
16	1	P01	A01	TSK41131	AMO-001	P01-A01-TSK41131-AMO-001			
17	2	P01	B01	TSK41131	AMO-002	P01-B01-TSK41131-AMO-002			
18	3	P01	C01	TSK41131	AMO-004	P01-C01-TSK41131-AMO-004			
19	4	P01	D01	TSK41131	AMO-005	P01-D01-TSK41131-AMO-005			
20	5	P01	E01	TSK41131	AMO-006	P01-E01-TSK41131-AMO-006			
21	6	P01	F01	TSK41131	AMO-007	P01-F01-TSK41131-AMO-007			
22	7	P01	G01	TSK41131	AMO-008	P01-G01-TSK41131-AMO-008			
23	8	P01	H01	TSK41131	AMO-009	P01-H01-TSK41131-AMO-009			
24	9	P01	A02	TSK41131	AMO-011	P01-A02-TSK41131-AMO-011			
25	10	P01	B02	TSK41131	AMO-012	P01-B02-TSK41131-AMO-012			
26	11	P01	C02	TSK41131	AMO-013	P01-C02-TSK41131-AMO-013			
27	12	P01	D02	TSK41131	AMO-015	P01-D02-TSK41131-AMO-015			

Our Experience

Receipt of the phenotypic data for the 450 selections

SPRING 2022														
Genotype	Visual Observation												Fruit	
	Flower bud swell	Open Flowers	1st pick	Senescence Beginning	Senescence End	Aphids	Rust	Powdery mildew	Cane Disease	Root Rot	Spur Blight	Red Spider Mite	Size	Firm
AMO-001	19/04/2022	04/05/2022	24/05/2022	09/11/2022		No	No	No	Yes	No	Yes	No	3,87	1
AMO-002	11/04/2022	29/04/2022	27/05/2022	25/10/2022		No	No	No	Yes	No	Yes	No	4,15	2
AMO-003	15/04/2022	03/05/2022	26/05/2022	25/10/2022		No	No	No	Yes	No	Yes	Yes	3,70	2
AMO-004	15/04/2022	29/04/2022	25/05/2022	04/10/2022		No	No	No	Yes	Yes	Yes	Yes	4,10	1
AMO-005	15/04/2022	29/04/2022	26/05/2022	09/11/2022		No	No	No	No	No	No	No	4,25	1
AMO-006	15/04/2022	29/04/2022	24/05/2022	09/11/2022		No	No	No	Yes	No	Yes	No	3,49	2
AMO-007	11/04/2022	03/05/2022	25/05/2022	04/10/2022		No	No	No	Yes	No	Yes	No	5,08	2
AMO-008	11/04/2022	22/04/2022	20/05/2022	18/10/2022		No	No	No	Yes	No	Yes	No	4,18	2
AMO-009	08/04/2022	22/04/2022	20/05/2022	09/11/2022		No	No	No	Yes	No	Yes	No	3,71	1
AMO-011	15/04/2022	29/04/2022	27/05/2022	17/11/2022		No	No	No	Yes	No	Yes	No	4,12	2
AMO-012	15/04/2022	29/04/2022	26/05/2022	25/10/2022		No	No	No	Yes	No	Yes	No	4,22	2
AMO-013	04/04/2022	19/04/2022	19/05/2022	17/11/2022		No	No	No	Yes	No	Yes	Yes	3,38	3
AMO-015	22/04/2022	03/05/2022	27/05/2022	31/10/2022		No	No	No	Yes	No	Yes	No	3,20	3
AMO-016	15/04/2022	29/04/2022	24/05/2022	31/10/2022		No	No	No	Yes	No	Yes	Yes	3,39	3
AMO-017	22/04/2022	03/05/2022	26/05/2022	25/10/2022		No	No	No	No	No	No	Yes	3,88	2
AMO-018	15/04/2022	26/04/2022	25/05/2022	04/10/2022		No	No	No	Yes	No	Yes	No	4,60	1

Our Experience

Completion of the training

In December 2024 we participate to a video meeting to discuss about the preliminary results

During the first part of the meeting we had the opportunity to analyze the genetic structure of the raspberry genotypes provide by the project members.

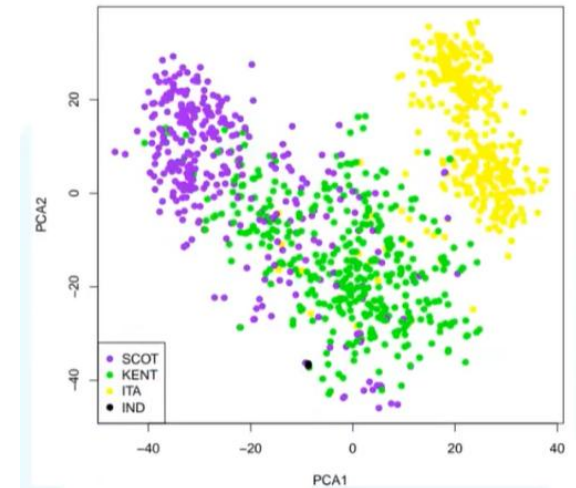
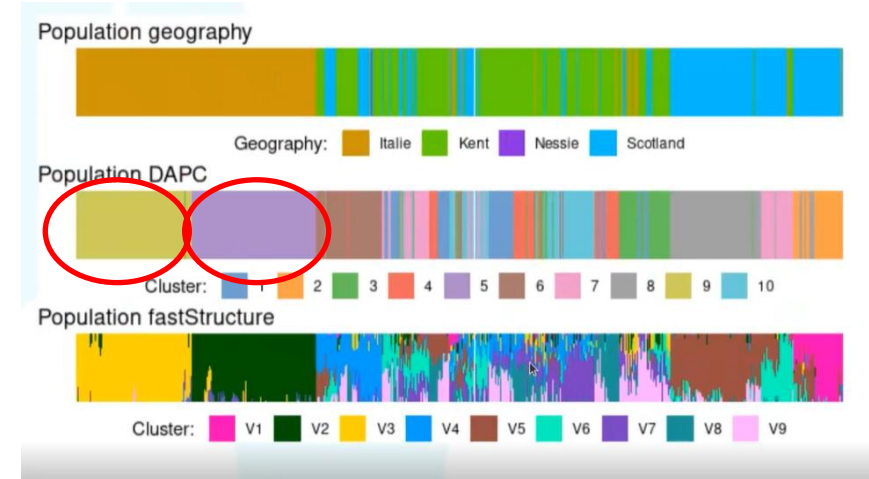
In the second part the results from the GWAS were presented and we discuss about the most important trait of interest for the different breeding program.



Results

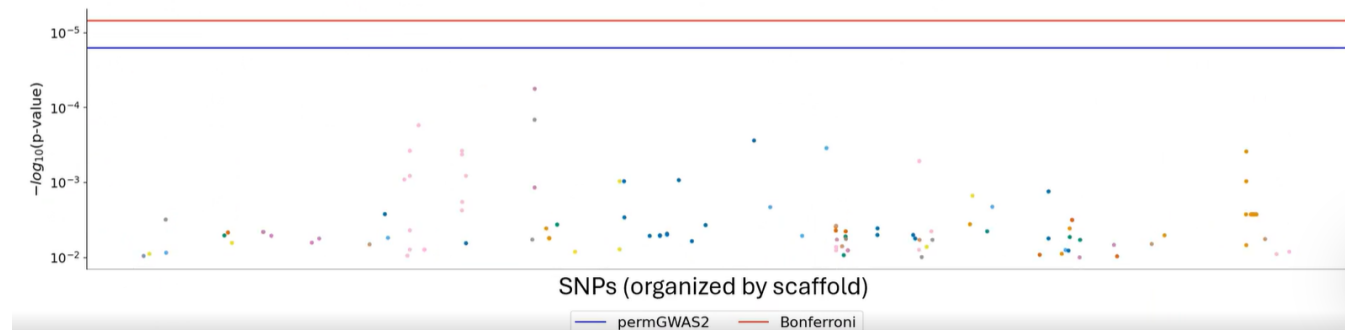
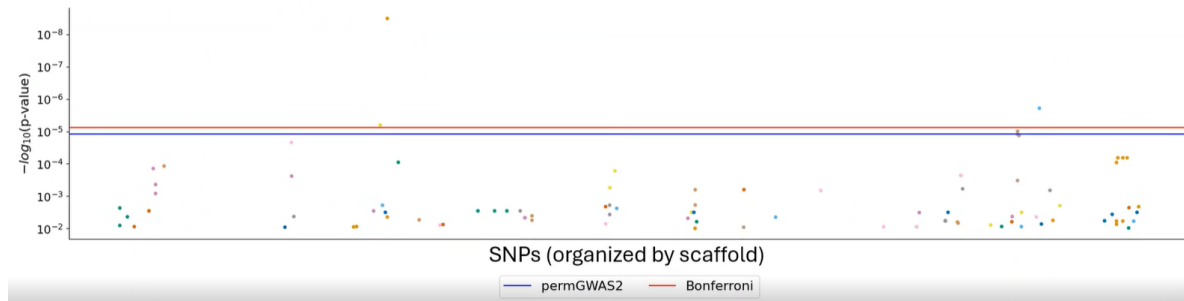
The preliminary results obtained showed that most of the G-Berries material are genetically similar and they can be grouped **in two cluster** while some raspberry genotypes are more genetically different from the rest.

These information are very useful because they will help us to take decision for our breeding program despite they are preliminary



Results

The results from the GWAS, a very important tool to find location in the genome that are important for different traits, are interesting and some potential SNPs for some traits were found for color, leaf out, flower bud swell



Impact

- The BreedingValue Open Call#3 provided a **huge added value** to our company
- Thanks to this project we have been able to **acquire a lot of knowledge** on plant genetic, especially on MAS and GWAS. These tools could be very useful to save time, space and speed the breeding process
- Opportunities to **network and exchange ideas** with other companies
- Allowed us **to improved our data collection method** by making it more effective

THANKS FOR YOUR ATTENTION