



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

Multi-model GWAS reveals key loci for horticultural traits in reconstructed garden strawberry

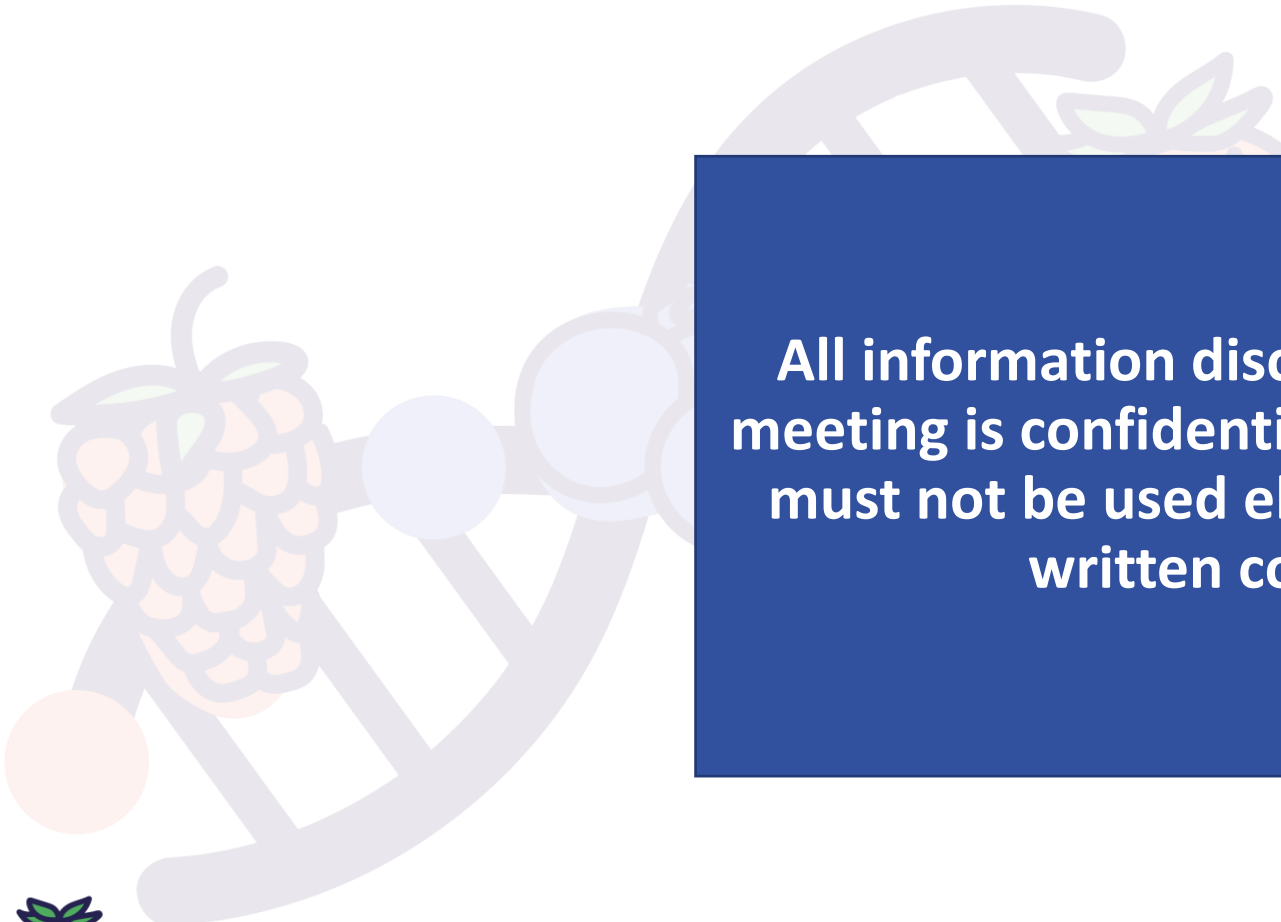
Ancona, Italy

Attiq ur Rehman
Luke, Finland



The BreedingValue project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 101000747.

Confidentiality

A faint, light purple illustration of a raspberry branch with several berries and leaves is positioned in the background, partially obscured by the central text box.

All information disclosed during this meeting is confidential information and must not be used elsewhere without written consent !

The birth of garden strawberry $\approx$ 300 years ago

Fragaria virginiana

$2n = 8x = 56$



Fragaria chiloensis

$2n = 8x = 56$



Interspecific hybridization

Breeding



Fragaria x ananassa

$2n = 8x = 56$

➤ Reproductive barriers among octoploid *Fragaria* taxa remain essentially nonexistent

03.04.2025



Breeding

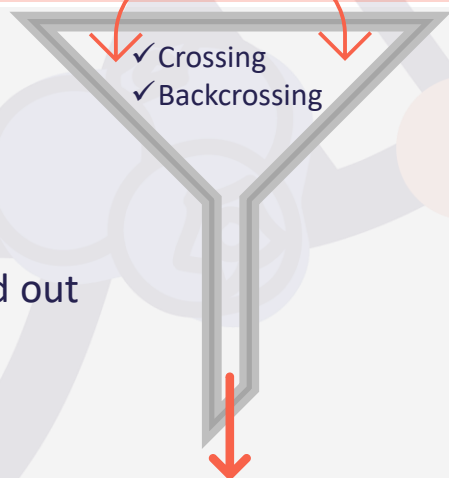
Base population

- Contain important genes
- Heritable genetic variation



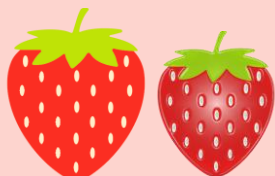
Selection breeding

- 8- 10 years
- Most plants get dropped out
- Costly



New Strawberry variety(s)

- New characteristics

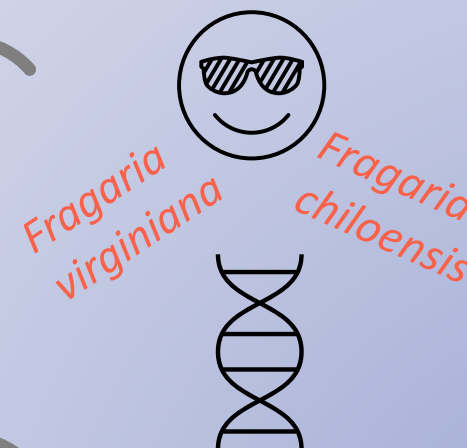


WHAT IF???



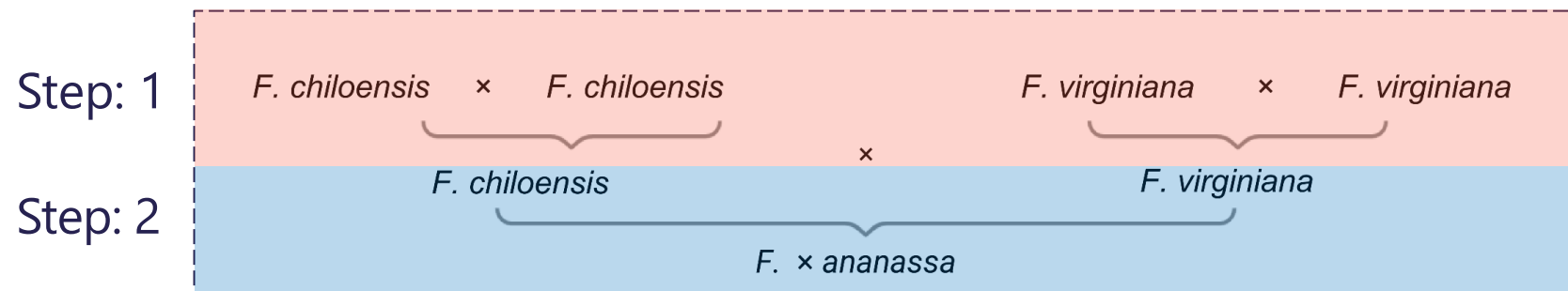
Pre-breeding

1. Progenitor species, wild relatives, and local accessions

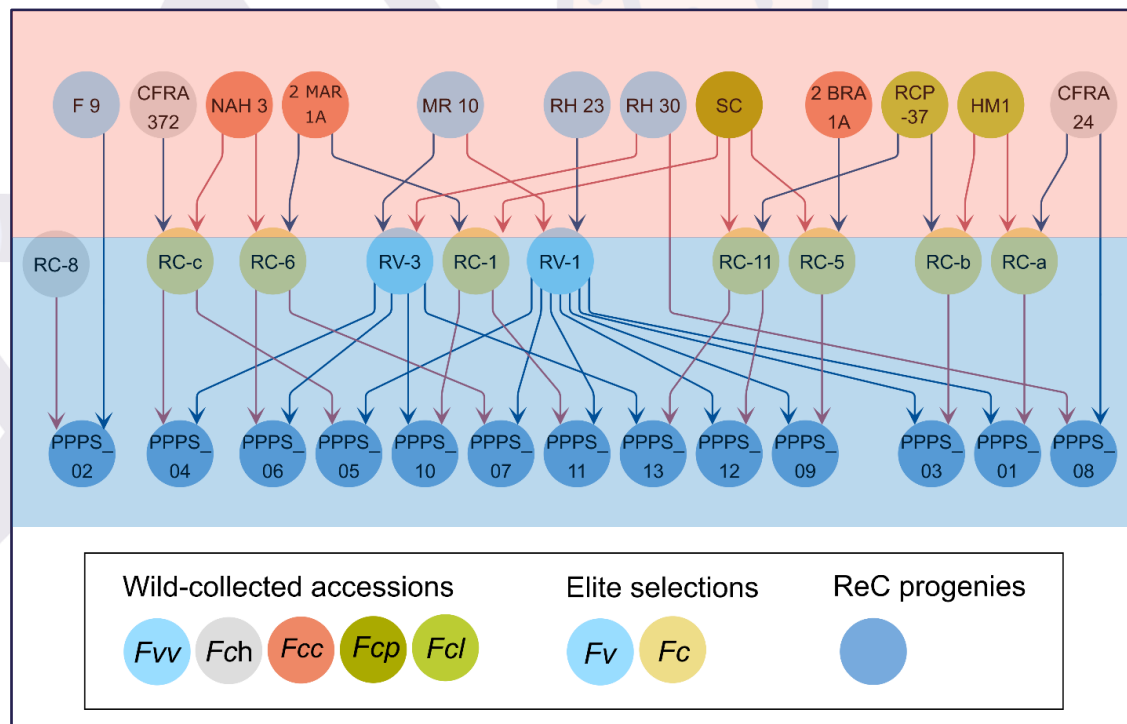


2. Implementing modern genomic tools such as GWAS and Genomic prediction

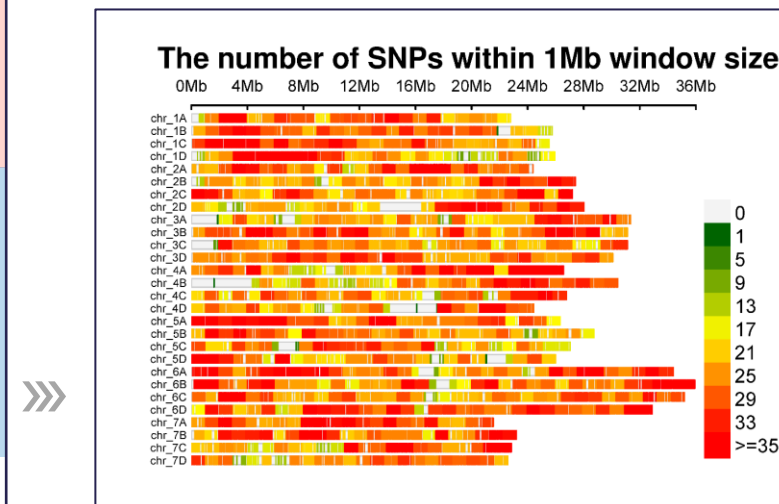
Reconstruction approach of strawberry pre-breeding



Reconstructed strawberry population (ReC)



Credits: Jakob Junkers

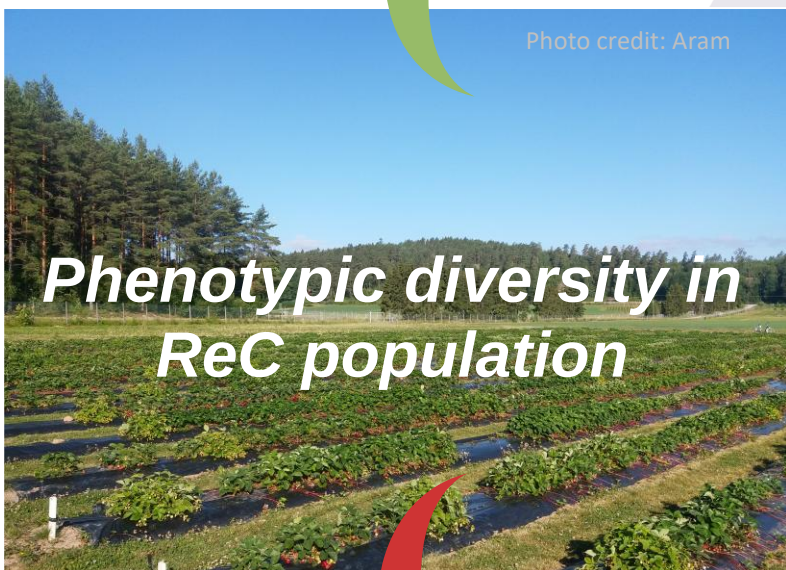
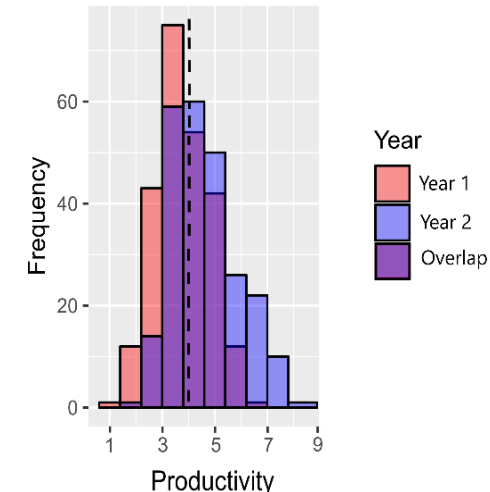
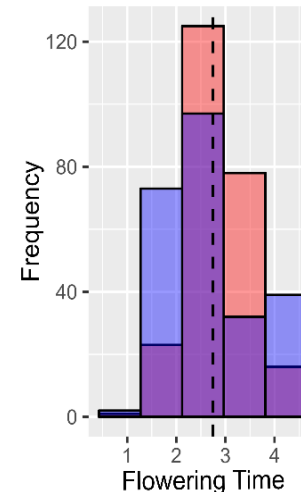
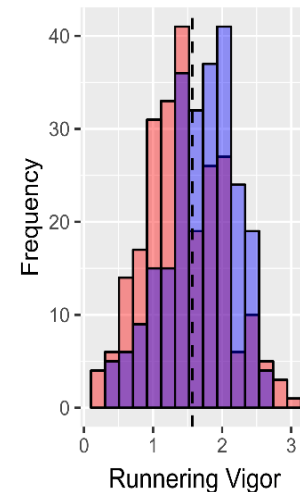
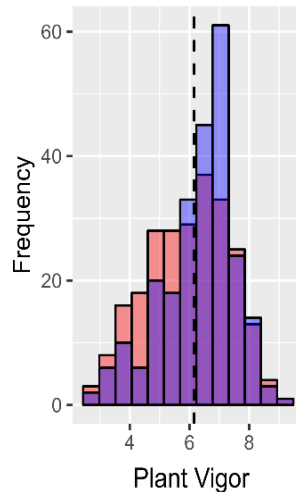
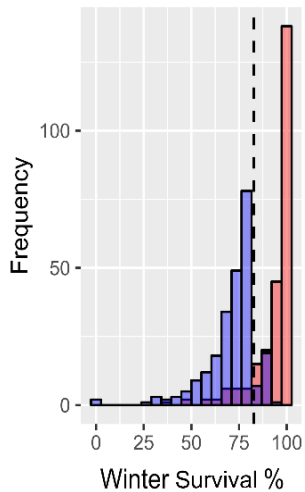


298 Rec individuals
genotyped with 50K array

1



**Plant
characteristics**



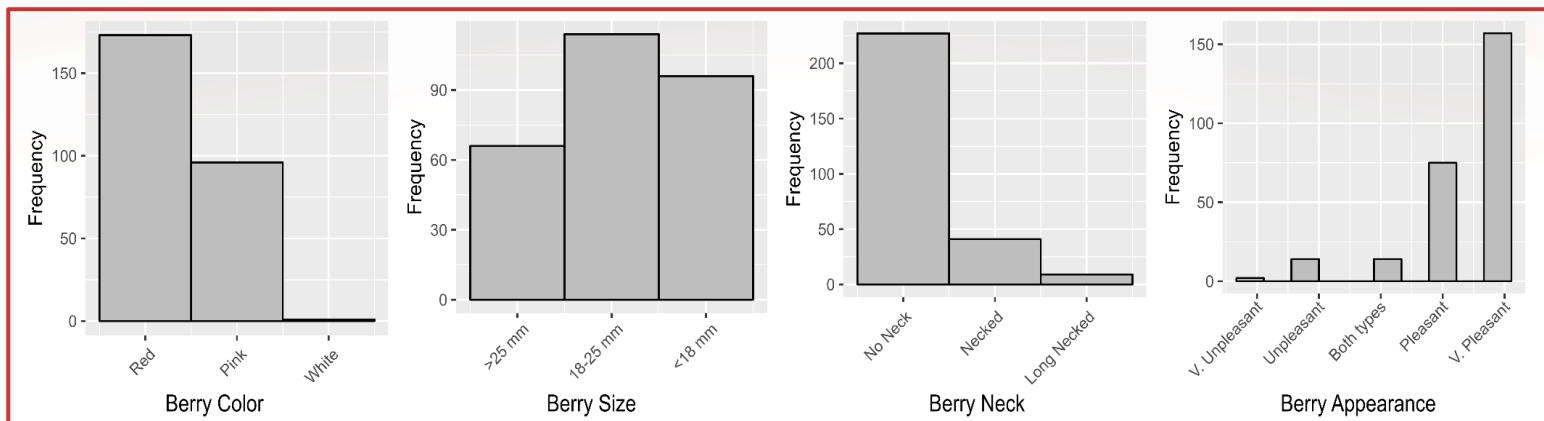
**Phenotypic diversity in
ReC population**



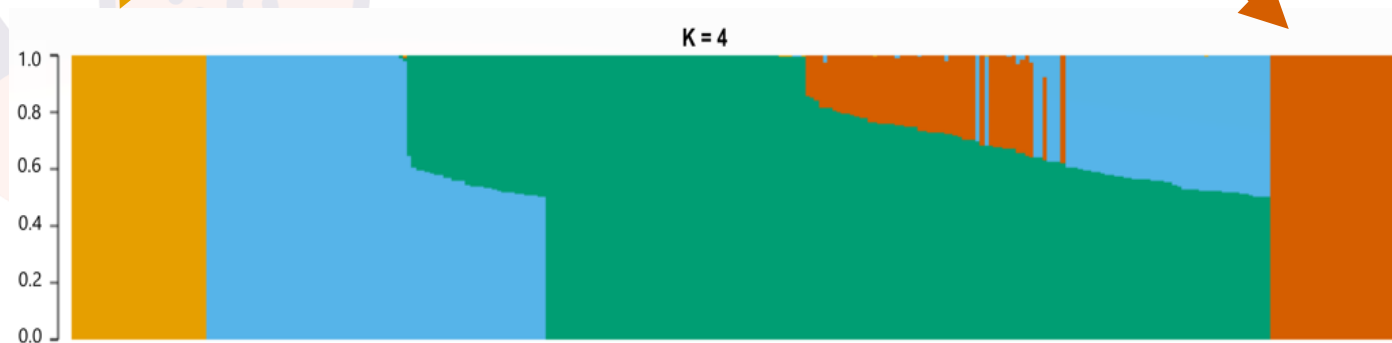
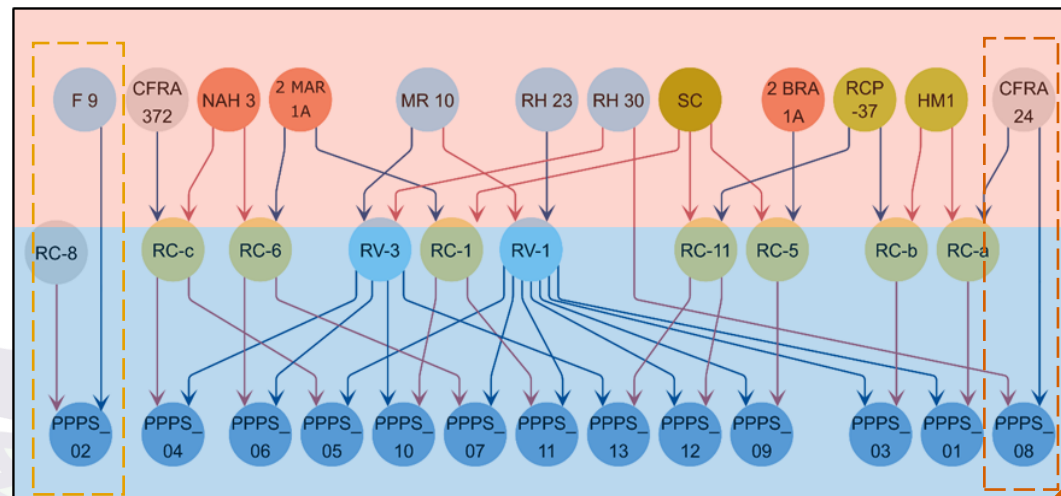
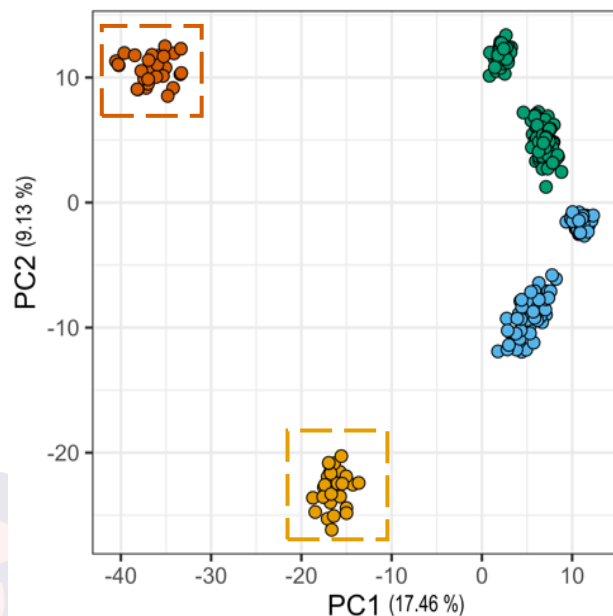
**Floral sex
characteristics**



**Fruit
characteristics**



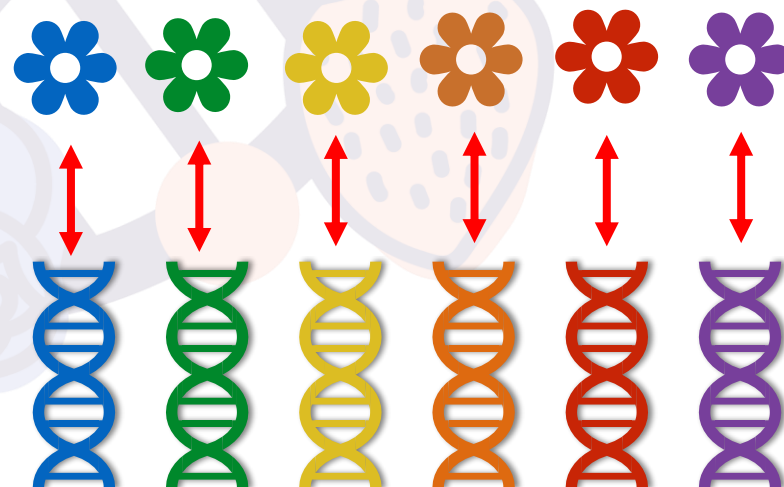
Population structure analysis



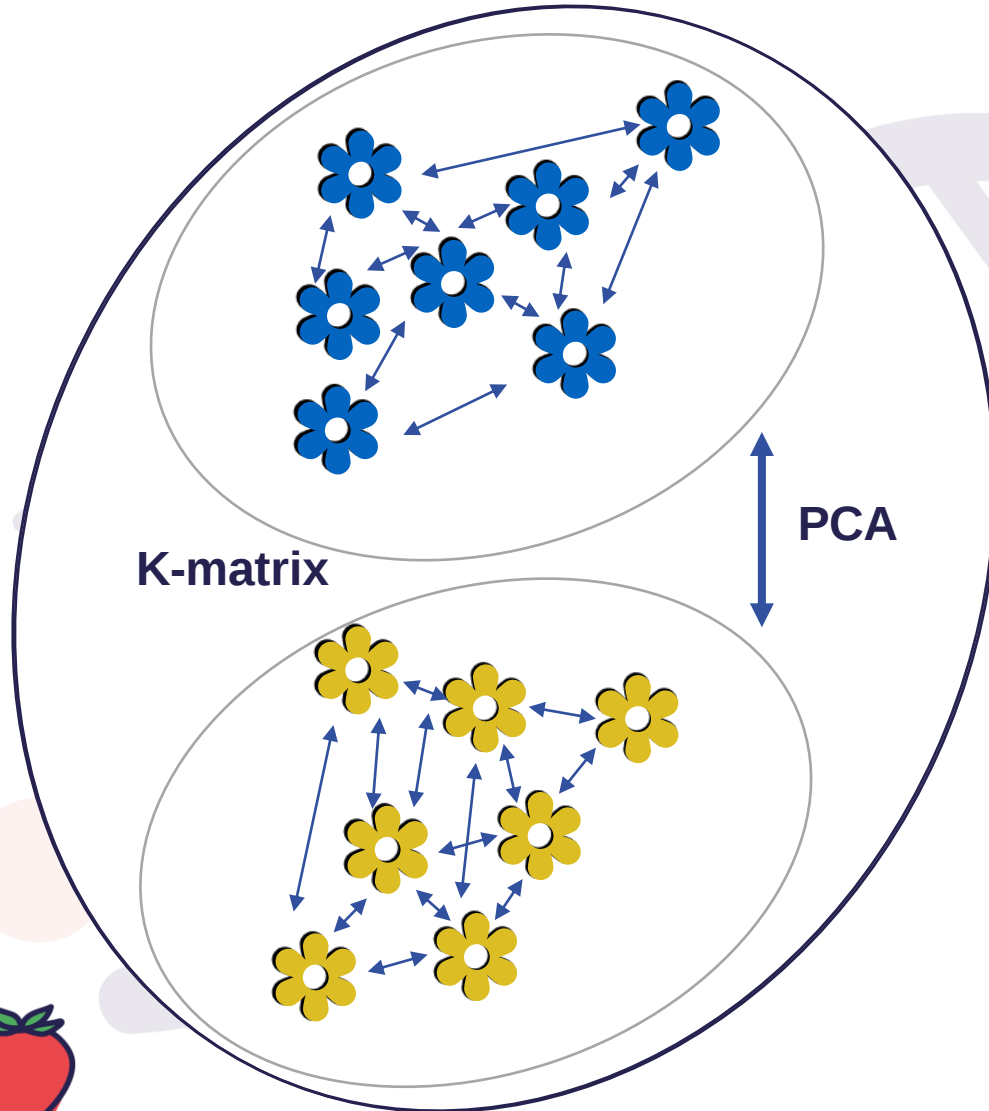
- ReC population is structured into 4 sub-populations.
- SNP based population structure analyses are in agreement with known pedigree information.
- **GWAS** was performed by accounting for **population structure**.

What is a GWAS?

Genome Wide Association Study
Link genetic differences to phenotypic differences



GWAS and Population structure



Individuals within a population / sub-population are often more related than those between populations.

Here, flowers in a population share not only causative variants, but also non-causative variants that are more common in the population (genetic background).

We take this background into account in GWAS to try to reduce the significance of non-causative variants.

PCA represents overall grouping while the **K-matrix** represents this background relatedness.

Main Results



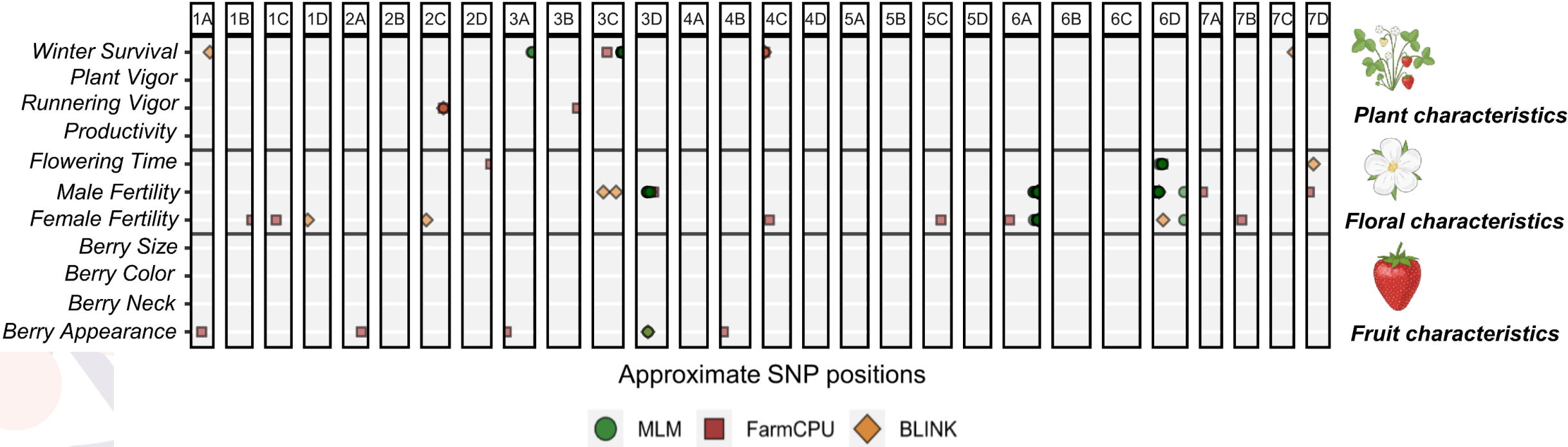
Received: 26 March 2024 | Revised: 8 June 2024 | Accepted: 10 June 2024
DOI: 10.1111/ppl.14440

ORIGINAL RESEARCH



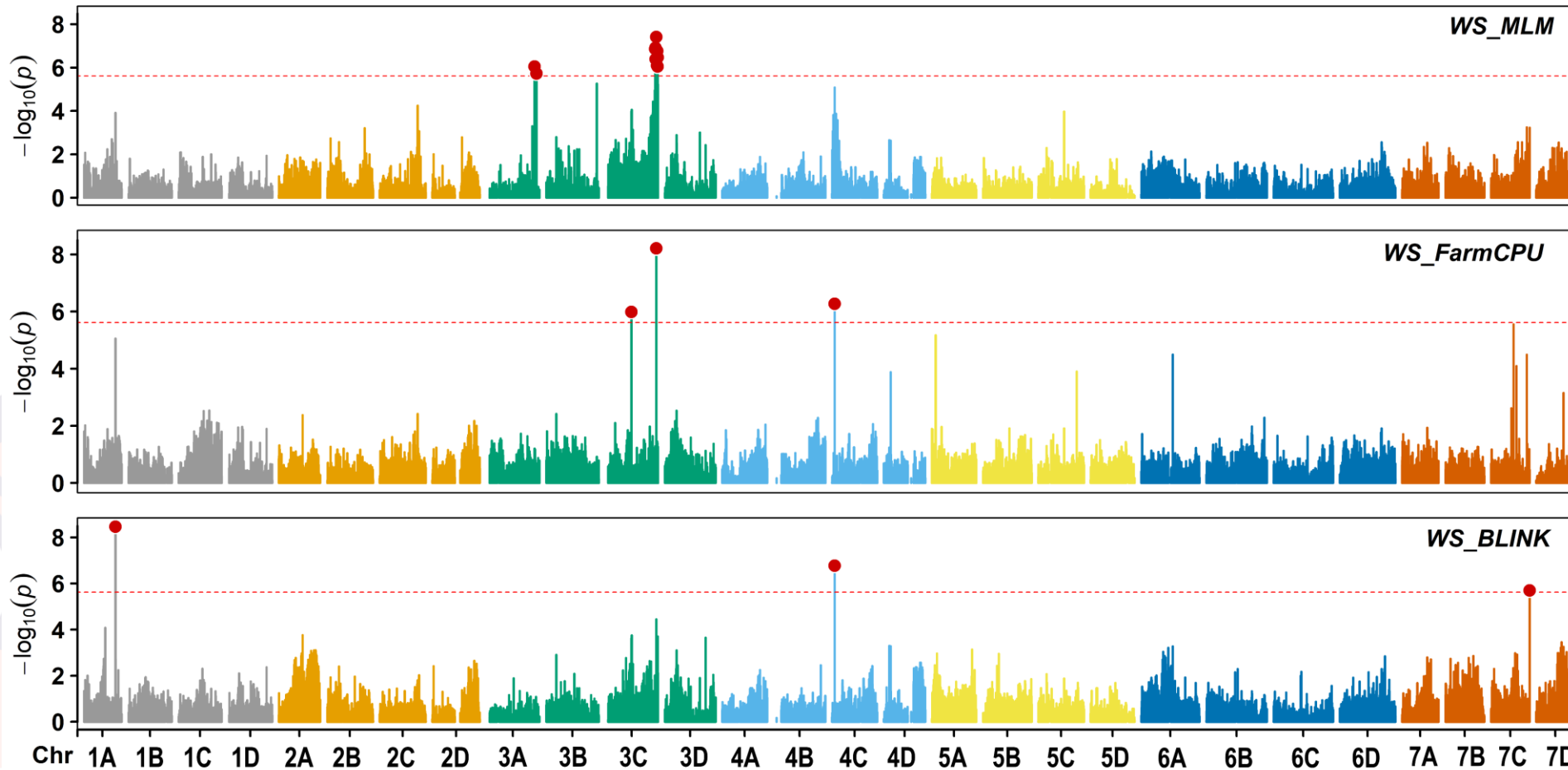
Multi-model GWAS reveals key loci for horticultural traits in reconstructed garden strawberry

Attiqu ur Rehman^{1,2} | Terhi Iso-Touru¹ | Jakob Junkers³ | Marja Rantanen¹ |
Saila Karhu¹ | Daniel Fischer¹ | Muath Alsheikh^{4,5} |
Stein Harald Hjeltne⁶ | Bruno Mezzetti⁷ | Jahn Davik³ |
Alan H. Schulman^{1,8,9} | Timo Hytönen^{8,10} | Tuuli Haikonen^{1,8}



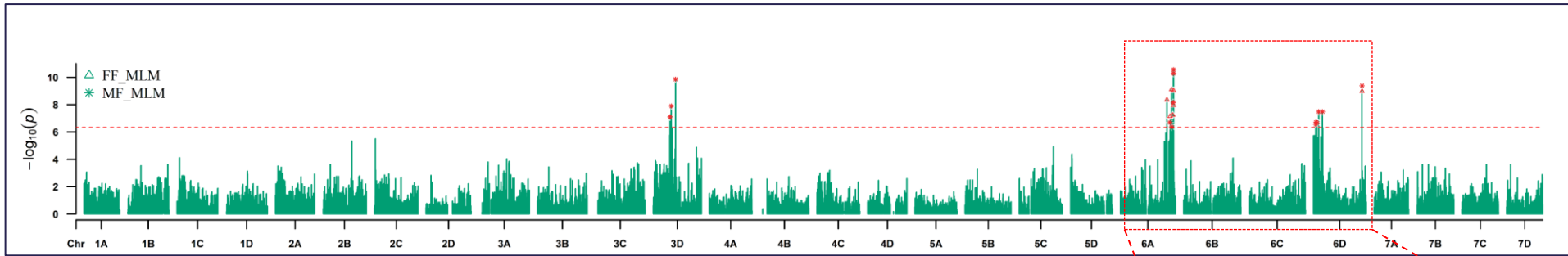
- ✓ In total, 39 QTL regions for eight traits distributed across 20 chromosomes
- ✓ 21 of these QTL regions were novel, rest were confirmed from previous studies

Winter Survival GWAS

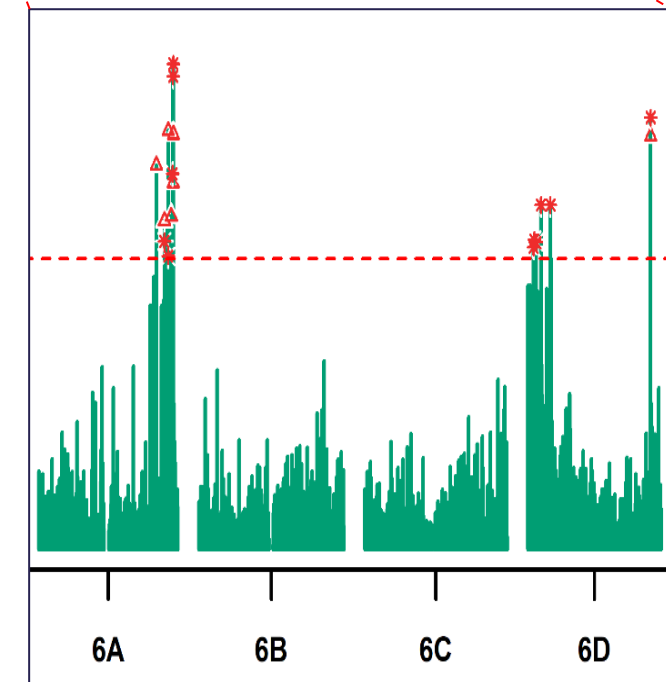


- 6 NOVEL QTL regions were identified for winter survival
- 19 plausible candidate genes were identified for winter survival in strawberry

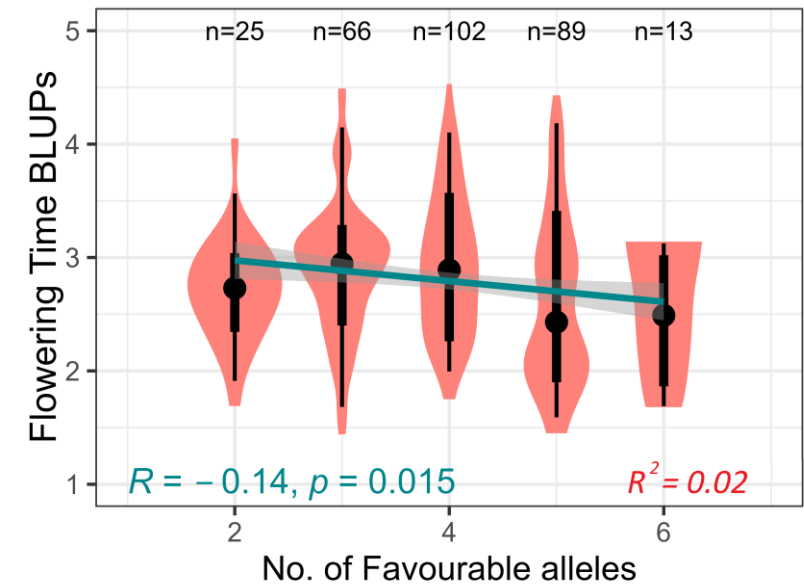
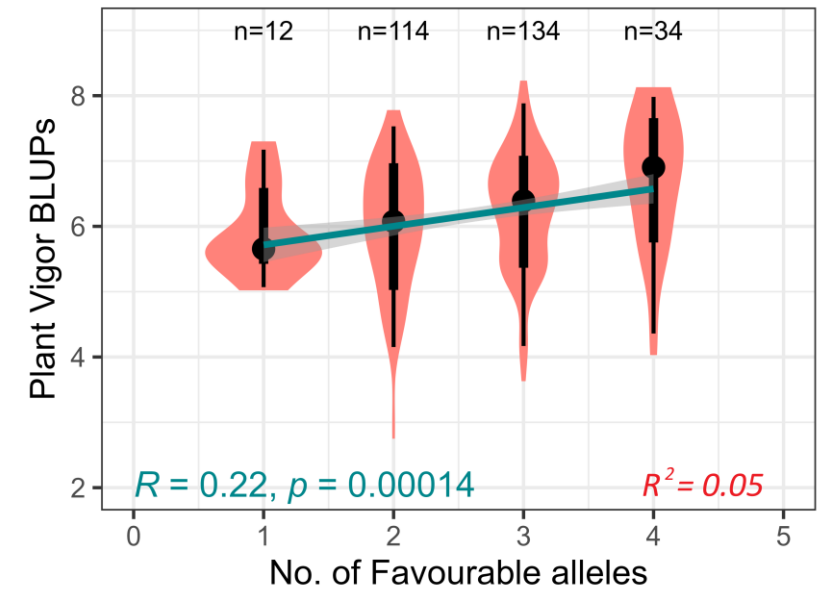
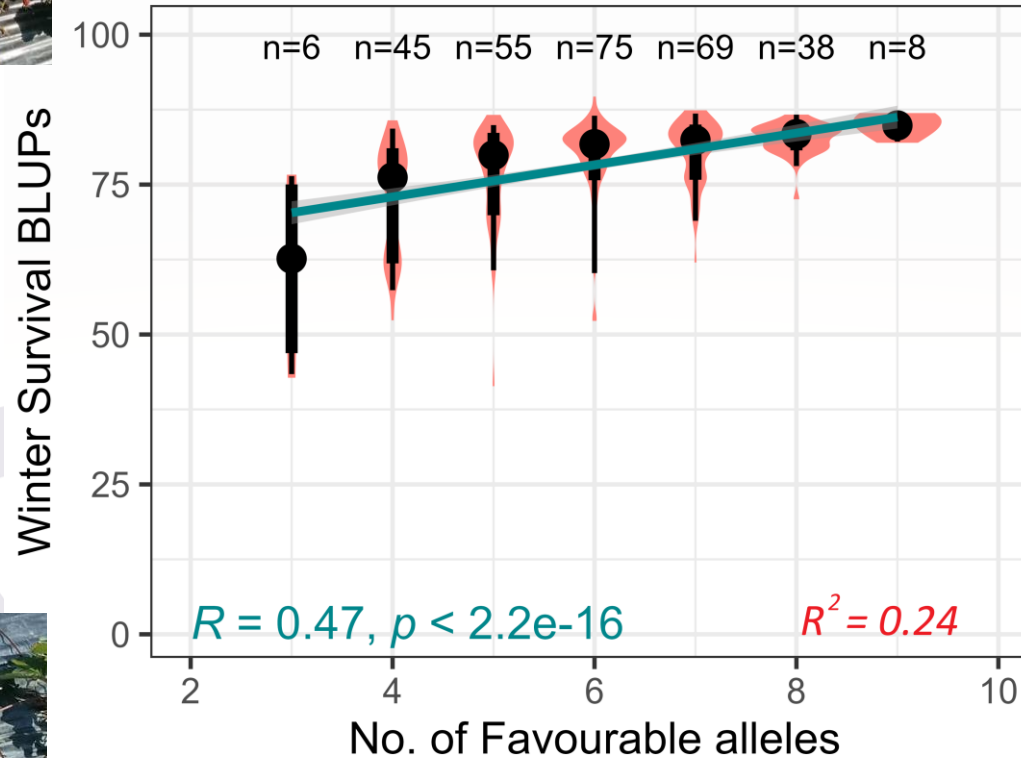
Same genomic region controlling Male and Female fertility



- Chromosome 6A and 6D harbor important loci associated with fertility traits in garden strawberry
- Previous studies have reported SDR (sex-determining region) on chromosome 6.



Were the QTLs any good for breeding?



2 Resistance to Powdery mildew in ReC population



0

a healthy plant
with no disease
symptoms



1

slight leaf curling
with no visible mycelium



2

leaf curling and
mottling



3

severe leaf curling,
reddening and visible
damage to lower surface



4

severe necrosis
and some leaf death

3
YEARS



2
YEARS



Main Results

✓ In total, 6 QTLs for Leaf and 2 QTLs for Fruit PM were discovered.

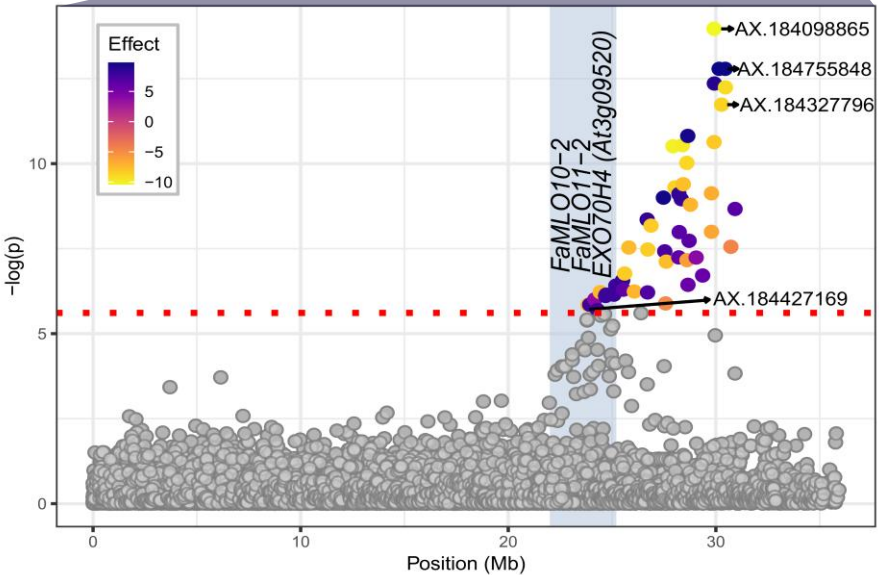
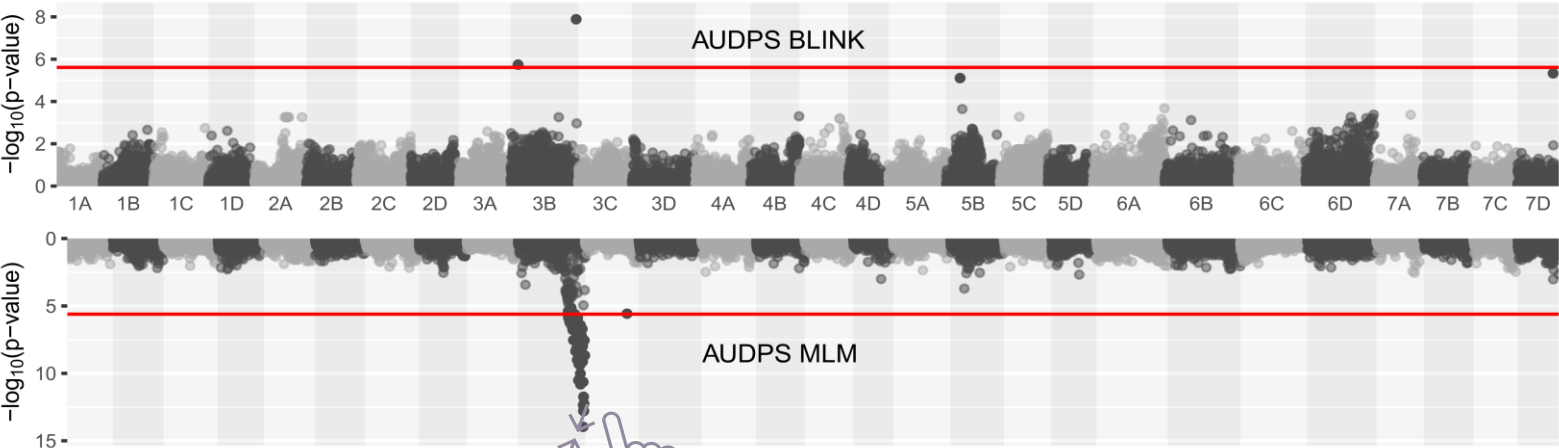
QTL	Top SNPs	Chr	Position	<i>p</i> Value	MAF	GWA model
<i>Leaf</i>						
<i>q.LPM.Rec-3B.1</i> *	AX.184227292	3B	3 705 268	2.39E−09	0.43	BLINK
				2.80E−06	0.08	BLINK
<i>q.LPM.Rec-3B.2</i> *	AX.184098865	3B	29 912 198	1.47E−15	0.21	MLM
				3.73E−09	0.21	BLINK
				1.37E−08	0.26	MLM
				1.57E−08	0.40	MLM
				1.80E−06	0.08	MLM
				2.11E−08	0.08	BLINK
<i>q.LPM.Rec-5B</i> †	AX.184751456	3B	29 787 819	2.49E−11	0.24	MLM
				1.45E−06	0.25	BLINK
<i>q.LPM.Rec-6A</i> *	AX.184960774	6A	34 273 789	1.54E−06	0.36	BLINK
				1.23E−08	0.25	BLINK
<i>q.LPM.Rec-6B</i> †	AX.184633416	6B	2 561 272	2.16E−06	0.22	BLINK
<i>q.LPM.Rec-7D</i> †3	AX.184357125	7D	19 668 633	1.80E−06	0.43	BLINK
				2.11E−07	0.07	BLINK

<i>Fruit</i>						
<i>q.FPM.Rec-3B</i>	AX.184327796	3B	30 278 425	1.18E−06	0.24	MLM
<i>q.FPM.Rec-4B</i>	AX.184557621	4B	10 404 300	1.17E−06	0.46	BLINK

Why different GWAS models?



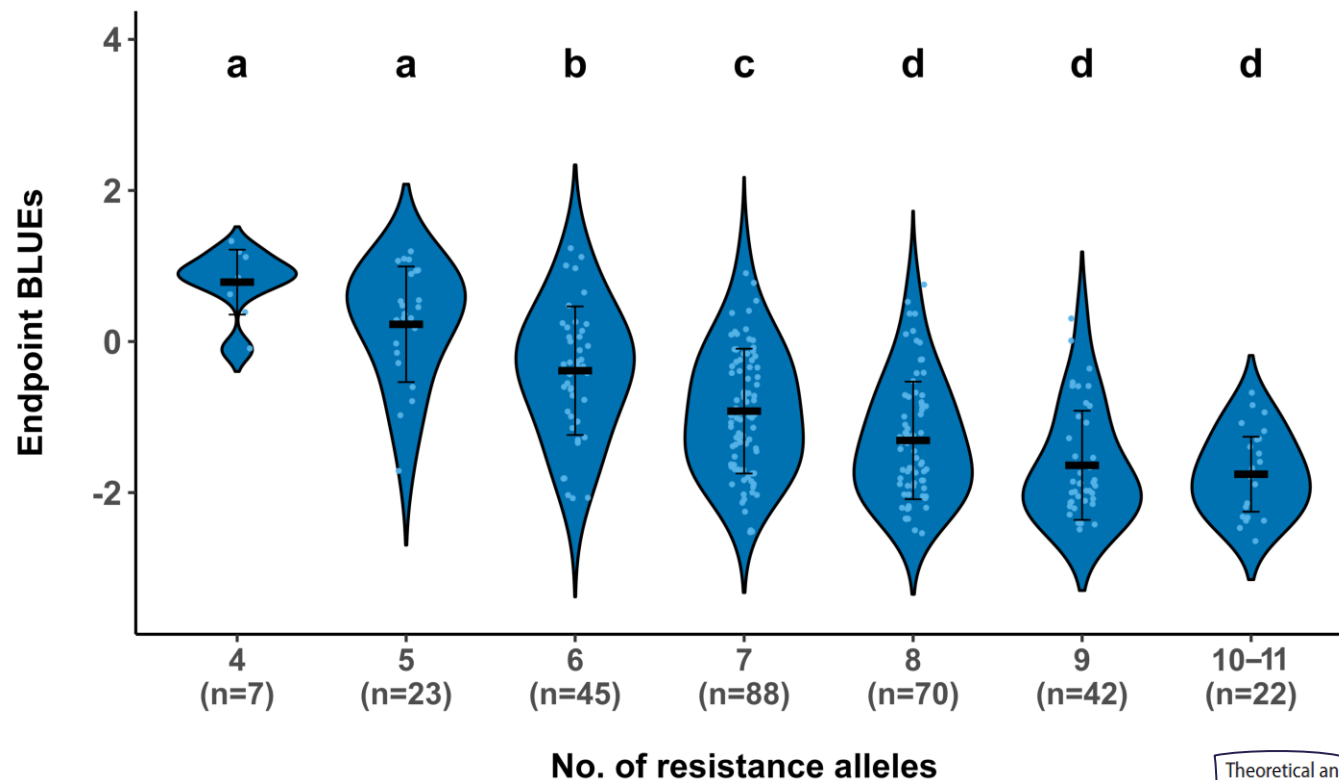
A major NOVEL QTL on Chr 3B for PM resistance in strawberry



Greenhouse leaf							
q.LPM_GH.Rec-3B	AX.184652123	3B	27 935 377	1.44E-11	0.26	BLINK	



Stacking of multiple alleles can help select against PM



Theoretical and Applied Genetics _#####_
<https://doi.org/10.1007/s00122-025-04871-6>

ORIGINAL ARTICLE

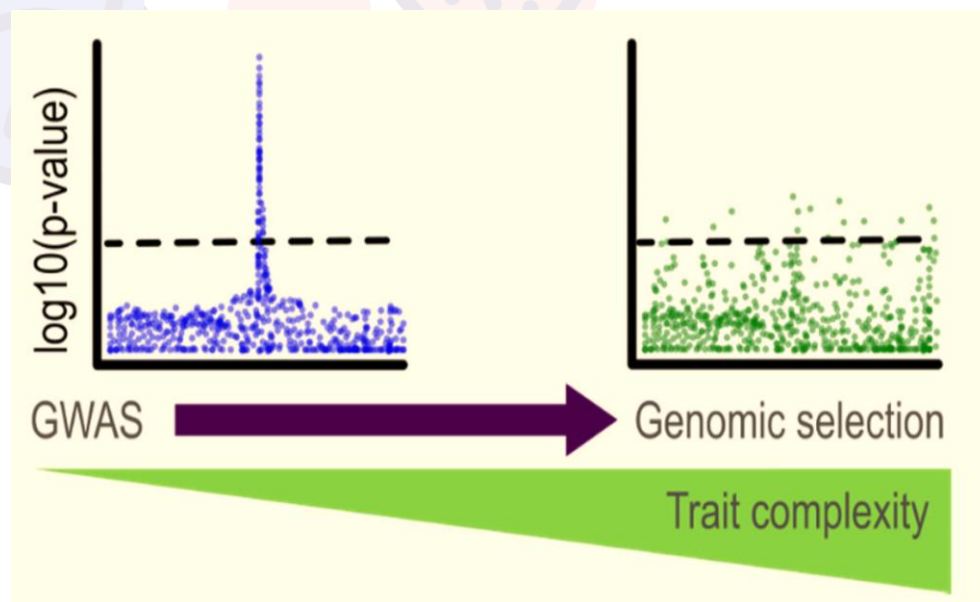


A major QTL region associated with powdery mildew resistance in leaves and fruits of the reconstructed garden strawberry

Attiq ur Rehman^{1,2,3} · Jahn Davik⁴ · Petteri Karisto¹ · Janne Kaseva¹ · Salla Karhu¹ · Marja Rantanen¹ · Ismo Strandén¹ · Timo Hytönen^{5,6} · Alan H. Schulman^{1,5,7} · Tuuli Haikonen^{1,5} 

Concluding remarks

- Reconstruction of strawberry provides a wide diversity for genetic studies and breeding in challenging climates.
- The ReC material is a potential resource for novel alleles for multiple breeding traits.
- Our GWAS results open new avenues for genome-informed breeding and deeper analysis of studied traits.
- Developing and testing KASP markers would be next potential step.
- Strategies must be devised to use ReC genotypes for next steps in breeding.



Acknowledgements

- My supervisors: **Tuuli Haikonen, Alan Schulman** and **Timo Hytönen**
- Luke's technical staff and support
- To all the co-authors and collaborators
- All the internal and external fundings



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Thank you for your attention!