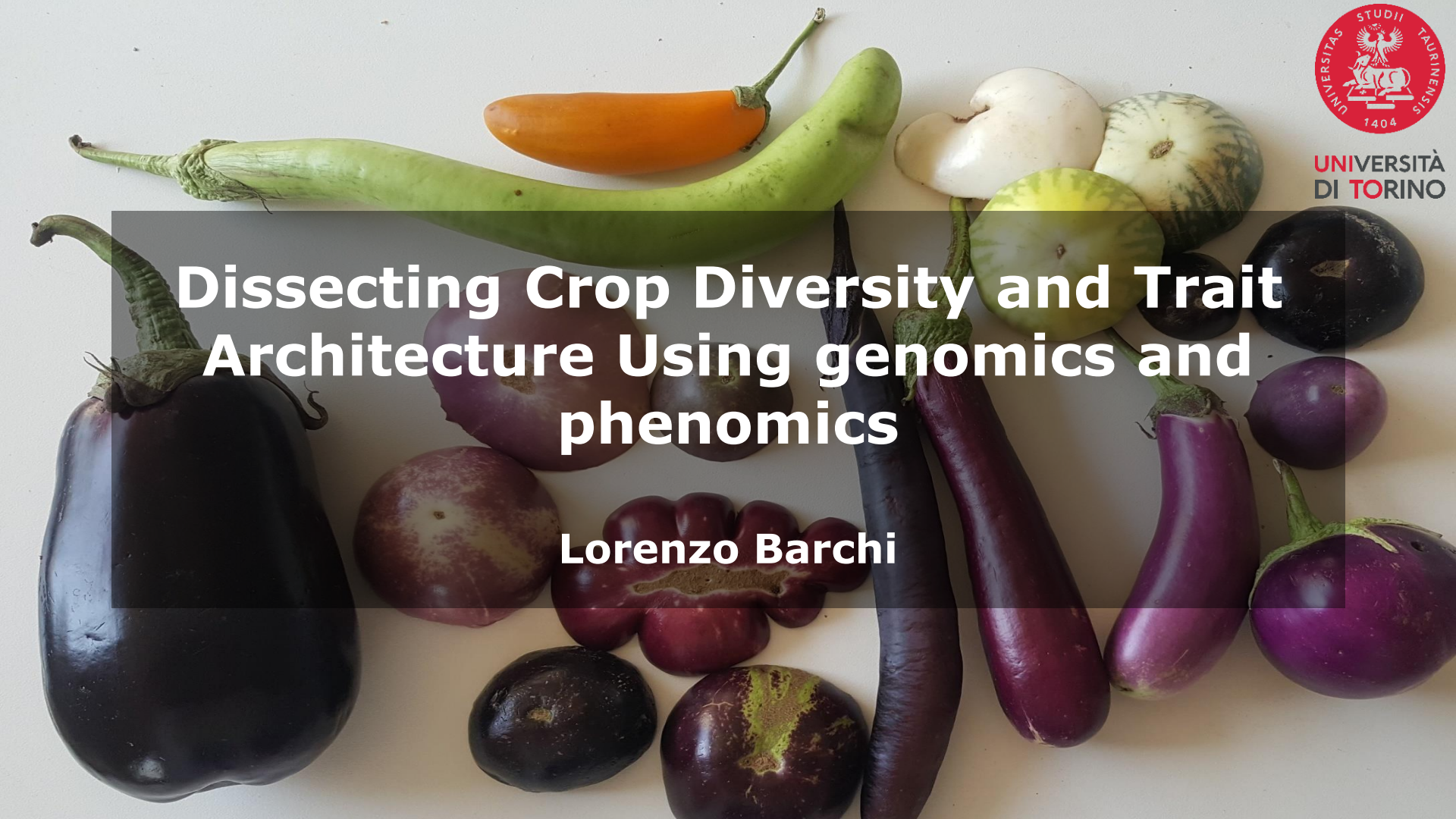


Dissecting Crop Diversity and Trait Architecture Using genomics and phenomics

Lorenzo Barchi

UNIVERSITÀ DI TORINO

Eggplant

Solanum melongena L. (2n = 2x = 24)

- **12 chromosomes**
- **Genome size 1.13 Gb**
- It belongs to the ***Solanaceae*** family and to the subgenus *Leptostemonum*, also known as **'spiny solanum' group**
- **High phenotypic diversity** observed in cultivated and wild eggplant species
- **Wild progenitor: *S.insanum***
- **Closest sister species: *S.incanum***
- **Crop wild relatives (CWR) harbor valuable genetic diversity**, including traits conferring environmental adaptability

EU-funded projects

http://www.g2p-sol.eu/

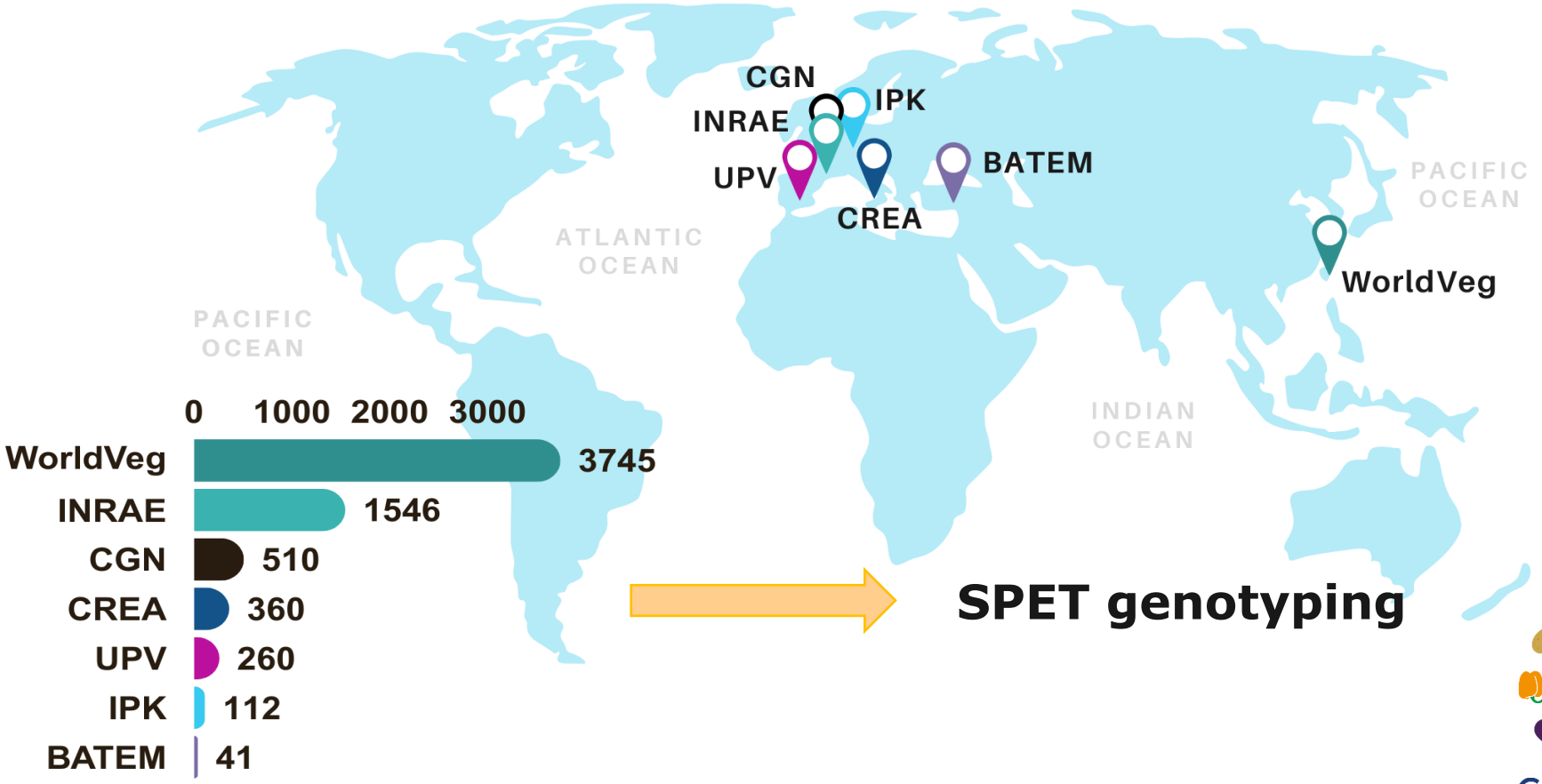
G2P-SOL (**G**enotype to **P**henotype) aimed to preserve and revive the genetic resources of the four main **Solanaceous crops, potato, tomato, pepper and eggplant**.

One of the main objectives was to build a **core collection for each crop** to perform **GWA** studies.

https://www.grace-ri.eu/pro-grace

PRO-GRACE aims to develop the concept for a novel European Research Infrastructure dedicated to cataloguing, describing, safeguarding and enhancing European plant genetic resources (**PGR**) for food and agriculture.

G2P-SOL Eggplant accessions



G2P-SOL

SPET genotyping

6,574 accessions

3,532 genotyped accessions

Single Primer Enrichment Technology (SPET) genotyping

the plant journal | SEB | SOCIETY FOR EXPERIMENTAL BIOLOGY

Original Article | Open Access

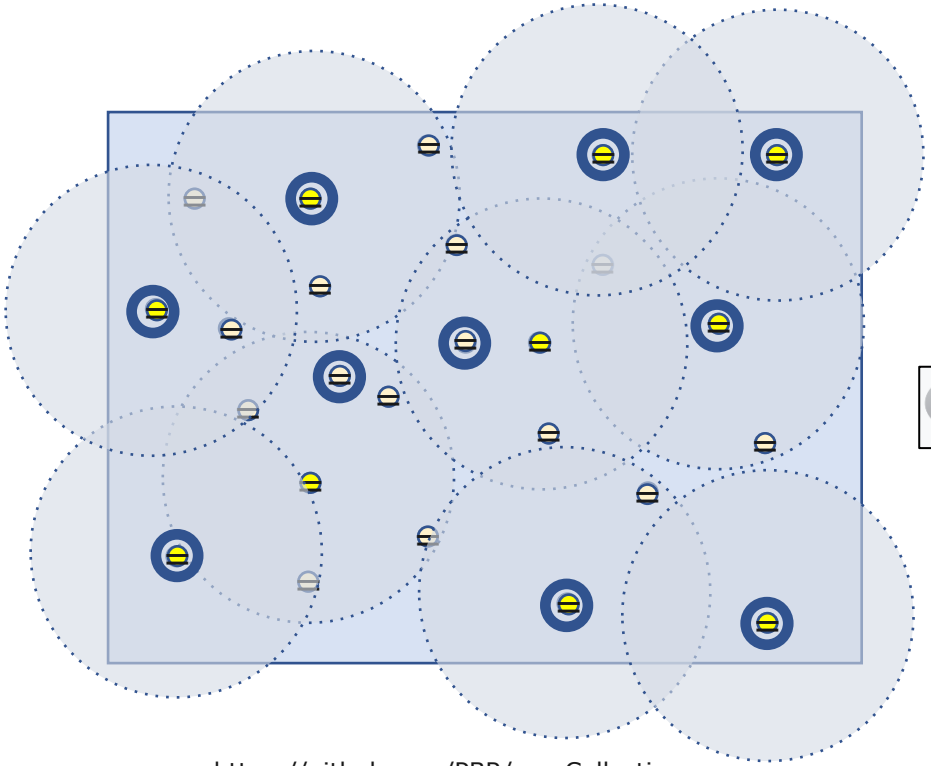
Analysis of >3400 worldwide eggplant accessions reveals two independent domestication events and multiple migration-diversification routes

Lorenzo Barchi, Giuseppe Aprea, M. Timothy Rabanus-Wallace, Laura Toppino, David Alonso, Ezio Portis, Sergio Lanteri, Luciana Gaccione, Emmanuel Omondi, Maarten van Zonneveld, Roland Schafleitner, Paola Ferrante, Andreas Börner, Nils Stein, Maria José Díez, Veronique Lefebvre, Jérémy Salinier, Hatice Filiz Boyaci, Richard Finkers, Matthijs Brouwer, Arnaud G. Bovy, Giuseppe Leonardo Rotino, Jaime Prohens, Giovanni Giuliano ... See fewer authors

First published: 08 September 2023 | https://doi.org/10.1111/tpj.16455

Build up the eggplant core collection

SPET genotyping



VCF

Distance Matrix

88 preselected individuals

WAGENINGEN UNIVERSITY & RESEARCH

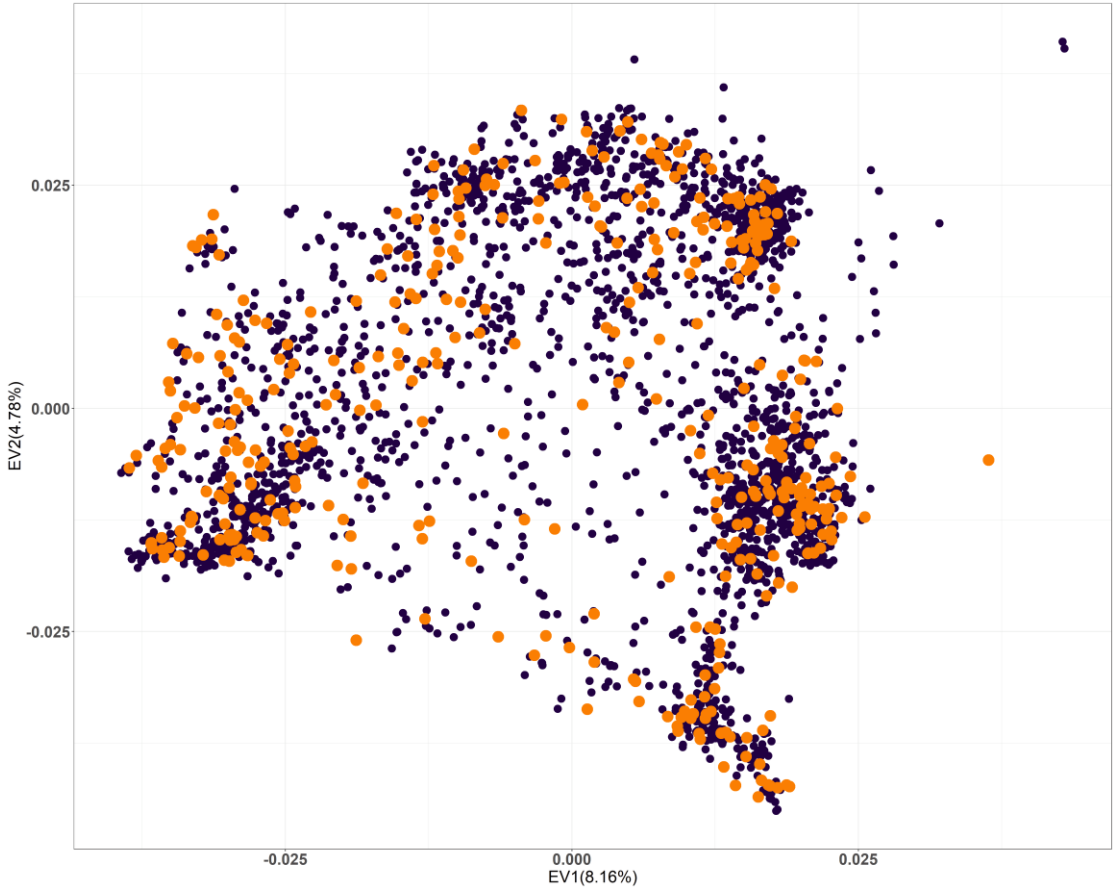
R

CoreCollection algorithm

Eggplant core collection 450 accessions

https://github.com/PBR/coreCollection

Build up the eggplant core collection

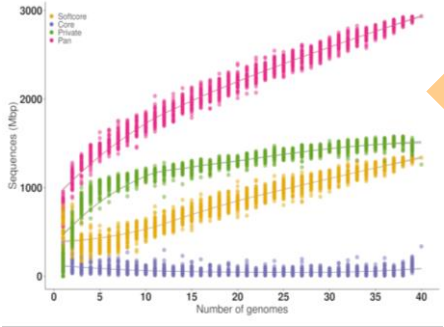


	Accessions
Initial Core collection	**450**
Phenotyped accessions	**415**
-*S. melongena*	390
-Wild species	25
Accessions excluded as heterogeneous	59
Genotyped accessions	**368**

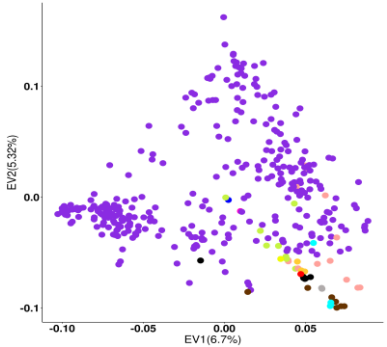
Eggplant core collection

Graph-based pangenomes and pan-phenome of eggplant and its wild relatives

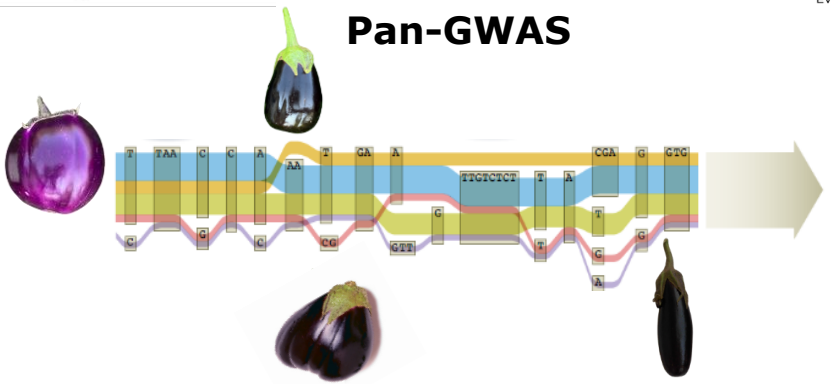
Modelling



Diversity



Pan-GWAS

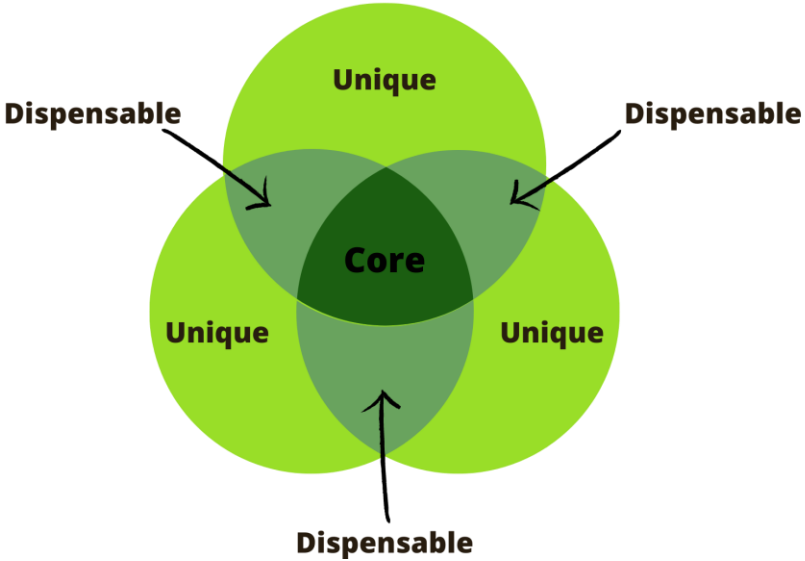


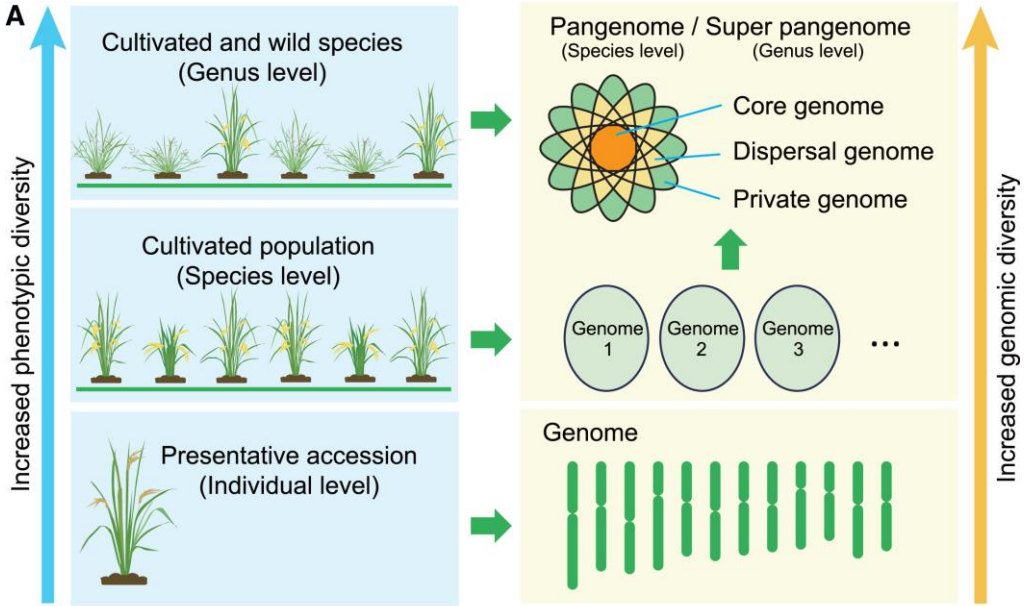
nature communications

"Graph-based pangenomes and pan-phenome provide a cornerstone for eggplant biology and breeding"

Gaccione *et al.* ***accepted***

Pangenome and super pangenome concepts

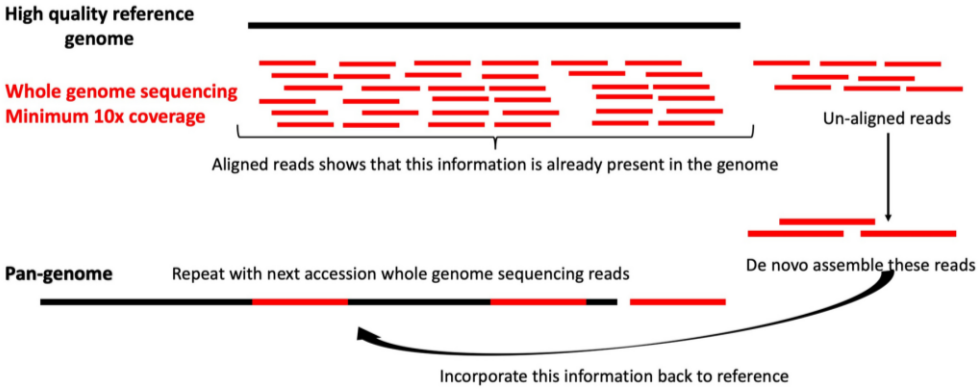




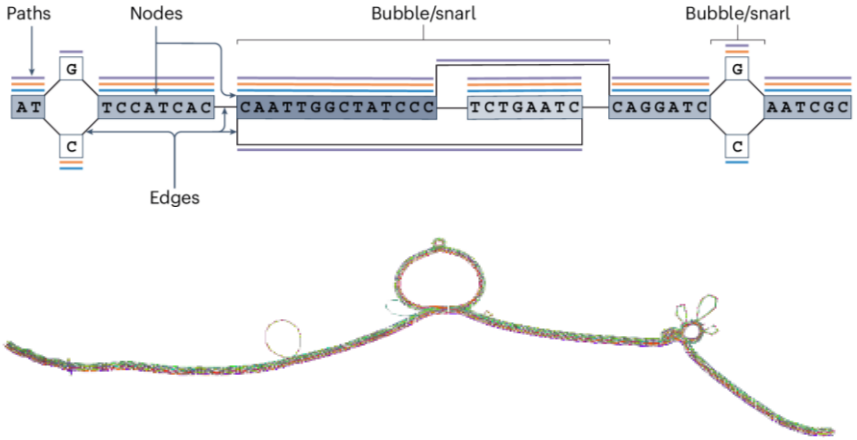
From He *et al.* 2025

Pangenome construction approaches

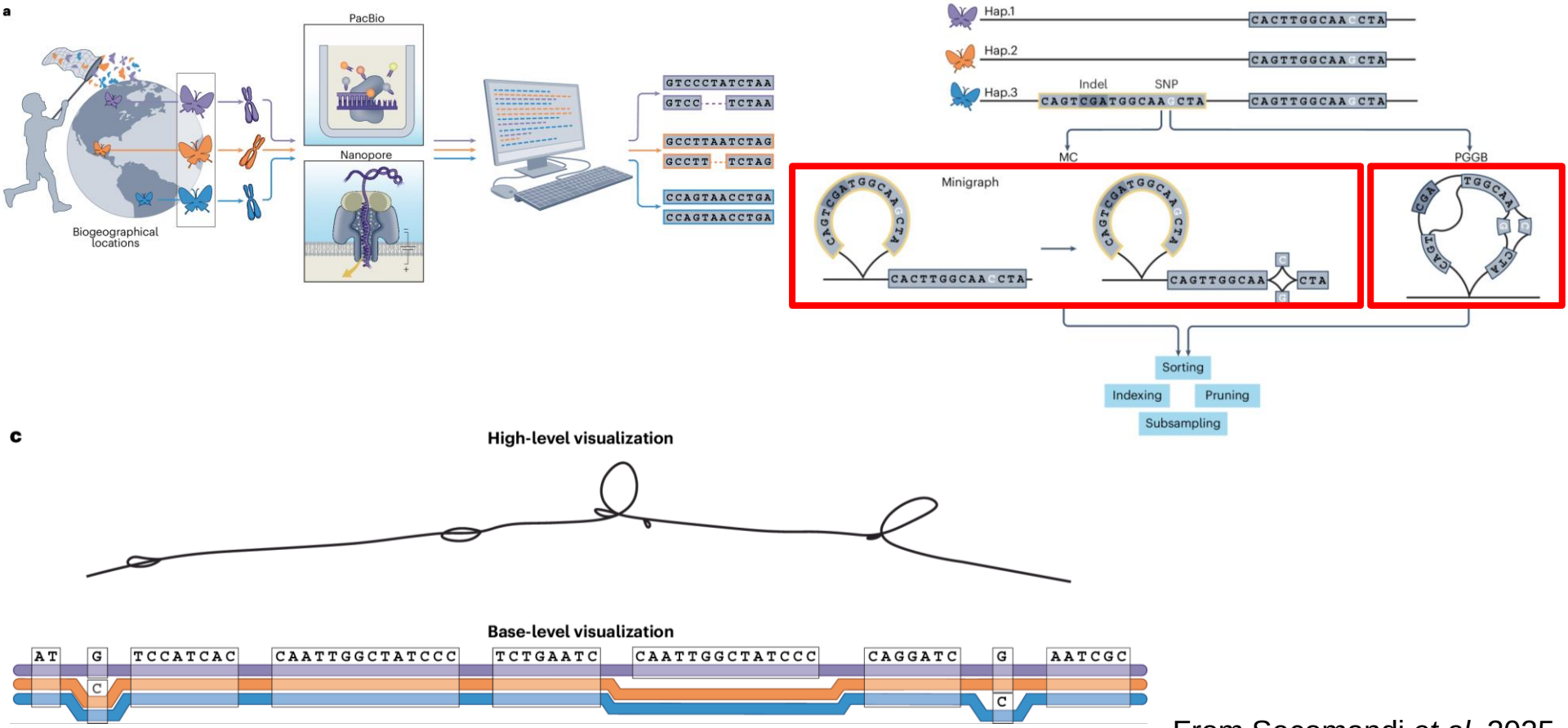
Linear Pangenome



Graph-based Pangenome



Pangenome graphs building pipeline

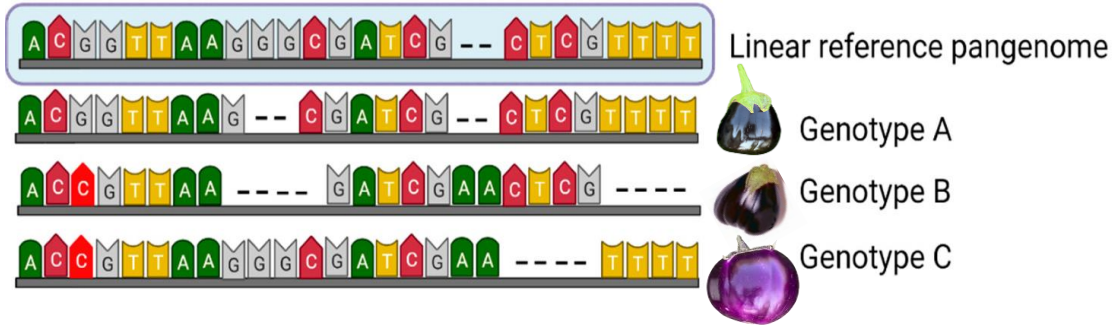


From Secomandi *et al.* 2025

Eggplant pangenome

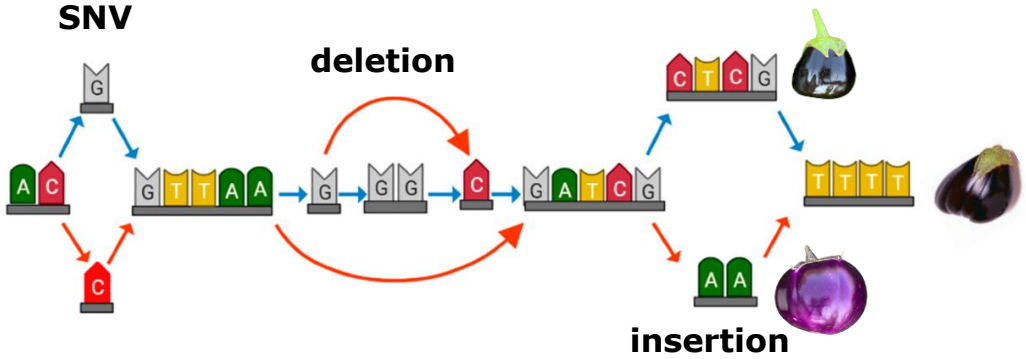
Linear pangenome

Already published
(24 *S.melongena, 1 S. incanum* and 1 *S. insanum* accessions)
Barchi et al., 2021



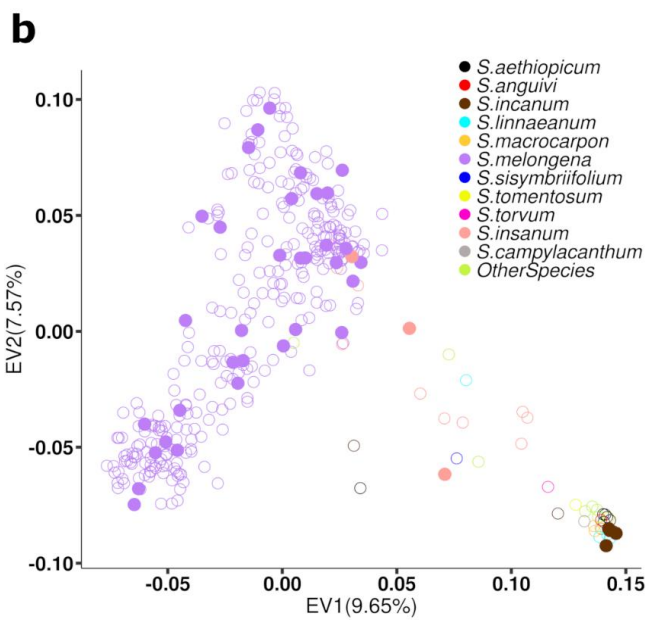
Graph-based pangenomes

33 *S.melongena, 4 S. incanum* and 3 *S. insanum*



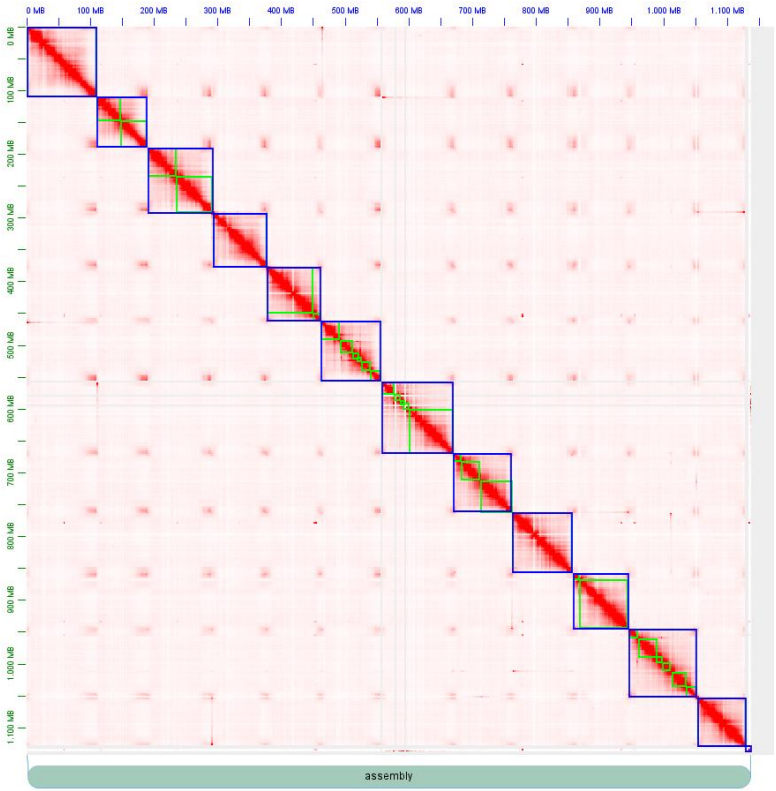
Pangenome backbone

Core collection = 368 accessions (*S. melongena, S. insanum, S. incanum* and other wild relatives)



Chromosome-scale genome assembly: GPE001970

6 *S.melongena*, 2 *S. insanum* and 2 *S. incanum* accessions



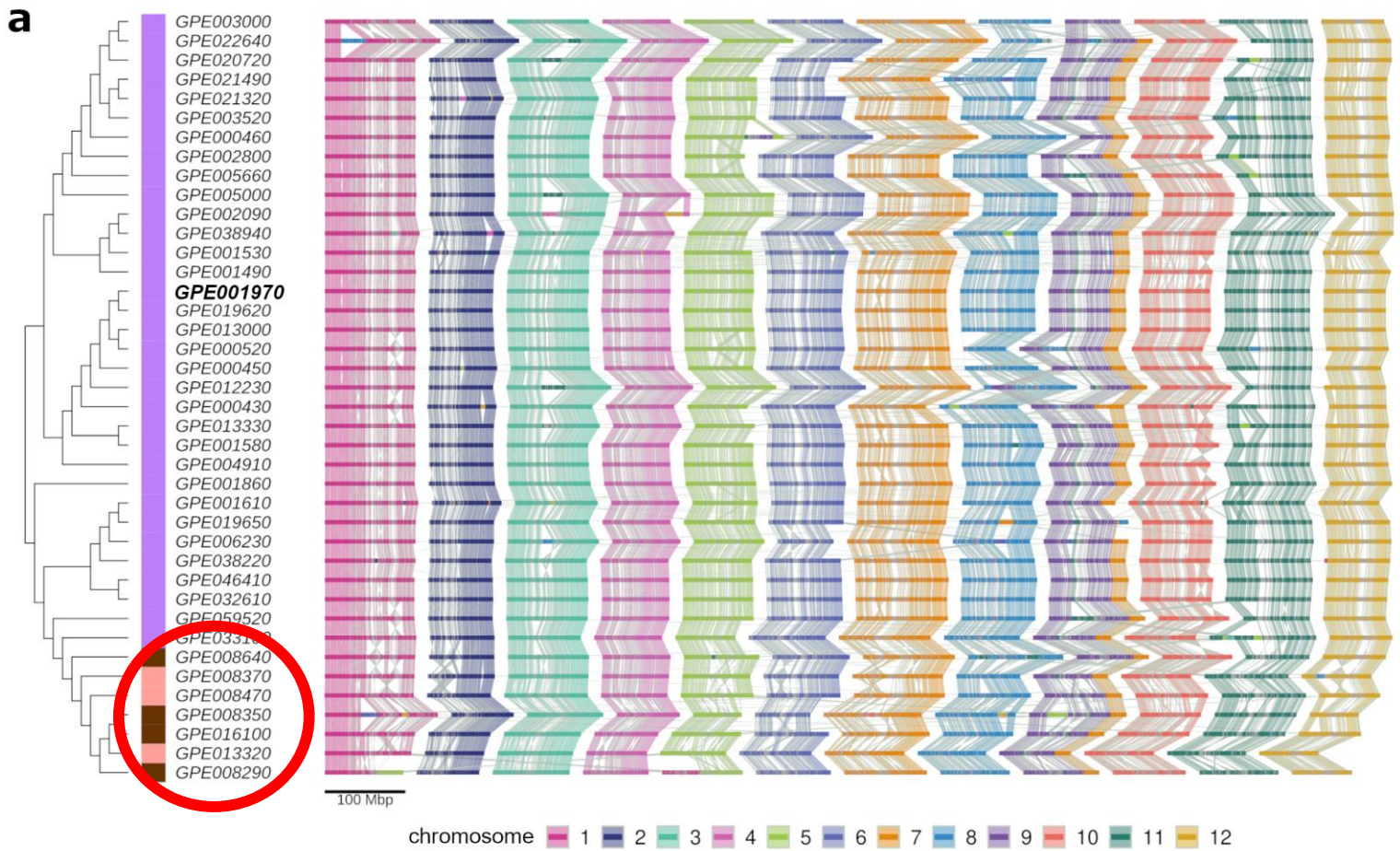
Reference line "67/3" Version 4.1

Chr	Length (bp)
1	114,254,532
2	78,087,157
3	98,477,688
4	82,644,910
5	82,765,812
6	96,735,250
7	108,824,248
8	90,718,205
9	92,127,910
10	87,162,497
11	105,637,937
12	76,208,483
0	**50,774,894**

Reference line "67/3" Version 5

Chr	Length (bp)
1	112,110,000
2	80,031,836
3	101,568,281
4	84,526,223
5	86,643,817
6	93,152,865
7	112,005,674
8	92,652,595
9	95,583,805
10	88,043,255
11	106,951,443
12	77,153,890
0	**6,122,066**

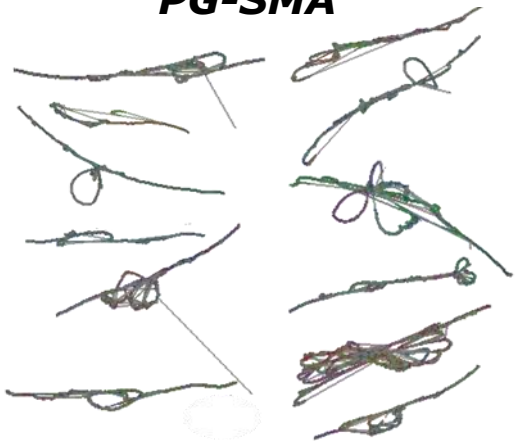
Synteny map of the 40 chromosome-scale eggplant accessions



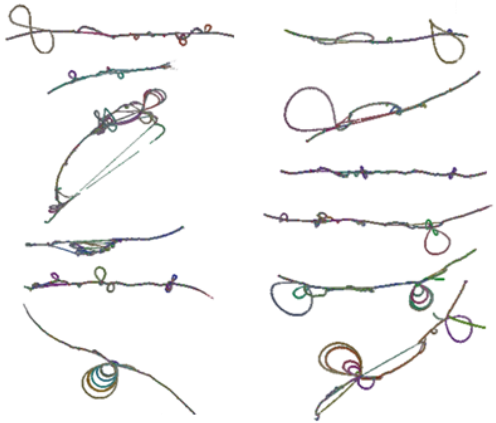
PGGB

Minigraph-Cactus

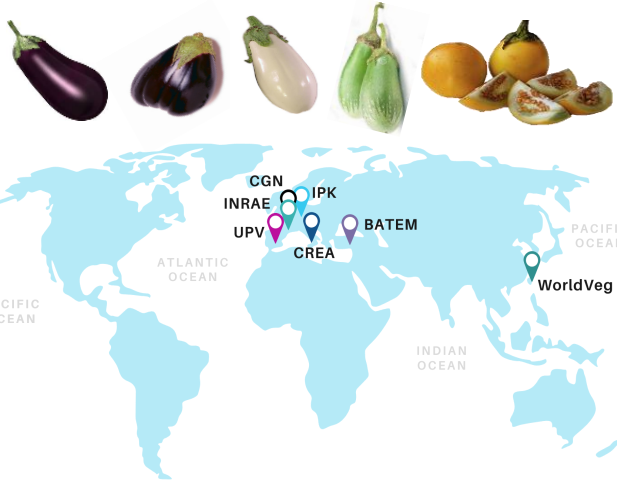
Super pangenome graph of the Eggplant clade "PG-SMA"



S. melongena pangenome graph "PG-SM"

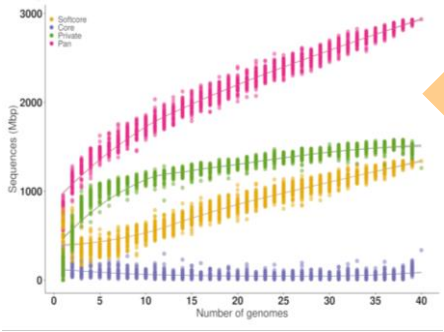


Eggplant core collection

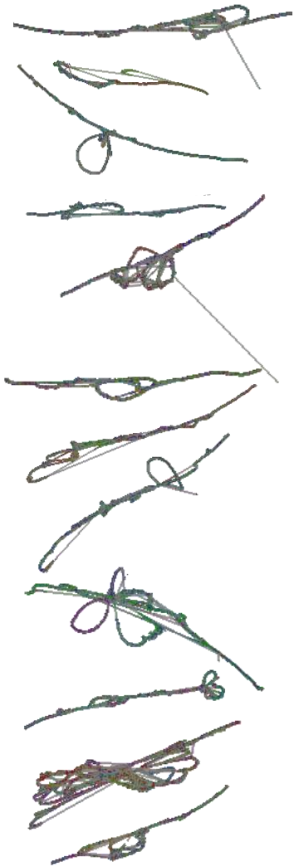


Graph-based pangenomes of eggplant and its wild relatives

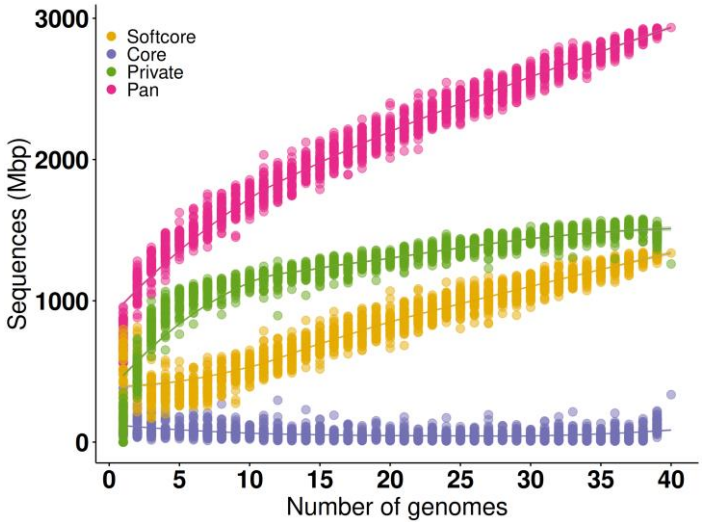
Modelling *PG-SMA*



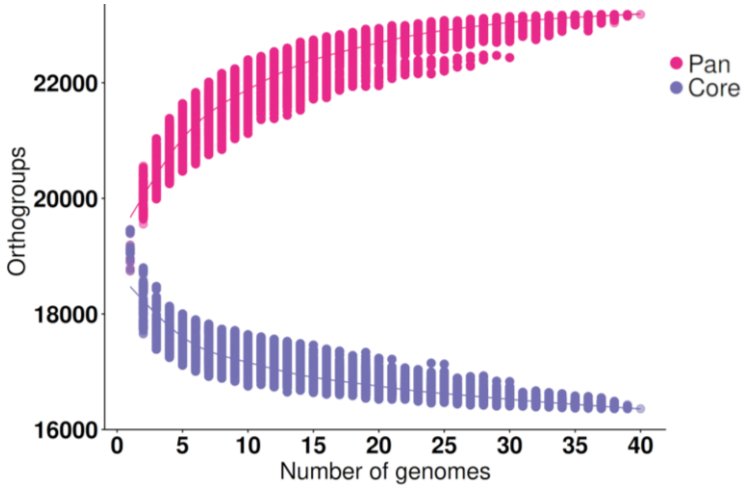
Graph-based pangenome of the ‘Eggplant’ clade (*PG-SMA*)



Sequence-level modeling



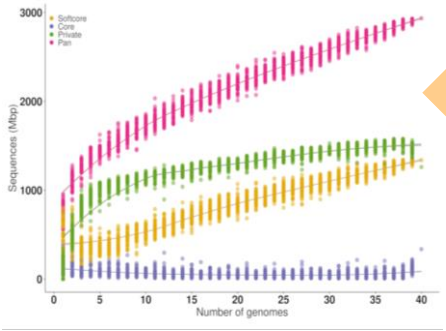
Gene-level modeling



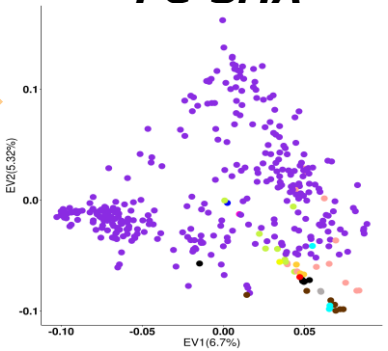
Eggplant core collection

Graph-based pangenomes of eggplant and its wild relatives

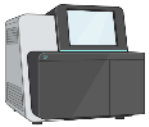
Modelling *PG-SMA*



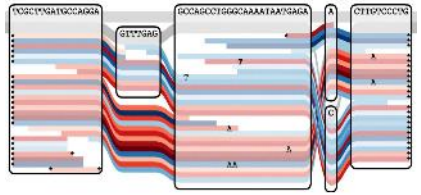
Diversity *PG-SMA*



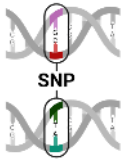
CC re-sequencing at 20X

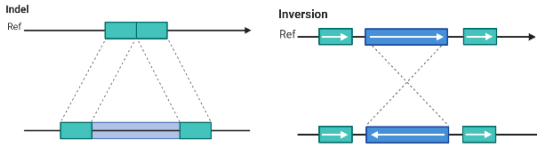


Align short reads to the *PG-SMA* graph
(vg giraffe)

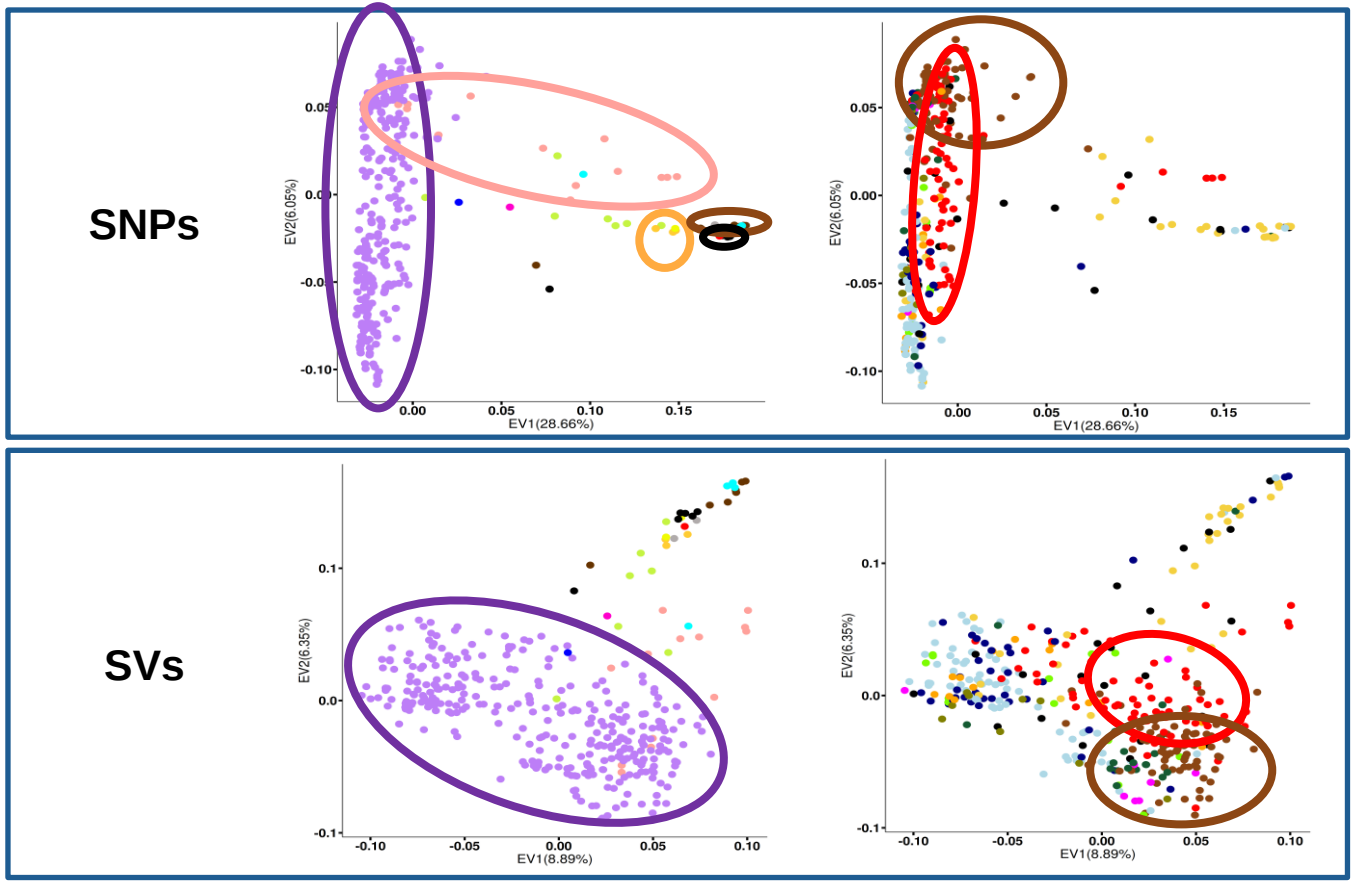


SNPs and SVs calling
(vg call)





Phylogeny and population structure of *S. melongena* and wild relatives using SNPs and SVs genotyped on *PG-SMA*

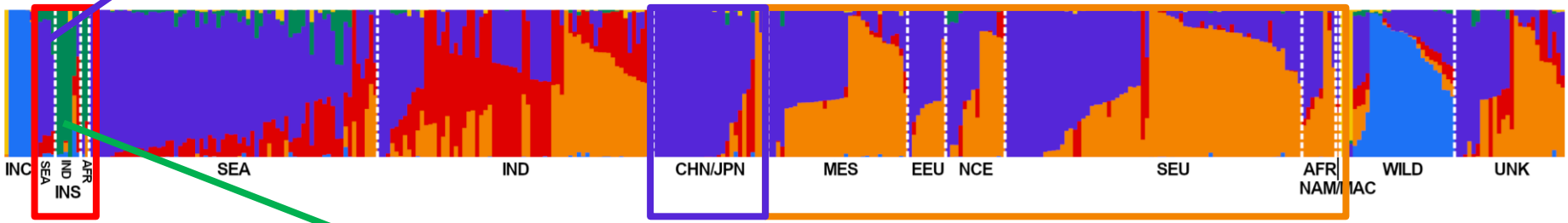


Population structure of *S. melongena* and wild relatives using SNPs genotyped on *PG-SMA*

snmf analysis: best k=6

Southeast Asian *S. insanum* genetic signatures remain detectable in SEA accessions

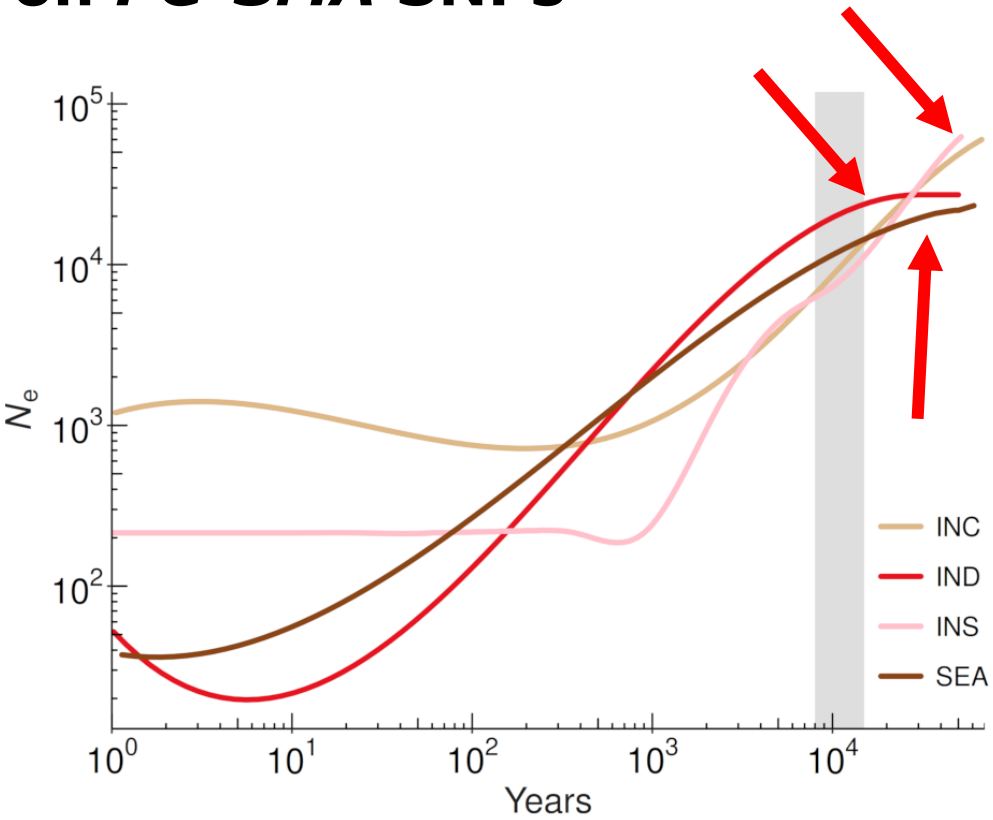
Southeast Asian ancestry



Indian eggplants largely lack genomic traces of Indian *S. insanum*

Signals from both domestication centers

Eggplant domestication from *Solanum insanum* based on *PG-SMA* SNPs

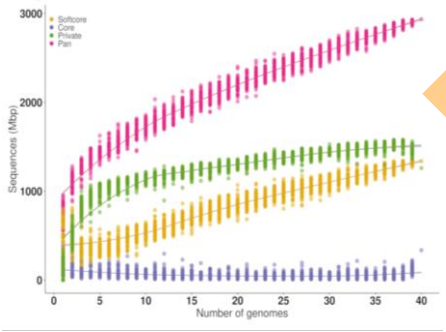


- SMC++ analyses recent bottolnecks
- For ***S.incanum*** **and** ***S.insanum*** a reduction of population size is already occuring at **40-45 kya**
- **SouthEast Asian** and **Indian *S. melongena*** accessions showed a more recent bottlneck (**15kya**)

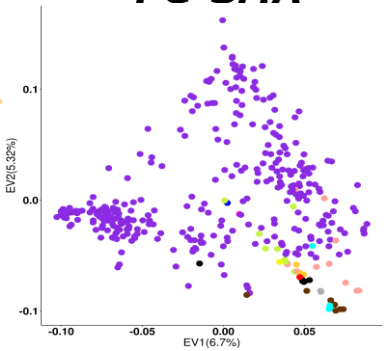
Eggplant core collection

Graph-based pangenomes of eggplant and its wild relatives

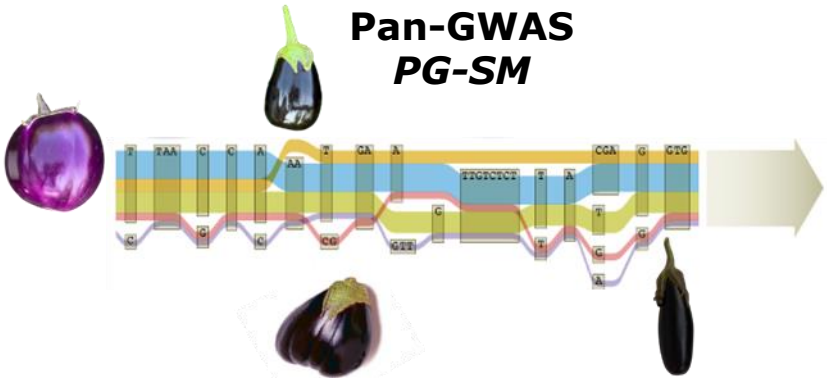
Modelling *PG-SMA*



Diversity *PG-SMA*



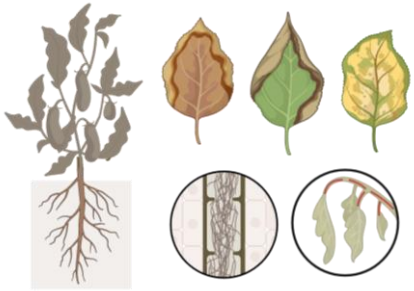
Pan-GWAS *PG-SM*



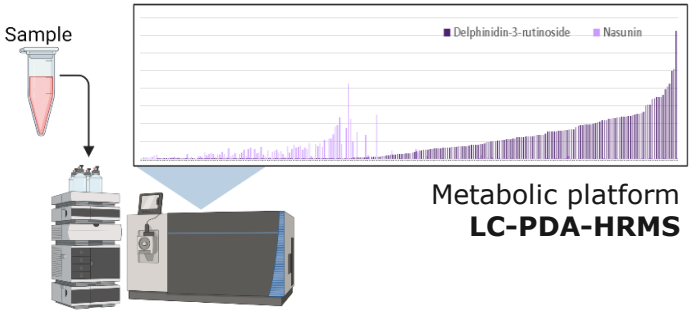
Pan-phenome

46 agronomic traits

10 biotic/abiotic stress



162 semi-polar fruit metabolites

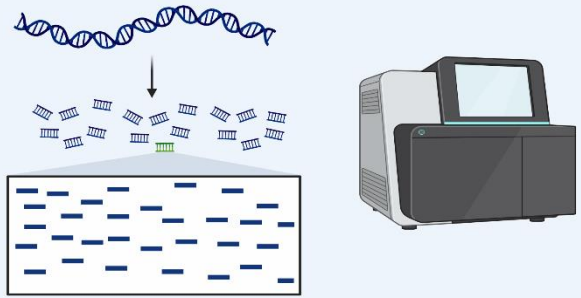


Metabolic platform
LC-PDA-HRMS

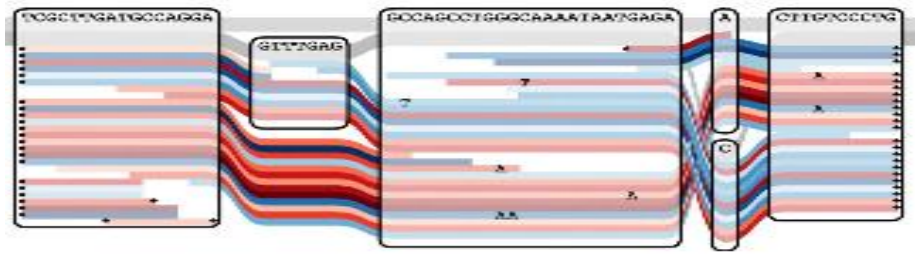
CREA (Italy) **UPV (Spain)** **BATEM (Turkey)**

Pan-GWAS – Genotyping

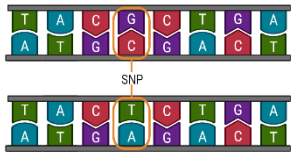
20X Resequencing

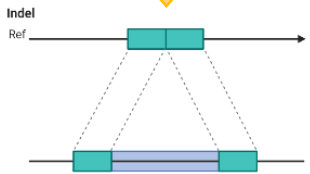


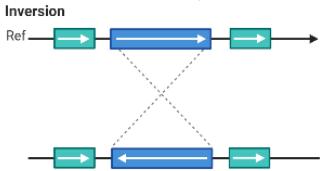
Align short reads to the *PG-SM* graph
(vg giraffe)



Variant calling
(vg call)







5.2M SNPs

1.2M short indels

13k SVs

Quality filters for GWA
Mean DP 15
missing 5%
MAF 0.05

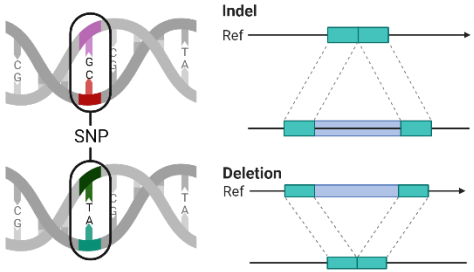
2.3M SNPs

186k short indels

4.5k SVs

Phenotype

Genotype

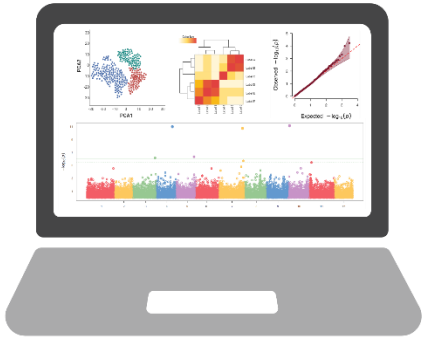


GAPIT

Genomic Association and Prediction Integrated Tool

(Version 3)

Blink

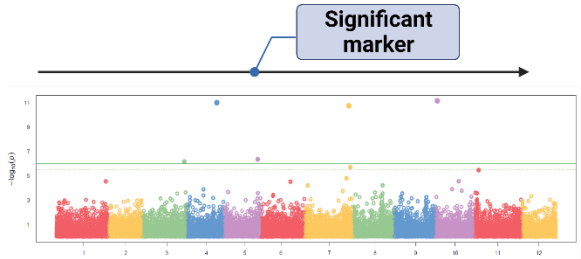


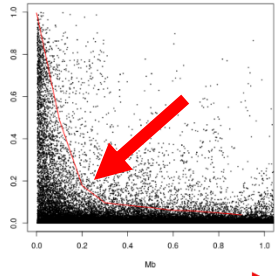
- **Single-environment**
- **Multi-environment**

CREA (Italy) **UPV (Spain)** **BATEM (Turkey)**

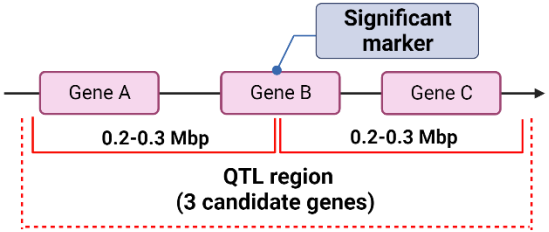
Pan-GWAS – Results QTLs

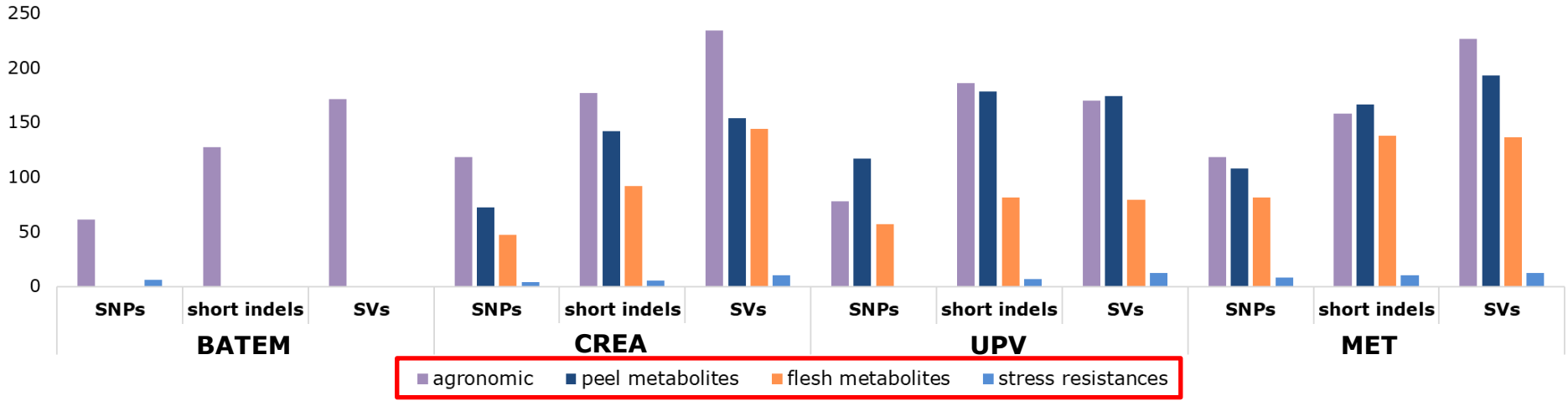
Eggplant LD decay: 0.2-0.3 Mbp



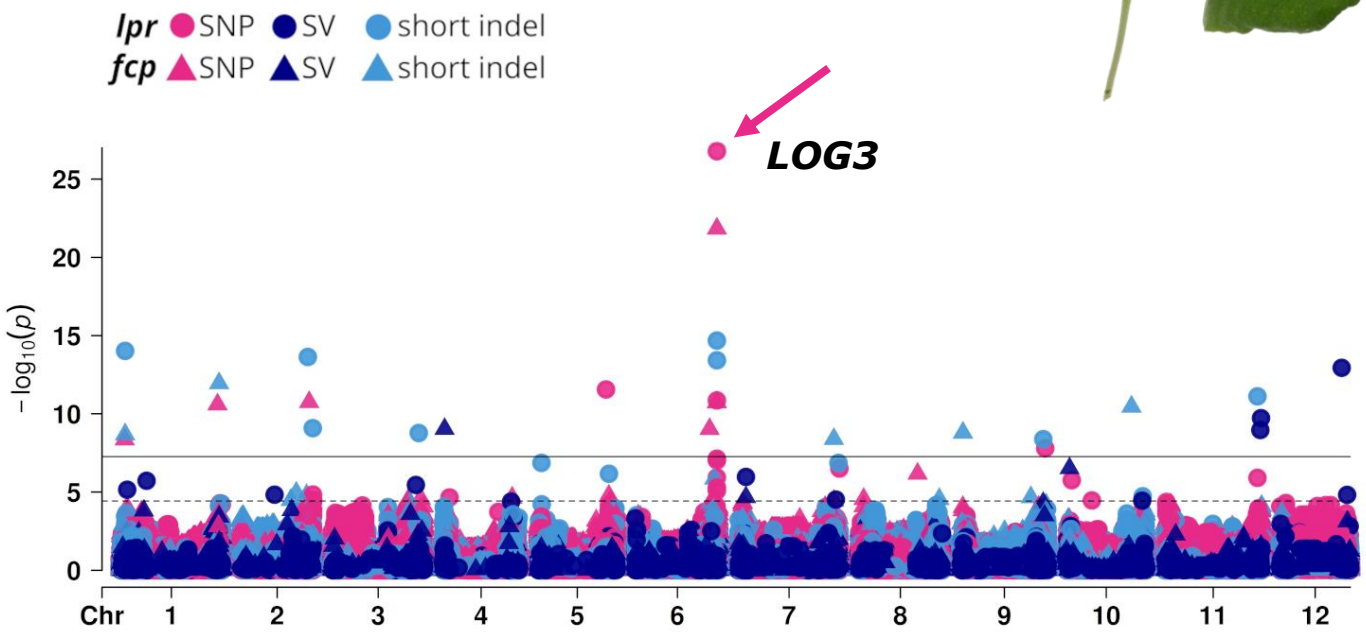


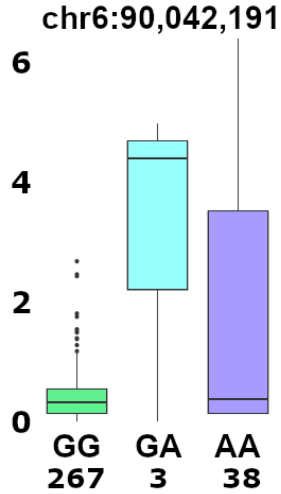
LD decay analysis





Pan-GWAS Results – *Prickliness*





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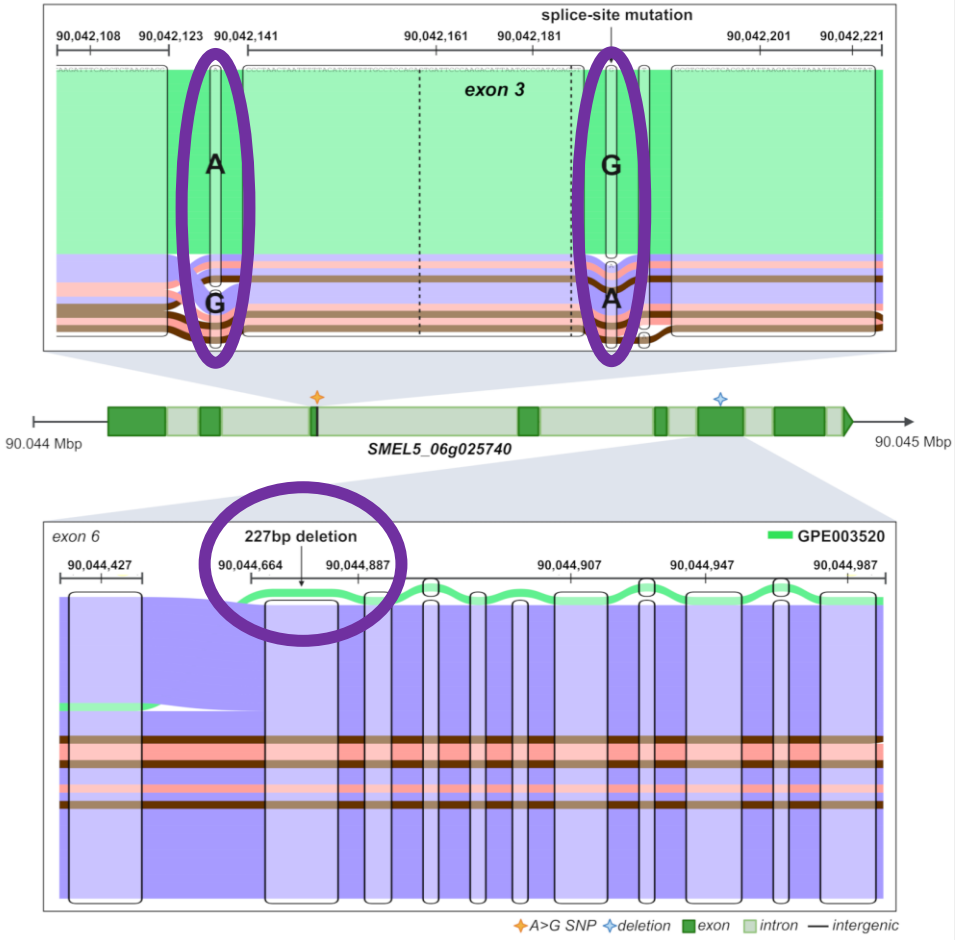

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RESEARCH ARTICLE | PLANT GENETICS

Convergent evolution of plant prickles by repeated gene co-option over deep time

JAMES W. SATTERLEE, DAVID ALONSO, PIETRO GRAMAZIO, KATHARINE M. JENIKE, JIA HE, ANDREA ARRONES, GLORIA VILLANUEVA, MARIOLA PLAZAS, SRIVIDYA RAMAKRISHNAN, [...], AND ZACHARY B. LIPPMAN

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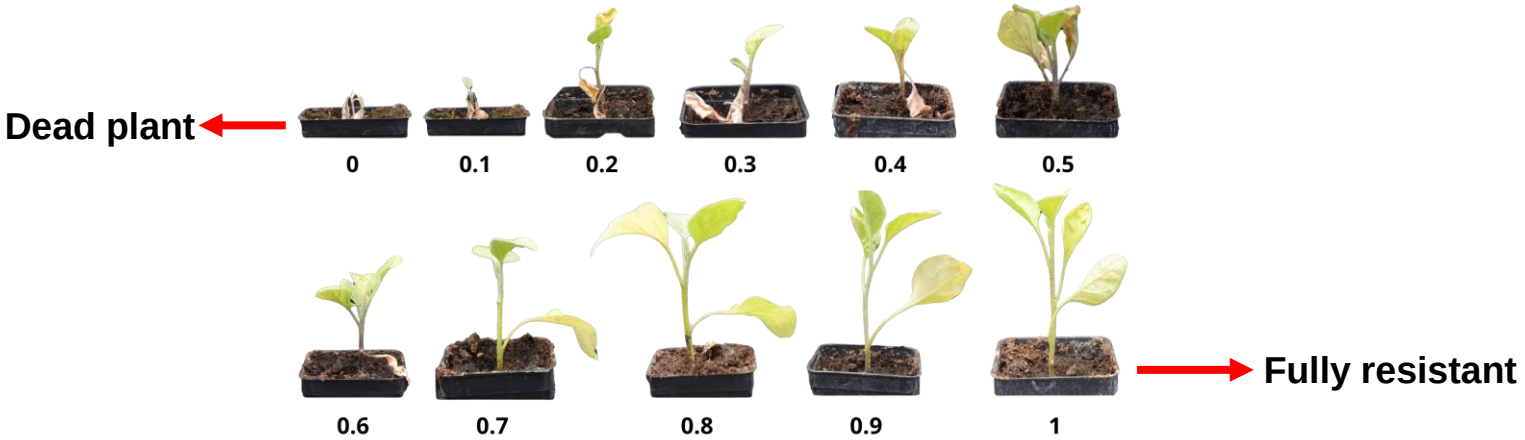
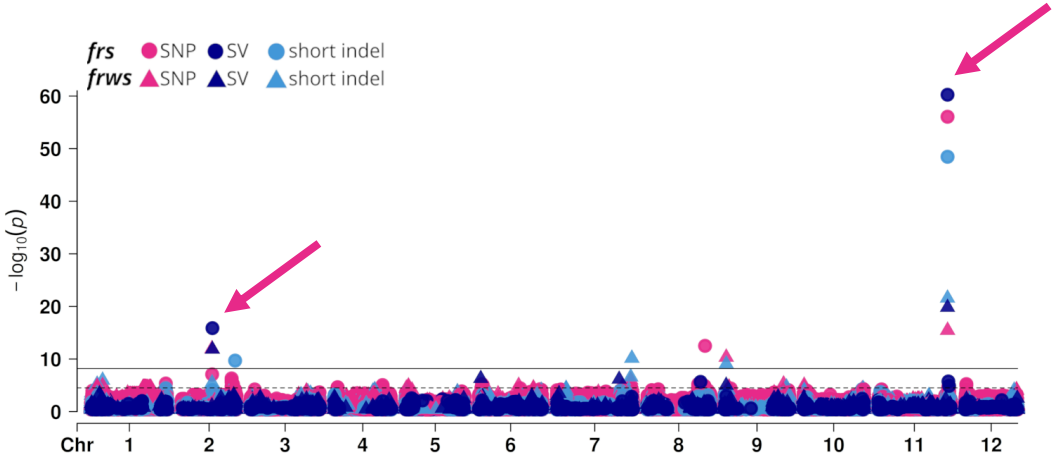
Transcriptomic evidence

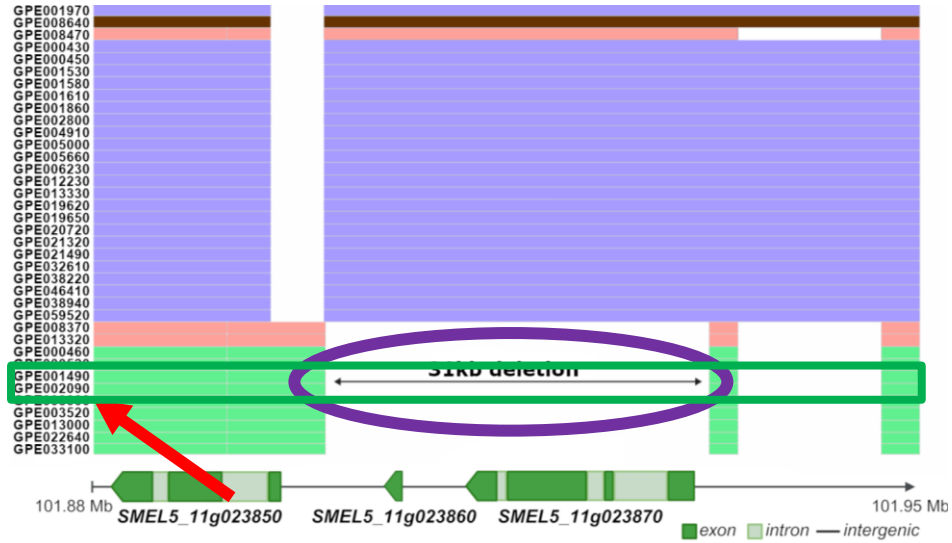
Pan-GWAS Results – *SVs as novel drivers of prickliness*

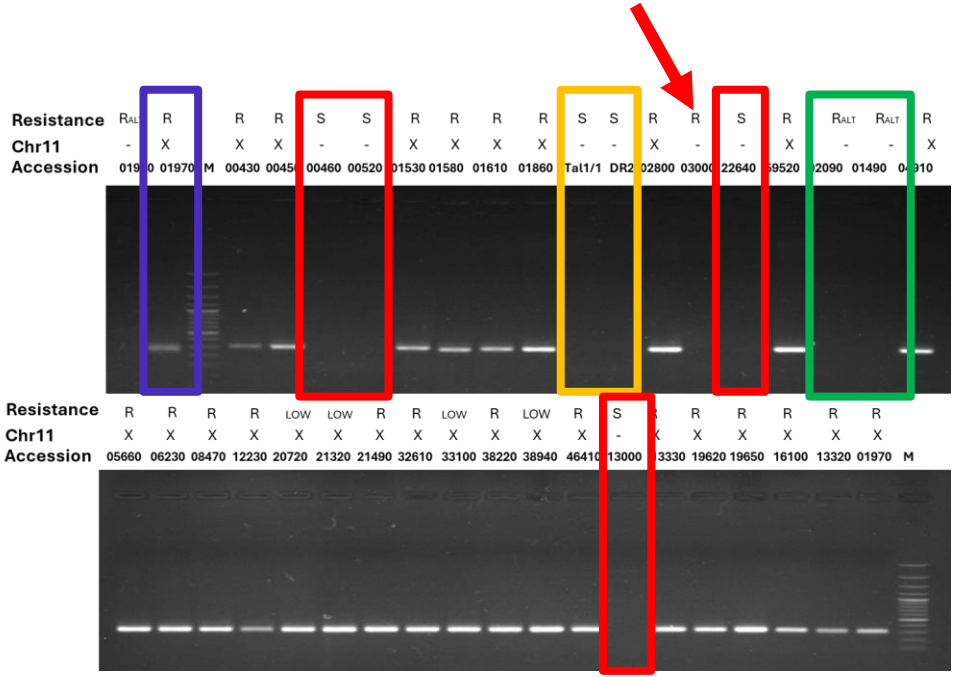
Pan-GWAS Results – *Fusarium* resistance



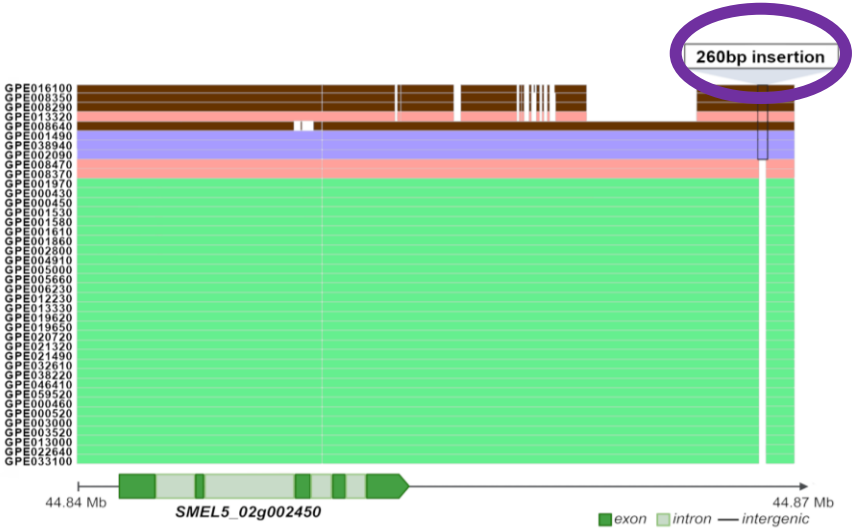


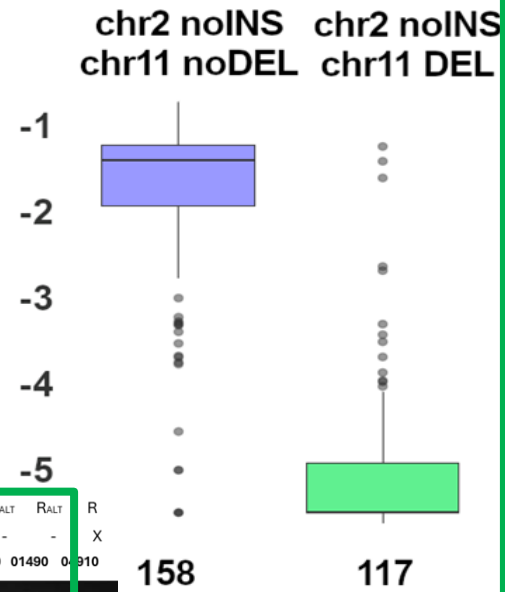
Pan-GWAS Results – *Fusarium* resistance
QTL on chromosome 11

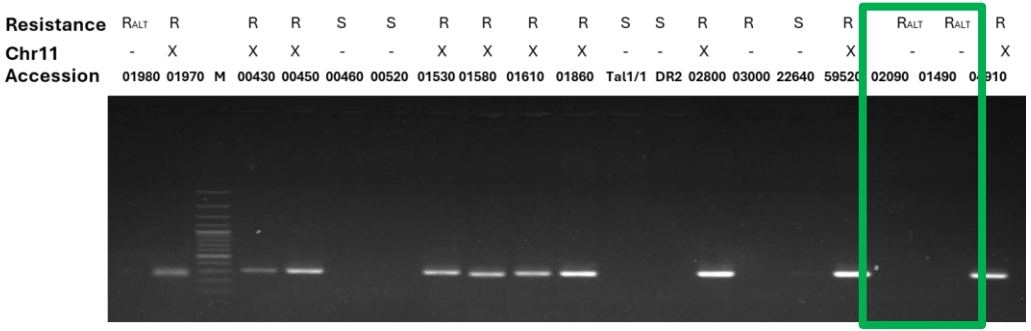




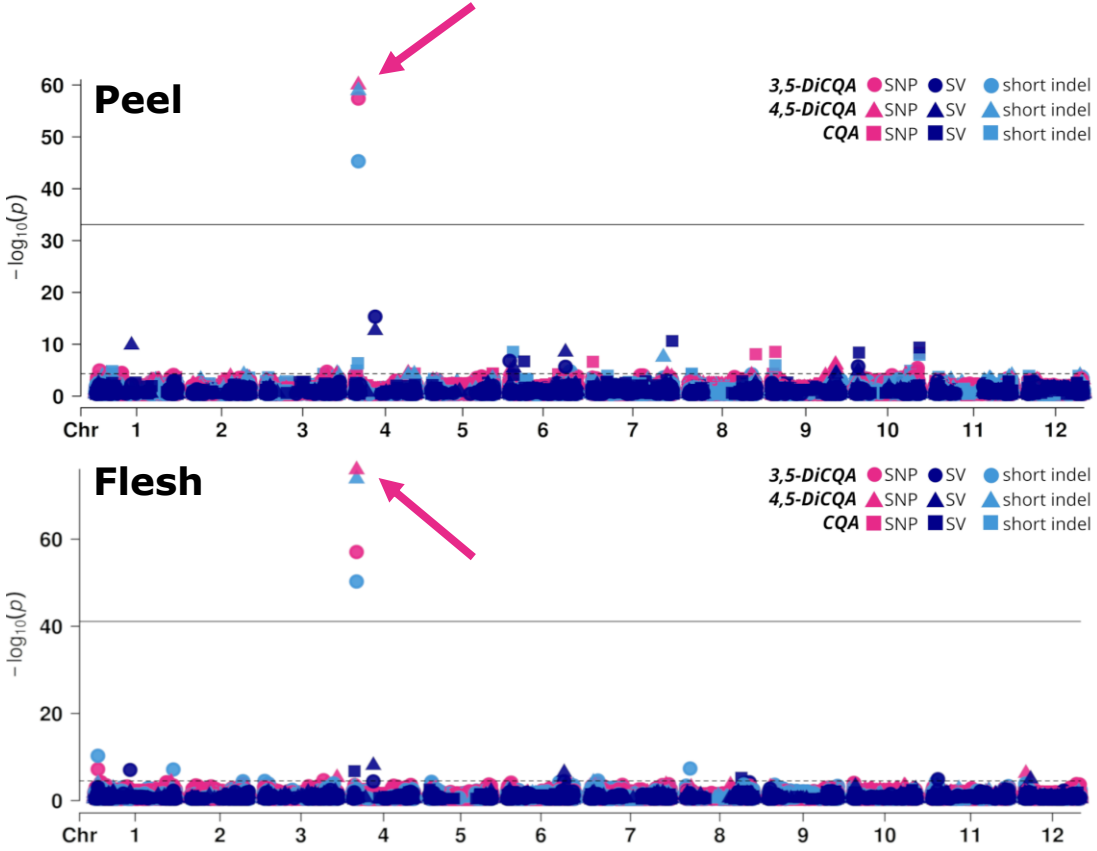
Pan-GWAS Results – *Fusarium* resistance
QTL on chromosome 2 – Alternative resistance to chr 11

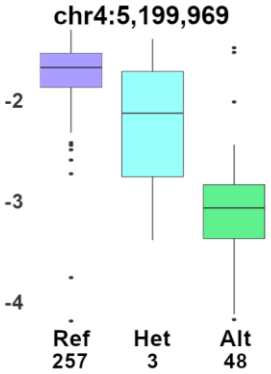


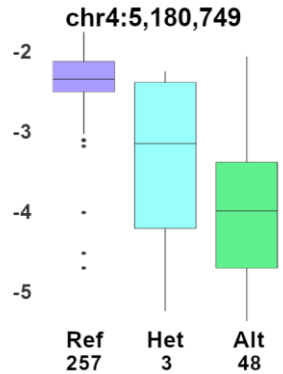




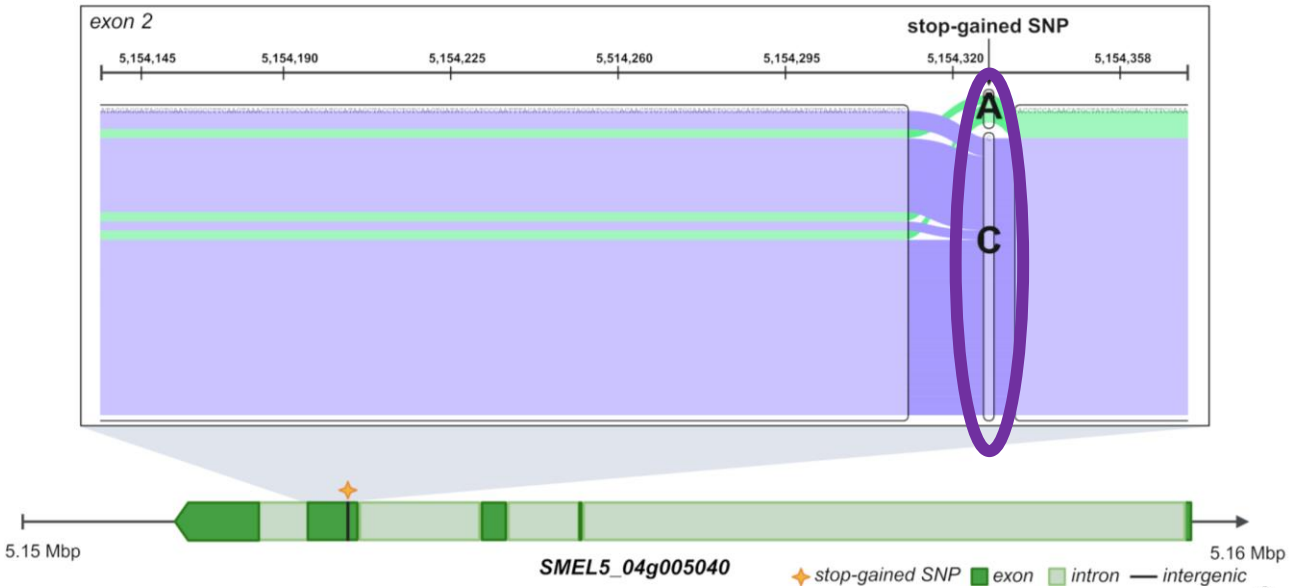
Pan-GWAS Results – Chlorogenic and isochlorogenic acids

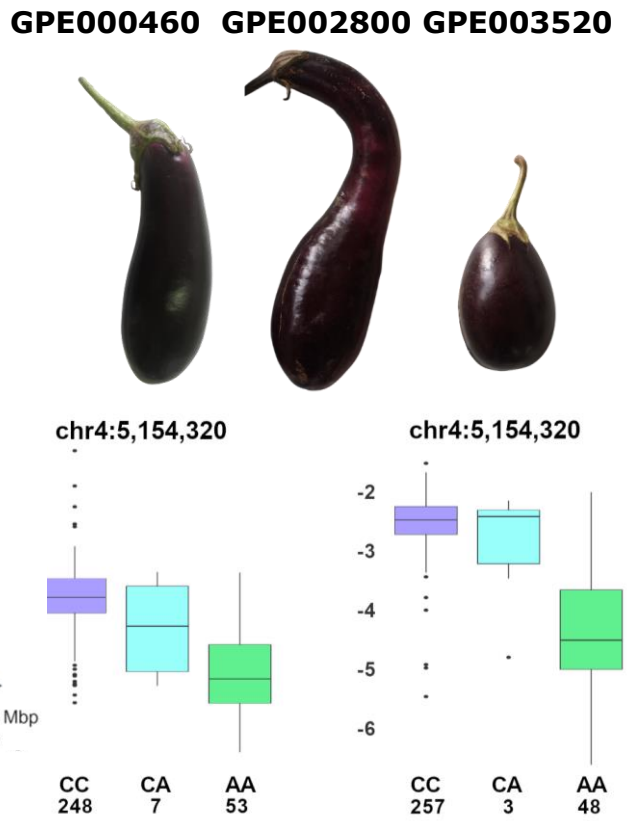






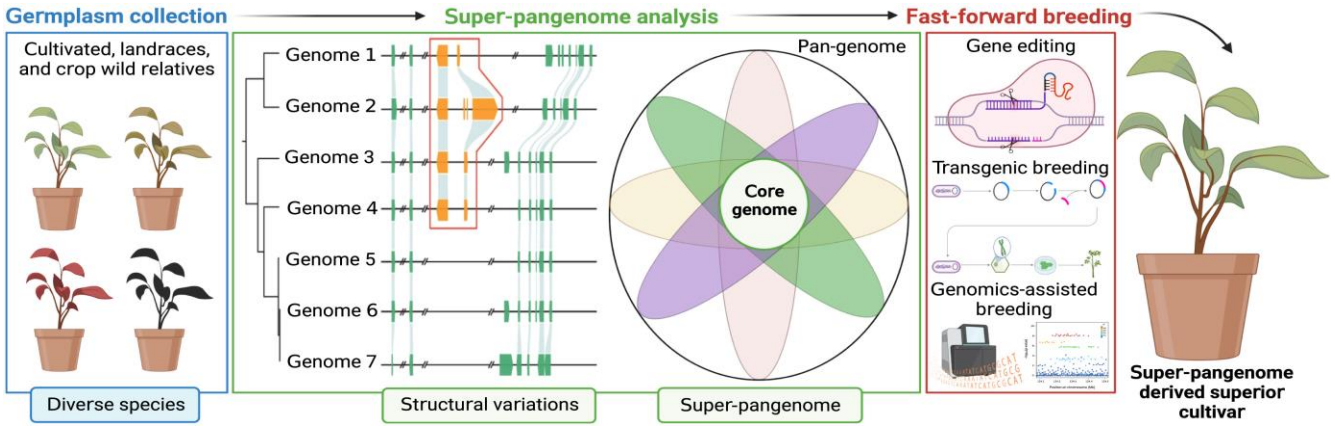
Pan-GWAS Results – *Chlorogenic and isochlorogenic acids*





Future perspectives

- **Exploit graph-based pangenome and pan-phenome to study other traits** addressing specific biological questions
- Apply the **pangenome-informed strategies in eggplant breeding** and genetic improvement
- **Refine breeding targets** by knocking out or modifying candidate genes
- **Expansion and refinement of the pangenome resources** to include accessions harboring alleles conferring resilience/resistance to abiotic/biotic stresses
- **Pan-transcriptome** to explore functional implications of genotypic diversity



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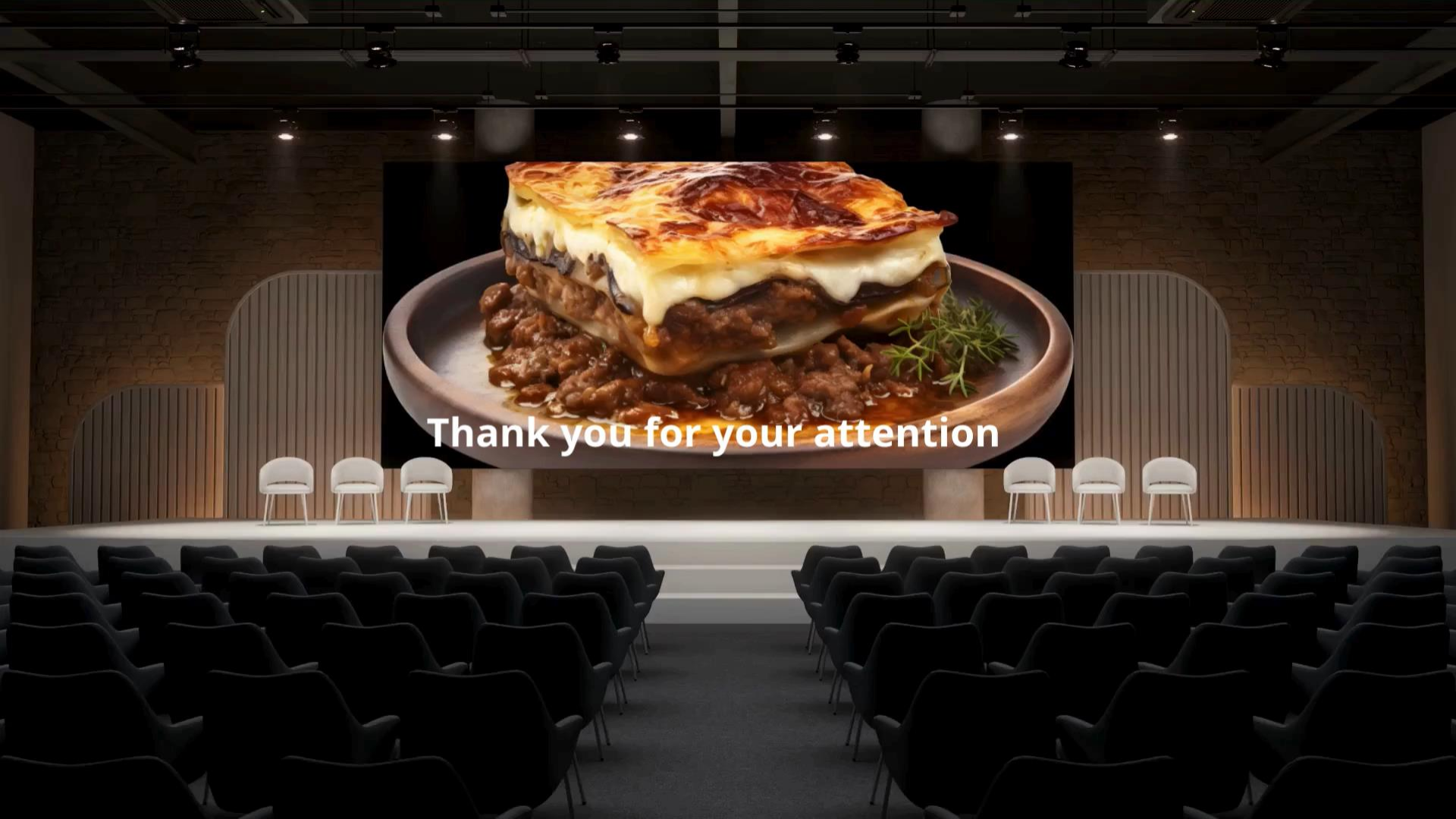
PRO-GRACE
PROMOTING A PLANT GENETIC RESOURCE COMMUNITY FOR EUROPE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