

Actividades divulgación Proyecto AGROALNEXT_2022

Lugar	Monasterio PoortAckere, Gante, Bélgica
Localidad	Gante
Provincia	Gante, Bélgica
Fecha	15-18 de mayo 2023
Proyecto:	ROOT4UE
Código proyecto	AGROALNEXT_2022/036
Grupo de investigación	 Instituto de Bioingeniería UNIVERSITAS Miguel Hernández 

INFORME DE LA ACTIVIDAD:

Durante los días 15 a 18 de mayo se celebró el 10th International Symposium on Root Development al que asistió José Manuel Pérez (IP1) en representación del grupo del proyecto ROOT4UE.

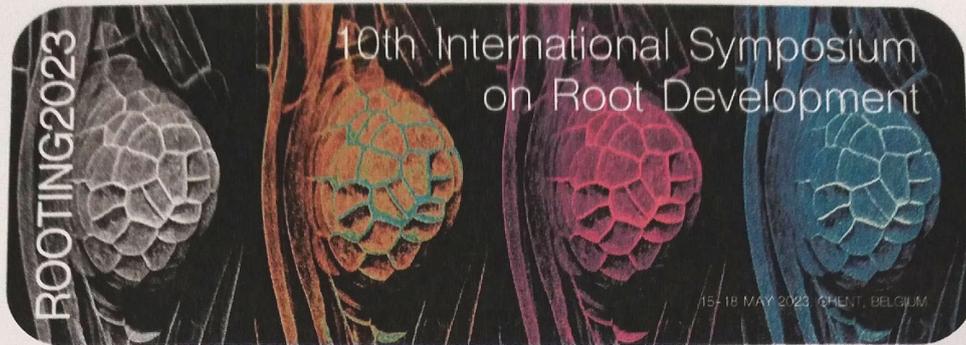
Comité organizador:

- Bert De Rybel VIB-UGent Center for Plant Systems Biology, BE
- Tom Beeckman VIB-UGent Center for Plant Systems Biology, BE
- Jenny Russinova VIB-UGent Center for Plant Systems Biology, BE
- Lieven De Veylder VIB-UGent Center for Plant Systems Biology, BE
- Barbara De Coninck Division of Crop Biotechnics, KU Leuven, BE

Lugar: <https://goo.gl/maps/GVack7M5HDZotf596>

El IP1 del proyecto ROOT4UE presentó algunos de los resultados obtenidos hasta la fecha en formato póster en el congreso internacional 10th International Symposium on Root Development.

JUSTIFICANTE DE ASISTENCIA:

**Proof of attendance:**

The organisers of the 10th International Symposium on Root Development meeting in Ghent, Belgium hereby officially declares that **José Manuel Pérez Pérez** attended and participated to this meeting.

Sincerely,
For all organizers,
Bert De Rybel

<https://www.vibconferences.be/events/10th-international-symposium-on-root-development>

PÓSTER PRESENTADO:

Natural variation during wound-induced adventitious root formation in diverse tomato genotypes

María Salud Justamante¹, Mariem Mhimdi¹, Eduardo Larriba¹, José Blanca², Joaquín Gañizares², José Manuel Pérez-Pérez¹



¹Instituto de Bioingeniería, Universidad Miguel Hernández de Elche, Elche, Spain
²Instituto de Conservación y Mejora de la Agrodiversidad Valenciana (COMAV-UPV), Universitat Politècnica de València, València, Spain
 mjustamante@umh.es, jmperez@umh.es



Introduction

Natural variation studies are an important tool for unraveling the genetic basis of quantitative traits in plants. Here we studied wound-induced adventitious root formation in two different tomato collections: a collection of introgression lines derived from the cross *Solanum pennellii* × *S. lycopersicum* [1], and a collection of 164 tomato accessions including *S. pimpinellifolium* (SP), *S. lycopersicum* var. *cerasiforme* (SLC) and *S. lycopersicum* var. *lycopersicum* (SLL), representing the genetic variability of tomato in its centers of origin and domestication [2].

Results

Contrasting rooting performances were identified during the wound-induced response in young shoot explants. Various root-related traits were analyzed to identify SNPs associated with the observed variation for further use in tomato breeding.

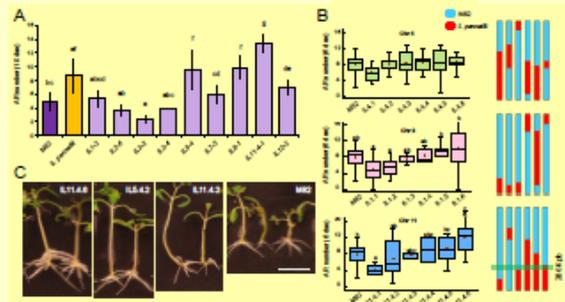


Figure 1. Characterization of introgression lines derived from the *S. pennellii* × *S. lycopersicum* cross. (A) Adventitious root (AR) number observed in nine tomato introgression lines (ILs) at 10 days after excision (dae). (B) AR number measured in 18 ILs within chromosomes 5, 8 and 11, at 6 dae. Letters indicate significant differences (LSD; p-value < 0.01). (C) Representative images for different ILs with extreme adventitious rooting values compared to M82; high (IL11.4.6), intermediate (IL5.4.2) and low AR number (IL11.4.2). Scale bar: 20 mm.

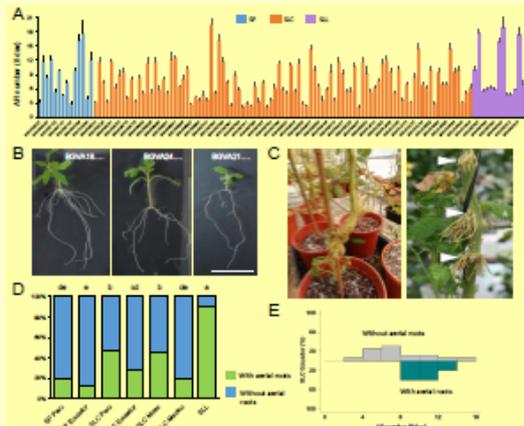


Figure 3. Natural variation in rooting performance in a defined collection of tomato accessions. (A) AR number measured in 164 accessions of the studied collection [2] at 8 dae. (B) Representative images for different accessions with extreme adventitious rooting numbers. (C) Aerial roots appear along the entire stem on fully developed plants of selected accessions. (D) Proportion of accessions with aerial roots in each subpopulation. Letters indicate significant differences (LSD; p-value < 0.01). (E) AR number in shoot explants at 8 dae and aerial root development are positively correlated in some of the studied subpopulations. Scale bar: 20 mm.

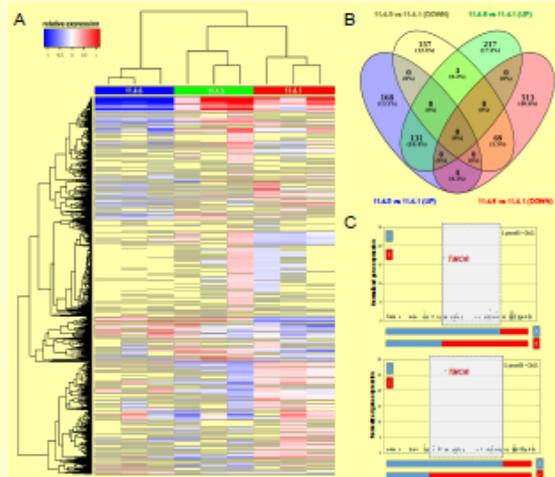


Figure 2. Transcriptome profiling of selected ILs. (A) Comparative transcriptome profiling of studied ILs at 10 dae. (B) Venn diagram with comparisons of differentially expressed genes (DEGs) between the lines 11.4.5, 11.4.5 and 11.4.1. (C) Differential expression of genes at chromosome 11 during AR formation in selected lines allowed us the identification of a candidate gene.

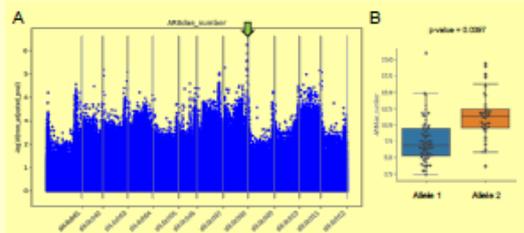


Figure 4. Genetic mapping of rooting traits using a genome wide association (GWA) approach. (A) Manhattan plot of associations between SNPs and AR number at 8 dae. (B) Scatterplot of average AR number values used for GWA mapping, sorted by the alleles, 1 and 2, at Chr06:61781934 position.

Conclusion

These studies allow us to map and characterize major effect QTLs and other loci involved in various rooting related traits. We have discovered an interesting correlation between several of the traits studied and the main steps followed during tomato domestication that deserve further investigation.

References

- Omer et al. (2016) *Plant J.* 87: 151.
- Mata-Nicolás et al. (2020). *Hortic. Res.* 7: 66.



Acknowledgements

Work in the laboratory of J.M.P.-P. is supported by the grants PID2021-126940GB-I00 and TED2021-132256B-C22 funded by MCIN/AEI/10.13039/501100011033, and AGROALNEXT/2022/036 funded by the Conselleria d'Innovació, Universitats, Ciència i Societat Digital of the Generalitat Valenciana, the "ERDF A way of making Europe", and the "European Union NextGenerationEU/PRTR". M.M. was a research fellow of the Generalitat Valenciana (GRISOLIAP/2019/006).



Y para que conste a los efectos oportunos

Firma del IP1.