“Successful edition of the Advanced Training School on Tomato Databases and their use to link genotypes to phenotypes”

The training school took place on line on September 28th and it was organized as part of the training activities of the EU-funded project HARNESSTOM (http://harnesstom.eu/). The advanced training school covered the latest developments on databases to link genotypes to phenotypes and it was exemplified by several presentations covering specific cases. Emphasis was made on the *S. pennelli* population, an important resource produced by partner HUJI and widely use in HARNESSTOM and elsewhere. The program is detailed below and basically covered talks about HARNESSTOM DB a PHENOME DB presented by the developers, both HARNESSTOM partners. These two Databases which include bioinformatics tools aim to serve as information gateways for tomato researcher in academia and private companies as well as breeders. More specific talks exemplified the importance of genetic resources and populations to dissect the diversity, and eventually zoom in to identify the genetic basis for various traits, from disease resistance to inflorescence traits. Speakers included leading scientist from 10 different institutions in 6 different countries.

Over 250 people registered to the course from both public or private institutions and covering over more than 50 countries. More than 80 % of the participants were staff scientists or PhD but also over 30 breeders from private companies while the rest were researchers and /or professors or students.

Outline of the HARNESSTOM Advanced On-Line Training School program that took place on line on Sept 28th at 09:00 -14:00 Central European Summer Time (~5 hours).:

Title: How to use the 2000 *Solanum pennellii* Backcross Inbred Lines (BILs) and databases to link G2P?

Part I Moderator: Toni Granell (presenting the course)
9:00 – 9:30 Björn Uadel: The *Solanum pennellii* genome.
9:30 – 10:00 Shai Torgeman: Population structure of the interspecific LOST BILs.
10:00 – 10:15 Shay Trigerman: Genetic mapping of forked inflorescence.
10:15 – 10:30 Break
Part II Moderator: Toni Monforte
10:30 – 11:00 Saleh Alseekh: BIL fruit metabolism.
11:00 – 11:30 Edan Rochsar and Aviv Dombrovsky: Fine mapping of TM1 – a gene for resistance to the Tomato Brown Rugose Fruit Virus.
11:30 - 11:45 Dani Zamir: Comparative BIL mapping of yield QTL under deficit irrigation from two accessions of *Solanum pennellii*.
11:45 – 12:00 Break
Part III Moderator: Mara Ercolano
12:00 – 12:30 Yaniv Semel: The Phenome Networks database.
12:30 – 13:00 Clara Pons Puig: Harnesstom DB and tools
13:00 – 13:20 Giovanni Giuliano: Genotyping for the management of large collections and reconstruction of domestication history.
13:20 – 13:50 Toni Granell, Yaniv Semel, Giovanni Giuliano, Dani Zamir, Mara Ercolano, Toni Monforte, Christian Bachem: Future Outlook

This project has received funding from the European Union’s Horizon 2020 research and innovation programme under grant agreement No *101000716*

HARNESSTOM Advanced On-Line Training School

Title: ***How to use the 2000 Solanum pennellii Backcross Inbred Lines (BILs) and databases to link G2P?***

Sept 28th at 09:00 -14:00 Central European Summer Time (~5 hours).

Program –

Moderator: *Toni Granell*

9:00 – 9:30 Björn Usadel: The *Solanum pennellii* genome.

9:30 – 10:00 Shai Torgeman: Population structure of the interspecific LOST BILs.

10:00 – 10:15 Shay Trigerman: Genetic mapping of forked inflorescence.

10:15 – 10:30 Break

Moderator: *Toni Monforte*

10:30 – 11:00 Saleh Alseekh: BIL fruit metabolism.

11:00 – 11:30 Edan Rochsar and Aviv Dombrovsky: Fine mapping of *TM1* – a gene for resistance to the Tomato Brown Rugose Fruit Virus.

11:30 - 11:45 Dani Zamir: Comparative BIL mapping of yield QTL under deficit irrigation from two accessions of *Solanum pennellii*.

11:45 – 12:00 Break

Moderator: *Mara Ercolano*

12:00 – 12:30 *Yaniv Semel*: The Phenome Networks database.

12:30 – 12:50 Mohamed Zouine: ***TomExpress*** and other useful tomato databases.

12:50 – 13:10 *Clara Pons Puig*: Harnesstom DB and tools

13:10 – 13:30 Giovanni Giuliano: Genotyping for the management of large collections and reconstruction of domestication history.

13:30 – 14:00 *Toni Granell, Yaniv Semel*, Giovanni Giuliano, Mohamed Zouine, Dani Zamir, Mara Ercolano, Toni Monforte, Christian Bachem: ***Future Outlook***

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No *101000716*

Fig 1. Snapshot of the programme held online on the 28th September 2023

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No *101000716*

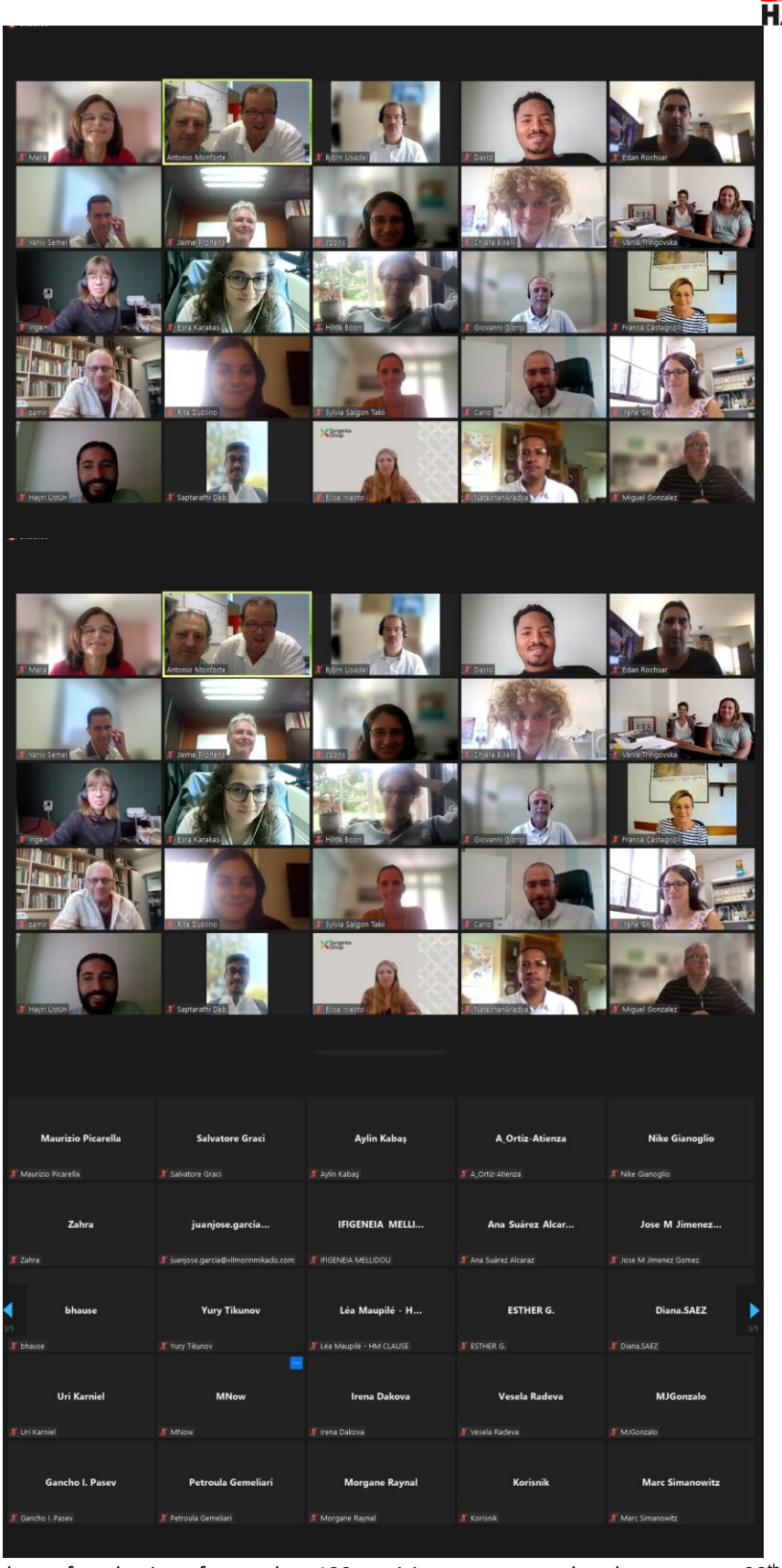
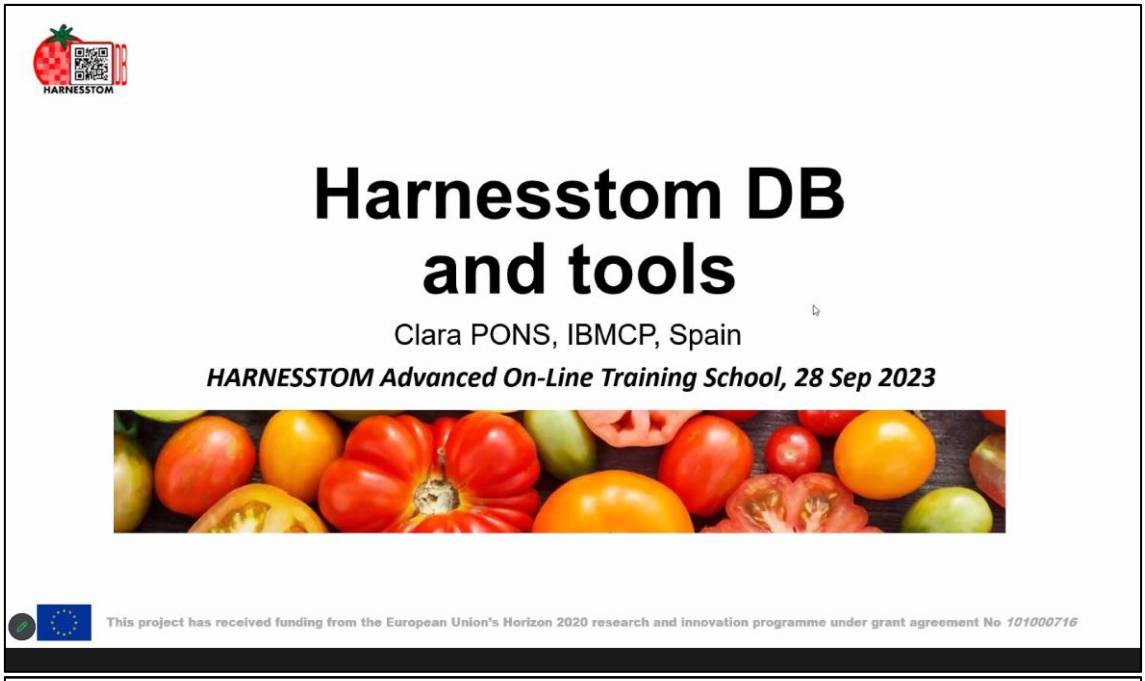
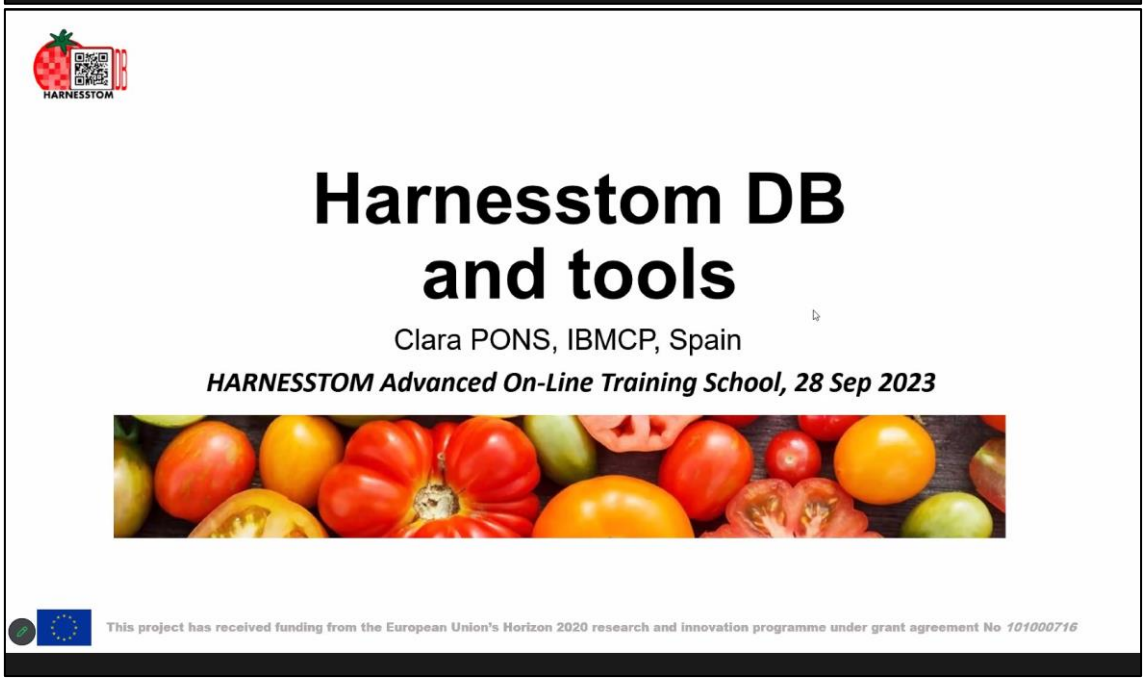


Fig 2. Snapshots of a selection of more than 120 participants connected to the course on 28th set 2023.

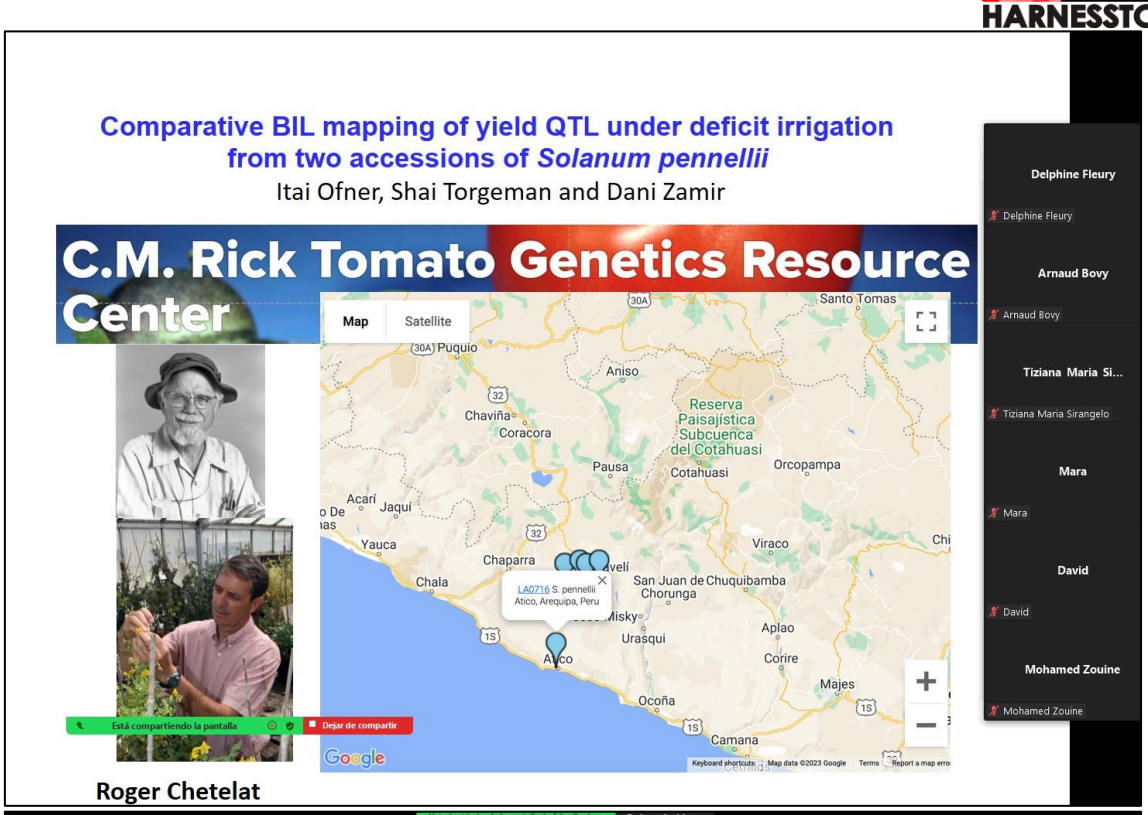
This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No *101000716*

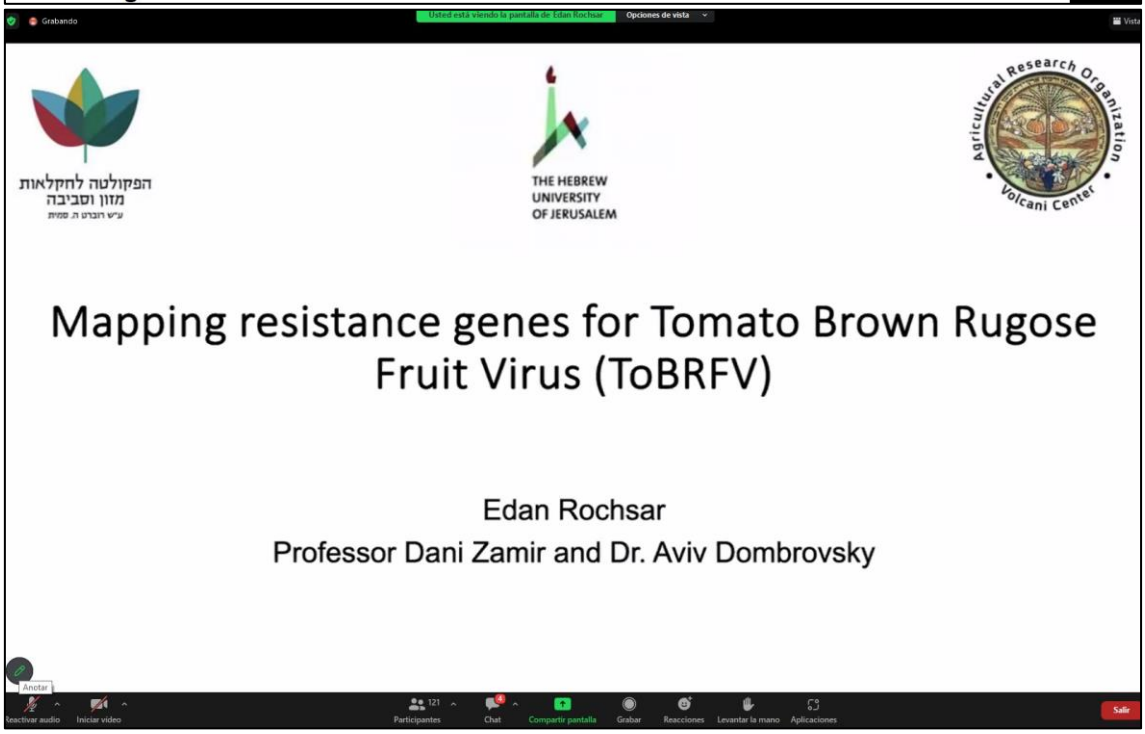
Some snapshots of the presentations are included below:



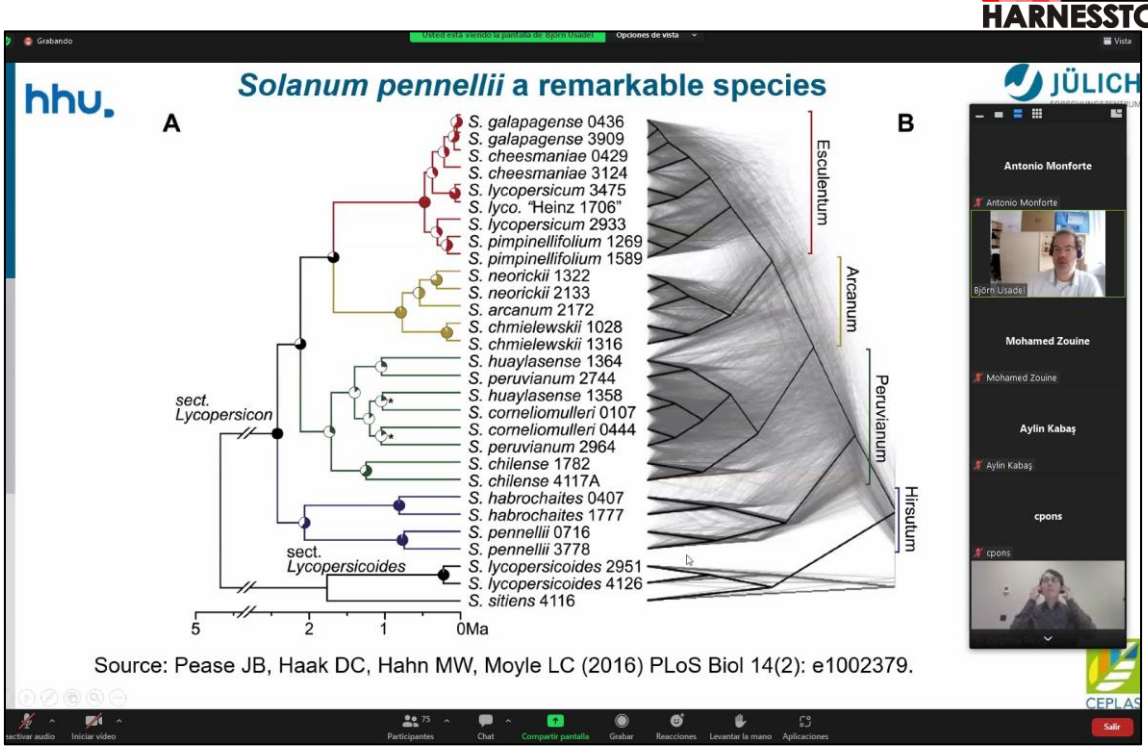


This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No *101000716*





This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No *101000716*



This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No *101000716*

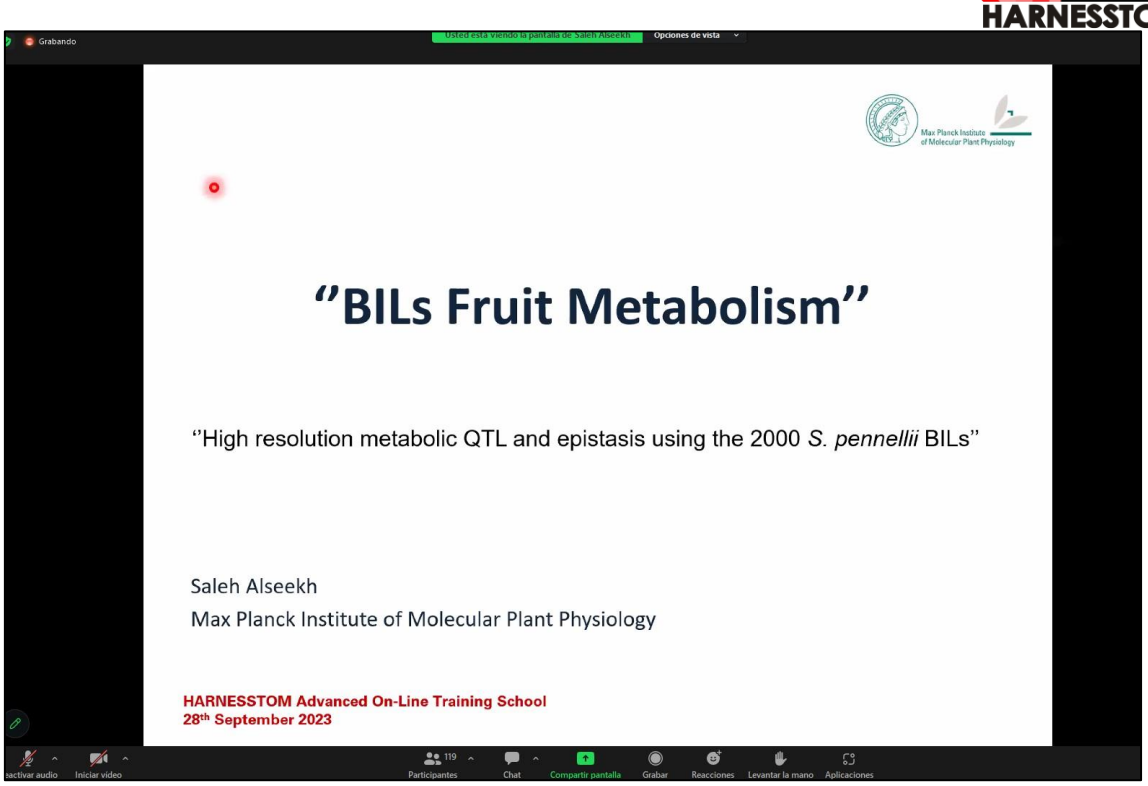


Fig 3. Snapshots of a selection of talks presented at the course on 28th set 2023.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No *101000716*