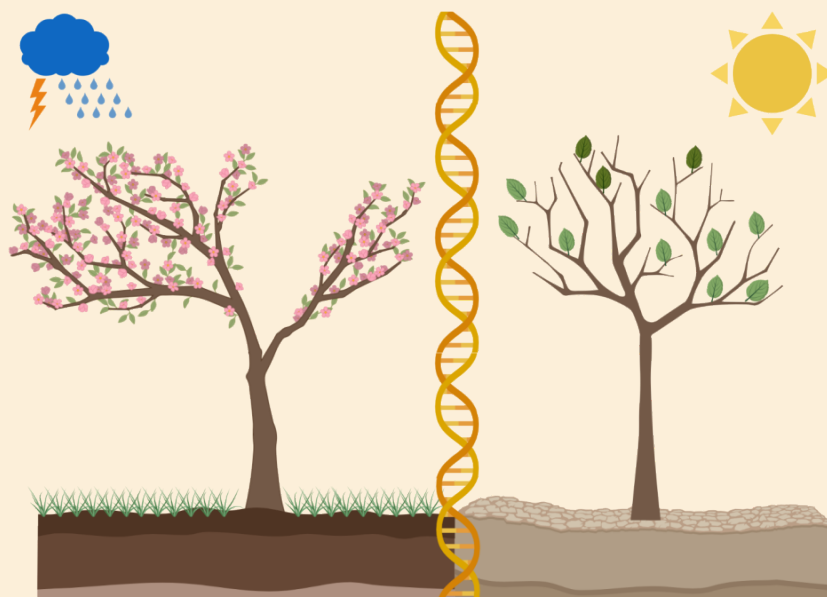




## A two-day webinar

11 speakers

13:00 CET

[illegible]

Organized by the project 'Fruit Crop Resilience to Climate Change-FREECLIMB'  
<https://primafreeclimb.com/>



C. Bazakos, P. Drogoudi, Institute of Plant Breeding and Genetic Resources,  
Dep. of Deciduous Fruit Trees, Naooussa, Greece  
G.Koubouris, Institute for Olive Tree, Subtropical Crops and Viticulture, Chania, Greece

## Wednesday, April 27th, 2022

12:45 CET Webinar connection

13:00 Welcome by organizers

13:15 Introduction on the PRIMA project 'Fruit Crop Resilience to Climate Change'  
-Daniele Bassi, University of Milan, Italy

### Session 1: *Vitis*

Chair: Gabriella De Lorenzis

#### 13:25 Exploring grapevine germplasm diversity to develop breeding programs

-*Gabriella De Lorenzis, University of Milan, Milan, Italy*

Grapevine (*Vitis vinifera* subsp. *sativa*) originated from their wild ancestor, the *Vitis vinifera* subsp. *sylvestris*. This process took place in the Caucasus (the cradle of grapevine domestication), around 6-8,000 years ago. From the Caucasus, the domesticated varieties were spread in different areas around the Mediterranean Basin, following mainly the migration routes of Mediterranean peoples. Today, the domesticated form includes a huge number of varieties, with more than 10,000 cultivars, related each other by a complex intertwining, believed to exist in the world. If on the one hand, the domestication process concerns how plants were modified by humans in the past, on the other, it allows us to understand how to design ideal crops for more sustainable viticulture. Indeed, it is from assessing the grapevine biodiversity that useful traits for the new breeding programs can be found, in order to make the modern viticulture more resilient to climate changes.

#### 13:45 Breeding for pathogen resistance in *Vitis* spp.

-*Silvia Vezzulli, Fondazione Edmund Mach, San Michele all'Adige, Italy*

The cross-breeding program for biotic stress resistance in grapevine began at FEM in 2010. After an initial phase of scouting a various and complex genetic pool of resistance (R) traits/loci to downy and powdery mildews (DM and PM), a group of accessions were selected as R-donors. Then, through Marker-Assisted Parental Selection (MAPS), various genotypes with stacked loci reached the open field and were then used for breeding purposes. Subsequently, the optimization of phenotyping and genotyping protocols was conducted for a highly efficient Marker-Assisted Seedling Selection (MASS). In 2018, approximately 650 progeny individuals were tested and characterized at nine R-loci, revealing a maximum of seven stacked loci and up to three loci in homozygous state. The optimized applied process in more than 20 segregating populations and the several detected R-loci arrangements allowed to unveil both inter- and intra- population effects. Thanks to these findings, starting from the 2019 a forward MAS process - without phenotypic screening - was established on the progenies derived from those parental lines with a known behavior within the FEM breeding program.

#### 14:05 The Greek vitis collection: genetic resources to meet modern challenges

-*Georgios Merkouropoulos, ELGO-'DIMITRA', Institute for Olive Tree, Subtropical Crops and Viticulture, Department of Viticulture, Athens, Greece*

The oldest and largest collection of Greek grapevine varieties is maintained in Lykovrysi (Athens) by the Hellenic Agricultural Organization DIMITRA. In addition, during the last 20 years more than one hundred new varieties have been created, using the traditional breeding technique of hybridization. Characterization of all this genetic material (autochthonous varieties and new varieties), in terms of molecular profiling, evaluation of oenological potential, and evaluation in response to biotic and abiotic factors, is under way, in order to distinguish superior the genotypes.

#### 14:25 Discussion



## Wednesday, April 27th, 2022

### *Prunus session*

Chair: Laura Rossini and Marco Cirilli

#### **14:40 Following the adaptive path of apricot domestication to improve Mediterranean crop resources**

*-Veronique Decroocq, INRAE, Bordeaux, France*

The specific traits that have recently evolved in domesticated organisms under strong and recent human-driven selection provide unique opportunities to understand adaptive processes as it leaves footprints in the genome. Here we studied the evolutionary history and selection footprints in apricots (*Armeniaca* section) using a population genomics approach. In addition to improving our fundamental knowledge on the processes of fruit tree domestication, we are currently assessing its potential to improve Mediterranean apricot resources.

#### **15:00 Prunus marker assisted introgression**

*-Ibo Eduardo, CRAG, Barcelona, Spain*

Every day we are discovering new evidence that indicate that interspecific crosses have been the rule during plant domestication. Recovering some interesting genes from the wild is not an easy task, specially in fruit trees with long juvenile phases. Marker Assisted Introgression (MAI) is a strategy based on whole genome selection using molecular markers that allow to introgress these useful genes from wild or exotic germplasm in an efficient way. An example of the introgression from a powdery mildew resistance gene from almond to peach will be presented and discussed.

#### **15:20 Breeding for climate resilience in Prunus/peach**

*-Ksenija Gasic- Clemson University, South Carolina, USA*

Climate fluctuation and its effect on peach production has emphasized the need to incorporate adaptive phenotypic plasticity in newly developed cultivars. Adaptive mechanism in temperate fruit trees, such as peach, include genotype specific chill and heat accumulation as cues for flowering. Ideal peach cultivar with climate resilience would have appropriate chilling requirement for the intended production region and high heat requirement for delayed bloom and avoidance of late spring frosts. The latest achievements in enabling breeding for climate resilient peach will be presented.

#### **15:40 Discussion**

#### **16:00 End of 1st day**



**Thursday, April 28th, 2022**

**12:45-13:00 CET Webinar connection**

**13:00 Introduction by organizers**

### *Olive session*

**Chair: Georgios Koubouris and Sihem Tellah**

#### **13:05 Molecular characterization of the worldwide olive germplasm bank of Marrakech : Towards innovative breeding for sustainable oliviculture**

*-Armed Elbakkali -INRA, Centre Régional de la Recherche Agronomique de Meknès, Meknès, Morocco*

The Worldwide Olive Germplasm Bank of Marrakech, Morocco, is currently the largest existing olive collection with almost 590 olive accessions originating from 14 Mediterranean countries. Molecular characterization of the collection, using both SSRs and SNPs markers, has provided useful information for preservation and management of genetic resources while bringing new insights into the history of olive domestication and diversification. To face the climate change effects and other associated risks that are threatening the olive growing sector, the genetic diversity within the collection represents valuable tool for conducting further studies through developing collaborations between olive research teams to assess Genotype x Environment interaction and to explore association mapping studies.

#### **13:20 Whole genome resequencing of a Mediterranean basin hotspot collection provides new insights into olive genetic diversity**

*-Christos Bazakos -ELGO 'DIMITRA', institute of Plant Breeding and Genetic Resources, Thessaloniki, Greece*

Olive tree is one of the most ancient domesticated species and olive oil is an important source of income in the agricultural community of the Mediterranean region. In the frame of the Greek research network "Olive Roads" we re-sequenced in high-depth 43 accessions from Greece Genbank collection, that span the traditional range of olive cultivation and represent the majority of variation (>95%) in Greece. To gain a better understanding of the patterns of genome-wide variation in olive, the newly re-sequenced genomes were analysed together with 46 accessions from a previous study. Furthermore, by conducting a genome-wide association study (GWAS), we identified genomic regions affected by breeding and genetic loci associated with phenotypic variation for agronomically important traits of relevance to olive breeding.

#### **13:35 Analysis of genomic resources for olive genetic research and breeding**

*-Aureliano Bombarely - Instituto de Biología Molecular y Celular de Plantas, Valencia, Spain*

The use of different genomic methodologies by the scientific olive community has brought different genome assemblies as well as dozens of re-sequenced accessions. Nevertheless, the choice of a reference as well as the re-use of publicly available data is not always an intuitive task. We have compared the different olive reference genomes as well as two types of genomic data: GBS and WGR. We also have used the publicly available data to identify the origin of the Vouves monumental olive tree as example of the use of the publicly available data.

#### **13:55 Discussion**

**Thursday, April 28th, 2022**

**Citrus session**

**Chair: Alessandra Gentile and Marco Caruso**

**14:15 Sequencing of the lemon genome and its application for high-throughput genotyping of segregating populations**

*-Mario Di Guardo, University of Catania (UNICT), Department of Agriculture, Food and Environment, Catania, Italy*

Lemon (*Citrus limon* (L.) Osbeck) is one of the most cultivated and appreciated Citrus species. The first reference genome of lemon (cv. Femminello Siracusano) has been recently released. The availability of the reference genomes of the ancestors of lemon, enabled the definition of the two haplotypes: the paternal (descending from citron, 312.8 Mb) and the maternal (inherited by mandarin and pumelo, 324.74 Mb). The availability of a high-resolution lemon genome was a prerequisite for the genotyping of two segregating populations ad-hoc developed for mapping candidate genes related to tolerance to malsecco disease. In both populations, the highly susceptible Femminello Siracusano 2kr was crossed with the malsecco tolerant Citrus clementina (125 accessions) or Citrus latipes (127 accessions). The genotyping of the two full-sib families was carried out employing a Single-primer Enrichment Technology (SPET) leading to the definition of 30,000 SNPs specifically designed to (i) cover evenly the entire lemon genome (ii) target coding sequences and (iii) anchor unmapped scaffolds on the lemon genome.

**14:30 Genomics insights on the evolution, domestication and breeding of citrus**

*-Manuel Talón, Valencian Institute of Agricultural Research, Valencia, Spain*

Citrus breeding is extremely limited by various physiological and genetic constraints inherent to the reproductive biology of commercial citrus. These include, for example, long periods of juvenility, or pernicious restrictive conditions of self-incompatibility and gametic sterility. In addition, modern citriculture also faces the current worldwide challenges, such as climate change, sustainability and resilience. Recent achievements in genomics, however, are providing an invaluable information on the structure of the citrus genome and, therefore, on the mysterious of origin, evolution, and domestication of citrus. In this talk, I will review our knowledge on these aspects, I will expose the genomic bases that support the development of promising breeding programs and present our approaches to implement genomic advances in citrus breeding.

**14:50 Discussion**

**15:15 End of 2nd day**



**Local organizers:**

C. Bazakos, P. Drogoudi, Institute of Plant Breeding and Genetic Resources,  
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**Genome-based characterization  
of Mediterranean fruit crop  
genetic resources for better  
resilience to climate extremes**