



COST Action
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INTEGRAPE

International Conference on Data integration for
grapevine research in the context of environmental transition

BOOK *of* ABSTRACTS

COST ACTION CA 17111
Lemesos (Cyprus), 14th-16th March 2022

Welcome

We are delighted to welcome you to attend the 4th Annual meeting of INTEGRAPE: Data integration to maximise the power of omics for grapevine improvement held under the auspices of COST (European Cooperation in Science & Technology).

The Conference is a joint initiative of the Cyprus University of Technology, Department of Agricultural Sciences, Biotechnology & Food Science and the University of Verona, Italy.

The theme of the meeting is “Data integration for grapevine research in the context of environmental transition” and the Scientific Program is comprised of 7 plenary talks and 20 oral presentations segregated into 7 Sessions.

We aspire to offer a high-quality and interesting scientific program.

The Convenor

George Manganaris

Cyprus University of Technology

The Chair of the COST Action

Mario Pezzotti

University of Verona, Italy

Scientific Committee

George Manganaris (convenor)
Mario Pezzotti (MC Chair)
Anne-Françoise Adam-Blondon (MC Vice-Chair)
Christopher Davies
Anne-Marie Digby
Astrid Forneck
Ana Margarida Fortes
Jérôme Grimplet
Daniela Holtgräwe
Fulvio Mattivi
José Tomás Matus
Camille Mietton
Nathalie Ollat
Camille Rustenholz
Reinhard Töpfer
Giovanni Battista Tornielli

Organising Committee

George Manganaris (convenor)
Vassilis Fotopoulos (co-convenor)
Egli Georgiadou
Anne-Marie Digby

Conference Program

Monday, March 14, 2022

16:00-18:00 **Attendee registration** (Royal Apollonia Hotel)

18:00-18:30 **George Manganaris** (Local Organiser) & **Mario Pezzotti** (MC Chair)
Welcome Remarks

18:30-19:15 **Cornelius Van Leeuwen** [Inaugural talk, PLE-1] *virtual*
Impacts of climate change in viticulture and potential adaptations

19:15-20:00 **Welcome Cocktail**

Tuesday, March 15, 2022

08:00-09:00 **Attendee registration** (Royal Apollonia Hotel)

09:00-10:45 **Session I: Adaptation / Mitigation to CC / Drought effects**
Moderator: Anne-Françoise Adam-Blondon

09:00-09:45 **Aaron Fait** [PLE-2]
Cultivar identity as a major determinant of wine grapevine response to impending consequences of global warming

09:45-10:00 **Eleni Tani** [OP-1]
Stress-related gene expression and epigenetic modifications in autochthonous grapevine varieties from the 'Epirus' region of Greece with differential responses upon consecutive drought stress

10:00-10:15 **Andreea Manolescu** [OP-2]
Maintenance and characterization of grapevine genetic resources in Romania

10:15-10:30 **Andreas Doulis** [OP-3]
Phenotypic characterization of Greek autochthonous *Vitis vinifera* varieties in different environments

10:30-10:45 **Anna Nebish** [OP-4]
Phenotypic variation and genetic origin of seedless grapevine varieties in Armenia

10:45-11:30 **Morning Tea/Coffee break & Group Photo**

11:30-13:15 **Session II: Rootstock responses, effect on berry composition**
Moderator: Jérôme Grimplet

11:30-12:15	Nathalie Ollat [PLE-3] Rootstock effects on berry composition in the context of climate change
12:15-12:30	Luis Gonzaga Santesteban [OP-5] Implications of the goodness of graft connection on vineyard performance
12:30-12:45	Elisa Marguerit [OP-6] The challenges to be met to unravel the mystery of the adaptation to drought conferred by grapevine rootstocks
12:45-13:00	Gayane Melyan [OP-7] Micropropagation of Grapevine Rootstock Cultivar '1103-Paulsen'
13:00-13:15	Ignacio Buesa [OP-8] <i>virtual</i> Rootstock effects on 'Tempranillo' grapevines performance under deficit irrigation conditions
13:15-14:45	Lunch
14:45-16:15	Session III: Data analysis for untargeted metabolomics: new tools and applications Moderator: José Tomás Matus
14:45-15:30	Justin van der Hooft [PLE-4] <i>virtual</i> Recent advances in computational metabolomics workflows for improved metabolite annotation
15:30-15:45	Angelos Kanellis [OP-9] Exploring the biosynthetic mechanism of aroma formation in grape berries of <i>Vitis vinifera</i> cv. Assyrtiko
15:45-16:00	Konstantina Leontaridou [OP-10] Uncovering the aromatic characteristics of two Greek red wine grape varieties of <i>Vitis vinifera</i> cv. Xinomavro and cv. Agiorgitiko
16:00-16:30	Afternoon Tea/Coffee Break
16:30-17:45	Session IV: Digital Viticulture Moderator: Nathalie Ollat
16.30-17:15	Javier Tardaguilla [PLE-5] High-Throughput Phenotyping Tools in Digital Viticulture
17:15-17:30	Stefania Savoi [OP-11] Phenological and transcriptomic characterization of individual grape berry during development
17:30-17:45	Elsa Chedid [OP-12] Genetic variability of grapevine vigor parameters as described with LiDAR data and associated quantitative trait loci

17:45 - 18:45	Roundtable on the COST Innovator Grant (CIG) [RT-1]
	GRAPEDIA - The Grapevine Genomics Encyclopedia: an innovative portal to integrate knowledge, resources and services for the grape scientific community and industry.
	Contributors: José Tomás Matus (CIG Chair), Camille Rustenholz (CIG Vice-Chair), Michael Alaux, Aureliano Bombarely, Dario Cantu, Pablo Carbonell, Marianna Fasoli, Jérôme Grimplet, Daniela Holtgräwe, Camille Mietton, Marco Moretto, Walter Sanseverino
19:30	Departure to Limassol Castle Area
20:00-00:00	Gala Dinner (Karatello)

Wednesday, March 16, 2022	
09:00-10:30	Core Group Meeting
10:30-11:00	Morning Tea/Coffee break
11:00-12:30	Management Committee Meeting
12:30-13:15	Session V: Grapevine diversity and evolution Moderator: Vassilis Fotopoulos
12:30-12:45	Ia Pipia [OP-13] Tracking the Plastid Genome Diversity of Wild Grapevines (<i>V. vinifera</i> ssp. <i>sylvestris</i>) around Georgia, Europe, Mediterranean basin and Asian and American species by the Next-generation Sequencing and Comparative Genomics
12:45-13:00	Herlander Azevedo [OP-14] Grapevine genomics and the domestication history of Western European varieties
13:00-13:15	Kristina Margaryan [OP-15] virtual The hidden biodiversity of <i>Vitis vinifera</i> L. in Armenia
13:15-14:45	Lunch
14:45-16:00	Session VI: Plant and Soil microbiome Moderator: Margarida Fortes
14:45-15:30	Virginie Lauvergeat [PLE-6] Soil and root-associated microbiomes in a context of vine decline

15:30-15:45	Michaela Griesser [OP-16] <i>virtual</i> Enhancing hydrolytic soil enzyme activity with under-vine vegetation in vineyards
15:45-16:00	Nicolas Vigneron [OP-17] <i>virtual</i> Deciphering the molecular mechanisms behind essential oil treatment against downy mildew in grapevine
16:00-16:30	Afternoon Tea/Coffee break
16:30-18:00	Session VI: Modelling / <i>in silico</i> plants Moderator: George Manganaris
16:30-17:15	Jim Haseloff [PLE-7] <i>virtual</i> Open tools for engineering biology
17:15-17:30	Diego Micheletti [OP-18] <i>virtual</i> FEMVitisDB: a FAIR data management system for data integration in grapevine
17:30-17:45	Marco Moretto [OP-19] Absolute vs relative normalizations to model transcriptomic responses: caveats and limitations
17:45-18:00	Stefania Pilati [OP-20] OneGenE inferred association networks can support experimental research in grapevine

Plenary Lectures, PLE

Code	Presenting Author - Title
PLE-1	Cornelius Van Leeuwen Impacts of climate change in viticulture and potential adaptations
PLE-2	Aaron Fait Cultivar identity as a major determinant of wine grapevine response to impending consequences of global warming
PLE-3	Nathalie Ollat Rootstock effects on berry composition in the context of climate
PLE-4	Justin van der Hooft Recent advances in computational metabolomics workflows for improved metabolite annotation
PLE-5	Javier Tardaguilla High-Throughput Phenotyping Tools in Digital Viticulture
PLE-6	Virginie Lauvergeat Soil and root-associated microbiomes in a context of vine decline
PLE-7	Jim Haseloff Open tools for engineering biology

PLE-1

Impacts of climate change in viticulture and potential adaptations

Cornelis van Leeuwen, Agnès Destrac-Irvine, Gregory Gambetta, Mark Gowdy,
Elisa Marguerit, Philippe Pieri and Nathalie Ollat

*EGFV, Univ. Bordeaux, Bordeaux Sciences Agro, INRAE, ISVV, Villenave d'Ornon, France
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Climate change will impose increasingly warm and dry conditions on vineyards worldwide. Wine quality and yield are strongly influenced by climatic conditions and depend on complex interactions between temperatures, water availability, plant material and viticultural techniques. In established winegrowing regions, growers have optimized yield and quality by choosing plant material and viticultural techniques according to local climatic conditions, but as the climate changes, these will need to be adjusted. Adaptations to higher temperatures include changing plant material (e.g. rootstocks, cultivars and clones) and modifying viticultural techniques (e.g. changing trunk height, leaf area to fruit weight ratio, timing of pruning) such that harvest dates are maintained in the optimal period at the end of September or early October in the Northern Hemisphere. Vineyards can be made more resilient to drought by planting drought resistant plant material, modifying training systems (e.g. goblet bush vines, or trellised vineyards at increased row spacing), or selecting soils with greater soil water holding capacity. While most vineyards in Europe are currently dry-farmed, irrigation may also be an option to grow sustainable yields under increasingly dry conditions but consideration must be given to associated impacts on water resources and the environment. Mediterranean countries have always been exposed to warm and dry conditions. Considerable resources do exist in this area in terms of plant material (heat and drought resistant varieties) and expertise to cope with these conditions. Until recently, these resources have been ignored by the scientific community and the mechanisms driving the heat and drought tolerance of Mediterranean varieties and training systems remain largely unknown. A better understanding of this plant material and cultivation practices would be particularly useful to adapt viticulture to the changing climatic conditions across all winegrowing regions in the world.

PLE-2

Cultivar identity as a major determinant of wine grapevine response to impending consequences of global warming

Kelem Gashu¹, Chao Song¹, Arvind Kumar Dubey¹, Tania Acuña¹, Moshe Sagi¹,
Nurit Agam¹, Amnon Bustan², **Aaron Fait¹**

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Exploiting consistent differences in radiation and average air temperature between two experimental vineyards in Israel arid Negev region, we conducted a multiple year study on the impact of climate shifts on fruit development, berry indices, total carotenoids (TC), redox status, and phenylpropanoid metabolism in the berries of 30 red and white wine grapevine (*Vitis vinifera*) cultivars. A significant interaction between cultivar, location, and season affected most parameters. The warmer RN site was generally associated with higher H₂O₂ levels and carotenoid degradation, and lower phenylpropanoid content than the cooler MR site. It was also generally associated with enhanced carotenoid degradation and advanced phenological course for the white cultivars, which reached harvest up to 2 weeks earlier than at the MR site. The white cultivars also showed stronger correlation between non-consecutive phenological stages than did the red ones. In contrast, the harvest time of red cultivars considerably varied according to seasons and sites causing berry shriveling and cluster collapse in a few cultivars. Phenylpropanoids were differently associated with climate indices at the two sites. For instance, flavan-3-ols were negatively correlated with radiation at RN, while flavonols were correlated with DDD at MR. Furthermore, flavonols, amino acids, and stilbenes were inversely correlated with H₂O₂ content in a cultivar-specific manner. Our results emphasize the potential of grapevine biodiversity to withstand global warming.

PLE-3

Rootstock effects on berry composition in the context of climate

Nathalie Ollat, Jean-Pascal Tandonnet, Gregory Gambetta and Elisa Marguerit

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The potential impacts of climate change on grapevine yield and berry composition have been studied for almost 20 years. Elevated atmospheric CO₂, increases in average temperature, extreme temperature events and more frequent droughts act individually and interact to modify grapevine yield and berry composition. The most frequently documented concerns are reduced yield, higher sugar content, lower acidity and high potassium content in berries, as well as modifications of secondary metabolism that would affect the polyphenolic and aroma profiles of the wines and induce a delay of anthocyanin accumulation in red grapes. Rootstocks are known to directly or indirectly affect these characteristics. Rootstock effects on yield, vegetative growth and fruit composition have been reported in wide-ranging climates and soil conditions, with different growing practices (including non-irrigated and irrigated vineyards), and various scion varieties and rootstock genotypes with a large contribution of interactions between parameters. The underlying mechanisms are complex and remain to be elucidated. Rootstock effects on berry composition are largely indirect via the strong general relationship between yield or reproductive/vegetative ratio and quality parameters such as sugar content, titratable acidity and pH. These allometric relationships may also be genotype dependent. However direct rootstock effects on berry amino acids and secondary metabolites have also been described with transcriptomic and metabolomics approaches. Mineral nutrition, especially nitrogen, is probably involved. A general survey of these direct and indirect effects will be presented with the objective to evaluate more precisely the potential role of rootstocks to adapt grapevine to climate change.

PLE-4

Recent advances in computational metabolomics workflows for improved metabolite annotation

Justin van der Hooft

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Specialized metabolites play key roles in regulating physiological processes in organisms related to growth and development and serve as communicators between organisms. Their encoded messages include cries for help, embrace yourself, as well as deadly kisses. However, only relatively few specialized metabolites are structurally characterized, and even less are connected to their genetic machinery in the organisms producing them. Making such links between genes and mass will help to elucidate specialized metabolite structures and infer their functions, for example through regulatory or functionally annotated genes neighboring biosynthetic genes. In this seminar, I will highlight recent advances in computational metabolomics workflows related to metabolomics mining and annotation tools in order to better understand the complex metabolite mixtures that specialized metabolites are typically part of as well as recent advances in combined analysis of genomics and metabolomics data. I recognize three paths to better understand complex metabolite mixtures: i) increased metabolite annotation power, ii) chemically-informed comparative metabolomics, and iii) linked metabolomics profiles to function and genotype/genomic information. During this keynote, I will present recent work from my group and close collaborators. I will indicate why we need improved metabolite annotation tools to empower untargeted metabolomics approaches, and touch upon the motivation behind and general background of molecular networking and MS2LDA substructure finding and the MolNetEnhancer workflow that brings everything together. I will explain what mass spectral embeddings are and how they have the potential to transform untargeted plant metabolomics analysis workflows. Furthermore, I will briefly introduce the Paired Omics Data Platform as a resource for paired omics datasets that facilitate the integrated analysis of genomics and metabolomics data. I will finish off by highlighting the importance of FAIRifying omics workflows and with my perspective on integrating genome and metabolome mining workflows to accelerate specialized metabolite discovery and their structural and functional characterization. I expect that the presented methodological developments will advance our understanding of the role of metabolites and their complex molecular interactions that underpin growth, development, and health. This will pave the way toward, for example, improved understanding of how grape grows, and how resilient and nutrient-rich grape can be grown in an eco-friendly manner.

PLE-5

High-throughput phenotyping tools in digital viticulture

Javier Tardaguilla

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High-throughput phenotyping tools based on emerging technologies are being developed and applied in digital viticulture. In this work, we describe several new phenotyping tools based on technologies as computer vision, chlorophyll fluorescence, thermography, spectroscopy and hyperspectral imaging for proximal or remote monitoring of the vineyards. The main objective of these new tools is to obtain and supply data and information to grape growers and wine producers as a basis for improving decision-making process in digital viticulture. The smart applications of these new high-throughput phenotyping tools in viticulture are discussed in relation nutrient and water status, pests and diseases, yield components and fruit composition.

PLE-6

Soil and root-associated microbiomes in a context of vine decline

Romain Darriaut¹, Guilherme Martins², Coralie Dewasme¹, Isabelle Masneuf-Pomarède², Elisa Marguerit¹, Livio Antonielli³, Guillaume Darrieutort⁴, Séverine Mary⁴, Patricia Ballestra², Philippe Vivin¹, Birgit Mitter³, Stéphane Compant³, Nathalie Ollat¹, **Virginie Lauvergeat¹**

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The soil microbiota plays a decisive role in soil quality by contributing to the biogeochemical cycles of carbon, nitrogen and phosphorus, but also by providing the plant with most of its rhizospheric and endospheric microbiota. Some of these micro-organisms are beneficial for the plant, contribute to its growth and promote its adaptation to environmental constraints. They allow better accessibility to water and mineral elements and/or induce defense mechanisms. It is the balance between these “good” microorganisms and the “bad” ones, those that are pathogenic, which would define the microbiological quality of the soil. It has thus been defined that the greater the diversity, the better the quality. However, it is necessary to acquire more data concerning the microbial biodiversity of soils and roots, and its functionality, in order to fully understand how to define the quality of the soil and root microbiota according to the environmental context and to understand how to restore it. This question is particularly interesting when vineyard is subjected to decline unrelated to identified pathogens, water or mineral stress. To investigate the role of the soil microbiota in such declines, a survey has been done in four vineyards in Bordeaux region. In each of the chosen plots, an area with vines with a lower vigor and yield, and a higher mortality was defined as the symptomatic area (S) and was compared to an area with a normal growth called asymptomatic (AS). The soil of the inter-row of the S area showed a disruption in microbial diversity and enzymatic activities compared to AS soil. Further analysis of the roots and rhizosphere of declining plants in one of these plots revealed a high presence of potentially pathogenic but also beneficial micro-organisms. In a second step, a greenhouse experiment with young grapevines planted on the S soil of a vineyard plot exhibiting signs of decline, showed that the rootstock modified the microbial composition of the roots and rhizosphere. Bacteria were isolated from the rhizosphere of these plants and their putative plant growth promoting activity was evaluated through enzymatic assays and *in vitro* bio-assays. This part allowed the identification of isolates modifying the aerial and root systems of vine plantlets. These results contribute to the understanding of vine-soil interactions, highlighting the role of the genetic dimension of the rootstock.

PLE-7

Open tools for engineering biology

Jim Haseloff

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Plant systems are characterised by complex genetic and cellular networks that are locked together by dynamic, parallel and non-linear feedback interactions that give rise to self-organised growth, repair and propagation. These evolved systems pose formidable barriers to rational engineering approaches. Yet, the challenge is compelling. Plants are capable of assembling harvestable materials, chemical and foodstuffs, and they can do this in a renewable fashion, cheaply and in up to gigatonne scale. We have adopted the liverwort weed *Marchantia polymorpha* as a simple plant system and testbed for bioengineering. Liverworts are characterised by morphological simplicity, matched by simple underlying genome structure. The ease of culture, transformation and analysis of *Marchantia* make it an ideal system for experiments with plant development and synthetic biology. We have developed a battery of computational, imaging and genetic tools to allow clear visualisation of individual cells inside living plant tissues, and developed a common syntax and assembly methods for plant DNA parts that can be used to reprogram metabolism and development. We have established the OpenPlant research initiative as a hub for interdisciplinary exchange and to establish technical frameworks for (i) open standards for plant synthetic biology, (ii) simple model systems for analysis of whole plant growth and metabolic engineering, and (iii) frugal technologies for international training and capacity building. This has led to the establishment of the Biomaker initiative as a means of distributing accessible engineering tools, and “gluing” together biologists, physical scientists and engineers in bioinstrumentation projects (<https://www.biomaker.org>).

RT-1

The Grapevine Genomics Encyclopedia: an innovative portal to integrate knowledge, resources and services for the grape scientific community and industry

Michael Alaux; Aureliano Bombarely; Dario Cantu; Pablo Carbonell; Marianna Fasoli; Jérôme Grimplet; Daniela Holtgräwe; Camille Mietton; Marco Moretto; Walter Sanseverino; Camille Rustenholz; **José Tomás Matus**
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Online tools and databases are key to exploit the potential offered by genomic advances to both research and industry. In plants, the final goal of these resources is to contribute towards crop improvement, which, whether achieved through selective breeding or biotechnological strategies, is largely dependent on the cumulative knowledge of a plant species' genome (and pangenome) and its containing genes. Acquiring this knowledge is specially challenging in grapevine (*Vitis vinifera* L.), one of the oldest fruit crops grown worldwide. Well-established research communities studying model organisms have created and maintained, through public and private funds, a diverse range of online tools and databases serving as repositories of genomes and gene function data. The lack of such resources for the non-model, but economically important *Vitis vinifera* species has driven the need for a standardized collection of assets within the grapevine community. Within the INTEGRAPPE COST Action CA17111, several resources destined to maximise genomics and phenotyping data have been established, using standardized and F.A.I.R. protocols. Among these efforts, the Action has (1) included the first grape gene reference catalogue, where genes are ascribed to functional data, including their accession identifiers from different genome-annotation versions, (2) enlisted all reference genome sequence assemblies and their functional gene annotations, and (3) created guidelines for the correct generation, upload and treatment of diverse omics data. Despite these advances, there is much space for innovation. The CIG will centralize the resources in a single database, with open access to the public but also offering customized services for the research community and industry, thus giving economic value to this platform. In order to assist the scientific community and grape/wine companies in designing next-generation cultivars that will adapt to new climate conditions, this database will combine omics, phenotypes and climate data to generate predictions. The CIG aims to implement innovative technologies such as deep learning and modelization methods to provide a service to the companies in order for them to adapt their production, being aware of the impact of climate transition. These tools will also allow growers to assess the level of sustainability of their vineyard. During the CIG grant period the CIG Team will gather in Working Group Meetings to decide on the best procedures to implement the GRAPEDIA database and will customize the web portal through the activity of Training Schools conducted in the form of jamborees and hackathons to work towards the same goal. Short-Term Scientific Missions will also be promoted to accomplish deliverables, where students and researchers will be nurtured by laboratories that have expertise in biological database construction. The structure of the database will consist of modules to manage and visualize omics and phenotypic data and will allow the implementation of new modules after the grant period ends to serve as a social data-driven platform for the grapevine community in which scientists, breeders, producers, and consumers will be able to exchange information.

Oral Presentations, OP

OP-1

Stress-related gene expression and epigenetic modifications in autochthonous grapevine varieties from the 'Epirus' region of Greece with differential responses upon consecutive drought stress

Grigorios Maniatis¹, Kimon Klouvatos¹, Stamatia Megariti¹, Efi Sarri¹, Maria Gerakari¹, Ioannis Papadakis², Theodora Pitsoli³, Aliko Kapazoglou³, **Eleni Tani^{1,*}**

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Vitis vinifera is a cultivation of great importance both for economical and historical reasons in Greece that stands under threat from the ongoing climate change. This study focuses on the response to drought stress of traditional grapevine varieties from the region of 'Epirus' in Northwestern Greece, aiming to assess the degree of stress-resilience among different genotypes and unravel the possible mechanisms of drought tolerance. By comparing the morphological and physiological parameters, two varieties (namely Debina and Dichali) were selected among a series of autochthonous varieties, as they present the more distinctive variation in the response, upon a two-phase drought stress experiment. Gene expression analyses were performed for several drought-related genes (*VvMYB*, *VvGATA*, *VvTOPLESS*, *VvCONSTANS*) as well as for two miRNAs (miRNA159, miRNA156) that possibly target the aforementioned genes. Preliminary results indicate that gene expression is upregulated in the variety Debina when subjected to different levels of drought stress. On the contrary, Dichali tends to preserve a more stable pattern of gene expression in all conditions. Further studies on the regulation of miRNA-target gene modules will contribute to our understanding of the molecular mechanism underlying grapevine response to drought and perhaps other abiotic stressors.

OP-2

Maintenance and characterization of grapevine genetic resources in Romania

Andreea E. Manolescu, Anamaria M. Dumitru, Dorin I. Sumedrea, Carmen F. Popescu*

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The national evaluation of the genetic diversity from the grapevine germplasm collections is a major objective for the research community. Over time (1895 - 1970) such collections were established in 4 university centres and 9 units with a research profile. The curators tried to comply with the international requirements regarding the following issues: a) providing registration documents of the accessions; b) applying of a unitary system for a complete characterization of the existing/introduced varieties in the germplasm collections; c) confirmation the authenticity of the accessions from the germplasm collections by ampelographic descriptions (from reference literature and *in situ* observations) and molecular analyses with 13 SSR markers (9 markers from the internationally recommended standard set - VVS2, VVMD5, VVMD7, VVMD25, VVMD27, VVMD28, VVMAG32, VVMD28, VVMD32, to which 4 markers were added - ISV2, ISV3, ISV4 and VMCNG4b9). Molecular analyses on a number of 52 accessions, considered autochthonous and at risk of extinction, proved the following: a) 15 accessions presented genetic profiles identical to those already registered in European databases; b) for 11 accessions the synonyms mentioned in the reference documents were confirmed; c) the synonyms for 3 accessions have not been confirmed; d) for 5 accessions, about which we do not have complete information in the reference literature, new synonyms have been identified; e) for other 4 accessions, about which we have complete information in the reference literature, new synonyms were documented; f) arguments were brought to prove that: *Bătută neagră* is synonymous with the *Negru românesc* variety; *Gordan*, *Iordană* and *Zemoasă* have the same SSR profile, so they are synonymous; *Zghihară de Huși* and *Galbenă de Odobești* are synonymous; g) the genetic profiles obtained for 3 accessions (*Moroștină*, *Negru mare* and *România*) proved the 'uniqueness' of these grape varieties in the European germplasm collections; h) for 4 accessions, differences were found both regarding the ampelographic description (compared to the descriptions in the reference literature) and the SSR profiles that did not correspond to any variety indicated as a possible synonym, so there were considered misnomers. All these results were confirmed in three laboratories (Centro di ricerca per la viticoltura Conegliano - Italy, Institut für Rebenzüchtung Geilweilerhof - Germany and The Vassal-Montpellier Grapevine Biological Resources Center - France), were published and included in the international databases. The genetic resources maintained in the germplasm collections are represented by genotypes guaranteed in terms of their authenticity and can be used as: - reference material for comparative studies in any research activity involving ampelographic characterization, phenology and the evaluation of the productive and oenological potential of the grapevine varieties or clones; - initial propagating plant material in order to restore the varietal assortment or to save endangered varieties. According to our knowledge, in the grapevine germplasm collections from Romania there are around 2580 different varieties, of which 30% are considered as local varieties, that could be valuable for the European heritage and need to be completely analyzed.

OP-3

Phenotypic characterization of Greek autochthonous *Vitis vinifera* varieties in different environments

Theodora Pitsoli¹, **Andreas Doulis²**, Aliko Kapazoglou^{1*}

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Viticulture is an important agricultural sector in Greece and in the wider region of the Mediterranean basin. Protecting the rich Mediterranean *Vitis* biodiversity in the era of ongoing climate change is a major goal among different countries for ensuring sustainable viticulture in adverse environmental conditions. In this context, the project “*MedVitis*-Protecting the diversity of Mediterranean *Vitis* in a changing environment” within the framework of the Arimnet2 programme, has implemented collaborative actions among three Mediterranean countries, Greece, Slovenia and Morocco, aiming at protecting Mediterranean *Vitis* biodiversity through detailed phenotypic and molecular-genetic analysis of grapevine genetic resources. In the present work phenotypic characterization was performed for a selection of autochthonous wine grapevine varieties from the prefecture of Preveza (region of Epirus), in Northwestern Greece. In particular, morphological characterization was performed for six wine grapevine varieties from two locations in Preveza characterized by different environmental conditions. Specifically, the varieties included in the study were: Dichali (N), Managiatiko (N), Korithi (N), Tourkopoula (Rs), Alpoura (N) and Koutsoupia (N) grown in the area of Oropos (average altitude 30 m) as well as Dichali and Korithi grown in the historical site of Zalongo / Kryopigi (average altitude 500 m). The aforementioned varieties exhibit very good adaptation to the agroclimatic conditions of the Epirus region and have low input requirements. Vinification at small-scale, by local viticulturists has shown promising potential for production of quality wines. Proper variety identification is vital for classification and for protecting the rich grapevine diversity and grapevine products of the Epirus region. This region is characterized by fragmented areas of cultivation, traditionally with low communication so it can be expected that varieties are not as well described as elsewhere in Greece. Localization and marking (a total of 27 independent vines) was followed by full photographic record acquisition. The Ampelographic description was based on 52 ampelographic descriptors of young shoots, young leaves and mature leaves, as specified by the OIV Descriptor List (OIV 2009). An exploratory statistical analysis of ampelographic measurements provided information on the hierarchical structure of phenotypic diversity among the grapevine varieties examined. A dendrogram was constructed utilizing the Manhattan dissimilarity index and the UPGMA clustering algorithm employing NTSYSpc software program. Diverse clustering was observed demonstrating inter-cultivar variability. Interestingly, same varieties from two different environments with different altitudes were grouped in discrete clusters. It may be suggested that during historical times, the two areas of cultivation formed the basis of different isolated genetic pools. This purported isolation could allow for a separate genetic drift of the two populations leading to genetic differentiation. Alternatively, it could be postulated that different cultural practices have allowed for the survival of different kinds of genotypes in each altitude (*on-farm breeding*), or that the diverse environments have led to different epigenetic landscapes in each genotype and consequently the establishment of different phenotypes. Our study provides initial morphological characterization of the autochthonous grapevine varieties of the area of Preveza to be followed by future phenotypic and molecular analysis and ultimately contribute to the overall effort of phenotypic and genetic assessment of the Mediterranean grapevine germplasm.

OP-4

Phenotypic variation and genetic origin of seedless grapevine varieties in Armenia

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During the last decades seedlessness became a new trend in commercially valuable table grapes and raisins production. Identification and characterization of seedlessness from different origins and in different genetic backgrounds could boost the success of table grape breeding and innovation. Recently, a missense mutation in the MADS-Box gene *VviAGL1* was confirmed as the major origin of stenospermocarpic seedlessness in grapes. Armenia is one of the countries of grape domestication and seedless grapes origin and is characterized by rich grape diversity. Armenian grapevine genetic resources show a clear genetic differentiation from European grapes and can carry unexplored sources of genetic variations for the development and innovation of seedless grape varieties. Searching for new sources of seedlessness, we analysed a set of 42 seedless grapevine accessions located in the Etchmiadzin Grape Collection (FAO Institute Code: ARM006), Nalbandyan Grape Collection (FAO Institute Code: ARM011) and within private orchards of the Armavir region. Genetic identification was performed with seven nuclear microsatellite loci and the genotypes obtained were compared with the *Vitis* International Variety Catalogue (www.vivc.de) database. Berry and seeds phenotypic characterization was performed on thirty berries from two plants per accession. Furthermore, molecular analysis of seedlessness was performed by the targeted sequencing of *VviAGL1*. Microsatellite analyses revealed the presence of 11 genotypes among the 42 accessions, namely 'Anush', 'Eskeri', 'Hrushaki', 'Karmir Kishmish', 'Karmir Yerevani', 'Kishmish Chernyi', 'Kishmish Khishrau', 'Kishmish Moldavskii', 'Parvana', 'Sultanina' and 'Ushahas Nazeli'. Based on available pedigrees data, 'Eskeri', 'Hrushaki' and 'Kishmish Moldavskii' are offspring of Sultanina, while 'Anush' and 'Ushahas Nazeli' have a second-degree relationship with it. Phenotypic analysis revealed a wide variation in berry weight as well as in the formation of seeds and seed rudiments. Mean berry weight ranged between 0.89g ('Karmir Yerevani') to 3.74g ('Parvana'). Berries with only rudimental seeds were detected in 'Karmir Yerevani', 'Karmir Kishmish', 'Sultanina' and 'Hrushaki'. By contrast, plants of 'Anush', 'Eskeri', 'Kishmish Khishrau', 'Kishmish Chernyi', 'Kishmish Moldavskii' and 'Parvana' mostly produced large and empty floating seeds, and only occasionally well-developed seeds. Berries of 'Ushahas Nazeli' showed 1.5 well-developed potentially viable seeds per berry (despite its seedlessness recorded in *VVC* database). Targeted sequencing of *VviAGL1* gene at the site of causative mutation showed that ten investigated seedless genotypes are heterozygous for the seedless allele with dominant point mutation (C>A) causing the stenospermocarpy present in 'Sultanina' and 'Sultanina'-derived seedless cultivars. As expected, 'Ushahas Nazeli' did not carry that mutation and was homozygous for the seeded allele (C:C). We are currently investigating whether the detected mutations in seedless genotypes are identical by descent or could have independently appeared in some cases.

OP-5

Implications of the goodness of graft connection on vineyard performance

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Graft union development is a relatively complex process that begins with the proliferation of a mass of undifferentiated parenchymatous cells at both the scion and the rootstock that initiate the healing process of the graft area as a wound response. The callus acts as a bridge between the scion and the rootstock until xylem and phloem tissues differentiate, enabling the vascular connection between the two plant individuals until they finally get connected. In viticulture, grafting was originally used to change varieties, but it became essential at the end of the 19th century due to the phylloxera crisis. In this study we focused on assessing the implications that the connection at the grafting junction has for grapevine performance in field. To evaluate the implication of the connection, plants with two different degrees of alignment between the rootstock and the scion were used, some where the alignment was optimum (CA, Complete alignment) and others for which it was suboptimum (PA, Partial alignment). These plants were bench grafted (omega graft) in the nursery one year before the experiment started, and the commercial process to obtain dormant rooted and grafted plants was followed. This is a realistic approach, since there is a diversity among nurseries on the degree of attention they pay to the perfect alignment between scion and rootstock. In 2018, the grafted plants obtained were planted following a factorial design. and their growth and yield monitored for four consecutive seasons. The results obtained demonstrate the negative implications that a poorer connection may have on vineyard development, particularly during the first seasons, and highlight the relevance of a careful alignment of rootstock and scion in the nursery.

OP-6

The challenges to be met to unravel the mystery of the adaptation to drought conferred by grapevine rootstocks

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Climate change will increase the frequency of water deficit situation in some European regions, by the increase of the evapotranspiration and the reduction of rainfalls during the growing cycle. This requires to find ways of adaptation, including the use of plant material which is more tolerant to drought. Over the varieties used as scion and involved in the typicality of our wines, rootstocks constitute a relevant way of adaptation to the more constrained environmental conditions. The rootstock genotype impacts the grapevine functioning at three levels: the absorption of water, the water transfer and the water consumption. The variability of root anatomy, root depth and water extraction capacity may explain differences observed or measured between rootstocks in pot experiment or in the field. Hydraulic conductivity differed between sensitive and tolerant rootstocks. Gas exchanges are related to the leaf area and the vigor conferred, but also with regulatory processes, partially independent during the day and the night. Gas exchanges regulation along the day and night but also with the variation of the water status, *i.e.* the transpiration plasticity to water status, is in fact controlled by rootstocks. Despite the empirical knowledge and the increasing interest dedicated to grapevine rootstocks in research, the mechanisms involved in all these responses to water deficit remains poorly understood. Data from the literature and recorded in Bordeaux will be synthesized. Some challenges have to be met to get further crucial information about the traits conferring a higher adaptation to water deficit in order to speed up the selection of new rootstocks tolerant to drought. These challenges discussed will be the variability of the responses due to water status scenario (the intensity and the occurrence in the cycle of the water deficit), the choice of the traits measured with particularly the interest to consider the plasticity of the traits usually measured and the rootstock scion interactions.

OP-7

Micropropagation of grapevine rootstock cultivar '1103-Paulsen'

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Grape is one of the major and ancient fruit crops in Armenia. Phylloxera (*Daktulosphaira vitifoliae*) is a very small (less than 1.0 mm) and dangerous pest (aphid) of grapes, that lives and feeds on the roots of grapevines, causing decline and often death of plants. Phylloxera spread all over the world, covering the main regions of viticulture. Now this insect is a serious threat to Armenian grape and wine industry also. The use of phylloxera - resistant rootstocks is the only real and effective way for control of that dangerous pest. Plant biotechnologies play a key role in the massive production of high quality, disease -free planting material of a wide range of crops. The objective of this study was to establish an efficient protocol for *in vitro* multiplication and rooting, as well as *ex vitro* acclimatization of phylloxera - resistant rootstock cultivar '1103-Paulsen' (*Vitis berlandieri* cv. Rösséguier 2 x *Vitis rupestris* cv. du Lot). The initial explants (nodal segments) were taken from new developing shoots of the plants grown under open field. The results showed that the maximum aseptic cultures with the highest percentage of explants survival were obtained when nodal segments treated with 1.0% sodium hypochlorite for 10 min + 70% ethanol for 1.0 min. For the culture initiation Gamborg (B5) medium was better than Murashige and Skoog (MS), Nitsch and Woody plant (WPM) media which showed rapid growth of axillary bud within 6 days. Numerous combinations of 6 - Benzylaminopurin (BAP), 6-furfuryl aminopurine (kinetin) and Giberrellic acid (GA₃) were carried out to optimize the proliferation phase. The highest shoot proliferation (4.30 ± 0.35) was obtained in medium fortified with 0.5 mg/L BAP + 0.2 mg/L Kin and the highest shoot length (4.50 cm) was obtained at 0.5 mg/L BAP + 0.8 mg/L GA₃. For *in vitro* rooting shoots were cultured on ½-strength B5 medium containing different concentrations of Indole-3-butyric acid (IBA) and Indole-3-acetic acid (IAA). '1103-Paulsen' rooted well in all rooting combinations, but the highest rooting (100%) was observed in medium containing 0.2 mg/l IBA + 0.1 mg/l IAA. The plant growth condition in the culture room were 16 h photoperiod, 3000 lux light intensity and a relative humidity of 60 ± 5.0 %. Acclimatization of *in vitro* plants to *ex vitro* is very hard and stressful phase during micropropagation. *In vitro* well-developed rooted plantlets with 6-8 cm height were acclimatized *ex vitro*. The maximum percentage (83%) of plant survival was on the potting medium consisted of equal quantities of perlite, soil.

OP-8

Rootstock effects on 'Tempranillo' grapevines performance under deficit irrigation conditions

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Grape production, quality and the profitability of viticulture largely rely on grapevine's responses to soil water deficit. Moreover, the typicity of Mediterranean viticulture depends on maintaining the cultivation of local varieties. However, with climate change increasing water needs in most semi-arid regions, preserving the sustainability of traditional viticulture requires adapting it to longer periods of water shortage. This can be achieved using both agronomical practices and plant material selection. In this regard, deficit irrigation and rootstock genotypes can be friendly strategies to address these challenges. This work aimed to evaluate the use of new grapevine rootstocks bred to perform better under drought conditions (M1 and M4) than the current ones (1103-Paulsen). The experiment was carried out during two seasons (2019-2020) on an experimental two-year old vineyard of 'Tempranillo' cultivar (*Vitis vinifera* L.) located in Moncada, Valencia. Two water regimes were imposed, Control, irrigated at 100% of estimated crop evapotranspiration for the entire season; and sustained deficit irrigation (SDI), irrigated at 50% of Control. Deficit irrigation had the expected effects on vine yield, water relations and leaf gas exchange rates. Nevertheless, rootstocks showed different responses to deficit irrigation on vine water status, but not on gas exchange parameters. This suggests possible differences in hydraulic capacity among rootstocks. The M1 showed the lowest leaf area, whereas the M4 the highest. Remarkably, pruning mass was significantly reduced on both M-series rootstocks in response to water deficit, while the 1103P did not. However, 1103-Paulsen yielded less than M4 due to smaller clusters and berries, with M1 showing intermediate values. Moreover, the berries from 1103-Paulsen showed lower total soluble solids content and pH values than those of the M-series, but significantly higher concentrations of phenolic compounds. These results evidence the potential of grapevine rootstocks for modulating vine performance and grape composition responses to drought and outline its physiological basis. Experiments are ongoing to corroborate these effects in the longer term.

OP-9

Exploring the biosynthetic mechanism of aroma formation in grape berries of *Vitis vinifera* cv. Assyrtiko

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We are interested in understanding the aroma formation in ripening berries of *Vitis vinifera* cv. Assyrtiko. Recently, this white wine cultivar originated from the Cycladic Island of Thira (Santorini) gained a worldwide popularity due to its acidity, fruity aromas, high alcoholic grade, full body, and characteristic metallic taste. Transcriptomic analysis of two clones exhibiting high and low aromatic bouquet as determined by a taste panel revealed several genes clustered in the high aromatic clone, such as carotenoid cleavage dioxygenases, enzymes of the MEP pathway and LOXA, involved in the lipoxygenase pathway. PCA, Volcano plot, Heat Maps, visualize the difference of the two clones and GO enrichment and KEGG analysis help to suggest the biosynthetic pathways involved in aroma formation. To this end, the following genes were functionally characterized by expressed either in yeast or by *in vitro* assays: raspberry ketone synthase (RZS1), contributing to the formation of 4-(4-Hydroxyphenyl) butan-2-one (raspberry ketone), coniferyl alcohol acetyl transferase (CAAT) and eugenol synthase (EGS1), both participating in the synthesis of eugenol, all belonging to the phenylpropanoid pathway. P450-CYP76F14, wine lactone synthase participating in the biosynthesis of precursors of wine lactone, namely E)-8-hydroxylinalool and E)-8-carboxylinalool.

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OP-10

Uncovering the aromatic characteristics of two Greek red wine grape varieties of *Vitis vinifera* cv. Xinomavro and cv. Agiorgitiko

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Two of the most well-known and widely consumed Greek red wine cultivars are Xinomavro and Agiorgitiko. Xinomavro from north Greece exhibits aromatic notes of olive and tomato paste, and violets. On the other hand, Agiorgitiko a native cultivar of Nemea is characterized by an aroma of fresh red fruit and spices. To understand the differences in the aromatic synthesis of these two varieties, GC-MS analysis of grapes from the two varieties helped to uncover the aroma characteristics of the two red varieties. Agiorgitiko is richer in furfural (Sweet, brown, woody, bread, caramellic aroma), acetic acid (sour, vinegar), cis-3-hexenol (green), beta-cadinene (woody, chamomile), whereas Xinomavro has higher concentration in 1-octen-3-ol (mushroom), hexanoic acid (cheesy) and linalool (citrus, floral). RNA-sequencing and bioinformatic analysis using Geneious platform was conducted to understand the mechanism of aroma formation at the gene level. Differential gene expression analysis between Xinomavro and Agiorgitiko showed that 16448 genes were differentially expressed in Xinomavro, while 17034 were in Agiorgitiko. GO enrichment analysis of those genes showed that the Xinomavro genes were localized in chloroplasts and plastids, with mostly transferase activity and related to defense response and photosynthesis. Agiorgitiko genes, however, belonged to aromatic or organic compound metabolic processes and gene expression, so their localization was mostly in nucleus and protein-containing complexes. KEGG pathway verified that the biosynthesis of secondary metabolism and especially the phenylpropanoids pathway and sulphur metabolism increased in the Agiorgitiko variety compared to Xinomavro. The latter had higher number of genes in the terpenoid pathway, carotenoids, and fatty acid metabolism such as (3S,6E)-nerolidol synthase 1, terpene synthase, (-)-germacrene D synthase, (E)-beta-caryophyllene synthase, carotenoid cleavage dioxygenase 4a and b.

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OP-11

Phenological and transcriptomic characterization of individual grape berry during development

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In recent years, the understanding of grapevine developmental physiology has often employed transcriptomic approaches that have generated an enormous amount of data from various experimental designs that have often considered different varieties, different growth conditions, and in some cases the concomitance of (a)biotic stresses. The identification of key molecular processes associated with transcriptomic remodeling and the knowledge of gene trajectories during grape development has always been considered the ultimate goal towards the definition of a detailed transcriptomic map together with their further modulation in case of different environmental conditions, presence of diseases, and/or use of agronomic practices. Although classical sampling of berries or portions of clusters aimed at representing the entire diversity of an experimental field currently predominates, it is recently becoming innovative to sample individual grape berries resynchronized according to their growth patterns, or sorted according to their sugar concentration to reduce the "noise" due to the high asynchrony and heterogeneity of grape development within clusters. In this study, the developmental period of a single fruit was revisited to investigate metabolic changes and their transcriptomic regulation from flowering to over-ripening. Individual growth measured over a three-month period by image analysis was fitted to a remarkably invariant double sigmoid model after fruit size normalization and synchronization of mean growth. For example, the transcriptomic study revealed a strong reprogramming of cell wall enzymes and structural proteins at the stop of phloem discharge, when berries might be considered physiologically ripe. Several sugar and aquaporin transporters on the plasma or tonoplast membranes, with the notable exception of H⁺/sugar symport transporters, which are rather weakly and constitutively expressed, behave as on/off switches for the discharge of processed sap into the ripening fruit, opening the water and sugar load in the berry and closing it at the growth max peak before going to initial dehydration. The prevalence of genes belonging to the SWEET gene family suggests that electrogenic transporters would play a minor role on the plasma membranes of the SE/CC complex and on that of the pulp, while sucrose/H⁺ exchangers dominate on its tonoplast, being the driving force behind all sugar accumulation in the vacuole. These very promising results clearly illustrate that a single berry sampling strategy can lead to a more complete and accurate understanding of the biology of fruit development and ripening.

OP-12

Genetic variability of grapevine vigor parameters as described with LiDAR data and associated quantitative trait loci

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Estimating growth traits of grapevine plants is common approach to describe the effects of cultural practices, training systems, environmental conditions, or genetic effects, both for rootstocks and scions varieties. Among these traits, the simple pruning weight is one of the most popular, while being time-consuming when hundreds of genotypes are to be characterized. To face the challenge of adaptation to climate change and the global demand for grapevine varieties resistant to disease, there is an increasing need for high throughput phenotyping methods. We studied the variability of the vineyard plant vigor in the progeny of the cross between two genotypes carrying resistance genes for powdery and downy mildew. In winter, the pruning weight was measured for more than 200 genotypes and, in parallel, we used a newly developed high throughput LiDAR acquisition system to characterize the plants. In summer, the exposed leaf area for the studied population was assessed using a RGB camera and canopy volume with the LiDAR system. We will present the LiDAR system and the comparison between LiDAR data and manually obtained data for pruning wood and exposed leaf area. Using “genotyping by sequencing” technology to describe the genetic heritage of the offspring, we performed quantitative trait loci (QTL) detection and identified several genomic regions associated with the genetic variability of plant vigor relying on electronic phenotyping.

OP-13

**Tracking the Plastid Genome Diversity of Wild Grapevines
(*V. vinifera* spp. *sylvestris*) around Georgia, Europe, Mediterranean basin
and Asian and American species by the Next-generation Sequencing
and comparative genomics**

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Vitis L. belongs to one of the oldest Vitaceae family of flowering plants. The origins of the grapevine remain uncertain, this family possibly were originated on the boarder of Jurassic and Cretaceous periods and was widely distributed in the Old and New World. Its great age is testified by fossilised grape leaves and seeds in Palaeocene and Eocene deposits. Glacial period destroyed most of *Vitis* habitats and only in a certain area (refuges) they were survived. Such areas in Europe were located around Mediterranean basin and Southern part of Black and Caspian Seas. The current distribution of genus *Vitis* habitat includes three centres of diversity: East Asia, Northern south America, Central America and North America, Europe and Central Asia. Recent chemical analyses of ancient organic compounds absorbed into the pottery fabrics from sites in Georgia in the South Caucasus region, dating to the early Neolithic period (ca. 6,000–5,000 BC), provide the earliest biomolecular archaeological evidence for grape wine and viticulture from the Near East, at ca. 6,000–5,800 BC. The discovery of early sixth millennium BC grape wine in this region is crucial to the later history of wine in Europe and the rest of the world (McGovern, 2017). We present the analyses of plastid genome diversity of wild grapevines (*V. vinifera* ssp. *sylvestris*) from Georgia, Europe, Mediterranean basin and Asian and American species by the Next-generation Sequencing and Comparative Genomics. In particular, in the frame of our research: 1). Next-generation Illumina Sequencing of more than 20 genomes of wild grapevine from different geographic origins were conducted; 2). SNPs and indel regions were detected in each sequenced genome; 3). By using of comparative genomic approaches, the phylogenetic linkage study of the analyzed plastid genomes was conducted. According to our results, it is shown that GTA haplotype dominates in Europe (i.e., France, Germany, Slovenia), ATA and ATT haplotypes were found in the Mediterranean basin and Anatolia (i.e., Morocco, Corsica, Greece and Turkey). Genetically unique AAA haplotype was found in Georgian samples and ATA haplotype was detected in Asian and American species. The obtained results will help to understand the genetic relationships between wild and cultivated grapes from different geographical locations and explain the molecular bases of grape origin and evolution.

OP-14
**Grapevine genomics and the domestication history of
Western European varieties**

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Expansion of human activity led to the creation of thousands of varieties with extensive phenotypic diversity. Unfortunately, the recent favoring of specific varieties/clones, and the globalization-driven exposure to pathogens, has led to extensive genetic erosion in this widely cultivated and economically significant crop. Fighting this genetic erosion whilst addressing issues of resilience to climate change, yield and other traits, requires a crucial understanding of the genetic basis of grapevine variation. This scientific field has witnessed significant advances due to the use of genome-wide approaches, enabled by Next Generation Sequencing. Here, NGS-driven whole genome resequencing strategies have been used to tackle multiple aspects associated with the extant biodiversity present in grapevine germplasm, including a clarification of different features of its recent evolutionary history. Results support a model in which a central domestication event in grapevine was followed by post-domestication hybridization with local wild genotypes, leading to the presence of an introgression signature in modern wine varieties across Western Europe. The strongest signal was associated with a subset of Iberian grapevine varieties showing large introgression tracts. Examination of underlying genes suggests that environmental adaptation played a fundamental role in both the evolution of wild genotypes and the outcome of hybridization with cultivated varieties, supporting a case of adaptive introgression in grapevine.

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OP-15

The hidden biodiversity of *Vitis Vinifera* L. in Armenia

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Armenia is considered an ancient origin of grapevine domestication and the cradle of wine-making, which is confirmed by remains of wild and cultivated grapes and wine-producing facilities found at archaeological sites of the country. The diverse climatic conditions, unique geography and existence of wild grapes were the main drivers in the formation of extensive diversity of cultivated varieties and the promotion of winemaking. After the 1990s and following two decades due to the socio-economic situation in the country, the genetic diversity of the cultivated grapevine in Armenia has drastically reduced, resulting in the vanishing of ancient autochthonous varieties. In the recent past, the national program forwarded on grapevine genetic resources recovery and conservation has been started. Significant efforts have been made and as a result, a huge number of neglected autochthonous varieties has been collected and conserved in the Armenian national grapevine collection. Prospections in traditional viticulture regions across Armenia provided insights into the hidden biodiversity of grape genetic resources existing in the country. To evaluate the autochthonous grapevine germplasm of Armenia, the plant material was collected from marginal areas and old vineyards across the country and genotype identity were determined combining 25 nuclear microsatellite markers (nSSR) and ampelographic descriptors in a combination of detailed analysis of bibliographic studies. The realized in-depth research started in 2017th included more than a thousand different genotypes and for hundreds of them assigned as unique genotypes, SSR profiles were never reported. Among analysed germplasm, more than 100 samples still remain as "unknown" varieties because of missing genetic profiles in SSR databases or lack of variety names. The clustering analysis was performed to evaluate genetic relationships among analysed grape varieties based on allele frequencies of 25 nSSR loci. Two main clusters were distinguished grouping most of the non-identified genotypes with old autochthonous varieties evidenced genetic relationships among analyzed grapevine genotypes and the second set of them clustered separately, assumed as feral types based on morphological characterization. Surprisingly, for this group, only female flower sex was determined based on observed phenotype and APT3 marker analysis. It is important to emphasize the dominance of an unexpectedly high number of female varieties, especially among old autochthonous and feral genotypes. Being cross-pollinated, most likely they have played a crucial role in the background of genetic diversity of Armenian grape germplasm. Nowadays, there is a deep interest in understanding the origin and investigating the genetic diversity and relatedness of grapevine germplasms bounded in isolated geographical regions as they represent untapped genetic resources. Obtained results evidenced the existence of a unique gene pool in Armenia characterized by a large genetic variability and specific molecular pattern. The hidden biodiversity of Armenian grapevine germplasm is considered an under-explored reservoir of beneficial alleles and a valuable source for breeding programs.

OP-16

Enhancing hydrolytic soil enzyme activity with under-vine vegetation in vineyards

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In terms of sustainability, alternative strategies for weed control below vines need to be developed and evaluated. In principle the space below vines is kept free from vegetation to reduce the competing effect for nutrient and water on vines and fruit development. Methods are applied, either individual or in combined, are the application of herbicides, soil tillage or the growth of spontaneous vegetation or cover crops. These methods affect the physico-chemical soil characteristics differentially as well as the soil biota and have therefore consequences on soil functions and ecosystem services. In the presented study we evaluated the effects of five under-vine treatments (herbicide application, rotary soil tillage, soil tillage with under vine weeder, mowed spontaneous vegetation, and spontaneous vegetation without mowing) on vine growth, yield and fruit quality, soil water content and the activity of soil hydrolytic enzymes in a vineyard in Lower Austria over three continuous seasons. Thereby we evaluate our hypothesis that a permanent under-vine vegetation coverage, either mowed or without mowing, supports the soil microbial communities and soil functions in a way to enhance water and nutrients availability which partly could compensate the effects of plant competition on vines. We observed a seasonal effect of the soil water balance in both treatments with a permanent vegetation with lower water availability until 20cm soil depth especially in periods of low precipitation. This may have led to the observed reduced photosynthetic activity of vines in the same treatments, the slightly lower shoot pruning weights and lighter berries. The grape juice parameters as total soluble solids or titratable acidity were similar in comparison with all treatments. While minor effects on vines were observed, the response of the soil microbial activity was significantly enhanced by a permanent vegetation cover below vines and this trend did increase with the years of the project. In conclusion, we observed a strong promotion of the soil microbial activity determined by the analyses of three hydrolytic soil enzymes without major consequences for vine vigor and grape quality. Nevertheless, further studies need to investigate the functional interactions between the species composition of a vegetation coverage, the soil microbial communities and water and nutrient cycles for plant growth and nutrition in order to specify site- or region-specific under-vine management strategies accordingly.

OP-17

Deciphering the molecular mechanisms behind essential oil treatment against downy mildew in grapevine

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Downy mildew, *Plasmopara viticola*, was accidentally introduced from North America and spread rapidly throughout all European winegrowing regions in the late XIXe century, strongly impacting grape quality and yield. To maintain economically sustainable yields and quality, winegrowers rely on high amount of copper and/or synthetic fungicides. On the long run, both of these strategies cause environmental damages, threaten consumer and producer health, as well as, for some synthetic pesticides (QoI), promote the emergence of resistant strains of *P.viticola*. To guarantee an environmentally sustainable and consumer friendly viticulture, natural fungicides need to be developed to reduce the dependency on synthetic pesticides and copper. Most essential oils are composite blends of volatile compounds exhibiting antimicrobial properties against a variety of micro-organisms. Rienth et al. (2019) highlights the effect against *P.viticola* of Oregano Essential Oil vapor phase (OEO) as a potential biological pesticide. The underlying molecular mechanisms of OEO on *P.viticola* and on *V. vinifera* as a potential elicitor remain unclear. We performed leaf disk experiments to investigate and discriminate between the potential direct antifungal and elicitor effects. We highlight that OEO strongly impacts *P. viticola* sporulation when leaf disks were treated after inoculation. OEO induced plant defense-related genes in *V. vinifera* for a short period enhancing its overall defenses against *P.viticola*. To deepen our understanding of OEO mode of action, we aim to decipher the molecular mechanisms behind its action combining RNA-seq and metabolomics approaches. Data from these experiments will help us to harness the potential of OEO and might provide clues to support alternative solutions to manage *P.viticola*.

OP-18

FEMVitisDB: a FAIR data management system for data integration in grapevine

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The grapevine germplasm maintained and preserved at the Foundation Edmund Mach (FEM, Italy) includes more than 2,000 unique genetic profiles (genotypes), represented by 1-20 accessions per genotype which are distinguished by their origin and/or distinctive phenotypic characteristics (e.g. berry skin color). New acquisitions from repositories around the world and wild collections were added to the historical set of about 1,000 cultivars of *Vitis vinifera* L. in the last decade. They consist of released or naturalized *Vitis* hybrids as well as *Vitis* species, useful to scout new genetic resources for diversity studies and breeding purposes (wine/table grapes and rootstocks). Most accessions were genotyped with the reference set of 9 microsatellite markers to verify their trueness-to-type against international and national databases; this process is still ongoing. Moreover, the entire germplasm collection has been phenotyped during three successive years for several traits related to ampelography, vine development (e.g. phenological stages, fertility), biotic stress response, berry and wine composition (e.g. chemical parameters). In parallel, cross-breeding programs have been carried out to obtain new genotypes coupling winemaking quality and resistance to different biotic stresses. We are developing the FEMVitisDB database to host all this information produced by the current and future grape breeding programs. This infrastructure is focused on the "FAIR" paradigm (Findable, Accessible, Interoperable, Reusable) which emphasizes the importance of organizing data and metadata to be accessed and used not only by human operators, but also by means of a computational system. The core of the data infrastructure is a PostgreSQL database compliant with the MIAPPE (Minimum Information About a Plant Phenotyping Experiment) standard. The database schema contains genotypic and phenotypic data in order to ease the link between the two kinds of information. The system is able to store heterogeneous datasets such as position of plants in the field (x-y coordinates), time course of variables and we are also actively working to insert images and related data. The database architecture is *ontology driven* (i.e. the semantics of all the terms can be specified by a suitable ontology) in order to provide a powerful system to integrate data originating from different experiments and platforms. Where feasible, the OIV code has been applied for the standardization of the phenotype description; alternatively, the grape or plant ontologies have been used. Such an approach allows the standardization of the entire data workflow and its use by non-expert users. The database is integrated with Standardized RESTful Web Service API based on BrAPI (brapi.org) which provides access to the data. The data management system is completed by the BrAPIViewer, a web frontend returning all the necessary information in a user-friendly way.

OP-19

Absolute vs relative normalizations to model transcriptomic responses: caveats and limitations

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Data normalization is a necessary step in order to ensure a fair comparison between samples measured across different experimental conditions. Since the advent of gene expression data analysis, several techniques have been proposed in order to account for unwanted sources of variation. The availability of a large collection of gene expression data, such as the one in VESPUCCI, the grapevine gene expression compendia, allows to perform comparisons between normalization techniques. In VESPUCCI two main categories of normalizations are proposed: an “absolute” one, through the (Transcript Per Million) TPM “normalization”, and a relative one, i.e. log ratios calculated using the LIMMA linear model package. Each of the two methods have advantages and drawbacks to take into consideration beforehand. The log ratios normalization offers a less trivial interpretation of the data since it represents a ratio between values measured in two different conditions, but it is better suited for comparing samples across different conditions while TPM, despite being more intuitive on the biological interpretation, should be used with caution when comparing samples with very different total mRNA levels or analyzed in different laboratories. TPM is unable to correctly remove batch-effects making a comparison between samples of different experiments less trustworthy since most of the observed variation might be due to technical differences instead of biological ones. Nevertheless, under conditions for which the transcriptomic responses are particularly different, such as different tissues, it is still possible to obtain valuable information from the TPM normalization such as, which are those genes highly expressed in a specific tissue compared to their average expression level. This information coupled with the relative information about how gene expression changes are driven by the shift in conditions and which other genes shows a similar behavior, might help better understand gene function and condition-specific gene expression.

OP-20

OneGenE inferred association networks can support experimental research in grapevine

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Vitis OneGenE is a tool to identify gene interactions and produce association networks starting from transcriptomic data. It represents a suitable approach to mine huge amounts of data and its architecture allows it to deal with the complexity of the system biology by taking advantage of a distributed computing platform. On the user side, the biologist can easily and rapidly obtain a list of directly associated genes or a visual representation of their gene network, due to the fact that these lists have been pre-computed and two tools have been implemented on the web interface. The ongoing effort of the grapevine community to update gene names and include them into a Grape Gene Reference Catalogue has been already integrated into Vitis OneGenE, to allow a more immediate understanding of the associated genes found by the tool. We recently published three case studies to show how the application of Vitis OneGenE can support the identification of new elements of a biological pathway, the description of three gene families also by integrating other “omics” data, and the prediction of gene function. In the first two cases, specific peroxidases, laccase and dirigent genes were found associated to stilbene synthases thus representing strong candidates for resveratrol oxidative oligomerization; in the latter, the abundance of genes related to pathogen response supported the involvement of VvDMR6-1 in plant defense. These results need experimental validation, that will also highlight strengths and limitations of this approach. An updated version of the VESPUCCI compendium -containing more than 7,000 samples from 271 experiments collected until December 2020- became recently available and allowed us to start a new project of OneGenE expansions.

