



COST Action  
CA 17111  
INTEGRAPE

# 1st Annual Meeting

## INTEGRAPE 2019

**Data Integration as a key step for future  
grapevine**

### Book of Abstracts



Chania, Greece  
25 - 28 March, 2019



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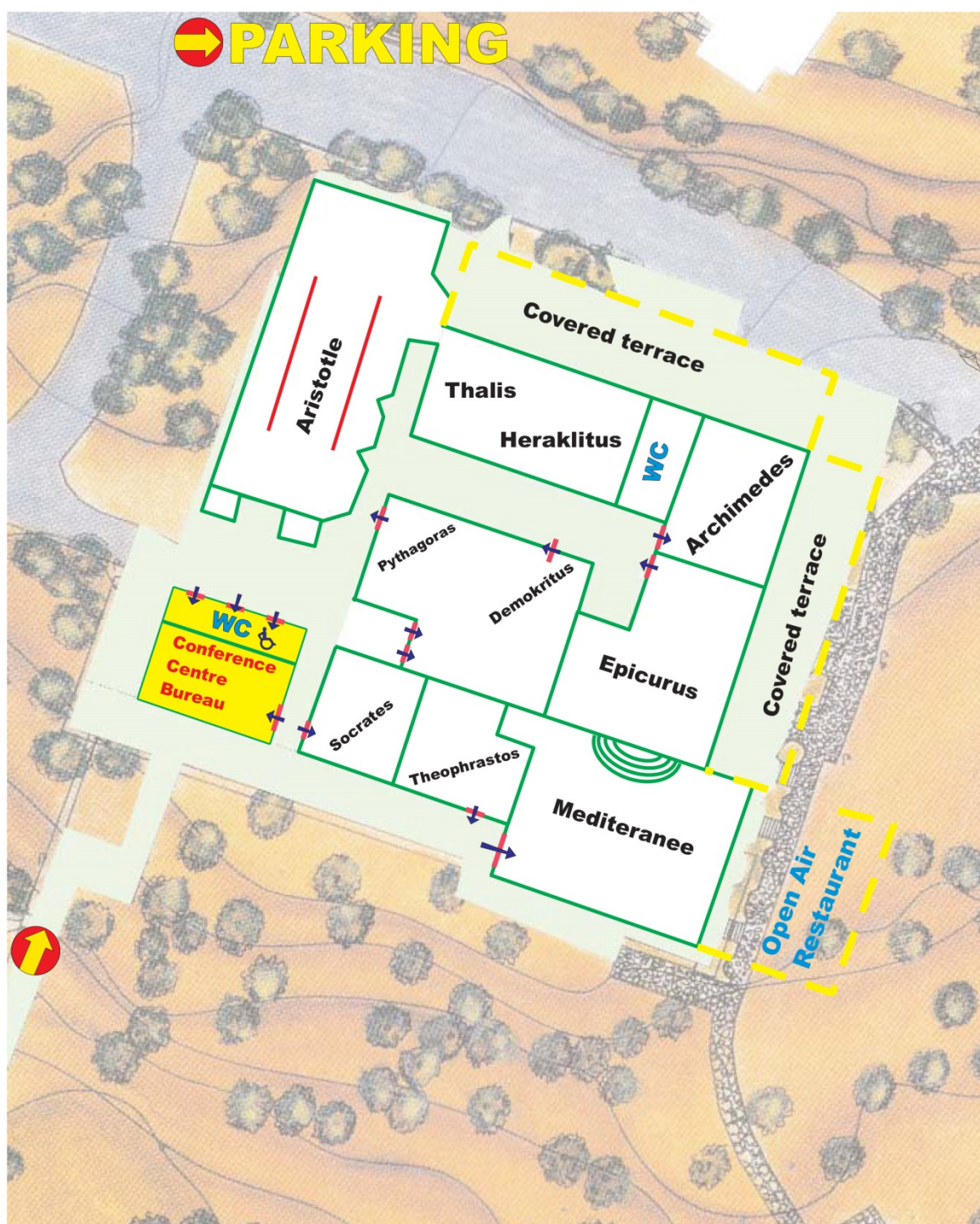
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# Programme Overview

MONDAY 25 March 2019	
19:00	Registration
19:00	Welcome Reception at the Conference Centre
TUESDAY 26 March 2019	
08:30-09:00	Registration
09:00-09:10	Local organisers welcome George Baourakis (Director of MAICh), Panagiotis Kalaitzis (Studies/Research Coordinator, Greece)
09:10-09:25	Welcome speech and introduction Mario Pezzotti (MC Chair, Italy)
09:25	<b>Session 1: Setting up the context</b>
09:25-09:45	Possibilities and needs of the participating countries in terms of infrastructure for bioinformatics Anne-Francoise Adam-Blondon (MC Vice Chair, France)
09:45-10:15	International initiatives to support open data in Life Sciences Paul Kersey (MC Member, WG2 Leader, UK)
10:15-10:45	Towards implementation of FAIR data management in life sciences - ongoing efforts in COST CHARME Kristina Gruden (Invited Speaker COST Action CHARME, National Institute of Biology, Ljubljana, Slovenia)
10:45-11:15	Coffee Break
11:15	<b>Session 2: External Views of Data Integration for grapevine improvement</b>
11:15-12:00	Characterization of genomic diversity in grapevines through whole-genome assembly Dario Cantu (Invited Speaker, College of Biological Sciences-UC Davis, USA)
12:00-14:00	Lunch and poster session
14:00	<b>Session 3: Status and example of databases in the grapevine community</b>
14:00-14:45	Developing Pan-Genome resources for grapevine Doreen Ware - GRAMENE (Invited Speaker, USDA-ARS & Cold Spring Harbor Laboratory, USA)
14:45-15:05	The Vitis International Variety Catalogue and the European Vitis database Ludger Hausmann (Julius Kühn-Institut (JKI), Institute for Grapevine Breeding, Germany)
15:05-15:25	Federations of information systems in the plant community and possible application to grapevine Anne-Françoise Adam-Blondon (MC Vice-Chair, INRA, France)
15:25-15:55	Coffee Break
15:55	<b>Session 4: Data Analysis and Best practices</b>
15:55-16:50	Methods for data generation, quality control, analysis and integration in wine research Johan Trygg (MC Members, WG3 Leader, Umeå University, Sweden)
16:50-17:10	The data standards in grapevine genomics from a user point of view Camille Rustenholtz (MC Member, WG1 co-leader, INRA, France)
17:10-17:30	The Vitis Ontology: sustainable and FAIR (Findable, Accessible, Interoperable, Reusable) for consistent and complete data description through biologist friendly ontologies Eric Duchêne (MC Member, INRA, France)
17:30	<b>Session 5: Example of large data sets managed by the community</b>

17:30-18:00	<b>Integration of large genetic and epigenetic data sets to identify causative factors of gene expression variation</b> Michele Morgante (MC Member, WG1 Scientific Advisor, University of Udine, Italy)
18:00-18:20	<b>Insights on grapevine (<i>Vitis vinifera</i>) biodiversity using NGS-enabled approaches</b> Azevedo Herlander (CIBIO, InBIO - Research Network in Biodiversity and Evolutionary Biology, Universidade do Porto, Portugal)

#### WEDNESDAY 27 March 2019

09:00	<b>Session 5 (continued): Example of large data sets managed by the community</b>
09:00-09:30	<b>Interoperability in metabolomics: the role of standardisation (co-authors: Alessandro Cestaro, Pietro Franceschi, Marco Moretto)</b> Fulvio Mattivi (MC Member, WG2 Scientific Advisor, University of Trento, Italy) (co-authors: Alessandro Cestaro, Pietro Franceschi, Marco Moretto)
09:30-09:50	<b>VESPUCCI: the integrated gene expression database for grapevine</b> Marco Moretto (Unit of Computational Biology, Research and Innovation Center, Fondazione Edmund Mach, S. Michele all'Adige, Italy)
09:50-10:10	<b>Ancient epialleles: a multi-omic view on wine quality</b> Carlos M. Rodriguez Lopez (University of Kentucky, USA)
10:10-10:30	<b>Whole genome sequencing and gene annotation of Georgian grape cultivars</b> Ia Pipia (Agricultural University of Georgia, Georgia)
10:30-11:00	<b>Coffee Break</b>
11:00-11:20	<b>EMPHASIS a European research infrastructure to integrate plant phenotyping and make data reusable</b> Roland Pieruschka (Forschungszentrum Jülich, Germany)
11:20-11:40	<b>Investigating grapevine x environment interactions: data integration is the corner stone!</b> Nabil Girollet (INRA, France)
11:40-12:00	<b>New integrated Hellenic Vitis resources available for further scientific collaboration</b> Aliko Kapazoglou (Department of Vitis, Institute of Olive Tree Subtropical Crops and Viticulture, Hellenic Agricultural Organization-Demeter, Greece)
12:00-12:20	<b>Determining the cistrome landscapes of the grape MYB transcription factor family: on the search of novel secondary metabolism regulators</b> Matus José Tomás (Institute for Integrative Systems Biology, Spain)
12:20	<b>Training Schools</b>
12:20-12:40	<b>Presentation of training schools (procedure and proposals)</b> George Manganaris (Training School Coordinator, Cyprus University of Technology, Cyprus)
12:40-14:00	<b>Lunch Break and poster session</b>
14:00-16:00	<b>Working Group's World café</b>
16:00-17:00	<b>Coffee Break and poster session</b>
17:00-18:00	<b>Wrap up of priorities for the next period</b>
20:00-24:00	<b>SOCIAL GALA DINNER &amp; LIVE MUSIC at Conference Centre</b>

#### THURSDAY 28 March 2019

09:00-10:00	<b>Conference Wrap up and Conclusions</b>
10:00-11:00	<b>Working Group's World café</b>
11:00-11:20	<b>Coffee Break</b>
11:20-13:15	<b>CA17111 - Management Committee</b>

# Orals

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# The Vitis International Variety Catalogue and the European Vitis Database

Hausmann Ludger<sup>1</sup>, Maul Erika<sup>1</sup>, Ganesch Alina<sup>1</sup>, Kecke Steffen<sup>2</sup>, Töpfer Reinhard<sup>1</sup>

<sup>1</sup>Julius Kühn-Institut (JKI) Institute for Grapevine Breeding, Siebeldingen, Germany, <sup>2</sup>Julius Kühn-Institut (JKI) Data Processing Department, Quedlinburg, Germany

Two international databases have been established at the Institute for Grapevine Breeding Geilweilerhof aiming to collect, maintain and update data of grapevine genetic resources: the Vitis International Variety Catalogue (VIVC) and the European Vitis Database (EU Vitis). Since its foundation in 1984, the number of cultivars, breeding lines and Vitis species in the VIVC ([www.vivc.de](http://www.vivc.de)) increased to about 23.000 with each of them linked to a 'variety number' as a unique identifier. Passport data with several interactively searchable data are provided together with photos, SSR marker data and links to the bibliography. To further increase the attractiveness for breeders and researchers, data were added about genetically mapped traits, initially as a PDF document and now also as an interactive search tool ('Table of Loci'; [www.vivc.de/loci](http://www.vivc.de/loci)). In addition, new features are currently programmed to integrate and visualize publically available data regarding specific trait loci of varieties. For clarity, traits will be presented by categories: resistance, morphology, phenology and metabolites. In particular, growers will obtain immediate information e.g. on multiple resistances of varieties. Associated SSR/SNP marker data and the corresponding allele sizes/bases will be included to facilitate marker-assisted selection. Therefore, it would be very helpful in the future if in coming publications relevant information for breeding and marker-assisted selection were presented in a standardized manner or even send via an online form directly to the database. The EU Vitis represents a database for grapevine accessions existing in European grapevine collections ([www.eu-vitis.de](http://www.eu-vitis.de)). Aside from the 'variety number' shared with VIVC, a unique 'accession number' is used in this database. This 'accession number' is a unique code number assigned to a sample/genotype entering a gene bank. It is used to unequivocally tag entering samples. The generated data from that accession e.g. characterization and evaluation data, genetic profiles and photos are linked to that number. In 2007 an online uploading and interactive modification system was implemented. This allows direct access of the EU Vitis partners to upload data from their repositories independently from the database manager. Germplasm investigation activities in grapevine collections are ongoing. Especially the identification process is a continuous activity. It is facilitated by the use of genetic fingerprints in combination with ampelography, which serves to increase trustiness of data. Thus, regular updating of the Multi Crop Passport Descriptor data of inventories in EU Vitis is desirable and grapevine repositories not yet registered in EU Vitis are welcome to do so. In the scope of European projects (e.g. GrapeGen06 and COST Action FA1003) formats for data input were determined. Descriptors and file formats (<http://www.eu-vitis.de/descriptors/dbDescriptors.php?retval=4000&PHPSESSID=5d7bea99af555de196df39de12ceee59>) can be downloaded. The addition of further trait data serves the grape community and upgrades EU Vitis. Standardization of descriptor recording and presentation is indispensable.

# The data standards in grapevine genomics from a user point of view

Rustenholz Camille

Université de Strasbourg - INRA Colmar, Colmar, France

As a scientist working in grapevine genomics, I am handling data of various nature. The DNA or RNA short-sequences, genome assemblies, genome annotations and genotyping data are the ones I am collecting, generating and analyzing the most. It is a perpetual challenge to collect all data information either from colleagues or from public databases, in order to select and to integrate the most relevant data to address a specific scientific question. Data standardization with minimal compulsory information, well-defined vocabulary and easy access seems appropriate to tackle this problem. As a user of data standards, some fields are not detailed enough or even not completed. For example, with sequence data, the protocol for the preparation of the library is not always mentioned or incorrectly. With RNA-seq data, biological sample information like organ or its precise developmental stage can often only be found in the related publication. On the other side, when I need to submit data to public databases, the process is like an obstacle course. I know that even if I have already done it several times, the submission protocol and the forms are regularly changing. In addition, I always miss a piece of information that is required and for which I do not understand the relevance from my grapevine genomics point of view. One solution may be that the whole grapevine community, me included, should be aware of the needs of all data users. Everyone in its field of expertise should understand the kind of information relevant for every step of the data processing starting with the plant material and ending with the final analysis like GWAS, QTL detection or gene identification. At this condition, everyone may better understand the relevance of the required fields. A special care should be taken to reduce the constraints for both data users and submitters and to make data standardization easy, relevant and stable over time. My opinion is that relevant data standardization should become an automatic reflex for all of us. Everyone should feel like an actor in the data analysis process and therefore take its part of responsibility towards the whole grapevine community.

# The Vitis Ontology: sustainable and FAIR (Findable, Accessible, Interoperable, Reusable) for consistent and complete data description through biologist friendly ontologies

Duchêne Éric

INRA, Colmar, France

Studies on perennial plants like grapevine would greatly benefit to use datasets that gather data collected over several years and locations. Datasets of observations and measures on plants can however be efficiently exploited only if their content is understandable at a large scale in the grapevine scientific community. This correct understanding of scientific datasets relies on biologist friendly data standards that allow i) to organize the data, like MIAPPE ([www.miappe.org](http://www.miappe.org)) or VCF (Variant Call Format, [www.internationalgenome.org/wiki/Analysis/vcf4.0/](http://www.internationalgenome.org/wiki/Analysis/vcf4.0/)), ii) to identify the important elements of the datasets, such as the plant material through MCPD (Multicrop Passport Descriptors <https://www.biodiversityinternational.org/e-library/publications/detail/faobiodiversity-multi-crop-passport-descriptors-v21-mcpd-v21/>), and iii) to give an extensive description on the experimental methods, through controlled vocabularies and ontologies. The Vitis Ontology ([https://www.cropontology.org/ontology/CO\\_356](https://www.cropontology.org/ontology/CO_356)) proposes a controlled vocabulary for describing phenotypic data obtained on grapevine plants, berries, musts or wines. This ontology follows the biologist friendly crop ontology framework to describe phenotypic variables through a triplet made of i) a trait, the phenotypic or environmental characteristic under study, like pruning weight or flowering date ,ii) a method that describes how the trait was measured (i.e. with a scale or computed through image analysis), and iii) a scale/unit (i.e. International system units like centimeter or meter, or notation scale like late, early, etc...). We will present how this ontology is organized and its interaction with existing standards like the OIV descriptors. We will also show how it is used in real Vitis datasets or in library for electronic devices used in the vineyard. (like <https://urgi.versailles.inra.fr/ephep/ephep/viewer.do#dataResults/trialSetIds=23>). We propose to extend the use of this ontology to the grapevine community following the example of the Forest trees community (<https://urgi.versailles.inra.fr/ephep/ephep/viewer.do#dataResults/trialSetIds=15> & <https://urgi.versailles.inra.fr/ephep/ephep/viewer.do#dataResults/trialSetIds=24>).

# Insights on grapevine (*Vitis vinifera*) biodiversity using NGS-enabled approaches

Freitas Sara<sup>1</sup>, Gazda Małgorzata Anna<sup>1</sup>, Rebelo Miguel<sup>1</sup>, Munõz-Pajares Antonio Jesús<sup>1</sup>, Azevedo-Silva David<sup>1</sup>, Beja-Pereira Albano<sup>1</sup>, Sottomayor Mariana<sup>1</sup>, Gonçalves Elsa<sup>2</sup>, Martins Antero<sup>2</sup>, Ferrand Nuno<sup>1</sup>, Carneiro Miguel<sup>1</sup>, Azevedo Herlander<sup>1</sup>

<sup>1</sup>CIBIO, InBIO - Research Network in Biodiversity and Evolutionary Biology, Universidade do Porto, Portugal, Vairão, Portugal, <sup>2</sup>LEAF, Instituto Superior de Agronomia, University of Lisbon, Portugal; Portuguese Association for Grapevine Diversity-PORVID, Portugal, Lisboa, Portugal

Grapevine (*Vitis vinifera* L.) is one of the most widely cultivated and economically significant crops in the world, with 7.5 mha of worldwide cultivated area generating 259 mhl of wine production. Since the early domestication period, expansion of human activity led to the creation of thousands of grapevine 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. Breeding for resilience to climate change, yield or other traits, requires a crucial understanding of the genetic basis of phenotypic variation, a field that has seen significant advances due to the use of genome-wide approaches. In this context, grapevine germplasm is a valuable natural resource, with strategic importance for future improvement and biotechnology efforts in this species. Portugal is a hotspot for grapevine varietal diversity. For instance, large grapevine collections of intra-varietal diversity have been established based on efficient experimental designs and adequate models to quantify diversity and to perform selection with high genetic gains. Despite the effectiveness of these methods, new developments are expected with the deployment of Next Generation Sequencing (NGS) technologies to quantify genetic diversity. Presently, we are using NGS strategies to unlock the biodiversity and evolutionary relationships associated with various grapevine varieties. Here, we report on the use of NGS-enabled Pool-Seq and Re-Seq strategies based on Illumina paired-end resequencing, and geared towards the characterization of extant biodiversity associated with grapevine germplasm. Work has been developed within the scope of project NORTE-01-0145-FEDER-000007, supported by Norte Portugal Regional Operational Programme (NORTE2020), under the PORTUGAL 2020 Partnership Agreement, through the European Regional Development Fund (ERDF). Work has also been supported by FEDER through COMPETE, and by FCT, for Rede de Investigação em Biodiversidade e Biologia Evolutiva [UID/BIA/50027/2013 and POCI-01-0145-FEDER-006821].

# VESPUCCI: the integrated gene expression database for grapevine

Moretto Marco<sup>1</sup>, Sonego Paolo<sup>1</sup>, Pilati Stefania<sup>2</sup>, Malacarne Giulia<sup>2</sup>, Costantini Laura<sup>2</sup>, Moser Claudio<sup>2</sup>, Engelen Kristof<sup>1</sup>

<sup>1</sup>Unit of Computational Biology, Research and Innovation Center, Fondazione Edmund Mach, San Michele all'Adige, Italy, <sup>2</sup>Department of Genomics and Biology of Fruit Crop, Research and Innovation Center, Fondazione Edmund Mach, San Michele all'Adige, Italy

VESPUCCI, the Vitis Expression Studies Platform Using COLOMBOS Compendia Instances, is an on-line gene expression compendium that integrates publicly available transcriptomic data for grapevine measured using both microarray and RNA-seq. It was originally developed in 2014 and has since grown from the initial ~1500 samples to the current ~2000 samples. Each sample has been manually annotated using a controlled vocabulary developed ad hoc to ensure both human readability and computational tractability to precisely describe which parameters have changed across different experimental conditions. VESPUCCI was created based on an approach for dealing with the large heterogeneity of data formats present in public databases, and to integrate cross-platform gene expression experiments in one dedicated, coherent database. The expression data in the compendium can be visually explored using several tools provided by the web interface, an exploratory tool meant to assist more dedicated research in grapevine genomics, biology, and physiology. The technology underlying VESPUCCI has recently been completely overhauled in order to simplify the data management. This update has involved both the compendium creation step and the data query step. Concerning the former, the new technology supports different normalization strategies within the same compendium, and thus the legacy normalization data in which samples were treated disregarding the fact that they were measuring the same biological condition will be available together with normalized data in which replicated measurement are taken into consideration. Then, the sample annotation has been revisited to better exploit existing ontologies such as the Plant Ontology, the Plant Trait Ontology, the Plant Experimental Conditions Ontology and the Unit of Measurement Ontology. Finally, the programmatic access to the compendium is going to be easier and more powerful, simplifying the integration of VESPUCCI with other services. All these improvements will be implemented in the new release of the VESPUCCI, which will include all publicly available expression experiment up to 2019, raising the number of collected samples to ~3000.

# Ancient epialleles: a multi-omic view on wine quality

Rodriguez Lopez Carlos Marcelino

University of Kentucky, Lexington, United States

The term terroir is used in the wine industry to relate wine's sensory attributes to its geographic origin. Abiotic and biotic regional differences coupled with differences in vineyard management have a significant impact on the grapevine fruit traits that ultimately affect wine quality. Advances in the area of genomics, epigenomics, transcriptomics, proteomics and metabolomics, have significantly increased our knowledge on the abiotic regulation of yield and quality in many crop species, including *V. vinifera*. The integrated analysis of multiple 'omics' can give us the opportunity to better understand how plants modulate their response to different environments. However, the analysis of multi-omic data from plants grown under natural conditions can be a daunting task. Here we present a web-based tool developed using R Shiny Framework, which allows for multi-omic data to be analyzed and visualized through interactive plots in order to identify the main drivers of DNA methylation and gene expression differentiation in grapevine. To showcase this tool, we present a case study integrating DNA methylation and gene expression data within the context of 25 environmental variables and 38 phenotypic traits retrieved from 22 commercial vineyards grown in the 5 wine subregions of the Barossa Region in Australia. We will finally discuss the potential contribution of epigenetic mechanisms in the regulation of the expression of fruit quality traits.

# Whole Genome Sequencing and Gene Annotation of Georgian Grape Cultivars

Pipia Ia<sup>1</sup>, Tabidze Vazha<sup>1</sup>, Beridze Tengiz<sup>1</sup>

<sup>1</sup>Agricultural University of Georgia, Tbilisi, Georgia

The genomes of four Georgian grape cultivars—Chkhaveri, Saperavi, Meskhetian green, and Rkatsiteli, belonging to different haplogroups, were resequenced. The shotgun genomic libraries of grape cultivars were sequenced on an Illumina HiSeq. The sequence of all 19 chromosomes of four Georgian grape cultivars was determined by resequencing using Pinot noir as a reference genome. Annotation of chromosomal DNA of Georgian grape revealed 17,409 candidate genes in Chkhaveri; 17,021 in Saperavi; 18,355 in Meskhetian green and 13,960 in Rkatsiteli. Among them, 106 predicted genes and 43 pseudogenes of Terpene synthase (TPS) and 44 candidate genes of Stilbene synthase (STS) were found in all studied Georgian cultivars. Several additional TPS and STS genes not present in the reference Pinot noir genome were detected. This work is the first attempt of a comparative whole genome analysis of different haplogroups of *Vitis vinifera* cultivars.

# EMPHASIS a European research infrastructure to integrate plant phenotyping and make data reusable

Pieruschka Roland

Forschungszentrum Jülich, Jülich, Germany

Quantitative assessment of the plant phenotypes provide the vital link between genetic information and biological structure and function needed to improve plant performance, tolerance to biotic or abiotic stress or quality related traits. Within the last decade, genomic data has been becoming easily accessible, the phenotypic information is not keeping pace with the explosion in available genomic information. The lack of reliable and available phenotypic data may limit the use methods to identify the associations between phenotypic and genotypic data. This phenotypic gap is a major challenge in biological understanding of plant processes their translation into practical application. Specifically phenotyping of perennial plants such as grapevine under field conditions represents challenge for quantitative non-invasive assessment of a variety of traits. In this presentation, I would focus on discussing the requirements and challenges to obtain FAIR (Findable, Available, Identifiable, Reusable) data in viticulture where relevant high-throughput field phenotyping platforms may support quantitative assessment relevant traits over vast areas. Specifically, addressing these challenges requires interaction within the community. The EU funded project EPPN2020 provides access to some plant phenotyping facilities in Europe (<https://EPPN2020.plant-phenotyping.eu/>), while the ESFRI listed project EMPHASIS aims at a synergistic development and long-term operation of phenotyping infrastructure in Europe (<https://emphasis.plant-phenotyping.eu/>) by developing infrastructures and providing access for multi-scale phenotyping to analyze genotype performance in diverse environments and quantify the diversity of traits.



# Investigating grapevine x environment interactions : data integration is the corner stone !

Delrot Serge<sup>1</sup>, Girollet Nabil<sup>1</sup>, Garcia Virginie<sup>1</sup>, Bert Pierre-François<sup>1</sup>, Barrieu François<sup>1</sup>, Cookson Sarah<sup>1</sup>, Dai Zhanwu<sup>1</sup>, Destrac Agnes<sup>1</sup>, Gallusci Philippe<sup>1</sup>, Gambetta Gregory<sup>1</sup>, Gomes Eric<sup>1</sup>, Guillaumie Sabine<sup>1</sup>, Hilbert Ghislaine<sup>1</sup>, Lauvergeat Virginie<sup>1</sup>, Lecourieux Fatma<sup>1</sup>, Lecourieux David<sup>1</sup>, Marguerit Elisa<sup>1</sup>, Merlin Isabelle<sup>1</sup>, Pieri Philippe<sup>1</sup>, Prodhomme Duyen<sup>1</sup>, De Resseguier Laure<sup>1</sup>, Stamitti Linda<sup>1</sup>, Teyssier Emeline<sup>1</sup>, Trossat-Magnin Claudine<sup>1</sup>, Van Leeuwen Cornelis<sup>1</sup>, Vivin Philippe<sup>1</sup>, Ollat Nathalie<sup>1</sup>

<sup>1</sup>EGFV, Villenave D'Ornon, France

Nowadays, the wine industry is facing several important challenges as adaptation to climate change and reducing inputs for grape growing and wine making. As a contribution to take-up these challenges, "Ecophysiology and Functional Genomics" research unit in Bordeaux, is developing integrative biology approaches from the vineyard to the gene. The scientific objectives are to analyze and simulate the development of the grafted grapevine, the ripening of the berries and their metabolism in response to environmental constraints and genetic background. For this purpose, the research unit has developed a full range of skills, tools, plant material and experimental designs to collect and store phenotypic and genotypic data. Phenotypic platforms and facilities are available to investigate whole plant responses to water and thermal stress, as well as root development. Simplified models such as fruiting cuttings, in vitro isolated berries and roots grown in rhizotrons are also commonly used. Since 2007, several inter and intraspecific populations were created and two major field experimental plots were planted to characterize a large set of *Vitis vinifera* and rootstock genotypes. Phenology, plant growth, as well as root and berry development, fruit composition (primary and secondary metabolites) are some of the most commonly recorded traits. Information systems were created to store these phenotypic data. In parallel, a full range of metabolomic, proteomic, transcriptomic, and more recently, epigenetic data have been collected on berry or root samples submitted to various growth conditions as drought, heat or mineral stresses. Genomic data as microsatellite markers, SNPs and full genome sequence are produced to characterize the plant material of interest. Dedicated workflows have been developed to analyze those data and to highlight key genes, networks and regulatory pathways. So far, data integration occurs mainly through genetic mapping and modelling. QTLs and putative genes have been identified for many traits. For some of these traits, candidate genes have been proposed and are currently studied. Several ecophysiological and metabolic models have been developed. A major challenge is now to integrate these models at plant level and fill the gap between genotypes and phenotypes. In this context, the development of a full data management system remains the challenge to overcome. It should be the main objective for the next decade, as well as to make data publicly available. It will be the only way to go further in the goal of data mining.

## New integrated Hellenic Vitis resources available for further scientific collaboration

Kapazoglou Alik<sup>1</sup>, Merkouropoulos Georgios<sup>1</sup>, Taskos Dimitrios<sup>1</sup>, Pitsoli Theodora<sup>1</sup>, Doupis Georgios<sup>2</sup>, Doulis Andreas<sup>2</sup>

<sup>1</sup>Hellenic Agricultural Organization DEMETER (ex. NAGREF), Institute of Olive Tree, Subtropical Plants and Viticulture, Department of Grapevine, Athens, Greece, <sup>2</sup>Hellenic Agricultural Organization DEMETER (ex. NAGREF) Institute of Olive Tree, Subtropical Plants and Viticulture, Department of Viticulture, Vegetables and Floriculture, Heraklion, Greece

Grape and wine production are major branches of the Greek agri-food sector. Total grapevine acreage accounts to approximately 110,000 ha (OIV-International Organisation of Vine and Wine-statistics <http://www.oiv.int/>) of which about 50% is dedicated to wine-and grape production. The Greek National Grapevine germplasm collection has been established in the early 70's and is maintained by the Department of Grapevine of the Institute of Olive Trees, Subtropical Crops and Viticulture (IOSV), Hellenic Agricultural Organization "Demeter" (HAO-D) at Lykovryssi, Athens, Greece. The collection, which is comprised of more than 500 autochthonous and about 300 international grapevine varieties, is the largest in Greece. Smaller collections in Thermi (Northern Greece) and Heraklion (Crete) are partial, safety, copies of the central National Collection. Considering the phenomena of genetic erosion and climate change the Greek National collection constitutes an invaluable genetic resource for characterizing and valorizing the rich grapevine germplasm. The two IOSV departments of Grapevine (Athens and Heraklion), recently empowered with new research personnel and funding from participation in more than six national and European research programs, have undertaken a comprehensive effort combining ampelographic, physiological, genotyping, and epigenetic studies for detailed phenotypic and molecular characterization of the majority of the Greek grapevine germplasm. Considering the potential impact of climate change scenarios on regional viticulture, studies are underway to unravel the tolerance/resistance of Greek varieties to abiotic and biotic stresses through a combination of physiological and molecular tools including epigenomics, transcriptomics, proteomics and metabolomics. Large datasets are the expected outcome of these research programs and an appropriate data maintenance, presentation, and interoperability model is being developed for maximum effectiveness. Together the aforementioned approaches, by exploiting the full potential of the Greek grapevine germplasm, through appropriate data integration, are expected to efficiently address issues related to varietal identification, genetic erosion, climate change and host biotic stress responsiveness thus contributing to viticulture sustainability.

# Determining the cistrome landscapes of the grape MYB transcription factor family: on the search of novel secondary metabolism regulators

Matus José Tomás<sup>1</sup>, Huang Shao-shan Carol<sup>2</sup>, Cantu Dario<sup>3</sup>

<sup>1</sup>Institute for Integrative Systems Biology (I2SysBio), València, Spain, <sup>2</sup>Center for Genomics and Systems Biology. Department of Biology. New York University., New York, United States,

<sup>3</sup>Department of Viticulture and Enology, University of California. , Davis, United States

Plants manufacture specialized metabolites that aid in the interaction and survival with their environment. These compounds, referred as 'secondary metabolites', influence quality traits in foods such as color, flavor, texture, aroma, and deliver many human health benefits once consumed. The processes controlling secondary metabolism in fleshy fruits are largely unknown and represent an enormous potential for the agro-industry sector. The project that we propose contributes in this knowledge by deciphering the gene regulatory networks of the R2R3-MYB transcription factor (TF) family and determining the roles of this family in the control of secondary metabolism. We propose that the regulatory processes that govern the accumulation of secondary metabolites can be straightforwardly studied by integrating genome-wide analyses that account for transcription factor genome occupancy and co-expression networks. By these means, our first objective uses ampDAP-Seq, a high-throughput TF binding site discovery method that interrogates genomic DNA with in vitro-expressed TFs. Despite ChIP-seq is the ultimate approach for TF binding site discovery, it is limited in scale as it is complicate to execute, depends on antibody quality and is rare for low abundant TFs. DAP-seq provides a scalable alternative for non-conventional model species where genetic transformation is difficult, to rapidly and inexpensively interrogate large number of TFs. We will also conduct intervarietal analyses by isolating a large set of MYB coding sequences from two red-skinned cultivars holding sequenced genomes: 'Pinot Noir' and 'Cabernet Sauvignon'. Both cultivar genomic DNAs will be challenged with their respective varietal TFs. We estimate an initial count of 40-50 transcription factors/per cultivar to analyse from a total of 134 family members. The integration of TF binding data, co-expression and transcriptome data in response to MYB overexpression should allow us to establish high confidence gene regulatory networks. All these activities are critical for elucidating complex transcriptional networks that underlie important processes in grapevine. To keep it cohesive with the INTEGRAPE consortium, we intend to develop a public web-based platform for inspecting MYB cistrome landscapes in association with genome sequences.

# Posters

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# EXPLOITATION OF THE GENETIC DIVERSITY OF GRAPEVINE (*Vitis vinifera* L) IN THE ADAPTATION TO SALT STRESS

Arroyo-Garcia Rosa<sup>1</sup>, Carrasco David<sup>1</sup>, Carazo Encina<sup>1</sup>, Ocete Rafael<sup>2</sup>, Revilla Angeles<sup>3</sup>

<sup>1</sup>CBGP, Madrid, Spain, <sup>2</sup>Dpto Entomología Aplicada, Sevilla, Spain, <sup>3</sup>Dpto Biología de Organismos y Sistemas, Oviedo, Spain

The climate change will involve a major water shortage and high salinity in soil that might affect the growth of the plant. A strategy to cope with these problems is the search of genotypes adapted to the conditions of the climate, taking advantage of the genetic diversity present in the cultivated ( *Vitis vinifera* L ssp *sativa*) and wild grapevine (*Vitis vinifera* L ssp *sylvestris*). The scientific interest of the highly endangered ancestor of cultivated grapevine, *Vitis sylvestris*, has so far been mostly confined to questions of conservation genetics, and a deeper understanding of the domestication history of the cultivated crop. However, since domestication traits such as higher yield, larger berries, and higher sugar content are usually accompanied by a loss of resilience factors these it is promising to search for such factors in the crop wild ancestor. In this research, salinity tolerance of *V. vinifera* subsp. *sylvestris* accessions derived from natural condition growing in the cliffs close to the sea, they were evaluated for various salinity levels. In addition we have included a rootstock (R110) as a control. We have identified natural genotypes tolerant to abiotic stress (salinity). Actually, we are performing the transcriptomic and physiological analyses in order to identified putative genes related to this abiotic stress.

# Grapevine cultivars performance and fruit metabolism in arid environments

Gashu Kelem<sup>1</sup>, Harcavi Eran<sup>2</sup>, Drori Elyashiv<sup>3</sup>, Agam Nurit<sup>1</sup>, Bustan Amnon<sup>4</sup>, Fait Aaron<sup>1</sup>

<sup>1</sup>Ben-Gurion University of the Negev, Jacob Blaustein Institutes for Desert Research, French Associates Institute for Agriculture & Biotechnology of Drylands, Midreshet Ben-gurion, Israel, <sup>2</sup>Ministry of Agriculture and Rural Development, Agricultural Extension Service - Shaham, Bet-Dagan, Israel, <sup>3</sup>Agriculture Research Department, Eastern Region Research and Development Center, Midreshet Ben-Gurion, Israel, <sup>4</sup>Desert Agriculture Research Center, Ramat Negev R&D center, Ramat Negev, Israel

Desert conditions are considered beyond the climate frame of traditional wine-producing belts due to water scarcity, high temperatures, and excess light/UV intensity, all negatively affecting phenology, fruit metabolism, and wine quality. However the semiarid to arid regions are inevitably becoming wine grapevine growing area in Israel, the Negev desert offers diverse topo climate conditions, with altitudes ranging from 250 to 900 m asl. The present study was aimed at identifying cultivars with crop quality potentials under desert environments. Experiments take place in two vineyards located in the middle of Negev Desert, Israel: Ramat Negev R&D Center, and Ramon, at 300 and 850m asl, respectively. Both vineyards share a similar experimental setup, comprising 30 (10 white, and 20 red) cultivars planted in a randomized blocks design. In the first two harvest years (2015 and 2016), Chenin Blanc and French Colombard among the white cultivars, and Petit Verdot and Malbec among the red ones, exhibited promising wine qualities, with some advantages to the relatively cooler region, Ramon. A consistent two-week difference in timing of phenological event between the two vineyards was preserved from bud break to véraison in both 2017 and 2018 growing seasons. We found that the phenological events from budburst to véraison significantly advanced at warmer Ramat Negev. Nevertheless, the berry ripening period was significantly longer in the warmer region, Ramat Negev compared to Ramon, with more pronounced effect during warmer growing season 2017, during which a considerable number of fruit clusters shriveled before reaching the BRIX harvest threshold. A significant decreasing in skin phenylpropanoids and pulp organic acids was observed at Ramat Negev, as the berry development continued from véraison to harvest. Also, the oxidative stress level was significantly higher at Ramat Negev cultivars than at Ramon. Metabolic data of berry skin and pulp are being processed to assess environmental and varietal interaction on primary and secondary metabolism.

# SAUVIGNON BLANC GRAPE AND WINE METABOLOMICS DATA SHOW IMPORTANCE OF SEASON OVER REGION

Greven Marc

Bordeaux Sciences Agro, Cadaujac, France

SAUVIGNON BLANC GRAPE AND WINE METABOLOMICS DATA SHOW IMPORTANCE OF SEASON OVER REGION Authors: Marc GREVEN<sup>1,4\*</sup>, Sergey TUMANOV<sup>2, 5</sup>, Claire GROSE<sup>1</sup>, Victoria RAW<sup>1</sup>, Abby ALBRIGHT<sup>1</sup>, Lily STUART<sup>1</sup>, Silas VILLAS-BOAS<sup>2</sup>, Damian MARTIN<sup>1</sup>, Roger HARKER<sup>3</sup>, Farhana PINU<sup>1</sup> <sup>1</sup>Viticulture and Oenology group, The New Zealand Institute for Plant and Food Research Ltd, New Zealand <sup>2</sup>School of Biological Sciences, University of Auckland, New Zealand <sup>3</sup>Food Innovation, The New Zealand Institute for Plant and Food Research Ltd, New Zealand <sup>4</sup>Currently at Bordeaux Sciences Agro, 1, Cours du Général de Gaulle, CS 40201 - 33175 Gradignan Cedex, France <sup>5</sup>Currently at the Institute of Cancer Sciences, University of Glasgow, Garscube Estate, Glasgow G61 1BD, Scotland. \*Corresponding author: marc.greven@agro-bordeaux.fr Abstract: Context and purpose of the study - Sauvignon blanc (SB), New Zealand's flagship grape and wine variety, is produced in wine growing regions throughout the country. However, only SB wines from the Marlborough region are well recognised because of their varietal combination of tropical and herbaceous aromas. Although volatile profiles of New Zealand, particularly Marlborough SB wines, are well characterised, not much is known yet about how much do these wines differ in quality among locations within the Marlborough region as well as from other regions in New Zealand. Moreover, only very small amount of data is available to show the seasonal differences in SB juice and wine composition. To fill this knowledge gap, we developed a unique database of New Zealand SB grape juices and wines to develop tools to help winemakers to better understand potential differences between vineyard blocks and assist in making blending decisions. Materials and Methods: - Over a period of three harvest seasons (2011–2013), about 400 SB juices were collected from Marlborough and several other grape growing regions in New Zealand. All these juices were then fermented under strictly controlled vinification conditions (700 mL; 15°C) using a commercial yeast strain *Saccharomyces cerevisiae* EC1118. Vineyard row orientation and vine density, vine age, clone and rootstock as well as phenological information and associated meteorological data was combined with detailed oenological parameters for each juice and wine. Comprehensive metabolite profiling of these juices and wines by gas chromatography-mass spectrometry was undertaken. Results: - These combined data sets, particularly metabolomics of juices and wines, clearly demonstrate that seasonal variation is more prominent than regional or vineyard management differences in both SB juices and wines. This was despite 95% of the samples used in this research were obtained from irrigated vineyard blocks. Additionally, using chemometric approaches, we identified different groups of juice and wine metabolites that play important roles behind the seasonal variations. Therefore, these metabolites may represent chemical signatures for SB juice and wine quality assessment. In addition, this database has the potential in creating a predictive tool for wine quality and innovation, especially when combined with mathematical modelling. Key words: Seasonal difference, aroma compounds, mass spectrometry, vineyard management.

# rhAmpSeq Core Genome Markers Improve the Coverage of a GBS-Based Genetic Map and Marker Transferability to Other Grapevine Populations

Karn Avinash<sup>1</sup>, Zou Cheng<sup>1</sup>, Sun Qi<sup>2</sup>, Alahakoon Dilmini<sup>3</sup>, Fennell Anne<sup>3</sup>, Londo Jason<sup>4</sup>, Reisch Bruce<sup>1</sup>, Cadle-Davidson Lance<sup>4</sup>

<sup>1</sup>Cornell University, Geneva, United States, <sup>2</sup>Cornell University, Ithaca, United States, <sup>3</sup>South Dakota State University, Brookings, United States, <sup>4</sup>Grape Genetics Research Unit, USDA ARS, Geneva, United States

Elucidating the genetic basis of traits in diverse and highly heterozygous crops like grapevine (*Vitis* spp.) benefits from genetic maps with good coverage and density. Previously, F2 genetic maps for *V. riparia* x 'Seyval' were constructed with 1,449 non-redundant SNPs identified through genotyping-by-sequencing (GBS). Relative to a previous SSR map, GBS markers covered 11.4% more of the genome and increased marker density 9-fold, but the GBS map had poor coverage in telomeric and repetitive chromosomal regions. In this study, we developed 2000 markers targeting the core genome based on rhAmpSeq technology, which uses RNA-containing primers for highly multiplexed amplification and nextgeneration sequencing. We integrated the GBS and rhAmpSeq markers to re-build the F2 genetic map using a custom pipeline and Lep-MAP3. The resulting integrated map has 2,663 markers (GBS=1449, and rhAmpSeq=1214) spanning 1524 cM in genetic length across 19 chromosomes, increasing genome coverage by 4% and marker density by 84%. Gaps greater than 3 Mb were reduced from 16 to 1. Accuracy of the integrated map was validated by correlation between genetic and physical position of markers (average R<sup>2</sup> of 80.9% across all chromosomes), and by QTL mapping of berry color, malic acid and cessation of summer lateral emergence. Thus, rhAmpSeq markers filled gaps in the GBS map and improved marker density particularly near repetitive regions, and significantly narrowing QTL confidence interval regions.



# How cover crops and mulching effect on soil biological and physical parameters in an erosion exposed vineyard

Kovacs Barnabas

University of Pannonia, Veszprém, Hungary

How cover crops and mulching effect on soil biological and physical parameters in an erosion exposed vineyard Barnabás Kovács<sup>1</sup>, László Kocsis<sup>1</sup>, Péter Varga<sup>2</sup>, János Májer<sup>2</sup> <sup>1</sup>Department of Horticulture, University of Pannonia, Keszthely, Hungary <sup>2</sup>NAIK-Research Institute for Viticulture and Oenology, Badacsony, Hungary E-mail address: kovacs.barnabas@georgikon.hu

Sustainable cultivation methods on sloping vineyard cultivation are becoming increasingly important within today's adaptation to climate change impacts on these lands much exposed to erosion. On the Balaton uplands more than a decade ago, the Viticulture and Oenology Research Station (SZBKI-NAIK) in Badacsony recognized this significant hiatus across Europe and established a long-term study of soil covering processes in a vineyard that was deliberately exposed to erosion. Their aim was to compare the effectivity and ecological aspects of these processes and find answers for viticulturists looking for more economical and ecological future ways of farming in this wine region. We present the results of our measurements taken in 2017 in soil enzyme activity, soil moisture and economic (yield) parameters of the studied soil and vineyard. As compared to the average sunshine duration, in 2017 there had been 20% more but the temperature level and the amount of precipitation were close to the average values of many years, therefore conclusions can be reached not just for this year but generally for the climate of this wine region. According to our results, mulching with organic plant wastes achieved the most positive effect on the parameters studied also effectively reducing exposure to erosion in the plantation. The publication is supported by the EFOP-3.6.3-VEKOP-16-2017-00008 project. The project is co-financed by the European Union and the European Social Fund. Keywords – sloping vineyard, erosion, cover crop, mulching, soil biology

# CHARACTERIZATION OF DELETIONS CAUSING BERRY COLOR VARIATION IN GARNACHA AND TEMPRANILLO.

MAURI PANADERO NURIA

ICVV, Logroño, Spain

CHARACTERIZATION OF DELETIONS CAUSING BERRY COLOR VARIATION IN GARNACHA AND TEMPRANILLO. Nuria Mauri<sup>1</sup>, Maite Rodríguez-Lorenzo<sup>1, 2</sup>, Pablo Carbonell-Bejerano<sup>1</sup>, Carolina Royo<sup>1</sup>, Félix Cibrián<sup>2</sup>, Julián Suberviola<sup>2</sup>, Ana Sagüés<sup>2</sup>, Javier Ibáñez<sup>1</sup>, José M. Martínez-Zapater<sup>1</sup> <sup>1</sup> Instituto de Ciencias de la Vid y del Vino (ICVV), CSIC-Universidad de La Rioja-Gobierno de La Rioja, 26007 Logroño, Spain <sup>2</sup> Sección de Viticultura y Enología, Dpto. Desarrollo Rural, Medio Ambiente y Administración Local. Gobierno de Navarra, 31390 Olite, Spain. Gray and white somatic variants occasionally appear in some black-berried grapevine cultivars. Genetic and molecular studies have associated color loss to the emergence of deletions at the grape color locus located on chromosome 2 in heterozygous colored cultivars carrying a functional and a null allele. Previous studies of this lab in Tempranillo cultivar have pointed that the color locus deletion is associated with other intra- and inter-chromosomal genomic rearrangements. In order to extend this study to more cultivars, we characterize this time the structural variation occurring in two different clones of white-berried Garnacha cultivars. In this study, we evaluate the variation effect at gene expression level and try to figure out the boundaries of possible variation through sequencing analysis loss of heterozygosity analysis. These markers were used to characterize white and gray isolates originated from Garnacha Tinta and Tempranillo Tinto and collected along the Ebro valley (NE Spain). Two main deletion classes were detected in Garnacha Blanca correlating with the geographical origin of the accessions, while Tempranillo gray berry variants showed higher variation. Comparative genomics of Garnacha variants after whole-genome re-sequencing was addressed to understand the mutational mechanisms generating color variation. The results show that these deletions are generally associated with more complex genome rearrangements. Additional structural variation between independent lines of Garnacha Blanca likely emerged in different ancestral clonal lines of Garnacha Tinta. These results can be exploited for the selection of color variants best suited for the development of new cultivars and can help to detect rearrangement hotspots in the grapevine genome.

# IRIS-EDA: An integrated RNA-Seq interpretation system for gene expression data analysis

McDermaid Adam<sup>1</sup>, Monier Brandon<sup>1</sup>, Wang Cankun<sup>1</sup>, Miller Allison<sup>2</sup>, Fennell Anne<sup>1</sup>, Ma Qin<sup>3</sup>

<sup>1</sup>South Dakota State University, Brookings, United States, <sup>2</sup>Saint Louis University, St. Louis, United States, <sup>3</sup>The Ohio State University, Columbus, United States

Next-Generation Sequencing has made available substantial amounts of large-scale Omics data, providing unprecedented opportunities to understand complex biological systems. Specifically, the value of RNA-Sequencing (RNA-Seq) data has been confirmed in inferring how gene regulatory systems will respond under various conditions (bulk data) or cell types (single-cell data). RNA-Seq can generate genome-scale gene expression profiles that can be further analyzed using correlation analysis, co-expression analysis, clustering, differential gene expression (DGE), among many other studies. While these analyses can provide invaluable information related to gene expression, integration and interpretation of the results can prove challenging. Here we present a tool called IRIS-EDA, which is a Shiny web server for expression data analysis. It provides a straightforward and user-friendly platform for performing numerous computational analyses on user-provided RNA-Seq or Single-cell RNA-Seq (scRNA-Seq) data. Specifically, three commonly used R packages (edgeR, DESeq2, and limma) are implemented in the DGE analysis with seven unique experimental design functionalities, including a user-specified design matrix option. Seven discovery-driven methods and tools (correlation analysis, heatmap, clustering, biclustering, Principal Component Analysis (PCA), Multidimensional Scaling (MDS), and t-distributed Stochastic Neighbor Embedding (t-SNE)) are provided for gene expression exploration which is useful for designing experimental hypotheses and determining key factors for comprehensive DGE analysis. Furthermore, this platform integrates seven visualization tools in a highly interactive manner, for improved interpretation of the analyses. It is noteworthy that, for the first time, IRIS-EDA provides a framework to expedite submission of data and results to NCBI's Gene Expression Omnibus following the FAIR (Findable, Accessible, Interoperable and Reusable) Data Principles. IRIS-EDA is freely available at <http://bmbi.sdstate.edu/IRIS/>.

# Grapevine collection of "El Encín". An integrated database

Muñoz Organero Gregorio<sup>1</sup>, De Andrés María Teresa<sup>2</sup>, Cabello Félix<sup>2</sup>

<sup>1</sup>Instituto Madrileño de Investigación y Desarrollo Rural, Agrario y Alimentario (IMIDRA), Alcalá de Henares, Spain, <sup>2</sup>Instituto Madrileño de Investigación y Desarrollo Rural, Agrario y Alimentario (IMIDRA), Alcalá de Henares, Spain

Grapevine Collections scientifically known as Germplasm Banks were first created in the late 19th century. The main reason was the spread of phylloxera in Europe in the mid-19th century from North America. The attack of that insect produced an important loss of autochthonous plant material as a result of the disappearance of millions of hectares. Therefore, conservation and identification of autochthonous grapevine varieties was started in Europe to avoid the severe genetic erosion that was occurring. The activities in the Grapevine Collection of "El Encín" are the prospection, establishment, conservation, identification and evaluation of genus "Vitis". The plant material collection was started in 1893 by Manso de Zúñiga, collecting 13 grapevine varieties from La Rioja and creating the collection of Haro. Nine of these 13 are now preserved in El Encín. Nicolás García de los Salmenes took over the material collection in 1904. He collected 1.699 varieties of which only 447 accessions including Spanish varieties and rootstocks are preserved in El Encín. Martínez-Zaporta was the first great promoter of vine varieties prospecting from Madrid: 636 varieties including Spanish and foreign wine grapes, table grapes and rootstocks remain from this time. The greatest incorporation of plant material occurred under the direction of Hidalgo and currently 966 grapevine varieties, mainly Spanish table and wine accessions are preserved. Since 2003 the viticulture team coordinated by Cabello has incorporated mainly Spanish minor varieties prospected in old vineyards from private or public institutions and wild grapes (collecting 648 individuals from 64 Spanish populations). Plant material is under use in national and international research projects. Currently the collection consists of 3.532 accessions. Database of the collection includes 153 fields including passport data, ampelographical and molecular information, photographic documentation, as well as data recorded during the evaluation of the material. They are grouped into 852 rootstocks, 69 interspecific hybrids (H.P.D.), 111 *Vitis* spp., 1.852 *Vitis vinifera* varieties, of which 1.178 are for wine use and 674 for table use and 648 de *Vitis vinifera sylvestris*. Some of this information is of public access in the website [www.madrid.org/coleccionvidencin/](http://www.madrid.org/coleccionvidencin/) and in the European Vitis Database ([www.eu-vitis.de](http://www.eu-vitis.de)). More information will be available online from now onwards as it is generated and in some cases published. Only the information supplied by private companies or used to meet public service activities is kept as confidential.

# Different strategies and approaches for studying of Armenian grapevine genetic resources

Nebish Anna<sup>1</sup>, Melyan Gagik<sup>2</sup>, Aroutiounian Rouben<sup>3</sup>

<sup>1</sup>1) Yerevan State University, Department of Genetics and Cytology, 2) Institute of Molecular Biology of NAS RA, Research group of Plant genetics and Immunology, Yerevan, Armenia,

<sup>2</sup>Armenian Academy of Viticulture, Wine-making and Fruit-growing NGO, Yerevan, Armenia,

<sup>3</sup>Yerevan State University, Department of Genetics and Cytology, Yerevan, Armenia

Armenia is famous as homeland of viticulture and winemaking, and germplasm sources are rich by *Vitis vinifera* L. cultivated ancient, *Vitis* newly bred inter- and intraspecific hybrids and *V. vinifera* subsp. *silvestris* wild genotypes. For Armenian viticulture nowadays the major challenge is complex characterization, conservation of genetic diversity and maintenance of a sustainable production of high quality grapes in a changing environment. In order to answer the new challenges faced by viticulture the main goal of grapevine breeding is to create new cultivars using high quality, resistant to diseases and unfavorable environmental conditions and healthy stock material. In our research multidisciplinary study of Armenian grapevine cultivars has been started for the creation of the first Armenian Grapevine database on the base of ampelographic, cytoembryological and genetic data by standardized protocols and according to OIV descriptors. For more than 70 cultivars genetic and phenotypic profiles were created for their characterization and identification. Grapevine reproductive biology strongly affects the fruit set, the berry quantity and quality. High sterility of male and female gametophytes leads to yield decreases. Cytoembryological study of reproductive biology revealed differences in sterility and morphometric traits of pollen and ovules between ancient and new bred cultivars, as well as between table and wine cultivars. 'Garan dmak' and 'Areni' cultivars characterized by highest pollen sterility up to 39%. Carpological analysis revealed significant differences in berries weight and sizes between table and wine cultivars. The largest berries were developed in table varieties with average berry weight up to 6,2 g for 'Shahumyani' and 'Itsaptuk', average sizes 20-30 mm and sugar content of the juice of ripe grapes up to 22g/L. In wine cultivars the values of morphometric traits were lower with average weight of berries in Muscats from 1.1 to 2.9 g and average sizes from 12.3 to 23.4 mm, but higher sugar content up to 28 g/L. Genetic characterization of Armenian grapevines using nine SSR molecular markers detected genetic diversity and genetic relations between accessions. Seven cases of identical genotypes and three cases of homonymy among studies genotypes were identified. In the frame of COST Action INTEGRAPe new strategies and approaches including genomics, epigenomics, transcriptomics, proteomics and metabolomics for the detailed characterization of Armenian grapevine cultivars and wild species will be carry out. Our data will give important information about useful sources of desirable traits and will be useful for improvement grape quality and saving costs in breeding programs.

# Dissemination tools to increase visibility of the Cost Action

## INTEGRAPE results

Nikolic Dragan

University of Belgrade, Faculty of Agriculture, Belgrade-Zemun, Serbia

Dissemination includes measures to achieve the visibility of the project and can be called simply by project marketing. In projects funded by EU funds, it is important for several reasons: contributing visibility and replication of project results, and thus improving the success of the project; raises interest in the use of EU funds by the general and interested public; increases the visibility of the project consortium/individual carrier of the project, as well as their activities, products and services; secures the visibility of the European Union as a source of funding. The Cost Action INTEGRAPE will create a strong link between the grapevine community and large international species-agnostic initiatives currently building open standards for plants. WG4 will disseminate the recommendations that will make by WGs 1-3 and will train the grapevine community to follow these recommendations, providing feedback from trainees to each WG. Dissemination will include the following audience (scientific community, industry, policymakers, national authorities, consumers, layperson). From communication channels to target audiences will be used (online / print / TV / radio and events). Disseminate the project outputs will be at local, regional, national and international level. The dissemination activities firstly will be focused on building a strong INTEGRAPE project visual identity (i.e., logo, flyer) to harmonize communication both internally to the consortium and externally to the general public and the scientific community. Besides the advertising (logo, flyer), electronic access (INTEGRAPE web site, facebook, twitter), dissemination will include other dissemination actions related to research in the Cost Action such as: TV spots, blogs, videos, banners, posters, brochures, books, conferences, workshops, seminars, exhibitions, articles in peer review journals, conference papers, workshop papers, magazines targeting industry, e-newsletters, interviews, info days, lectures, press releases, etc. The INTEGRAPE web site, webinars and hands-on sessions will be the main deliverables of dissemination. The ultimate goal of the dissemination of this project is how the results achieved will be expanded and thus will enhance the project's effect on the wider grapevine community.

# Genomics of flower identity in grapevine (*Vitis vinifera* L.)

Palumbo Fabio<sup>1</sup>, Vannozzi Alessandro<sup>1</sup>, Magon Gabriele<sup>1</sup>, Lucchin Margherita<sup>1</sup>, Barcaccia Gianni<sup>1</sup>

<sup>1</sup>University of Padua, Legnaro, Italy

The identity of the four characteristic whorls of typical eudicots, namely, sepals, petals, stamens and carpels, is specified by the overlapping action of homeotic genes, whose single and combined contributions have been described in detail in the so-called ABCDE model. Continuous species-specific refinements and translations resulted in this model providing the basis for understanding the genetic and molecular mechanisms of flower development in model organisms, such as *Arabidopsis thaliana* and other main plant species. Although grapevine (*Vitis vinifera* L.) represents an extremely important cultivated fruit crop globally, studies related to the genetic determinism of flower development are still rare, probably because of the limited interest in sexual reproduction in a plant that is predominantly propagated asexually. Nonetheless, several studies have identified and functionally characterized some ABCDE orthologues in grapevine. The present study is intended to provide a comprehensive screenshot of the transcriptional behavior of 18 representative grapevine ABCDE genes encoding MADS-box transcription factors in a developmental kinetic process, from preanthesis to the postfertilization stage and in different flower organs, namely, the calix, calyptra, anthers, filaments, ovary, and embryos. The transcript levels found were compared with the proposed model for *Arabidopsis* to evaluate their biological consistency. With a few exceptions, the results confirmed the expression pattern expected based on the *Arabidopsis* data.

# NES2RA: A TOOL FOR GRAPEVINE TRANSCRIPTOMIC DATA MINING

PILATI STEFANIA<sup>1</sup>, MALACARNE GIULIA<sup>1</sup>, VALENTINI SAMUEL<sup>2</sup>, MORETTO MARCO<sup>3</sup>, ASNICAR FRANCESCO<sup>2</sup>, MASERA LUCA<sup>2</sup>, SONEGO PAOLO<sup>3</sup>, CAVECCHIA VALTER<sup>4</sup>, BLANZIERI ENRICO<sup>2</sup>, MOSER CLAUDIO<sup>1</sup>

<sup>1</sup>FONDAZIONE EDMUND MACH, Department of Genomics and Biology of Fruit Crops, Research and Innovation Centre, SAN MICHELE ALL'ADIGE, Italy, <sup>2</sup>UNIVERSITY OF TRENTO, Department of Information Engineering and Computer Science, TRENTO, Italy, <sup>3</sup>FONDAZIONE EDMUND MACH, Unit of Computational Biology, Research and Innovation Centre, SAN MICHELE ALL'ADIGE, Italy, <sup>4</sup>CNR, Institute of Materials for Electronics and Magnetism, TRENTO, Italy

The development of “omics” technologies to study gene expression has revolutionized our perspective from the single gene to the gene network level. However, the complexity of the system biology approach requires appropriate mathematical, computational and statistical tools to analyze data and extract information. Grapevine transcriptomic data are currently collected in two databases: the ViTis Co-expression DataBase (VTCdb, Wong et al., 2013) dedicated to data obtained with microarray technology and the Vitis Expression Studies Platform Using COLOMBOS Compendia Instances (VESPUCCI, Moretto et al., 2016) including data from both microarrays and RNAseq experiments. Here, we present the application of the algorithm of Network Expansion by Subsetting and Ranking Aggregation (NES2RA, Asnicar et al., 2016) to expand Local Gene Networks (LGN) in grapevine using transcriptomic data stored in the VESPUCCI compendium. NES2RA is based on the PC-algorithm (Spirtes and Glymour, 1991), a gaussian graphical model (GGM) that finds causal relationships from observational data. It is based on a systematic test for conditional independence to retain significant relations between pairs of genes. It starts from a fully connected network and removes interactions between genes, whenever it finds a set of genes that supports that interaction (i.e., separation set). Due to the computational power requirement of NES2RA algorithm, it has been running as part of the gene@home project, a distributed computation project which relies on thousands of volunteers' computers by means of the TN-Grid, an infrastructure based on BOINC system (Asnicar et al., 2015). NES2RA has been used to expand four LGNs related to the grapevine response to climate changes (Malacarne et al., 2018). The obtained expansion gene lists have been analyzed by means of statistical tools - such as gene annotation and functional categories enrichment to assess the functional coherence between LGNs and expansion gene lists and promoter analysis to test co-regulation among output genes - and compared with experimental results, when available, and literature. These analyses produced promising results in support of the meaningfulness of this approach. Moreover, the LGNs expansions can be visualized as networks, thus providing the biologist with a prompt information about the significant relationships retained by NES2RA, highlighting positive or negative correlations within gene pairs. We are currently developing NES2RA algorithm to make it available as a web tool to be used in real time and exploring new applications.



# Phenotypic variation of autochthonous Greek Vitis varieties

Pitsoli Theodora<sup>1</sup>, Kapazoglou Aliko<sup>1</sup>

<sup>1</sup>Department of Vitis, Institute of Olive Tree Subtropical Crops and Viticulture (IOSV), Hellenic Agricultural Organization-Demeter (HAO-Demeter), , Athens, Greece

Phenotypic variation of autochthonous Greek Vitis varieties Pitsoli Theodora 1, Kapazoglou Aliko 1  
1Department of Vitis, Institute of Olive Tree, Subtropical Crops and Viticulture (IOSV), Hellenic Agricultural Organization-Demeter (HAO-Demeter) Sofokli Venizelou 1, Lykovrisi, Athens, Greece, GR-14123 The Ampelographic National Collection of the Department of Vitis, Institute of Olive Tree Subtropical Crops and Viticulture (IOSV), Hellenic Agricultural Organization-Demeter (HAO-Demeter), composed of more than 700 local varieties, constitutes an invaluable genetic resource for characterizing and valorizing the Greek grapevine germplasm. As part of a larger effort toward phenotypic characterization of the national grapevine germplasm, the present study investigated a series of 26 autochthonous wine grapevine varieties, originally collected in the 1980s, from different geographic regions in Greece. The Ampelographic characterization was based on 117 ampelographic descriptors including young shoot, herbaceous shoot, leaf, inflorescence, bunch, berry, woody shoot as specified by the OIV Descriptor List (OIV 2009). Statistical analysis of ampelographic measurements was performed utilizing the Manhattan dissimilarity index and UPGMA method to determine the degree of phenotypic variability and generate the corresponding dendrograms displaying the degree of relatedness among varieties. In addition, Principal Component Analysis (PCA) was used to evaluate the ampelographic characteristics with the highest contribution to the clustering of varieties into different groups. The analysis revealed that the biotypes examined constitute different grapevine varieties. However, despite their large dispersion in different viticultural regions of Greece, their different names (Alpitsa, Zacharokokkinouda, Aspromandilaria, Potamissi, Vranizades, Svourdouli etc.), and their individual differences in ampelographic characters, they are closely related varieties derived from a single parent, either from the original genealogical center of *Vitis vinifera caucasica* or from a secondary center related to the wider cultivation region. In addition, the most significant ampelographic characteristic indicating phenotypic variability is associated with hair formation of young and mature leaf. This study comprises a significant contribution to the characterization of the Greek grapevine germplasm and the datasets produced will be integrated in the National and European Vitis Databases. Moreover, it shows that ampelographic description, when based on a large number of ampelographic characters, is an effective and reliable method for proper identification and discrimination of cultivated grapevine varieties.

# Intergrative analysis of micrometeorology and metabolomics to explore the regulation of grape metabolism by environmental cues

Reshef Noam<sup>1</sup>, Agam Nurit<sup>1</sup>, Fait Aaron<sup>1</sup>

<sup>1</sup>Ben-Gurion University of the Negev, Jacob Blaustein Institutes for Desert Research, French Associates Institute for Agriculture & Biotechnology of Drylands, Midreshet Ben-Gurion, Israel

Micrometeorological conditions such as solar irradiance and temperature are important factors affecting fruit composition. In recent years, their effect on the composition of wine grapes received much attention, owing to the paramount influence of abiotic defense-related compounds on fruit and wine quality. Nevertheless, to this day we are unable to anticipate compositional consequences of a given set of conditions, and are uncertain to whether they represent acclimatization, or are imposed by the environment. In addition, the fundamental question of how grapes respond to the extensive spatiotemporal variations accompanying the diurnal path of the sun, remains largely unexplored. To address these questions, we harnessed the strong and stable solar irradiance in the Negev desert to create an extensive gradient of irradiance levels in the cluster-zone, using commercially available shading-nets. We integrated high-resolution micrometeorological measurements with seasonal, spatial, and diurnal analyses of grape metabolic profile. We found that grapes successfully acclimate to strong solar irradiance by repartitioning within primary metabolites and the major flavonoid groups. However, this leads to inferior sensorial characteristics commonly associated with warm/arid climate. We show that the spatiotemporal solar regime in a vineyard is a major factor driving spatial variability and diurnal fluctuations in fruit composition. Taken together, precise solar irradiance management is a central element of improving fruit quality and homogeneity and mitigating the detrimental consequences of warm and arid conditions.

# MICROPROPAGATION OF GRAPEVINE (VITIS VINIFERA L.)

## VARIETY 'HAGHTANAK'

Sahakyan Aghvan<sup>1</sup>, Sahakyan Narek<sup>1</sup>, Dangyan Kima<sup>1</sup>, Barsegyan Andranik<sup>1</sup>, Melyan Gayane<sup>1</sup>

<sup>1</sup>ANAU, Scientific center of Agrobiotechnology, Etchmiadzin, Armenia

Grapevine (*Vitis vinifera* L.) is one of the most widely grown crops in Armenia. The use of in vitro culture for vegetative multiplication, termed micropropagation, offers an important alternative to conventional methods of plant propagation. A protocol for the micropropagation of the wine grape variety 'Haghtanak' was developed. Shoot tips (0.3-0.5 cm) were used as explants. The explants were disinfected with calcium hypochlorite, either alone or in combination with ethanol. Maximum survival response (63.7 %) was observed when explants were exposed to 1.5% Calcium hypochlorite followed by 70 % ethanol for 20 second. The effect of various concentrations and combinations of plant growth regulators N6 benzylaminopurine (BAP) and kinetin (kin) on plant regeneration was used. Growth medium was supplemented with 2% sucrose and 0.5% agar. The maximum number of proliferated shoots (2.6) was obtained on MS medium containing 1.5 mg/l BAP. For rooting stage, microshoots were transferred in MS; MS/2, MS/3 media supplemented with different concentrations and combinations of Indol-3-butyric acid (IBA) (0.0; 0.3; 0.5; 1.0; 1.5; 2.0 mg/l) and Naphthaleneacetic acid (NAA) (0.0; 0.3; 0.5; 1.0; 1.5; 2.0 mg/l). A high frequency of rooting (81.0 %) with early root initiation and maximum growth response was obtained when in vitro shoots were transferred onto half strength MS/2 medium supplemented with IBA (1.0 mg/l) + NAA(0.3 mg/l). The plantlets were successfully acclimatized (survival rate-82.0%) when transferred to pots containing peat moss and sand (1:1 v/v).

# Progress in integration of data and knowledge in the frame of international projects –based on example of Grapevine

## Genofond of the Republic of Moldova

Savin Gheorghe<sup>1</sup>, Baca Ivan<sup>1</sup>, Cornea Vladimir<sup>1</sup>

<sup>1</sup>Research and Practical Institute for Horticulture and Food Technologies, Chisinau, Moldova,  
Republic of

Towards the end of the 80s in the Republic of Moldova had been created an Ampelographic Collection which after the number of accumulated genotypes and their diversity held the 3rd place in the world (after USA and France). Based on this diversity of genetic resources, a wide program of grapevine breeding has been developed in order to create modern varieties with enhanced (advanced) resistance to abiotic and biotic unfavourable factors of the environment. As a result a number of new varieties have been created that complemented the grapevine assortment both in Republic of Moldova, as well as in other countries. Since 1985, the OIV Descriptor List has been accepted for description and this format has been used to create a Database (since 1991). The last decade of the 20th century have been created the conditions for wider international cooperation, including through participation in multilateral research projects (regional, European). This cooperation has evolved progressively under the aspects of the development and adoption of the methods of inventory, recording, description and research of the ex situ, in situ and on farm grapevine genetic resources, also accepted and introduced as formats of information in existing traditional database (projects GENRES 081, IPGRI-BIOVERSITY International, GrapeGen06, SEEDNet, COST FA1003). As a result database was completed with the characteristic of our genotypes, especially of the old autochthonous varieties. We also contributed to the projects with SSR analysis (INTAS, SEEDNet, COST FA1003) which, in our opinion, significantly have changed the visions of phylogenetic relationships of the grapevine in the last decade. At the same time, the impact of these collaborations on the development and updating of our Database and Information System has evolved: starting from the Database elaborated in dBase-III (late in FoxBase+ and FoxPro) and in format in accordance with the OIV Descriptor List (1983), Information System is currently developed on Visual Foxpro 9.0 and allows management of accesses present in Genofond (according MCPD), obtaining and keeping information in formats according to internationally accepted methodologies (in the frame of mentioned projects) and OIV Descriptor List (2009), the possibility of delivering information in accordance with the European Vitis Database formats. The web-availability of data, possibilities of on-line exchange and interoperability of information at international level are some of the objectives formulated for future researches and development.

# Haplotype Markers Developed from the Vitis Core Genome and Their Applications for QTL Mapping and MAS Breeding in Hybrid Grape Populations

Sun Qi<sup>1</sup>, Zou Cheng<sup>1</sup>, Karn Avinash<sup>2</sup>, Reisch Bruce<sup>2</sup>, Nguyen Allen<sup>3</sup>, Sun Yongming<sup>3</sup>, Bao Yun<sup>3</sup>, Campbell Michael S.<sup>4</sup>, Church Deanna<sup>4</sup>, Williams Stephen<sup>4</sup>, Smith Timothy P. L.<sup>5</sup>, Fennell Anne<sup>6</sup>, Clark Matthew<sup>7</sup>, Ware Doreen<sup>8</sup>, Londo Jason<sup>9</sup>, Cadle-Davidson Lance<sup>9</sup>

<sup>1</sup>Cornell University, Ithaca, United States, <sup>2</sup>Cornell University, Geneva, United States, <sup>3</sup>Integrated DNA Technologies, Redwood City, United States, <sup>4</sup>10x Genomics, Inc., Pleasanton, United States, <sup>5</sup>USDA-ARS, Clay Center, United States, <sup>6</sup>South Dakota State University, Brookings, United States, <sup>7</sup>University of Minnesota, Saint Paul, United States, <sup>8</sup>USDA-ARS & CSHL, Cold Spring Harbor, United States, <sup>9</sup>USDA-ARS, Geneva, United States

This study is part of VitisGen2, a multi-disciplinary, collaborative project that incorporates the latest genomics technology and socioeconomic research into the grape breeding and evaluation process. One of the goals of the project is to develop a low-cost and high density genotyping technology. The Vitis genus has a very diverse genomic structure among the different species, which is demonstrated by very poor marker transferability when doing marker assisted selection in hybrid grape breeding. The structural variation also compromises genetic studies in non-vinifera populations when using the V. vinifera genome as the reference. In this study, a pan-genome graph was developed from nine de novo assemblies, representing diversity from six wild species and three vinifera cultivars. Conserved syntenic regions were identified from the pan-genome graph. PCR primers were developed from regions of the genome which are structurally stable but contains 2-7% SNPs. This is to ensure unique haplotype identification from the sequence of PCR amplicons. In collaboration with Integrated DNA Technologies (IDT), a novel RNase H2-dependent PCR technology (rhAmpSeq) was used to amplify targeted regions, followed by Illumina sequencing. This set of markers target 2000 loci, with an average distance of 200 kb between markers. Validation in one F2 and three F1 families shows that 92% of markers were amplified in all four families, and 83% of the markers are informative for linkage map construction. The pan-Vitis marker system allows us to build a consensus map across very diverse hybrid populations, systematically study haplotype variations, segregation distortions and other genetic features across families. By incorporating the latest developments in genome assembly, high throughput genotyping and phenotyping technologies, the VitisGen2 project is developing a systematic approach for QTL and marker discovery, sample tracking and breeding decision making. Grape is one of the five focus crops of the USDA Breeding Insight Project (BIP). The VitisGen2 teams will work together with BIP developers on the breeding IT platform development, and progress will be presented.

# BIOCHEMICAL AND TRANSCRIPTIONAL ANALYSES OF A SUSCEPTIBLE AND A TOLERANT GRAPEVINE ROOTSTOCK UNDER HIGH SALINITY CONDITIONS

Vannozzi Alessandro

DAFNAE - University of Padova, Legnaro, Italy

Nowadays, modern viticulture is entirely based on the use of scions grafted onto interspecific rootstocks. This widespread practice is based on the fact that rootstocks are not only able to confer resistance to a vast range of pathogens, but they also impart many advantages by altering numerous physiological processes at the scion level, including biomass accumulation, fruit quality, and the ability to respond to many abiotic stresses. All of these characteristics make the use of rootstocks and breeding strategies aimed at the production of new rootstock genotypes, of crucial importance for the future of viticulture. Due to the uninterrupted climate changing in wine-growing regions, the selection of drought and salinity tolerant rootstocks has now developed into one of the main factors to develop a sustainable viticulture. In this study a new selected genotype, recently registered in the Nation Register of Grapevine Varieties and designed as M4 ((*V. vinifera* x *V. berlandieri*) x *V. berlandieri* cv. Resseguier n. 1), has been compared to the commercial and widely used rootstock 101.14. In particular, a physiological, transcriptomic, ionomic and metabolomic survey was conducted on M4 and 101.14 genotypes showing contrasting drought and salinity tolerance. The experimental plan was based on a gradual exposure to salinity in potted plants under controlled environmental conditions. Physiological analyses indicated a better ability of M4 to respond to the salinity stress in term of photosynthetic activity, showing higher levels of transpiration and assimilation respect to 101.14. Transcriptional analyses were performed at different time points (4, 10 and 20 days from stress imposition) and led to the identification of differentially expressed genes (DEGs) specifically induced by the tolerant genotype respect to the susceptible one, whereas biochemical analyses were conducted exclusively at T3 by mean of LC-GS. The multivariate statistical analysis on RNA-Seq data indicated that the "genotype" component represents the main factor driving the differential gene expression in roots, whereas the kinetic of stress appear to be the dominant component in leaves. Under stress conditions, M4 leaves showed an enrichment in many GO categories, mainly tied to regulation of circadian rhythm and the neutralization of reactive oxygen species (ROS). In roots, induced gene categories in M4 belong to stress responses, transcription factors and response to abscisic acid stimulus. Meanwhile roots in M4 go against salinity, initially identifying stress and increasing the ABA content, leaves activate a series of genes responsible for transporter activity and the neutralization of free radicals. Regarding biochemical analyses, most of the metabolites more accumulated in M4 roots under stress were amino acids or their derivate (phenylalanine, glutamine, alanine, isoleucine, serine, pyroglutamic acid, aspartic acid) whereas leaves of the tolerant genotype seem to activate a wide range of pathways in response to stress. Many of the metabolites are sugars, but other potentially important metabolites are coumaric acid (in common with the roots), and I-Quercitol, known to play a well-defined role in NaCl stress.

# Bioinformatics of wet lab procedures for wine varietal composition assessment

Vignani Rita<sup>1</sup>, Lio Pietro<sup>2</sup>, Scali Monica<sup>3</sup>

<sup>1</sup>University of Siena - Dept. Life Science, 53100, Italy, <sup>2</sup>Computer Laboratory, Cambridge, United Kingdom, <sup>3</sup>University of Siena - Dept. Life Science, SIENA, Italy

The varietal authentication of wines is fundamental for assessing wine quality, and it is part of its compositional profiling. The availability of historical, cultural and chemical composition information is extremely important for quality evaluation. DNA-based techniques are a powerful tool for proving the varietal composition of a wine. SSR-amplification of genomic residual *Vitis vinifera* DNA, namely Wine DNA Fingerprinting (WDF) is able to produce strong, analytical evidence concerning the monovarietal nature of a wine, and for blended wines by generating the probability of the presence/absence of a certain variety, all in association with a dedicated bioinformatics elaboration of genotypes associated with possible varietal candidates. Together with WDF we could exploit Bioinformatics techniques, due to the number of grape genomes grown. From monovarietal, experimental ones, to commercial monovarietals, to blended commercial wines, the results demonstrate that WDF, after calculation of different distance matrices and Neighbor-Joining input data, followed by Principal Component Analysis (PCA) can effectively describe the varietal nature of wines. In the unknown blended wines the WDF profiles were compared to possible varietal candidates (Merlot, Pinot Noir, Cabernet Sauvignon and Zinfandel), and the output graphs show the most probable varieties used in the blend as closeness to the tested wine. This work favors in perspective the multidisciplinary building-up of on-line databanks and bioinformatics toolkits on wine.

# Study the interrelation between the flavonoid and stilbene pathways in *Vitis vinifera* cv. Gamay Red cell suspension

Wang Ru<sup>1</sup>, Oliva Moran<sup>2</sup>, Sikron-Persi Noga<sup>3</sup>, Gashu Kelem<sup>3</sup>, Fait Aaron<sup>3</sup>, Oren-Shamir Michal<sup>4</sup>

<sup>1</sup>The Hebrew University of Jerusalem & Agricultural Research Organization - the Volcani Center, Rishon LeZion, Israel, <sup>2</sup>Weizmann institute, Rehovot, Israel, <sup>3</sup>The Jacob Blaustein Institutes for Desert Research, Ben Gurion University of the Negev, Sede Boker, Israel, <sup>4</sup>Agricultural Research Organization - the Volcani Center, Rishon LeZion, Israel

Grape (*Vitis vinifera* L.) is an important source of health-promoting bioactive compounds including phenolic compounds such as stilbenes and flavonoids. Extensive studies have been conducted to modify flavonoid and stilbene biosynthesis by metabolic engineering strategies; however, such engineering requires knowledge of the pathways involved, their regulation, interrelation and competition. Thus, to enhance the nutritional quality of engineered fruits, we aimed to elucidate the molecular and metabolic interrelations between the flavonoid and stilbene pathways in *Vitis vinifera* cv. Gamay Red cell suspension. We developed double-transformed cell cultures expected to modify these two pathways. The two pathways, branching from their common substrates (p-coumaroyl-CoA and malonyl-CoA) were manipulated by enhancing either AroG\* + FLS or AroG\* + STS in *Vitis vinifera* cv. Gamay Red cell suspension. AroG\* is a gene encoding a feedback-insensitive bacterial form of 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase enzyme of the shikimate pathway that enables to increase the production of AAAs and in particular of phenylalanine. FLS (flavonoid synthase) and STS (stilbene synthase), separately, are expected tools to drive the metabolism to flavonol and stilbene pathways. We hypothesize that by genetically targeting this metabolic interception in a grape cell suspension originating from red grapes, we will have an effective tool to challenge the phenylpropanoid metabolism and tackle the interrelation between flavonoids and stilbenes pathways. Our preliminary metabolic analysis of transgenic cell suspension lines, AroG\* + FLS and AroG\* + STS suggest that the interrelation between the two pathways may be complex, since AroG\* + FLS, directing the carbon flux towards flavonoid production, also caused a significant accumulation of stilbenes, vice versa. Our unique materials will be characterized by metabolic profiling and RNA-seq analysis, meanwhile metabolic fluxes will be quantified via stable isotope enrichment analysis, from this integrative analysis we expect to acquire comprehensive knowledge of the pathways involved, their regulation, interrelation and competition. This knowledge will help us to improve fruit nutritional quality.



# Multidisciplinary characterization of Armenian grape germplasm

Margaryan Kristine<sup>1</sup>

<sup>1</sup> Institute of Molecular Biology, NAS RA, Research Group of Plant Genetics and Immunology

The conservation and sustainable use of grapevine genetic resources depend on efficient management of germplasm collections and the precise description of the maintained accessions. Application of rules and adapted procedures are needed to ensure their survival and to make the material available to breeders, researchers and farmers. A general strategy for Armenian grapevine germplasm conservation encompasses the collection of the still existing diversity and the use of protection techniques to minimize the losses over time. Being studied mainly by ampelography, the genetic diversity of Armenian grapevine needs to be re-investigated in accordance with modern requirements and international scales. The multidisciplinary study of Armenian grape cultivars and its wild ancestor, the subspecies *Vitis sylvestris*, by standard ampelographic and molecular methods, permit to estimate their breeding potential which is of great practical importance. In the proposed research, one of the main concerns is the comprehensive characterization of Armenian grapevine genetic diversity, based on its ampelographic, eno-carpological, genetic characteristics and the assessment of trueness to type. With this purpose, Armenian-German cooperation highly supports the management of Armenian grapevine genetic resources. The realization of the project help to identify endangered, rare and unique genotypes and to promote their duplicates preservation in the grapevine collection at the Institute for Grapevine Breeding Geilweilerhof. The duplicate preservation is done in accordance with the objectives in the initiative of "A European Genebank Integrated System" (AEGIS), implemented by the European Cooperative Programme for Plant Genetic Resources (ECPGR). The project permits to optimise and ensure duplication of local varieties in further Armenian grapevine collections as well. The available genetic diversity and its multidisciplinary study still allow us to identify valuable grape genetic resources, with possible resistance to pathogens and abiotic stresses and high wine and table grape quality. In many countries breeding activities are increasingly directed to produce cultivars resistant to the most spread fungal pathogens such as powdery and downy mildew (*Erysiphe necator* Schwein. Burr, *Plasmopara viticola* Berk. et Curtis). Downy and powdery mildew cause severe problems in Armenian viticulture. For a small number of Armenian grapevines molecular and infection tests were earlier performed and there is no complete information about the existence of cultivars with resistance to downy and powdery mildew. Application of DNA-based molecular markers related with resistance genes of downy and powdery mildew and phenotypic evaluation of Armenian grape cultivars for downy and powdery mildew resistance according to the international standards carried out and promising genotypes were determined. On the base of realized research, a true to type inventory of accessions preserved in Armenian grapevine collection are created. The inventory will be uploaded in the European Vitis Database ([eu-vitis.de](http://eu-vitis.de)) and documented in the Vitis International Variety Catalogue ([www.vivc.de](http://www.vivc.de)) All accession specific data produced within the projected work will be uploaded in the first Armenian Vitis Database ([www.vitis.am](http://www.vitis.am)). Multidisciplinary characterization of Armenian grapevine genetic resources will provide new knowledge about germplasm diversity and possibly further sources for breeding.

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Conference Centre Bureau of Mediterranean Agronomic Institute of Chania-MAICH  
PO Box 85, 73 100 Chania, Crete, Greece  
T: +30 28210 35080 F: +30 28210 35001 E: [confer@maich.gr](mailto:confer@maich.gr)





