

Short Term Scientific Missions (STSM) Reports

Establishment of network construction pipelines to identify gene regulatory networks.

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The massive amounts of data generated by omics technologies in grapevine is being stored in public databases considerably exceeding the analytical capacities of humans, making imperative the use of computational resources to extract relevant information. Despite different grape specific platforms have been developed, there is no established method adopted to construct gene co-expression networks derived from publicly available data in this species. Based on this premise, the main goal of the STSM was to learn how to represent large transcriptomic data in networks for elucidating different biological processes in grapevine, by using two platforms developed or adapted in FEM, namely the Vitis Expression Studies Platform Using COLOMBOS Compendia Instances (VESPUCCI) and NES2RA. The VESPUCCI is an integrated gene expression database for grapevine that originally included 1,500 transcriptomic samples at the time of its first release and now has doubled in size including most of publicly available transcriptomic data (<http://vespucci.colombos-dev.fmach.it/>). On the other hand, the NES2RA algorithm is a mining tool for transcriptomic data used to expand a known local gene network (LGN) by finding new related genes, and it has been applied to the grapevine transcriptomic dataset using VESPUCCI as data source. An additional purpose of the STSM was also to discuss a strategic plan to integrate these freely available platforms in the community and disseminate their use among grapevine researchers. The use of VESPUCCI and NES2RA allowed to generate lists of co-expressed samples and genes of interest to my research but most importantly, I learned the importance of using these platforms and discussed with their developers the best way to incorporate them in the grapevine research community. As a short-term result from this discussion I believe that the INTEGRAPPE Action should create within a Grape Information System a centralized hub where all these resources are posted. One of VESPUCCI's biggest effort and most notable feature is the manual curation and quality check of samples. Each sample has been annotated by curators using controlled vocabularies to ensure both human readability and computational tractability. One of the biggest problems of the community in terms of metadata handling is the poor and inconsistent annotation of experiments. To completely fulfill the properties of the FAIR (Findable Accessible Interoperable Reusable) principles, we need to exploit standards and bio-ontologies for data annotation. We need to considerate about the importance of correctly annotating experiments. The importance of early annotation of experiments as soon as (or even before) data are available is underrated. It is often considered as an annoying request to fulfill before the publication, while it should be treated as an integral part of the experimental design. This is something that we need to address urgently and I believe that it should be a main pillar to address within the INTEGRAPPE COST Action.



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STSM conducted in
Fondazione Edmund Mach di
San Michele all'Adige (FEM).
Italy.

Host: Dr. Giulia Malacarne



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Targeted metabolomics to study the effect of mineral supplements in grape berry phenolics.

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The purpose of this STSM was performing targeted metabolomic analysis on grape berry samples collected from grapevines cv. “Vinhão” located in the DOC Region of “Vinhos Verdes” (Portugal), and evaluate the effect of the application of mineral supplements throughout the fruiting season on berry phenolics. UPLC-MS analyses using selected ion monitoring (SIM) mode were conducted to identify specific molecular targets affected by the treatments, and to understand the effects in key secondary compounds that greatly account for grape berry quality. The ultimate goal was to understand the potential of mineral supplements to improve fruit properties and provide a starting point to implement innovative management strategies in viticulture. In addition, the mission allowed exchange of valuable scientific know-how between the two research groups and originated a solid partnership for continuing the collaborative work in this research line. Data obtained will be further processed and stored following a proposed FAIR Data Management Plan, in accordance to the goals of the Cost Action CA17111.

STSM conducted in
Laboratoire de biologie
cellulaire et biochimie
végétale Biomolécules et
Biotechnologies Végétales
(BBV), Tours, France

Host: Prof. Arnaud Lanoue



Source: Wikipedia

Short Term Scientific Missions (STSM) Reports



Analysis of cuticular waxes and cutin compounds in grape berry along ripening process under water and heat stresses.

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The aim of the STSM was the identification of the different epicuticular and intracuticular waxes compounds at different phenological stages of grape berries in order to detect any difference in their accumulation due to cluster position and/or irrigation treatment. In addition we aimed at the quantification of oleanolic acid in berry waxes. To achieve these goals, different methods of extraction and analysis by the mean of GC-MS at the mass spectroscopy unit facility (CAI Espectrometría de Masas, UCM) at the University of Madrid were performed. Results from GC-MS analysis showed no differences in the chromatogram profile of waxes along berry ripening and under the different treatments. The berry epicuticular waxes of Aragonez (syn. Tempranillo) variety are composed by alcohols, fatty acids esters, alkanes, triterpenoids and steroids, as well as other non identified compounds. In the present investigation, alcohols were the most abundant compounds found in berry waxes. However their abundance changed along berry developmental stages: 90% at pea size, 80% at veraison and between 70 to 85% at full maturation. Based on previous gene expression data, in which we observed a significant regulation by irrigation treatments on the expression of transcripts encoding for enzymes responsible for oleanolic acid biosynthesis, we decided to quantify oleanolic acid in cuticular waxes. Oleanolic acid was quantified using MRM analysis. Results showed that oleanolic acid content slightly changed along berry ripening, but both irrigation treatment and cluster position had a significant impact on its content. Additionally, the different extraction procedures performed during the STSM, showed that the oleanolic acid compound was much present at intracuticular waxes than at epicuticular ones.

STSM conducted in
Universidad Politécnica de
Madrid, Madrid, Spain

Host: Dr. Victoria Fernández



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Short Term Scientific Missions (STSM) Reports

Documentation and molecular characterization of grapevine genetic resources in Armenia.

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In the scope of Cost Action CA 17111 STSM project the large-scale molecular characterization and documentation of 170 grapevine accessions collected during autumn 2018 in the main vine-growing regions in Armenia was realized. The genetic diversity of grape accessions was analyzed by 25 simple sequence repeat markers encompassing the nine SSR markers recommended by the European project GrapeGen06.

The determination of the 170 accessions identity requires a combination of molecular data and morphological features. Molecular analysis of Armenian grape varieties revealed the following three main cases: synonyms: different cultivar names, but identical fingerprints, homonyms: identical or very similar cultivar names, but different fingerprints, questionables: for some cases the variety, being true-to-type on the basis of ampelographic descriptors, turned out to be critical after comparison of their SSR profiles; or obvious differences between morphological descriptions in bibliography and the accessions features in the collection were detected.

The SSR profiles comparison based on *Vitis* International Variety Catalogue (VIVC) (<http://www.vivc.de/>) database assisted to determine accessions identities and provided in some cases unexpected information. Unique profiles, additional synonyms and homonyms also were identified.

On the basis of the realized molecular analysis it turned out that 110 distinct genotypes are maintained in the collection and 60 accessions revealed to be synonyms, homonyms and duplicates. Regarding the identification of 110 distinct genotypes, for 78 distinct genotypes a matching profile existed in the VIVC database. The genetic profiles of the 32 accessions represent 32 distinct varieties, mainly losted and rare varieties. In the scope of already realized projects (COST Action FA1003, DAAD, BMBF) accessions from the previous collection were genotyped and thus further genetic profiles from Armenian varieties were available. During Soviet Union times Armenian grape breeders were actively creating new table and wine grape varieties. In the scope of the prospection some of them were discovered as well. Although no matching profile was found and descriptive references were lacking, their identity was considered as true to type if the parentage given by the breeders was corresponding. Genetic identification is followed by ampelographic confirmation to ascertain the true identity of the variety and to ensure that no errors occurred during sampling. Owing to the fact that no living references are available, morphological features of the varieties need to be compared with descriptions and photographs available in bibliography. Three toms of Armenian (published in 1947; 1962; 1981), three toms of Russian (published in 1946–1956; 1963–1970; 1984) ampelographies and the Caucasus and Northern Black Sea Region Ampelography (2012) are the most valuable sources for this purpose.

The results obtained in the scope of the proposed project are proving the effectiveness of genotyping as a reliable and convenient tool for supporting ampelography in the correct identification of varieties maintained in the germplasm collection. By application of these approach similarities among accessions from Armenian collection and the varieties cultivated in other, mainly in post-Soviet Union countries were found and incorrect records of the accessions were discovered. Using molecular fingerprinting in our research we were able to document inconsistencies and inaccuracies in ampelographic descriptions, which is prerequisite for complete and precious description of all varieties preserved in germplasm collection. The inventory will be uploaded in the European *Vitis* Database (www.eu-vitis.de) and documented in the *Vitis* International Variety Catalogue (www.vivc.de) and Armenian *Vitis* database (www.vitis.am).



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STSM conducted in
Julius Kühn-Institut (JKI)
Federal Research Centre for
Cultivated Plants, Institute
for Grapevine breeding,
Geilweilerhof, Germany

Host: Prof. Reinhard Töpfer



Source: Wikipedia

Short Term Scientific Missions (STSM) Reports



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The profiles of anthocyanins, polyphenols, peroxidase and polyphenoloxidase from two autochthonous grape varieties in Bosnia and Herzegovina wine region.

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The aim of this research was to evaluate and characterise polyphenolic and anthocyanin profiles, antioxidative capacities and peroxidase (POD, EC 1.11.1.7) and polyphenoloxidase (PPO, EC 1.10.3.1) activities in the berries of two autochthonous grapevine cultivars from Bosnia and Herzegovina, Blatina and Trnjak. The samples were collected in the experimental fields in Herzegovina wine region (Čitluk, Bosnia and Herzegovina) and have been stored frozen in laboratory until their analyses. For all analyses the extractions have been done separately from the berries' skins and pulps of both cultivars. The anthocyanin and polyphenolic profiles were characterized by HPLC/MS technique, while enzyme assays and antioxidative capacities of extracts have been analysed using spectrophotometric methods. All results were compared between grape cultivars, but also among the skins and pulps at each variant. According to obtained results there is no significant variation of the anthocyanin profiles between analyzed grape varieties. The most dominant anthocyanins in both genotypes are the glucoside derivatives of pelargonidine and peonidine. Both genotypes have similar distribution of phenolic compounds between skin and pulp. The most dominant phenols in the skin are flavonoid glucosides and phenolic acids, while in the pulp prevail catechin derivatives and gallic acid. At both varieties total antioxidative capacity of berry extract was higher in the skin in comparison to the pulp. The pulp of both grape varieties has bigger PPO activity in comparison to their skins, while POD activity in reactions with phenolic acids was more expressed in pulps. Generally, taking into consideration all analyzed metabolites no big differences were found between Blatina and Trnjak, even Blatina has somewhat higher content of polyphenolics, anthocyanins and antioxidative activity. In all performed analyses, more significant differences have been observed between skin and pulp in both grape varieties with the similar trends.

STSM conducted in
Institute for Multidisciplinary
Research, Belgrade, Serbia

Host: Dr. Vuk Maksimović



Source: Wikipedia