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**GBG
2026**

**XIV. International
Symposium on Grapevine
Breeding and Genetics**

■ ■ ■ ■ **ZAGREB CROATIA**

28 June – 3 July 2026 • Zagreb (Croatia)

Book of Abstracts



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**XIVTH INTERNATIONAL
SYMPOSIUM ON GRAPEVINE
BREEDING AND GENETICS**

INFORMATIONS

This book of abstracts comes from a collaboration between the XIVth International Symposium on Grapevine Breeding and Genetics, held in Zagreb, Croatia, from 28 June to 3 July 2027 and the International Viticulture and Enology Society. The book is available online with open access on the *IVES Conference Series* platform.



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XIVTH INTERNATIONAL SYMPOSIUM ON GRAPEVINE BREEDING AND GENETICS

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EDITORIAL

Dear Participants,

On behalf of the Organizing Committee, it is our pleasure to welcome you to the XIV International Symposium on Grapevine Breeding and Genetics. Organized under the auspices of the International Viticulture and Enology Society, this symposium continues a long-standing tradition of promoting international collaboration and scientific exchange among researchers, breeders, students, and industry stakeholders.

This Book of Abstracts compiles the scientific contributions presented at the symposium, reflecting the diversity, innovation, and excellence of contemporary grapevine research. The collected abstracts highlight recent advances across a broad range of disciplines, including breeding, genetics, genomics, biotechnology, germplasm conservation, climate-change adaptation, disease resistance, and fruit quality.

The assessment and preservation of grapevine genetic diversity remain fundamental priorities viticultural research. Traditional cultivars represent an irreplaceable reservoir of genetic resources and cultural heritage, having shaped viticultural landscapes and wine identities for generations. At the same time, development of new cultivars that combine high fruit and wine quality with enhanced resistance to biotic stress with enhanced resistance biotic stresses, such as drought, heat, cold injury, sunburn, and other extreme weather conditions, has become increasingly important. By integrating the valuable traits of traditional cultivars with modern breeding approaches and genomic technologies, researchers are helping to create resilient grapevine cultivars that support productive, environmentally responsible, and economically viable viticulture.

We hope that the scientific presentations, discussions, and interactions throughout the symposium will inspire new ideas, strengthen existing collaborations, and foster the development of future partnerships. We trust that this collection of abstracts will serve as a valuable resource for participants and contribute to the dissemination of knowledge within the international grapevine research community.

Finally, we hope that your stay in Zagreb will be both scientifically enriching and personally enjoyable.

Sincerely yours,
The Organizing Committee
July 2026

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ORAL
SESSION:
GENETIC RESOURCES



ORAL KEYNOTE

Exploring grapevine genetic resources in a changing climate

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ABSTRACT

Plant genetic resources have sustained human societies throughout history. Through selection and propagation, humans have shaped plant gene pools to enhance productivity, local adaptation, and diversity of products across continents. This long-term process relied on the inherent genetic variability and plasticity of plants, leaving detectable signatures in their genomes that we can now decipher, interpret, and harness.

Unlike annual crops, modern cultivated grapevines (*Vitis vinifera* var. *vinifera*) result from a unique combination of sexual reproduction and long-term vegetative propagation, with some widespread varieties attested to be more than one thousand-year-old. They are highly heterozygous, and their genomes encode information about the history of domestication, introgression, as well as their potential of response to selective pressure.

Recent research has capitalized on extensive grape genetic resources, through two approaches. Paleogenomics has compared ancient grape genomes - recovered from archaeological excavations - with large modern germplasm collections. These studies elucidate the arrival, dispersal, and genetic evolution of grape types in Europe. In France, viticulture expanded rapidly during the early Roman period, with swift emergence of red and white *V. vinifera* types bearing small or large berries, and showing both Eastern

and Western ancestry. Archaeological evidence and genomic comparisons confirm early clonal propagation and long-distance exchanges during this era. The resulting datasets enable deeper investigations into introgression patterns, rates of haplotypic change over time, and selection of adaptive gene clusters.

A second ongoing approach leverages the resources of a large network of living collections, to forecast grape adaptation to climate change. Landscape genomics integrates genomic and geographic data to identify statistical associations between alleles and climatic variables. Models predictive of the phenotypes are constructed from the distribution of climate-associated alleles across individual genomes, and their goodness-of-fit validated against traits observed in common-garden experiments. Genomic offset - the predicted mismatch between current genetic composition and future climatic conditions - can then be estimated, informing targeted management and breeding strategies.

Together, these advances underscore the immense value of conserving and managing our grape genetic resources heritage. Precise identification, traceability, and comprehensive characterization remain essential to support both scientific understanding and a sustainable viticulture in a changing world.

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ORAL

Archaeogenomics reveals few generations separating ancient Eastern Mediterranean and modern Iberian grapevines over three millennia of viticulture

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Keywords: grapevine domestication, ancient DNA, Iberian viticulture, hybridisation

ABSTRACT

Viticulture became central to most western Mediterranean civilisations only a few millennia after grapevine (*Vitis vinifera* L.) was domesticated in the South Caucasus and the Near East. To elucidate the origins of the grapevines that enabled this westward spread over the past 3,000 years, we analysed 28 grapevine seeds from seven archaeological sites in the Iberian Peninsula and Sardinia. Ancient DNA analyses from the oldest seeds with domesticated-like morphology (ca. 1,000 BCE) found in southwestern Spain showed nuclear and chloroplast genome signatures of Eastern Mediterranean cultivars. In contrast, seeds from the same and later Iron Age Iberian sites exhibited signatures of hybridisation between local wild grapevines and eastern cultivars. Ancestry analyses of Sardinian and northeastern Spanish seeds suggest that historical diversification processes differentiating Central European and Iberian wine genetic groups likely occurred

already in the early Iron Age. In Iberia, Roman-period seeds were inferred as first-degree relatives of both the earliest eastern-introduced domesticates and a Medieval seed whose genetic profile matches that of the extant Iberian variety 'Pasa Valenciana'. Another Medieval seed was predicted as the offspring of the prolific Iberian cultivar 'Hebén', supporting that this major founder of the Iberian germplasm has been continuously propagated for over 1,100 years. These results indicate that Western Mediterranean viticulture likely began with Phoenician settlers who introduced eastern domesticated grapevines. Early hybridisation with local Iberian wild grapevines could have facilitated adaptation to the new environment. Through only a few sexual generations, followed by long-term reliance on clonal propagation, these early introductions laid the foundation for a lineage of modern Iberian cultivars.

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ORAL

Documenting and mining disease resistance alleles in the USDA *Vitis* repositories

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Keywords: *Erysiphe necator*, *Plasmopara viticola*, rhAmpSeq, Blackbird

ABSTRACT

The USDA Agricultural Research Service maintains *Vitis* germplasm repositories in Geneva, NY and Davis, CA collectively preserving approximately 5,000 unique accessions representing 30 *Vitis* species. Over the past two decades, biparental mapping families derived from selected accessions have been evaluated for resistance to powdery mildew and downy mildew, resulting in the discovery of numerous quantitative trait loci (QTL) and resistance alleles that are now actively used in breeding programs. Over this time, genotyping and phenotyping technologies have evolved to enable higher throughput approaches to allele mining, driven by innovations in the VitisGen projects. Given the allelic diversity at resistance loci, QTL mapping remains the most reliable approach for discovering novel resistance alleles. Currently, the primary bottleneck is generating sufficient seedling populations to support accelerated allele mining pipelines. Open data initiatives like the VIVC database (<https://www.vivc.de/>) and the Grapevine QTL Browser (<https://grapedia.org/qtl-browser/>) are leading the way to making genetic discoveries accessible to breeding programs. In USDA, we plan to use the GRIN database (<https://www.ars-grin.gov/>) to document known resistance alleles and chromosome painting of species representation for each accession. The next challenges are to rapidly introgress multiple novel resistance alleles into high quality genetic backgrounds for grape breeding and cultivar release.



ORAL

Study of ancient north-east Italian grape varieties taking advantage of an optimized aDNA extraction protocol

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Keywords: aDNAextraction, seeds remains, grape varieties

ABSTRACT

Grapevine (*Vitis vinifera* L.) is one of the most extensively cultivated fruit trees in the world. It is cultivated primarily for wine production but also for fruit fresh consumption. Its domestication started in the Near East approximately 11,000 years ago and since then many different varieties evolved through multiple historical pathways. Population genetic studies have been used to infer relatedness and migrations routes, highlighting a key role of Italy in grapevine spreading from Greece to Central and Western Europe.

In this project we have applied a complimentary paleogenomic approach relying on 146 ancient grape pips from 13 different archaeological sites from North-east in Italy, dated from Bronze age up to middle-age. First of all, we explored the possibility to improve the aDNAextraction step to recover good quality and processable extracts from grapevine pips. We developed the SPE-method exploiting reagents against soil inhibitors coupled with an aDNAsilica binding step. Our optimized method demonstrated a higher yield and more consistent performance across sites compared to previous extraction methods, significantly improving the library production step, particularly in challenging sites. So far, the protocol allowed to get 52 good quality libraries from 10 of the 13 sites. We also conducted target-enriched genome-wide sequencing for 10K SNPs on at least one samples from each archeological site and explored the genetic relationships of the ancient samples with modern grapevine varieties. Tailored analytical approaches were applied according to sequencing coverage gained at each site. The developed pipeline allowed to identify one archaeological sample from XIII century as an identical clone variety to our days. Additional close genetic relationships to varieties still present locally were also highlighted, pointing out migration and local adaptation trajectories of grapevine's cultivars connected to the territory.



ORAL

What 2,900 wild grapevines reveal about the genetic diversity of *Vitis vinifera* L. subsp. *sylvestris*

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Keywords: genetic resources, SSR marker, population genetics, population structure, conservation

ABSTRACT

Vitis vinifera L. subsp. *sylvestris* is the wild ancestor of the European cultivated grapevine (*V. vinifera* L. subsp. *sativa*). The recent identification of valuable alleles associated with abiotic stress tolerance and disease resistance in this subspecies has led to coordinated efforts towards the identification, characterization and preservation of the few remaining populations still present in river valleys, forest margins, and humid habitats throughout Europe, Western Asia, and North Africa. Previous genetic studies indicated the presence of two major *sylvestris* ecotypes, with genomic signatures differentiating populations of western and eastern origin. These works also indicated strong genetic differences between *sylvestris* and *sativa* populations, as well as important gene flow between them due to their prolonged coexistence.

However, an in-depth characterization of this subspecies is still needed to fully resolve its population structure, useful to inform effective conservation and management strategies.

In this cooperative work, we performed the genetic characterization of 1,460 newly sampled *sylvestris* individuals by a set of standard SSR markers, which were merged with those already available in the literature. Following rigorous data curation and allele size standardization based

on reference cultivars and allelic frequency patterns, this approach generated the largest dataset of genetic profiles for this subspecies available to date, compiling over 2,900 unique genetic profiles from 21 countries falling within its natural habitat range. Population structure analyses divided these genetic profiles into two ancestral genetic groups, broadly corresponding to the division of this subspecies into western and eastern ecotypes, and supporting the approach adopted in this study. Finer levels of resolution revealed a more complex genetic structure, identifying up to five well-defined genetic subgroups that correspond to the geographic origins of the sampled genotypes: the Southern Caucasus, the Middle East, the Maghreb and Iberian Peninsula, Central Europe and the Balkans, and a narrowly distributed group restricted to Central European regions of Austria and Slovenia. Complementary phylogenetic and dissemination modelling analyses supported this subdivision level, and facilitated inference of the relationships and potential evolutionary pathways among the identified genetic subgroups. Overall, this study provides an updated global assessment of the genetic diversity of this endangered subspecies and delivers valuable information for its effective management and conservation.

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This work was supported by the European Cooperative Programme for Plant Genetic Resources (ECPGR, <https://www.ecpgr.org/>).

ORAL
SESSION:
GENOMICS AND
FUNCTIONAL GENETICS



ORAL KEYNOTE

Structural and regulatory variation in the grapevine genome

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ABSTRACT

The grapevine genome harbors considerable levels of structural variation that represent an important source of functional variation and could result in high levels of cis-regulatory variation. For structural variation we focused on the elucidation of the elusive structure of centromeres in grapevine species. Centromere specific haplotypes belonging to 3 cultivated grapevine accessions, one wild accession of the same species and one interspecific hybrid have been reconstructed using PacBio HiFi and ONT long-reads. ChIP-seq data of centromere specific histone variant CENH3 has also allowed us to identify the functional domains of the centromeres and study their evolution throughout the domestication process. Considerable variation in repeats arrays dimensions and repeat composition in centromeric haplotypes was present both within the same individual and between accessions. The variation mostly involved non-functional satellite repeats, namely the very abundant 107 bp repeat, while the functional part composed of small arrays of a 59-mer monomer and a solo-LTR Gypsy element was conserved overall when comparing the same chromosome in different accessions. The comparison of identical by descent haplotypes has also uncovered recent events of TE insertions

and generation of solo-LTR, giving hints on the underlying mechanisms of diversification and homogenization of these regions.

For cis-regulatory variation, we developed a new theoretical and experimental approach to identify the cis-regulatory alleles present in a population of individuals and to estimate their cis-regulatory value that we named Estimated Genetic Contribution (EGC) of alleles. We have applied our approach to analyse transcript abundances in leaves and berries of >90 whole genome sequenced grapevine genotypes. We observe that the cis-regulatory variation of individual genes is mostly due to the presence of a multiallelic system with many different levels of expression related to the presence of multiple haplotypes in the population and that the EGC of individual haplotypes is highly variable between organs both in terms of the magnitude of relative differences among haplotypes (dynamic range of expression variation) as well as in terms of relative expression values of different haplotypes (ranking of the different haplotypes in terms of EGC). We also observe different levels of cis-regulatory variation between leaves and berries.



ORAL

A NAC-centered transcriptional network as a core regulatory module controlling the onset of grape berry ripening

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Keywords: berry ripening, functional genetics, cistrome, hierarchical intra-family regulatory network, NAC transcription factors

ABSTRACT

The onset of fruit ripening represents a major developmental transition characterized by extensive transcriptional and metabolic reprogramming that determines fruit texture, color, flavor, and aroma. In grapevine (*Vitis vinifera* L.), rising temperatures due to global warming advance the onset of ripening and reshape berry physiology, underscoring the need to resolve the transcriptional regulatory network controlling this transition. NAC transcription factors constitute a prominent component of these regulatory circuits, with VviNAC33, VviNAC60, and VviNAC03 implied in cooperative regulation of ripening-related processes, and VviNAC61 linked to later stages of ripening. Moreover, numerous additional NAC genes are specifically induced during grape berry development and ripening, yet their functional roles and network connectivity remain largely unexplored. Here, we investigate twelve berry-specific NAC genes as candidate master regulators driving large-scale transcriptome reprogramming during grapevine development. By integrating gene regulatory network inference based on co-expression, homologous overexpression coupled with transcriptomic profiling, cistrome mapping by DNAaffinity purification sequencing (DAP-seq), and complementary molecular approaches, we dissect intra-family regulatory interactions and the ripening-related processes they control. Based on temporal expression profiles in early- and late-ripening cultivars, together with transient overexpression in *Fragaria vesca* and *Fragaria × ananassa* fruit, VviNAC60 and VviNAC18 emerge as the earliest NAC transcription factors involved in the initiation of ripening. Collectively, our results define a NAC-centered transcriptional network as a core regulatory module controlling the onset of grape berry ripening.



ORAL

Dissection of the Rpv12 locus: from the genetic basis to the phenotype

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Keywords: defense mechanism, downy mildew, molecular cloning, *Plasmopara viticola*, Rpv12

ABSTRACT

Modern viticulture relies predominantly on traditional European grapevine cultivars (*Vitis vinifera*) and is therefore heavily dependent on fungicide use to mitigate crop losses from downy (*Plasmopara viticola*) and powdery mildew (*Erysiphe necator*), the two most widespread grapevine diseases. The breeding of new fungus-resistant grapevine cultivars by crossing European elite cultivars with wild *Vitis* species, that possess genetic resistance loci, is one chance to reduce fungicide applications in viticulture.

To date, over thirty loci mediating resistance to downy mildew are known. However, only few of them are used in the breeding programs and little is known about their defense mechanisms and the genes responsible for them. Since the long-term goal of resistance breeding is to pyramid multiple resistance loci, these loci should rely on different resistance mechanisms to enhance durability in the vineyard. Therefore, detailed knowledge of the defense mechanisms and resistance genes associated with the respective Rpv loci is essential for sustainable resistance management and for achieving durable and stable resistance in breeding programs.

Rpv12 originating from *Vitis amurensis* on chromosome 14 is one of the strongest resistance loci against downy mildew. The defense mechanism mediated by this locus was compared to Rpv3 and Rpv10 carrying cultivars through assessment of the downy mildew sporulation, onset of programmed cell death (PCD) and production of defense metabolites like hydrogen peroxide and stilbenes. Additionally, resistance breaking isolates of *P. viticola* were used to prove that the resistance loci rely on different resistance mechanisms. The carried out experiments revealed a clear temporal difference between Rpv10 and Rpv12 cultivars, which exhibited an early and localized defense response in comparison to Rpv3 cultivars that displayed a delayed and diffuse response. These temporal differences were associated with increased transveratrol accumulation and hydrogen peroxide formation shortly before the onset of PCD and may explain the observed

cultivar specific variation in hyphal growth, sporulation and in the vineyard.

We were able to narrow down, the originally described Rpv12-locus (Venuti *et al.* 2013) through new resistance markers. Bioinformatic analysis of an Rpv12-carrier (Frommer *et al.* 2023) led to the identification of two putative diseases resistance R-genes. For functional characterization the two candidate genes will be cloned into expression vectors for stable and temporary expression. Additionally, we were able to design CRISPR-Cas9 knock-out constructs specifically for the two candidate genes. Infiltration experiments will show which of the genes is responsible for resistance.



ORAL

Epigenetic regulation of APT3 seems to explain the masculinized phenotype of a floral mutant of Listán Prieto

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Keywords: sex determination, somatic mutation, DNAmethylation, APT3 gene, cytokinin regulation

ABSTRACT

While most cultivated grapevines (*Vitis vinifera* L.) possess perfect flowers, their wild ancestors were dioecious. Genomic analyses of commercial cultivars and wild grapevines have identified the structure of the sex-determining region, where an ancient recombination event enabled the expression of genes required for hermaphrodite flower formation. To preserve their agronomic properties, cultivated grapevines are clonally propagated; consequently, somatic mutations represent the primary source of genetic variability. The accession Criolla Chica N°2 (CCN2), a floral somatic mutant of Criolla Chica (the Argentine synonym for cv. Listán Prieto) is characterized by predominantly masculinized flowers as compared to Criolla Chica Ballista (a Listán Prieto accession with hermaphrodite flowers -CCBA-). Exogenous application of cytokinins to early-stage CCN2 inflorescences induced the reversion of the phenotypic mutation. To elucidate the molecular mechanisms underlying this mutant phenotype, we sequenced and annotated the cv. Listán Prieto genome. Using Listán Prieto as reference genome, we evaluated differential gene expression between CCN2 and

CCBA in inflorescences at a pre-anthesis stage (E-L 14 stage). Among the differentially expressed genes (DEGs), cytokinin dehydrogenase 3 and adenine phosphoribosyltransferase-3 (APT3) were significantly upregulated in CCN2. APT3 is associated with male flower development and is proposed to interfere with cytokinin metabolism and to be responsible for pistil development suppression. To further investigate the cause of this upregulation, Nanopore long-reads from the CCN2 and CCBA accessions were obtained and used to analyze structural variants (SVs) and methylation profiles. None of the identified SVs were directly associated with the phenotype of interest. However, we identified a differentially methylated region upstream of the APT3 gene on the hermaphrodite haplotype, where CCN2 showed significant hypermethylation. We propose that this epigenetic modification increases APT3 expression, interfering with the cytokinin metabolism and the female organs' development, ultimately resulting in the masculinized phenotype observed in CCN2.

ACKNOWLEDGEMENTS:

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ORAL

Functional dissection of grapevine resistance loci against *Plasmopara viticola* (Rpv) using a comparative multi-omics approach

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Keywords: *Vitis vinifera*, *Plasmopara viticola*, Rpv loci, downy mildew, multi-omics

ABSTRACT

Grapevine resistance breeding relies on a limited number of major resistance loci (Rpv) to control *Plasmopara viticola*. Although previous findings suggest locus-specific resistance patterns, we currently lack comparative multi-omics data conducted within a uniform, genetic background and standardized laboratory conditions.

In this work, we analysed the resistance conferred by Rpv1, Rpv3.1 and Rpv10 in a dedicated biparental population, using a single pathogen strain and standardized infection conditions. By integrating transcriptomic analyses across several early infection time points with metabolomics, we characterized the temporal dynamics of the defence responses deployed by each locus.

Before 1 day post inoculation (dpi), a small core of common infection-responsive genes was identified, although most transcriptional changes differed between Rpv backgrounds. Indeed, the three loci exhibited distinct gene expression patterns and temporal dynamics, indicating that Rpv-mediated resistance is not controlled by a single common programme but instead reflects locus-specific regulatory strategies. At the metabolic level, significant changes associated with the Rpv responses emerged after 1 dpi in terms of the time and amplitude of compound accumulation. However, many grapevine-associated resistance metabolites were common to all three Rpv loci, whereas some changes were shared by only two loci or were locus-specific.

In conclusion, our results show that major Rpv loci differ not only in resistance level but also in the regulatory mechanisms underlying the temporal evolution of resistance responses. This comparative multi-omics approach improves our functional understanding of grapevine responses to *P. viticola* and supports breeding strategies aimed at combining loci to achieve effective and durable resistance.



ORAL

Functional dissection of NPR3 by genome editing highlights its role in grapevine defense and root symbiosis

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Keywords: grapevine, genome editing, mycorrhizal symbiosis, resilience, sustainability

ABSTRACT

New Plant Breeding Techniques (NPBTs), and particularly genome editing, represent a powerful avenue to enhance disease resilience in perennial crops. However, their practical implementation in grapevine remains constrained by the species' complex biology, recalcitrance to transformation, and long breeding cycles. In this study, we explored the potential of targeted genome editing of key susceptibility and regulatory genes to reinforce disease resistance while preserving beneficial plant–microbe interactions. Simultaneous disruption of the mildew susceptibility genes VvMLO6 and VvMLO7 resulted in a marked reduction of powdery mildew incidence, reaching approximately 80% compared with wild-type plants under controlled infection conditions. In parallel, editing of the salicylic acid signaling regulator VvNPR3 led to a substantial decrease in disease severity (up to 70%) and conferred enhanced tolerance to the oomycete pathogen *Plasmopara viticola*. These resistance phenotypes were associated with pronounced metabolic adjustments, including increased accumulation of stilbenes such as resveratrol and piceid, suggesting a broader reprogramming of defense-related pathways and secondary metabolism. Beyond pathogen resistance, we investigated whether NPR3 also plays a role in modulating interactions with beneficial microorganisms in the root environment. Notably, roots of NPR3-edited lines displayed significantly increased colonization by the arbuscular mycorrhizal fungus *Rhizophagus irregularis*, characterized by a higher abundance of functional arbuscules and a more developed intraradical mycelium. Integrated transcriptomic and metabolomic profiling revealed extensive remodeling of defense signaling networks, cell wall dynamics, and specialized metabolism, collectively contributing to a more permissive root environment for symbiosis establishment.

Consistently, strong induction of the mycorrhizal marker VvPT4, together with the activation of fungal genes involved in nutrient exchange processes, confirmed the establishment of a more efficient symbiotic interface. Overall, our findings

identify NPR3 as a central regulatory hub coordinating immune responses and symbiotic compatibility in grapevine, providing a conceptual framework for genome editing strategies that simultaneously enhance disease resistance and beneficial microbial partnerships in this economically and culturally important perennial crop.



ORAL

Haplotype diversity and marker development at grapevine (*Vitis*) disease resistance loci

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ABSTRACT

Studying disease resistance loci in grapevines (*Vitis*) is a complex process because resistance QTL often coincide with highly-repetitive NLR gene clusters that are difficult to analysis bioinformatically, requiring extra time and attention to fully characterize. With the ever-increasing use of next generation sequencing, long-read genome assemblies, and efforts like the USDA-funded VitisGen3 grape breeding and genetics project, these regions have become more accessible to researchers and breeders alike. A hallmark endeavor of VitisGen3 has been to identify and characterize resistance loci, test candidate gene function, develop markers for marker-assisted selection, and create bioinformatic pipelines to expedite selection on these loci for breeding programs world-wide. This effort wouldn't be possible without the

creation of the *Vitis* colinear core genome rhAmpSeq panel. Available as a service to anyone in the world, the panel has been used to genotype more than 80,000 grapevines since its publication in 2019, including the accessions from the USDAgermplasm repository. To date, rhAmpSeq alleles have been utilized for the prediction of more than 30 resistance loci and other traits of interest for marker-assisted selection. With rhAmpSeq discovery and screening of resistance QTL now routine, VitisGen3 has expanded into QTL fine mapping, KASP marker development, chromosome painting, and studies on haplotype diversity. In this talk, I aim to highlight the strategies used by VitisGen3 for characterizing the haplotypes at resistance loci such as Rpv3, among others, and the development of low-cost KASP markers.

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ORAL

Haplotype-resolved genome assembly and implementation of VitExpress, an open interactive transcriptomic platform for grapevine

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Keywords: haplotype genome sequencing, transcriptomic data mining platform

ABSTRACT

In contrast to most crops, *Vitis vinifera* has benefited little from classical breeding due to its high heterozygosity. Remarkably, the main cultivated grapevine varieties grown today remain largely unchanged from those cultivated centuries ago and have been only marginally improved to cope with evolving environmental constraints. However, climate change and environmental concerns now demand a transition toward knowledge-based viticulture supported by advanced genomic tools. Here, we report haplotype-resolved genome assemblies for two heterozygous *V. vinifera* cultivars, Chasselas and Ugni Blanc, generated by combining high-fidelity long-read sequencing with high-throughput chromosome conformation capture (Hi-C). Telomere-to-telomere chromosome assemblies enabled the separate reconstruction of both haplotypes for each cultivar and revealed substantial structural variation between homologous chromosomes. Integration of full-length transcript isoforms obtained by Iso-Seq significantly improved genome annotation. Building on these resources, we developed VitExpress, an open and interactive transcriptomic platform providing a genome

browser and integrated web tools for expression analysis. VitExpress incorporates more than 3,500 curated Vitis RNA-Seq datasets, whose metadata are standardized using Plant Ontology (PO) and Plant Experimental Conditions Ontology (PECO). This rigorous semantic framework enables reliable cross-project comparisons and underpins the Dual Selection DEG tool, which identifies differentially expressed genes between conditions, even when derived from independent studies. The “Search by Profile” tool further supports hypothesis generation by identifying genes whose expression patterns match user-defined profiles. In addition, ExpressionManager, a dedicated submission portal, allows the community to securely analyze private datasets against the public reference atlas while preserving data confidentiality until publication. By combining high-quality genomic resources with standardized transcriptomic integration and interactive analytics, VitExpress provides a comprehensive framework to accelerate gene discovery and support next-generation grapevine breeding strategies.

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ORAL

Large-scale variant identification and annotation from whole-genome-sequencing data enables functional prediction in grapevine

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Grapevine (*Vitis vinifera*) is amongst the world's most cultivated fruit crops, and of global and economic significance. The genus *Vitis*, encompassing approximately 70 naturally occurring inter-fertile species, exhibits extensive genetic and phenotypic diversity, highlighted by the global cultivation of thousands of predominantly *Vitis vinifera* cultivars. Despite the importance of harnessing its naturally occurring genetic diversity to pursue traits of interest, the systematic characterization of available functional genetic variants remains limited. Such characterizations hold the potential not only as a critical tool for directed breeding, including the identification of molecular markers for genetic selection, but would also enable the functional characterization of genes that may exert influence over key functional traits. With over 5,000 Illumina-sequenced accessions available, detecting and comparing sequence variation (*e.g.*, single nucleotide polymorphisms; SNPs) across the grapevine germplasm presents a unique opportunity to integrate heterogeneous sequencing information and improve candidate gene exploration. To this end, we developed Vinotype, a Nextflow-based pipeline for efficient and reproducible large-scale variant identification and

annotation of *Vitis* whole-genome-sequencing (WGS) datasets. We validated Vinotype's performance using genomic regions with known functionally characterized variants within DXS1 and AGL11, and benchmarked results against a commercially available SNP-array, demonstrating high concordance (> 95 % genotyping accuracy) in variant discovery capabilities. Analysis of over 177,000 putatively high-to-moderate impact SNPs identified several candidate variants linked to genes associated with specialized metabolism, fruit-related characteristics and development, in addition to biotic and abiotic stress responses. To further demonstrate the pipeline's scalability and efficiency, we processed over 3,000 publicly available WGS datasets providing a valuable resource for allele-mining and candidate gene prioritization in grapevine. This large-scale cataloguing of coding region sequence variation provides the foundation for future predictions regarding the impact of genetic variations on protein structure and function, facilitating the identification of beneficial alleles and novel sequence-trait associations, ultimately aiming to accelerate genetic improvement programs and the development of cultivars with enhanced attributes.

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ORAL

Mapping of five loci for black rot resistance in four breeding populations and identification of candidate genes associated with Rgb1

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Keywords: biotic stress, *Guignardia bidwellii*, *Phyllosticta ampellicida*, QTL analysis, resistance breeding

ABSTRACT

Black rot, caused by *Phyllosticta ampellicida* (*Guignardia bidwellii*), is a serious fungal disease in viticulture. Incidences increased in recent years due to reduced pesticide treatments, neglected phytosanitary measurements, and effects of climate change. Until recently, grapevine cross breeding focused primarily on the development of new varieties with resistances to powdery and downy mildew. More than forty resistance loci were described for the mildew diseases, several of these loci were frequently used in breeding through marker-assisted selection (MAS), and a few resistance genes were identified and characterized. However, only three loci have been described conferring resistance to black rot. Therefore, we used four biparental populations based on the resistance donors 'Börner', 'Merzling', 'Calardis Musqué', 'Villard Blanc' and 'Calardis Blanc' for quantitative trait locus (QTL) analysis to identify new resistance loci. In addition to Rgb1 and Rgb2, three previously unknown QTL were mapped on chromosome 6 (Rgb5), 13 (Rgb6) and 17 (Rgb7), indicating several independent sources of black rot

resistance. Because Rgb1 on chromosome 14 appears to be a very frequently occurring black rot resistance in current breeding material and some disease-resistant varieties, we focused on the refinement of this locus. The genetic maps of the four populations were aligned, comprising the phenotypic and genetic results of more than 750 F1 individuals. With this approach, the Rgb1 locus could be validated and a genomic region around the simple sequence repeat marker UDV-095 was defined as the putative core of the resistance locus. The haplotype-resolved and annotated genomes of the cultivars 'Calardis Musqué' and 'Börner' were compared with PN40024 and analyzed at the Rgb1 locus. Structural variations and possible candidate genes will be discussed, like a gene cluster of pattern recognition receptors. The results obtained enable the development of tightly linked molecular markers for MAS and finally the introgression of Rgb1 into elite breeding lines. The additional resistance loci can be used for pyramiding to strengthen overall resistance to black rot and to prevent a possible resistance breakdown.

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ORAL

miR7122-3p is a key regulating factor of the photosynthetic process in grapevine

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Keywords: functional analysis, miR7122, *Vitis vinifera*, water stress, VvDAHPS

ABSTRACT

Plant microRNAs are small regulatory RNAs that control gene expression and play key roles in plant development and stress adaptation. The miR7122 locus produces two strands: miR7122-5p, previously associated with the synthesis of phased small interfering RNAs, and miR7122-3p, whose biological function is still unclear. To gain experimental evidence on the role of vvi-miR7122-3p, an in-depth physiological and molecular characterization of transgenic grapevines was carried out, in which this miRNA was either over-accumulated or sequestered using the short tandem target mimic approach. Transgenic lines of two *Vitis vinifera* cultivars, ‘Bragat rosa’ and ‘Chardonnay’, overexpressing (OE) or silencing (STTM) vvi-miR7122-3p, were subjected to water stress and recovery, and their physiological and molecular responses were analyzed. Modulation of vvi-miR7122-3p significantly affected leaf gas exchanges upon drought. Particularly, STTM plants exhibited reduced carbon assimilation and abnormal high substomatal CO₂ levels, pointing to a strong impairment of carbon fixation. Notably, these alterations occurred without significant changes in photosystem II efficiency, suggesting that the limitation was mainly biochemical and associated with the Calvin cycle

rather than photochemical damage. Such physiological adjustments were genotype-dependent, as ‘Bragat rosa’ STTM plants displayed stronger stress sensitivity than ‘Chardonnay’ STTM vines. Additionally, under water stress, silencing of vvi-miR7122-3p triggered a large-scale transcriptional reprogramming, leading to the repression of genes involved in photosynthesis and carbon assimilation together with activation of respiration, secondary metabolism, and defense-associated pathways. Network and correlation analyses identified the 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase (VvDAHPS), a key enzyme of the shikimate pathway, as main target of vvi-miR7122-3p. Experimental validation confirmed that the miRNA directly regulates this gene, further supporting a model in which vvi-miR7122-3p contributes to drought acclimation through regulation of the shikimate pathway. When the miRNA amounts are reduced, VvDAHPS is derepressed, activating shikimate-derived secondary metabolism and redox-related pathways. This metabolic shift could reallocate carbon sources toward the production of antioxidant and defensive compounds, therefore lowering the photosynthetic processes and leading to elevated internal CO₂ concentrations.

ACKNOWLEDGEMENTS

This study was carried out in the frame of the project “TEA4IT_Tecnologie di Evoluzione Assistita per le filiere agroalimentari italiane” funded by the Italian Ministry of Agriculture, Food Sovereignty and Forestry (MASAF). Part of the work was carried out within the project “SHIELD4GRAPE: Breeding and integrated pest management strategies to reduce reliance on chemical pesticides in grapevine,” funded by the European Union through the Horizon Europe Research and Innovation Programme (Grant number 101135088). Views and opinions expressed are, however, those of the authors only. Neither the European Union nor the granting authority nor the European Commission can be held responsible for them.



ORAL

QTL mapping and transcriptomics reveal complex and conserved regulation of graft union formation

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Keywords: wounding, grafting, scion, rootstock, regulation

ABSTRACT

Understanding how grafts form has fascinated scientists for over a century, and numerous transcription factors (TFs) involved in wound healing, callus formation, and graft development have been identified in model plants. However, despite the importance of grafting for cultivating many crops, the genetic architecture underlying grafting-related traits remains poorly characterised.

To address this gap, we mapped quantitative trait loci (QTLs) associated with grafting-related traits in grapevine, including callus formation, mechanical strength of the graft union, and post-grafting growth. However, we were unable to detect QTLs associated with grafting success rate itself. To further investigate the genetic basis of grafting, we integrated transcriptome data comparing grafted and intact tissues, which led to the identification of 36 candidate TFs that may regulate grafting-related traits. Many of these were

orthologues of genes known to control defence and wounding responses, callus formation, and tissue regeneration in model species.

We also demonstrated that two TFs previously shown to regulate callus formation and grafting in *Arabidopsis* perform similar functions in grapevine. This was confirmed by silencing their grapevine orthologues using exogenous double-stranded RNAs, which affected grafting-related processes.

Together, these findings highlight both the difficulty of detecting QTLs for highly complex traits such as grafting success rate and the value of breaking these traits down into simpler component traits. The identification of candidate TFs within QTL regions, combined with functional evidence from gene silencing, suggests that key regulators of grafting are conserved across diverse plant species.

ACKNOWLEDGEMENTS

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ORAL

Targeted long-read sequencing reveals function-restoring MYBA1 and MYBA2 mutations in white-to-red grape color somatic variants

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Keywords: grape color, long-read sequencing, RNA-seq, MYBA1 and MYBA2, somatic variation

ABSTRACT

To diversify production, vinegrowers select somatic variants in grape color that arise spontaneously during the propagation of cultivars. This is the case of the red-berried bud sports that recently arose in the white-berried cultivars Albariño and Verdejo. To understand the molecular basis of grape color recovery, we combined real-time targeted Nanopore sequencing of a panel of anthocyanin metabolism and regulation genes, and a berry skin RNA-seq transcriptome comparison of the red variants and their corresponding ancestral white cultivars. In the red variant of Albariño, we identified overexpression of VviMYBA1 associated with the excision of the Gret1 retrotransposon that suppresses expression in the canonical white-grape allele. In the red variant of Verdejo, the frameshift InDel of the VviMYBA2 white-grape allele was restored, likely due to gene conversion between the two CR domains of the gene. Restoration

of either VviMYBA1 or VviMYBA2 function activated the phenylpropanoid biosynthesis pathway, including the upregulation of VviPAL, VviCHS, VviFH3, VviLDOX, and VviUFGT in both red variants. Targeted UPLC-QqQ-MS/MS metabolomics confirmed specific accumulation of anthocyanins—predominantly dihydroxylated forms—in both red variants, with higher concentration in red Albariño than in red Verdejo. Among colorless flavonoids, the accumulation of trihydroxylated flavonols also increased in both red variants, whereas proanthocyanidins increased only in red Albariño and dihydroxylated flavonols only in red Verdejo. Our results reveal a recurrent recovery of VviMYBA1 expression and a rare restoration of the VviMYBA2 reading frame in independent white-to-red grape variants, suggesting potentially distinct roles of the two master regulators of anthocyanin biosynthesis in grapevine fruits.

ACKNOWLEDGEMENTS

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**ORAL
SESSION:
GENETIC IMPROVEMENT
AND BREEDING STRATEGIES**



ORAL KEYNOTE

Prediction-based approaches for grapevine improvement

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¹ Hochschule Geisenheim University, Department of Plant Breeding, Germany**Keywords:** genomic prediction, phenomic prediction, predictive breeding

ABSTRACT

Grapevine breeding is fundamentally constrained by long generation times, perennial growth and clonal propagation. These characteristics limit the rate of genetic gain and make selection decisions both critical and uncertain.

Advances in genomics, phenomics and quantitative genetics are creating new opportunities to accelerate breeding progress via prediction-based approaches. The increasing availability of large-scale and multi-environment datasets is offer the possibility of shifting grapevine breeding from descriptive data generation towards prediction-driven decision making.

This presentation will discuss how predictive approaches may reshape grapevine improvement across different stages of breeding programs. Examples from genomics, phenomics, clonal evaluation and genotype-by-environment modelling will illustrate how increasingly integrated datasets enable new forms of biological inference and predictive modelling in grapevine.

The talk will further explore concepts and emerging modelling frameworks designed to improve information transfer across populations, environments and breeding cycles. Perspectives on scalable prediction systems and new computational approaches will also be discussed. The central message is that future progress in grapevine breeding will depend not only on generating increasingly complex datasets but on integrating and transforming these data into robust and continuously improving prediction systems.



ORAL

A Portuguese grapevine breeding program focused on enhancing resistance to *Plasmopara viticola* and *Erysiphe necator*

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Keywords: grapevine breeding, disease resistance, *Plasmopara viticola*, *Erysiphe necator*, Marker-Assisted Selection, resistance loci

ABSTRACT

Downy mildew (*Plasmopara viticola*) and powdery mildew (*Erysiphe necator*) are among the most destructive diseases affecting grapevine (*Vitis vinifera* L.). To address this challenge, several breeding programs have been established worldwide with the goal of developing resistant genotypes. In Portugal, PLANSEL Lda., with continuous support of the University of Évora, has been at the forefront of these efforts, leading a grapevine breeding program since the 1980s aimed at enhancing resistance to both pathogens. The program was initially co-financed by the German state bank KfW and later supported by the Portuguese State through national R&D initiatives, including the AGRO 8.2 project and, fifteen years later, the PDR 784 project (2019–2022). More recently, the PEPAC project (PEPACC115) has continued advancing the program. Within these initiatives, resistance genes against powdery and downy mildew were introgressed into Portuguese autochthonous grapevine varieties through controlled crosses with multiresistant, largely homozygous material (kindly provided by the Julius Kühn Institute, Geilweilerhof, Germany). This work led to the registration of the new cultivar ‘Defensor’ in the Portuguese Catálogo Nacional de Variedades. At present, PLANSEL

Lda. maintains a collection of more than 700 F1 hybrid plants currently under evaluation. These genotypes will be further characterized through marker-assisted selection (MAS), aiming to pyramid resistance loci for downy mildew (Rpv1 and Rpv3.1) and powdery mildew (Run1, Ren3, and Ren9). In parallel, 184 PIWI genotypes selected within the breeding program have already been grafted and established in a vineyard for advanced field assessment, including wine quality evaluation through microvinification. In its ongoing breeding program, PLANSEL Lda. collaborates with three Portuguese partners, University of Évora, ATEVA, and INIAV, as well as the German institution JKI-Geilweilerhof, which provides genetic material from its breeding programs. These programs target not only downy and powdery mildew but also additional pathogens, such as black rot (Rgb) and *Xylella fastidiosa* (Rxf), which will be incorporated into new crosses at PLANSEL Lda. The ultimate objective is to develop new cultivars resistant to both pathogens (known as PIWI) while maintaining close genetic and oenological similarity to Portuguese *Vitis* germplasm. This approach promotes more sustainable viticulture while enhancing and valorising the identity and quality of Portuguese wines.

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ORAL

Evaluation of 21 new disease-resistant winegrape varieties (PIWI) for viticultural suitability in north-eastern Italy

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Keywords: grapevine, yield, fruit composition, phenotype, climate change

ABSTRACT

The cultivation of disease-resistant winegrape varieties (PIWI) is gaining interest worldwide, particularly in viticultural areas where the use of fungicide is limited. Most breeding programs have focused primarily on resistance to pathogens, while yield performance and fruit composition across different environments, especially under global warming conditions, have received much less attention. This study evaluated yield components and fruit composition of 21 disease-resistant grapevine varieties grown under three training systems over ten consecutive vintages (2015–2025) in an experimental vineyard in Castelfranco Veneto, north-eastern Italy. The 11 white varieties included Aromera, Bronner, Fleurtaï, Johanniter, Muscaris, Sauvignon Kretos, Sauvignon Nepis, Sauvignon Rytos, Solaris, Soreli and Souvignier gris. The 10 red varieties were Monarch, Cabernet Carbon, Cabernet Volos, Cabernet Eidos, Julius, Merlot Kantus, Merlot Korus, Prior, UD 31-103 and Vinera. Mean yield was similar between white and red varieties, averaging 2.65 kg per vine. Among white varieties, the lowest yields were recorded for Sauvignon Nepis and Aromera (1.72 and 1.81 kg per vine, respectively), while among red varieties the lowest values were observed for Cabernet Carbon, Merlot Korus and Merlot Kanthus (1.93, 2.19 and 2.14 kg per vine, respectively). These varieties were characterized by smaller clusters and lower cluster numbers, which accounted for their reduced yield. At harvest, average total soluble solids were 20.5 °Brix in white varieties and 20.1 °Brix in red varieties, while titratable acidity averaged 7.1 g L⁻¹ and 7.6 g L⁻¹, respectively. The lowest acidity levels were found in Soreli and Fleurtaï (5.8 and 6.2 g L⁻¹). Overall, all resistant varieties reached technological maturity with adequate sugar levels while maintaining acceptable acidity. The resistant varieties proved well suited to the local environment, characterized by high annual rainfall (> 1000 mm) and warm growing conditions (~1900 °C growing degree days). Bronner and Sauvignon Rytos (white), as well as Cabernet Carbon and UD 31-103 (red), showed high phenotypic stability across all the productive traits evaluated, as indicated by regression

coefficients close to or below 1. In contrast, Sauvignon Rytos (white) and Merlot Kanthus (red) exhibited low phenotypic stability, displaying a strong response to vintage conditions and high inter-annual variability. However, in particularly hot vintages, such as 2016, white varieties showed rapid sugar accumulation accompanied by a marked decline in acidity (2.6 g L⁻¹ in Fleurtaï), raising concerns about their future suitability under projected climate warming.



ORAL

Genomic and epigenomic contributions to trait variation, genotype-by-environment interactions, and stability in grapevine clones

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Keywords: grapevine clones, DNAmethylation, genotype-by-environment interaction (G×E), yield stability, multi-omics integration

ABSTRACT

Clonal selection remains central to grapevine improvement, yet consistent yield and fruit quality across vintages are challenged by pronounced genotype-by-environment interactions (G×E). While genomic markers are increasingly used to characterise clonal diversity, the extent to which epigenomic variation contributes to trait performance and stability in grapevine remains unclear.

Here, we integrate genomic (SNP) and epigenomic (DNAmethylation-derived) features with 11 years of phenotypic data from 210 Riesling clones to quantify their relative contributions to yield and juice quality traits. Genomic and epigenomic relationship structures differed substantially, indicating that methylation profiles capture patterns of clonal relatedness not fully explained by DNAsequence variation.

Multi-kernel linear mixed modelling and subsequent variance partitioning revealed that epigenomic features contributed strongly to trait variation and explained a greater proportion of G×E interaction variance than genomic markers for yield and key fruit quality traits. Notably, the two molecular layers exhibited distinct G×E patterns, with epigenomic features explaining a greater proportion of interaction variance, indicating that they capture components of performance not fully represented by genomic markers.

Aggregating marker effects to genomic regions identified segments associated with both high mean performance and reduced year-to-year variability, providing a framework to prioritise stability-associated regions in clonal selection.

These findings demonstrate that integrating epigenomic information can enhance the dissection of trait stability in grapevine and offers new opportunities to refine clonal selection strategies for consistent performance under variable growing conditions.



ORAL

Grapevine breeding for the development of multi-disease-resistant cultivars through marker-assisted selection and resistance gene pyramiding

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Keywords: grape, genetics molecular markers, resistant varieties, microvinification

ABSTRACT

The climatic conditions of southern Brazil favor the incidence of fungal diseases in grapevines, which hampers the cultivation of *Vitis vinifera* varieties. In addition to downy mildew and powdery mildew, anthracnose and bunch rots are major diseases that require control by fungicides. More recently, resistant cultivars (“PIWIs”) have been developed that consist largely of a *V. vinifera* genetic background but include the introgression of a few resistance genes, thereby reducing dependence on chemical products. Abreeding program with this objective is being conducted in the state of Santa Catarina, Brazil (Epagri/UFSC program), aiming to develop high-quality wine grape cultivars resistant to the main grapevine diseases (downy mildew, powdery mildew, anthracnose, and grape ripe rot (*Colletotricum* sp.)). The genetic basis of the program includes currently available resistant varieties and additional sources of resistance to fungal diseases. Selection for downy mildew resistance is carried out at the early seedling growth stage using molecular markers. For downy mildew, the loci Run1/Rpv1, Rpv3,

Rpv10, and Rpv12 are monitored, with the goal of selecting individuals carrying at least three of these genes. Selection for powdery mildew resistance is based on the Run1 gene. Selected seedlings are evaluated for anthracnose resistance through artificial inoculation under controlled conditions. The source of anthracnose resistance originates from *V. amurensis* and was initially identified in the cultivar Sibera. After evaluation for resistance to the three diseases, selected materials are grafted and multiplied for planting under commercial vineyard conditions, where they are assessed for agronomic traits, resistance to bunch rots, and oenological quality. Initial evaluations have shown that canopy health in pyramided multi-resistant materials is superior to that of most resistant cultivars currently under testing. Enological evaluations started in 2024. The program will continue in the coming years through successive cycles of crosses, marker-assisted selection, and field evaluation for agronomic and oenological traits.

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ORAL

Improving grapevine traits via gene editing

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Keywords: gene editing, prime editing, VviMybA1, VviDXS1, VviBR6OX

ABSTRACT

Significant progress has been made recently leveraging the gene editing technology for trait development in grapevine (*Vitis* spp.), alongside the emergence of innovative methodologies for non-transgenic gene editing. We at the USDA-Agricultural Research Service Grape Genetics Research Unit have made significant progress in both areas of targeted trait modification and development of gene-editing methods. In this presentation, we will highlight our success in editing VvMybA1 for restoring skin color by removal of a 10.5-kb Gret1 transposon from the VviMybA1 promoter in *Vitis vinifera* cv. Chardonnay, editing VviDXS1 for the creation of muscat flavor by changing one single nucleotide in VviDXS1 in *V. vinifera* cv. Scarlet Royal, and modifying VviBR6OX1 and VviBR6OX2 for the creation of short-statured vines. In addition, we will share our recent progress in developing and adapting innovative delivery and selection methods for creating transgene-free edited events for improving disease resistance and fruit quality traits in grapevines.



ORAL

Induced mutagenesis as a tool for intra-varietal improvement: increased diversity in vegetative, fruit and phenological traits in *Vitis vinifera* cv. Pinotage

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Keywords: induced mutation, morpho-colourimetric analysis, phenotyping, phenology

ABSTRACT

Climate variability and rising biotic pressure threaten global viticulture. Modern wine production depends on a limited number of grapevine cultivars, represented by multiple clones that differ slightly in their agronomic, oenological, or stress-tolerance traits. Broadening the genetic base within wine grape cultivars (identifying, conserving and deploying useful phenotypes) is therefore essential for long-term resilience. Induced mutation, using chemical or physical mutagens, could expand the intra-varietal diversity, allowing for the identification of enhanced, heritable traits.

The red-wine cultivar Pinotage is relatively young, compared to well-established cultivars such as Pinot noir, and therefore lacks clonal diversity. An intra-varietal improvement scheme was implemented using gamma irradiation to increase the diversity of current Pinotage planting materials. Gamma irradiation was applied to in vitro plantlets of three widely planted Pinotage clones (Pi7B, Pi45R and Pi48I), resulting in a collection of ~ 1400 putatively mutated plants. A subset of 500 individuals (irradiated treatment vines and unirradiated somaclonal controls) was pre-selected and field-planted in 2021. Morpho-colourimetric analysis during the juvenile

phase assessed leaf and petiole size, shape and colour, with irradiated vines displaying more extreme phenotypes than unirradiated control vines. This trend was also seen when the population bore fruit (since 2023). Phenotyping techniques (using OIV descriptors, image analysis and agronomic measurements), along with phenological scoring (using E-L scale), and ripeness monitoring, were employed to perform the initial characterisation of the fruiting putative mutant grapevines. Diverse phenotypical variation observed in the population included variation in berry skin and flesh colour and bunch compactness. Image analysis focused on differing bunch architectures and compactness, given the links with improved ripening and reduced fungal infections in less compact bunches. The population also displayed a wide range of phenological progressions and ripening periods, with increased variation in the véraison-to-harvest period. This could promote climate resilience, allow balanced phenolic accumulation, and thereby uphold wine quality. Our results on this population will be shared to highlight the potential of gamma irradiation and induced mutagenesis for increasing intra-varietal diversity in grapevine cultivars and clones.

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ORAL

Reviving grapevine massal selection in the context of climate change: A strategy for resilient vineyards in the 21st century

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Keywords: massal selection, climate change resilience, intra-cultivar diversity, precision viticulture

ABSTRACT

Modern viticulture faces a critical paradox. The widespread adoption of clonal selection in the mid-20th century successfully standardized production and reduced viral incidence through sanitization and certification, but unintentionally created a genetically simplified vineyard landscape. Today, as climate change imposes unprecedented pressures (from heat waves to emerging pests) reduced intra-cultivar diversity can constrain adaptive responses to heat, drought, and emerging pests/pathogens.

This work synthesizes historical, genomic, and epigenetic evidence to argue that massal populations serve as dynamic genetic reservoirs, turning the “imprecision” of the past into the buffering capacity required for future vineyards. We synthesize evidence indicating that massal populations preserve rare alleles, structural variants, and adaptive trait combinations (including somatic variation and epigenetic modifications) that are systematically lost in clonal systems. Furthermore, we redefine the “clone” not merely as a genetic entity, but as a holobiont where the phenotype is modulated by the interaction between the genotype, the epigenome, and the virome.

To implement this diversity, we propose a new framework: “Precision Massal Selection”. By leveraging high-throughput genotyping tools (such as GBS and Amplicon-seq) and metagenomics (High-Throughput Sequencing for virome analysis), it is now possible to fingerprint massal populations and characterize their sanitary status with high resolution. This enables “surgical sanitation” (the removal of vines with detrimental viruses while preserving the adaptive complexity of the population). Precision Massal Selection represents the ultimate expression of precision viticulture, matching diverse populations to specific terroirs to ensure yield stability and stress tolerance without altering varietal identity.



ORAL

Strategic advancement of the Korean table grape breeding program for consumer-preferred cultivars

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Keywords: grape breeding, molecular marker, table grape, phenotyping, cultivar

ABSTRACT

In Korea, summer rainfall and comparatively less favorable growing conditions than major grape-producing countries have influenced the direction of table grape breeding. Until around 2010, the primary objective of the Korean grape breeding program was to develop interspecific hybrids combining the environmental adaptability of American species with the superior fruit characteristics of European species. Interspecific hybrid cultivars such as ‘Campbell Early’ and ‘Kyoho’ were widely used as parental materials in the breeding program.

With increased exposure to imported grapes, consumer preferences shifted toward seedless cultivars with non-slip berry skin that can be eaten whole without peeling or removing seeds. Consequently, breeding targets expanded beyond large berry size, high soluble solids content, and attractive appearance to include more refined fruit quality traits.

Current breeding objectives emphasize genetically seedless cultivars with firm flesh, strong berry–pedicel attachment, and reduced skin astringency. The breeding program utilizes crossing populations such as ‘Tano Red’ × ‘Ruby Seedless’, as well as approximately 800 germplasm accessions. Using these materials, fruit traits phenotyping, genome-wide association studies (GWAS) and QTL analyses are performed to identify associated loci. SNP-based markers related to seedlessness are applied in the breeding program, while markers associated with other traits are being validated across germplasm resources.

In addition to fruit quality traits, bud fruitfulness and stable coloration have been incorporated as breeding objectives, and breeding populations are being developed with continuous data accumulation. Through the refinement of breeding objectives, intensive phenotyping, and routine SNP-based selection, the Korean table grape breeding program continues to advance toward the development of consumer-preferred cultivars.

ACKNOWLEDGEMENTS

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ORAL

VitisGen3: completing the grapevine powdery mildew pipeline

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Keywords: disease resistance, hybrid grapevine, gene identification, consumer adoption, marker assisted selection

ABSTRACT

Past VitisGen projects (VitisGen, 2012-2017, and VitisGen2, 2017-2022) generated groundbreaking technologies for the grapevine breeding community, from low-cost DNA marker platforms to advances in computer vision phenotyping. With a focus on powdery mildew resistance, VitisGen3 has leveraged these resources to complete the pipeline all the way from QTL identification to consumer adoption using a multidisciplinary approach. We will discuss progress on our

objectives including candidate gene validation, new disease resistant selections, cutting edge imaging technologies, updated production guidelines, and consumer behavior studies. Creating durable resistance is a key target of most crop breeding programs, and so we will also address our strategy for safeguarding long term genetic disease resistance through Extension and outreach efforts.

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ORAL
SESSION:
DISEASE RESISTANCE AND
PLANT-PATHOGEN INTERACTIONS



ORAL KEYNOTE

Progress toward less susceptible grapevines to vector-borne diseases

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¹ INRAE² Université de Bordeaux**Keywords:** grapevine diseases, vector-borne organisms, resistance

ABSTRACT

Grapevine diseases pose a major threat to viticulture worldwide, causing substantial yield losses and jeopardizing the long-term sustainability of vineyard systems. They are caused by a wide range of pathogens with contrasting epidemiologies. Airborne pathogens, such as many fungi, can often be managed through direct chemical control, mainly based on fungicide applications. However, this strategy depends heavily on chemical inputs and is increasingly challenged by environmental, economic, and societal constraints.

In contrast, many of the most destructive grapevine diseases are caused by vector-borne pathogens, including viruses, bacteria, and phytoplasmas, some of which are quarantine organisms, such as *Xylella fastidiosa* and the Flavescence dorée phytoplasma. In these pathosystems, disease development depends on a complex tripartite interaction between the host plant, the pathogen, and a biological vector, mainly hemipteran insects and nematodes. Unlike airborne pathogens, direct control of the pathogen itself is generally not feasible. Current management strategies therefore focus on removing infected plants to limit inoculum sources and reducing pathogen spread through vector control, most often using insecticides or nematicides. However, chemical control of vectors raises significant concerns related to resistance development, non-target effects, and increasingly stringent regulatory restrictions. As a result, the sustainable management of vector-borne grapevine diseases remains a major challenge.

An alternative and promising strategy is the development of resistant, or at least less susceptible, grapevine varieties. Nevertheless, this approach faces several limitations, including quarantine regulations that restrict experimental work and the inability to culture some agents in vitro. Moreover, breeding for resistance to vector-borne pathogens is particularly complex and time-consuming due to the involvement of multiple biological partners, difficulties in phenotyping, and the long generation time of grapevine. Resistance may target either the pathogen itself – as illustrated by recent advances in resistance to *X. fastidiosa* – or the vector, as exemplified by the Nemadex rootstock, which confers resistance to the nematode *Xiphinema index*, the vector of Grapevine fanleaf virus.

This presentation will provide an overview of current research efforts and strategies aimed at developing grapevine varieties resilient to complex, vector-borne disease threats.



ORAL

Are specific microbiota from the phyllosphere of American *Vitis* species involved to their resistance to downy mildew?

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Keywords: microbiome-mediated disease resistance, native host–pathogen interactions, wild and cultivated plants, basidiomycete yeasts

ABSTRACT

The oomycete *Plasmopara viticola* (Berk. & M.A. Curtis) Berl. & De Toni, the causal agent of grapevine downy mildew, originated in the northeastern United States and was accidentally introduced into Europe in the mid-19th century. It has since caused major economic losses in viticulture worldwide. All its invasive populations outside the US belong to the narrow clade *P. viticola* f. sp. *aestivalis*, to which cultivated grapevine (*Vitis vinifera* L.) is highly susceptible. *P. viticola* f. sp. *aestivalis* naturally parasitizes two North American wild *Vitis* species, *V. aestivalis* and *V. labrusca*, whose accessions display variable levels of susceptibility but are consistently more resistant than *V. vinifera*. These species are therefore considered the original hosts of the *P. viticola* populations that have invaded worldwide vineyards. We hypothesized that a longer coevolutionary history between these wild hosts and the pathogen has led to the evolution of resistance genes in the plant genome, but also to the establishment of a specific foliar microbiota contributing to disease resistance.

During 2023, we sampled leaves from wild populations of *V. labrusca* and *V. aestivalis* along the eastern coast of the United States as well as repository-grown plants of *V. vinifera*, *V. labrusca*, *V. aestivalis*, and their interspecific hybrids in the USA and France. Leaves collected in USA were phenotyped for downy mildew resistance in a controlled experiment, and both epiphytic and whole-leaf microbiota were characterized for fungal and bacterial communities. In total, 329 leaf samples were collected, 122 from wild populations and 207 in repositories. A continuous gradient of susceptibility to downy mildew was observed across plant genotypes and environments, ranging from complete resistance to high susceptibility. Differential abundance and TITAN analyses revealed that resistant plants harbored higher relative abundances of specific taxa within their microbiota. In particular, basidiomycete yeasts, known as biocontrol agents, were consistently associated with resistance phenotypes in plants grown under repository conditions in the United States.

Ongoing analyses aim to determine whether these microbial associations are conserved in repository-grown plants in France. Genome-wide association analyses are currently underway to identify host loci influencing microbiota composition, particularly those involved in the recruitment of microorganisms associated with downy mildew resistance.



ORAL

Deciphering the hormonal regulatory networks underlying grape berry resistance to *Botrytis cinerea*

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Keywords: *Botrytis cinerea*, phytohormones, transcriptomics, metabolomic profiling, *Vitis vinifera*, resistance

ABSTRACT

Botrytis cinerea is a major fungal pathogen affecting viticulture, causing substantial economic losses due to reduced fruit quality and subsequent yield. While the physical and chemical barriers of the grape berry are essential components of defence, the signalling mechanisms coordinating response to infection, particularly the interplay between cell wall remodelling and hormone-mediated pathways, are not yet fully understood. Here, we investigate the regulatory networks governing grape berry resistance by integrating metabolomic profiling with high-throughput transcriptomic analyses.

To characterise the hormonal fingerprint of *B. cinerea* infection, we analysed two *Vitis* genotypes displaying contrasting resistance phenotypes: the highly susceptible *V. vinifera* cultivar 'Teroldego' and the resistant interspecific hybrid 'Souvigner gris'. Using mass spectrometry-based techniques (UHPLC-MS/MS and PTR-ToF-MS), we quantified the temporal accumulation of key phytohormones and their derivatives, including salicylic acid (SA), jasmonic acid (JA), abscisic acid (ABA), and volatile organic compounds. These measurements provided a dynamic metabolic profile of the stress response, revealing marked differences in signalling dynamics between the resistant and susceptible genotypes. To further elucidate how these hormonal cues activate downstream defence mechanisms, elicitation experiments were conducted using *V. vinifera* liquid cell cultures. Identified phytohormones were applied individually, and RNA-seq analyses were performed in a time-course experimental design to capture transcriptional responses associated with each signalling pathway. This approach enabled the identification of hormone-responsive gene modules and key regulatory nodes involved in the biosynthesis of specialised metabolites and potential cell wall modifications.

By integrating quantitative hormone profiling with transcriptomic network analysis, this study aims to bridge the gap between pathogen perception and physiological resistance. The identification of core regulatory networks provides a molecular framework for future breeding strategies and supports the development of cisgenic grapevine lines with enhanced and durable resistance to *B. cinerea*.



ORAL

Decoding lipid signaling in grapevine – *Plasmopara viticola* interaction: from host membrane remodeling to oomycete-derived lipid elicitors

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Keywords: downy mildew, RPV loci, C18:3

ABSTRACT

Over the past decades, lipids and fatty acids have emerged as pivotal regulators of plant–pathogen interactions. Their functions span a broad spectrum, ranging from the formation of structural barriers to the activation of signaling pathways and immune priming. Increasing evidence also identifies specific lipid species as potential biomarkers of resistance or susceptibility to diverse pathogens. Furthermore, studies examining extracellular dynamics during plant–pathogen interactions have highlighted the role of lipids in mediating intercellular communication and contributing to the establishment of systemic acquired resistance. In the context of grapevine downy mildew, lipid signalling plays a surprisingly central role in determining the outcome of the interaction, despite the biotrophic lifestyle of *Plasmopara viticola*. We have demonstrated that jasmonic acid biosynthesis is rapidly induced during the early hours of infection in tolerant grapevine genotypes. This response is associated with enhanced membrane lipid biosynthesis, elevated levels of

C18:3, and the activation of fatty acid desaturation processes, along with increased chloroplast membrane lipid hydrolysis. Key lipid-processing enzyme gene families have also been characterized in grapevine, including phospholipases A, C, and D, as well as fatty acid desaturases and stearyl-ACP desaturases. Ultimately, we showed that the specific activation of lipid signalling pathways may be linked to the resistance locus Resistance to *Plasmopara viticola* locus 3 (RPV3), suggesting a mechanistic connection between lipid-mediated signalling and genetically determined resistance.

From the pathogen’s perspective, several lipid species accumulate during infection, playing pivotal roles in life cycle completion and pathogenicity. Moreover, we have demonstrated that selected *P. viticola*-derived lipids can prime grapevine immune responses both in pot and in field trials. The use of these lipids as elicitors represents a promising strategy to address disease management through more sustainable, non-chemical approaches.

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ORAL

Multi-dimensional characterization of grape berry cuticles and their usability for an improved breeding of *Botrytis* bunch rot resilience

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Keywords: phenomics, epicuticular wax, physical barriers, biotic resistance, metabolomic analysis

ABSTRACT

For one of the major fungal diseases in cool-climate viticulture, *Botrytis* bunch rot (BBR), management practices as well as plant protection possibilities reach their limits. In contrast to downy and powdery mildew or black rot, no active defense mechanisms by major R-genes are available conferring resistance towards BBR. However, the cuticle and its epicuticular waxes proved to be one of the most powerful physical barriers increasing BBR resistance. Therefore, berry impedance (BI) was previously identified as a sensor-based indicator for high-throughput and reliable phenotyping of cuticle and berry surface characteristics. Aiming at the development of molecular markers for BBR-associated traits, a fine mapping approach was done based on the F1 progeny of 'Dakapo' x 'Cabernet-Sauvignon' (DxC) using 364 genotypes, 348 SSR marker mapped on 19 linked groups (LG) and three-years of phenotypic data. This resulted in QTLs on the chromosomes 6, 11, 15 and 17 with narrowed confidence intervals. The data further indicated that the presence of QTLs for BI seems to have an additive effect, i.e., genotypes with combinations of several QTLs show much higher berry impedance values.

However, as BI is naturally affected by the thickness and permeability of the cuticle as well as the hydrophobicity of epicuticular waxes, berry surfaces of varieties differing in BBR susceptibility and BI were investigated regarding the microscopic structure of epicuticular waxes and corresponding metabolomic profile. On the basis of Cryo Scanning Electron Microscopy in two consecutive seasons, five different epicuticular wax classes (EWC) could be identified. The EWC of different varieties is hereby correlated to BI ($r = 0.65$) and is comparable between years. In addition, the chemical composition of berry cuticles from the same varieties were analyzed by high-resolution mass spectrometry. By this, one specific compound was for instance detected in Calardis Blanc, a white variety with high BI values and BBR resilience. In addition, genotypes (F1 progeny of DxC) with very high and very low impedance values were selected for further metabolomic analysis of the berry cuticle, aiming

to identify molecular markers linked to crucial chemical compounds. All of these findings will contribute to a better understanding of BBR resilience and allow the integration of measurable parameters into the breeding process to enhance the natural protection of grapevines against BBR.



ORAL

Uncovering novel epigenetic traits in grapevine resistance against downy and powdery mildew – A multi-omics approach

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Keywords: grapevine, immunity, DNAmethylation, small RNA, transcriptome

ABSTRACT

As one of the most important crop plants in the world, securing grapevine yields and production quality is a top priority. This, however, needs to be reconciled with a move towards greater sustainability, which may prove to be an issue due to the extensive use of phytopharmaceuticals in viticulture to fend off against common diseases¹. Epigenetics may prove to be extremely useful in the search of the immunity mechanisms of grapevine, due to the prolific and ubiquitous roles. From being one of the key players in orchestrating transcriptional reprogramming to possibly being implicated in immune memory, it is a currently understudied component of grapevine immune responses with tremendous potential². While studying the epigenome can be elucidative, integrating it with other omics, namely transcriptomics and small RNA (sRNA)-seq only serves to strengthen analysis and future discovery of molecular resistance traits³. This is the mission of the Horizon2020 SHIELD4GRAPE project, starting with multi-omics analysis of grapevine responses and culminating with the development

of integrated pest management strategies, promoting viticulture sustainability.

In this work, we performed an infection assay with *Plasmopara viticola* and *Erysiphe necator*, causal agents of downy and powdery mildew, using seven minority cultivars from Portugal, Spain, Italy, and Greece, and ‘Chardonnay’ as a susceptible control. We then perform whole-genome bisulfite sequencing, RNA-seq and sRNA-seq, and perform multi-omics integration. By comparing the responses of the tolerant genotypes to infection against ‘Chardonnay’, we uncovered epigenetically-regulated genes, DNAmethylation-sRNAcrossstalk and microRNA(miRNA)-mediated gene silencing. From this Big Data approach, we can elect new resistance marks linked to DNAmethylation or small RNAs, as well as elucidate fundamental mechanisms of epigenetic regulation in this valuable crop plant. Future work is being developed to integrate proteomics and metabolomics data, other scopes of analysis within SHIELD4GRAPE, and capture the complete picture of grapevine immune responses.

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reflect those of the European Union. Neither the European Union nor the granting authority can be held responsible for them. JPP was supported by a FCT PhD Studentship (reference 2024.00649.BD).

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ORAL
SESSION:
CLIMATE CHANGE AND
ABIOTIC STRESS TOLERANCE



ORAL KEYNOTE

The role of genetics in adapting grapevine production to environmental challenges

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ABSTRACT

The wine producing sector currently faces major challenges, particularly adapting to climate change and transitioning toward agroecological practices - notably reducing the use of plant protection products and synthetic fertilizers. The choice of plant material (grapevine varieties, clones, and rootstocks) is a key lever to address these challenges. While breeding programs have successfully produced varieties resistant to downy and powdery mildew, selecting genotypes tolerant to abiotic stresses has proved to be far more difficult. Difficulties include defining the target traits that determine tolerance to abiotic stresses, choosing and applying relevant abiotic stress scenarios, and using the timescales necessary to assess tolerance in a perennial crop species. For example, maintaining yield is a complex trait that requires long-term monitoring, always directly in the vineyard.

Abiotic stresses relevant to viticulture include water deficit, high and extreme temperatures, and soil salinity (often caused by intensive irrigation in dry climates). Although the genetic contribution to the variability of grapevine responses to these stresses has been demonstrated, the underlying genetic architecture remains poorly understood and is often complex, potentially involving additional mechanisms, including epigenetic regulations. In rootstock breeding programs, these results are not yet consolidated between different genetic backgrounds, and the underlying physiological mechanisms remain poorly characterized.

Research in this field faces significant challenges. The wide range of stress scenarios (applied at different developmental stages, intensities, and durations) leads to a large variability in results. Furthermore, rootstock $\times$ scion $\times$ environment interactions add layers of complexity to interpreting results. Beyond studying individual stress factors, multi-stress studies (both in controlled conditions and in the field) are essential and need to be developed. Ultimately, it is crucial to consider the combined genotype of the scion/rootstock chimera under stress conditions that are likely to be experienced in the future.



ORAL

Chloroplast-related pathways involved in grapevine drought responses

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Keywords: grapevine, drought stress, RNA-seq, chloroplasts

ABSTRACT

Water scarcity is an increasing constraint for viticulture in Mediterranean regions, making the identification of molecular mechanisms underlying drought tolerance a key objective for grapevine breeding and management. While transcriptomic studies have revealed strong cultivar-dependent responses, the regulatory networks supporting these differences remain poorly characterized.

This study investigated drought-responsive transcriptional regulation in six Portuguese *Vitis vinifera* L. cultivars grown under field conditions and subjected to contrasting irrigation regimes (irrigated vs. rainfed). At the end of the ripening period, leaf samples were collected from three biological replicates per cultivar and irrigation regime. Total RNA was sequenced using paired-end Illumina sequencing. RNA-seq data was analyzed using a combination of cultivar-specific differential expression analysis and weighted gene co-expression network analysis (WGCNA) performed across all cultivars.

The gene co-expression module most strongly correlated with the rainfed condition was predominantly composed of genes encoding proteins localized to chloroplasts and thylakoids, although not directly enriched in photosynthesis-related biological processes. Guided by this pattern, cultivar-specific responses were explored to assess how chloroplast-associated responses were manifested at the cultivar level.

Pronounced cultivar-dependent differences were observed in the regulation of chloroplast-related genes under water deficit. Cultivars exhibiting broader transcriptional responses showed a markedly higher proportion of up-regulated genes associated with chloroplasts and thylakoids. Photosynthesis-related biological processes were exclusively detected among up-regulated genes in four of the six cultivars, with no photosynthesis-associated down-regulation. These included core components of photosystem II and photosystem I, light-harvesting complexes, electron transport and NDH complex elements. Consistent with the WGCNA module, additional up-regulated genes were involved in thylakoid architecture and photosystem assembly, chloroplast gene expression and protein synthesis, protein folding and quality control mechanisms, redox regulation and oxidative stress control.

These findings support a conceptual framework in which chloroplasts act not only as sites of photosynthesis but as metabolic centers that integrate environmental signals and coordinate cellular responses to water stress through adjustments in photosynthetic capacity, structural organization, protein homeostasis, and antioxidant defenses. The identification of both conserved chloroplast-centered responses and cultivar-specific regulatory patterns provides valuable insights for grapevine breeding strategies aimed at improving drought tolerance in Mediterranean viticulture.

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ORAL

CRISPR/Cas9-induced trehalase knockout for drought resistance in grapevine

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ABSTRACT

Climate change is predicted to alter the water availability where grapevine is cultivated, potentially impacting grape yield and quality [1]. Conventional grapevine breeding requires long periods of time and may alter a cultivar's distinctive characteristics [2]. These factors make CRISPR/Cas9 molecular breeding techniques an attractive tool in limiting the effects of drought [3]. Trehalose is a well-known osmoprotectant sugar, with known functions in reducing reactive oxygen species levels (ROS), preserving membrane stability and accumulating of starch and other soluble sugars in leaves of plants under drought stress [4]. Exogenous application of trehalose has been shown to improve abiotic stress tolerance in many plants, including grapevine, thus increasing its content endogenously should enhance grapevine productivity in water-limited environments [5]. Woody plants generally biosynthesize small quantities of trehalose, which is later degraded by the trehalase enzyme. By utilising CRISPR/Cas9 to induce a knockout mutation, trehalase activity can be inactivated, thus allowing the accumulation of

trehalose [6]. Agrobacterium-mediated transformation was used to transform Chardonnay embryogenic callus with a CRISPR construct containing sgRNAs targeting the trehalase gene.

Lines of grapevine were regenerated and confirmed, with next generation sequencing, containing complete knockout edits of trehalase. Gas chromatography-mass spectroscopy (GCMS) analysis performed on leaf tissue of the edited and control plants, showed an accumulation of trehalose and other soluble sugars in the edited lines. A population of the control and edited lines have been hardened off and will undergo more comprehensive phenotyping to evaluate growth and morphology, as well as water stress under greenhouse conditions. To confirm that the edited grapevine lines are less susceptible to water stress, physiological water-related parameters will be monitored throughout the trial, and biochemical tests and RT-qPCR analysis of drought and sugar-metabolism related genes are to be performed on leaves of the plants under water stress conditions.

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ORAL

Evidence of trans-annual epigenetic memories of stresses in grapevine

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Keywords: DNAmethylation, biotic stress, abiotic stress, perennial plants

ABSTRACT

Epigenetics refers to the layer of genetic information carried in chromatin beyond the DNasequence, including histone modifications, DNAmethylation and small RNAs. Studies in Arabidopsis, tomato and other plants have shown the influence of epigenetic mechanisms on development, agronomic traits, genome stability, and plant responses to stresses, including their memory. However, most studies have focused on annual plants, while epigenetic research in perennials remains limited. As a woody perennial, clonally propagated and commonly grafted, grapevine offers unique features that make it an attractive model for epigenetic investigations.

Here, we examine the complex response of grapevine to both biotic and abiotic stresses. We demonstrate that Esca-symptomatic plants, that display sectors with leaf symptoms alongside sectors without symptoms, present change in leaf metabolite content and gene expression profiles strictly associated with symptom development. In contrast, DNA methylation patterns are altered in leaves from both

symptomatic and asymptomatic sectors compared to plants showing no disease symptoms. Some DNAmethylation changes conserved between sectors of symptomatic plants are also detected in young leaves before any visible symptom, suggesting a trans-annual memory of esca in grapevine.

We also investigate the long term consequences of drought and heat stress on clones derived from a single mother plants. Clones were grown during 4 years in contrasted environments, and were then transferred in the same growing conditions. Results indicate that the clone methylomes are clearly different after 4 years in contrasting growing conditions. In addition, some of these differences are maintained when plants are subsequently grown in the same conditions.

These data support the idea that perennials maintain a trans-annual epigenetic memory of their environment, a process likely essential for their long term adaptation to environmental challenges.

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ORAL

Root system architecture plasticity in *Vitis* plants under progressive soil drying

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Keywords: grapevine, rootstock breeding, root system architecture, drought tolerance

ABSTRACT

Prolonged water deficits driven by climate change are increasingly affecting the viticultural sector highlighting the need for drought-tolerant rootstocks. Rootstocks contribute to grapevine responses to water stress throughout the entire lifespan of the vineyard and represent a sustainable strategy to enhance cultivar adaptation while reducing reliance on additional agronomic practices. However, the availability of drought-tolerant rootstocks is limited, as only a few genotypes are widely used, and their genetic base is narrow. Exploiting the genetic variability within the genus *Vitis* could enable the selection of new drought-tolerant rootstocks. As the below-ground part of the plant, rootstocks and their root system architecture (RSA) play a central role in soil water foraging and regulating plant responses under water deficit. In particular, RSA plasticity to water-limiting conditions is considered a key trait for drought-adaptation. This study aimed to investigate the RSA of a large set of *Vitis* genotypes under progressive soil drying through a smartphone-based phenotyping approach. Plants were grown in rhizotrons under controlled conditions and water use and physiological responses at both aerial and root levels were monitored throughout the soil-drying cycle. Four groups exhibiting contrasting physiological responses to soil drying and distinct RSA patterns were identified. Number of lateral roots emerged as the most influential trait in group differentiation indicating its importance in RSA plasticity under decreasing soil water availability. Among the identified groups, Group 1 exhibited the most promising behaviour for drought prone environments combining reduced water consumption through tight stomatal regulation, with sustained growth under water deficit, and a well-developed root system. The adopted smartphone-based image acquisition system proved suitable for high-throughput phenotyping, allowing rapid and reliable root traits determination. These findings reinforce the central role of RSA plasticity in grapevine adaptation to soil drying and support future rootstocks breeding programmes that exploit the largely unexplored genetic variability within *Vitis*.



ORAL

VvRefPanel field trial reveals new genetic determinants for abiotic stress tolerance in *Vitis vinifera*

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Keywords: GWAS, QTL, genotype x environment interaction, phenology, leaf ecophysiology

ABSTRACT

Despite the urgent need for boosting grapevine breeding to face the threat of climate change, the genetic determinism of key traits related to phenology and leaf physiology have yet to be explored in a large diversity panel in the field. To fill this gap, we established near Narbonne (South of France) a representative panel of > 250 *V. vinifera* varieties, the VvRefPanel, in four randomized complete blocks. We measured budburst, flowering and veraison dates, as well as traits related to carbon gain and water loss at the leaf level, including morphological and ecophysiological traits. We performed GWAS with resequencing data and millions of

markers. We found several new phenology QTLs, most with limited individual effects.

For leaf traits, the QTLs detected in the field experiment differed from those previously found in a greenhouse experiment involving the same panel. However, multi-environment GWAS revealed shared QTLs with similar or opposite effects across experiments. These results emphasize the potential of this large diversity field trial, but also of joint analysis in several environments, to decipher the genetic architecture of key traits useful for breeding better adapted grapevine varieties.

ACKNOWLEDGEMENTS

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**ORAL
SESSION:
PHENOTYPING**



ORAL KEYNOTE

Supporting grapevine breeding and research through sensor-based phenotyping applications

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ABSTRACT

Phenotyping refers to the description of phenotypes and can range from morphological characteristics to plant compounds. It plays a central role in both grapevine breeding and grapevine research, as it represents the only direct access to the expression of genetic traits under real environmental conditions. Only with precise and reproducible phenotype data genetic effects can be identified and genotypes can be reliably compared and selected. It thus forms the basis for marker development, breeding progress, and thus the transfer of genetic knowledge into practice. Against the backdrop of climate change, objective, high-resolution phenotyping is becoming increasingly important.

Traditional methods, especially for phenology and morphological characteristics, are often based on manual recording and classification using pre-defined scales (*e.g.*, OIV, BBCH). These methods are cost-effective and easy to implement but predominantly time-intensive, subjective, and therefore restricted for a small amount of plant material. In addition, many phenotypic studies using manual methods or wet chemistry analysis, such as for the extraction of plant metabolites, are also destructive. Sensor-based automatic phenotyping enables fast, objective detection of traits and can increase sample throughput and thus efficiency.

Sensor-based phenotyping can be carried out on various scales, from individual plant organs or even individual cells to individual vines or even entire vineyards. In the area of breeding and breeding research, we usually range from the laboratory scale under controlled, standardized conditions to the field scale, including handheld sensors, ground-based, or airborne platforms.

This keynote presentation will highlight traits and topics that can be supported by sensor applications, the components and required setup steps of such pipelines, and successful solutions.

One example of such an application in grapevine breeding is the support of breeders by data provided by a field phenotyping platform with a multispectral camera system. This high-throughput-platform can support the pre-selection of breeding material at an early breeding stage. In the field of breeding research, digital tools can help evaluate plant material for the development of QTLs, for example, the

classification of resistance levels on leaf discs using imaging techniques.

Sensor applications will broaden our options in grapevine breeding beyond individual characteristics to complex relationships between genetics, environment, and management. It is crucial that sensor technology is not seen as an end in itself, but as a tool that opens up new perspectives for grapevine breeding when used consciously, critically, and in dialogue with viticulturists.



ORAL

A morphological approach for the early selection of grapevine rootstocks tolerant to water stress

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Keywords: grapevine rootstocks, drought tolerance, morphological markers, rootstock breeding, genotype classification

ABSTRACT

Over the past two decades, grapevine rootstock breeding programs have increasingly favored genotypes with a tendency toward anisohydric behavior, which are better adapted to hot and arid conditions. However, drought tolerance is a complex trait that is difficult to evaluate during the early stages of selection. In this context, the present study investigates whether specific morphological traits can predict hydraulic behavior in *Vitis* spp., thereby supporting the identification of new parental genotypes.

Nine rootstocks from the University of Milan collection (four anisohydric and five isohydric) were analyzed by evaluating ten anatomical traits potentially associated with drought response, including leaf absorbance spectrum, shoot xylem area, leaf surface hydrophobicity, and stomatal density. Traits were examined individually through analysis of variance

(ANOVA) and jointly through multivariate discriminant analysis.

ANOVA identified four traits that differed significantly between the two physiological classes: mean shoot xylem lumen area, petiole diameter, leaf area, and areole size. These parameters allowed the construction of a significant discriminant function, achieving an accuracy of 83% in correctly classifying genotypes as isohydric or anisohydric.

The resulting model enables the rapid discrimination of genotype hydraulic behavior using a limited set of easily measurable morphological traits. It is currently being validated on an independent collection of American progenies not yet characterized for their response to water stress. This approach represents a relevant advancement for the selection of resilient rootstocks and for the development of more efficient breeding programs.

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ORAL

Early-stage phenomic prediction in grapevine (*Vitis* spp.) using near-infrared (NIR) reflectance spectra

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ABSTRACT

Recent advances in high-throughput phenotyping, particularly near-infrared (NIR) spectroscopy, have prompted interest in phenomic selection as a powerful tool for breeding. NIR spectra capture tissue- and family-specific biochemical signatures and have been used to predict agriculturally relevant traits such as yield or fruit quality in a range of crop species. To explore the use of phenomic selection models for early-stage selection in grapevine, seeds and seedlings of 1,618 individuals from six families were evaluated using hyperspectral reflectance data. For seedlings, spectral signatures were collected under two irrigation treatments (well-watered and water-stressed) in the greenhouse.

Reflectance spectra were used to assess within- and among-population variation and to develop predictive models for early life-stage traits including germination success, germination rate, seedling morphology (above- and below ground-biomass, plant height, leaf number, and root-to-shoot ratio), and developmental shift (indicated by the first tendril). Using phenomic prediction models from seeds and seedlings, with five-fold cross-validation, we observed moderate to high ($r = 0.3 - 0.8$) predictive abilities in germination success, all morphological traits, and first tendril development (seed spectra only) across both irrigation treatments. Together, these results demonstrate that NIR reflectance data collected at the earliest stages of development can be used to predict seedling traits in grapevine. This work provides a proof of concept for phenomic prediction in grapevine seedlings and highlights the potential of low-cost, high-throughput spectral data to supplement genomic selection and accelerate decision-making in grapevine breeding programs.



ORAL

High-throughput cnn-based phenotyping of grape berry heat stress as an objective indicator of sunburn sensitivity

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Keywords: *Vitis vinifera*, grape sunburn phenotyping, environment-independent test system, machine learning, artificial intelligence

ABSTRACT

Ongoing climate change poses increasing challenges for viticulture, as higher temperatures, more frequent heat extremes, and intensified ultraviolet (UV) radiation expose grapevines to severe abiotic stress conditions. One critical consequence of these conditions is grape berry sunburn, an abiotic disorder resulting from complex interactions between environmental stressors and plant physiological responses. Sunburn leads to substantial yield losses and reduced berry quality, thereby compromising the economic sustainability of grape production. Reliable phenotyping approaches are therefore essential to objectively evaluate varieties for their risk of developing grape sunburn, enabling meaningful comparisons across genotypes and environments. However, the appearance of natural sunburn symptoms in the field is strongly influenced by environmental variability. To overcome this limitation, we established a controlled laboratory-based heat stress (HS)-treatment of young berries that induces varying degrees of brown lesions. The proportion of lesion area depends on the genotype and is correlated to the sensitivity to grape sunburn in the field. This method was further optimized through the development of a fully automated phenotyping pipeline to enable objective and high-throughput lesion quantification. The pipeline comprises automated acquisition of up to 1,800 high-resolution berry images per hour, followed by automated image analysis using convolutional neural networks (CNNs). Accordingly, a modified DenseNet architecture was trained using image patches extracted from 25 representative single-berry images selected to cover the full sunburn severity range (five images per severity class from low to high). The CNN classified image patches into 'background', 'lesion', and 'non-lesion' categories and achieved an overall classification accuracy of 97.41%. Model performance was evaluated in two independent validation steps: (i) analysis of an additional set of 25 berry images acquired in a different season, and (ii) analysis of berry images from 50 genetically diverse *Vitis vinifera* cultivars (one image per cultivar). Highly significant correlations (above, $r > 0.94$) were observed between CNN-based predictions and independent assessments by three expert evaluators across both validation datasets. Furthermore, CNN-based results revealed clear differences in

HS sensitivity among varieties, indicating which genotypes are likely to exhibit a higher risk of grape sunburn under field conditions. Overall, the presented methodological framework provides a robust, objective, and scalable solution for grape sunburn phenotyping and generates high quality phenotypic datasets suitable for improved variety characterization, linkage-based QTL mapping, genome-wide association studies, and the training of genomic prediction models.



ORAL

Which potential for Near Infrared Spectroscopy-based phenomic selection of grapevine rootstocks?

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Keywords: NIRS, phenomic prediction, rootstock, scion/rootstock interaction

ABSTRACT

Developing rootstocks adapted to environmental constraints constitutes a key lever for grapevine adaptation to climate change. In this context, Near Infrared Spectroscopy (NIRS) could be used as a high-throughput phenotyping technique to simplify the selection of rootstocks and predict their performance in grafted situations. This study is an exploratory analysis that aimed at evaluating the potential of NIRS spectra acquired ex- and in-situ in different tissues and stages of the vegetative cycle on ungrafted and grafted plants to reveal rootstock effects and their plasticity in response to scion/rootstock combination of to better characterize these interactions, and to predict phenotypes of grafted plants from data acquired on ungrafted material.

Through the study of 25 combinations (5 scions × 5 rootstocks), performed in 2023 in a dedicated experimental vineyard, we showed that NIRS obtained from ex-situ and in-situ measurements on scion tissues of grafted captured some rootstock and scion/rootstock interaction signals (up to 20% of the total variance at specific wavelengths). Yet, the scion effect on the spectra remains dominant over the rootstock effect,

which is also the case for agronomic traits measured in the same experimental vineyard. Using NIRS data collected ex-situ on dried leaves, spectral wavelengths specific to the rootstock effect could be identified.

Predictions at the plant level were carried out on twenty-eight phenotypic traits recorded over several seasons (2019-2022), showed variable predictive abilities (0.2 to 0.8) between traits, those related to all phenological stages recorded in 2023 and pruning weight in 2021 and 2022, being the best predicted. For NIRS data collected on dried leaves, three spectral regions were consistently identified as contributing to predictions and to differences between scion/rootstock combinations. No significant difference was detected in the prediction ability between the whole spectrum and these specific regions for their predictive ability. Considering these promising findings, NIRS data have been collected similarly on leaves of a non-grafted and grafted progeny (as rootstocks). Their predictive ability will be tested, and preliminary results will be presented during the conference.

ORAL
SESSION:
FRUIT DEVELOPMENT, GRAPE
AND WINE COMPOSITION



ORAL

Oenological identity and technological challenges of PIWI varieties

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¹ University of Zagreb, Faculty of Agriculture**Keywords:** PIWI varieties, wine production, sensory profile

ABSTRACT

Disease-resistant grapevine varieties (PIWI) represent one of the most relevant achievements of contemporary grapevine breeding, developed in response to increasing environmental pressures, climate change, and the need to reduce pesticide inputs in viticulture. Created through interspecific crosses between *Vitis vinifera* and other *Vitis* species carrying multiple resistance loci, these cultivars incorporate genetic traits that enhance tolerance not only to downy mildew (*Plasmopara viticola*) and powdery mildew (*Erysiphe necator*) but also contribute to improved resilience against additional fungal pathogens, certain pests, and emerging abiotic stresses linked to climate change. While their agronomic and ecological benefits are well established, their oenological identity and technological performance leave many scientific and practical questions open, with many aspects still insufficiently understood requiring further research.

The oenological identity of PIWI varieties is shaped by their unique and genotype-dependent metabolic composition. Differences in sugar accumulation dynamics, total acidity, pH values, and nitrogen content directly influence fermentation kinetics and wine overall expression. Their phenolic profiles often diverge from traditional *V. vinifera* cultivars, particularly in terms of tannin structure, anthocyanin composition as well as extractability. Certain genotypes exhibit elevated concentrations of specific aroma precursors, including volatile thiols and terpenes, while the main problem of the first generations of PIWI varieties was related to the higher concentration of methyl anthranilate associated with “hybrid” sensory notes has been successfully overcome. These well-defined characteristics call for carefully tailored vinification strategies to fully express their potential and achieve balanced organoleptic harmony.

Technological challenges arise during harvest timing, maceration and fermentation management, oxygen control and defined wine style. In red PIWI varieties, optimizing phenol maturity and ensuring color stability demand precise extraction protocols and balanced micro-oxygenation. In white cultivars, reductive vinification techniques are often essential to preserve primary aromas and prevent the development of atypical notes. The interaction between genotypes, terroir, and climate further influences metabolic

expression, making site-specific approaches crucial for quality optimization.

Beyond technical considerations, issues of typicity and consumer perception remain decisive. So, consumers must be reassured that wines made from PIWI varieties can match the sensory quality of international wines, while offering the added advantage of more sustainable production. This, in turn, can stimulate market demand for wines produced from disease-resistant cultivars. However, given that wine consumers are generally conservative in their purchasing decisions, substantial communication and educational efforts are essential to break through this resistance and encourage greater acceptance and interest in these emerging disease-resistant varieties. Luckily, recent research and commercial experience demonstrate that, when supported by appropriate oenological practices, PIWI varieties can produce wines of high quality, structural balance, and distinctive character.



ORAL

Enhancing fruit quality of cold-hardy interspecific table grapes through gibberellic acid applications

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Keywords: gibberellic acid, berry size, interspecific, cold-climate

ABSTRACT

The University of Minnesota has been breeding interspecific grapes for cold-climate production over the past 125 years. Recent efforts in table grape breeding have resulted in three new cold-hardy table grape cultivars that exhibit excellent fruit quality characteristics, such as seedlessness, flavor, and texture. However, their berry size is relatively small compared to commercial table grapes. Gibberellic acid (GA) is a plant growth regulator that can enhance fruit quality, such as increasing berry size and berry firmness. GAs typically applied pre- and/or post-bloom, and its efficacy varies based on dosage, timing, and cultivar. While extensively tested on *Vitis vinifera* cultivars, GA has never been evaluated on interspecific grapes. Our aim was to evaluate the effects of GA treatment in the vineyard on fruit quality of three new cultivars and three commercial cultivars. Clusters were treated at flowering and berry set (5mm) with 0, 25, or 50 ppm GA in two growing seasons. Results showed that all six cultivars exhibited significantly larger berry diameter and weight at 50 ppm. A similar trend was observed at 25 ppm, but statistical significance varied by cultivar and season. GA treatment generally reduced berry count per cluster, but cluster weight remained unchanged. These results demonstrate that GA application is an effective strategy to enhance berry size in cold-hardy interspecific table grapes.



ORAL

Evaluation of fermentation kinetics and wine quality parameters of distinctive Florida muscadine wines fermented with autochthonous yeast strains

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Keywords: muscadine grape, native yeast, fermentation, microbial diversity, wine quality

ABSTRACT

Commercial *Saccharomyces cerevisiae* starter cultures dominate modern wine fermentation; however, reliance on genetically uniform strains may limit expression of regional characteristics, particularly in non-*Vitis vinifera* species such as the native American muscadine grape (*Muscadinia rotundifolia*). As Florida's wine industry expands, characterization of endemic microbial resources represents an opportunity to enhance fermentation performance and regional wine identity.

This study established a repository of native yeast populations associated with Florida muscadine grapes and evaluated their fermentative potential for enological application. Spontaneous fermentations were conducted using juice from the cultivars 'Floriana,' 'Noble,' and 'Carlos,' enabling isolation of indigenous yeast communities throughout fermentation.

Molecular identification recovered more than 250 yeast accessions representing five genera, including *Pichia*, *Saccharomyces*, *Starmerella*, *Hanseniaspora*, and *Nakaseomyces*.

Representative isolates were assessed in controlled fermentations of muscadine juice and compared with a commercial *S. cerevisiae* strain using a composite fermentation quality index integrating ethanol production, residual sugar utilization, glycerol formation, and volatile acidity. Native *Saccharomyces* species demonstrated efficient sugar depletion and favorable metabolite profiles, while select non-*Saccharomyces* isolates exhibited elevated glycerol production and moderated volatile acidity while maintaining desirable fermentation kinetics.

These findings confirm the presence of diverse autochthonous yeast communities adapted to Florida vineyard environments and identify promising candidates for tailored fermentation strategies. Development of a curated culture collection integrating genotypic and phenotypic characterization provides a foundation for mixed-culture fermentations and technology transfer supporting innovation and product differentiation in emerging warm-climate wine regions.

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ORAL

Integrated genetic and functional analyses reveal PEPC and cMDH as antagonistic regulators of grape acidity

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Keywords: berry acidity, functional genomics, cell culture, genome editing, climate-resilience

ABSTRACT

Breeding grape cultivars with optimized acidity is a priority for climate resilience, yet identifying causal regulators of malate metabolism remains challenging due to the complexity and long generation time of whole-vine functional studies. Multiple molecular and genetic studies, including QTL mapping, have highlighted the cytosolic malate dehydrogenase (cMDH) and phosphoenolpyruvate carboxylase/carboxykinase (PEPC/PEPCK) pathways as primary candidates for malate regulation. To dissect their specific roles, we integrated comparative transcriptomics with rapid functional characterization.

Compared to *V. vinifera* cultivars, high-malate wild species (*V. riparia*, *V. cinerea*) exhibited a distinct expression signature during ripening, characterized by elevated PEPC and reduced cMDH expression. To translate these findings to causal evidence, we utilized grape-derived cell cultures as a rapid reverse-genetics platform. Wild-type cultures reproduced the sugar-malate dynamics and coordinated expression of malate metabolic and transport genes characteristic of pre-veraison berries, supporting their suitability for functional studies of malate regulation.

Stable overexpression (OE) lines exhibited clear and opposing effects. PEPC OE increased malate accumulation by 47–50 % and enhanced biomass, while inducing PEPCK expression, linking these enzymes as highlighted by transcriptomic (PEPC) and QTL (PEPCK) analyses. Metabolite profiling revealed shifts in organic acids and amino acids, consistent with enhanced carbon flux into malate biosynthesis. In contrast, cMDH OE reduced malate levels by 25–30 % and increased sugars, mirroring the metabolic shift characteristic of berry ripening.

PEPC and cMDH emerge as antagonistic “push–pull” regulators of the malate-sugar balance and as promising targets for modulating fruit acidity under climate change. Gene-function validation remains a major bottleneck in grape genetics, particularly in the era of genome editing. Our results demonstrate that grape-derived cell cultures provide a rapid, valuable strategy for establishing gene-trait relationships and prioritizing editing targets prior to whole-vine transformation.

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ORAL CANCEL

SHORT COMMUNICATION
SESSION:
GENETIC RESOURCES



SHORT COMMUNICATION

Genetic insights into Georgian grapevine germplasm

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Keywords: genotyping, grapevine diversity, simple sequence repeat (SSR), single nucleotide polymorphism (SNP), South Caucasus

ABSTRACT

The South Caucasus is widely recognized as a primary center of grapevine domestication (*Vitis vinifera* L.). Genetic studies highlight the singularity and uniqueness of the Georgian grapevine genetic pool, characterized by varieties exhibiting exceptional phenotypic diversity across important traits related to crop yield, grape quality, and resistance to a range of biotic and abiotic factors. Recognizing their significance, we have characterized the genetic resources preserved at the National Grapevine Collection of the SRCA at Jighaura (GEO 038), the largest grapevine collection in Georgia. The systematic genetic profiling of 782 accessions of putative Georgian origin at 13 SSR and 240 SNP loci differentiated 319 unique genetic profiles, with 162 preserved twice or more in the Collection, some as misnamed accessions or under local synonyms. Among the 319 differentiated genotypes, 160 were found to match the grapevine genetic profiles stored in international databases, most of them of alleged varieties of Caucasian origin. This is the case of the Georgian varieties ‘Chinuri’, ‘Argvetula Sapere’, and ‘Tkupkvirta’, which were the most frequently identified genotypes in the Collection, in 19, 14 and 13 accessions, respectively. On the other hand,

159 of the genetic profiles differentiated in this study were not found in the bibliography, so they could be useful for the identification and management of these putative local varieties.

The integration of genetic and phenotypic data revealed some somatic variants, further contributing to intra-varietal diversity and offering potential for varietal innovation. Additional genetic analyses confirmed the clear differentiation of Georgian germplasm from European varieties previously reported, and revealed a major subdivision of local varieties into two genetic groups, likely reflecting contrasting environmental and orographic conditions between western and eastern Georgia. The study of parentage relationships revealed a large number of first-order kinship relationships, some of them not previously reported. Altogether, this work provides a significant contribution to the current knowledge of the Georgian germplasm. This information is useful to address questions regarding grapevine domestication and diversification processes, and its singularity can be harnessed to enhance both oenological and key agronomic traits, essential to face current viticultural challenges.

ACKNOWLEDGEMENTS

This work was supported by project GCP/GEO//EC “FAO support to Georgian agricultural sector under ENPARD III”. JT acknowledges funding from the Ramón y Cajal Programme (RYC2022-037758-I), supported by MCIU/AEI/10.13039/501100011033 and the European Social Fund Plus (ESF+).



SHORT COMMUNICATION

Genetic insights into recently discovered indigenous grapes from historical Armenian vineyards: implications for conservation and breeding

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Keywords: grapevine, genetic diversity, Armenia

ABSTRACT

Grapevine (*Vitis vinifera* L.) is one of the most ancient and culturally significant plant species, domesticated over 11,000 years ago. Throughout history, grapevines have played a fundamental role in shaping agricultural traditions, economies, and cultural practices worldwide. Armenia is recognized as one of the earliest centers of grapevine domestication, where viticulture has thrived uninterrupted for millennia. This rich and continuous viticultural legacy has contributed to developing an exceptionally diverse grapevine gene pool, shaped by natural selection, human cultivation, and complex ecological interactions.

Over the past decade, extensive nationwide prospections have been conducted to recover, document, and characterize minor indigenous grapevine germplasm across Armenia's traditional viticultural regions, including Ararat, Aragatsotn, Vayots Dzor, Tavush and Syunik. Inventoried vineyards were distributed across an exceptionally broad altitudinal gradient, ranging from approximately 420 m above sea level in Tavush Province to elevations exceeding 1,800-2,000 m in Vayots Dzor Province. The surveys were carried out during both the vegetative and harvest periods, with a primary focus on historical vineyards established in the early 20th century or earlier, many of which had remained abandoned or minimally managed for prolonged periods.

These integrated investigations led to the establishment of a rigorously validated, true-to-type inventory of Armenian grapevine germplasm, encompassing more than 3,300 genotyped accessions. Currently, 400 genetically distinct Armenian varieties are officially documented in the Vitis International Variety Catalogue (VIVC), while a further 50 accessions are undergoing final validation prior to registration. Despite significant progress, over 230 accessions forming the core of the present investigation remained unassigned, primarily due to the absence of corresponding SSR profiles in reference databases and the lack of documented historical varietal denominations. To address these gaps, continued bibliographic research and enhanced collaboration with international germplasm collections preserving Armenian grapevine diversity is in progress.

The combined application of molecular fingerprinting by 24 microsatellites and classical ampelographic assessment proved highly effective for the identification and validation of accessions recovered from historical vineyards and home gardens. This integrative approach enabled the resolution of numerous cases involving synonyms, homonyms and misnomers. The establishment of well-documented grapevine genetic resources with confirmed identity and controlled phytosanitary status represents a fundamental prerequisite for their sustainable utilization and long-term conservation within germplasm repositories.

ACKNOWLEDGEMENTS

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SHORT COMMUNICATION

Sativa introgression in Croatian wild grapevine

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ABSTRACT

The wild grapevine, *Vitis vinifera* L. subsp. *sylvestris* (Gmelin, Hegi), is spontaneous to Europe and has gained increasing scientific attention in recent years due to its rapidly declining populations and its valuable, yet largely unexplored, genetic pool. Over the past few years, considerable efforts have focused on the characterization and evaluation of natural populations, revealing crop-to-wild gene flow from *V. vinifera* subsp. *sativa*. In recently published studies, Croatian *sylvestris* populations have been extensively characterized using SNP markers. Marinov *et al.* (2024) reported the presence of a domestication-related *sativa* haplotype associated with white berry colour among 41 individuals from four analysed populations, occurring at a frequency of 21%. In this study, we show relations between white berry haplotype, dioecious flower phenotypes and *sativa* ancestry estimates reported by Dong *et al.* (2023). Consistent with most wild grapevine

populations, male individuals predominate, representing approximately 60% of the sampled population.

Female individuals showed higher average *sativa* estimate (19%) than males (14.48%). Despite this, one third of the male individuals carried the white *sativa* haplotype, including one homozygote, whereas 23.5% of females carried the haplotype exclusively in heterozygous form. The *sativa* ancestry estimates in these individuals ranged from 2.68% to 62.75%, which suggests that the introgression of recessive *sativa* alleles originated during the early cultivation of white cultivars and continues to shape wild populations today. This case demonstrates that the introgression of recessive *sativa* alleles into wild populations—exemplified by the white berry haplotype—often remains undetected by expert prospectors, as these alleles are predominantly present in a heterozygous state or are phenotypically masked by flower dimorphism.

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SHORT COMMUNICATION
SESSION:
GENOMICS AND FUNCTIONAL GENETICS



SHORT COMMUNICATION

A population-scale analysis of genetic, epigenetic, and phenotypic variation in Pinot clonal populations

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¹ Department of Plant Breeding, Hochschule Geisenheim University, Geisenheim, Germany**Keywords:** clonal selection, long-read sequencing, epigenetics, somatic mutations, Pinot

ABSTRACT

Clonal selection has been used for centuries to improve major grapevine varieties, yet the molecular mechanisms responsible for phenotypic variation among clones remain poorly understood. While somatic mutations accumulate during vegetative propagation, recent evidence suggests that epigenetic variation, particularly stable DNAmethylation changes, may be an equally important and heritable source of clonal diversity. Understanding the relative contributions of genetic and epigenetic variation to agronomic and oenological performance is essential for developing molecular breeding strategies in clonally propagated crops.

In this ongoing work, we have performed Oxford Nanopore long-read sequencing of 202 clones from the Pinot family (P. noir, P. blanc, P. gris, and P. précoce) to characterize somatic genetic variation, including SNPs and structural variants, alongside single-base DNAmethylation patterns. These molecular data were integrated with extensive two-year field evaluations of phenology, proximal sensing-derived cluster, berry architectural traits and fruit quality parameters. To the best of our knowledge, this represents the most extensive integration of genomic, epigenomic and phenotypic data within a single grapevine cultivar group to date. In ongoing analyses, we dissect the relative contributions of somatic mutations and stable DNAmethylation differences to key agronomic traits. This allows us to resolve molecular drivers of clonal diversity within the Pinot family and to quantify trait variation that cannot be explained by genetic sequence differences alone. By linking specific molecular features to agronomic performance, this work provides a foundation for incorporating epigenetic information into clonal evaluation and selection, and for defining molecular targets that can inform precision breeding strategies in grapevine and other vegetatively propagated crops.



SHORT COMMUNICATION

Diploid genome assembly and annotation provide insights into allele-specific variants underlying fruit-quality QTLs

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Keywords: diploid genome assembly, gene annotation, allele-specific variants, fruit-quality QTLs

ABSTRACT

Fruit-quality traits including berry aroma and bunch architecture are major targets for improvement in both the wine and table grape industry. However, our current understanding of their underlying genetic architecture is limited due to the complex polygenic nature of these fruit traits. To identify and characterise genetic variants related to berry aroma and bunch architecture, we utilised a biparental mapping population derived from a cross between the wine grape ‘Deckrot’ (‘Pinot gris’ x ‘Teinturier’) and a table grape selection, G1-7720 (‘Black Rose’ x ‘Muscat Seedless’). Diploid chromosome-scale genomes were assembled with PacBio HiFi reads for the parents of the population. Each diploid genome comprised of 19 pseudochromosomes for both haplophase (hap 1 and hap2) assemblies. Reference-based scaffolding generated assemblies with a length of 504.14 Mb for Deckrot hap 1, 490.18 Mb for Deckrot hap2, 496.07 Mb for G1-7720 hap1, and 489.16 Mb for G1-7720 hap2. Scaffold N50 value for all assemblies exceeded 25 Mb with a mean BUSCO score of 98.4%. Additionally, transcriptome-based gene annotation of Deckrot hap1, Deckrot hap2, G1-7720 hap1, and G1-7720 hap2 predicted 42215, 40766, 43207, and 40418 gene models, respectively. Comparative analysis of the annotated genomes identified structural variants, single nucleotide polymorphisms, and gene copy number variation potentially underlying QTLs for berry aromatic profiles and bunch phenotypes segregating in the population. Furthermore, the assembly of diploid genomes facilitated allele-specific expression (ASE) analysis with RNA-seq data generated from flower tissue of the progeny. Thus, allowing us to distinguish parental alleles, detect genes showing ASE, and provide insights into the regulatory mechanisms influencing candidate genes identified in the QTLs. Among the candidate genes interrogated in this analysis, the gene VvTPS29, found in a QTL associated with sesquiterpene biosynthesis, showed ASE in the population and a possible loss-of-function allele in G1-7720. This study provides high-quality genome assemblies and annotations to dissect fruit-quality QTLs, identify putative candidate genes, and streamline genetic marker development. By implementing whole genome sequencing in this study, we demonstrated the utility of this approach in deciphering genetic variation and biological mechanisms underpinning key grapevine breeding targets.



SHORT COMMUNICATION

Identification and functional validation of a grapevine downy mildew resistant NLR gene through biparental graph-based forward genetics

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¹ Shanghai Jiao Tong University**Keywords:** grapevine, grape downy mildew, NLR resistance gene, biparental genome graph**ABSTRACT**

Grape downy mildew, caused by the oomycete *Plasmopara viticola*, is one of the major diseases threatening the viticulture industry. Discovery and functional characterization of resistance genes are key factors for enhancing DM resistance in grapevine. In this study, F1 and BC1 crossing populations were generated by crossing *V. vinifera* ‘Cabernet Sauvignon’ and *V. amurensis* ‘Shanghong’. Resistant/susceptible individuals were observed and scored among the BC1 population. In the mean time, we assembled the haplotype-resolved genomes of the parents for the mapping population. Genome-wide synteny analysis revealed extensive SNVs and SVs between haplotypes, highlighting the high heterozygosity and structural complexity of *Vitis* genomes. In addition, BiPG provides a more comprehensive representation of genomic variation between *V. vinifera* and *V. amurensis*, enabling finer mapping resolution. As a result, a DM resistant QTL was mapped on chromosome 7, and a group of resistant candidate genes were identified in this locus. Using bioinformatic analysis and gene mining strategy, a canonical CC-type NLR gene was, designated as Rpv-vnf1 was identified and isolated in the putative DM locus region. Functional analysis revealed that this gene can confer grapevine resistance to downy mildew. This research provides an efficient framework for high-resolution genotyping and gene mining in the complex grape genome. Identification, isolation and characterization of Rpv-vnf1 provides a valuable target of grapevine resistance breeding and basis for elucidating effector-triggered immunity (ETI) mechanisms.



SHORT COMMUNICATION

Origin of hemizygosity in grape: the case study of cv. Merlot

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Keywords: haplotype-resolved genome, hemizygosity, clonal propagation, structural variation

ABSTRACT

Hemizygous genes, are genes present on only one copy of the genome (only one allele) and should not be confused with homozygous genes. Grapevine genome display a relatively high rate of hemizygous genes, varying between 13,5% and 15% (Peng *et al.*, 2025). What is the origin of these hemizygous genes? Are they inherited, due to the cross between two highly heterozygous and structurally diverging parents or acquired along the clonal life, through segment loss?

To answer this question, we analyzed the cultivar 'Merlot' which is the result of a cross between 'Cabernet franc' and 'Magdeleine noire des Charentes' (Boursiquot *et al.*, 2009). First mention of this cultivar dates back to the late XVIIIth century in France (Viala and Vermorel 1902–1910). Since that time 'Merlot', being one of the most planted cultivars worldwide, have been extensively propagated and many clones exist today in public or private collections.

We sequenced three clones of Merlot and both its parents using PacBio Hifi technology. We then assembled each genome, using trio-binning for the Merlot, resulting in haplotype resolved chromosome scale genomes. Merlot assemblies present many homozygous regions, the longest being on chromosome 4 with a length of 23Mb. We annotated genes for each genome and identified the hemizygous genes in Merlot (Sichel *et al.*, 2023).

We characterized the transmitted genome regions from each parent and compared it to the corresponding 'Merlot' haplotype and we show that since its obtention, around 250 years ago, Merlot has accumulated few structural variants. Historical parental relationships within the grape gene pool may generate homozygous regions in current varieties and these regions may be confounded with hemizygous regions. We will present and discuss the origin of the hemizygous genes in 'Merlot'.

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SHORT COMMUNICATION
SESSION:
GENETIC IMPROVEMENT
AND BREEDING STRATEGIES



SHORT COMMUNICATION

Breeding for climate adaption should avoid a widely distributed allele within the *Ver1* veraison locus

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Keywords: climate change, cool climate viticulture, marker development, Frühburgunder, Spätburgunder

ABSTRACT

In the past breeding programmes for grapevine varieties for cool climate focused on developing early ripening cultivars that are better adapted to the prevailing climatic conditions. In the context of the ongoing climate change many of these cultivars are now ripen earlier than desired. This results in a decline in quality and typicity of the final wines. The very early ripening phenotype in nearly all of the developed cultivars was found to be inherited from Pinot Precoce Noir' (PPN), an early-ripening clone of 'Pinot Noir' (PN). The phenological differentiation is evident in the onset of veraison about two weeks earlier, which is known to be induced by the *Ver1* locus on chromosome 16, first identified in 'Calardis Musqué' and then traced back to PPN. A functional SSR marker for early ripening was developed to incorporate a new trait into the marker-assisted selection (MAS) pipeline, as well as to support the selection of cross parents. A crucial step forward was the identification of a marker that enables the functional differentiation between PN and PPN, which could not be achieved with any of the previously available markers. To validate the marker, the

allelic status of 72 important international and German cultivars was investigated within the *Ver1* locus. Functional confirmation was based on 12 years of data for veraison assessments (BBCH 85) for these cultivars grown at JKI Geilweilerhof in Siebeldingen, Germany.

The identified characteristics make this marker a highly valuable tool for tracing individual Pinot descendants back to their respective founder (PN or PPN), as well as for screening viticulturally relevant cultivars. The results suggest that there was high selective pressure for the early ripening phenotype in cool-climate breeding programmes in previous decades, and that this success is primarily due to the PPN allele. The marker provides now a simple tool for screening genetic resources and selection for or against the early ripening phenotype in today's breeding programs. By helping breeders adapt their breeding programmes to future climate conditions, the marker will contribute to the development of more resilient varieties and promote sustainable viticulture and quality wine production.

ACKNOWLEDGEMENTS

The authors are grateful to the German Federal Ministry of Research, Technology and Space (BMFTR) for funding of the "SelWineQ" project (FKZ 031B1306) within the program "PLANT BREEDING RESEARCH III".



SHORT COMMUNICATION

Building an integrated, high-throughput pipeline to accelerate grapevine improvement in New Zealand

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Keywords: mutagenesis, genotyping, phenotyping, Sauvignon blanc

ABSTRACT

The value that perennial crop improvement can offer is constrained by the lag between when growers define a problem and when genetic solutions reach the vineyard. During this period, production systems, markets, and growing environments can shift. Reducing this delay requires accelerating progress on two technical challenges: (i) generating populations with novel trait combinations and (ii) identifying improved individuals at scale.

New Zealand's Sauvignon Blanc 2.0 programme has used somatic embryo mutagenesis to rapidly address a diversity bottleneck, producing >8,000 novel Sauvignon Blanc clones in three years. A field-ready database links unique vine identifiers to provenance, treatment history, and batch genotyping metadata, providing traceability from plant production through screening.

We describe progress towards an integrated pipeline that combines early-stage genotyping with scalable phenotyping for traits prioritised by the New Zealand wine industry. DNA samples are collected early using automated extraction from young leaves. Genomic and epigenomic data are generated by multiplex nanopore sequencing and mapped to a phased reference genome for variant calling. In parallel, careful plant management in the nursery and vineyard accelerates maturation to advance phenotyping.

Phenotyping spans phenology (*e.g.*, timing of budburst and flowering), disease sensitivity, and abiotic stress responses including drought tolerance and frost susceptibility. With thousands of vines and no replication, measurements must be both accurate and efficient. For each trait, we begin with controlled, targeted stress challenges on a subset of the population to develop biomarkers and calibrate scalable assays. Once these are established, automated imaging and batch scheduling help increase throughput and comparability.

Common trait targets provide opportunities to adapt and standardise assays among international breeding teams. We discuss how shared data, methods, and functional genomic knowledge can shorten feedback loops between discovery and selection to accelerate progress, particularly through counter-season collaboration.



SHORT COMMUNICATION

Polyclonal selection in ancient grapevine varieties: genetic gains and stability across environments

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Keywords: intra-varietal variability, polyclonal selection, genetic gains

ABSTRACT

Conserving and exploiting intra-varietal diversity in ancient grapevine varieties is essential to secure their future use whilst preserving the genetic heritage of historical winegrowing regions. Two complementary strategies are recommended: (i) conserving representative samples of intra-varietal variability to safeguard genetic resources; and (ii) deploying that variability through polyclonal selection to enhance and promote the cultivation of each variety. In Portugal, this approach includes the conservation of more than 50,000 accessions from over 300 Portuguese varieties by PORVID, together with their utilisation in polyclonal selection schemes. By maintaining heterogeneous plant material—often from rarely cultivated varieties with underexplored potential—and by implementing polyclonal selection, this approach enhances viticultural sustainability, responds to evolving producer and consumer requirements, and improves adaptation to climate change, whilst supporting stable varietal performance across environments. This study aims to (1) formulate a theoretical framework for genetic gains in polyclonal selection and (2) demonstrate the flexibility of selection criteria, the precision of predicted

genetic gains, and the stability of selected polyclonal material across environments. Multi-environment field trials of ancient grapevine varieties were established using resolvable row–column experimental designs and were phenotyped for agronomically and economically relevant traits, including yield, must quality parameters. Linear mixed models were fitted to predict selection gains under alternative criteria. Stability across environments was evaluated using prediction intervals for genetic gains. The flexibility of defining selection targets and optimising gains was further illustrated using the R package *maxRgain*: Maximising Polyclonal Selection Gains Using Integer Programming.

Overall, the results show that polyclonal selection enables accurate and precise prediction of genetic gains and promotes stability across environments. These findings support polyclonal selection as an effective breeding and conservation-oriented strategy to valorise intra-varietal variability in autochthonous grapevine germplasm and to strengthen the resilience of viticulture under current and future challenges.

ACKNOWLEDGEMENTS

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SHORT COMMUNICATION
SESSION:
DISEASE RESISTANCE AND
PLANT-PATHOGEN INTERACTIONS



SHORT COMMUNICATION

Grapevine *DMR6-1 DMR6-2* double mutants display constitutive systemic acquired resistance and altered gibberellin metabolism

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Keywords: downy mildew, gene editing, salicylic acid, gibberellin

ABSTRACT

Achieving disease resistance in grapevine (*Vitis vinifera*) without compromising plant growth is a significant challenge for viticulture. A strategy to reduce susceptibility to Downy Mildew (DM) is through dual inactivation of the salicylic acid (SA) hydroxylases *VviDMR6-1* and *VviDMR6-2* by gene editing, which leads to elevated endogenous SA levels and enhanced immunity. Unlike other SA-overaccumulating mutants, these double mutants exhibit no observable growth defects during the juvenile stage and in greenhouse conditions. Through gene-network and expression analyses, we identified a constitutive activation of genes involved in Systemic Acquired Resistance (SAR) in the double *DMR6-1 DMR6-2* mutant but not in the single *DMR6-1* mutant, suggesting functional synergy between these two genes in grapevine. Our analyses revealed also the interaction between SA and gibberellin metabolism. By unraveling this hormonal crosstalk, this research provides strategies to mitigate potential growth penalties when developing transgene-free grapevine varieties with reduced susceptibility to pathogens.



SHORT COMMUNICATION

Proteomic insights into early grapevine defense responses to downy and powdery mildew

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Keywords: grapevine, immunity, proteomics, *Plasmopara viticola*, *Erysiphe necator*

ABSTRACT

Grapevine is a globally significant crop whose productivity is constantly threatened by fungal and oomycete diseases. At the same time, increasing environmental and regulatory pressures demand a substantial reduction in pesticide use in viticulture¹. Achieving durable disease control under these constraints depends on improving our understanding of the molecular basis of grapevine tolerance, thereby enabling the development of more resilient cultivars and sustainable crop protection strategies.

Multi-omics approaches are particularly suitable to unravel the complex signalling networks underlying grapevine immunity². This is a central objective of the Horizon Europe SHIELD4GRAPE project, which combines multi-omics analyses with breeding and integrated pest management strategies to promote viticulture sustainability.

Within the multilayer framework of the Horizon Europe SHIELD4GRAPE project, we focused on early proteome reprogramming associated with grapevine responses to *Plasmopara viticola* and *Erysiphe necator*. Proteins play a fundamental role in grapevine development, stress responses, and immune regulation, acting as key effectors of metabolic pathways and defence signalling and their characterization

can be particularly important in grapevine breeding programs facilitating the identification of tolerance-associated traits^{3,4}.

In this work, we selected tolerant minority genotypes from Mediterranean regions and compared them with the susceptible genotype ‘Chardonnay’ under controlled inoculation conditions. Leaf samples were collected at 24 hours post-inoculation, a critical stage for defence activation and pathogen establishment. Ashotgun proteomics LC-MS/MS approach allowed the analysis of differentially accumulated grapevine proteins 24h post inoculation. Tolerant genotypes displayed some overlap in protein accumulation tendencies, while simultaneously showing genotype-specific response, demonstrating the complexities of proteome remodelling upon pathogen challenge. Gene ontology enrichment analysis reflected this complex accumulation pattern, revealing a concerted effort at the proteome level with the biological goal of stress amelioration and response to disease. Ongoing integration of proteomics with transcriptomic, epigenomic and metabolomic datasets generated within SHIELD4GRAPE will contribute to reconstructing regulatory networks underlying disease tolerance and to identify candidate molecular markers for breeding more resilient grapevine cultivars.

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SHORT COMMUNICATION

SESSION:

**CLIMATE CHANGE AND
ABIOTIC STRESS TOLERANCE**



SHORT COMMUNICATION

Bridging *in vitro* and *in planta* models: metabolic insights into grapevine stress responses

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Keywords: *in vitro* cell culture, *Vitis vinifera*, jasmonic acid, stress responses, Fourier-Transform Ion Cyclotron Resonance Mass Spectrometry (FT-ICR MS)

ABSTRACT

Rapid climate changes and increasing biotic pressures compromise grapevine production systems by threatening grape quality and production yields, thus increasing phytochemical dependence as a widely adopted mitigation strategy.

Reducing phytochemical dependence, while maintaining production and quality standards, requires an improved understanding of the mechanisms underlying stress adaptation and defence responses.

Perennial woody species, including grapevine, may present temporal, physiological and logistical constraints that limit their usage in the study of specific aspects of plant defence mechanisms. This also constrains the preliminary evaluation of potential biostimulants and elicitors. To improve experimental efficiency while preserving biological relevance, complementary systems that allow reliable knowledge transfer to intact plants should therefore be considered.

Plant cell suspension cultures offer a promising, simplified, tightly controlled, and highly reproducible platform with a homogenous cellular background suitable for dissecting specific response mechanistic aspects. However, their applicability depends on the extent to which *in vitro* responses reflect plant responses, an aspect never assessed. Thus, to address this, cell suspension cultures from two wine grape cultivars of *Vitis vinifera* with contrasting pathogen susceptibility, the susceptible cv. ‘Cabernet Sauvignon’ and the tolerant cv. ‘Chambourcin’ were established. To bridge biological scales, detached leaves from the same cultivars were considered as a simplified plant model. Thus, both systems were elicited with jasmonic acid, and their metabolic profiles were analysed at 2 and 5 days after elicitation using Fourier-Transform Ion Cyclotron Resonance Mass Spectrometry (FT-ICR MS).

A comparative metabolic analysis revealed a metabolic overlap between systems concerning oxidative stress defence, stress signalling, and secondary metabolism.

These findings support the use of grapevine cell suspension cultures as a reliable complementary platform in the study of stress response mechanisms. This approach provides a suitable framework for developing new sustainable disease management and resilience-oriented strategies in viticulture.



SHORT COMMUNICATION

Physiological performance and targeted gene expression dynamics in ‘Italia’ table grapevine under prolonged water deficit

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Keywords: table grape, abscisic acid signaling, osmoprotection mechanisms, stomatal regulation, drought responsive genes

ABSTRACT

Water availability constraints are becoming a defining factor in Mediterranean viticulture, which requires a deeper understanding of cultivar-specific adaptive mechanisms to sustain yield and fruit quality. The widely cultivated table grape (*Vitis vinifera* L.) cv. ‘Italia’ is particularly relevant in this context, yet its integrated physiological and molecular responses to prolonged water deficit remain insufficiently characterized.

This study evaluated the response of ‘Italia’ grapevine subjected to 37 days of controlled drought stress, combining ecophysiological measurements with targeted gene expression analysis. Leaf water potential, transpiration rate, and net CO₂ assimilation were monitored to assess plant water status and photosynthetic performance. In parallel, the expression of six drought-responsive genes was quantified by qRT-PCR: *VvPP2C4* and *VvPP2C8*, involved in abscisic acid (ABA) signaling; *VvGolS1* and *VvGolS2*, associated with osmoprotectant biosynthesis; *VvHSP18*, encoding a small heat-shock protein linked to cellular protection; and *VvRD26*, a NAC transcription factor implicated in dehydration responses.

Water deficit progressively reduced leaf water potential and gas-exchange parameters, indicating a conservative strategy based on stomatal limitation to minimize water loss, albeit at the expense of carbon assimilation. Gene expression profiling revealed significant upregulation of *VvPP2C4*, *VvGolS2*, *VvHSP18*, and particularly *VvRD26*, which exhibited up to a 60-fold increase at the end of the stress period. Conversely, *VvPP2C8* and *VvGolS1* showed limited modulation, suggesting differential regulatory roles within the same functional pathways.

These findings highlight a coordinated adjustment between physiological regulation and selective activation of ABA-dependent signaling, osmoprotection, and stress-responsive transcriptional control. The identified expression patterns provide potential molecular indicators of drought responsiveness in ‘Italia’ and contribute to the development of targeted strategies for improving resilience in Mediterranean table grape production systems.



SHORT COMMUNICATION

Seasonal dynamics in grapevine physiological and transcriptomic responses to combined water and nitrogen limitation

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Keywords: drought, nutrient, Grenache, Cabernet-Sauvignon

ABSTRACT

The increasing occurrence of drought events poses a major challenge for viticulture, as water deficit negatively affects vine yield and berry quality. Although grapevine responses to water deficit and nutrient supply have been widely characterized, their combined effects are still not well defined. This study investigated the physiological, ionic, and transcriptomic responses of two *Vitis vinifera* L. cultivars subjected to water deficit and nitrogen (N) availability. Two-year-old Cabernet Sauvignon (near-anisohydric) and Grenache (near-isohydric) plants grafted onto SO4 rootstock were grown in soil-filled pots under semi-environmental conditions. Vines were either maintained well-watered or subjected to a controlled water deficit irrigation and received different N fertilization rates. Water deficit significantly reduced vegetative growth in both cultivars, with Grenache exhibiting a slower growth rate than Cabernet Sauvignon. At flowering, water availability emerged as the dominant factor regulating physiological performance, as water deficit reduced stomatal conductance (gs) and increased leaf nutrient

concentrations. From veraison onward, N supply strongly modulated gs and leaf ionic composition in Cabernet Sauvignon, with decreased nutrient accumulation under high N rates. Conversely, Grenache displayed a more stable physiological status and a delayed nutritional response, with major changes occurring mainly at maturity. Transcriptomic analyses revealed cultivar- and stage-specific activation of abiotic stress-related genes (including heat shock proteins and stress-responsive transcription factors), with greater modulation observed at maturity than at flowering. Notably, N treatment strongly influenced the transcriptomic response to water deficit. Overall, these results showed that grapevine responses to combined water and nutrient constraints are strongly dependent on genotype and phenological stage, and involve coordinated physiological, nutritional, and molecular adjustments. This integrative approach provides valuable insights for optimizing irrigation and fertilization practices, contributing to a more resilient and sustainable viticultural system.

ACKNOWLEDGEMENTS

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SHORT COMMUNICATION
SESSION:
PHENOTYPING



SHORT COMMUNICATION

Dissecting the role of *EPFL9-2* in grapevine root system architecture through rhizotron-based phenotyping

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Keywords: phenotyping, roots, drought stress, *EPFL9-2*, genome editing

ABSTRACT

Epidermal Patterning Factors (EPFs) constitute a family of small, highly conserved peptides that regulate diverse physiological and developmental processes in plants. In grapevine (*Vitis* spp.), *EPFL9-2* has been identified as a positive regulator of stomatal development and a critical determinant of root system architecture (RSA). Unlike aboveground organs, roots present significant challenges for non-invasive phenotyping. This study aimed to establish a root phenotyping system to deeply characterize the RSA of *epfl9-2* knockout (KO) lines of the 'Kober 5BB' (*Vitis berlandieri* x *Vitis riparia*) rootstock.

Two distinct *epfl9-2* KO lines and wild-type (WT) control were cultivated in a greenhouse using a rhizotrons (25 x 50 x 4 cm). Root growth was monitored at three time-points using standardized digital imaging. Furthermore, the RSA was imaged also in grafted plants where an *epfl9-2* KO line and Kober WT were grafted with a 'Syrah' (WT) scion. Images were processed using RhizoVision Explorer software to quantify key parameters, including total area covered by roots, root length density, and lateral root branching angles.

Our results indicate that *epfl9-2* mutants exhibit a more compact RSA compared to the WT, characterized by reduced total length and lateral expansion. Notably, KO lines showed a significant reduction in the gravitropic angle and total root length, while simultaneously displaying increased root diameters and higher density per unit area. Grafting experiments demonstrated that the *epfl9-2* root phenotype persists regardless of the presence of a WT scion, suggesting that these altered root traits are independent of the shoot apparatus. This phenotyping approach provides a robust framework for further evaluating the performance of *epfl9-2* genotypes under simulated environmental stress. Future research will investigate how these specific root traits may impact scion resilience to abiotic stress in grafted grapevine varieties of economic interest.

SHORT COMMUNICATION

SESSION:

**FRUIT DEVELOPMENT, GRAPE
AND WINE COMPOSITION**



SHORT COMMUNICATION

Development of a wine with controlled origin from PIWI grape varieties

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ABSTRACT

On the international wine market, wines that have a controlled (and guaranteed) origin from a specific wine-growing region enjoy special attention. They are considered particularly typical of an area and represent the pinnacle of wine quality. For this type of wine, only well-established grape varieties, mostly of a traditional nature, have been used so far. The regional committee for the Kamptal wine-growing region has decided to test Piwi varieties in the form of a project to see if they are suitable for such a wine of origin.

From a pool of new breeds, most of which have not yet been named, those genotypes were selected that are genetically particularly closely related to the traditional varieties used so far. In the case of the Kamptal, this mainly affects crosses with Grüner Veltliner, Rhine Riesling and Pinot Blanc. Eight genotypes were propagated and released in various plantations in the wine-growing area. Observations were made with regard to the viticultural suitability of the varieties under reduced plant protection. Considerable differences between the individual genotypes could be identified. The grapes were used to process classic fruity white wines. These have been subjected to extensive sensory and analytical tests. In particular, aroma-relevant ingredients and phenols were analysed. With the help of these results, a selection is to be made as to which varieties can be used for wine of origin in the future.

POSTER
SESSION:
GENETIC RESOURCES



POSTER

A *Vitis vinifera* L. core collection suitable for association studies of fruit quality and resilience traits

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Keywords: association mapping, genotyping, grapevine diversity, high-throughput phenotyping

ABSTRACT

The wide genetic and phenotypic diversity of *Vitis vinifera* L. varieties represents a valuable resource for improving grapevine fruit quality traits and crop resilience to biotic and abiotic stresses. The development of well-structured core collections that capture the maximum diversity of the species while maintaining a manageable number of varieties is therefore a key step toward efficient genetic mapping studies. Starting from the *V. vinifera* accessions preserved in the ICVV germplasm collection, we designed a core collection of 150 varieties suitable for association studies. Using available genotypic data from 240 SNP markers, we first investigated the genetic structure of the entire collection, which revealed three major genetic groups consistent with current knowledge of grape usage and geographic origin: wine grapes from the Iberian Peninsula, wine grapes from Central Europe, and table grapes of diverse origins. Within each genetic group, individuals showing low levels of admixture were retained, generating three datasets that were subsequently used to construct independent core collections of 50 varieties each. After their assembly, the final core collection comprises 150 varieties with limited genetic relatedness, and represents the three genetic backgrounds in

a balanced manner. To evaluate its suitability for association studies, we assessed the extent of phenotypic variation for different traits of interest. The use of a high-throughput berry image acquisition platform coupled with an automated image-processing pipeline revealed substantial diversity for berry size and shape traits in the collection, with berries varying between 3.1 and 0.7 cm in length and 2.1 and 0.7 cm in width. An image-based approach to quantify sunburn-like damage in whole clusters subjected to a standardized heat stress treatment under controlled conditions further highlighted wide phenotypic variation, identifying varieties that were nearly unaffected and others with massive necrotic damage. In addition, controlled inoculation of individual berries with *Botrytis cinerea* revealed marked differences in susceptibility, with varieties ranging from low to extensive mycelial growth under identical experimental conditions.

Altogether, this *V. vinifera* core collection and the established phenotyping methods provide a robust and efficient resource for association studies aimed at dissecting the genetic basis of fruit quality and resilience traits, for adaptation of grapevine cultivation to current viticultural challenges.

ACKNOWLEDGEMENTS

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POSTER

Ampelographic and SSR-based characterization of drought-adapted grapevine accessions from Deir El Ahmar, Lebanon

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Keywords: grapevine landraces, diversity, variety identification, East Mediterranean viticulture

ABSTRACT

Deir El Ahmar, Bekaa Valley, Lebanon (1000 – 1100 m a.s.l.), is a semi-arid viticultural region characterized by harsh agroclimatic conditions. Grapevine varieties traditionally cultivated there represent germplasm that has persisted under long-term heat, often exceeding 40 °C during summer, making this area a potential reservoir of climate-adapted diversity. Thirteen grapevine accessions collected in Deir El Ahmar were characterized using standardized ampelographic descriptors (OIV) and SSR molecular markers. Evaluation of leaf, bunch, and berry traits revealed substantial morphological variability, while SSR analysis identified nine distinct genetic profiles among the studied accessions.

Genotypic comparisons indicated the presence of four Lebanese-origin varieties as well as five previously unreported profiles, with cases of synonymy and homonymy reflecting local naming dynamics. The results highlight the genetic and morphological diversity maintained in a drought-prone environment and emphasize the importance of prospecting marginal viticultural areas in the context of climate change. Such germplasm constitutes a strategic resource for breeding climate-resilient wine and table grape varieties in Mediterranean environments.

ACKNOWLEDGEMENTS

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POSTER

Enhancing grapevine rootstock genetic diversity through novel American *Vitis* progenies

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Keywords: genetic diversity, non-vinifera germplasm, rootstock, viticulture

ABSTRACT

Grafting is the predominant propagation method for vineyard establishment worldwide, strongly affecting grape and wine quality. Since their introduction in the late XIX century, grapevine rootstocks have been subjected to genetic improvement primarily aimed at enhancing tolerance to environmental stresses, such as pests, limestone and drought. However, breeding activity drastically declined over the XX century, leading to a limited number of rootstocks available today.

Moreover, most currently used rootstocks derive from a narrow set of founders, further limiting the existing genetic base. Although current rootstock supports viticulture across various pedoclimatic conditions, expanding their genetic base is crucial to address future environmental conditions, especially in the context of climate change.

The preservation of grapevine rootstocks germplasm represents a valuable resource for breeding programs. One of the largest Italian rootstock collection, consisting of about 500 accessions and representing most of the rootstocks used worldwide, has been genotyped with SSR markers, revealing 232 unique genetic profiles. A core-collection of 70 genotypes was identified to represent the overall genetic diversity of this collection.

The present study aims to evaluate how much the genetic diversity of the rootstock collection can be enhanced by introducing new genotypes derived from American *Vitis* spp. progenies that have not yet been exploited for rootstock breeding. The existing core-collection and 30 additional genotypes from American progenies were analyzed using an 18k SNP array. Considered genotypes originated from open pollination of *V. arizonica*, *V. acerifolia*, *V. monticola*, *V. aestivalis*, *V. cinerea*, *V. champinii* and *V. rotundifolia*. Genetic diversity was assessed by estimating heterozygosity and characterizing genetic structure through SNP based multivariate and clustering analyses.

Results showed an increase in genetic variability and a more complex genetic structure after introducing the new American genotypes, enabling the integration of this expanded diversity into an updated SNP-based core-collection. Furthermore, the analyzed American genotypes are currently undergoing phenotyping to determine how this broader genetic base may contribute to enhanced abiotic stress tolerance under future climate scenarios.



POSTER CANCEL



POSTER

Genetic identification of *Vitis vinifera* L. old traditional cultivars in ancient vineyards of the "vinodol" area (Croatia)

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Keywords: grapevine, varieties, identification

ABSTRACT

The Vinodol area is located about forty kilometers southeast of the city of Rijeka (Croatia). It is a small area that is dominantly located on the steep slopes of the associated mountain massif. The area is traditionally known as a wine-growing area, as evidenced by the toponym ("vino" - wine, "dol" - valley). Due to some historical and economic reasons, steep and karst terrain, vineyard areas in the last fifty years have been almost completely neglected. Viticulture has been reduced to a small number of hobby winegrowers and one larger winery. The first variety identification was carried out in the early 2000s by the Faculty of Agriculture in Zagreb, when several autochthonous varieties were identified: 'Bilan bijeli',

'Ošljčina', 'Plavica', 'Verdić', 'Žumić', 'Malvazija istarska' and the most widespread 'Žlahtina' variety. Through the activities of the National Program for the Conservation and Sustainable Use of Plant Genetic Resources for Food and Agriculture in 2022, 2023, and 2025, inventories were conducted in nine old, previously unexplored vineyards still existing in this area. A total of 22 samples of presumed old and unknown varieties were collected with the aim of genetic identification. The genetic analysis was carried out at the Institute for Adriatic Crops and Karst Reclamation in Split by genetic analysis of the "SSR" marker technique ("Simple Sequence Repeat"). The analysis was performed on 9 standard gene-loci (VVS2, VVMD5, VVMD7, VVMD25, VVMD27, VVMD28, VVMD32, VRZAG62, VRZAG79) prescribed by the International Organization for Vine and Wine ("OIV") grapevine identification. Genetic profiles were compared with the Vitis International Variety Catalog ("VIVC") database for identification purposes. The following varieties were identified by comparison: 'Žlahtina', 'Bljuzgavac' (syn. 'Vulpea'), 'Kuć' (syn. 'Mostosa'), 'Mejsko belo', 'Kraljevina', 'Zelenika' (syn. 'Hainer Gruen'), 'Chardonnay blanc', 'Cabernet Franc' and 'Brajdica bijela'. Nine samples were confirmed to be unique genotypes. One genotype was confirmed by three samples (H4, Jel8, Pl2), one genotype by two samples (Pl4, Pl23_1). Other seven were confirmed with one sample (Brajda1, Brajda2, Cr1, Jel7, B1, B3, Bl1). This research confirmed

that this is an area with a much larger grapevine gene pool than was determined by previous research. A wider cultivation area was confirmed for the varieties 'Bljuzgavac', 'Kuć', 'Mejsko belo' and 'Brajdica bijela', as they were previously established in some neighboring areas but not in the observed one. Also, 'Zelenika' variety was confirmed for the first time in the Republic of Croatia.



POSTER

Genetic resources as a foundation for more successful viticulture: A case study of indigenous grapevine variety revitalization in Croatia

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Keywords: genetic resources, revitalization, indigenous cultivars, economic value, wine tourism, Croatia

ABSTRACT

Over the past 30 years, systematic ampelographic and genetic research in Croatia has led to the identification and collection of approximately 130 grapevine cultivars (*Vitis vinifera* L.) considered to be indigenous. Many of these genotypes were rediscovered in extremely limited numbers—sometimes as single remaining vines in old, abandoned vineyards.

While the initial focus was on preserving biodiversity and preventing genetic erosion, subsequent evaluation has revealed the immense economic and viticultural value of some genotypes. This paper argues that many autochthonous varieties were historically marginalized due to phytosanitary issues or changing agricultural/market trends, despite their high enological potential.

The study presents the successful revitalization models of three key cultivars: Tribidrag (syn. Crljenak kaštelanski, Zinfandel), Malvasija dubrovačka bijela (syn. Malvasia delle Lipari), and Belina starohrvatska (syn. Heunisch Weiss). Through these case studies, we demonstrate how scientific efforts—ranging from DNA identification and parentage analysis to clonal and sanitary selection—have transformed “forgotten” genotypes into commercially successful pillars of regional wine economies.

The results show that the revitalization of these varieties has enabled winemakers to differentiate their products in a globalized market, increase profitability through “premium” branding, and utilize genotypes naturally adapted to local terroirs. Furthermore, in a country like Croatia, dominated by small-scale family wineries and a thriving tourism sector, story-driven wines based on unique genetic heritage offer a crucial competitive advantage. This Croatian model serves as a proof of concept that investing in the preservation of old and rare genetic resources is not merely a matter of heritage, but a strategic tool for building a more competitive, authentic, and sustainable modern viticulture.



POSTER

Genome-wide genetic diversity in grapevine rootstocks and wild *Vitis* reveals adaptive potential in rootstocks breeding

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Keywords: genetic diversity, *Vitis*, rootstocks, drought, grapevine

ABSTRACT

Grapevine rootstocks are a key determinant of vineyard performance, yet the genetic diversity supporting rootstock relevant phenotypes and environmental adaptation in commercial rootstocks remains poorly characterized. In this study, we compared the genetic diversity between 59 commercial rootstocks and a germplasm collection of 280 wild *Vitis* accessions using whole-genome sequencing data. We identified 3M highly reliable single nucleotide polymorphisms across all genotypes and used this information to assess genetic diversity. Measures of nucleotide diversity, heterozygosity, and linkage disequilibrium permitted to quantify and compare genomic diversity between commercial and wild groups, while population structure and phylogenomic analyses were conducted to assess genetic relationships. We compared commercial rootstocks genetic diversity relative to wild *Vitis* accessions, to estimate the impact of targeted selection during breeding. We hypothesize that wild accessions carry high allelic diversity with adaptive potential, especially in genomic regions where QTLs related to stress tolerance were previously identified. This study investigate how wild *Vitis* germplasm can be a potential reservoir of adaptive genetic variation that remains underutilized in rootstock breeding. Our findings provide a genomic framework for identifying candidate alleles and introgression targets to improve resilience and adaptive capacity in future grapevine rootstock breeding programs, supporting viticulture under increasingly variable environmental conditions.



POSTER

Georgian wild grapevine germplasm: A genetic and phenotypic characterization

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Keywords: SNP, OIV descriptor, biodiversity, genetic resources, conservation

ABSTRACT

The wild progenitor of the cultivated grapevine, *Vitis vinifera* subsp. *sylvestris*, represents a crucial reservoir of genetic diversity and adaptive traits of significant value for conservation and breeding programs. Georgia, recognized as one of the primary centers of grapevine domestication, still harbors remnant populations of wild grapevines that preserve unique and ancient genetic lineages. In this study, the genetic diversity and population structure of 23 wild Georgian grapevine accessions were investigated using 18k SNP loci and compared with 112 additional wild genotypes from across the Mediterranean Basin. Genetic analyses revealed that wild grapevine populations from Eastern Georgia form a single, highly diverse genetic pool with limited overall stratification. However, cluster analyses detected geographically associated substructures, particularly within the Kakheti region. Within the broader Mediterranean context, Georgian wild grapevines displayed marked genetic distinctiveness. Both clustering approaches and PCA consistently identified the Georgian samples as a coherent and genetically differentiated group, with minimal overlap with Mediterranean accessions.

Population structure analyses supported the presence of three ancestral populations: the Georgian group formed an independent cluster (POP2), while North African and Iberian Peninsula samples grouped together (POP1), and Western–

Central European genotypes constituted a third cluster (POP3). A minimum spanning network further highlighted the presence of three main populations, with the North African group acting as a genetic bridge between Georgian and Western–Central European wild grapevines. TreeMix analysis indicated a clear tree-like divergence pattern among the three populations, with POP1 and POP2 forming sister groups and POP3 diverging earlier. Georgian samples exhibited the highest level of genetic drift, and no evidence of admixture or post-divergence gene flow was detected. In addition to genomic analyses, a phenotypic characterization of the Georgian wild grapevine germplasm was carried out in order to assess morphological variability and adaptive traits. Forty one accessions, included also those 21 genotyped, available in the collection and described by 52 OIV ampelographic descriptors, demonstrated presence of 8 homogenous descriptors and 44 heterogeneous ones. These descriptors, selected by the COST FA1003 project and covering all organs of grapevine, together with photos became the basis for producing of the detailed ampelographic cards. Altogether, these results underline the genetic uniqueness of Georgian wild grapevine populations and emphasize the importance of preserving this germplasm as a valuable resource for future conservation strategies and grapevine breeding programs.

ACKNOWLEDGEMENTS

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POSTER

Molecular identification of neglected grapevine varieties from the Georgian vineyards

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Keywords: SSR markers, local and foreign varieties, ampelography

ABSTRACT

The conservation of grapevine genetic resources in Georgia dates back to the late 19th century, when the first field collections were established. The major milestone was achieved in the early 1930s, when the Institute of Viticulture and Winemaking established the largest collection of local varieties at the Telavi Testing Station and initiated their characterization. The most extensive collection, comprising more than 3000 accessions of both Georgian native and introduced varieties, was later settled at the Dighomi collection of the Georgian Agricultural Institute. Currently, Georgian collections, including the largest, the Jighaura Collection of the Scientific-Research Center of Agriculture and the Shumi Collection, maintain a large number of local and introduced grape varieties.

Experience gained over of the past few years has demonstrated that, despite the high concentration of varieties preserved in these collections, some varieties could still be recovered from old and amateur vineyards, using combined ampelography and molecular genetic approaches. The aim of this study was to identify grapevine varieties

currently spread in the Georgian vineyards lacking precision identification.

Eight interesting accessions from various Georgian viticultural regions (Racha, Lechkhumi, and Kakheti) were selected based on the preliminary information and basic ampelographic data. These varieties were subjected to molecular analysis using 12 SSR markers at the CREA-VE Genetics Laboratory in Conegliano (TV-Italy). The obtained results were verified against the Center's internal database (the largest and most comprehensive currently available) and the Vitis international Variety Catalogue (VIVC).

The results confirmed the presence of five known local Georgian and foreign varieties recorded in the databases. In addition, three accessions of putative Georgian origin, not previously documented in any databases, were identified. Further ampelographic description of these varieties during subsequent vegetative seasons is recommended. For two of the newly identified varieties– Rkatsiteli Mtsvane and Rkatsiteli Shavi –hypotheses regarding their putative parent pairs were provided.

ACKNOWLEDGEMENTS

The National Wine Agency of Georgia supported this work within the framework of the “Research Project for the Study of Georgian Grapes and Wine Culture”.



POSTER

Plant propagation in ancient times: possible impacts on cultivar selection during grapevine domestication

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Keywords: *Vitis vinifera sylvestris*, Caucasus, rhizogenesis, seed germinability, prehistoric agriculture

ABSTRACT

Propagation techniques played a significant role in the early domestication of plants. It probably contributed to the key transition for early humans from a nomadic hunter-gatherer existence to settled agricultural communities based on cultivating their plant resources.

The propagation (vegetative and sexual) aptitudes of the two subspecies (*sylvestris* and *sativa*) of *Vitis vinifera* were compared. To test whether domestication has had an effect on the grapevine's capacity for rooting and therefore vegetative propagation, 1,061 grapevine cuttings from 9 different accessions were studied for 200 days in two different experimental sites in Georgia. Considering sexual propagation, germination of 13200 seeds coming from 6 accessions in Italy and 19 accessions in Georgia was tested, after exposure to different ways for conservation or processing (fresh, drying, and fermentation).

The results demonstrate the greater aptitude for vegetative propagation of the *sativa* subspecies, contrasted with the greater efficiency in sexual reproduction of wild vines. This shift in propagation aptitudes can be considered one of the symptoms of the domestication syndrome, and it is consistent with the hypothesis that already in prehistoric times the grapevine was propagated by vegetative means.

During domestication, therefore, there was a selective pressure focused on traits (e.g. rooting of cuttings and ethanol tolerance of seeds) that are less interest today, while for the last 150 years *Vitis vinifera sativa* is propagated exclusively by grafting for the establishment of the vineyards, and the seeds are used only by the breeders making complex evaluation of the seedlings before selection. The aptitude for propagation techniques during the domestication phase may therefore have created a bottleneck in varietal selection, needlessly reducing the genetic variability of the cultivated grapevine.

ACKNOWLEDGEMENTS

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POSTER

Revival of neglected Istrian grapevine varieties: genetic authentication, ampelographic characterization and wine style definition of Duranija, Surina, Garganja and Hrvatica

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Keywords: neglected varieties, SSR genotyping, on-farm conservation

ABSTRACT

Several traditional grapevine varieties that were historically widespread in Istria region (Croatia) until the mid-20th century have undergone severe genetic erosion following profound changes in viticultural practices from the 1960s. Duranija, Surina, Garganja and Hrvatica, once integral components of regional viticulture, were progressively displaced by varieties characterized by more uniform and reliable ripening, ultimately leading to their near disappearance from commercial production and the wine market.

The present study aimed to genetically authenticate these neglected varieties through SSR genotyping of individual vines collected from various different old-sourced vineyards and to support their conservation and sustainable reintroduction as valuable elements of regional grapevine germplasm. A total of nine different old vineyards were surveyed and 20 vines were genotyped. The resulting allelic profiles were compared with those in the SSR database of native Croatian varieties and the international VIVC database. For two samples, the SSR profiles did not match any of the four investigated varieties, highlighting the need to establish their true-to-type identity. The obtained molecular profiles confirmed that all four varieties represent unique and distinct genotypes, clearly differentiated from internationally cultivated varieties, thus validating their status as autochthonous Istrian grapevine genetic resources.

Molecular data were integrated with detailed ampelographic descriptions and phenotypic observations to assess varietal characteristics and key agronomic traits relevant for reintroduction. On this basis, experimental vinifications were conducted in order to define technologically appropriate and economically viable wine styles for each genotype. Duranija was identified as suitable for producing fresh, young white wines intended for early consumption, Surina for sparkling wine production with potential for both short- and long-term ageing, Garganja for high-acid base wines intended for long-

aged sparkling wines, and Hrvatica for rosé wine production, either as still wines or sparkling wines.

This integrated approach demonstrates how molecular characterization combined with applied viticulture and oenology can effectively counteract genetic erosion and facilitate the on-farm conservation and commercial revival of endangered grapevine germplasm. As a direct outcome of this work, all four varieties have recently been replanted in Istria, contributing to the preservation of viticultural biodiversity and the long-term safeguarding of regional genetic heritage.



POSTER

The FEMVitisDataset: from germplasm collection to an Open FAIR Data resource

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Keywords: germplasm bank, genetic diversity, grapevine breeding, phenotypic data, SSR fingerprinting

ABSTRACT

The preservation and strategic exploitation of grapevine genetic resources are essential to sustain viticulture under accelerating climatic and phytosanitary pressures. Here we present the FAIR-compliant digitalization and genetic characterization of the FEM grapevine germplasm, one of the largest curated collections in Europe. The publicly released FEMVitisDataset comprises 2,904 accessions from 51 Countries, including cultivated *Vitis vinifera* and wild relatives, interspecific hybrids, and pure wild species, capturing extensive taxonomic and functional diversity.

All accessions were genotyped using nine international reference SSR loci, enabling multilayer True-To-Type validation through comparison with major international databases. The analysis identified 1,937 unique genetic profiles, of which 894 were previously unreported, highlighting the substantial originality and unexplored value of the germplasm. Beyond molecular fingerprinting, the dataset integrates multi-year phenotypic observations—phenology, fertility, ampelography, and biotic stress responses—structured according to MIAPPE standards and semantically harmonized through plant and crop ontologies. The wide phenotypic variability recorded across accessions, including large offsets in phenological timing and reproductive traits, illustrates the adaptive potential retained within the germplasm and its relevance for breeding under climate change scenarios. The standardized data structure provides a transferable framework that can support other germplasm repositories in FAIR digitalization workflows.

The coexistence of historical cultivars, somatic variants and breeding selections provides a unique bridge between conservation and modern genetic improvement pipelines. Approximately one third of the validated profiles correspond to novel genotypes, underscoring the global relevance of this resource for germplasm discovery.

All unique genetic profiles have been genotyped with the High-density Axiom®Vitis22K SNP array, enabling genome-wide association studies, population structure analyses and genomic prediction approaches aimed at accelerating

trait dissection and increasing breeding efficiency. Overall, the FEMVitisDataset represents a quantitatively rich and qualitatively validated resource, demonstrating how curated germplasm banks can evolve into digital infrastructures supporting biodiversity research, data-driven breeding and future viticulture resilience.



POSTER

When the grapevine diversity reveals us some secrets of resilience in old vineyards and in gene pool germplasm in Portugal

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Keywords: grapevine diversity, Portuguese origin, phenotype-genotype, biotic and abiotic stresses

ABSTRACT

Vitis vinifera L. is the main European grapevine species used for wine production. It is characterized by the production of grapes and wines with unique organoleptic properties, distinguished by high quality and the absence of strong “foxy” aromas. This quality results from the long-term evolution of grapevine diversity driven by human selection through both seed propagation and vegetative reproduction using cuttings.

In recent years, advances in the search for grapevine varieties that are more resilient to biotic and abiotic stresses have led to the further exploitation of selected varieties identified in old vineyards across diverse environments and preserved in ampelographic collections.

The aim of this study arises from the identification of resilience to environmental stresses, either within the gene pool of the collection or in ancient vineyards.

Twenty-two accessions were selected for this study and subjected to morphological and molecular (SSR) characterization using OIV descriptors. Among nine accessions previously classified as unknown (uKn), it was possible to correctly identify seven.

uKn R was identified as Mollar Cano Rose (VIVC 26543); uKn Mte_Barr corresponds to Montua B (VIVC 2520); uKn Mte_Cor 1 and uKn Mte_Cor_2 are both synonyms of Ahmeur Bou Ahmeur R (VIVC 140); uKn_4 B BrSousa was identified as Síría B (VIVC 2742); uKn_2 BrSousa corresponds to Samarrinho B (VIVC 15684) and uKn (14111) corresponds to Alvadurão B (VIVC 20806).

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For two of the uKn accessions— uKn_2 N and uKn_(14213), it was not possible to establish an identification. In the latter case, SSR analysis was inconclusive; however, leaf morphology showed similarities with varieties from the Couderc family.

Mosc_Banana 1 and Mosc_Banana 2 were found to be homonyms: the 1st correspond to Ferdinand de Lesseps B (VIVC 4088), while the 2nd match with Nuno Gomes B (VIVC n°. 15066). None of these grape varieties had previously been described in Portugal, although Nuno Gomes is a Portuguese name, and this variety is preserved on FRA139 collection, with Portuguese origin. July Pearle B was identified as a synonym of Presentabil B (VIVC 23192).

Considering biotic and abiotic stress responses, Presentabil B was classified with a score of 7 for both downy mildew and powdery mildew in 2024, and scores of 7 and 9, respectively, in 2025. For uKn (14213), the phenotype was also classified with scores of 7 or higher in both 2024 and 2025. Interestingly, similar results were observed for Síría B (VIVC n°. 2742). In 2024, this variety exhibited a score of 7 for downy mildew and 5 for powdery mildew, whereas in 2025 it reached a score of 7 for both diseases.

Overall, the results highlight the importance of preserving old grapevine varieties from ancient vineyards in Portuguese Ampelographic Collection (CAN – PRT 051) and of conducting further in-depth studies of these gene pools, with the aim of identifying levels of tolerance or resistance to biotic and abiotic stresses and linking specific phenotype-genotype characteristics to the diverse territories of cultivation.

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POSTER
SESSION:
GENOMICS AND FUNCTIONAL GENETICS



POSTER

A curation framework for a genome-anchored grapevine QTL browser: insights from phenology

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Keywords: complex trait genetics, data integration, FAIR data principles, QTL database and browser, phenology

ABSTRACT

Over the past few decades, Quantitative Trait Loci (QTL) mapping has been widely applied in grapevine to investigate the genetic architecture of complex traits. However, this extensive body of information has been only partially exploited in genetic research and breeding programs, mainly due to poor data accessibility, heterogeneous reporting formats, limited QTL mapping resolution, and variable robustness of QTL detection. To address these limitations and promote FAIR (Findable, Accessible, Interoperable and Reusable) use of existing data, QTL experts from around the world have joined forces, building on the CIG GRAPEDIA initiative, to lay the foundation for a community-accessible Grapevine QTL Browser (<https://grapedia.org/qtl-browser/>).

QTL data from more than 150 peer-reviewed studies published between 2000 and 2025 were manually surveyed and curated, comprising several thousand QTLs spanning seven major trait classes (abiotic stress, agronomical, biochemical, biotic stress, morphological, phenological, and technological traits). To this end, a structured annotation scheme comprising approximately 70 standardized descriptors was defined, covering phenotypic variables and protocols, genetic materials, and QTL mapping parameters and outputs. Annotations were harmonized, whenever

possible, with existing ontologies and public databases. A dedicated web-based frontend was developed to support structured data upload and expert curation.

As a proof of concept, phenology-related QTLs were analyzed in a pilot study. The dataset comprised approximately 500 QTLs associated with five major developmental stages (budbreak, flowering, veraison, ripening, and end of the vegetative season), derived from 13 biparental populations and three association panels. This case study highlights the potential of the Grapevine QTL Browser for trait-specific QTLome compilation, cross-study QTL validation, and refinement of genomic intervals for candidate gene prioritization. Additional key developments enabled by this framework include the extension of the Vitis Ontology and the integration of the Grapevine QTL Browser with the Grapevine Gene Catalogue.

Overall, the Grapevine QTL Browser represents a scalable resource for systematic QTL integration and provides a foundation for linking bi-parental population studies, GWAS (Genome-Wide Association Studies), and functional genomics resources to support grapevine research and breeding.



POSTER

A telomere-to-telomere genome assembly of *Vitis vinifera* cv. Glera to support grapevine breeding and genetic research

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Keywords: *Vitis vinifera*, telomere-to-telomere genome assembly, long-read sequencing, structural variation, pangenome

ABSTRACT

Grapevine (*Vitis vinifera* L.) is a clonally propagated crop of high economic value and remarkable genetic complexity, characterized by extensive structural variation and heterozygosity. These features make the generation of contiguous and accurate genome assemblies challenging, often leaving important genomic loci unresolved. Advances in sequencing technologies have enabled the generation of a high-quality telomere-to-telomere (T2T) genome references, which provide complete, gapless representations of chromosomes and allow the resolution of highly repetitive and structurally complex regions that remain inaccessible in fragmented assemblies. Here, we present a T2T genome assembly for *Vitis vinifera* cv. Glera, the main cultivar used for Prosecco production and one of the most economically relevant grapevine cultivars in Italy. Despite its agronomic importance and the presence of numerous clonal lines displaying phenotypic variability, genomic resources for Glera remain limited. The assembly integrates complementary sequencing technologies, combining PacBio high-

fidelity (HiFi) long reads and ultra-long Oxford Nanopore Technologies (ONT) reads with chromatin conformation capture (Hi-C) data. The resulting genome provides a high-quality reference for functional genomics and breeding studies, enabling improved detection of structural variants and gene duplications, and supporting the investigation of relevant genomic regions that were previously unavailable. In a broader perspective, this work will represent a key step toward the construction of a grapevine pangenome. Using this high-quality T2T genome as a foundation, it becomes possible to move beyond single-reference frameworks and develop graph-based genomic representations capable of capturing both core and variable genomic components by integrating multiple assemblies from different cultivars. Such approaches will provide a more comprehensive view of grapevine genomic diversity and support advanced applications in population genomics, trait mapping, and genomic-assisted breeding.

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POSTER

An advanced genotyping tool to inspect grapevine variability: the Axiom®Vitis22K SNP array

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Keywords: genome-wide analysis, high-throughput genotyping, marker/genome assisted breeding, genetic diversity, *Vitis* spp

ABSTRACT

Grapevine is one of the most relevant fruit crops worldwide, owing to its extensive distribution and considerable socio-economic significance. While the cultivated Eurasian species *Vitis vinifera* dominates global grape production, wild *Vitis* species from Asia and North America constitute essential genetic reservoirs, offering allelic diversity associated with tolerance or resistance to several biotic and abiotic stresses. Genotyping is a key tool in grapevine genetics, as it enables the assessment of genetic diversity, the elucidation of the molecular basis of agronomic and adaptive traits, and the implementation of marker-assisted selection. SNP (single nucleotide polymorphism) arrays provide an efficient genotyping tool, combining high-throughput capability, cost-effectiveness, and dense genome-wide marker coverage.

Here, we report the development and validation of the Axiom®Vitis22K SNP array, implemented within a broader multi-species 70K SNP platform. The array includes informative SNPs from the GrapeReSeq 18K *Vitis*

genotyping chip, SNPs and small InDels (insertions and deletions) putatively associated with phenotypic traits from literature, and novel SNPs obtained from the resequencing of 12 samples representing seven different grapevine species. Validation was performed by genotyping 144 genotypes from two diversity panels. Genotyping data were processed with the Axiom Analysis Suite and the newly developed AxioSAFE pipeline revealing a total of 10,314 robust polymorphic markers, together with 13 manually curated variants. These markers were successfully employed to study the genetic diversity and genetic relationships within the sample panels. Integration of genotypic and phenotypic data also enabled the validation of candidate SNPs associated with target traits such as flower sex type, seed content, berry color and taste. Overall, the results demonstrate the potential of the Vitis22K array to support large-scale genetic studies and breeding programs in grapevine.

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POSTER

Beyond the reference genome: A grapevine pangenome reveals hidden genetic architecture of agronomic traits

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Keywords: pangenome, structural variants, Pan-GWAS, phenology, berry development

ABSTRACT

Pangenomes capture the genetic diversity included in several genome assemblies. We can then use these pangenomes as a new reference for genomic studies. In this work, we sequenced and assembled nine cultivated grapevine genomes. We completed this dataset with six publicly available genomes and the PN40024 T2T, which resulted in 16 high quality assemblies of *Vitis vinifera* subsp. *vinifera* distributed within the genomic diversity of the species as defined previously.

From these genomes, we built a 1.1 Gb pangenome graph including 600 Mb of sequence absent from the reference genome and used it to genotype SNPs and structural variants in a diversity panel of 277 grapevine cultivars. As a proof of concept, we demonstrated that using this pangenome increases GWAS power for traits related to phenology, berry development and berry composition.

ACKNOWLEDGEMENTS

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POSTER

Characterisation of novel berry colour mutants originating in South Africa

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Keywords: berry colour, somatic mutations, R2R3 MYB, *Vitis vinifera*

ABSTRACT

Grapevine (*Vitis vinifera*) is considered as one of the most economically important crops worldwide. Throughout the course of its domestication history, grapevine growers have routinely relied on vegetative propagation and the subsequent natural accumulation of somatic mutations as a valuable source of phenotypic diversity. These mutations influence important agricultural traits, driving the development of new cultivars. Specifically, somatic mutations affecting berry skin colouration represent one of the major contributors of diversity in cultivated grapevine. Genetic studies have linked berry colour variation to mutations at the berry colour locus on chromosome 2, particularly in the VvMYBA1 and VvMYAB2 genes, which are the main determinants of berry pigmentation. Within the South African context, Sémillon and Cinsaut, and their colour mutants (Sémillon gris; Cinsaut gris and Cinsaut blanc) represent unique viticultural and genetic resources.

Notably, white-skinned Sémillon gave rise to the pink-skinned Sémillon gris. Similarly, purple-skinned Cinsaut has mutated to yield both the white-skinned Cinsaut blanc and the grey-pigmented Cinsaut gris mutant. However, the molecular basis underpinning the colour-related changes in these cultivars have not been elucidated. In this study, Pac-Bio HiFi long read whole genome sequencing was employed, followed by confirmatory molecular, chemical and histological analyses. Anovel layer (L1/L2) specific deletion of over 4 Mb was found to be responsible for the Cinsaut mutants. This deletion included the entire berry colour locus as well as approximately 100 additional genes, and was identified in the superepidermal (L2) cell layer of Cinsaut gris, resulting in a triallelic profile of the berry colour locus for this cultivar. Moreover, the exact same deletion is evident in both cell layers of Cinsaut blanc, leading to only one non-functional copy of VvMYBA1, and indicative of a sequential mutation event, where Cinsaut blanc arose from the displacement of the deletion from the L2 layer of Cinsaut gris to its outer L1 epidermis. In the case of Sémillon gris it was found that colour formation is due to the partial excision of the retrotransposon Gret1, retaining a solo-LTR (long terminal repeat) upstream of VvMYBA1, and leading to the recovery of VvMYBA1 expression. Significantly, while Gret1 excision is considered a rare event across grapevine cultivars in general, it has occurred independently multiple times in Sémillon gris.

The discovery and analysis of these unique colour mutants could help shed light on the mechanisms underlying somatic mutations, and their phenotypic implications in vegetatively propagated crops.



POSTER

Characterization of the LATERAL ORGAN BOUNDARIES Domain gene family in *Vitis vinifera*

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Keywords: *Vitis vinifera*, Downy mildew, LATERAL ORGAN BOUNDARIES DOMAIN, S genes

ABSTRACT

The LATERAL ORGAN BOUNDARIES DOMAIN (LBD) family is a group of plant transcription factors characterized by the presence of a conserved LOB domain, which facilitates DNA binding. First described in *Arabidopsis thaliana*, the LBD family has been identified in many plant species and has been seen to play a crucial role in a wide variety of processes, from plant development to the response to biotic and abiotic stresses. Up to nowadays, 50 VviLBD genes have been identified in grapevine.

To further investigate the role of the LBD family in grapevine, we have explored the expression profile of 46 VviLBD genes in 186 samples, coming from 6 organs at different developmental stages, and under abiotic (light-exposed/light-excluded berries) and biotic (inoculation with *Plasmopara viticola*, the causal agent of downy mildew) stress conditions. The experiment was performed in parallel on two *Vitis vinifera* cultivars, one susceptible (Pinot noir) and one resistant (Mgaloblishvili) to downy mildew. Gene expression was measured by a TaqMan

Gene Expression Assays based on the TaqMan Array Cards technology.

While the expression of most genes was found across different organs, the expression pattern varied among the different developmental stages and conditions, suggesting the role of specific subsets of these genes as developmental switches. For instance, VviLBDId6 showed regulated expression during berry ripening, whereas other members of the same family responded to the inoculation of *P. viticola*. Among the genes responding to the biotic stress condition, VviLBDId4 and VviLBDIIa1 were identified, as they display an expression profile typical of susceptibility (S) genes, indicating them as potential novel candidates. In addition, VviLBDIf7 showed an S-gene-like expression profile, and its involvement in the interaction with *P. viticola* was further validated through the use of dsRNA.

The results obtained present a detailed overview of the role of the LBD members across a wide range of conditions, providing insights relevant to future breeding programs.

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POSTER

CRISPR knockout reveals dual role of DMR6 in grapevine

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Keywords: *Vitis vinifera*, salicylic acid, DMR6 Water limitation

ABSTRACT

Grapevine (*Vitis vinifera*) faces increasing pressure from combined abiotic and biotic stressors. Achieving dual stress tolerance through editing of a single target offers a promising strategy for the development of robust, climate-resilient crops. Several studies have reported on the successful inactivation of host susceptibility genes for obtaining improved disease resistance in grapevine. Specifically, silencing of the well-described DOWNY MILDEW RESISTANT 6 (DMR6) gene leads to enhanced downy mildew (DM) resistance through the modulation of salicylic acid (SA) accumulation.

Beyond this, recent evidence has revealed that the inactivation of DMR6 also confers improved abiotic tolerance in tomato and potato. Therefore, the present analysis investigated whether editing of VvDMR6.1 could extend to abiotic stress resilience. VvDMR6.1-edited plants were obtained through CRISPR/Cas9-genome editing and Vvdmr6.1-mutant lines were assessed for DM resistance and subjected to water deficit conditions. Physiological and molecular analyses revealed that mutant lines exhibit a distinct water-saving strategy, maintaining high stomatal conductance under well-watered conditions, while a significant decrease was observed under water limitation. This was accompanied by elevated abscisic acid (ABA) accumulation, upregulation of major ABA biosynthesis genes (VvNCED1 and VvNCED3), and enhanced antioxidant defences (VvSOD, VvAPX, VvSTS). Additionally, VvDMR6.1-mutants demonstrated decreased susceptibility to DM, consistent with previous findings. Taken together, these results establish VvDMR6.1 as a promising target for developing dual-stress resilient cultivars.



POSTER

Deciphering the genetic determinants associated with key phenological stages of berry development in table grapes

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Keywords: GWAS, MAS, molecular markers, phenology traits, plant breeding

ABSTRACT

Grapevine (*Vitis vinifera* L.) is one of the most economically important fruit crops at worldwide level, and its development is highly dependent on environmental conditions. Characterizing the genetic basis of key phenological stages could support the development of new selection tools for table grape breeding aiding adaptation to climate change. In this study, a diverse collection of 116 genotypes was evaluated across three seasons to identify the genetic determinants of major vegetative and reproductive stages, from woolly-bud to harvest. Vigor-related traits such as effective leaf area index, photosynthetic efficiency, and internode number related were also gauged.

Genotyping-by-sequencing (GBS) identified 116,751 high-quality biallelic SNPs, which were used for genome-wide association studies (GWAS). Multiple genomic regions, or hotspots, associated with vegetative and reproductive phenological stages were identified, with significant SNPs clustering on specific chromosomes (chr.), notably chr. 2, 4,

5, 13, 16, and 18. This finding suggests that certain genomic regions act as regulatory hotspots controlling key transitions on budbreak, flowering, and veraison. Significant SNPs associated with hormonal signaling and stress responses highlight the interplay between developmental regulation and environmental adaptability, related to phenology progression.

Significant SNPs associated to reproductive stages revealed a strong over-representation of transmembrane transport, receptor-like kinase activity, ATP-binding, and nucleic acid-binding functions categories, highlighting the importance of membrane-associated perception and gene regulatory control during the reproductive development. Overall, this study reveals the polygenic architecture of grapevine phenology and provides a foundation for marker-assisted selection strategies to optimize phenological timing and quality traits under climate change scenarios.

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POSTER

Decoding grapevine somatic embryogenesis through 3D spatial transcriptomics

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Keywords: *Vitis vinifera*, spatial transcriptomics, somatic embryogenesis, cellular plasticity, grapevine biotechnology

ABSTRACT

Somatic embryogenesis refers to the process through which differentiated plant cells reacquire totipotency and regenerate into whole plants. In grapevine (*Vitis vinifera* L.), this developmental reset represents a crucial regeneration pathway supporting vegetative propagation, genetic transformation and, increasingly, DNA-free genome editing approaches whose successful application depends on robust and predictable regeneration systems. Despite its relevance, embryogenic competence remains incompletely understood, as the complex regulatory networks underlying totipotency are typically inferred from bulk transcriptomic analyses that lack cellular resolution and obscure spatial heterogeneity. Although single-cell RNAsequencing increases resolution, it disrupts tissue architecture and positional information that are central to plant developmental regulation. Spatial transcriptomics (ST) overcomes these limitations by enabling in situ gene expression profiling while preserving spatial relationships between neighbouring cells. Recent technological advances allow the integration of serial sections into three-dimensional reconstructions, generating combined molecular and histological tissue

atlases at subcellular resolution (Schott *et al.*, 2024). However, 3D ST has not been implemented in grapevine and remains largely unexplored in plant developmental reprogramming. Here, we propose the first adaptation of this approach to grapevine somatic embryogenesis to generate spatially resolved expression maps of embryogenic calli and developing embryos. This strategy will allow the identification of transcriptional domains, embryogenic niches and cellular microenvironments associated with the transition from differentiated cells to totipotent embryogenic states, with a particular focus on the spatial coordination of transcription factors and hormone-related pathways shaping embryogenic reprogramming. Preliminary optimization of the workflow in grapevine embryogenic tissues provides encouraging evidence of technical feasibility and enabling subsequent spatial analyses.

More broadly, the implementation of 3D ST in grapevine represents a significant methodological advance for perennial crops, expanding the frontiers of spatial gene expression studies and strengthening the innovation capacity of viticulture research.

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POSTER

Dissecting the genetic basis of susceptibility to Flavescence dorée in a *Vitis vinifera* progeny

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Keywords: Flavescence dorée, susceptibility, markers, GWAS, predictive modelling

ABSTRACT

Flavescence dorée (FD) is one of the most destructive epidemic diseases affecting yields of cultivated grapevine (*Vitis vinifera* L.) in Europe. FD is caused by a phytoplasma (FDp) classified as quarantine organism and transmitted by the leafhopper vector *Scaphoideus titanus* Ball. As no curative treatment against FDp is available, FD control relies on vineyard surveys, the uprooting of symptomatic grapevines, chemical control of the vector, and the use of disease-free propagation material. In the context of sustainable viticulture, alternative control strategies are therefore urgently needed. Several studies have reported differential susceptibilities among grapevine cultivars, although none are resistant.

Interestingly, the highly susceptible Cabernet Sauvignon (CS) and poorly susceptible Merlot (M) share a common parent, Cabernet Franc (CF), which displays intermediate susceptibility to FD. In contrast, the second parent of CS, Sauvignon Blanc, is highly susceptible, whereas the second parent of M, Magdeleine Noire des Charentes (MAG), exhibits low susceptibility. Therefore, the following question arises: is the reduced susceptibility observed in M heritable from MAG? To answer this question, we investigated

the genetic determinism of two phenotypic traits: (i) the proportion of FD-infected plants and (ii) the mean of FDp titer in infected plants. Crosses between MAG and CF (MAG x CF; CF x MAG) and resulting from a self-fertilization of MAG (MAG x MAG) were performed to generate a progeny of 125 individuals. We determined the susceptibility of the progeny, for both phenotypic traits, using a controlled FDp transmission assay by *S. titanus* under confined greenhouse conditions. In parallel, genomic analyses were conducted on healthy progeny plants using a genotyping-by-sequencing approach to identify potential constitutive biomarkers. Phenotypic assays revealed a wide range of susceptibility levels within the progeny. After filtering of the genotyping data, 11,942 SNP markers were retained, and genomic heritability values for both phenotypic traits were high (> 0.8). GWAS analyses and predictive modelling were then performed to identify SNP markers associated with low susceptibility to FD. These results will contribute to a better understanding of the genetic basis of grapevine susceptibility to FD and provide valuable perspectives for grapevine breeding.

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POSTER

Elucidating the transcriptomic bases of floral alterations hindering fruit set rate in Malbec clones

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Keywords: Malbec, fruit set, clonal variation, RNA-seq, flower mutation

ABSTRACT

Fruit set is the transformation of flowers into berries, a major component of yield in grapevines. The efficiency of this process depends on multiple factors, including plants' reproductive performance. In Malbec, it has been shown that fruit set rate is highly variable and clone dependent. Furthermore, extremely low fruit set rates were associated with morphological and functional floral alterations. Here, we aimed to elucidate the transcriptomic bases of such flower alterations by analyzing three Malbec clones. Clones Mb510 and Mb515 were selected for exhibiting consistently low fruit set rates, and clone Mb508 was selected as a high fruit set rate control. Total RNAs were extracted from flowers sampled before anthesis (stage EL-14), and each clone was represented by three biological replicates. RNA-seq was performed with Illumina technology to obtain stranded short-reads (average coverage 20x). Differential gene expression analyses were performed using a pipeline based on the R package DESeq2. Two pairwise analyses were performed to identify differentially expressed genes (DEGs): Mb508 vs Mb510 and Mb508 vs Mb515. In both comparisons several statistically significant DEGs were detected ($p < 0.05$), some of them relevant for flower development and functionality. In clone Mb510 low fruit set rate was linked to anthers indehiscence and low pollen viability. This phenotype was explained by the downregulated genes DEHYDRATION INDUCED PROTEIN (Vitvi10g00491) and EXPANSIN-A10 (Vitvi17g01251), involved in anthers' cell wall dehydration, loosening and opening. Furthermore, flavonoids are needed for the correct pollen maturation and a key enzyme for flavonoid biosynthesis was downregulated in Mb510: FLAVONOID 3'5' HYDROXYLASE (Vitvi06g01890). In regard to clone Mb515, low fruit set was associated with malformations such as stamen-pistil fusions, as well as decumbent/crinkled stamens. Two transcription factors associated with the described phenotypes were significantly downregulated in Mb515: CYCLOIDEA (Vitvi17g00374) involved in flower symmetry determination, and bHLH021 (Vitvi18g04102) involved in masculine organogenesis and gametogenesis. Overall, downregulation of key genes involved in floral development and functionality provided insight into the molecular mechanisms impairing fruit set rate and yield in specific Malbec clones.



POSTER

Engineering seedlessness in grapevine: insights from INNER NO OUTER gene functional studies

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Keywords: grape, seedlessness, gene-editing

ABSTRACT

Seedlessness is a key quality trait in table grapes. In *Vitis vinifera*, seedlessness can originate from different biological processes: parthenocarpy, the fruit formation without fertilization, or steno-spermarpy, when fertilization occurs but is followed by aborted seed development. A major genetic determinant for seedlessness from Sultanina, SdI, widely exploited in breeding, was shown to be associated to a missense mutation in the MADS-box gene VvAGL11. Alternative seedless phenotypes have been described in other species, including the ‘Thai seedless’ mutant of *Annona squamosa* and *Arabidopsis thaliana*, linked to mutations at the INNER NO OUTER (INO) locus. The INO gene AT1G2340 was characterized in *Arabidopsis ino-1* mutant. It encodes a YABBY-family transcription factor that regulates abaxial development of the ovule outer integument. Our previous study identified VviINO as the grape YABBY ortholog of AT1G2340. Functional complementation experiments demonstrated that VviINO fully restores the *ino-1* mutant phenotype, suggesting conserved activity. Despite that a functional characterization in grapevine is still required to assess its potential relevance for breeding of grape seedless cultivars.

Here, we used *A. thaliana ino-1* lines complemented with VviINO CDS developed in our previous study to assess a set of RNAguides for an efficient CRISPR/Cas9 knockout of the grapevine gene. Cas9 cleavage tests *in vitro* were first conducted. In parallel, floral dip transformation of *Arabidopsis* complemented lines enabled *in vivo* assessment of five guide RNAs constructs (three single guides and two tandem guides). Cas9-free T2 edited individuals exhibiting the rescued *ino-1* phenotype and altered seed set were rescued for two of the three single guides as well as for one of the tandem guide constructs, bearing different classes of mutations. Following assessment in model system, embryogenic calli of the grape cultivars ‘Bragat Rosa’ and ‘Chardonnay’ have been transformed with constructs of the more successful guides.



POSTER

EpiGRAPE: decoding histone acetylation in grapevine resistance to downy mildew

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Keywords: plant-pathogen interaction, *Plasmopara viticola*, epigenetics, histone acetylation, disease resistance

ABSTRACT

Epigenetic mechanisms, particularly post-translational histone modifications, are pivotal regulators of phenotypic plasticity in perennial crops. In *Vitis vinifera*, histone acetylation acts as a dynamic molecular switch that modulates chromatin accessibility, governing the transcriptional reprogramming required to cope with biotic stress. This regulation is especially critical during the interaction with *Plasmopara viticola*, the causal agent of downy mildew, which severely impacts grapevine productivity. To understand these defense mechanisms, this study explores the epigenetic landscape of two contrasting genotypes upon inoculation with *P. viticola*: Chardonnay (highly susceptible) and C19 (a Portuguese *Vitis vinifera* selection with enhanced resilience). We aim to characterize the acetylation status of Histone H3 and the transcriptional profile of its regulatory enzymes in these distinct genetic backgrounds. The experimental work followed a multi-level approach starting with the extraction of nuclear proteins from leaves to evaluate the levels of total versus acetylated

Histone H3 via Western Blot, complemented by protein quantification using ImageJ. Simultaneously, transcriptional activity is assessed through RNA extraction and RT-qPCR to monitor the expression patterns of Histone Acetyltransferases (VhATs) and Histone Deacetylases (VhDACs) during the compatible and incompatible interaction.

The data obtained will be instrumental for subsequent large-scale analyses, including Transcriptomics, ChIP-seq, and ChIP-MS, aimed at mapping genome-wide histone modifications and identifying the specific proteins associated with chromatin remodeling. These insights open new frontiers for precision viticulture, potentially leading to the development of epigenetic biomarkers for early resistance screening and the use of epi-priming agents. Ultimately, EpiGRAPE aims to provide a molecular blueprint for breeding or gene-editing programs focused on enhancing the natural defenses of *Vitis vinifera* against downy mildew, reducing the reliance on chemical fungicides.

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POSTER

Evolution and diversity of grapevine COP1 homologs

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Keywords: grapevine, genomics, phylogeny, evolution, COP1

ABSTRACT

Grapevine (*Vitis vinifera* L.) is a versatile organism and a key worldwide crop. One well-studied aspect of grapevine biology concerns the important agricultural trait of fruit color variation. In grapevine, the modulation of the berry color trait has been amply associated with the role of specific MYB transcription factors, yet the importance of upstream regulatory elements has been understudied. Here, we initiated a Pool-Seq genomics strategy to screen for additional genes associated with berry color variation. Our analysis highlighted a tentative role for CONSTITUTIVE PHOTOMORPHOGENIC1 (COP1) homologs in grapevine, prompting further examination of COP1 in this crop. The phylogenies performed within the present study confirmed

SUPPRESSOR OF PHYA-105 (SPAs) and REPRESSOR OF UV-B PHOTOMORPHOGENESIS (RUPs) as the WD40-repeat domain proteins most closely related to COP1 proteins. Notably, our results traced the emergence of SPA proteins to more basal species than previously reported, and suggested that the evolution of SPA and RUP proteins was not a parallel event. We annotated COP1, SPA, and RUP genes in grapevine, which were surveyed from an evolutionary and topological perspective. A possible sub-functionalization of the grapevine COP1 paralogs (VvCOP1a and VvCOP1b) is suggested through gene expression analysis across grapevine tissue and berry development.

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POSTER

Genomic diversity patterns linked to berry color variation

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Keywords: berry color, grapevine, genomics intra-varietal diversity

ABSTRACT

Grapevine (*Vitis vinifera* L.) is one of the most widely cultivated and emblematic crops in the world. Understanding the biology of grapevine, and how plant genetics determines the general performance of a variety is crucial for its optimization and quality monitoring. Advancements in genomic studies have enabled the use of refined technologies to explore the influence of genome-wide variations and evolutionary dynamics. Pool-Seq is a cost-effective genomics strategy that enables the generation of important information on genetic variation within a population. In the present work, we implemented a Pool-Seq strategy to characterize the clonal diversity of 18 ancient varieties. We carried out an extensive characterization of genetic diversity within each

variety, assessed genetic differentiation between varieties, and inferred on signatures of selection within the grapevine genome. A particular focus was placed on identifying selection signatures associated with berry color variation, by contrasting red versus white grape varieties. We detected several genes underlying selective sweeps for berry color variation, including the canonical MYB genes that compose the well-established berry color locus. However, the strongest selection signals were present in a downstream genomic tract that included multiple genes of interest, suggesting a more complex relationship between berry color variation, selection, and the aromatic profile of grapes.

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POSTER

GRASP (Genomic Region Affinity Sequestration by CRISPR purification): A plant transformation-independent CRISPR–Cas9 system for affinity purification of specific chromatin loci in isolated plant nuclei

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Keywords: grapevine, DAP-seq, gene regulation, CRISPR-Cas9, chromatin targeting

ABSTRACT

DNA–protein interactions play a fundamental role in essential cellular processes such as transcriptional regulation, DNA replication, recombination, and repair. Investigating these interactions is therefore crucial for understanding gene regulatory networks. Existing methodologies can broadly be classified into two conceptual frameworks: protein-centered approaches, which identify genomic regions bound by specific transcription factors (TFs), and gene-centered approaches, which aim to identify the proteins associated with specific DNA loci. In grapevine (*Vitis vinifera*), we first exploited previously generated DAP-seq datasets covering 197 transcription factors, mainly from the MYB and WRKY families, to develop an in silico platform for exploring TF–DNA interactions. This framework enables both protein-centered analyses, allowing visualization of genomic targets for individual TFs, and gene-centered queries, where a selected gene can be interrogated to identify candidate TFs potentially binding its regulatory regions. While this resource is necessarily limited to the transcription factors included in the dataset, it provides a practical example of how gene-centered interrogation of regulatory interactions can be implemented computationally. Independently from

this computational framework, we developed a gene-centered experimental strategy based on CRISPR/Cas-mediated chromatin targeting, designed to enable the in situ purification of specific genomic regions. This approach aims to capture chromatin fragments associated with defined loci and ultimately identify proteins and potential long-range DNA interactions linked to these regions. The method was initially validated using telomeric repeats, which represent highly repetitive genomic targets, and subsequently extended to more complex loci including members of the stilbene synthase (STS) gene family, as well as single-copy genes such as Stay-Green and actin. At the current stage, the method allows efficient enrichment and recovery of DNA associated with the targeted chromatin regions for all tested loci. Proteomic characterization of associated proteins has so far been successfully performed only for telomeric regions, while optimization of protein recovery for less repetitive targets is currently ongoing. Together, these approaches highlight the potential of combining computational resources and CRISPR-based chromatin targeting strategies to move from protein-centered analyses toward truly gene-centered investigations of regulatory interactions in plant genomes.

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POSTER

Haplotype-resolved genomics reveals structural variation and parental haplotypes in global grapevine rootstocks

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Keywords: rootstocks, structural variation, parental haplotypes, pangenome

ABSTRACT

Grapevine rootstocks remain the primary defence against phylloxera and soil-borne stresses in viticulture. However, increasing climatic variability and emerging environmental constraints demand the development of improved, climate-resilient rootstock varieties. Conventional rootstock breeding is slow due to long generation times and complex hybrid backgrounds, highlighting the need for genomics-assisted strategies. Despite their importance, genomic resources for rootstocks remain limited compared with scion cultivars.

Rootstocks are predominantly derived from wild *Vitis* species and interspecific hybrids, resulting in high heterozygosity, complex ancestry and extensive structural variation. To capture this diversity, we analysed a panel of 27 grapevine rootstock cultivars used across the globe, including two newly developed rootstock lines from the Department of Plant Breeding, HGU. All genotypes were sequenced using Oxford Nanopore long reads (> 100 × coverage) and assembled into haplotype-resolved genomes. The assemblies achieved an average N50 of ~ 26 Mb across 54 haplotypes with mean assembly sizes of ~ 529 Mb, enabling high-resolution comparison of both inter-cultivar and intra-cultivar haplotypic variation.

Initial comparative analyses indicate substantial structural variation and haplotypic divergence among rootstocks, including large presence-absence variants and introgressed haplotype blocks derived from distinct *Vitis* parental lineages. This framework enables the assessment of how structural variants, introgressed segments and haplotype blocks of parental origin are inherited, reshaped, or lost across F1-derived clonal generations. Ongoing analyses aim to quantify the gain, loss and rearrangement relative to gene space. These results and analytical approaches will be presented and discussed.

Using these new genomic resources, we are constructing a graph-based rootstock pangenome, which will also be presented as a developing framework for haplotype-guided breeding. By enabling direct haplotype-aware marker development and the targeted selection of structurally conserved or variable genomic regions relevant for rootstock breeding this work will provide a foundation for the development of molecular tools to accelerate the design of rootstocks adapted to future environmental challenges.



POSTER

Homozygosity of the berry color locus on chr 2 in *Vitis vinifera* cv. Dornfelder, Domina and Probus

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Keywords: VvmybA1c allele, berry color locus, anthocyanin biosynthesis, cultivar differentiation

ABSTRACT

Achieving intense berry coloration and high phenolic ripeness represents a major challenge in cool climate viticulture, where lower temperatures often limit anthocyanin accumulation and the production of full-bodied red wines. Therefore, the selection of grapevine varieties capable of synthesizing and accumulating sufficient levels of anthocyanins, while maintaining desirable agronomic and oenological traits, is of great importance for wine-growing regions under such climatic conditions. This study investigated the genetic and biochemical basis of enhanced berry coloration in the grapevine varieties 'Dornfelder', 'Domina', and 'Probus'. All three cultivars were identified as homozygous for the VvmybA1c allele at the berry color locus on chromosome 2, known as the black color allele. Homozygosity at this locus was associated with a significant increase in total anthocyanin concentration in berry skins compared to their parental varieties. The increased anthocyanin accumulation led to wines with higher color density, indicating an additive effect of color alleles on the regulation of anthocyanin biosynthesis. Statistical analysis confirmed positive correlations between total anthocyanin content, wine color density, and alcohol level, which could be described by a regression model. Among the studied cultivars, 'Domina' and 'Dornfelder' exhibited the highest color density in the resulting wines. Anthocyanin profiling demonstrated cultivar-specific composition patterns. Mono-glucosides were the predominant compounds in all three varieties, while secondary anthocyanin forms differed among cultivars. In 'Probus' and 'Domina', anthocyanin dimers were the second most abundant group, whereas in 'Dornfelder', 3-coumaroyl derivatives were present in higher amounts. Cluster analysis based on anthocyanin concentrations in berry skins and wines confirmed the close genetic relationship between the homozygous cultivars and their parental lines. Overall, the results highlight the importance of genetic background in determining anthocyanin accumulation and wine color intensity, and demonstrate that anthocyanin composition can serve as a reliable biochemical marker for grapevine cultivar differentiation.



POSTER

Identification of genomic regions associated with powdery mildew resistance in grapevine

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Keywords: *Erysiphe necator*, powdery mildew resistance, genome-wide association study (GWAS), quantitative trait loci (QTL), marker-assisted selection

ABSTRACT

Vitis vinifera L. is a perennial woody vine of global importance, both in terms of economic value and geographical distribution. Over the last decade, the progressive availability of genomic data has significantly advanced research in this field, fostering the integration of molecular breeding approaches into genetic improvement programs. These strategies, based on hybridization and Marker Assisted Selection (MAS) processes, aim to identify and characterize genes involved in phenotypic traits of interest, such as apireny (seedlessness), which is particularly valued in the table grape sector, and resistance to major fungal pathogens. In production contexts such as Italy, *Erysiphe necator*, the causal agent of powdery mildew, causes annual production losses of between 1 % and 25 %, with significant economic repercussions. The objective of this study is to identify genomic regions associated with powdery mildew resistance and to support marker-assisted selection in grapevine breeding. A full-sib population named FS-POP was established, crossing a Hungarian cultivar showing resistance to powdery mildew ('Terez') and a susceptible, seedless, table grape cultivar ('Autumn Giant'). To evaluate the segregation of the resistance/susceptibility trait in the FS-POP progenies, the genotyping and phenotyping results have been obtained. *Erysiphe* resistance assessments were conducted during peak disease pressure in the field, and observations included all individuals, using a susceptible cultivar as a control. Each plant was inspected for symptoms and scored according to the OIV (International Organization of Vine and Wine) descriptor lists, using the OIV455-1 (OIV, 1984) scoring scale from 1 to 9 to assess disease susceptibility or resistance. The phenotyping in the open field has been carried out for 3 different years. QTL mapping and GWAS analyses were performed to identify genomic regions associated with powdery mildew resistance. Preliminary analyses revealed segregation of resistance within the population and identified genomic regions potentially associated with the trait. The objective of this study is to identify genomic regions associated with powdery mildew resistance and to support marker-assisted selection in grapevine breeding.



POSTER

Identification of novel QTLs for black rot resistance derived from *Vitis rotundifolia* in grapevine pseudo-backcross populations

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Keywords: grapevine, black rot, *Vitis rotundifolia*, QTL mapping, Rgb4

ABSTRACT

Grapevine black rot, caused by the ascomycete *Phyllosticta ampellicida* (Engelm.), formerly known as *Guignardia bidwellii*, is re-emerging as a major disease in European vineyards. This resurgence is particularly pronounced in low-input production systems and in varieties carrying resistance to downy and powdery mildew, where fungicide use is reduced.

Despite its increasing agronomic importance, the genetic basis of black rot resistance remains poorly characterized, with only three quantitative trait loci (QTLs) reported to date, located on chromosomes 14 and 16. The limited number and moderate effects of these loci constrain the development of grapevine cultivars with durable resistance, underscoring the need to identify additional resistance sources.

This study aimed to identify new black rot resistance loci derived from *Vitis rotundifolia* and to characterize their effects under vineyard conditions. A pseudo-backcross 2 population, derived from the muscadine accession ‘22-8-78’ crossed with *Vitis vinifera* cv. Syrah, was evaluated under natural infection in an untreated vineyard over three consecutive seasons. The population was genotyped using

genotyping-by-sequencing (GBS)-derived SNP markers and subjected to QTL mapping. A major and highly significant QTL was consistently detected on chromosome 9, explaining up to 47% of the phenotypic variance for leaf resistance. This locus exhibited stable effects across years, observation dates, and plant organs. The resistance allele originated from *V. rotundifolia* and was associated with a marked reduction in symptom severity on both leaves and berries. Additional minor QTLs were identified on chromosomes 15 and 18, showing more limited and environment-dependent effects.

The major chromosome 9 locus, designated Rgb4, represents a previously undescribed source of black rot resistance, distinct from known loci on chromosome 14. These results demonstrate that *V. rotundifolia* remains a valuable reservoir of genetic variation for black rot resistance and confirm the relevance of vineyard-based phenotyping for identifying stable resistance factors. Rgb4 constitutes a strong candidate for marker-assisted selection and for pyramiding with other resistance loci to enhance the durability of grapevine cultivars in sustainable viticulture systems.

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POSTER

Investigating the black rot resistance locus Rgb7 in the cultivar ‘Villard blanc’ and its progeny

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Keywords: black rot, *Guignardia bidwellii*, *Phyllosticta ampellicida*, molecular markers, resistance loci

ABSTRACT

Grapevine is grown under extensive fungicide use, mainly due to two diseases native to North America that were introduced to Europe in the nineteenth century, downy mildew and powdery mildew. Breeding programs aim to combine desirable properties for wine production from the European *Vitis vinifera* with resistance loci from North American or Asian wild *Vitis* species in new cultivars. The cultivation of these new disease-resistant varieties, so called “PIWIs”, allow the winegrowers to reduce the utilised amounts of fungicides as well as the number of applications needed. These changes in plant protection measures lead to an increasing number of infections with black rot (*Guignardia bidwellii*, synonym: *Phyllosticta ampellicida*), as the fungicides applied also controlled black rot. This fungus infects all green tissues in the plant including young berries in multiple infection cycles, resulting in reduced or complete loss of harvest.

In previous work, a cross-population of two cultivars resistant to black rot (‘Calardis Musqué’ x ‘Villard Blanc’) was investigated to further understand black rot resistance in grapevine. Quantitative Trait Locus (QTL) analysis revealed the resistance loci Rgb1, Rgb5 and Rgb6 in ‘Calardis Musqué’ as well as the resistance locus Rgb7 in ‘Villard Blanc’. ‘Villard Blanc’ is a resistant French cultivar that was frequently used for breeding in the twentieth century and gave rise to several pathogen-resistant varieties such as ‘Bianca’ and ‘Felicia’.

The current project aims to further analyse Rgb7 in ‘Villard Blanc’ and its progeny, as well as to potentially find additional resistance loci in ‘Villard Blanc’. Therefore, a cross-population of ‘Villard Blanc’ x *V. vinifera* is analysed. F1 plants were phenotyped for the degree of resistance after artificial infection. Genotyping of the plants was carried out with rhAmpSeq-markers, enabling the generation of a dense genetic map and QTL analysis. F1 individuals of the cross-population carrying the Rgb7 locus will be further analysed to better understand this specific resistance locus and develop Rgb7-associated markers for marker-assisted selection in breeding programs. The overall goal is to make this novel locus accessible for breeding of new cultivars with stacked black rot resistances.



POSTER

It's a berry story: integrating cistromics and co-expression to decode the MYB14/15 regulon in grapevine

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Keywords: DAP-seq, transcriptomics, co-expression, stilbene synthesis

ABSTRACT

The R2R3-MYB transcription factors VviMYB14 and VviMYB15 are established master regulators of the stilbene biosynthetic pathway in grapevine, directly modulating stilbene synthase (STS) genes. Despite their characterized roles, the broader regulatory network—including downstream effectors and pathway-coordinating genes—remains largely unresolved. The differential accumulation of stilbenes in early- versus late-ripening cultivars provides a unique transcriptomic window into how these MYBs govern metabolic shifts during fruit maturation.

To decode this complexity, we developed PETAL, an interactive R/Shiny web-platform that integrates DNAaffinity purification sequencing (DAP-seq) data with multi-tissue gene co-expression networks, bridging the gap between in vitro binding potential and in vivo functional relevance. A private version of PETAL was constructed utilizing grapevine DAP-seq data from 187 transcription factors (TFs) in Cabernet franc (a collaborative effort of the Universities of Padova and Verona) and the extensive Vitviz co-expression network. By applying stringent filters for binding affinity, promoter proximity, and tissue-specific expression, PETAL enabled the identification of the MYB14/15 regulon with unprecedented stringency.

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Notably, the identification of C4H2 and ERF110 as direct targets suggests a dual-level control mechanism: MYB14/15 may simultaneously prime upstream phenylpropanoid flux via C4H2 while initiating a regulatory cascade through the ethylene-responsive factor ERF110 to coordinate stilbene synthesis with the broader ripening program.

Our current objective is to cement these computational predictions by evaluating them against an independent, berry-specific transcriptomic dataset. This ongoing work focuses on berry development in two varieties with contrasting phenologies: Pinot grigio (early-ripening) and Raboso piave (late-ripening). By cross-referencing PETAL-derived regulons with the expression trajectories of these varieties, we aim to determine if these regulatory modules represent a conserved core across different genetic backgrounds. This validation step, alongside ongoing dual-luciferase assays and metabolite-transcript correlations, seeks to anchor the identified nodes in the physiological reality of fruit ripening. We also announce the imminent public release of the PETAL platform on Plantaeviz.

The coexpression data for the PETAL app was taken from the Plantaeviz platform where PETAL will eventually be integrated.



POSTER

Localization of genomic region associated with the leaf resistance to grapevine phylloxera (*Daktulosphaira vitifoliae*)

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Keywords: *Vitis*, breeding, QTL analysis, pest resistance

ABSTRACT

The present study aimed to identify genomic regions associated with leaf resistance to grapevine phylloxera (*Daktulosphaira vitifoliae*). A mapping population (MP), derived from a cross between 'Moscato Giallo' (*Vitis vinifera*) and the rootstock 'IAC766' {106.8 Mgt' [*V. riparia* × (*V. rupestris* × *V. cordifolia*)] × *V. caribaea*}, was used for this study. The MP and parental genotypes were grown under greenhouse conditions, and phylloxera infestation occurred naturally. The MP population was evaluated for phylloxera incidence, number of leaf galls, and damage severity on the fourth and fifth leaves from the shoot apex toward the base. The MP was genotyped using 2,000 rhAmpSeq DNA molecular markers in collaboration with Dr. Lance Cadle Davidson. PCR amplicons were purified, quantified, and sequenced using an Illumina platform (Illumina, San Diego, CA, USA). Genotypic data were initially converted into a VCF file and imported into TASSEL 5 software for genotype and marker filtering. Markers were further filtered using Lep MAP3 v.0.2, assigned to 19 linkage groups, and ordered. These linkage groups were used to construct genetic maps with MapChart software. For the identification of genomic regions associated with resistance, genetic map data were combined

with phylloxera phenotypic data. QTL mapping was performed in R using the R/qtl package. Interval mapping was conducted using the scanone function, based on a binary model (incidence data) and Haley–Knott regression. The significance threshold for the logarithm of the odds (LOD) score was determined by 1,000 permutation tests at $\alpha = 0.05$. Approximately two-thirds of the population exhibited complete resistance to phylloxera, frequently characterized by the presence of necrotic spots on leaves. Among progenies showing infestation, quantitative variation was observed for gall number and damage severity.

These results indicate the presence of a major resistance gene associated with additional genes of minor effect. QTL analysis identified a genomic region located on chromosome 18 significantly associated with leaf resistance to phylloxera. The QTL was detected in the same genomic region for all three evaluated traits ($\alpha = 0.05$), with LOD values up to 15.9. This study identified a novel source of leaf resistance to grapevine phylloxera and paves the way for the gene(s) underlying the resistance and the development of molecular markers for marker-assisted selection.

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POSTER

Microvine as a model system for functional gene characterization in grapevine berries

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¹ Department of Biotechnology, University of Verona, Strada Le Grazie 15, 37134 Verona, Italy**Keywords:** microvine, gene functional analysis, stable genetic transformation, berry ripening regulation, gene expression modulation/regulation

ABSTRACT

Despite significant progress in grapevine research, conducting functional genetic studies at the berry level remains challenging due to the species' physiological and developmental limitations, including its perennial growth habit, large plant size, and long juvenile phase. In this context, microvine offers a valuable alternative model by combining a dwarf stature, continuous flowering, and an accelerated reproductive cycle that enable rapid berry development under controlled conditions. Therefore, the microvine mutant represents a powerful platform for fruit-focused functional genomics and targeted genetic manipulation in grapevine.

In our group, inflorescences from microvine fruit cuttings grown under controlled environmental conditions were used to produce inflorescences for isolating stamens with immature pollen, which were then cultured in-vitro to induce embryogenic calli. Two distinct media, MSII and PIV, were tested for embryogenic callus induction, resulting in callus formation efficiencies of 2.8 % and 0.48 %, respectively. The embryogenic calli were subsequently subjected to in vitro regeneration assays using two different culture media, NN and X6, achieving whole-plant regeneration efficiencies of 42.35 % and 13.75 %, respectively. Regenerated plants were monitored for vegetative growth and development and were later successfully acclimated.

Through *Agrobacterium*-mediated stable transformation, we are currently using the microvine platform for the functional characterization of key genes involved in grape berry development and ripening. The VvAGL11 gene, a major regulator of seed development, is being knocked out to induce a seed abortion-like phenotype, providing a controlled system to investigate stenospermocarp mechanisms. Meanwhile, for the functional analysis of transcription factors VvNAC33, VvNAC60, and VvNAC18, recognized as key regulators of grape berry ripening, stable overexpression lines are being regenerated. Additional constructs, based on serial deletions of the NAC gene and promoter regions, are being developed to finely modulate their expression during berry ripening.

Overall, this work establishes microvine as a versatile and efficient platform for fruit-focused functional gene analysis in grapevine, enabling the dissection of molecular networks involved in berry development and maturation and supporting future strategies for genetic improvement in grapevine.



POSTER

Multi-omic dissection of interspecific grapevine rootstock-scion-environment interactions in the United States

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Keywords: hybrid, environment, transcriptome, metabolome, epigenetics

ABSTRACT

Gene regulation in grapevine emerges from interconnected above- and below-ground responses to the environment. Bulk molecular profiling has largely focused on scion cultivars, primarily *Vitis vinifera*, and has provided important insights for genotype-by-environment (G×E) interactions. As viticulture adapts to increasing climatic pressures, it is essential to evaluate these approaches in newly adopted interspecific hybrids and across the distinct climates where they are cultivated. Here, interspecific hybrid ‘Marquette’ scions were replicated across three experimental vineyard sites in the United States and

grafted to multiple rootstocks (1103P, 3309C, SO4, 5C), alongside homografted ‘Marquette’ and own-rooted ‘Marquette’ individuals. Leaf, berry, and root tissues were collected for multi-omic and phenotypic profiling, including transcriptomics, metabolomics, anatomy, epigenetics, and ionomics, to quantify the relative contributions of site and environment to scion genotype × rootstock genotype × environment interactions. Together, these datasets span distinct climatic regimes that strongly influence phenotypic plasticity and provide a mechanistic framework linking genotype, gene regulation, and observed phenotype.

ACKNOWLEDGEMENTS

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POSTER

QTL mapping of juice color in a *Vitis* interspecific hybrid ‘Chambourcin’-based population

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ABSTRACT

Berry juice color plays a critical role in determining grape and wine quality, influencing consumer preferences and market appeal. While most prior research has concentrated on berry skin pigmentation, studies examining juice color remain limited. This work explores the genetic basis of juice color in an F1 population of 273 genotypes derived from the *Vitis* interspecific hybrid ‘Chambourcin’ and *V. vinifera* ‘Cabernet Sauvignon.’ To evaluate juice color, a nine-category visual scoring system was developed based on OIV 225 and complemented by quantitative, image-based measurements of CIELAB parameters (L*, a*, b*), Hue, and Chroma. Additionally, a high-density linkage map was constructed with 421 simple sequence repeats (SSR) and 2,011 RNase H2-dependent amplicon sequencing (rhAmpSeq)-derived haplotype markers that clustered into 19 linkage groups (LGs). Across four harvest years, a stable quantitative trait locus (QTL) for juice color was identified on LG 2 within a 4.8 cM interval. Two rhAmpSeq-derived

markers within this QTL region (rh_chr2_14239122 and rh_chr2_14464718) flank three MYBA genes associated with anthocyanin biosynthesis.

Haplotypes at these two markers were used to screen 1,512 genotypes from the USDA–ARS cold-hardy *Vitis* Collection in Geneva, NY, resulting in the identification of 72 accessions carrying at least one of the target haplotype combinations.

Among these, 70 (97.2 %) were classified as Noir-skinned based on data from the *Vitis* International Variety Catalogue (IVVC). This high level of concordance was achieved despite the potential influence of the Gret1 retrotransposon and the possibility of recombination events in the region, both of which can affect berry juice color. Collectively, these findings facilitate marker-assisted selection and enhance insight into the genetic regulation of anthocyanin-related traits.

ACKNOWLEDGEMENTS

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POSTER

REDEL-shiny: A user-friendly interface for exploring differential expression landscapes integrating clustering, ontology, and co-expression-based enrichment

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Keywords: RNA-seq, differential gene expression, functional enrichment, co-expression, grapevine

ABSTRACT

RNA-seq is a standard approach for studying gene expression in grapevine, yet downstream bioinformatics remains a bottleneck. Existing tools cover only parts of the workflow and require varying expertise. Scripted R tools such as DiCoExpress support differential and co-expression analysis but require programming skills (1). Standalone web services such as g:Profiler, DAVID, Enrichr, and ShinyGO provide functional enrichment but are disconnected from analysis workflows and optimized for model organisms with well-curated databases (2–5). More advanced web interfaces for omics integration, co-expression, and network inference (RFLomics, AskoR, DIANE) still lack grapevine-specific support for multiple genome and annotation versions, limiting access to specialized resources (6–8). No existing tool provides an integrated, code-free solution addressing these species-specific needs.

We present REDEL-shiny, built on REDEL (R project for Exploring Differential Expression Landscapes), an R package integrating differential expression, clustering, ontology enrichment, and co-expression analysis. REDEL-shiny provides a workflow from raw counts to interpretation: data upload and validation, quality control (PCA, sample correlation), TMM normalization, and differential gene

expression analysis using edgeR (9) and limma-voom (10). Visualizations include volcano plots, MAplots, and heatmaps. The tool supports complex designs with up to three biological factors and one batch factor.

Functional analysis is integrated in the same interface: Gene Ontology enrichment (topGO (11), clusterProfiler (12)), gene set enrichment analysis (fgsea (13)), KEGG pathway visualization (pathview (14)), GO term reduction (rrvgo (15), GOSemSim (16)), and co-expression clustering (coseq (17)). Planned features include MapMan pathway mapping using Mercator annotations (18,19). Built-in grapevine gene identifier conversion simplifies access to organism-specific databases.

The application is containerized with Docker and validated with 3 grapevine datasets representing factorial, paired, and two-group designs. The differential expression module is functional, with functional enrichment and network analysis modules under active development. This tool aims to lower the bioinformatics barrier for grapevine researchers, enabling autonomous transcriptomic analyses.

Source code: REDEL R package: <https://forge.inrae.fr/egfv/bioinfo/redel>; REDEL-shiny: <https://forge.inrae.fr/egfv/bioinfo/redel-shiny>

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POSTER

SPET-based linkage maps for traits associated with berry texture and seedlessness in grapevine

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Keywords: *Vitis vinifera*, berry texture, seed size, QTL mapping, candidate genes

ABSTRACT

Berry texture and seed size are major components of grapevine fruit quality, influencing both consumer perception and technological performance; however, the genetic bases of these traits remain incompletely understood. In this study, Single Primer Enrichment Technology (SPET)-based high-resolution linkage mapping was used to dissect the genetic architecture of berry texture, berry color, and seed traits in a grapevine F₁ population of 200 individuals derived from crossing the seeded red wine cultivar Raboso Veronese and the seedless white table grape Sultanina. Dense pseudo-testcross genetic maps were independently constructed for both parents, each including over 1,200 molecular markers, and integrated with an extensive automated phenotyping dataset encompassing berry color, 28 texture-related traits, and 12 seed traits.

Quantitative trait locus (QTL) analysis confirmed major, known loci associated with berry color on chromosome 2 and with berry texture and seedlessness on chromosome 18. In addition, several minor-effect QTLs for berry texture components were detected in both genotypes: in Raboso Veronese they were found on chromosomes 11, 17, and 18, while in Sultanina they were detected on chromosomes 4 and 11. Although each of these loci individually explained a limited proportion of phenotypic variance, their combined effects contributed to the fine-scale modulation of berry mechanical properties.

Candidate gene analysis within QTL confidence intervals revealed contrasting, genotype-specific genetic architectures. In Raboso Veronese, berry texture was mainly associated with structural genes involved in cell wall remodeling and sugar transport. In Sultanina, regulatory genes related to

hormonal signaling and transcriptional control, including the seedlessness-related locus VvAGL11 and genes encoding NAC, AP2/ERF, SAUR, and F-box proteins, played a predominant role in coordinating berry texture and seed development.

Despite moderate map inflation likely resulting from residual genotyping inaccuracies inherent to highly heterozygous genomes, strong collinearity between genetic and physical marker positions supported the reliability of marker ordering and QTL localization.

Overall, this study represents the first application of SPET for linkage mapping in grapevine and provides novel insights into the genetic mechanisms underlying berry texture and seed traits, offering valuable targets for functional validation and marker-assisted breeding.



POSTER

Targeting genes involved in the organic acid metabolism of grape berry

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ABSTRACT

Global warming accelerates the loss of acidity in grape berries (*Vitis vinifera*), a critical parameter for wine quality and sensory freshness. During early development, organic acids (mainly malate and tartrate) are accumulated at high levels in the vacuole compartment of mesocarp cells, whereas at the onset of ripening, a sharp decline in acidity and a concomitant rise in pH occur. This decline is driven by two primary factors: the respiratory degradation of malate during ripening and its chemical neutralization by potassium ions (K⁺) accumulating in the vacuole. This PhD project aims to explore three strategic intervention points for stabilizing or enhancing grape acidity through the identification and functional characterization of candidate genes involved in enhancing vacuolar sequestration, reducing K⁺-driven neutralization and preventing malate efflux from the vacuole. Leveraging knowledge from model systems like tomato and apple, promising candidates to target have been prioritized through comparative genomics and analysis of existing grape berry transcriptomic datasets. For vacuolar loading,

the Aluminum-Activated Malate Transporter (ALMT) family and their potential transcriptional repressors (*e.g.*, members of the WRKY family) are key candidates for investigation. To counteract K⁺ influx, potassium transporters belonging to the Shaker (*e.g.*, VvK1.2) and KUP/HAK/KT families represent promising targets. For the still poorly understood mechanism of malate efflux, the Tonoplast Dicarboxylate Transporter (TDT) family in grape (VvTDTs) and tonoplast-associated protein kinases that may regulate their activity are promising targets for investigation. Preliminary expression analysis of these candidates across publicly available RNA-seq datasets reveals distinct temporal patterns during berry development. Some of these candidates show interesting expression profiles, with peaks at early ripening stages, as observed for certain potassium transporters or TDT family members. This project will validate the function of selected targets through heterologous systems and, ultimately, via targeted mutagenesis in grape, aiming to develop climate-resilient cultivars with superior and stable acidity.

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POSTER

Transcriptome profiling of genotypes showing contrasting bunch compactness subtraits reveals differential expression of genes involved in cell wall organization and terpene metabolism

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Keywords: bunch compactness, fruit quality, transcriptomics, wine and table grapes

ABSTRACT

Bunch compactness (BC) is a complex trait which can influence several aspects of fruit quality given its role in disease susceptibility, ripening heterogeneity and consumer acceptance (in the case of fresh grapes). It is determined by the simultaneous expression of several attributes, many of which are influenced by seasonal effects. High throughput phenotyping methods has enabled the study of BC variation and opened new avenues for its study in a more precise fashion. At the same time, GWAS analyses helped to identify some candidate genes, related to growth regulators metabolism. In this work we characterized the transcriptional profiles at early developmental stages and in two seasons, considering two genotypes (Dodrelyabi and Crimson seedless) with contrasting phenotypes for BC. Inflorescence samples were taken in 2024 and 2025 seasons at two stages: 10 leaves stage (E-L 16) and beginning of flowering (E-L 20). Then, RNAseq analyses were performed using EdgeR (FDR < 0.05, TREAT log2 fold-change:1) revealing that only a small portion of differentially expressed genes (DEGs) were common to both seasons (*e.g.* at E-L16 stage: 296 common genes of 1418 total DEGs and 271 common genes of 1250 total DEGs, for upregulated and downregulated

genes, respectively). The gene set enrichment analysis of the DEGs displayed several significant Gene Ontology terms in each case, suggesting a strong response for cell wall organization in Dodrelyabi and an elicited defense response along with redox-related processes in Crimson seedless, at both developmental stages. In fact, similar results are reported when applying weighted co-expression network analysis. Module identification with CEMiTool assembled a total of eight modules. Particularly, two modules (M2 and M4) were related to immune response and redox response, respectively. The M1 module was also enriched in several terms associated with pollen-based processes and cell wall, highlighting the importance of these processes within the developmental timeframe considered in this study. Finally, lists for the most expressed genes identified by RNAseq analysis, and the hub genes and co-expressed modules, are presented. Overall, this is one of the few works addressing transcriptional variation over consecutive seasons with focus in BC trait/subtraits. More conditions should be explored to identify conserved responses associated to BC, considering a larger set of grapevine cultivars.

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POSTER

Unravelling the genetic determinants of anthocyanin and polyphenol content in grapevines integrating genome wide association studies and metabolomic profiling

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Keywords: anthocyanin content, polyphenol content, metabolomic profiling, molecular markers, GWAS

ABSTRACT

The quality and productivity of grapevines are highly dependent on environmental factors. Climate change is altering grapevine physiology and wine production conditions, thus, winegrowers need to adapt to maintain optimal production and wine quality. Flavonoids and other phenolic compounds such as anthocyanins and flavonols constitute critical determinants of wine quality, affecting color, stability, and sensory profile of the wine. Our goal is to determine the genetic basis of sensory characteristics by integrating genome-wide association studies (GWAS) and comparative metabolite profiling. To address this issue, a diverse panel of 109 grapevine individuals, including varieties of different genetic backgrounds and segregant lines from the breeding program of the Instituto de Investigaciones Agropecuarias (INIA-La Platina), was characterized for anthocyanin and polyphenol total content in berries at harvest. Phenotypic variation for both traits was analyzed and analysis of variance (ANOVA) results showed significant differences due to genotype effect ($p < 0.001$). Subsequently, this panel was genetically characterized by genotyping-by-sequencing (GBS) approach, and GWAS were performed for the polyphenol and anthocyanin total

content, using a set of 116,751 good quality SNPs, the mixed linear model (MLM) and LIMMA software. Our preliminary results showed significant association of a genomic region for the former at the chromosome (chr.) 6, while for the latter, highly associated SNPs were identified at chr. 1, 7, 13, and 17. In parallel, a set of 22 varieties exhibiting contrasting phenotypes for polyphenol content (*i.e.* low content vs. high content) was analyzed to characterize the metabolomic profiling of anthocyanin and polyphenolic compounds by HPLC. The ANOVA results revealed significant genotypic effects for syringetin-3-O-glucoside ($p < 0.05$) and resveratrol ($p < 0.05$). Also, significant genotype $\times$ phenotype group interactions were determined for ellagic acid ($p < 0.001$), gallic acid ($p < 0.05$), procyanidin B1 ($p < 0.01$), hyperoside ($p < 0.05$), quercetin-3-O-glucoside ($p < 0.01$), syringetin-3-O-galactoside ($p < 0.01$), and syringetin-3-O-glucoside ($p < 0.05$). Further studies including transcriptional and metabolite characterization are currently under development. Our ultimate goal is to identify biomarkers associated to polyphenol and anthocyanin metabolites biosynthesis pathways, and evaluating their potential application in MAS breeding programs.

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POSTER CANCEL

POSTER
SESSION:
GENETIC IMPROVEMENT
AND BREEDING STRATEGIES



POSTER

A multi-species DArTag genotyping panel for grapes: design and validation across *Vitis* and *Muscadinia*

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Keywords: DNAMarker, microhaplotype, marker-assisted selection, linkage mapping, GWAS

ABSTRACT

Grapevine breeding and germplasm curation require a scalable, cost-effective genotyping solution that performs robustly across wine, table, raisin, juice, and muscadine grapes from diverse *Vitis* species. We designed and validated a targeted genotyping panel covering germplasm from both *Muscadinia* and *Euvitis* subgenera using the DArTag platform (<http://www.diversityarrays.com/>). To ensure multi-species performance, candidate variants were filtered to exclude sites in transposable elements, within 5 bp of indels, and low-quality or low-frequency variants, and to include variants in conserved genic regions that passed in-silico specificity checks via BLAST alignments of the 75 bp flanking sequences. The resulting 3K panel comprises 1000 high-quality rhAmpSeq core genome loci, 1000 *Muscadinia*-polymorphic loci, 1000 *Vitis vinifera*-polymorphic loci, and 40 trait-related markers, which include powdery mildew resistance (RUN1, REN3/4/6/9/11/12), downy mildew resistance (RPV3 and RPY10.3), sex determination (YABBY, APT3), seedlessness (VviAGL1), and muscat aroma (VvDXS1). We evaluated its performance on a broad, taxonomically diverse sample set that included *Muscadinia*, *Muscadinia* × *Vitis* hybrids, *V. vinifera* cultivars, wild *Vitis* species, and *Euvitis* interspecific hybrids.

Across samples, the panel delivered consistent, high-quality genotypes with low marker missingness and high replicate concordance. The results file (missing allele discovery count, MADC) reports read counts of 109 bp microhaplotypes for all marker loci. These microhaplotypes combine target variants (used in assay design) with tightly linked off-target variants within the same short sequencing fragment. Using microhaplotypes and target and off-target SNPs independently, we created linkage maps for a *Muscadinia* × *V. vinifera* introgression population. Additionally, high polymorphism in *V. vinifera* confirms its utility for cultivar breeding. The DArTag panel is available to the grape community through Diversity Arrays.

Because this panel is modular, it can be updated as new markers and targets emerge, supporting continued community adoption and interoperable, multi-species grape genotyping.



POSTER

Advancements in genetic and environmental factors for grapevine breeding against grape ripe rot

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Keywords: *Vitis*, selection criteria, *Colletotrichum* spp., phenotyping, biological control

ABSTRACT

Completed or ongoing projects were designed to identify, refine, and optimize phenotypic and molecular criteria for genetic improvement and management practices, aiming to reduce the incidence and severity of grape ripe rot (GRR). When GRR occurs, winegrowers harvest the grapes before physiological maturity or when the infected berries, leading to low wine quality in both cases. In addition, no effective chemical control of GRR is currently available, as it is caused by multispecies pathogens. Importantly, the disease is caused by multiple pathogen species and is highly aggressive in Southern Brazil, highlighting the need for genetic and sustainable solutions. So far, research activities related to GRR have enabled: discrimination of grapevine genotypes according to the degree of resistance to GRR, selection of parents for future crossing, generation of segregating populations for future resistance genes mapping, quantification of the genotype × environment interaction in three grow grapevine regions of Santa Catarina,

characterization of the genetic diversity of *Colletotrichum* spp., development of a diagrammatic scale for disease assessment, identification of differential responses of genotypes to distinct *Colletotrichum* spp. isolates, association between anthocyanin and polyphenol concentrations with GRR incidence and aggressiveness, mycoparasitism and antagonism of *Trichoderma* spp. against *Colletotrichum* spp., among others. The obtained results increased the scientific knowledge about the interaction between grapevine × *Colletotrichum* spp. and added additional criteria to support genetic breeding concerning the selection efficiency. Along-term purpose, a new grapevine variety with resistance genes to multiple diseases, including GRR, which is underway between UFSC and Epagri, will allow for lower production costs, reduced environmental and human health risks due to decreased fungicide use, and better alignment with consumer demands.

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POSTER

Agrobacterium-free genome editing in grapevine: biolistic transformation of somatic embryos

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¹ University of Zagreb, Faculty of Science, Division of Molecular Biology, Horvatovac 102a, 10000 Zagreb, Croatia**Keywords:** genome-editing, VvPDS, Cas9, biolistic, somatic embryogenesis

ABSTRACT

Grapevine cultivation is heavily dependent on chemical pesticides to manage biotic or abiotic stressors. However, increasing environmental and health concerns, alongside climatic and economic pressures, necessitate the development of more sustainable agricultural practices. Traditional grapevine breeding is hindered by long generation times and high heterozygosity, making the development of improved cultivars both time-consuming and costly. To enhance biotic and abiotic stress tolerance while reducing pesticide dependence, next-generation genetic engineering, specifically genome editing, offers a rapid and precise alternative. In this study, we demonstrate a proof-of-concept for targeted mutagenesis in grapevine somatic embryos (SE) using a single-plasmid CRISPR-Cas9 system. The use of an SE-based in vitro system ensures the maintenance of the desired genotype and facilitates efficient whole-plant regeneration. We targeted the VvPDS locus, an established marker gene in carotenoid biosynthesis whose disruption should result in a clearly observable phenotype. Transformation was achieved via biolistics (particle bombardment) to deliver DNA-coated microparticles into the embryonic tissues. Following bombardment, we successfully regenerated grapevine plants and analysed sequence alterations at the VvPDS target site. The induced mutations were found not to be biallelic, which was a necessary for the appearance of visible bleached sectors. The reason for that was a hidden heterozygosity at the target locus which was not immediately obvious from the genome sequence. Our findings underscore a critical bottleneck in grapevine editing: despite the availability of quality reference genomes, there is a fundamental necessity for initial, cultivar-specific biallelic genotyping of any targeted genomic region. Nevertheless, we demonstrated that somatic embryogenesis provides a valuable platform upon which more precise and efficient genome-editing strategies can be developed.



POSTER

Application of New Genomic Techniques (NGTs) to reduce the pathogen susceptibility in grapevine

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Keywords: grapevine, *Vitis vinifera*, DNA-free genome editing, S-genes, NGT plants

ABSTRACT

Preserving the genetic heterogeneity of grapevine provides a valuable reservoir of allelic combinations that can offer genetic traits to contrast biotic and abiotic stresses, highly advantageous for breeding programs. Next-generation viticulture will need to intensify the contribution of genomics and biotechnologies to solve phytosanitary and qualitative problems. The control of pathogens in viticulture often relies on the application of massive amounts of pesticides, especially fungicides, which comes at great costs for viticulture and poses a considerable risk for human health and the environment. Conventional breeding has played a key role in domesticating grapevine varieties, but it is a time-consuming process to develop new cultivars with desirable traits for cultivation, such as pathogen resistances. New plant genomic techniques (NGTs) offer a potential revolution in grapevine cultivation, and genome editing has been shown promising for targeted mutagenesis. The success of these biotechnological approaches relies on efficient in vitro regeneration protocols, particularly through somatic embryogenesis (SE). Although this method has proven to be successful in some *Vitis vinifera* species, its effectiveness varies due to the genotype-dependent nature of many cultivars. Considering the heterozygous nature and the widespread use of vegetative propagation of grapevine, protoplasts have proven to be particularly suitable for transgene-free genome editing applications. Despite, plant regeneration from protoplasts remains generally considered challenging in grapevine, DNA-free approaches preserve the genetic identity of the cultivars, which would otherwise be altered through crossing.

The focus of this study is to enhance in vitro plant regeneration process via SE and isolate and regenerate plants from protoplasts derived from embryogenic calli of Corvina and Garganega, two grapevine varieties of significant economic importance for wine production in the Veneto region, Italy. Protoplasts represent a versatile platform for DNA-free genome editing via the CRISPR/Cas9 system, enabling the targeted knockout of MLO and DMR susceptibility (S) genes associated with powdery mildew and downy mildew susceptibility in grapevine. This

research aims to accelerate the development of grapevine varieties with improved traits, overcoming the limitation of conventional breeding methods and this advancement aligns with European legislative demand about NGT plants.



POSTER

Comparative evaluation of regenerable cell systems in ‘White Riesling’ for future genetic modification approaches

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Keywords: grapevine, suspension culture, somatic embryogenesis, genetic modification

ABSTRACT

‘White Riesling’ is the flagship grapevine cultivar of the Rheingau region. However, due to climate change, its cultivation faces increasingly challenging conditions, including drought stress, high solar radiation, and heightened pathogen pressure. Biotechnological approaches provide a powerful toolkit to investigate and potentially modify the underlying physiological responses of the grapevine. Furthermore, anticipated changes in EU regulations are expected to open new opportunities for these technologies.

The Department of Plant Breeding at Geisenheim University possesses extensive expertise in anther-derived somatic embryogenesis across more than 40 varieties, achieving regeneration frequencies of up to 60 % in ‘White Riesling’.

Focusing on this cultivar, various synchronized cell culture systems are available in our lab as starting material for genetic modification: synchronized proembryogenic masses (PEMs), protoplasts (currently under development), and long-term suspension cultures with inducible regenerative potential. To minimize the inherent risk of chimerism, our recent research emphasizes the use of these synchronized materials.

Our in-house expertise in cryopreservation allows for the continuous provision of regenerable material, ensuring that PEMs and suspension cultures are available for transformation regardless of the season.

The objective of this study is to evaluate the suitability of ‘White Riesling’ suspension cultures for genetic modification and to determine whether these cultures indeed represent the most effective starting material compared to our other systems. This is a prerequisite for developing a platform for precise genome editing to support future functional genomics and targeted trait improvement in ‘White Riesling’.



POSTER

Effect of minor allele frequency on the predictive accuracy of genomic selection models optimized by grid search

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Keywords: *Vitis vinifera* L., feature selection, machine learning, genomic prediction, plant breeding

ABSTRACT

Although the grapevine (*Vitis* spp.) is among the oldest and most economically significant fruit species globally (Candar *et al.*, 2021), its genetic improvement faces major bottlenecks due to long juvenile periods and extended cycles for phenotype evaluation (Allewelt & Possingham, 1988; Camargo *et al.*, 2011; Bharati *et al.*, 2023). In this context, Genomic Selection (GS) has emerged as an effective alternative to traditional phenotypic selection, offering a robust framework to optimize breeding programs by significantly reducing generation intervals while enhancing predictive accuracy (PA) and expected genetic gains (EGG) (Souza *et al.*, 2019; Francisco *et al.*, 2021; Aono *et al.*, 2022; Bharati *et al.*, 2023). This study evaluated the effect of data dimensionality reduction on GS performance by selecting single-nucleotide polymorphisms (SNPs) based on Minor Allele Frequency (MAF) thresholds. The experimental design tested the predictive capacities of four machine learning (ML) algorithms (ElasticNet, K-Neighbors, Support Vector Machine Regression, and XGBoost) alongside the conventional Genomic Best Linear Unbiased Prediction (gBLUP) model. These were validated using three SNP datasets (11,115, 9,494, and 6,100 markers) filtered by MAF levels of 0.05, 0.1, and 0.2 across six genetic traits, while also comparing EGG between conventional breeding and GS via the breeder's equation. Results revealed that ML models

exhibited remarkable stability, with no significant differences in PA across different MAF-based SNP densities, except for Berry Length, which showed a substantial difference with XGBoost at MAF 0.2. Conversely, gBLUP demonstrated high sensitivity to dimensionality reduction, with MAF filtering significantly affecting its performance across all traits. This suggests that ML-based approaches offer greater flexibility in feature reduction than traditional GS models that rely on a genomic kinship matrix. Morphological traits generally achieved higher predictive capacities than chemical ones, with peak accuracies identified as: 0.79 for Berry Length (Support Vector Machine Regression, MAF 0.05), 0.61 for Cluster Length (gBLUP, MAF 0.1), 0.60 for Cluster Width (gBLUP, MAF 0.05), 0.55 for Rachis Fresh Weight (gBLUP, MAF 0.1), 0.58 for Maturation Index (gBLUP, MAF 0.1), and 0.35 for Total Soluble Solids (gBLUP, MAF 0.05). Furthermore, the trained models were applied to an external population, yielding results that were highly consistent with those obtained during training, underscoring their robustness. Ultimately, all GS models yielded genetic gains superior to those of traditional breeding, with improvements ranging from an 8.90-fold increase in Berry Length to a 2.86-fold increase in Total Soluble Solids, confirming that GS integration is exceptionally promising for enhancing efficiency in global viticulture.

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POSTER

Enhancing competitiveness through independent table grape breeding programs

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Keywords: seedlessness, downy mildew, powdery mildew, resistance, marker-assisted selection

ABSTRACT

Freeing seedless table grape producers from paying royalties on patents held by international breeding companies is a primary objective of the breeding programs promoted by the IVC (Italian Variety Club) network, an association of 20 grape producers in collaboration with SINAGRI s.r.l., a spin-off of the University of Bari “Aldo Moro” and research center CRSFA “Basile Caramia”. The initiative focuses on breeding new seedless table grape varieties specifically adapted to the soil and climatic conditions of southern Italy, while also ensuring resistance to powdery mildew (PM) and downy mildew (DM), the two most destructive diseases affecting grapevines. To date, approximately 30,000 seedlings have been obtained from seedless × seedless crosses and around 10,000 seedlings derived from 120 crosses aimed at introducing disease resistance. Selection for seedlessness and disease resistance has been supported by MAS (marker assisted selection). The first evaluation fields have been established over a total area of five hectares. In addition, a potted field trial of progenies has been set up to enable rapid screening for disease resistance. Evaluation has been carried out on both qualitative and quantitative performance and on the degree of resistance to the diseases, with multiple observations according to the different levels of precocity of the plants. Two comparison vineyards have been planted to support the registration of new varieties in the National Catalogue, and primary propagation sources have been established in a greenhouse. Procedures have also been initiated to secure European patent protection for the first five selected genotypes, one of which shows resistance to powdery mildew.



POSTER

Multi-omics – enabled next-generation breeding in native American muscadine grapes: translational genomics for improved fruit quality and stress resilience

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Keywords: grape, wine, germplasm, gene-editing, genetics, hormonomics

ABSTRACT

Native American muscadine grape (*Muscadinia rotundifolia*) represents a strategically important reservoir of allelic diversity for grape improvement. This species combines exceptional nutraceutical value with inherent resilience to biotic and abiotic stresses common in warm, humid production regions. As climate variability intensifies and disease and pest pressures evolve, muscadine-derived traits provide a complementary pathway to enhance the sustainability and stress tolerance of common grape (*Vitis vinifera*) while maintaining market standards for fruit and wine quality.

This presentation highlights how integrated multi-omics technologies enable a next-generation breeding framework that connects genetic variation to biochemical and physiological phenotypes with unprecedented resolution.

Genomic resources—including chromosome-scale reference assemblies, high-density SNP genotyping platforms, genome-wide association studies (GWAS), and structured breeding populations—are accelerating quantitative trait locus (QTL) discovery for complex traits related to fruit quality, stress adaptation, and reproductive development. These efforts are strengthened by transcriptomic profiling, which elucidates gene regulatory networks across developmental stages and environmental conditions. Integrating expression dynamics with genetic mapping allows precise prioritization of candidate genes within QTL intervals, facilitating marker-assisted selection and genome-informed breeding.

Metabolomics further advances genotype-to-phenotype translation by quantifying dynamic changes in nutraceutical and stress-responsive metabolites that influence berry composition,

ripening, antioxidant capacity, and environmental adaptation. When combined with genomics and transcriptomics, metabolomic datasets enable multilayered trait modeling and improve predictive accuracy for complex phenotypes. The addition of hormonomics introduces a regulatory dimension by linking hormone signaling networks to developmental and stress-response pathways.

To bridge discovery and deployment, gene-editing platforms validate high-confidence candidate genes identified through multi-omics analyses. Seedlessness serves as a case study within this pipeline, illustrating how QTL mapping and transcriptomic signatures converge on regulatory genes controlling seed and embryo development, followed by targeted CRISPR/Cas9-mediated editing to confirm causality and accelerate trait integration. This iterative discovery-to-validation framework reduces breeding cycle time and increases selection efficiency.

By USDA charter, the Florida A&M University (FAMU) Viticulture Center maintains the public germplasm collection of *Muscadinia* species and American native Pierce's Disease-tolerant *Vitis* species and serves as one of five National Clean Plant Centers for Grapes. Implementation of an accelerated, omics-guided breeding pipeline has led to the release of three patented cultivars in the past five years: two muscadines—'Floriana' (red wine) and 'Florida Onyx' (fresh fruit)—and one *Vitis* hybrid cv. 'Blanc du Soleil.' We are not only improving grapes—demonstrating that genomic discovery can translate directly into market-ready innovation.

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POSTER

New *in vitro* culture techniques for molecular editing programs in grapevine

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Keywords: *Vitis vinifera*, organogenesis, seedlessness, genome editing

ABSTRACT

Grapevine breeding programs have traditionally focused on the development of seedless table grape cultivars combining high berry quality with resistance to major pathogens, in response to both market demand and sustainability goals.

Maintaining the competitiveness of Italian viticulture also requires the introduction of innovative cultivars suitable for modern production systems. In this context, new breeding techniques (NBTs), including genome editing, offer promising opportunities for the genetic improvement of grapevine.

The successful application of genome editing approaches relies on efficient *in vitro* regeneration systems, which remain a major bottleneck for many grapevine genotypes. In particular, the induction of embryogenic callus and somatic embryogenesis from plant explants is a key prerequisite for genetic transformation and genome editing. Among the genes potentially involved in reproductive development, INO (INNER NO OUTER) has been identified as a candidate regulator of ovule development in grapevine.

This study aimed to develop an efficient protocol for callus induction from immature inflorescences and leaf explants of different table grape cultivars to support future genome editing applications targeting genes involved in seed development. Immature inflorescences and leaf explants from several *Vitis vinifera* table grape cultivars were *in vitro* cultured to evaluate their capacity for callus induction. The selected genotypes include commercially important cultivars widely appreciated in the table grape market, making them particularly relevant targets for genetic improvement. Different culture media were tested by modifying plant growth regulator combinations based on protocols reported in the literature. Media derived from Nitsch and Nitsch and Murashige and Skoog formulations, together with additional callus induction media, were compared to identify the most suitable conditions for embryogenic callus development.

Embryogenic responses were obtained from both immature inflorescences and leaf explants. The modified MS medium showed the highest efficiency for callus development from immature inflorescences in the Muscat Timpurium and Bolgar Rezy cultivars, whereas the best embryogenic callus

induction from leaf explants was observed on CIM medium in the Regal cultivar. These results provide a useful basis for the development of regeneration systems supporting genome editing approaches aimed at the generation of improved seedless grapevine cultivars.



POSTER

Next-generation genome editing and breeding genomics in *Vitis vinifera* and *Malus × domestica*

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Keywords: *Vitis vinifera*, *Malus × domestica*, CRISPR, genome editing, DNA-free editing; protoplasts, RNP delivery, single-cell systems, somatic embryogenesis, climate resilience, breeding genomics

ABSTRACT

The accelerating effects of climate change on perennial crops demand transformative approaches in plant biotechnology, particularly for grapevine (*Vitis vinifera*), a species historically constrained by limited genetic improvement and low transformation efficiency. Here, we present the newly established Breeding Genomics Group at the Laimburg Research Centre, focused on developing next-generation genome editing platforms for *Vitis* and *Malus*. Our work pioneers innovative CRISPR-based strategies aimed at generating transgene-free, precisely edited grapevine plants using single-cell systems and ribonucleoprotein (RNP) delivery.

By combining protoplast-based editing with advanced regeneration protocols, we aim to overcome current

bottlenecks in grapevine transformation and enable efficient, DNA-free genome editing. These platforms are integrated with multi-omics technologies, including transcriptomics and genome annotation, to identify key regulators of stress resilience and developmental traits. Additionally, we are establishing robust in vitro systems to support high-throughput screening and functional validation of candidate genes.

Through interdisciplinary research and international collaboration, this initiative seeks to position grapevine as a model for cutting-edge plant biotechnology, accelerating the development of climate-resilient cultivars adapted to Alpine and global viticultural systems.

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POSTER

Preliminary works on varietal selection for resistance to *Xylella*

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Keywords: interspecific crossbreeding, Pierce's disease, varietal selection, *Vitis arizonica*, *Xylella fastidiosa*

ABSTRACT

At the beginning of 2024, an outbreak of *Xylella fastidiosa* subsp. *fastidiosa* (Xff), ranked among the twenty priority pests, was intercepted on *Vitis vinifera* in Apulia (Cornara *et al.*, 2025), well-known to be the causal agent of Pierce's Disease (PD) of grapevine in California (Hopkins & Purcell, 2002). Given the high susceptibility of *V. vinifera* cultivars and the absence of genetic traits associated with the resistance to the bacterium, genetic improvement programmes should be activated at European level to develop resistant grape germplasm. The aim of this research is to analyse sources of resistance within the *Vitis* genus in order to plan a crossbreeding programme, supplemented by phenotypic selection protocols, for the introgression of resistance genes into *V. vinifera* plants.

Therefore, to address this aim, a systematic review of the literature publicly available, was carried out to identify American species potentially resistant to the pathogen. Indeed, the co-evolution with the pathogen has led native American species to develop resistance traits. Sources of resistance were found not only in *V. arizonica*, but also in *V. berlandieri*, *V. × champinii*, *V. aestivalis*, *V. rotundifolia*, *V.*

vulpina, *V. mustangensis*, *V. shuttleworthii*, *V. popenoei* and *V. nesbittiana* (Dimaglie *et al.*, 2025).

In 2024, a breeding programme was launched involving crosses between male plants obtained from *Vitis arizonica* seeds (by open pollination) and female-flowering of bunch grape cultivars Lambrusco di sorbara, Picolit, Moscato rosa and Kharistvala tetri. At the same time, the susceptibility of *V. arizonica* genotypes, used as parents, was investigated by artificially inoculating plants with bacterial suspension and monitoring the progression of the infection. Preliminary data on the response to infection of *V. arizonica* genotypes indicate a variable and differential behaviour, spanning from plants with milder symptoms to ones completely dead over a 6-months observation period.

The first filial generation (F1), resulting from the first crosses, comprises 256 hybrids and is currently undergone the phenotypic characterisation for selection for backcrossing. Future prospects include the evaluation of resistance to *X. fastidiosa* in the new obtained populations and the use of additional *Vitis* species in the breeding programme, in order to broaden the genetic base useful for the selection of resistant materials.

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POSTER

Relaunch of the PIWI grapevine breeding program at Geisenheim University

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Keywords: PIWI breeding, disease resistance, predictive breeding, resistance markers

ABSTRACT

The development of disease-resistant grapevine cultivars (PIWI) has become a key strategy to reduce fungicide inputs, increase climate resilience, and meet regulatory and societal demands for sustainable viticulture. While substantial progress has been achieved in recent decades, further genetic gain and accelerated breeding cycles are required to ensure practical implementation and market acceptance.

In 2023, the grapevine breeding program at Hochschule Geisenheim University (HGU) was relaunched, continuing a long-standing tradition that began in the 1960s and was interrupted between 2000 and 2023. The renewed program builds on valuable legacy breeding material with strong resistance backgrounds and favorable viticultural traits, complemented by the integration of modern PIWI parents to broaden genetic diversity and performance.

The main breeding objectives are stable resistance to downy mildew (*Plasmopara viticola*), powdery mildew (*Erysiphe necator*), and black rot (*Guignardia bidwellii*), combined with high wine quality and agronomic suitability, including yield stability, growth habit, and favorable phenological traits. A multi-stage breeding funnel is implemented, combining targeted parental selection, classical cross-breeding, and large seedling populations with successive phenotypic and genotypic selection steps. Early selection is based on artificial inoculation and natural infection, supported by established resistance markers (Rpv, Ren, Rgb). To accelerate genetic gain, innovative approaches such as early parental recycling and location-based grafting are applied to shorten generation intervals.

In parallel, the program is developing a structured reference population that will serve as the basis for future data-driven breeding. Systematic multi-site phenotyping and standardized trait recording are being established to capture genetic variation for disease resistance, agronomic performance and quality traits under diverse environmental conditions. These data will gradually be complemented by high-throughput genotyping and digital phenotyping approaches implemented at HGU. The long-term goal is to enable the use of predictive breeding approaches to support parental selection and early-stage seedling evaluation, particularly for complex traits that are costly or time-consuming to measure directly.

Since its restart, the program has expanded from a single cross in 2023 to 35 successful crosses in 2025, with initial resistance screenings already identifying highly resistant seedlings. Although advanced field trials are still under establishment, the program provides a foundation for a modern, predictive breeding strategy contributing to long-term sustainable viticulture and regional breeding capacity.



POSTER

Scaling disease-resistant grape varieties adoption: optimization of the ampelographic platform and management practices in Switzerland and Europe

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Keywords: grape breeding, varietal selection, grapevine resistance, disease control, sustainable viticulture

ABSTRACT

Grape breeding has benefited from a long and worldwide effort to develop new varieties able to control major diseases such as downy mildew, caused by *Plasmopara viticola*, and powdery mildew, caused by *Erysiphe necator*. The cultivation of disease-resistant grape varieties (DRV, also known as Pilzwiderstandsfähige, or PIWI) is expanding to reduce the negative health, environmental, and socio-economic impacts of plant protection products (PPP) in viticulture. However, viticultural regions are characterized by different climatic conditions and wine production typicity, highlighting the need for adapted varieties and viticultural-oenological practices. With the aim of scaling grape DRV-PIWI adoption, more than 40 recent grape varieties obtained across breeding centres in Europe (Switzerland, Germany, France, Italy, Austria, and Hungary) are under evaluation in three environmentally different regions in Switzerland: the hilly Lake Geneva coast (Changins College for Viticulture and Enology), the Aargau-Jura hills (FiBL) and the hilly Lake Zurich coast (Weinbauzentrum Wädenswil-Agroscope). The agronomic traits and oenological qualities of the varieties, and disease protection tools are evaluated in parallel vintages under the challenge of variable temperatures, rainfall and soil conditions. The efficacy and durability of grapevine resistance are monitored using the OSCAR EU protocol, which includes disease assessments and, for *P. viticola*, the genotyping of population virulence. The research will develop cross recommendations to support Swiss and European grape-wine growers in choosing suited grape varieties (Swiss national project 'OenoPIWI'), monitoring mildew epidemics and populations, and deploying decision support systems (DDS) and PPP (EU project 'GrapeBreed4IPM') to produce more sustainable wines.



POSTER

The Cornell Grapevine Breeding Program: developing disease-resistant cultivars for more sustainable wine production

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¹ Cornell University**Keywords:** breeding, marker assisted selection, disease resistance, digital phenotyping

ABSTRACT

The Cornell Grapevine Breeding Program (CGBP), based at Cornell AgriTech in Geneva, New York, develops new wine grape cultivars adapted to the northeastern United States (US) and other cool-climate regions. The program's goal is to breed cultivars that produce exceptional wines while thriving under challenging environmental conditions. A central focus is durable resistance to major grapevine diseases, including powdery mildew, downy mildew, and black rot, combined with winter cold hardiness and superior wine quality. Growers in the northeastern US face persistent challenges from high disease pressure, variable weather patterns, and rising labor and input costs. Humid summers and proximity to the centers of origin for major grape pathogens drive some of the most intensive fungicide spray programs in the US. As climate variability and disease pressures increase, growers urgently need cultivars that combine reliable environmental adaptation, durable disease resistance, reduced input requirements, and high wine quality. To meet these needs, the CGBP integrates traditional breeding with modern genomic and phenotyping tools to accelerate the development of resilient, high-value cultivars. Strategic crosses are made among elite parents with the goal of stacking multiple resistance genes for broad, durable disease resistance. Seedlings are grown in greenhouses and screened using marker-assisted selection for key resistance loci. Selected seedlings are planted in no-spray nurseries where they are exposed to natural disease pressure and evaluated for early vigor and resistance. Surviving vines are then planted in low-spray vineyards for further evaluation. Promising selections advance to replicated vineyard trials where mature vine performance, cold hardiness, and fruit traits are evaluated across multiple seasons. The program increasingly employs digital imaging and computer-vision tools, including the Cornell-developed PhytoPatholoBot, to generate standardized high-throughput phenotyping data for disease and vine traits. Fruit from early and advanced selections is harvested, analyzed for juice chemistry, and vinified in small experimental lots. Wine quality is evaluated using instrumental analyses alongside structured sensory evaluation. A trained sensory panel, complemented by industry and consumer tastings, provides feedback on aroma, flavor, mouthfeel, and overall quality

to ensure alignment with market preferences. Through this integrated breeding pipeline, the program is developing and releasing new cultivars that enable a reduction in fungicide use by up to 90%, improve grower profitability, and support sustainable cool-climate viticulture.



POSTER

The use of mutagenesis to generate variation: A case study in Pinot gris

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Keywords: clonal selection, cultivar improvement, grapevine breeding, cluster compactness, field trial

ABSTRACT

Genetic variation is the cornerstone of plant breeding. In traditional grapevine cultivars, intra-varietal diversity has declined due to decades of selection for elite genotypes, shifting breeding goals, the widespread replacement of diverse germplasm with high-performance clones, and environmental pressures. Historically, mutagenesis introduced novel genetic variation and economically relevant clones.

Buds of grafted grapevines from several traditional cultivars were irradiated with X-rays and fast neutrons. Among forty newly created clones, the long-term agronomic performance of three Pinot gris clones (1-31 Gm, 1-32 Gm, and 1-33 Gm) was assessed four decades after their creation. Across four consecutive years, yield, pruning wood weight, and key technical juice parameters showed only minor differences between clones, as evaluated using best linear unbiased estimates. In contrast, clone 1-31 Gm consistently exhibited higher concentrations of macronutrients (N, P, K, Ca, Mg) in the juice compared to the other two clones. Performance was strongly influenced by environmental conditions, and clones differed in the stability of individual traits across years, highlighting both the sensitivity of specific traits to changing conditions and the genotypic control of climate-responsive characteristics.

Cluster morphology was quantified using a 3D-based phenotyping pipeline, providing precise measurements of cluster compactness and shape. All three clones displayed a relatively loose cluster architecture.

The subtle yet meaningful differences in performance of the three clones tested offer growers the opportunity to select plant material tailored to production goals and to manage challenges such as *Botrytis* bunch rot under warmer, faster-ripening seasons. This highlights the long-term relevance of induced variation and provides insights into clone-specific performance and trait stability for informed selection in viticulture.



POSTER

Three new cold-hardy seedless table grapes released by the University of Minnesota

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Keywords: cold hardy, table grape, hybrid grape, seedless

ABSTRACT

The University of Minnesota grape breeding program is releasing three new cold-hardy, seedless table grapes. MN1296 (marketed as EmberGlo[®]), bred in 2004 from a cross between ‘Louise Swenson’ and MN1213, is a red grape cultivar with light, fruity flavors. MN1325 (marketed as ShadowGlo[®]), developed in 2007 from MN1130 MN1213, is a black grape cultivar with crunchy texture, slightly thicker skin, and a mild labrusca flavor. Its berry size and shape resemble blueberries, making it a potential substitute for blueberry in smoothies and baked goods. MN1369 (marketed as LumiGlo[®]), originating from a cross between MN1104 and ‘Petite Jewel’, is a green grape cultivar with a pleasant tropical aroma and flavor. Clusters can be harvested over a 3-4 week window, providing growers flexibility to meet market demand. In Minnesota, MN1369 typically ripens first (late August to early September), followed by MN1296 (early September), and MN1325 (mid-September). All three cultivars are seedless with only minor seed traces, show moderate resistance to downy and powdery mildews, and are rated hardy to USDA Zone 4. These new releases expand options for cold-climate grape and fruit growers, offering diversification in color, flavor, and harvest timing.



POSTER

Vinid'Occ – A multidisciplinary research program supporting grapevine variety innovation to shape the viticulture and oenology of tomorrow

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Keywords: varietal innovation, climate change, input reduction, multidisciplinary research, from gene to bottle

ABSTRACT

The 'Défi Clé Vinid'Occ' is a multidisciplinary research program—supported by the Occitanie Region and led by the University of Montpellier—which aims at responding to the major challenges faced by the wine sector, in a context of climate change in Occitanie and the reduction of viticultural and oenological inputs.

The programme focuses on the development of fundamental research of international scope from the gene to the bottle to the consumer. It enables the acquisition of the knowledge needed to support varietal innovation and accelerate changes in viticultural practices throughout the entire chain of plant material-production-processing markets.

The research work focused on four main themes:

- 1. The study of grapevine genome diversity in order to determine genes of interest for stress response or wine quality, specifically through a pan-genomic approach, the study of the plasticity of grapevine and its behaviour in response to water stress. It aims to guide future breeding programs to identify new interesting grape varieties at an early stage.
- 2. The experiments on soil management, the mobilisation of biodiversity in plots, the use of beneficial insects, and

trials of different training systems under stressful conditions, all of them coupled with varieties resistant to powdery mildew and downy mildew. The development of digital tools is also considered, facilitating vineyard management and winemaking, thanks to the acquisition of information, data processing and modelling.

– 3. The production of wine from resistant grape varieties has yet to be fully evaluated. With a particular focus on microbiological and technological issues, the project is aimed at gaining a better understanding of the oenological potential of resistant varieties, but also to determine the oenological criteria that are important for assessing the final quality of wines and the impact on the microbiota of the berries.

– 4. Finally, one of the current challenges is the transfer and application of innovations in the industry. Indeed, the Vinid'Occ initiative consults with economic stakeholders in the region and supports industry players in changing their practices. It studies market and consumer expectations, including to identify barriers to the implementation of new practices

ACKNOWLEDGEMENTS

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POSTER

ViniGWAS – towards the development of climate-resilient grapevine varieties

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Keywords: GWAS, markers, climate

ABSTRACT

One possible strategy to face the increasing challenges of climate change in viticulture is the breeding of new climate-resilient grapevine varieties using modern breeding techniques, *e.g.* marker-assisted-selection. The limiting factor in facilitating this is that the genetic background of the desired traits for climate-adaptation has not been sufficiently elucidated yet, like it has been for example for fungal resistance. To characterize these genomic regions, we are combining high coverage whole-genome sequencing (WGS) in a genome-wide association study (GWAS). Over 250 genotypes of the JKI Grapevine breeding institute have been genotyped with Illumina paired-end 150 bp WGS at IPK Gatersleben, yielding an average coverage of 30–35 ×. Several categories of phenotypic data have been collected: a) phenological data at different developmental stages, b) analysis of multiple grape must quality parameters at harvest time with FTIR and c) 3D-Scans of the grape clusters at harvest time. The phenotypic data has been collected for several years and exists for different traits from 2019 onwards. First calculations with the phenotypic data showed a high broad-sense heritability and a high correlation between the years. With the changing climate, developing grapevine varieties with later phenological development is more and more preferred. Hence the focus in this research is foremost the phenological development, mainly the time of budburst ($H^2 = 0.87$), time of flowering ($H^2 = 0.85$) and time of veraison ($H^2 = 0.92$). Over the years, more and more GWAS models have been developed, each having its own advantage for detecting different kinds (*e.g.* single-locus *vs.* multi-locus) of traits. We used different models to combine the WGS genotypic data with the phenotypic data to investigate the traits of interest. Uncovering the genetics of these traits is needed to develop corresponding genetic markers to make breeding climate-resilient varieties possible.

POSTER
SESSION:
DISEASE RESISTANCE AND
PLANT-PATHOGEN INTERACTIONS



POSTER

Characterization of the soil fungal microbiome associated with mildew-resistant grapevine varieties in La Rioja

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Keywords: downy mildew, powdery mildew, *Erysiphe necator*, *Plasmopara viticola*, PIWI varieties, filamentous fungi

ABSTRACT

The study was conducted using 9 fungal-resistant varieties planted at the “Finca Valdegón,” belonging to the Government of La Rioja. Specifically, the white varieties Fleurtaí, Soreli, Sauvignon Rytos, Sauvignon Kretos, and Sauvignon Nepis were analyzed, along with the red varieties Cabernet Eidos, Cabernet Volos, Julius, and Merlot Khoros. Tempranillo and Viura varieties were used as controls.

Four samplings were carried out between June and July, two in 2023 and two in 2024: the first without disease incidence and the second when infection was already present in the plants. A total of 0.5 kg of soil was sampled from the root zone (between 5 and 20 cm depth, corresponding to the area of greatest microbial activity) at 50 cm from the base of the plant along the row. DNA extractions were performed with the PowerSoil Pro Kit (QIAGEN) on the 66 samples corresponding to the two samplings (11 varieties × 3 blocks) each year. Fungal DNA was amplified using primers ITS86F and ITS4 which amplify approximately 300 bp of the internal transcribed spacer region of the 18S rRNA–5.8S rRNA (ITS). Purification, library preparation, and sequencing were performed using the DADA2 method, which generated amplicon sequence variants (ASVs). Taxonomic identification from phylum to genus level for each sample was performed using the QIIME2 algorithm by Novogene.

To compare phylum and order data among samples, mean comparisons were performed using ANOVA with Duncan’s test at a significance level of 0.05. The same test was used to compare alpha diversity parameters based on genus-level data. The alpha diversity parameters analysed were richness (R), abundance (N), Shannon (H), Simpson 1/D (S1/D, values between 0 and 1), dominance (D, values between 0 and 1), evenness (E, values between 0 and 1), equitability (J), and Berger–Parker (d, values between 0 and 1). Beta diversity was analysed using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA), based on the Bray–Curtis

(dis)similarity index. Anon-metric multidimensional scaling (NMDS) analysis using the Prefscl algorithm was used to position samples in a two-dimensional space based on their similarity in genus composition, highlighting the genera with the greatest weight in the analysis. Past 4.03 and SPSS v28 software were used for these analyses.

The analysis of the filamentous fungal microbiome, after applying a filtering process to remove singletons, allowed the identification of 238 genera belonging to 66 orders across 6 phyla. The phylum Ascomycota predominated in all samples, followed by Basidiomycota, as is typical in agricultural soil samples. Cryptomycota was detected only in samples from Fleurtaí and Julius. Zoopagomycota was the least abundant phylum, although it was present in approximately half of the samples, with higher incidence in those originating from healthy plants. Hypocreales and Eurotiales were the two most abundant orders, representing more than 50% of total reads in most samples. Order level analysis revealed 11 orders with relative abundances above 1% of total reads: Sporidiobolales, Eremomycetales, Rhizophydiales, Auriculariales, Botryosphaerales, Cantharellales, Chaetothyriales, Microascales, Cystofilobasidiales, Orbiliales, and Glomerales.

In summary, the fungal microbiome exhibited populations characterized by the co dominance of the orders Hypocreales and Eurotiales (which together accounted for more than 50% of all reads), as well as by the marked presence of a core of saprotrophic and antagonistic genera. The greatest variability observed among fungal populations could be attributed primarily to the health status of the plant, outweighing factors such as variety or sampling year. The fungal communities of the two varieties most susceptible to pathogens, Tempranillo and Viura, showed the greatest divergence from the rest.

Implications for further research will be discussed.

ACKNOWLEDGEMENTS

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POSTER

Comparative analysis of infection and defensive strategies associated with powdery mildew disease in grapevine and strawberry

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Keywords: powdery mildew, grape, strawberry, CRISPR-Cas9, omics, *in vitro* culture

ABSTRACT

Domesticated strawberry and grape are fruits of very significant commercial and nutritional importance worldwide. However, they are, respectively, highly susceptible to infection by *Podosphaera aphanis* and *Erysiphe necator* fungi causing powdery mildew. Fungicide application has effectively controlled powdery mildew; however, fungicides cause pathogen resistance and affect environmental and human health. Additionally, loss of active ingredients associated with stricter European regulations created new challenges.

Previously, we showed that susceptible grapes activate defence responses associated with PAMP-triggered immunity and effector-triggered immunity, together with salicylic acid- and jasmonate-related pathways and the accumulation of defence-associated metabolites, although these responses were insufficient to restrict fungal progression. Some of these responses were shared with leaves, while others were organ-specific. A similar workflow strategy (transcriptomics coupled with metabolomics and targeted metabolic profiling) is being used with strawberry leaves and fruits to understand the basis of organ susceptibility and resistance/ tolerance across two non-climacteric fruits challenged by two different PM fungi with the same lifestyle. These data will support the selection of candidate genes for CRISPR-Cas9-based mutagenesis aiming at improving powdery mildew resilience. Optimisation of *in vitro* culture processes required for plantlet transformation and regeneration is under investigation. Additionally, *in silico* analysis of the *Podosphaera aphanis* and *Erysiphe necator* secretome, and identification of putative powdery mildew-specific core effectome assisted by RNAseq data is being carried out to decipher the mechanisms of fungal virulence under host defensive strategies.

Altogether, this data will contribute to mitigate the impact of powdery mildew in two important fruit species.



POSTER

Early transcriptional responses associated with downy mildew resistance in grapevine

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¹ Höhere Bundeslehranstalt u. Bundesamt für Wein und Obstbau, Klosterneuburg**Keywords:** *Plasmopara viticola*, transcriptional response, RNA sequencing, Rpv-Loci

ABSTRACT

Downy mildew caused by *Plasmopara viticola* remains a central challenge in grapevine production, particularly under conditions aiming at reduced fungicide input. For this reason, breeding strategies increasingly focus on resistance loci (Rpv) derived from wild *Vitis* species. Although these loci are widely used in modern breeding programmes, the early molecular processes underlying their resistance response are still not fully clarified.

In this work, we examined transcriptional responses following infection with *P. viticola* in grapevine cultivars differing clearly in their resistance background. Leaf disc assays were performed using Grüner Veltliner as a susceptible *Vitis vinifera* cultivar and Seyval blanc as a genotype with established Rpv-mediated resistance. Samples were collected at early time points after inoculation and analysed by RNA sequencing.

After pathogen exposure, Seyval blanc displayed marked and rapid changes in gene expression. Grüner Veltliner, in contrast, reacted only weakly. Moreover, a considerable number of genes showed opposing regulation patterns between the two cultivars. Defence-associated transcripts, including genes related to stress signalling, reactive oxygen species metabolism and pathogenesis-related proteins, were strongly induced in the resistant genotype. In particular, numerous RPP13-like disease resistance transcripts were differentially regulated, often with opposing expression trends between cultivars, suggesting genotype-specific modulation of NLR-associated defence components.

In parallel, a subset of transcripts associated with chloroplast function and primary carbohydrate metabolism showed reduced expression or opposing trends in Grüner Veltliner relative to the resistant genotype, consistent with an early separation of basal metabolic adjustment and defence-related transcriptional activation.

Altogether, the data indicate that Rpv-mediated resistance is accompanied by an early and coordinated transcriptional adjustment. The candidate genes identified here will be further analysed by qRT-PCR and may support ongoing efforts to functionally characterise resistance loci relevant for grapevine breeding.



POSTER

Evaluation of novel cold-hardy rootstocks for phylloxera and nematode resistance across contrasting environments

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Keywords: rootstock, phylloxera, nematode

ABSTRACT

Pest- and disease-resistant rootstocks are foundational to sustainable global viticulture, offering a strategy to mitigate edaphic stressors and climatic variability while optimizing scion performance. This study evaluated four elite grapevine rootstock selections (i.e., RT24, RT40, RT50, and GE0937-18) developed by the University of Minnesota for growth morphology, propagation efficiency, phylloxera resistance, and cold hardiness.

These selections, along with own-rooted *Vitis vinifera* ‘Chardonnay’ as a control, were established in a randomized complete block design with three replicates in two geographically distinct regions in the U.S.: Minnesota and Washington. Viticultural metrics, including stem diameter, pruning weights, and number of acceptable propagative units, were generally higher in the Washington trials. Among the selections, GE0937-18 consistently exhibited the lowest vigor and the greatest propagation difficulty.

Resistance to plant-parasitic nematodes was validated through controlled greenhouse inoculations using three nematode species: *Meloidogyne hapla*, *M. incognita*, and *Mesocriconema xenoplax*. Results demonstrated a high degree of resistance across the new selections compared to the control. For instance, own-rooted ‘Chardonnay’ supported average densities of 27,375 (*M. hapla*) and 85,373 (*M. incognita*) eggs per gram of root, whereas the most susceptible new selection (RT50) restricted densities to just 75 and 252, respectively.

A comprehensive data matrix will be presented, providing a framework for researchers to integrate these rootstocks into future scion-interaction trials and sustainable production systems.



POSTER

Evaluation of resistance to powdery mildew (*Erysiphe necator*) in twelve Croatian grapevine cultivars (*Vitis vinifera* L.)

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Keywords: *Vitis vinifera* L., powdery mildew, OIV 455, leaf disc, SSR markers

ABSTRACT

The fungus *Erysiphe necator* causes powdery mildew (PM), one of the most significant diseases of grapevine. Observing visual disease symptoms is essential in virtually all pathosystems. Consistent phenotypic evaluations that accurately reflect the biology are of paramount importance for understanding disease resistance, even at the genotypic level.

Croatian grapevine germplasm represents an important portion of Mediterranean grapevine diversity, shaped by centuries of interaction between eastern and western gene pools. Despite its historical and genetic significance, it remains poorly studied in relation to PM resistance. In Croatia, only wild grapevine (*Vitis vinifera* subsp. *sylvestris*) germplasm has previously been evaluated for PM resistance, confirming partial resistance associated with Ren1-linked SSR markers and a notable presence of R-alleles. In this study, twelve cultivars were initially assessed for PM resistance through visual evaluation of spontaneous infection in vivo and by in vitro inoculation using the leaf disc method, applying the OIV 455 descriptor (inverted scale). Selected genotypes were further screened using three SSR markers linked to the Ren1 gene (UDV124, SC8-0071-014, and SC47-18). Two white cultivars, 'Malvazija istarska' and 'Kujundžuša', demonstrated elevated partial resistance under both greenhouse (open-style) and laboratory conditions over two consecutive seasons. 'Malvazija istarska' did not carry R-alleles at the analyzed SSR loci, whereas 'Kujundžuša' harbored R-alleles at two markers (UDV124/208 and SC47-18/246–246). 'Malvazija istarska' exhibited higher average phenotypic resistance than 'Kujundžuša' in the leaf disc assay (3.9 vs. 4.9), despite the absence of detected R-alleles. The leaf disc assay provided a more accurate assessment of the susceptibility of sensitive genotypes than observations based on spontaneous PM infection. This likely reflects differences in the source, quantity, and distribution of natural inoculum, as well as variation in infection dynamics and environmental conditions. Furthermore, it is essential to investigate the early responses of both resistant and susceptible genotypes to PM, particularly at stages before visible symptoms develop.



POSTER

Expanded host range of grapevine virus A in vineyard ecosystems

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Keywords: grapevine virus A, alternative hosts, vector transmission, vineyard weeds, epidemiology

ABSTRACT

Grapevine virus A (GVA), a member of the genus *Vitivirus* (family *Betaflexiviridae*), is an economically important pathogen associated with grapevine wood diseases and significant yield losses. While both cultivated and wild *Vitis* species are recognised as natural hosts, the role of alternative hosts in virus epidemiology remains poorly understood. This study investigated the ability of the vine mealybug (*Planococcus ficus*) to transmit GVA from infected grapevines to non-grapevine plant species commonly found in Croatian vineyards.

Transmission experiments conducted under greenhouse conditions over three consecutive years demonstrated successful vector-mediated infection of several herbaceous hosts. Serological and molecular assays (DAS-ELISA, end-point RT-PCR, real-time RT-PCR), complemented by electron microscopy and sequencing in selected cases, confirmed GVA infection in velvetleaf (*Abutilon theophrasti*), redroot pigweed (*Amaranthus retroflexus*), field poppy (*Papaver rhoeas*), nettle-leaved goosefoot (*Chenopodium murale*), and the previously known host *Nicotiana benthamiana*. Infection rates varied among species and experimental years.

Infected plants exhibited a range of symptoms including leaf reddening, chlorotic spotting, vein clearing, foliar deformation, reduced lateral shoot growth, and dwarfism, although infections in *A. theophrasti* remained asymptomatic. Attempts to transmit GVA back from infected herbaceous hosts to virus-free grapevines were unsuccessful under the conditions tested.

The identification of new alternative hosts suggests that weeds in vineyards may act as reservoirs of GVA inoculum and contribute to virus persistence and spread. These findings expand the known host range of GVA and provide new insights into its epidemiology, highlighting the importance of considering non-*Vitis* species in disease management strategies.



POSTER

Field performance of fungal resistant crop varieties under diverse integrated pest management approaches in northern Spain

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Keywords: grapevine, *Plasmopara viticola*, *Erysiphe necator*, disease management

ABSTRACT

Grapevine production in the EU faces increasing pressure from climate change, high pesticide dependence, and the need to maintain grape and wine quality while reducing environmental impact. Within this context, the SHIELD4GRAPE project aims to develop sustainable Integrated Pest Management (IPM) strategies and exploit resilient or resistant grapevine genotypes to reduce reliance on synthetic fungicides against downy mildew (DM), powdery mildew (PM) and trunk diseases.

This study focused on grapevine disease management through the combined use of powdery and downy mildew-resistant varieties and low-risk plant protection products. The objective was to assess the impact on yield, vine balance, disease control, and oenological traits of two treatments (orange oil and potassium bicarbonate, and Cu and S were used as controls) in two resistant varieties, with Viura included as a susceptible control, across two experimental locations (Valdegón and Arkaute). The interaction between variety, treatment, and environment was also evaluated.

Treatments significantly influenced must and wine composition. Linear discriminant analysis, using treatment as the grouping factor, clustered samples with the same

treatment together in the two-dimensional representation. In must samples from Valdegón, the orange oil treatment increased yeast assimilable nitrogen (YAN) in resistant varieties, while wines produced under this treatment showed lower alcohol content and volatile acidity. Wines from Cu-S treatments exhibited lower malic acid concentrations, whereas those treated with potassium bicarbonate showed higher total SO₂ levels. In the Arkaute samples, the IPTs were much higher for the Cu-S treatment, and the tartaric acid and volatile acidity was lower in the samples treated with orange oil.

Multivariate analysis of variance (MANOVA) demonstrated a notable interaction between variety and location, yield-related parameters were consistently higher in Valdegón compared to Arkaute. YAN value in the musts and the ethanol content in wines were also different between the two locations. The interaction between variety and treatment was not significant for either the productivity variables or the physicochemical parameters of the must or wine.

Implications of these results will be further discussed. The expected results will help the transition to a more diverse, environmentally-safer viticulture in the EU.

ACKNOWLEDGEMENTS

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POSTER

GLRaV-3 infection induces a metabolic reconfiguration of sugar transport and secondary metabolism in *Vitis vinifera* cv. Malbec

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Keywords: anthocyanin biosynthesis, hexose transport, source-to-sink relationship, virus

ABSTRACT

Grapevine leafroll-associated virus 3 (GLRaV-3) represents a significant threat to viticultural productivity. This study analyzed the impact of this pathogen on the expression of genes involved in hexose transport and flavonoid biosynthesis in leaves of Malbec, a cultivar of great enological importance. Research was conducted on a vineyard located at the Mendoza Agricultural Experiment Station of the National Institute of Agricultural Technology (INTA). Using RT-qPCR, we evaluated the expression of HT1 (active hexose transporter), F3H1 (flavanone 3-hydroxylase), FLS1 (flavonol synthase), and F3'H and F3'5'H (flavonoid 3'-hydroxylase and 3'5'-hydroxylase, responsible for the synthesis of di- and tri-hydroxylated anthocyanins, respectively). Evaluations were performed in leaf tissues of healthy and GLRaV-3-infected plants at four phenological stages: pea-size berry, veraison, 18° Brix, and 24° Brix.

Results revealed that at veraison, infected plants showed overexpression of HT1, F3H1, and FLS1, suggesting an early activation of hexose transport compensation and antioxidant defenses in response to viral-induced stress. As veraison marks the onset of active secondary metabolite transport from source to sink, this compensation is likely linked to sugar accumulation in leaves due to phloem transport defects. In later stages, lower expression of F3'5'H and F3'H indicated altered biosynthesis of di- and tri-hydroxylated anthocyanins. Tri-hydroxylated synthesis was the first to be affected at 18° Brix, coinciding with visual leafroll symptoms.

These expression changes may be related to a redirection of carbon fluxes toward other metabolic pathways or to the inhibition of key enzymes in the flavonoid pathway. These metabolites are energetically expensive for the plant. When combined with accumulated oxidative damage in the photosynthetic apparatus, normal leaf function is impaired, affecting berry phenolic accumulation. These findings suggest that GLRaV-3 infection induces a complex metabolic reconfiguration in Malbec grapevines. Understanding the molecular mechanisms underlying

these plant-pathogen interactions is crucial for developing sustainable management strategies and elucidating how the virus disrupts source-to-sink metabolite transport.



POSTER

Grapevine sanitation: A mini-review

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ABSTRACT

As other vegetatively-propagated species, grapevine (*Vitis vinifera* L.) can be subjected to contamination, throughout the multiplication cycles, with a number of pathogenic agents, including viroids and viruses. As to viruses, over a hundred can affect grapevine, some leading to severe plant damages or even vine death. It is therefore of considerable importance to ensure a healthy sanitary status of vineyards and particularly of repository accessions.

A literature review showed that virus elimination in *Vitis* species has been achieved through various methods, viz. chemotherapy, meristem culture, micrografting, thermotherapy, cryotherapy or electrotherapy. Virus elimination has also been reported following somatic embryos regeneration, albeit genetic/epigenetic modifications are then more likely to occur. Still according to the literature, the elimination of all *Vitis* viruses regulated in the EU, i.e. fanleaf-associated viruses (GFLV, ArMV), leafroll associated viruses (GLRaV-1, GLRaV-3) and rupestris stem-pitting virus (Rupestris stem pitting-associated virus, GRuSPV) plus Grapevine fleck virus (GFkV) was achieved using one or more of the above methods. As observed in other non-*Vitis* species, combining sanitation methods – one typically being thermotherapy – is at times used for increased efficacy. Among these sanitation methods, cryotherapy is being increasingly mentioned in the literature, with successful results as, to date, GFLV, Grapevine virus A, leafroll-associated viruses (GLRaV-1, -2 and -3) have reportedly been eliminated.

As an illustration, we will present early cryotherapy results obtained within the sanitation programme linked to the transfer of the Vassal grapevine repository; they show thus far that our current protocol, provided that genetic stability of the sanitized regenerants is clearly established, could indeed largely advance this sanitizing effort.



POSTER

Intra-varietal difference in *Plasmopara viticola* susceptibility under field conditions

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Keywords: downy mildew, climate change, clonal susceptibility, grapevine diseases, intra-varietal diversity

ABSTRACT

Intra-varietal diversity has been widely studied to improve the adaptability of *Vitis vinifera* cultivars to climate change, which is altering cultivation conditions, agricultural practices and suitable growing areas. Downy mildew (*Plasmopara viticola*), one of the most damaging diseases in vineyards, is increasing in regions traditionally considered dry due to shifts in rainfall patterns that concentrate precipitation during periods of high susceptibility. While varietal susceptibility has been studied in depth, clonal susceptibility remains largely unexplored. The objective of this work was to assess intra-varietal differences in the susceptibility to *Plasmopara viticola* in four grape varieties. In order to achieve this objective, a field study was conducted in 2025, a year marked by climatic conditions highly favourable to the development of downy mildew and associated with severe yield losses across the DOCa Rioja.

A total of 33 Tempranillo, 15 Graciano, 24 Viura and 28 Garnacha Blanca clones were evaluated in an experimental vineyard. Disease incidence was assessed as the percentage of affected bunches. Results showed the highest downy mildew incidence in Tempranillo and the lowest incidence in Garnacha Blanca. Furthermore, significant intra-varietal variability was observed. The incidence of the disease exhibited significant variation among the different grape varieties, with a range of 61% in Tempranillo, 41% in Graciano, 50% in Viura, and 36% in Garnacha Blanca. For instance, the clone most susceptible to this disease was identified as VN11 (cv. Tempranillo), while the less susceptible was the clone 942 (cv. Graciano).

These findings indicate clear differential clonal susceptibility and support the development of further investigations aimed at identifying clones with lower susceptibility to this disease within the framework of clonal selection programs.

ACKNOWLEDGEMENTS

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POSTER

Metabolic responses of grapevine leaves to grapevine leafroll-associated virus 3-infection

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ABSTRACT

Grapevine leafroll disease, primarily associated with grapevine leafroll-associated virus 3 (GLRaV-3), significantly affects grapevine physiology and productivity. However, its effects on grapevine leaf secondary metabolism remain incompletely understood. This study investigated metabolic responses of grapevine leaves of the Croatian cultivar 'Plavac mali' to GLRaV-3 infection by integrating analyses of photosynthetic pigments, oxidative stress markers, phenolic compounds and volatile organic compounds (VOCs). Virus-free and GLRaV-3-infected plants were established under controlled conditions and compared using targeted chromatographic analyses and multivariate statistics.

GLRaV-3 infection significantly reduced chlorophylls and carotenoids, indicating impaired photosynthetic capacity, while hydrogen peroxide, malondialdehyde and proline levels increased, reflecting enhanced oxidative stress. Concomitantly, the phenolic profile of infected leaves revealed a pronounced accumulation of hydroxycinnamic and hydroxybenzoic acids, flavonols and stilbenes, suggesting activation of phenylpropanoid metabolism. In contrast, p-coumaric acid was higher in virus-free leaves, indicating a possible metabolic shift toward downstream defense compounds in infected plants.

VOCs analysis demonstrated strong induction of fatty acid-derived green leaf volatiles, including C6 aldehydes and alcohols, as well as methyl salicylate, a key signal molecule in systemic acquired resistance. Conversely, several benzenoid and carotenoid-derived volatiles were reduced in infected leaves. Principal component analysis clearly separated virus-free and infected samples based on both phenolic and VOC profiles, highlighting a distinct metabolic signature associated with GLRaV-3 infection.

Overall, GLRaV-3 infection induced a coordinated metabolic reprogramming in grapevine leaves characterized by reduced photosynthetic capacity, oxidative stress and enhanced allocation of carbon and redox resources toward defense-related secondary metabolism. The combined phenolic and VOC changes define a characteristic defense-oriented chemical phenotype and identify potential non-invasive biomarkers for the detection and monitoring of grapevine leafroll disease.

These findings contribute to a better understanding of grapevine-virus interactions and provide a biochemical framework for future metabolomics-based diagnostics and resistance-oriented breeding strategies.



POSTER

Metabolomic profiling of grapevine leaf apoplast upon pathogen infection

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Keywords: plant-pathogen interaction, apoplast, dynamics, metabolic, biomarkers

ABSTRACT

Grapevine is one of the most important crops worldwide. In a climate change scenario, vineyards face not only abiotic challenges, but also recurrent annual outbreaks of diseases, such as downy mildew and grey mould, caused by the oomycete *Plasmopara viticola* (PV) and the fungi *Botrytis cinerea* (BC), respectively. By regulating several metabolic pathways, the grapevine can defend itself and survive from pathogens attack.

In our previous studies [1,2], upon PV and BC infection, our results showed that grapevine's metabolic dynamics has a pivotal role on the activation/shutdown of specific defence pathways. Flavonoids, carbohydrates, and lipids are the metabolic classes with higher modulation, exhibiting distinct temporal regulation patterns. Further analysis, using mass spectrometry imaging, revealed that stilbene phytoalexins and carbohydrates strongly accumulate near PV and BC infection sites, with levels determined by both post-infection timing and molecular complexity [3,4].

These observations raise the possibility that specific metabolites within these classes are not only responsible for *Vitis* species' tolerance/susceptibility, but also play an active role in pathogen recognition and plant defence mechanisms.

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In this context, exploring the metabolic content of grapevine leaves apoplast (APF) is essential, as this compartment is the first hub of plant-pathogen communication playing a key role in pathogen recognition, activation of signalling cascades, and pathogen counterattack. Preliminary team studies [5] at the constitutive level revealed a broad spectrum of metabolic classes, being the most represented ones 'Lipids', followed by 'Phenolic compounds' and 'Carbohydrates'; however, the metabolic characterisation of the APF during grapevine-pathogen interactions has never been reported.

To gain a better understanding of these metabolic dynamics, we performed a metabolic characterisation of grapevine leaves APF following infection with PV and BC, using ultra-high-resolution mass spectrometry. In this study, we integrated intracellular and extracellular (apoplast) untargeted metabolomics data to provide a comprehensive view of grapevine's metabolic response to pathogen invasion, with the goal of identifying crucial metabolites involved in grapevine's defence. This knowledge is fundamental for elucidating the role of metabolites in grapevine defence and paves the way for new sustainable disease control strategies.

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POSTER

Molecular, metabolic, hormonal, and cell wall profiling of ripe grapes exhibiting esca disease

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Keywords: esca disease, transcriptome, metabolome, hormonal profiling, cell wall profiling

ABSTRACT

Esca is a major grapevine trunk disease caused by a consortium of xylem-colonising and wood-degrading fungi, including *Phaeomoniella chlamydospora*, *Phaeoacremonium minimum* and *Fomitiporia mediterranea* and poses a growing threat to vineyard longevity. While its aetiology and effects on vegetative tissues have been extensively studied, the impact on grape berries remains poorly characterised. Previous findings from our research indicate a more pronounced metabolic shift in fruits compared to vegetative organs. In the present study, ripe grapes (EL38) of *Vitis vinifera* cv. Aragonese (syn. Tempranillo) from infected plants with and without Esca foliar symptoms were analysed using an integrative approach combining RNAsequencing, two complementary mass spectrometry-based metabolomics techniques — gas chromatography–time-of-flight mass spectrometry (GC-TOF-MS) and ultra-high-performance liquid chromatography coupled to high-resolution mass spectrometry (UHPLC-HRMS) — and Fourier-transform infrared spectroscopy with attenuated total reflectance (FTIR–ATR). Despite limited differential expression of genes, pathway enrichment analysis revealed a coordinated transcriptional reprogramming related to activation of oxidative stress and proteostasis pathways together with broad repression of translation, vesicle trafficking, cell wall organisation, and central metabolism in grapes from symptomatic plants. These transcriptional patterns were consistent with the metabolomic profile, which showed

a tendency toward reduced levels of hexose sugars and several amino acids, together with increased accumulation of polyols and organic acids. Hormone profiling further revealed lower abscisic acid content in these grapes, consistent with altered hormonal signalling when Esca foliar symptoms are present. Cell wall analysis indicated increased contributions of pectic and hemicellulosic matrix glycans, higher O-acetylation, and enrichment of wall-associated phenolics in grapes from symptomatic vines, with differences largely confined to alkali-labile matrix polysaccharide decorations rather than to the cellulose scaffold. Collectively, these findings reveal a coordinated systemic response in grapes from plants displaying Esca symptomatology, characterised by the activation of stress-associated pathways, together with the repression of primary metabolism and the restructuring of cellular processes, despite the absence of direct pathogen colonisation. This response is consistent with a physiological shift in the whole plant associated with Esca-related vascular dysfunction, providing new insight into the impact of Esca disease on grape composition and structure, with possible implications in wine quality.



POSTER

Phenotypic and genotypic assessment of black rot resistance in a grapevine diversity panel

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Keywords: black rot, *Guignardia bidwellii*, PIWI cultivars, *Rgb1*, *Rgb3*

ABSTRACT

Black rot, caused by the ascomycete *Guignardia bidwellii* (anamorph *Phyllosticta ampellicida*), is an important fungal disease of grapevine (*Vitis vinifera* L.) and can lead to severe yield losses, particularly under warm and humid conditions. While genetic resistance represents a promising strategy for sustainable disease management, the diversity and distribution of black rot resistance within cultivated germplasm are still insufficiently characterized.

In this study, we investigated black rot resistance in a comprehensive diversity panel maintained at Hochschule Geisenheim University (HGU). The panel includes a wide range of international cultivars, traditional and historical varieties, as well as fungus resistant cultivars (PIWIs).

The experiment was conducted as a randomized block design across independent inoculation runs. Each genotype was tested in a single run with three biological replicates, arranged in three spatial blocks in the greenhouse. Fifteen control genotypes were included in all runs to account for temporal variation between inoculation dates. Plants were inoculated with conidia of *P. ampellicida*, and disease response was assessed after the end of the incubation period by visual scoring of disease severity and characterization of symptoms on leaves and shoots (lesion size, coloration, and overall symptom morphology). In parallel, selected accessions were screened for the presence of known black rot resistance alleles at the *Rgb1* and *Rgb3* loci using molecular markers.

The overall aim of this project is to systematically evaluate the level of black rot resistance across a broad and genetically diverse grapevine collection. By combining phenotypic and genotypic data, we seek to determine whether observed resistance patterns can be explained by previously described resistance loci or whether additional, potentially novel sources of black rot resistance are present. This study provides a systematic phenotypic and genotypic baseline that will serve as a foundation for future genetic analyses and breeding efforts aimed at improving black rot resistance in grapevine.



POSTER

Profiling of miRNA responses to viral coinfections in grapevine (*Vitis vinifera* L.)

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ABSTRACT

Grapevine (*Vitis vinifera* L.) is one of the most widely cultivated fruit crops worldwide and is susceptible to numerous pathogens, including viruses. To date, more than 100 viruses have been identified in grapevine, several of which cause severe disease symptoms that negatively affect yield and fruit quality (1). Viral infections can also alter the expression of microRNAs (miRNAs), a class of small non-coding RNAs that regulate gene expression at the post-transcriptional level (2, 3). In this study, we investigated how viral infections influence miRNA expression in the grapevine cultivars Refošk and Zeleni Sauvignon. In addition, degradome sequencing was performed to identify and analyze potential miRNA target transcripts.

Small RNAs were extracted from virus-free and virus-infected plants of two cultivars, Zeleni Sauvignon and Refošk. Sequencing was performed on the Ion Proton™ platform (Ion Torrent™, Life Technologies). In sRNA-seq datasets, viruses were detected using the VirusDetect

pipeline. miRNA expression was analyzed using three miRNA prediction tools: miRador, ShortStack and miRDeep2, and the integrated outputs from all three tools were used for differential expression analysis. Expression of selected miRNAs was further assessed by stem-loop RT-qPCR, and degradome sequencing was performed to confirm cleavage of target transcripts.

Small RNA sequencing generated between 6.3 and 25 million reads per library. No viruses were detected in virus-free samples, whereas infected samples contained viruses GPGV, GRSPaV, and GRVfV. Differential expression analysis identified 6 differentially expressed miRNAs in Refošk and 16 in Zeleni Sauvignon. Stem-loop RT-qPCR confirmed differential expression for 10 of 12 tested miRNAs in Refošk and 5 of 15 in Zeleni Sauvignon. Degradome sequencing identified miRNA-mediated cleavage of numerous transcripts, including transcripts involved in hormone signaling and plant-pathogen interaction pathways.

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POSTER

Simultaneous detection of grapevine viruses, viroids, and satellite RNAs by high-throughput and targeted assays

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Keywords: *Vitis vinifera* L., virome, sRNA-seq, mRT-PCR

ABSTRACT

Grapevine (*Vitis vinifera* L.) is considered to be among the most widely grown and major fruit crops worldwide with high economic importance. Viruses and virus-like organisms cause considerable economic losses in vitiviniculture, and considering that they cannot be controlled by conventional plant protection methods, the use of healthy vegetative propagation material is crucial. Metagenomic approaches for virus diagnostics enable rapid and accurate detection of viral pathogens in plants. To investigate the presence of viruses and virus-like organisms infecting grapevine from the Ampelographic Collection Kromberk in Slovenia, Ion Torrent small RNA sequencing (sRNA-seq) was performed, and the resulting data were analyzed using the VirusDetect pipeline. This approach revealed the presence of grapevine leafroll-associated virus 1 (GLRaV-1), grapevine leafroll-associated virus 2 (GLRaV-2), grapevine leafroll-associated virus 3 (GLRaV-3), grapevine rupestris stem pitting-associated virus (GRSPaV), grapevine fanleaf virus (GFLV) and its satellite RNA (satGFLV), grapevine fleck virus (GFkV), grapevine rupestris vein feathering virus (GRVFV), grapevine Pinot gris virus (GPGV), grapevine satellite virus (GV-Sat), hop stunt viroid (HSVd), and grapevine yellow speckle viroid 1 (GYSVd-1). To validate the infections predicted by sRNA-seq, multiplex reverse transcription-polymerase chain reaction (mRT-PCR) assays were developed, allowing simultaneous detection of different combinations of viruses, viroids, and satellite RNAs. The mRT-PCR assays represent a rapid and cost-effective tool for routine molecular diagnostics and could be applied for the detection of widespread, emerging, and rarely tested grapevine viruses, as well as viroids, which are often overlooked in standard diagnostic testing.



POSTER

Spatio-temporal dynamics of wound-induced defence responses in grapevine revealed by multiple approaches

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Keywords: pruning, xylem, metabolites, RNA sequencing

ABSTRACT

Grapevines are continually wounded throughout their cultivation, particularly during winter pruning. To prevent pathogen attack and tissue dehydration, plants have evolved a wide range of wound responses to protect their tissues. These responses include changes in gene expression and the synthesis of protective molecules such as polyphenols. In addition to these molecular responses, plants are known to occlude damaged xylem vessels in response to wounding and pathogen infection. Different types of occlusions can be produced, including gels, gums, and tyloses.

In this study, we explored grapevine responses to winter pruning in two different varieties. First, we studied the dynamics of xylem vessel occlusion formation at different dates during the winter months and at different depths from the wound.

Second, we characterised the gene expression changes triggered by pruning and the polyphenols that accumulated

in response. Finally, we used Raman microscopy to analyse the composition of xylem vessel occlusions.

We found that the two grapevine varieties studied showed very comparable responses to winter pruning. The genes upregulated in response to pruning were highly similar between varieties and highlighted the coordinated expression of genes involved in polyphenol biosynthesis, transport processes, cutin, suberin, and wax production, as well as cell wall modifications. We also observed coordinated upregulation of stilbene synthase genes together with the accumulation of stilbenes. Raman microscopy showed that winter xylem vessel occlusions in both genotypes were gel- or gum-type structures rich in polyphenols. To our knowledge, this is the first study to combine multiple approaches to investigate grapevine responses to winter pruning.

ACKNOWLEDGEMENTS

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POSTER

The epigenetic response of a resistant and a susceptible variety of *Vitis vinifera* to downy mildew

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Keywords: *Vitis vinifera*, downy mildew, epigenetics, nanopore

ABSTRACT

Plant-pathogen interactions can trigger extensive epigenetic modifications in the host genome. These include local changes to DNA methylation that may mediate host defence responses by altering the expression of key genes involved in disease resistance or susceptibility. This study characterises and compares the epigenetic response of a resistant and a susceptible grapevine variety to *Plasmopara viticola* infections, with the aim of identifying new candidate genes for resistance breeding.

The experimental design included two *Vitis vinifera* varieties, one susceptible (Pinot noir) and one resistant (Mgaloblishvili) to downy mildew. Plants were artificially inoculated with a sporangia suspension of *P. viticola* (I) or water as a non-inoculated control (NI). Three biological replicates were used per treatment. Disease incidence was scored at 7 days post inoculation (dpi). Genomic DNA was extracted from I and NI leaves at 12, 24, 48 and 72 hours post inoculation (hpi) and sequenced on an Oxford Nanopore Technologies PromethION, followed by whole-genome methylation analysis. Local and genome-wide epigenetic differences were evaluated in the three methylation contexts: CG, CHG and CHH (where H can be either an A, C or T). Genetic and phenotypic data were also compared.

Phenotypic analysis confirmed Mgaloblishvili's resistance to downy mildew. At a genome-wide level, the two varieties contrasting methylation profiles at 12 hpi: global CHH methylation increased significantly in Pinot noir following inoculation, whereas in Mgaloblishvili it decreased. Local differentially methylated regions associated with infection will be discussed for 12, 24 and 48 hpi in both varieties.

Overall, this study provides insights into the temporal dynamics of epigenetic responses in grapevine to *P. viticola* infections. The comparison of a susceptible and a resistant variety, demonstrates epigenetic features associated with different responses to disease infection. It also supports the identification of novel candidate genes for susceptibility and resistance to downy mildew, that may be applied in future grapevine breeding programs.



POSTER

Grapevine varietal influence on leaf bacterial and fungal communities across phenological stages

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Keywords: climate adaptation, inter-varietal diversity, high-throughput sequencing, leaf microbiome, *Vitis vinifera* L.

ABSTRACT

With the increasing frequency and intensity of extreme weather events, viticulture is expected to face progressively drier and warmer conditions, increasing the need for sustainable adaptation strategies such as the identification of resilient *Vitis vinifera* L. varieties. Grapevine leaves host complex microbial consortia composed of bacteria and fungi that interact with each other and the plant host, influencing stability and resilience to (a)biotic stresses. Understanding the structure of microbial communities is essential to elucidate varietal adaptation under climate change scenarios.

This study aimed to evaluate the dynamics of fungal and bacterial communities in leaves of six different grapevine varieties ('Alicante Bouschet', 'Donzelinho Tinto', 'Malvasia Preta', 'Tinto Cão', 'Touriga Franca' and 'Touriga Nacional') between veraison (BBCH 81) and harvest (BBCH 89) grown during the 2024 season in the Douro Demarcated Region-subregion Douro Superior. Leaves were sampled from a grapevine variety library located at Quinta do Ataíde of Symington Family Estates, in Vale da Vilarça, Northern Portugal. Metagenomic libraries (ITS and 16S) were prepared and sequenced using Illumina platform.

For the bacteria community, the phyla Actinomycetota and Pseudomonadota, as well as the genera *Protofrankia* and

Paraburkholderia, were the most abundant across all varieties and phenological stages. At both phenological stages, the highest number of reads was detected in 'Touriga Franca' whereas the lowest was observed in 'Alicante Bouschet'. The highest richness was also detected in 'Touriga Franca' and the lowest in 'Tinto Cão', both at veraison. The Shannon–Wiener diversity index revealed a significant decrease from veraison to harvest in 'Donzelinho Tinto' and 'Touriga Franca'. As for fungal community, the phyla Ascomycota and Basidiomycota and the genera *Alternaria* and *Filobasidium* were the most abundant among all varieties and phenological stages. At harvest, 'Donzelinho Tinto' showed the highest number of reads, whereas the lowest was observed in 'Tinto Cão' at veraison. The highest richness was observed in 'Touriga Nacional', statistically higher than all varieties except 'Touriga Franca', while the lowest was observed in 'Tinto Cão', both at veraison. The Shannon–Wiener index revealed a significant increase from veraison to harvest in 'Alicante Bouschet' and a significant decrease in 'Malvasia Preta'.

These results suggest that grapevine genotype influences leaf microbiome composition, with bacterial community showing stronger varietal differentiation than fungal community, potentially contributing to differential varietal resilience.

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POSTER
SESSION:
CLIMATE CHANGE AND
ABIOTIC STRESS TOLERANCE



POSTER

A comprehensive isoform catalogue to investigate transcriptional responses to water stress in grapevine

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Keywords: alternative splicing, drought stress, isoform transcriptome

ABSTRACT

Climate change is increasing the frequency and duration of droughts, leading to water deficits strongly affecting grapevine berry and wine quality. Alternative splicing mechanism allows the production of multiple isoforms from a single gene.

Therefore, it plays a role in adjusting gene regulation in response to abiotic stresses, drought in particular. However, isoform-level resources remain limited for *Vitis vinifera*.

Our project aimed to: (1) build a comprehensive catalogue of isoforms expressed in grapevine across tissues, cultivars and conditions, and (2) identify genes showing isoform-level changes under drought stress conditions.

We generated an extensive reference using PacBio Iso-Seq data complemented by public datasets. The dataset spans five tissues and twelve cultivars, including leaf and berry samples exposed to drought stress for 9 cultivars. A dedicated annotation workflow identified 23,411 genes with a median of four transcripts per gene, providing a high-resolution view of isoform diversity across tissues, cultivars and conditions. With this new resource, we identified that around 70% of the multi-exonic genes of *Vitis vinifera* undergo alternative splicing.

Expression of genes and isoforms was quantified from short-read RNA-seq of berries and leaves grown under contrasting drought stress conditions. This analysis highlighted splicing events affecting genes associated with drought responses.

The resulting isoform catalogue constitutes a unique reference for the grapevine community and supports future work on the molecular mechanisms underlying adaptation and cultivar specific response at the isoform level in grapevine. In addition, the isoform catalogue will be accessible to the community through VitExpress expression atlas platform to allow public consultation of the expressed isoforms.



POSTER

Avoidance or tolerance: late frost resilience mechanisms in grapevine

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Keywords: budbreak, climate change, cold stress, hybrids, physiology

ABSTRACT

Climate change has compressed grapevine phenology, advancing budbreak without a corresponding reduction in the probability or timing of late frosts. Consequently, late frost risk has increased in Trentino and is projected to rise across many European viticultural regions. This research aims to identify resilience mechanisms to mitigate such damage.

Sixteen interspecific hybrids (*Vitis vinifera* × *Vitis* spp.) and a *V. vinifera* Nosiola clone were analyzed over two seasons. We monitored: (i) phenology at budbreak, (ii) survival rates in controlled frost simulations, and (iii) the accumulation of primary metabolites and polyphenols. Additionally, a comparative RNA-Seq experiment and parallel metabolomic analysis were conducted on tolerant versus sensitive genotypes.

Two distinct strategies emerged: frost avoidance and frost survival. Avoidance genotypes reach sensitive phenological stages only after higher thermal accumulation, exhibiting plasticity and varying degrees of budbreak synchrony. Tolerance genotypes withstand freezing temperatures through specific anatomical traits, metabolic profiles, and transcriptomic regulation. These results were interpreted in the context of the genotypes' pedigree.

The existence of these distinct mechanisms underscores the necessity of an integrated study approach. While budbreak dynamics are key targets for breeding programs, tolerance mechanisms can be exploited through agronomic innovations, such as UV-C radiation treatments.



POSTER

Characterization of xylem anatomy and gas exchange traits in selected Croatian grapevine cultivars and wild grapes

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Keywords: grapevine, xylem, gas exchange, drought

ABSTRACT

Grapevine (*Vitis vinifera* subsp. *vinifera* L.) is one of the crops most affected by drought, and climate projections indicate that both the frequency and intensity of drought events will increase further in the future. Although grapevine is a Mediterranean plant species with well-developed mechanisms of adaptation to water deficit, including reprogramming of physiological and metabolic processes, osmotic adjustment, and enhanced tolerance to reactive oxygen species, these processes remain insufficiently understood. Although the influence of xylem anatomy on grapevine drought resistance has been documented in some *Vitis* cultivars, studies are primarily focused on hydraulic vulnerability and embolism resistance; the relationship between xylem structure, transpiration, and stomatal conductance in grapevine remains poorly understood. This study aimed to assess the effects of xylem anatomy on stomatal conductance and transpiration in Croatian grapevine and wild grape genotypes, thereby elucidating the relationship between anatomical traits and physiological responses under drought.

In this research, transpiration rate and stomatal conductance were measured in 13 Croatian grapevine (*Vitis vinifera* subsp. *vinifera* L.) and 3 wild grapevine (*Vitis vinifera* subsp. *sylvestris* Gmel Heg) genotypes, comparing control plants with those subjected to a drought treatment. At the same time, xylem structure was analyzed on cross-sections of canes, and pit density and aperture area were measured. Significant differences in xylem anatomy were observed among genotypes. Belina starohrvatska genotype showed the highest pit density (mean = 41.13 pits/mm²), whereas the genotype Plavina exhibited the largest pit aperture area (mean = 0,009 mm²). Treatment effects were significant also for transpiration and stomatal conductance, with a notable genotype × treatment interaction. Post-hoc analyses revealed significant genotype effects on transpiration and stomatal conductance. In *Vitis sylvestris* genotype Paklenica 120, transpiration averaged 0.871 mmol m⁻² s⁻¹

and stomatal conductance 0.056 mol m⁻² s⁻¹. In genotype Paklenica 122, these values were 0.746 mmol m⁻² s⁻¹ and 0.035 mol m⁻² s⁻¹, respectively.

This study represents the first research on the influence of xylem anatomy on drought-adaptive physiological processes in Croatian grapevine genotypes, particularly wild grapevine. The results may contribute to a better understanding of the mechanisms driving grapevine drought tolerance.



POSTER

Comparison among different Cannonau clones in northeast Sardinia (Italy)

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Keywords: viticulture, clone, water availability, phenotype

ABSTRACT

The intra-varietal variability of ancient grapevine varieties allows to identify individuals (i.e. clones) whose phenotype might be interesting for the winemaking industry. The process of clonal selection aims to check whether the phenotype of these clones is strongly modified by environmental deviations or instead reflects the genotype. In Italy, the clonal selection is carried out, but there are still few studies concerning the GxE interaction of the selected clones. Selected clones might be cultivated far away from the original environment without knowing their behavior in a different environment. Moreover, the comparison of different selected clones of the same variety into the same environmental and agronomical conditions has often been lacking.

In this work, it was performed a field phenotyping of 14 selected clones of Cannonau variety for the environmental conditions of northeast Sardinia. Cannonau is a widely spread variety in Sardinia and it is also cultivated in other regions of the Mediterranean basin, such as in Spain and France. The aim of the work was to detect differences among these clones and better assess their viticultural model and winemaking target.

Phenotyping of the selected clones (of which seven coming from Italy, four from France and three from Spain) was conducted over two consecutive seasons (2024 and 2025) in the same vineyard. Clones were allocated within the vineyard following a four-block completely randomized design. The evaluation focused on vine balance traits (vegetative growth and grape productivity), physiology at veraison and post-veraison (leaf nitrogen, flavonols and chlorophyll content, leaf gas exchange, stem water potential) and the technological parameters of the grape musts.

Results showed an overall significant dependence of the intrinsic water use efficiency (WUEi) over stomatal conductance (gs) ($R^2 = 0.6$). By fitting clone-specific regressions of WUEi over gs, significant differences in the slopes were found between the Spanish clone ARA2 and the French clone 135 (-36.6 and -14.7, respectively, for a decimal increase of gs). Therefore, ARA2 can be predicted as higher photosynthesis performer under moderate to severe water stress (which is common in Sardinia), while 135 is more efficient under mild and no water stress. These findings are corroborated by the PCA on the vegetative growth traits,

which showed that ARA2 was much more vigorous than 135. Finally, data harvest in 2025 revealed that ARA2 was the ripest must and the richest in Malic acid (1.2 g/L), while 135 was one of the less ripen and the lowest in Tartaric acid (6.3 g/L).

In this work, phenotypic differences arose between some clones, and these differences might be driven by a clone-specific water efficiency. For instance, ARA2 provides a better fitness to the environmental conditions of north-east Sardinia than 135, therefore it might be more advisable for most of the local wine productions.



POSTER

CRISPR/Cas9 functional characterization of grapevine glutathione S-transferases VvGST40 and VvGST30 reveals a role in drought resilience

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Keywords: *Vitis vinifera*, drought resilience, genome editing, GST

ABSTRACT

Increasing climate variability and the rising frequency of drought events are intensifying the demand for grapevine (*Vitis vinifera* L.) genotypes with improved performance under water-limited conditions. In this context, New Plant Breeding Techniques (NPBTs), and particularly CRISPR/Cas9-mediated genome editing, enable targeted manipulation of candidate genes involved in abiotic stress adaptation, aligned with EU sustainability objectives for agriculture.

We describe a genome editing strategy to functionally characterize two grapevine Glutathione S-transferase genes, VvGST40 and VvGST30, selected based on homology to an *Arabidopsis thaliana* GST previously associated with enhanced drought tolerance. Candidate gene prioritization was further supported by transient VvGST40 downregulation using spray-induced gene silencing (SIGS) via dsRNA delivery, which was associated with improved performance under water deficit.

Sixteen CRISPR-Cas9-positive lines were generated by *Agrobacterium*-mediated transformation. Targeted mutagenesis was validated by molecular analyses, and four independently edited lines carrying stable mutations were selected for downstream characterization. Preliminary in vitro screening assessed root system architecture traits potentially relevant to water uptake. Subsequently, drought stress assays were performed to quantify plant performance under water deficit, integrating morphological and physiological parameters. Edited lines displayed improved drought-responsive phenotypes relative to controls, supporting a functional contribution of VvGST40 and VvGST30 to grapevine water-stress adaptation.



POSTER

Deep learning reveals regulatory logic of water stress adaptation in grapevine

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Keywords: deep learning, transcriptional regulation, water stress

ABSTRACT

Predicting how sequence variants affect regulatory activity is critical for crop improvement, but confidence in these predictions, especially for diverse varieties, remains insufficient for breeding applications. Reference genomes collapse natural genetic diversity, creating reference bias that limits prediction accuracy across heterozygous crop genomes. We demonstrate the application of interpretable deep learning to a non-model perennial crop, *Vitis vinifera* (grapevine), and explore how layering computational evidence can build confidence in regulatory predictions.

We retrained the DeepCRE convolutional neural network on 163 public RNA-seq samples from water-stressed grapevine to predict genome-wide gene expression (high versus low) from flanking sequence. The model learns sequence-to-expression relationships, which we then interpret using gradient-based methods to extract the regulatory motifs driving predictions. Using chromosome-wise cross-validation to prevent homology inflation, the model achieved 91% accuracy and 92% F1 score. TF-MoDISco interpretation revealed 29 expression-predictive motifs organised into two functional meta-clusters.

Multiple lines of computational evidence support these predictions: genome-wide motif mapping shows enrichment consistent with expected expression patterns; gene ontology analysis reveals significant enrichment of co-occurring motifs in canonical drought response pathways including ABA signalling, osmotic stress response, and flavonoid biosynthesis; integration with co-expression networks identifies candidate hub transcription factors. Comparative analysis between water stress and control models reveals patterns of regulatory rewiring under drought conditions.

This work explores how integrating multiple computational approaches can support confident prioritisation of regulatory elements and variants for targeted validation - a critical step toward explainable AI predictions for breeding applications in heterozygous crop genomes.



POSTER

Determining conserved xylem response to drought in woody plants for use in grapevine editing

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ABSTRACT

Grapevine is a relatively drought-tolerant crop that adopts a variety of strategies in response to water deficit [1]. Hydraulic traits linked to water transport efficiency and xylem embolism vulnerability are especially important and show a large degree of variation between cultivars [2]. How exactly these traits influence the performance of grapevine plants under drought stress conditions is difficult to decipher, as they are closely associated with other water-use related traits like stomatal conductance, and can also vary in effectiveness based on the length and intensity of the drought stress [3]. The variation in hydraulic traits is strongly influenced by xylem cell wall structure and composition, and trade-offs are made between xylem vessel roles as a hydraulic conduit and structural scaffold [4]. Genome editing can be used to study how the altering of xylem characteristics affects drought response, but identifying targets in grapevine is challenging, as tissue-specific gene expression data of grapevine xylem tissue under water deficit conditions is

under-researched. To circumvent this limitation and identify potential targets, conserved responses between woody plants under water deficit conditions were investigated. Publicly available transcriptomic data from *Citrus macrophylla* [5], *Eucalyptus grandis* [6] and *Populus trichocarpa* [7] xylem tissue undergoing water stress trials were used. Conserved differentially expressed genes were identified, and gene ontology (GO) enrichment was performed to find over-represented GO terms that were conserved.

Additionally, a maximum relevance minimum redundancy network was constructed from the transcriptomic data of one of the *Eucalyptus* studies to assist in selecting potential targets. A list of targets was generated from these analyses that can be used for further validation with grapevine genome editing. Rapid plant genetic transformation systems such as hairy root transformation and protoplast editing can be used as models to assess alterations in xylem development, and cell wall and structure properties.

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POSTER

Drought tolerance in grapevine (*Vitis vinifera* cv. Chardonnay) clones

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Keywords: viticulture, Chardonnay, grapevine clones, climate change, drought stress

ABSTRACT

Viticulture's global significance enhances the concerns arising from the impending climate changes, with recently studies emphasizing prolonged drought periods. In grapevine drought stress can negatively impact key physiological traits, affecting both yield and quality across major wine growing regions. A way of dealing with these issues lies on the spontaneous somatic mutations that give rise to intra-varietal diversity, a pool of genotypic, morphological and physiological diversity within a single variety. Three clones belonging to the Chardonnay variety were studied. The two-year-old graftings were grown in the greenhouse and transferred to the phenotyper room with controlled conditions where two treatments were applied: "control" with daily watering and "drought" with water deficit for 14 days plus a recovery period of four days. During the experiment, phenotypical measurements and sampling for isotopic analysis were done weekly.

The results from the experiment aim to reveal differences in grapevine clones' tolerance to water deficit, highlighting variations in physiological responses and water use efficiency. Phenotypic changes, including reductions in plant height and leaf count, are seen among studied clones, with some showing faster post-drought recovery. Further results, from autonomous and continuous sources, regarding phenotypical traits are forthcoming. The study hopes to provide valuable insights into the role of intra-varietal diversity in grapevine drought resilience. The identification of clones with superior stress tolerance will be critical for developing sustainable viticultural practices in response to climate change; by leveraging natural genetic variability, the findings will aid the identification of materials and improve viticulture management.



POSTER

Evaluation of budbreak regulation on grapevine genotypes with extreme behaviour

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Keywords: grapevine, budbreak, dormancy, physiology, cold hardiness

ABSTRACT

Vitis vinifera enters dormancy in autumn to face adverse winter conditions and, then, resumes growth and budbreak (BB) in spring, when optimal climate conditions occur.

Climate change can cause yield damage due to phenology advances and spring frosts. Genes and pathways involved in dormancy and BB progression were previously enquired in grape, but an extensive understanding of the whole regulatory network is still lacking.

Here, we focused on a segregating population that was evaluated in the field for 6 years for phenological traits. BB timing in the parents was similar, whereas in the progeny it spanned a long interval (71 days in 2025). The transgressive behaviour was strongly correlated across replicates and across years, and individuals consistently breaking earlier or later than the parents were identified.

Based on BB timing data, few individuals showing opposite behaviour (3 early and 2 late BB timing genotypes) were chosen, along with the parents, for further phenotypic characterization. BB forcing assay (BFA) was performed over winter to test dormancy progression. Cold hardiness (CH) was also evaluated with differential thermal analysis (DTA). For these analyses, samples were collected every 3 weeks from November to March over two years. Moreover, the dynamic development of grapevine buds under natural field conditions was monitored over BB by microscopy observation of vascular connection rebuild progression in the different genotypes. Based on BFA all genotypes already exited endodormancy in January with no obvious differences between early and late ones. The different CH and cold de-acclimation behaviours in the genotypes appeared also not clearly correlated to the extreme field BB behaviours.

Altogether, the physiological characterization will provide useful insights in dissecting the extreme BB phenotype, paving the way for future studies on the underlying molecular mechanisms.



POSTER

Field-based insights into global grapevine methylation under conditions of recurring water constraint

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Keywords: epigenetics, DNA methylation, drought, adaptation, field-based study

ABSTRACT

Water limitation is a major environmental constraint affecting grapevine productivity and fruit quality worldwide. While DNA methylation has been widely implicated in drought responses in herbaceous species, its role in woody perennials such as grapevine remains underexplored under field conditions. Using a long-term, field-based model vineyard established to investigate grapevine adaptation and resilience under water limitation, an initial comparative global DNA methylation analysis was performed using an ELISA-based assay to provide a first description of potential epigenetic changes. The vineyard comprises 90 sampling points, representing five biological replicates of three scion cultivars—Cabernet Sauvignon (CAB), Pinotage (PIN), and Shiraz (SHI)—each grafted onto two rootstocks, Richter 110 (110R) and US87, and exposed to three irrigation regimes (well-watered, reduced irrigation, and dryland) since establishment. Leaf samples were collected during the 2021/2022 season across contrasting within-season conditions and again in the 2023/2024 season across six key developmental stages to capture seasonal methylation dynamics. DNA methylation data were contextualized using soil moisture and plant physiological metadata generated within the broader multidisciplinary study. Global DNA methylation varied across sampling periods and genetic backgrounds. A ~10% decrease occurred between the first sampling under non-limiting soil moisture and the second sampling following differential irrigation. Pronounced genotype effects were observed: Shiraz grafted onto 110R showed ~30% higher methylation than Cabernet Sauvignon on 110R, and ~30% higher than Shiraz on US87. Developmental stage further contributed to variability, with fluctuations of up to ~15%. Methylation showed strong associations with physiological and soil parameters in specific scion–rootstock–irrigation combinations, most notably with stomatal conductance ($r = -0.93$) and total soil moisture ($r = 0.99$). Together, these findings provide one of the first field-based global methylation profiles of grapevine under long-term water limitation and demonstrate that epigenetic responses are shaped by environmental, developmental, and genetic factors. Building on this foundation, a subset

of samples will be analyzed using whole-genome bisulfite sequencing (WGBS) to characterize DNA methylation at single-base resolution and identify differentially methylated regions associated with irrigation regime, developmental stage, and scion–rootstock combination.



POSTER

Genomic and phenotypic plasticity as a clue for grapevine adaptation to climate change?

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Keywords: climate change, adaptation, plasticity, genome, phenotype

ABSTRACT

In order to maintain grapevine production and quality under fluctuating and stressful environments, we urgently need some innovative genetic solutions. By characterizing the plasticity of grapevine functioning under different environments, the structural plasticity of its genome, the regulation of gene expression and alternative splicing events occurring in response to drought stress, we may identify genes and innovative genetic markers associated to adaptive traits, useful to breed climate-smart varieties.

A consortium of laboratories in Occitanie region (France), as part of “PlastiVigne” project, developed research activities in order to identify and characterize genomic and

phenotypic plasticity within a core collection of cultivated grapevines from different origins. We will present some outputs of “Plastivigne” and more particularly those of three PhD students, including a pangenome of the cultivated compartment of *Vitis vinifera*, a derived genotyping matrix including base substitutions and structural variants, a catalog of alternative spliced variants, the measurement of phenotypic variation for some adaptive traits and the genetic determinism underlying their plasticity. Combining this information will give us some clues related to the potential involvement of genomic plasticity in adaptive phenotypic plasticity in grapevine.

ACKNOWLEDGEMENTS

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POSTER

Genotypic variation in xylem vessel anatomy in a replicated F₂ grapevine (*Vitis* spp.) population under field conditions in California

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Keywords: xylem anatomy, quantitative trait loci (QTL)

ABSTRACT

Breeding for complex quantitative traits remains a major challenge in perennial crop systems, particularly for traits related to water use efficiency (WUE), which are strongly influenced by environmental variation and difficult to phenotype at scale. As water limitation intensifies in major grape-growing regions, identifying genetically controlled components of hydraulic architecture may provide new avenues for improving WUE in grapevine. We evaluated xylem vessel anatomy in a replicated VRS-F2 grapevine population produced from a selfed F1 (*Vitis* sp. '19-9-2') derived from a cross between *Vitis* riparia 'Manitoba 37' and *Vitis* sp. 'Seyval blanc'. The resulting population consisted of 183 genotypes, each with three clonal replicates, which were planted in Greenfield, California and commercially managed. This population was expected to segregate for hydraulic traits, providing an opportunity to evaluate genetically driven differences in xylem structure under field conditions. Cane samples were collected in 2024 and 2025 during winter pruning, cross-sectioned, and imaged using UV light microscopy. ABiodock AI model was trained to annotate images and extract vessel size (area) and density. Leaf-level physiological measurements were collected at two time points in 2024 and 2025 growing season, and petioles of same leaf collected, cross-sectioned and imaged. Pruning weight and cane diameter were collected to monitor vine vigor. Analyses indicate consistent genotypic differences in vessel size and density across years, suggesting xylem architecture is under partial genetic control. Variation in xylem traits is associated with differences in leaf physiological performance, indicating functional consequences for water transport and use. QTL mapping for xylem traits has been completed, and ongoing analyses will identify genomic regions associated with vessel size and density. These results lay the groundwork for integrating hydraulic traits into grapevine breeding programs aimed at improving water use efficiency under increasingly water-limited conditions.



POSTER

Impact of heat and drought stress on Vranec grape quality in the Tikveš wine-growing region

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Keywords: Vranec variety, climate change, grape quality, mechanical composition, chemical composition

ABSTRACT

Although the grapevine (*Vitis vinifera*) is a thermophilic plant which is well adapted to regions with warm and dry summers, it is increasingly affected by climate change. Rising average temperatures, more frequent drought periods, and extreme weather conditions lead to significant heat and water stress, which can negatively affect grape yield and quality.

The aim of this study was to evaluate the impact of extreme weather conditions during the 2024 growing season on the quality of grapes of the Vranec variety, the most widely cultivated red wine grape variety in the Republic of Macedonia. The research was conducted at eight locations in the Tikveš and Veles wine-growing regions using two experimental variants: irrigated and non-irrigated vineyards. At technological maturity, the mechanical composition of clusters and berries, the chemical composition of the must, and the chemical composition of the produced wine were analyzed. The results were compared with multi-year standard values for the Vranec variety.

The results show a significant influence of heat and water stress on the yield and quality of the Vranec variety. The average cluster weight decreased by 16.3% in the irrigated variant and by up to 48.1% in the non-irrigated variant, while the theoretical yield decreased by 6.4% and 14.8%, respectively. The must showed a pronounced imbalance in the chemical composition, characterized by high sugar content (up to 310 g/l) and low total acidity (4–5 g/l), accompanied by insufficient phenolic maturity of the seeds and the presence of ethanol, which indicates that the vines were exposed to considerable stress during the growing season.



POSTER

LED spectra to improve cuttings in *Vitis vinifera* cv. 'Nebbiolo' and 'Barbera'

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Keywords: light emitting diode, nursery propagation, single-bud cuttings, rooting

ABSTRACT

High-quality planting material is important for sustainable viticulture, and the early establishment of grapevine cuttings depends on rapid adventitious rooting and vigorous shoot growth. Light is an environmental factor that can influence plant development, including root and shoot formation. In recent years, LED technology has been increasingly used in plant research and propagation systems because it allows precise control of light spectrum and intensity, reduced heat emission, and stable light conditions compared to conventional lamps. Studies in different species have shown that specific LED spectra can improve rooting and shoot growth. For this reason, here we tested two LED spectra, Red:Blue:Far-red (RBFr) and Red:Blue:Green:Far-red (RBGFr), against a white LED control in single-bud cuttings of *Vitis vinifera* L. cvs 'Nebbiolo' and 'Barbera'.

Cuttings were standardized for size and rooted in deionized water under the three light treatments (60 $\mu\text{mol m}^{-2} \text{s}^{-1}$). The

basal end was immersed for 24 h in an aqueous indole-3-butyric acid (IBA) solution (0, 120, or 250 mg L⁻¹), after which the solution was replaced with fresh deionized water.

The experiment was randomized and combined cultivar, light treatment, and IBAdose, with 20 cuttings per treatment combination. After 30 days in water, rooting and callusing percentages, number of roots per cutting, and root length were analysed. Root system traits, including total root length and branching, was analysed using ImageJ software. After transplanting to perlite, survival, bud break, shoot length, leaf number, leaf area, and SPAD were monitored. This study aims to identify light and hormone combinations that improve rooting efficiency and promote shoot development in two important grapevine cultivars, providing useful information for nursery propagation.

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POSTER

Resilience of grapevine berries to sunburn necrosis and secondary infections

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ABSTRACT

Climate change increasingly challenges viticulture through heatwaves and drought on the one hand as well as high precipitation levels on the other. Several conventional cultivars are thus affected by damage to grapes such as sunburn necrosis and rot infestation, which can severely impair yield and wine quality. While grapevine breeding has traditionally focused on resilience to biotic stress, tolerance to abiotic stress is becoming equally important. In this context, the identification of stress-resilient traits is essential for modern breeding strategies.

The conventional cultivar ‘Riesling’ and the genetically related, fungus-resistant cultivar ‘Calardis Blanc’ were selected to investigate grape susceptibility to sunburn necrosis and its influence on secondary infections by *Botrytis cinerea*. In order to determine the extent of sunburn necrosis, bunch zones of the cultivars were completely defoliated on both sides of the canopy from bunch closure onwards, prior to the respective heatwave events. At harvest, berries without visible injuries as well as berries affected by sunburn necrosis at bunch closure or at véraison were selected, inoculated with a *B. cinerea* spore suspension and incubated for a minimum of three weeks. The extent of sunburn necrosis on grapes and *B. cinerea* on berries was assessed for each cultivar across two growing seasons.

‘Riesling’ exhibited a higher severity of sunburn necrosis than ‘Calardis Blanc’, although the extent varied between years. Uninjured berries of both cultivars showed no differences in susceptibility to *B. cinerea*. In contrast, berries damaged at véraison revealed a markedly higher level of *B. cinerea* infestation in ‘Riesling’ compared to ‘Calardis Blanc’. Sunburn necrosis occurring at bunch closure did not promote secondary infections in ‘Riesling’, likely due to the smaller size and higher firmness of sunburn damages on berry skin. The differences between cultivars were not attributed to the sugar content of the berries. Previous studies have shown that ‘Calardis Blanc’ is characterised by a looser grape architecture and an increased firmness of berry skin

compared to ‘Riesling’, which could prevent *B. cinerea* infections. Moreover, the antioxidative capacity of berries may contribute to differences in the resilience to sunburn necrosis between cultivars.

The results suggest that grape architecture and berry skin thickness display promising traits for breeding programs, which aim at improving grapevine adaptation to abiotic and biotic stress under future climatic conditions.



POSTER

Shared genetic control of seasonal bud freezing tolerance and winter endurance in an F₂ grapevine population

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Keywords: low temperature exotherm, winter survival, freezing tolerance QTL

ABSTRACT

Freezing tolerance is an important trait affecting grapevine winter survival in the Northern United States. This study investigated seasonal grapevine bud freezing tolerance and overall vine winter tolerance in grapevine using an F₂ population derived by selfing a single F₁ developed from a cross of *V. riparia* 'Manitoba 37' × 'Seyval blanc' (VRS-F₂). F₂ genotypes (113) were established in a vineyard at the N. E. Hansen Research Station, Brookings, SD, USA. Low temperature exotherm analyses (LTE) of 3 replicate buds was measured in November, December, January, February, and March of 2017/18 and 2020/2021 to identify immediate freezing tolerance. A second study evaluated overall winter endurance by scoring vine vigor at budbreak eight and nine years after planting. ArhAmpSeq-GBS genetic map was used for QTL identification. The monthly LTE analyses identified three stable QTL, in November and December,

on chromosomes 10, 13, and 14, which explained 16 to 27% of the variation. Analysis of the genes underlying the narrowest colocation of each QTL's 95% Bayesian interval found genes in the early-responsive to dehydration, circadian rhythm, floral development and MADS box transcription factor gene pathways. Whole vine winter endurance measured by vine vigor at budbreak identified a stable QTL on chromosome 4. Analysis of genes underlying the overall winter tolerance loci indicated calcium signaling, flower development, circadian rhythm, and WRKY transcription factor gene pathways. A whole vine winter endurance QTL on chromosome 14 collocated with LTE QTL in December and November suggesting shared genetic control of the monthly freezing tolerance and overall winter tolerance in the VRS-F₂ population.

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POSTER

SUSTEMICROP project: evaluation of grapevine varieties as agroecological innovations for climate change adaptation in sustainable viticulture

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Keywords: grapevine diversity, Mediterranean viticulture, phenology, technological potential, disease-resistant varieties

ABSTRACT

Mediterranean viticulture faces increasing pressure from rising temperatures, altered phenology, and intensified disease incidence. The use of plant material adapted to future climatic conditions represents a promising strategy. Within the SUSTEMICROP project, grapevine genetic resources were evaluated under field and controlled environments in France, Lebanon, and Greece as diversity-based adaptation approaches.

First, traditional Lebanese grapevine cultivars, shaped by long-term exposure to Mediterranean stress conditions, were prospected and characterized. Phenological stages were monitored over multiple growing seasons to evaluate developmental patterns under local environments, while microvinifications assessed technological potential for wine production. In parallel, ten Lebanese table-grape accessions were evaluated for agronomic performance and quality attributes, linking adaptive capacity to both wine and

fresh-market uses. To extend the comparative framework, experimental plots in France and Greece monitored the phenology of ten Greek, international, and disease-resistant cultivars under open-field conditions, allowing comparison of developmental timing and varietal responses across genetic groups. Under greenhouse conditions, controlled-environment experiments simulated current (2025) and projected 2050 climate scenarios, combining elevated CO₂ (~650 ppm) and increased temperature (+2.5 °C). The adaptive responses of conventional cultivars and breeding lines under selection were evaluated under these conditions. The combined results highlight complementary mechanisms of varietal performance, including historical adaptation, genetic resistance, and developmental plasticity. These findings identify key adaptive traits and provide a scientific basis for breeding and selection strategies aimed at securing Mediterranean viticulture under ongoing climatic change.

ACKNOWLEDGEMENTS

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POSTER

The hidden outcomes of clonal selection: cultivar-specific water-use efficiency dynamics in grapevine (*Vitis vinifera* L.)

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Keywords: clonal variation, somatic variants, stomatal conductance, transpiration efficiency

ABSTRACT

Clonal selection represents a key approach in the genetic improvement of grapevines. Its primary objective is to fix, within commercial clones, the cumulative somatic variations that have arisen over time in vegetatively propagated vineyards and that confer valuable agronomic traits. Traditionally, breeding programs have emphasized traits such as yield, berry composition, and sanitary status; however, it is plausible that certain, yet largely unexplored, adaptive responses to abiotic stress have also been unintentionally preserved in distinct genetic backgrounds. In the present study, ten *Vitis vinifera* varieties—represented by their most commercially relevant Italian clones—were evaluated under uniform field conditions in an experimental vineyard. Measurements of isotopic composition ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) and proximal physiological traits (stomatal conductance, g_s , and SPAD readings) were collected across three consecutive seasons (2022–2024) to investigate intra-varietal diversity in intrinsic water-use efficiency (iWUE). Results revealed significant variation ($p < 0.001$) across all traits examined, with the Year factor frequently significant, reflecting strong interannual fluctuations in temperature and precipitation. REML analyses indicated that both Variety and Clone contributed substantially to total variance, and broad-sense heritability (H^2) was high for $\delta^{13}\text{C}$ (0.75), $\delta^{15}\text{N}$ (0.58), and SPAD values (0.48). Conversely, in vivo g_s measurements showed lower heritability estimates. Intra-varietal BLUPs for the heritable parameters highlighted marked within-cultivar variability—particularly in Sangiovese, Pinot noir, and Cabernet Sauvignon—for $\delta^{13}\text{C}$, suggesting the coexistence of clones exhibiting distinct strategies for stomatal regulation and transpiration efficiency. Correlation analyses also revealed temporal patterns of selection, with more recently developed clones tending to display lower iWUE combined with higher average bunch weights. Overall, this work demonstrates substantial intra-varietal genetic variability for traits linked to stress tolerance while identifies discernible trends in clonal selection associated with reduced water-saving behaviour in later selections.

POSTER
SESSION:
PHENOTYPING



POSTER

Correction of environmental interference in field applications of handheld NIR spectroscopy for grape quality assessment

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Keywords: NIR, field assessment, breeding, sugar, acid

ABSTRACT

Sugar accumulation and organic acid degradation are key indicators of grape quality and require monitoring throughout the breeding process in the field. However, traditional methods are labor-intensive and limited by destructive sampling and laboratory-based chemical analyses, which pose a major challenge in the early breeding stage when younger vines produce limited quantities of grapes. Handheld near-infrared (NIR) spectroscopy offers a rapid, non-destructive alternative but its performance is strongly influenced by external environmental factors, particularly variable illumination, when applied in the field.

To address this challenge, the correction potential of External Parameter Orthogonalization (EPO) for grape quality assessment under vineyard conditions was evaluated in the present study. Paired dataset of NIR spectra were acquired under controlled laboratory conditions and in the vineyard from the same biological samples. Partial Least Squares Regression (PLSR) was used as a baseline modeling approach to quantify the improvement. The result showed that EPO significantly improved model performance for the field acquired data, reducing the root mean square error of prediction (RMSEP) from 142.18 g/L to 17.49 g/L and increasing the R^2 from -5.15 to 0.74 . These findings demonstrate the effectiveness of EPO in correcting environmental interference, enabling accurate and reliable field-based grape quality assessment using calibration models developed under laboratory conditions, which can accelerate the evaluation process in the breeding program and allow select grape material from early-stage vines to be used for further evaluations.



POSTER

Development of a high-performance platform based on computational vision for grape leaf rust phenotyping

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Keywords: viticulture, diseases, *Neophytopella tropicalis*, breeding, computational vision, phenotyping

ABSTRACT

Fungal diseases are one of the major causes of economic losses in agriculture. Here we present a high-throughput system for automatic phenotyping of foliar discs inoculated with Asian Leaf Rust (ALR), caused by *Neophytopella tropicalis* (Ono). Foliar discs with 10 mm diameter were inoculated with ALR and photographed by an automatic capture image system, called “BlackBird”. The images were manually phenotyped using an image editor software and used to train a Mask R-CNN model on framework Detectron-2 to collect leaf rust severity, number of pustules, and pustule mean area. After training, we manually

phenotyped a subset of images and compared these data with our trained Mask R-CNN model. Convolutional Neural Networks (CNNs) were also trained and used to classify these images. The mean difference between real and automatic severity, calculated by Mask R-CNN and CNN, was 0,37% and 19,30%, demonstrating that the Mask R-CNN model has great accuracy for image classification. To our knowledge, this is the first high-performance platform for phenotyping grapevine leaf rust. This methodology can also be used to phenotype rust from other hosts and be adapted to other pathogens.

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POSTER

Enhanced *in vitro* bud sprouting of field-derived grapevine material

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Keywords: *Vitis vinifera*, activated charcoal, bud sprouting, rooting, micropropagation

ABSTRACT

Improving the *in vitro* establishment of grapevine buds is important for micropropagation, sanitation programs, and germplasm conservation. Bud sprouting from field material can vary depending on the variety and the composition of the culture media. This study analysed the *in vitro* sprouting and rooting of nodal buds from two *Vitis vinifera* varieties, It18 and It5, grown in four culture media containing two benzyladenine (BA) concentrations ($\text{mg}\cdot\text{L}^{-1}$) with or without activated charcoal (2.2BA, 4.4BA, 2.2BACA and 4.4BACA). Data were analyzed using t-Student test ($p<0.05$).

The buds were disinfected using a standard protocol, and placed in the four experimental media. After 21 days of culture, we measured sprouting percentage, shoot length, number of leaves, presence of apical necrosis and rooting percentage.

It18 variety reached a percentage of sprouting of 75% in most treatments, with the longest shoots in 4.4BA and without apical necrosis in media containing activated charcoal. In It5 variety, sprouting was about 80% in all treatments, showing the longest shoots in 2.2BACA. Apical necrosis occurred only in media without activated charcoal. Regarding the number of leaves did not show significant differences among the different media in the It18 variety. However, in the It5 variety, significant differences were found between 2.2BA and 2.2BACA, and also between 2.2BA and 4.4BA.

Rooting results indicated that BA alone did not induce roots in either variety (0%), whereas BA combined with activated charcoal (BACA) promoted rooting. In It18, 2.2BACA achieved the highest rooting percentage (67%), followed by 4.4BACA (27%); whereas, in It5, both BACA media reached 18%.

In conclusion, these results suggest that the addition of activated charcoal is a key factor in reducing apical necrosis, promoting rooting and improving the quality of the regenerated material, but its effect on shoot length and sprouting depends on the variety and the BA concentration. These findings might help refine micropropagation protocols and support sanitation programs and the preservation of table grape varieties.



POSTER

Genetic and developmental regulation of leaf senescence in grapevine rootstocks and grafted scions

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Keywords: leaf senescence, rootstock, scion, photoperiod, genetic regulation

ABSTRACT

Leaf senescence in grapevines is a key developmental process influencing photosynthesis and carbon allocation from source tissues to sinks, with important implications for vineyard productivity. This study investigated the initiation and progression of leaf senescence in response to daylength changes and examined the underlying genetic regulation. Two presentations of an F1 rootstock population derived from *Vitis rupestris* 'B69' × *Vitis riparia* 'HP1' were evaluated: own-rooted individuals and individuals grafted with the common *Vitis* hybrid 'Marquette' scion. Time-series digital imaging was used to monitor leaf color change, and longitudinal phenotypic data were analyzed using functional principal component analysis. RGB pixel variation enabled

identification of leaf position along the shoot and genetic associations with daylength-responsive senescence patterns. Differences between the two population presentations suggest that the scion and/or its interaction with the rootstock influences senescence dynamics in grafted plants. Basal and apical leaves showed the strongest phenotypic responses to declining daylength, potentially reflecting differences in temporal leaf age. Functional QTL analysis identified genetic loci and enriched pathways associated with senescence across leaf positions, demonstrating the value of developmental trajectory-based approaches for dissecting complex traits.

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POSTER

Less effort, improved results: the potential of sensor fusion to optimize grape cluster phenotyping

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ABSTRACT

Sustainability and the consequences of climate change challenging today's viticulture resulted in a high demand for new disease resistant varieties (DRVs). However, breeding of DRVs with multiple resistances to biotic and abiotic stresses and high wine quality is a time-intensive task. An expanded availability of molecular markers especially for complex traits like grape cluster architecture or berry quality might accelerate the breeding of DRVs significantly and improve breeding efficiency. The application of user-friendly, preferably non-invasive, sensor techniques has proven them to be promising tools for facilitating high-throughput phenotyping of large biparental populations. This, in turn, enabled the detection of new Quantitative Trait Loci (QTLs), the base for the development of trait-linked molecular markers. However, most of the established user-friendly methods focus on one specific trait like grape cluster architecture or sugar content by using one sensor modality like 3D, Red-Green-Blue (RGB) or Near-Infrared (NIR) imaging. We aim to overcome the need for individual sensor-based methods by fusing optical and spectral sensors for combined phenotyping of geometric and spectral grape cluster traits using a single handheld tool for both laboratory and field applications. The major challenges from a biological point of view are: (i) the reliable linkage of normalized spectral reflectance at specific wavelength bands with analytical and chemical ground truth, such as phenolic compounds, acidity, or cuticle waxes; (ii) reproducibility of results in different years and material; as well as (iii) data analysis and prediction model development. Finally, the connection of data from up to twelve spectral bands fused with geometry will support fast assessments of berry ripening and berry skin traits as well as the detection of stress indicators for phenotyping of DRVs, mapping populations or genetic resources with less effort and improved outcomes.



POSTER

Phenotyping of heat response traits in a grapevine segregating population (Rhine Riesling × Cabernet-Sauvignon)

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Keywords: *Vitis vinifera*, heat stress, chlorophyll fluorescence, thermal imaging, BLUPs

ABSTRACT

Climate change is increasing the frequency and severity of heat waves, posing a major challenge to grapevine cultivation across Europe. Therefore, the development of tolerant genotypes may represent a viable strategy to enhance the sustainability of viticulture.

In this context, a segregating population (Rhine Riesling × Cabernet Sauvignon) has been evaluated at the experimental fields of Fondazione Edmund Mach. Phenotyping of key physiological traits associated with heat stress responses was carried out, including stomatal conductance (gs), chlorophyll fluorescence (Fv/Fm and non-photochemical quenching, NPQ), leaf temperature, and environmental drivers such as ambient radiation (PAR) and vapor pressure deficit (VPD).

Proximal measurements were conducted using a LI-COR LI-600 porometer on both sides of the vine rows and at different times of the day to capture side-specific and diurnal variability in plant physiological responses to combined heat and radiative stress.

Preliminary analyses revealed consistent relationships among environmental variables and plant physiological responses; gs showed significant correlations with PAR and VPD, while leaf temperature was related to both radiation

levels and stomatal behavior. These results highlight the interaction between atmospheric demand, stomatal regulation, and leaf thermal dynamics under field conditions. Thermal imagery of the vineyard canopy was reconstructed from UAV flights and will be integrated with proximal physiological measurements to evaluate the potential of canopy temperature as a proxy for vine physiological status. Additionally, NPQ was evaluated and compared with the relative reduction of Fv/Fm under heat stress conditions, allowing the estimation of genotypic performance using BLUP values. The associated standard deviation across years (2021–2023) was considered to assess the stability of genotypic responses over time.

This approach led to the identification of contrasting genotypes that will be used in further experiments under controlled conditions, aiming to improve our understanding of heat resilience mechanisms. These phenotypic evaluations are designed to complement QTL identification studies associated with heat stress tolerance, contributing to the development of scalable phenotyping strategies applicable both to vineyard management and grapevine breeding.

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POSTER

Predictive metabolomics of root traits across environments in *Vitis* spp.

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Keywords: breeding, drought, grafting, rootstock, wild species

ABSTRACT

Root traits are key determinants of plant performance and represent important targets for crop improvement. However, their phenotyping remains challenging due to limited accessibility and the labor-intensive nature of root measurements. Metabolomics-based approaches offer a promising avenue for high-throughput prediction of root system architecture (RSA), but they have been rarely explored as a proxy of complex root phenotypes, especially in perennial crops, such as grapevine.

In this study, we evaluated the ability of root metabolic profiles to predict 15 root traits related to RSA and osmotic adjustment in 12 wild *Vitis* species relevant for grapevine rootstock breeding programs. We further assessed the stability of these predictions across contrasting biotic contexts (cuttings vs. grafts) and environmental conditions (well-watered vs. water-deficit). Metabolomic data showed

moderate predictive power for specific traits, particularly the number of adventitious roots and root biomass, while overall predictability remained limited for most traits. Covariation analyses between metabolism and RSA or root osmotic adjustment uncovered species-specific relationships that shifted across biotic and environmental contexts. These inconsistencies between metabolism and other root phenotypes variation patterns suggest that phylogenetic structure strongly constrains metabolomics-based prediction of complex root traits.

Together, our results highlight both the potential and the current limitations of metabolomic approaches for root trait prediction in *Vitis* spp. and emphasize the need to account for evolutionary relationships when developing predictive models.

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POSTER

Spectral differences of grapevine leaves and clusters affect prediction accuracy of cluster architecture and juice traits

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Keywords: *Botrytis* bunch rot, grapevine breeding, phenomics, spectral reflectance

ABSTRACT

Grapevine productivity is increasingly threatened due to climate change. Grapevine clusters are especially sensitive to fungal infections such as *Botrytis* bunch rot and to abiotic stresses including sunburn damage. In this study, we evaluated how hyperspectral reflectance from different grapevine organs contributes to the prediction of cluster architecture and juice quality traits to support high-throughput phenotyping in Riesling and Pinot clonal populations. Using partial least squares regression (PLSR), we assessed the prediction accuracy of eight cluster architecture traits and six juice traits under two data analysis strategies: data splitting by population and by cluster type. Both sets of traits exhibited strong population-specific trends, as prediction accuracy depended on the data split strategy and the organ reflectance measurements used to train the model. Cluster reflectance models consistently outperformed those trained on dry leaf reflectance for most traits, except pH. Cluster type data split increased variance and improved calibration results for several traits, including number of berries ($R^2 = 0.53$), berry diameter ($R^2 = 0.79$) and total acidity ($R^2 = 0.48$), whereas population-based splits resulted in lower prediction accuracy. Variable importance in projection (VIP) scores indicated that visible (400-700 nm) and red-edge (680-760 nm) spectral regions contributed most to cluster architecture predictions, while near- and shortwave infrared spectra (700-1200 nm) were more relevant for juice trait prediction. Overall, our results demonstrate that organ-specific hyperspectral reflectance combined with appropriate data analysis strategies can enable scalable, non-destructive screening of cluster architecture and fruit quality traits to support early selection decisions for more efficient allocation of labour and costs in grapevine breeding programs.

POSTER
SESSION:
FRUIT DEVELOPMENT, GRAPE
AND WINE COMPOSITION



POSTER

Analysis of grape secondary metabolites in disease-resistant grape cultivars grown in central Croatia

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Keywords: disease-resistant cultivars, secondary metabolites, grape chemical profile

ABSTRACT

Breeding programs have been launched in the leading wine-growing countries and have been successful since there are multiple new disease-resistant cultivars on the market available to the vine growers. Furthermore, these new cultivars offer substantial reduction in the fungicide use while maintaining high fruit and wine quality. This study investigated the grape secondary metabolites (polyphenolic and volatile organic compounds) in 21 disease-resistant cultivar and compared them to the three widespread vinifera varieties.

White cultivars were subjected to the analysis of volatile organic compounds, and their aroma profiles were compared to Chardonnay. The results revealed high variability among cultivars, with 81 individual compounds analysed. The PCA based on the aroma profiles confirmed this variability, and singled out cultivars Muscaris, Hiberna, and Voltis, which were characterized by high content of terpenes and C13-norisoprenoids. Cultivars that grouped closely to Chardonnay were Souvignier gris, Johanniter, Soreli, indicating similar aroma profile, which was characterized by higher content of alcohols. Polyphenolic profiles were analysed in red cultivars and compared to Merlot and Cabernet Sauvignon. The most distinct differences, as expected, were observed in the anthocyanin profiles. The disease-resistant cultivars showed presence of diglucoside forms of anthocyanins, whereas Merlot and Cabernet Sauvignon were characterized by acylated forms. The PCA based on the polyphenolic compounds revealed clear separation of vinifera and disease-resistant cultivars, later being characterized by higher concentrations of stilbenes and flavan-3-ols.

These findings affirm the oenological potential and chemotaxonomic distinctiveness of PIWI varieties, supporting their adoption for sustainable production and enhanced disease management in regions vulnerable to fungal pathogens.



POSTER

Autochthonous yeasts from Florida vineyards produce distinct aroma profiles and support regional identity development in Muscadine wines

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Keywords: Muscadine grape, autochthonous yeast, wine fermentation, volatile organic compounds, regional wine identity

ABSTRACT

Florida's wine industry generates more than \$20 billion in annual economic activity, placing the state among the top three wine markets in the United States. Consumer research further indicates that wine buyers increasingly value locally produced products, with several generations demonstrating a willingness to pay premiums for wines labeled with regional origin. Muscadine grapes (*Muscadinia rotundifolia*), which are well adapted to the region's warm, humid climate and tolerant of endemic diseases, represent the primary wine grape grown in Florida and serve as the foundation of the state's growing wine sector. Despite this unique regional identity, most wineries rely on commercial *Saccharomyces cerevisiae* starter cultures developed for vinifera wines, which may limit the expression of regional wine character and distinctive aroma characteristics. The wine research program at the Center for Viticulture maintains the "Database of Southern Wines" and, since 2022, the "Reference Biorepository of Autochthonous Florida Yeast" with more than 200 isolates to support studies on fermentation performance and aroma development.

This study evaluates the functional enological potential of this collection and examines volatile organic compound (VOC) production during controlled microfermentations of muscadine must with selected FL autochthonous yeast isolates.

Representative strains from both *Saccharomyces* and non-*Saccharomyces* genera were compared with a commercial *Saccharomyces cerevisiae* reference strain. Volatile profiles were analyzed using solid-phase microextraction coupled with gas chromatography–mass spectrometry (SPME–GC–MS) to examine differences in fermentation-derived aroma metabolites among yeast strains.

Clear strain-dependent differences were observed among several fermentation-derived aroma metabolites. Native *Saccharomyces* and non-*Saccharomyces* isolates produced distinct aroma profiles relative to the commercial control, suggesting differences in the regulation of metabolic pathways involved in fatty acid and ester biosynthesis. These results indicate that utilizing native yeast strains can diversify aroma expression and provide new fermentation options for muscadine wine production.

Together, these findings highlight the functional importance of indigenous yeast populations associated with Florida muscadine vineyards. Continued integration of volatile metabolite analysis with the characterization of regional yeast biodiversity will support targeted strain selection and fermentation strategies that contribute to the development of regional identity in Florida muscadine wines.

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POSTER

Basal defoliation at berry set modulates berry weight, must composition, and secondary metabolite profile in 'Muscat Hamburg' grapes

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Keywords: 'Muscat Hamburg', basal defoliation, polyphenols, volatiles

ABSTRACT

Grape yield and quality largely depend on achieving an optimal balance between crop load and sunlight exposure, which is essential for the development of a desirable phenolic and aromatic profile in grapes. Improving canopy microclimate conditions and adjusting the ratio between older, less photosynthetically active leaves and younger, more active leaves may enhance grape composition. Basal defoliation is expected to improve grape and wine quality by increasing the concentration of polyphenolic and volatile compounds. The aim of this study was to evaluate the effect of basal defoliation performed at berry set on yield parameters, basic must composition, and the profile of polyphenolic and volatile compounds in grapes of 'Muscat Hamburg' grown on the Croatian hillside (2023.). At berry set, six leaves per shoot were removed in the cluster zone in the defoliation treatment, while no leaf removal was applied in the control. The trial was arranged in a randomized block design with three replicates of eight vines each. At harvest, yield per vine and average cluster weight were determined. From each replicate, 10 clusters were sampled for basic must analysis and 100 berries were collected for secondary metabolite analysis. Volatile compounds in grapes were analyzed by GC–MS and polyphenolic compounds were determined by HPLC. Data were subjected to one-way ANOVA. Basal defoliation at berry set did not affect total yield but significantly reduced cluster and berry weight. It increased sugar concentration and decreased total acidity in the must. Defoliation at berry set enhanced the content of total polyphenols, flavonols, flavan-3-ols, and resveratrol-3-O-glucoside, while no effect was observed on total anthocyanins, hydroxycinnamic acids, or hydroxybenzoic acids. It also increased the concentration of total volatile compounds, particularly terpenes and aldehydes, without affecting higher alcohols, fatty acids, esters, or C13-norisoprenoids, and reduced volatile phenols in berries.



POSTER

Biochemical markers for grape berry splitting resistance: prospects for targeted breeding

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Keywords: cutin monomers, epidermal cell density, fruit splitting, pectin, *Vitis vinifera*

ABSTRACT

Berry splitting is a major physiological disorder in fleshy fruits that undermines quality, yield, and shelf life. In table grapes (*Vitis vinifera* L.), susceptibility to splitting is a primary cause of sour rot disease, resulting in significant commercial and economic losses.

Due to the lack of effective agrotechnical practices to prevent grape berry splitting, breeding split-resistant cultivars is a priority objective in modern viticulture. However, genetic progress is constrained by a lack of reliable biochemical markers and a limited understanding of the structural and chemical mechanisms governing this trait.

This study addresses the knowledge gap by evaluating six distinct table grape cultivars grown under identical environmental conditions that exhibit a wide range of splitting susceptibility. Through comprehensive histological and biochemical analyses, we quantified skin epidermal cell density, cell wall polysaccharides, and cuticle thickness. We found that neither epidermal cell density nor cuticle thickness was associated with splitting susceptibility. Instead, cell wall pectin content was the only polysaccharide to exhibit a significant negative correlation with splitting, suggesting its potential role in mitigating the disorder by enhancing exocarp structural integrity.

Furthermore, utilizing GC MS analysis, we performed the first comprehensive profiling of grape berry cutin monomers. This analysis uncovered a dynamic, developmentally regulated metabolic shift in cutin biosynthesis, characterized by a transition from aliphatic components in early development to a predominance of phenolic monomers during the ripening stage.

Notably, the accumulation of specific phenolic monomers, especially cinnamic acid-3,5-dimethoxy and methyl-3,4-dihydroxybenzoate, alongside C16 and C18 fatty acids, was significantly associated with enhanced splitting resistance. These findings highlight cell wall pectin content and cutin monomer composition as key determinants of grape splitting susceptibility. These biochemical traits offer promising new selectable markers and provide clear molecular targets for developing resilient table grape cultivars.



POSTER

'Chocolat noir': A new Teinturier red wine grape cultivar with superior enological suitability

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Keywords: grape breeding, wine grape, Teinturier cultivar

ABSTRACT

In Korea, red wine has often been produced from table-grape cultivars such as 'Campbell Early' and 'Muscat Bailey A'. However, their use has limited the production of deeply colored, phenolic-rich red wines. To overcome these constraints, the National Institute of Horticultural and Herbal Science, Rural Development Administration (RDA), developed 'Chocolat Noir', a new teinturier wine grape cultivar.

The cultivar is characterized by a teinturier phenotype (pigmented skin and flesh) and a high tannin content. It originated from a cross between 'Bailey Alicante A' and 'Merlot' in 2011. Among the progenies, line W-11-01-33 was first selected in 2016 for favorable enological traits. For the evaluation of vine growth and fruit characteristics, regional adaptation trials were conducted at eight locations from 2022 to 2025, where the line showed consistently favorable vine performance and fruit characteristics across different growing regions. And the cultivar was finally selected in 2025. An application for plant variety protection was submitted to the Korea Seed & Variety Service (KSVS) in Nov. 2025.

'Chocolat Noir' blooms in late May and ripens in early September, approximately 5 d later than 'Campbell Early'. The average berry weight is 2.4 g. Because both the skin and flesh are intensely pigmented, wines produced under experimental winemaking conditions showed a color intensity of 14.9, approximately 7.5 times that of 'Campbell Early' (2.0). Soluble solids reached 21.6 °Bx, indicating that chaptalization may not be required under typical winemaking conditions. Titratable acidity was 5.8 g·L⁻¹ (tartaric acid equivalents), suggesting that acid adjustment may be needed to ensure balanced sensory properties and microbiological stability.

The cultivar is suitable for spur pruning and showed a relatively low incidence of physiological disorders, including berry cracking, even under non-thinned conditions, indicating manageable vineyard performance. High levels of polyphenols and tannins support its potential for varietal use or blending purposes. However, elevated phenolic content may increase astringency and bitterness, requiring careful harvest timing and winemaking management.

Overall, 'Chocolat Noir' is well adapted to Korean growing conditions and produces wines with markedly greater color density and high phenolic potential.

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POSTER

Environmental effects on the secondary metabolites of PIWI cultivars across different locations in Italy

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Keywords: sustainable viticulture, PIWI cultivars, metabolomics, disease resistance, wine quality

ABSTRACT

Grapevine breeding programs aim to develop cultivars that combine high productivity, oenological quality, disease resistance, and adaptability to diverse environmental conditions. In the context of climate change and increasing pressure from pathogens such as *Plasmopara viticola*, traditional viticultural systems face significant sustainability challenges, reinforcing the need for innovative varietal strategies. Metabolomics has emerged as a powerful approach to elucidate plant responses to biotic and abiotic stresses by integrating complex metabolic pathways. Thus, this study aimed to characterize the secondary metabolite profiles of four PIWI grapevine cultivars (Termantis, Nermantis, Charvir, and Valnosia) grown across six viticultural regions in Italy, using metabolomic analyses of polyphenols, volatile organic compounds, and anthocyanins. The results revealed a strong genotype × environment interaction shaping the metabolic profiles of the cultivars. Charvir, Valnosia, and Nermantis exhibited high phenotypic plasticity, with marked variations in secondary metabolite composition across environments, whereas Termantis displayed greater metabolic stability, suggesting

higher technological predictability. PIWI cultivars showed wide diversity in polyphenolic compounds, volatiles, and anthocyanins, including flavonoids, phenolic acids, and stilbenes such as resveratrol, which are directly associated with grape and wine color, astringency, acidity, stability, and aromatic complexity. Volatile compounds were key determinants of cultivar-specific aromatic profiles, reinforcing their relevance to sensory quality. Overall, the findings demonstrate that edaphoclimatic conditions play a decisive role in modulating grape metabolite composition and highlight phenotypic plasticity as a crucial adaptive trait in PIWI cultivars. Moreover, the reduced fungicide requirements associated with these cultivars underscore their strong potential for sustainable viticultural systems. The metabolic stability of Termantis and the adaptive flexibility of the other cultivars provide valuable insights for cultivar selection across diverse production contexts. These results offer robust scientific support for the adoption of PIWI cultivars in both traditional and emerging viticultural regions, including Brazil, contributing to innovation, resilience, and sustainability in the wine sector.

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POSTER

Impact of the enzymatic activity of autochthonous non-*Saccharomyces* yeasts on wine volatile profiles

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Keywords: β -glucosidase, proteolytic activity, Maraština, *Metschnikowia*, *Hanseniaspora*

ABSTRACT

Yeasts significantly influence wine aroma through various mechanisms, particularly by producing volatile aroma compounds. Yeasts contain genes that encode enzymes that play multiple roles during alcoholic fermentation (Romano et al., 2019). Non-*Saccharomyces* yeasts produce and release various enzymes, such as esterases, glycosidases, lipases, β -glucosidases, and proteases, into the periplasmic space and surrounding medium (Styger et al., 2011). These enzymes can interact with grape precursor compounds to generate aroma-active compounds, thereby significantly influencing the wine's aroma and flavour profile. A significant concentration of the aromatic compounds that shape the wine's aroma is produced by yeasts during fermentation (Carpena et al., 2021).

This research investigates the enzymatic activity of indigenous non-*Saccharomyces* yeasts and their influence on the volatile aroma profile of Maraština white wine. Selected indigenous yeast strains isolated from 11 vineyards across Dalmatia wine region were evaluated for their enzymatic potential and their impact on wine volatile composition during fermentation. In vitro enzymatic screening revealed significant variability among strains, with *Hypopichia pseudoburtonii* N-11, *Metschnikowia sinensis/shanxiensis* P-7, and *Hanseniaspora pseudoguilliermondii* V-13 showing

enhanced esterase activity. Strong proteolytic activity was observed within *Hanseniaspora* species, particularly leucine and valine arylamidase activity associated with aromatic amino acid metabolism and aroma precursor transformation. β -glucosidase activity, linked to terpene release, was also detected in several *Hanseniaspora* strains. Cluster analysis suggested that enzymatic profiles were more strongly influenced by yeast genus than species. Fermentation trials demonstrated that non-*Saccharomyces* yeasts significantly modified the volatile profile of Maraština wines. *Metschnikowia pulcherrima* K-6 and *Hanseniaspora guilliermondii* N-29 promoted the formation of terpenes and C13-norisoprenoids, contributing to enhanced floral and fruity aroma characteristics. *Pichia kluyveri* Z-3 and *Starmerella apicola* VP-8 showed increased ester production. Emerging strains such as *M. chrysoperlae* K-11 and *M. sinensis/shanxiensis* P-7 reduced the concentration of volatile phenols associated with undesirable "Brett" aromas. The results highlight the oenological potential of indigenous non-*Saccharomyces* yeasts as multifunctional starter cultures capable of improving aroma complexity and typicality of Maraština wines through specific enzymatic activities and modulation of volatile compounds.

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POSTER

Phenological characteristics of grapevine varieties released in Sremski Karlovci

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Keywords: phenology, created varieties, Morava, Probus, Petra

ABSTRACT

At the experimental field for viticulture in Sremski Karlovci, Serbia, grape breeding started 70 years ago. During that period three breeding programs resulted in 24 created varieties. First breeding program aims to improve the wine quality of the native pontica-balcanica varieties, by crossing them with occidentalis galica varieties. As a result 7 varieties were released. Second breeding program started in 1970s and aims to improve the tolerance to low winter temperatures. In their genetic base, they have 87.5% *Vitis vinifera* and 12.5% *Vitis amurensis*. In this program 6 varieties were released. In third breeding program, which is still in progress, the primary goal is to increase the tolerance to fungal diseases. As a result 11 wine varieties have been released.

The aim of this paper is to analyse phenological stages (budburst, flowering and veraison) of the varieties from the

three breeding programs recorded during the period 2019-2025 and to compare the phenology data for varieties released in first two breeding programs with available historical data. Following varieties were examined - First breeding program (Neoplanta, Probus, Sirmium and Župljanka); Second (Lela, Liza, Mila and Petra); Third (Bačka, Dionis and Morava).

Beginning of budburst occurred in first decade of April, which is more than one week earlier compared to historical data. The highest shift in budburst within the variety groups showed Probus and Lela. Flowering occurred in last decade of May which is in line with historical data. The earliest beginning of ripening showed varieties Bačka and Neoplanta. On the other hand Liza, Mila and Morava showed the latest entrance to veraison which was occurred in the first decade of August.

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POSTER

Sensory analysis of wines made from selected genotypes obtained from crosses involving Croatian native grapevine germplasm

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Keywords: breeding, disease-resistant cultivars, native grapevine, MFA, RATA

ABSTRACT

Acceptance of new disease-resistant cultivars in viticulture and winemaking remains limited, despite their enhanced resistance to major fungal diseases. This reluctance is primarily connected to the strong association between viticulture and the traditional varieties of a given area, and the historically inferior quality of early generation disease-resistant cultivars. Consequently, new cultivars are expected to produce wines comparable to traditional vinifera varieties. Therefore, the early evaluation of wine quality and sensory properties represents a crucial step in the breeding and selection of new disease-resistant cultivars.

The study was conducted on genotypes obtained from crosses Grk x Panonia (GRP) and Dišeća ranina x Panonia (DRP). Wines made from selected genotypes were produced in the 2024 and 2025 vintages and were subjected to sensory evaluation. The sensory evaluation was based on detailed sensory profiling using RATA (Rate-All-That-Apply) method, while the obtained data was used to perform MFA (Multiple Factor Analysis). For both vintages, results showed no presence of undesirable aromas or flavours,

such as 'foxy' aromas. Furthermore, the average scores for overall impression for most genotypes were 3.5 (out of 5) or higher, indicating good wine quality. Detailed sensory profiling combined with MFA revealed that both GRP and DRP genotypes clustered into two groups. One group was characterised by flower aromas, such as acacia, linden, honeysuckle, and elderflower, while the second group was characterised by fruity and herbaceous aromas, such as apple, lemon, grass, and herbs. The MFA also revealed that some of the genotypes showed similarities to the vinifera parent varieties. Moreover, the major influence of the vintage was also observed. Wines from the 2025 vintage displayed higher intensity of the aromas, especially flower and stone fruit aromas. These results indicate a good potential for producing wines that would appeal to consumers, along with the possibility of producing a wide range of wine styles, since the genotypes displayed variability in their sensory profiles. Furthermore, this study confirms the importance of including detailed sensory evaluation in the breeding program for the selection of genotypes with positive sensory profiles.

ACKNOWLEDGEMENTS

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POSTER

Spring phenology and bud fruitfulness of a grapevine segregating population (Rhine Riesling × Cabernet-Sauvignon)

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Keywords: *Vitis vinifera* L., budbreak bud fruitfulness, transgressive segregation, climate change

ABSTRACT

The rise of average temperatures worldwide influences grapevine (*Vitis vinifera* L.) phenology by accelerating its development, starting from anticipated budbreak dates. This shift exposes buds to an increased risk of late spring frosts exposure, which are expected to persist in the future despite global warming. Beyond phenology, bud fruitfulness is also significantly influenced by climate-driven environmental factors, such as radiation, water availability, and temperature. The genetic control of these complex traits remains largely unknown; a better understanding of these mechanisms would benefit selection efforts for slow- or late-developing varieties.

The primary objective of this study, carried out in the 2025 and 2026 seasons, was to characterize the phenotypic variation of traits associated with bud phenology and fruitfulness in a segregating population of 166 individuals derived from a controlled cross between internationally renowned Rhine Riesling (RR) and Cabernet Sauvignon (CS), performed in 2005. All plants are currently located at Fondazione Edmund Mach in San Michele all'Adige (46°18'N, 11°13'E, Italy). Specifically, budbreak date, intended as reaching of stage BBCH 07 ("green tip"), was recorded for each genotype. Bud fruitfulness was assessed in the second week of May at stage BBCH 57 ("inflorescences fully developed"). Overwintering buds on the fruiting cane alone were considered, and the number of inflorescences was counted for each node. Temperature, radiation and precipitation data were collected by a weather station in the vicinity of the vineyard and used for thermal requirements (GDD10) calculations.

Budbreak across the RR×CS population spanned an interval of approximately 20 days. Since RR and CS exhibited intermediate phenotypes, the substantial variation observed in budbreak DOY and thermal requirements indicates transgressive segregation in the progeny, with several individuals exceeding the parental range. Fruitfulness of the entire cane was compared to that of basal buds; values appeared normally distributed in both cases, highlighting the complexity of the genetic control of these traits. Bud fruitfulness of the entire fruiting cane was found to span from a minimum of 0 to a maximum of 3 inflorescences per shoot. The number of lowly fruitful buds was substantial

when fruitfulness of basal buds alone was considered, despite the presence of extreme individuals displaying high positive values. Residual bud fruitfulness, namely of apical and median buds combined, and that of basal buds appeared positively correlated.

This study provides a comprehensive screening of the spring phenology of the RR×CS segregating population, revealing significant diversity in phenological and fruitfulness characteristics. It establishes the foundation for subsequent genetic analyses, as well as for the employment of notable individuals for focused physiological studies.



POSTER

Varietal differences in berry biometrics, skin structure, and wax biosynthesis of red grapevine varieties: A two-year study

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Keywords: *Vitis vinifera* L., varietal selection, climate change adaptation, fruit histology, cuticular waxes

ABSTRACT

Climate change poses a major threat to vitiviniculture, particularly in Mediterranean regions, where increasing temperatures and drought events are reshaping berry development and composition. However, comparative information on varietal-specific responses under identical environmental conditions remains limited. Therefore, this two-year (2021 and 2022) field study aimed to identify morphological, histological, and biochemical traits associated with climate resilience across grapevine varieties. Twenty-seven red *Vitis vinifera* L. varieties grown in Northern Portugal were evaluated for berry biometrics (weight and dimensions), technological quality parameters (total soluble solids, pH, titratable acidity), cuticle thickness, epidermal and hypodermal structure, and cuticular wax accumulation. The expression of key genes involved in aliphatic wax biosynthesis, namely ERF045, CER10 and WSD1, was also evaluated on agronomically relevant varieties: ‘Cabernet Sauvignon’, ‘Tinto Cão’ and ‘Touriga Nacional’. The warmer and drier conditions observed in

2022 resulted in a widespread reduction in berry weight and size, with marked declines in some varieties, accompanied by increases in pH and higher cuticular wax content in several varieties, suggesting a coordinated stress response. Histological analyses revealed varietal-specific structural adjustments, with cuticle thickness generally decreasing in 2022. Gene expression analysis in ‘Cabernet Sauvignon’, ‘Tinto Cão’, and ‘Touriga Nacional’ demonstrated upregulation of the transcription factor ERF045, with varietal-specific modulation of the genes CER10 and WSD1, supporting enhanced wax-related protective responses in the berry skin.

By integrating berry morphology, tissue structure, and molecular regulation, this study identifies cuticular traits and wax biosynthetic pathways as potential markers of climate resilience. These findings contribute to evidence-based varietal selection and provide physiological targets for breeding strategies aimed at sustaining grape production under future climate scenarios.

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POSTER

Wine chemical profiling of genotypes obtained from crosses involving Croatian native grapevine germplasm

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Keywords: breeding programs, Croatian native varieties, secondary metabolites, chemical profiles

ABSTRACT

One of the goals of the breeding program launched at the Faculty of Agriculture in Zagreb is to create new varieties resistant to fungal diseases suitable for growing in Croatian wine regions. Moreover, the newly created varieties should have acceptable chemical profiles that are comparable to traditional vinifera varieties. Selected genotypes included in this study were obtained by crossing 'Grk' x 'Panonia' (GRP genotypes) and 'Dišća ranina' x 'Panonia' (DRP genotypes). After genotyping, 14 genotypes were confirmed to inherit resistant genes, and are now subjected to chemical profiling.

After harvesting at technological maturity, microvinification was carried out, and the resulting wines were subjected to physicochemical analyses and volatile profiling. Physicochemical analyses included basic chemical parameters of the wine, such as the alcohol content, extract, and total acidity, as well as individual acids present in the wine. The results revealed significant variability among genotypes, with several genotypes showing promising oenological characteristics. Wines produced from genotypes DRP-4, DRP-7 and GRP-17 showed significantly higher alcohol content and extract, while GRP-17 showed the lowest total acidity. This variability indicates that it would

be possible to produce different wine styles in accordance with the basic chemical characteristics.

Analysis of volatile organic compounds confirmed the presence of esters, higher alcohols, and other aroma-active compounds in concentrations comparable to those found in vinifera wines, without the presence of undesirable 'foxy' aromas typical for earlier generations of resistant cultivars. Results also revealed high concentrations of esters, norisoprenoids and terpenes in comparison to wines made from at least one parent variety. The PCA analysis further explained the variability. Among GRP genotypes, GRP-33 was singled out by its high presence of terpene compounds, while GRP-16 and GRP-36 grouped closely to Grk. Among DRP genotypes, genotype DRP-4 was singled out by high concentrations of terpenes, fatty acids, and volatile phenols. Other DRP genotypes were situated between parent genotypes, indicating similarity to both parents.

In conclusion, this study confirmed that the listed genotypes combine favourable physicochemical composition with desirable resistance to fungal diseases. This proves that resistance breeding does not necessarily compromise wine quality and that new grapevine varieties are suitable for wine production.

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