Summary of the *Vitis*Gen2 Project Meeting 2022

The 2022 annual *Vitis*Gen2 project meeting, just like the previous year 2021, was held online due to the rising cases of COVID-19. The meeting brought together the advisory panel, scientists, collaborators, students, and guest speakers for the final time before the termination of the project in August 2022. The meeting was held from January 5 to January 7, 2022, from 11:30 am ET and lasted about 3.5 to 4 hours each day. A total of sixty-three people attended at least one of the sessions across the three days of the meeting. The major highlights of the meeting included team reports from the six project teams; postdoc and student talks; and special seminars from two invited speakers (Dr. Margaret Worthington and Dr. Harlene Hatterman-Valenti). There were discussions following presentations and an evaluation session from the advisory panel members and the speakers for the special talks.

Highlights of the project accomplishments included the continued utilization of the rhAmpSeq genotyping technique developed by the project in various genomic studies and the dissection of important traits in grapes. This genotyping platform continues to be adopted by public and private research centers within and outside the USA. Many new mapping populations have been added to the list of previously generated populations across partner institutions. Advanced technologies in computer vision, computation and high-throughput phenotyping have been adopted in rapid and accurate assessment of traits both in the laboratory and in the field. Project outputs and resources remain accessible to the public and target audiences through trade publications, journals, the project website, social media, etc. Strategic engagement efforts to consumers and end-users remain an important part of the project to address future research approaches and communications. Through concerted efforts from different teams, the project has proudly released genetic materials with stacked powdery mildew resistance genes into the public domain through Foundation Plant Services. Also, numerous discoveries and results from different teams in the project are being processed for publication that will arguably advance the grape industries.

The first invited speaker – Dr. Margaret Worthington, an Assistant Professor of Fruit Breeding and Genetics at the University of Arkansas, Department of Horticulture, gave a talk on the ***"Opportunities for Collaboration between the Muscadinia and Vitis Research Communities"***. While stressing the objectives of the muscadine and grape breeding program at the University of Arkansas, including texture, flavor, disease resistance, seedlessness, etc., her talk and ensuing discussion after her talk focused on the various breakthroughs of *Muscadina* x *Vitis* hybrid breeding, the existing market for *Muscadina*, consumer preferences for *Muscadina* varieties and the call for more collaborations between the *Muscadina* and *Vitis* research communities in improving disease resistance, color, sex, cold hardiness, morphological, quality, and many other important traits. The second invited speaker, Professor Harlene Hatterman-Valenti, presented on the title ***"All Quiet on the Northern Front: VitisGen2's Role in Recent Breeding for Extreme Viticulture at North Dakota State University"*** and reviewed the impact of the *Vitis*Gen2 project on the improvement efforts for wine quality, powdery mildew resistance, cold acclimation, fruit composition and many other traits in the North Dakota State breeding program. Using a diallel mapping population, she underscored the benefits of using the rhAmpSeq markers of the *Vitis*Gen2 project in quantitative trait loci mapping for many traits.

Daily discussions at the meeting centered around the need to publish broadly the impacts and synthesis of the project, release more technical information on haplotypes, quantitative trait loci (QTL), and other resources on the project website, scientific meetings, and domains. The first day of the meeting featured team updates from the Extension and Outreach team, Powdery Mildew team, and a presentation from a postdoc on a DNA haplotype marker system for genome phasing and QTL fine-mapping in grape. Preserving and periodic updating of the project website was advocated. A skim-seq sequencing technique currently being evaluated by the genetics team was confirmed to validate and increase the accuracy of QTLs identified with rhAmpSeq markers. The breakdown in resistance of some genetic materials carrying resistant genes, especially REN3 and RPV3 genes, in the U.S. and Europe was discussed and ongoing collaboration between the US, the center of origin of PM disease, and Europe was reported. Other ongoing efforts to understand any possible co-evolution of grape and disease pathogens and identify other sources of resistance, especially from Israel and Asian regions, received attention. While it has become common practice to release new varieties with stacked resistance against multiple disease strains, the adoption of such materials in the US should be done with caution. It was suggested that different grape varieties with different architecture be used for computer vision for disease detection to ensure wide-range application across breeding programs and genetic backgrounds.

Day two internal presentations were from the Genetics and the Fruit Quality teams and two postdoc seminars. There were discussions on the adoption of the RipTide platform for expression profiling and genotyping, as well as KASP and DArTseq methods. While more information on RipTide was sought, the shortfalls of KASP technology were reported on grapes and there was an update on the collaboration with the Breeding Insight team to transfer the rhAmpSeq markers into the DArTseq platform and possible commercialization of the markers. Genotyping vendor services and turnaround time from DNA submission to the return of data to breeders received attention. The need to take advantage of the 80% discount on the rhAmSeq services for the project which ends in April 2022 was highlighted. The suitability of the rhAmpSeq technology for grapes research based on the long read haplotype compared to short and single sequencing technologies was emphasized. Screening for various odorants and furaneol was discussed and the details of the diglucoside (5GT) markers used for selection at Cornell were provided. There was interest in future exploration of the effect of circadian rhythms on the variability of malate and associated gene expression; to-date, consistency has been maintained in sampling to account for possible variation in the daytime.

The Breeding/Local Phenotyping and the Trait Economics teams presented on the final day of the meeting. Most of the talking points from the presentations were centered around the future of marker-assisted selection and the adoption of other modern techniques such as genomic selection in grapes. The major discussion from the consumer survey was the plans to get the results of the studies to the public and wider industry using outreach venues (e.g., trade publications).

The Advisory Panel commended the project for the high level of cooperation, coordination, and collaboration among members of the project and with industry partners. They were impressed by the infrastructural progress and products developed and released, as well as capacity development

(ie. training of scientists) undertaken by the project. Examples highlighted included the many mapping families and QTL, continual improvements in analytical and computational methodologies, including to track both haplotypes and refine genome locations in developing translatable markers and candidate genes. There was enthusiasm for the active role of all co-PIs in Extension products. They emphasized the need to sum up and broadcast the impressive project impact. There was a further emphasis to publish some technical information such as haplotypes and marker information on the project website and that the sooner marker information is shared, the broader the impact. Private breeders asked for translation of markers to platforms used at commercial vendors. The panel advised establishing measures to sustain the current developments, knowledge and processes after the lifespan of the project, and proposed conducting a retrospective analysis of the data management plan to help guide the development of future proposals, including the continued pursuit of FAIR data standards. The meeting ended with closing remarks from the project directors, Bruce Reisch and Lance Cadle-Davidson, and Advisory team representatives, Donnell Brown, and Nick Dokoozlian.

A few notable developments in the project include the hiring of a new postdoc, Robert Richter, to help facilitate the processing and publication of project outputs. A few scientists will be retiring soon including Tim Martinson and Craig Ledbetter; thanks go to them to their dedication and hard work. Lastly, a committee is working closely with the NGRA on submitting a proposal for a successor project.

Ugochukwu Ikeogu
Postdoctoral Associate and *Vitis*Gen2 Project Manager