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Oral Communication Abstract - 1.03

THE GENOMES OF 204 DOMESTICATED AND WILD VITIS VINIFERA ACCESSIONS REVEAL THE HISTORY AND THE GENETIC ANCESTRY OF EUROPEAN WINE GRAPES

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Vitis vinifera, DNA-Seq, domestication, allele-specific transcriptome analysis

We describe 204 genomes of Vitis vinifera from the Mediterranean range of viticulture and from the southern Caspian Sea Basin, the center of diversity of the species. Genetic ancestry analysis identifies two major ancestry components that are related to genetic differentiation between eastern and western accessions of the wild progenitor and were both passed on to the domesticated germplasm. All data support a single domestication event as the origin of all cultivated varieties followed, however, by pervasive across the genome introgressions from western populations of the wild progenitor into cultivars of eastern origin. This admixture has historically generated the botanical group of occidentalis wine grapes that have diffused from Alpine countries worldwide since the sixteenth century. Two minor additional components are mainly found within the cultivated germplasm and differentiate between table grapes and varieties from the Levant and from Europe's Mediterranean peninsulas, on one hand, and varieties with Muscat ancestry, on the other hand. Across Europe, we identified marked differences in the proportion of ancestry components in autochthonous varieties from different wine producing countries, largely explained by latitudinal clines, with France and especially Italy showing

the largest diversity among and within varieties. Very limited genetic effects of the domestication and improvement processes are detectable in cultivated varieties based on nucleotide level diversity. However, three regions of limited diversity are visible, presumably as a consequence of selective sweeps. In the genomic region showing lowest diversity, we used allele-specific transcriptome analysis to identify two candidate genes that showed a gain of function mutation in domesticated varieties, leading to a marked increase in expression in the berry. This mutation may have contributed to the change in berry size and morphology that made the fruit attractive for human consumption and adapted for winemaking.