

GENOMIC CHARACTERIZATION OF EXTANT GENETIC DIVERSITY IN GRAPEVINE

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Abstract:

Context and purpose of the study – Dating back to the early domestication period of grapevine (*Vitis vinifera* L.), expansion of human activity led to the creation of thousands of modern day genotypes that serve multiple purposes such as table and wine consumption. They also encompass a strong phenotypic diversity. Presently, viticulture faces various challenges, which include threatening climatic change scenarios and an historical track record of genetic erosion. Particularly with regards to wine varieties, there is a pressing need to characterize the extant genetic diversity of modern varieties, as a means to deliver knowledge-based solutions under a rapidly evolving scenario, that may enable improved yields and profiles, resistance to pathogens, and increased resilience to climate change. Here, we are using whole genome resequencing and Pool-Seq strategies to tackle multiple aspects associated with the extant genetic diversity present in grapevine germplasm, with an emphasis on the species's domestication history and the rich Portuguese/Iberian genetic pool.

Material and methods – Work revolves around the use of genomics strategies for the genome-level analysis of genetic diversity. Specifically, strategies employed the use of the Illumina short-read next generation sequencing platform, to generate either whole genome resequencing data of individual genotypes, or PoolSeq data of multiple individuals of the same variety. Subsequent analysis involved bioinformatics characterization of population structure, genetic variation and introgression.

Results – Our analysis incorporates, to the best of our knowledge, the first PoolSeq analysis of intra-varietal diversity associated with multiple grapevine varieties, which is being used to quantify genetic variation and detect the presence of selection signatures. Meanwhile, individual genomes are being used to address important features of the domestication history of grapevine, namely the presence of adaptive introgression and a tentative significant role for the Iberian Peninsula in grapevine domestication.

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