

Genomics and bioinformatics strategies to tackle diversity and domestication in grapevine

Freitas, Sara^{1,2,3}; Sottomayor, Mariana^{1,2,3}; Martins, Antero^{4,5}; Gonçalves, Elsa^{4,5}; Carneiro, Miguel^{1,2,3}; Azevedo, Herlander^{1,2,3,*}.

¹CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, Vairão, Portugal

²Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, Porto, Portugal

³BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, Vairão, Portugal

⁴LEAF- Linking Landscape, Environment, Agriculture and Food, Instituto Superior de Agronomia, Universidade de Lisboa, Tapada da Ajuda, Lisboa, Portugal

⁵Portuguese Association for Grapevine Diversity-PORVID, Tapada da Ajuda, Lisboa, Portugal

*hazevedo@cibio.up.pt

Abstract

Grapevine (*Vitis vinifera* L.) diversity richness results from a complex domestication history over multiple historical periods. Expansion of human activity led to the creation of thousands of varieties with extensive phenotypic diversity. Unfortunately, the recent favoring of specific varieties/clones, and the globalization-driven exposure to pathogens, has led to extensive genetic erosion in this widely cultivated and economically significant crop. Fighting this genetic erosion whilst addressing issues of resilience to climate change, yield and other traits, requires a crucial understanding of the genetic basis of grapevine variation. This scientific field has witnessed significant advances due to the use of genomics approaches, enabled by Next Generation Sequencing. Here, NGS-driven whole genome resequencing strategies have been used to tackle multiple aspects associated with the extant genetic diversity present in grapevine germplasm, including a clarification of different features of its recent evolutionary history that suggest a meaningful role of the Iberian Peninsula in grapevine domestication. These different aspects of grapevine biology, which require genome-level analysis, employ multiple genomics and bioinformatics strategies that help bridge the gap between population history, genomic variation and gene function. Funding: Fundação para a Ciência e Tecnologia (FCT/MCTES) for project GrapeVision (PTDC/BIA-FBT/2389/2020) and support to H.A. (CEECIND/00399/2017/CP1423/CT0004); FCT/MCTES and POCH/NORTE2020/FSE for support to S.F. (SFRH/BD/120020/2016); FCT/MCTES and POPH-QREN/FSE for support to M.C. (CEECINST/00014/2018/CP1512/CT0002).

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