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The grapevine QTLome is ripe: QTL survey, databasing, and first applications

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Abstract

Overarching surveys of QTL (Quantitative Trait Loci) studies in both model plants and staple crops have facilitated the access to information and boosted the impact of existing data on plant improvement activities. Today, the grapevine community is ready to take up the challenge of making the wealth of QTL information F.A.I.R.. To ensure that all valuable published data can be used more effectively, the myriad of identified QTLs have to be captured, standardised and stored in a dedicated public database.

As an outcome of the GRAPEDIA initiative, QTL-dedicated experts from around the world have gathered to compile the grapevine QTLome: the complete information (e.g., map positions, associated phenotypes) describing all experimentally supported QTLs for a specific trait. This has led to the collection of more than 150 published QTL papers and to the FAIRification of the fields relevant to the grapevine QTL database. A grapevine-QTL frontend application for uploading data has been developed to support QTL curators.

For each specific trait, the QTLome will be anchored firstly to the grapevine reference PN40024.T2T(v5) genome/annotation and secondly to the published diverse genome assemblies. The generated “Grapevine QTL browser” will (i) enhance the understanding of the genetic architecture of diverse phenotypes, (ii) reveal consistent QTLs across studies (consensus genomic intervals), which are particularly valuable for marker-assisted breeding, (iii) assist the identification of candidate genes (relevant alleles) and their integration into biological/biotechnological applications. The potential of this resource will be demonstrated by a case study.

Keywords: QTL browser, database, manual curation, Vitis ontology, FAIR