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**XIV. International
Symposium on Grapevine
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■ ■ ■ ■ **ZAGREB CROATIA**

28 June – 3 July 2026 • Zagreb (Croatia)

Book of Abstracts



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**XIVTH INTERNATIONAL
SYMPOSIUM ON GRAPEVINE
BREEDING AND GENETICS**

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POSTER

A curation framework for a genome-anchored grapevine QTL browser: insights from phenology

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ABSTRACT

Over the past few decades, Quantitative Trait Loci (QTL) mapping has been widely applied in grapevine to investigate the genetic architecture of complex traits. However, this extensive body of information has been only partially exploited in genetic research and breeding programs, mainly due to poor data accessibility, heterogeneous reporting formats, limited QTL mapping resolution, and variable robustness of QTL detection. To address these limitations and promote FAIR (Findable, Accessible, Interoperable and Reusable) use of existing data, QTL experts from around the world have joined forces, building on the CIG GRAPEDIA initiative, to lay the foundation for a community-accessible Grapevine QTL Browser (<https://grapedia.org/qtl-browser/>).

QTL data from more than 150 peer-reviewed studies published between 2000 and 2025 were manually surveyed and curated, comprising several thousand QTLs spanning seven major trait classes (abiotic stress, agronomical, biochemical, biotic stress, morphological, phenological, and technological traits). To this end, a structured annotation scheme comprising approximately 70 standardized descriptors was defined, covering phenotypic variables and protocols, genetic materials, and QTL mapping parameters and outputs. Annotations were harmonized, whenever

possible, with existing ontologies and public databases. A dedicated web-based frontend was developed to support structured data upload and expert curation.

As a proof of concept, phenology-related QTLs were analyzed in a pilot study. The dataset comprised approximately 500 QTLs associated with five major developmental stages (budbreak, flowering, veraison, ripening, and end of the vegetative season), derived from 13 biparental populations and three association panels. This case study highlights the potential of the Grapevine QTL Browser for trait-specific QTLome compilation, cross-study QTL validation, and refinement of genomic intervals for candidate gene prioritization. Additional key developments enabled by this framework include the extension of the Vitis Ontology and the integration of the Grapevine QTL Browser with the Grapevine Gene Catalogue.

Overall, the Grapevine QTL Browser represents a scalable resource for systematic QTL integration and provides a foundation for linking bi-parental population studies, GWAS (Genome-Wide Association Studies), and functional genomics resources to support grapevine research and breeding.