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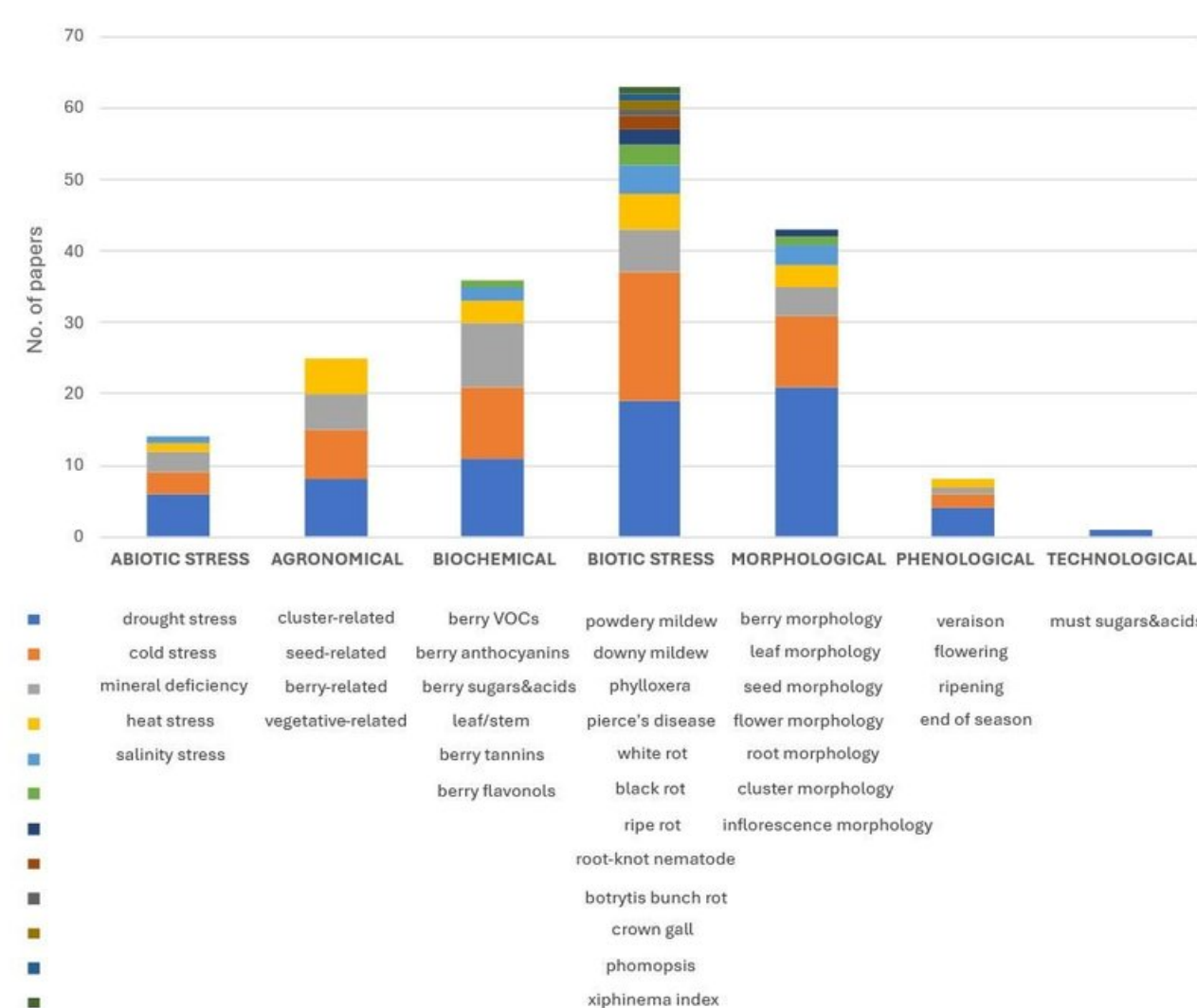
Contacts @GBG2026: Costantini, Bellin, Vezzulli

AIM OF THE WORK

Decades of grapevine Quantitative Trait Loci (QTL) mapping have generated vast data, yet its application in research and breeding remains limited by poor accessibility, diverse formats, low resolution, and inconsistent robustness. To overcome these barriers and ensure FAIR data principles, an international expert network has undertaken the compilation of a comprehensive grapevine QTL database, meant to evolve into a QTL browser (<https://grapedia.org/qtl-browser/>).

LITERATURE SEARCH

A total of 190 papers on grapevine QTLs in bi-parental populations and association mapping panels (published by February 2025) were collected and assigned to one of the seven trait classes described in Vitis Ontology.



QTL ANNOTATION AND MAPPING

Manual QTL curation was based on a standardized scheme of approximately 70 descriptors covering phenotypes, protocols, genetic materials, and mapping parameters. Wherever possible, annotations were harmonized with existing ontologies and public databases. Each QTL was mapped to the reference genome PN40024.T2T (v5) within a confidence interval.

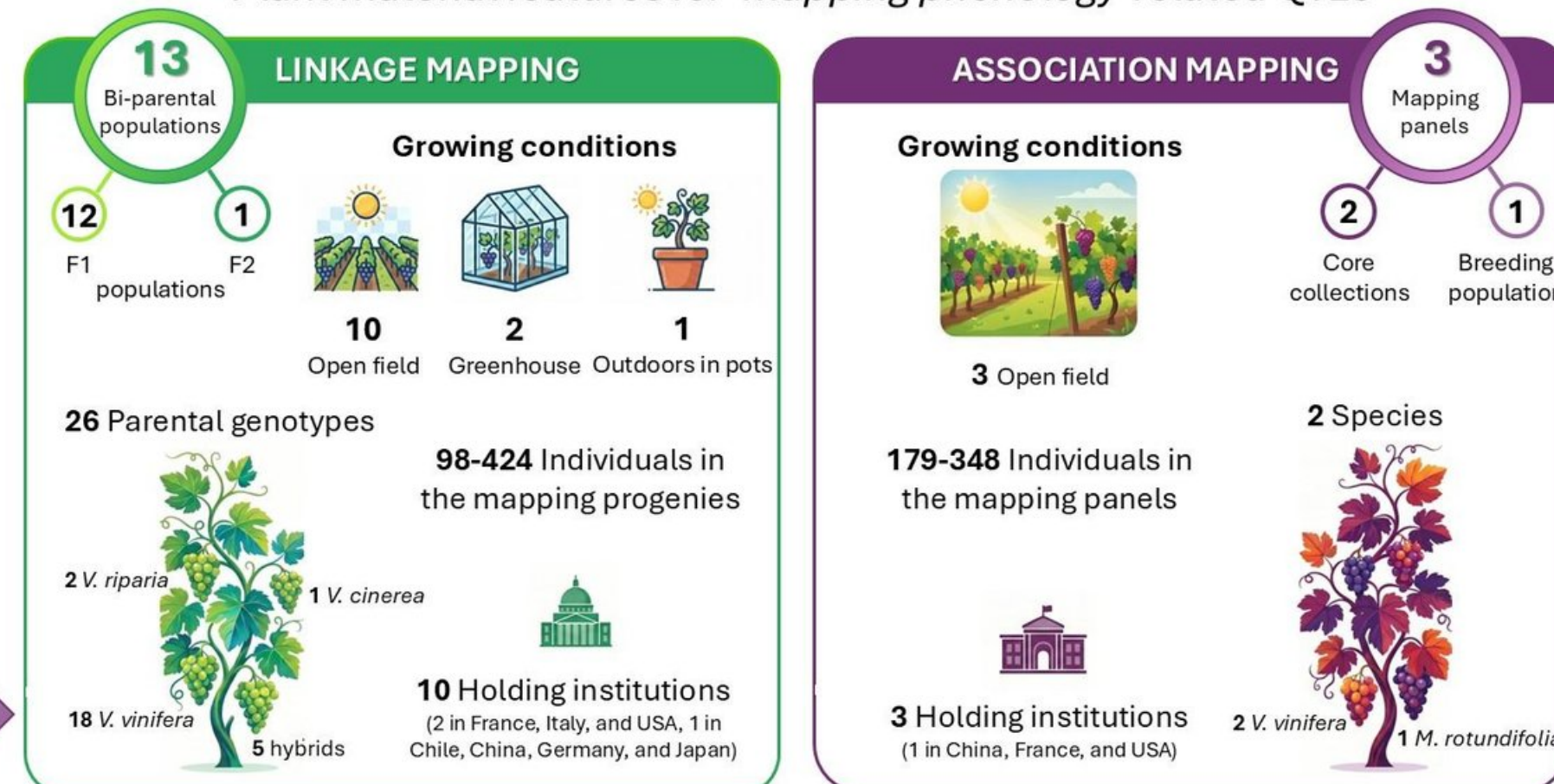
CANDIDATE GENES

Functional candidate genes with a validation level above 2 (according to the Grapevine Reference Gene Catalogue) were retrieved from the literature and mapped onto PN40024.T2T (v5) to assess their co-localization with QTLs.

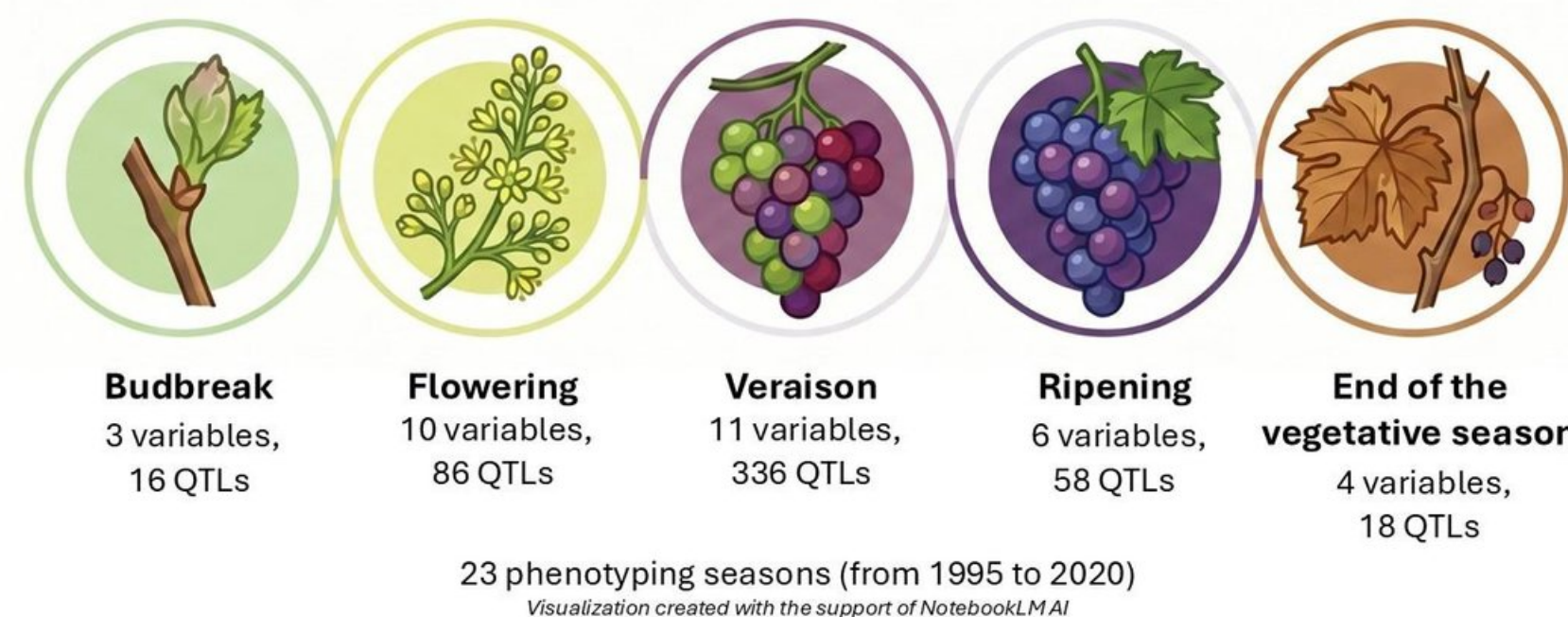
PHENOLOGICAL CASE STUDY

As a proof of concept, a pilot study was conducted on phenology-related QTLs. The dataset comprised **514 QTLs** derived from 13 biparental populations and three association panels, which were associated with five major developmental stages.

Plant material features for mapping phenology-related QTLs



QTL mapping across grapevine phenological stages



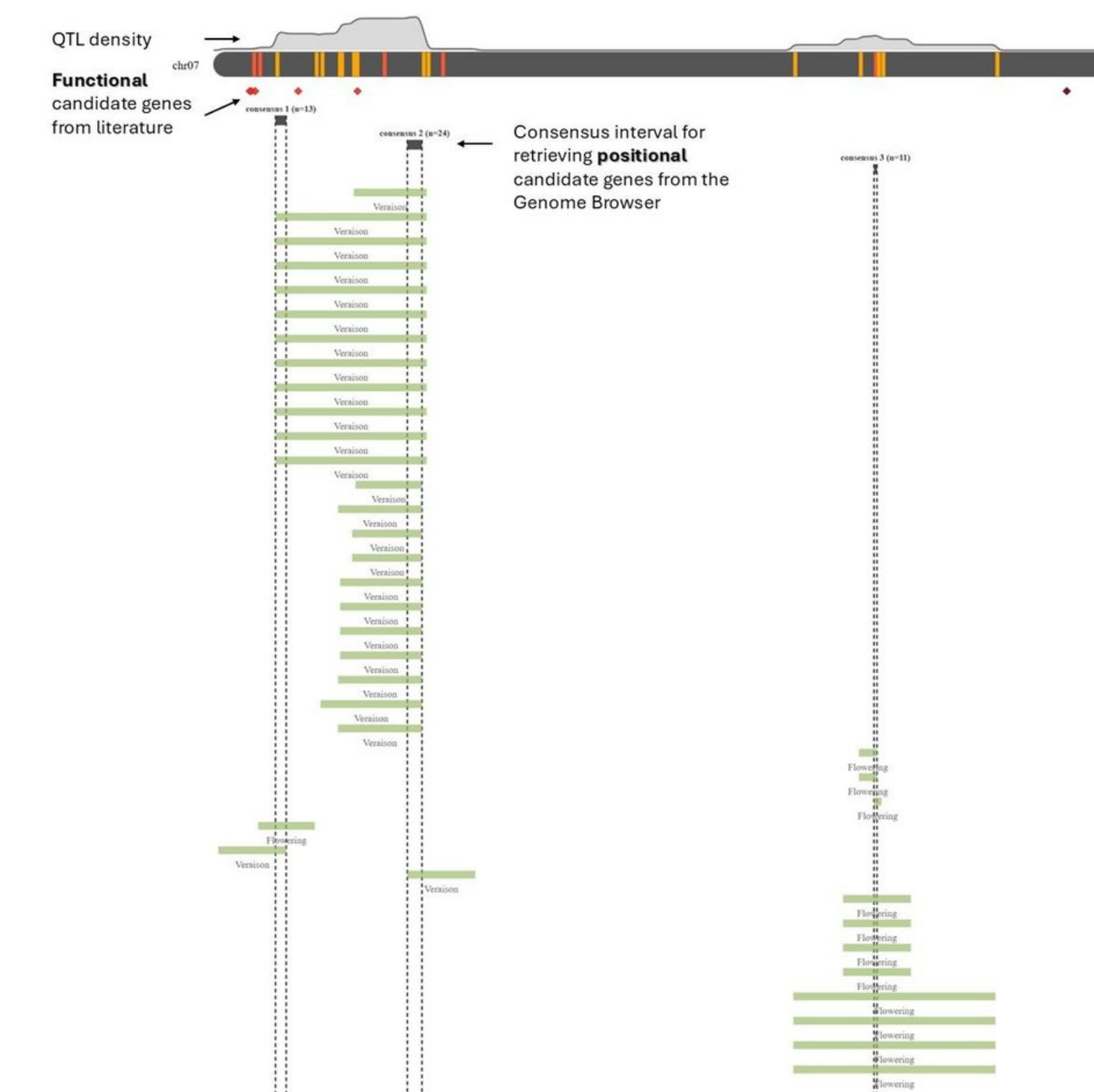
A QTL browser prototype was developed to explore QTL data, featuring various filtering options (by trait, QTL properties, genomic location), tools to visualize QTL density and co-localizations, and a link to the PN40024.T2T (v5) Genome Browser.

Explore This Topic Further: Don't miss the Grapedia QTL Browser workshop

 Tuesday, 30 June 2026 | **16:30 - 17:20**

The grapevine phenology QTLome

The phenology-related QTLs were mapped on all chromosomes (ranging from 1 QTL on chromosomes 3 and 9 to 129 QTLs on chromosome 16). QTL regions were defined by marker-flanked confidence intervals (n=362) or a ± 5 cM window around single markers (n=152), with the window converted to physical sizes via the dense map of Vervalle et al. (2022, TAG 135:4371-4390). The partial overlap of QTLs (for the same or different developmental stages) on single chromosomes enabled the pinpointing of **consensus genomic intervals** for candidate gene identification (see example below).



CONCLUSION

The Grapevine QTL Browser offers an interactive environment to leverage existing QTL data. This case study demonstrates its utility in defining trait QTLomes, refining genomic intervals for candidate gene prioritization, and identifying potential pleiotropic regions.