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**XIV. International  
Symposium on Grapevine  
Breeding and Genetics**

■ ■ ■ ■ **ZAGREB CROATIA**

28 June – 3 July 2026 • Zagreb (Croatia)

# Book of Abstracts



**IVES**

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**XIV<sup>TH</sup> INTERNATIONAL  
SYMPOSIUM ON GRAPEVINE  
BREEDING AND GENETICS**

## INFORMATIONS

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# **XIV<sup>TH</sup> INTERNATIONAL SYMPOSIUM ON GRAPEVINE BREEDING AND GENETICS**

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## POSTER

# An advanced genotyping tool to inspect grapevine variability: the Axiom®Vitis22K SNP array

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**Keywords:** genome-wide analysis, high-throughput genotyping, marker/genome assisted breeding, genetic diversity, *Vitis* spp

## ABSTRACT

Grapevine is one of the most relevant fruit crops worldwide, owing to its extensive distribution and considerable socio-economic significance. While the cultivated Eurasian species *Vitis vinifera* dominates global grape production, wild *Vitis* species from Asia and North America constitute essential genetic reservoirs, offering allelic diversity associated with tolerance or resistance to several biotic and abiotic stresses. Genotyping is a key tool in grapevine genetics, as it enables the assessment of genetic diversity, the elucidation of the molecular basis of agronomic and adaptive traits, and the implementation of marker-assisted selection. SNP (single nucleotide polymorphism) arrays provide an efficient genotyping tool, combining high-throughput capability, cost-effectiveness, and dense genome-wide marker coverage.

Here, we report the development and validation of the Axiom®Vitis22K SNP array, implemented within a broader multi-species 70K SNP platform. The array includes informative SNPs from the GrapeReSeq 18K *Vitis*

genotyping chip, SNPs and small InDels (insertions and deletions) putatively associated with phenotypic traits from literature, and novel SNPs obtained from the resequencing of 12 samples representing seven different grapevine species. Validation was performed by genotyping 144 genotypes from two diversity panels. Genotyping data were processed with the Axiom Analysis Suite and the newly developed AxioSAFE pipeline revealing a total of 10,314 robust polymorphic markers, together with 13 manually curated variants. These markers were successfully employed to study the genetic diversity and genetic relationships within the sample panels. Integration of genotypic and phenotypic data also enabled the validation of candidate SNPs associated with target traits such as flower sex type, seed content, berry color and taste. Overall, the results demonstrate the potential of the Vitis22K array to support large-scale genetic studies and breeding programs in grapevine.

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