

Proceedings of the LXV SIGA Annual Congress

Piacenza, 6/9 September, 2022

ISBN: 978-88-944843-3-5

Poster Communication Abstract – 6.32

INTRAVARIETAL GENETIC DIVERSITY OF THE GRAPEVINE (VITIS VINIFERA L.) CULTIVAR 'GRECO BIANCO'

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biodiversity, clonal selection, genotyping

In 2020, Italy ranked first among EU grape-producing countries. Part of these grapevines is registered on the national list, although a more prominent part is made by local varieties unknown or uncharacterized. They represent a valuable raw material for future selection and breeding goals. DNA markers are essential tools to definite these varieties, avoiding cases of synonymy and homonymy, and so protecting growers' and breeders' rights. Here, we present the use of phenological and genetic markers to generatethe first deep investigation of one of the most cultivated grape varietiesin Southern Italy, Greco Bianco. Twenty-four clones of *V. vinifera* cv. Greco Bianco and three clones of *V. vinifera* cv. Asprinio (synonym for Greco Bianco) were sampled in different areas of Southern Italy. The plant material was phenotyped using ampelographic and ampelometric traits and genotyped with SSR, transposon-based (REMAP), and SNP markers. Four (bunch compactness index, titratable acidity, and berry juice pH) out of six ampelometric traits displayed significant differences among clones. The SSR results showed 29 alleles ranging from 111 bp (VRZAG29) to 320 bp (VVIp60) and an average of 3 alleles per locus. Nine alleles were clone-specific. The analysis of retroelement insertional polymorphisms revealed 28 discriminant bands, two of which were specific to Asprinio and 13 to Greco Bianco. The ddRADseq genotyping generated a total of 196,950 SNPs, filtered and subjected to LD pruning ($r^2=0.50$) until a 3,293 high-quality SNP dataset. A slight intra-varietal genetic diversity was found (the identity-by-descent values ranging from 0.85 to 0.97), and 1,139 SNPs fell within annotated genes. The data generated in this study deepened our understanding of the existing diversity within the grape germplasm, providing valuable information for their exploitation and conservation.