

INVESTIGATION ON THE GENETIC DIVERSITY OF GRAPEVINE CLONES FROM APULIAN AND CAMPANIAN VARIETIES

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The genetic diversity of the cultivated grapevine (*Vitis vinifera* L.) arises from a large population of varieties, with sexual reproduction being a major contributor to inter-varietal variability. Additionally, spontaneous somatic mutations have played a role in shaping the vast array of grape varieties. Over the centuries, farmers have collected and propagated various selections of grapevine, labelling them as "clones". These clones often represent underexplored genetic resources that can be used to achieve successful conservation strategies and improve economically important traits. This study aimed to investigate the population structure and detect divergent loci in the genomes of 138 clones of six grapevine varieties from Campania (AGLIANICO LASCO, CAMAIOLA, and GRECO BIANCO) and Apulia (MALVASIA NERA, MINUTOLO and UVA DI TROIA). The samples from Campania and Apulia were genotyped using double-digested restriction site-associate DNA sequencing (ddRADseq) and Genotyping-by-sequencing (GBS), respectively. In both cases, the Pinot Noir PN40024 reference genome was used for calling single nucleotide polymorphisms (SNPs). Population genetic analysis indicated that all the varieties grouped their own clones,

except for AGLIANICO LASC0 which was separated into two sub-populations (AL1 and AL2). AL2 clones can be considered the true AGLIANICO LASC0, whereas AL1 individuals are homonyms of AGLIANICO. Genetic differentiation among the seven populations was further investigated by fixation index (F_{st}). At $F_{st} \geq 0.80$, a total of 1,016 divergent SNPs were detected, of which 285 were non redundant. Among the latter, 200 were in gene regions. The largest number of divergent SNPs was found in CAMAIOLA (N. = 453), while AL1 showed the lowest number (N. = 117). CAMAIOLA also had the largest number of divergent genes than the other varieties (> 81%).

In this study, we have shown that merging different SNP datasets is possible and valuable to study the inter- and intra-specific genetic diversity of grapevine populations. This provided a repeatable framework to streamline future computational studies based on retrieving information from partial analyses performed at different times and with different techniques.

Our results also demonstrated the value of advanced genomic methods in the study of synonymy/homonymy detection (as exemplified by AGLIANICO LASC0). Finally, signatures of divergence were identified among cultivars and between Campanian and Apulian accessions, some of which were involved in environmental adaptation and linked to key traits useful for grapevine breeding, such as budding, flowering and berry ripening time. These findings emphasize the importance of exploiting the vast untapped genetic variability that characterizes the minor grape varieties and the urgent need to conserve their genetic resources using them more effectively in breeding programs.