Genetic traceability of 'Nebbiolo' musts and wines by single nucleotide polymorphism (SNP) genotyping assays

AIM: 'Nebbiolo' (*Vitis vinifera* L.) is one of the most ancient and prestigious Italian grape cultivars. It is renowned for its use in producing monovarietal high-quality red wines, such Barolo and Barbaresco. Wine quality and value can be heavily modified if cultivars other than those allowed are employed. The fight against fraud to safeguard high-quality productions requires an effective varietal identification system applicable in musts and wines. METHODS: Single-nucleotide polymorphisms (SNPs) are considered the newest type of molecular marker for grapevine identification. We developed and investigated the efficiency of SNP TaqMan® assays in the varietal authentication of 'Nebbiolo' musts and wines. 'Nebbiolo'-specific SNPs were identified starting from available databases and 260 genotypes analysed by Vitis18kSNP array. RESULTS: Only two markers (SNP_15082 and SNP_14783) were sufficient to distinguish 'Nebbiolo' from more than 1,100 genotypes. In experimental vinifications, these SNP TaqMan® assays correctly identified 'Nebbiolo' in all wine-making steps, including wines 1 year after bottling. The high sensitivity of the assays allowed identifying, for the first time, mixtures of 1% in musts at the end of maceration, blends of 10% in musts at the end of malolactic fermentation and wines contamination of 10–20% with non-'Nebbiolo' genotypes. In commercial wines, the amplification efficiency of these SNPs was partially limited by the low amount of grapevine DNA and the presence of PCR inhibitors in DNA extracts. However, at least one SNP amplified correctly in all the commercial wines tested. CONCLUSIONS: The TaqMan® genotyping assay is a rapid, highly sensitive and specific methodology with remarkable potential for varietal identification in wines.

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Keywords: grapevine, musts, wines, genetic traceability, snp, blends

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