



An integrated technology platform to support the quality and safety of typical Piedmont wines

Aim of the study

The aim of the project was to provide an integrated technology platform supporting the production of typical wines of Piedmont, in terms of quality and safety.

Analyte

Proteins, nucleic acids, viruses, fungi

Methodology

Three registered Nebbiolo clones grown under different sanitary status (healthy vs virus-infected) and under different environmental conditions (clay vs. sand and slope vs. plain) were considered. The effect of different environments and virus infection on phenological stages, vegetative behaviour and yield of clonal vines were recorded. Berry samples were collected at harvest for the determination of juice qualitative composition (soluble solids, pH, tartaric and malic acids), focusing the evaluation on berry skin and seed polyphenols (anthocyanins, flavonols, catechins, stilbenes, etc.) and aromatic precursors (norisoprenoids, etc.). On the same berry samples, a proteomic analysis was performed. 2D protein maps of grapes were produced and compared. Differentially expressed proteins were examined in order to identify those whose expression is associated with cultivation environment or virus infection. Soil and roots sampling were performed in order to evaluate the mycorrhization status of grapevine roots of healthy or infected plants, grown in the two environments. Arbuscular Mycorrhizal (AM) fungi, present in vineyards planted to Nebbiolo clones, were characterised by morphological and molecular techniques. The phytosanitary status of vineyards under observation were screened, with special focus on grapevine viruses and grapevine yellow-phytoplasmas.

The wines were analyzed, with particular regard for the type and the amount of phenols, and ranked by means of sensory evaluations (colour, bouquet and taste). Specific protein markers of Nebbiolo identity were characterized by performing protein screening and identification by 2DE and LC-MS/MS.

System Wines, grapes and soils

Customer This study was performed in collaboration with the Agro-Food Department of CNR; Enocontrol; Enosis; S.A.F.AN. BIOINFORMATICS; Fondazione per le Biotecnologie; Vignaioli Piemontesi.

Results

An integrated approach involving the use of both genomic and proteomic techniques allowed to identify the relationships between 1) the virus infection in vines and grapes and wine quality of Nebbiolo; 2) the different environments (slope, soil and climate) and the vine growth, yield and wine quality of Nebbiolo; 3) the sanitary status of clonal vines, the different cultivation environments and the grape and wine protein fingerprintings, with special reference to identification of typicality markers in grape and of allergenic proteins in wine; 4) the soil arbuscular mycorrhizal (AM) fungal composition and the clonal vine performances in different cultivation environments; 5) the sanitary status of vines and the quality of grapes and wines in terms of their protein fingerprintings and soil fungal AM composition in the vineyards.

Advantage of the methodology

An integrated approach allowed to better investigate some of the factors that may affect the quality and safety of DOC and DOCG wines based on Nebbiolo grapes (i.e Barolo, Barbaresco, Roero, Gattinara, etc.), by characterizing the areas of production, the crop and the final product.

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