



A molecular approach to study the arbuscular mycorrhizal fungi community in a typical Piedmont grapevine cultivar

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Viticulture and wine production represent one of the most relevant agro-food sectors for the Piedmont Region (Italy) in terms of value, with more than 400 millions € a year (12 % of total agricultural production of the Region and the 10 % of the national grape and wine production).

The soil where grapevines (*Vitis* spp.) grow is one of the first parameters influencing the complex grapevine-wine chain. Arbuscular mycorrhizal fungi (AMFs), a main component of soil microbiota in most agrosystems, are considered crucial biomarkers of soil quality because of their biofertilisers role. As mutualistic symbionts, they colonize the roots of the majority of plants. Benefits in symbiosis are well showed as an improvement in shoot/root growth, mineral transport, water-stress tolerance and resistance to certain diseases.

Grapevines roots are often heavily colonized by AMFs under field conditions and in some cases AMFs appear to be necessary for their normal growth and survival. Even so, little information are until now available about composition of AMFs communities living in the vineyards soil and in associations with grapevine roots, mainly related to morphological characterization.

Vineyard of Nebbiolo, one of the most important Piedmont cultivar, was selected in order to study the AMFs community using a molecular approach. Soil samples and roots from an experimental vineyard located in Lessona (Biella, Piedmont, Italy) were analyzed using AM fungal-specific primers to partially amplify the small subunit (SSU) of the ribosomal DNA genes. Much more than 650 clones were sequenced. Phylogenetic analyses identified 32 OTUs from soil, clustered into *Glomus* groups Aa, Ab, Ad and B, *Diversisporaceae* and *Gigasporaceae* families. Thirteen OTUs from roots were determined, clustered into *Glomus* groups Ab, Ad and B, and *Gigasporaceae* family. In particular, *Glomus* group Ad was the best represented in both compartments, suggesting a correlation between intra and extra radical communities.

On the bases of AMFs families that we have found, grapevine culture shows a high rate of species richness, compared with similar studies already published on others plant cultures. These data will be useful to explain the possible relationship between AMFs communities and quality in the grapevine/wine chain.

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