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Regional scale analysis of arbuscular mycorrhizal fungi: the case of Burgundy vineyards

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Abstract

Vitis vinifera (L) is an economically important crop, in particular in France, the first producer of wine in the world. However, grape production and quality is highly dependent on soil quality, in term of physical and biological properties. In Burgundy, a region producing high-quality vines, vineyards are subject to soil erosion and diseases, and it is necessary to find a way to preserve this area, while adopting agricultural practices more respectful for the environment and especially soil biodiversity. We assessed AMF diversity, using 454 pyrosequencing based on the ITS marker, in 16 plots across Burgundy in vine roots under contrasted soil properties and agricultural practices. The results show that AMF could be retrieved from all plots across Burgundy, both in biologically-managed and conventional vineyards with high chemical inputs. From the sequences obtained 99% were affiliated to molecular species-level taxa in the Glomerales, including six core species, *i.e.* species found in all plots, corresponding to 77% of total sequences, suggesting a relatively low diversity of the species in vine roots. Among all sequences, some could be assigned to known species in the genera *Rhizophagus* and *Septoglomus*, a large part of the taxa had no close similarity to previously-reported sequences. This is the first large-scale study of arbuscular mycorrhiza fungal diversity in France for this important culture crop, and it provides essential knowledge basis for future applications in sustainable management of vineyards.