

## Exploring new biodiversity hotspots in *Tuber aestivum* natural distribution

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*Tuber aestivum* is associated with a wide range of tree species and is the most widespread edible truffle. Its capability of colonizing many different areas along with a long reaping period, increased in the last decades scientific studies and commercial interest.

A number of large- and fine-scale population genetics studies have been conducted to explore its genetic diversity and genetic structure.

Recent investigations based on ITS sequence analyses revealed a strong phylogenetic pattern and a higher level of genetic diversity in Turkish and southern European populations than in northern European populations, suggesting that Turkey and southern Europe may have acted as glacial refugia for this species.

Despite these findings, the southernmost distributional range of the species is not yet fully explored. With the aim of evaluating other potential diversity hotspots in this study we expand previous investigation, extending the sampling to other southernmost natural *T. aestivum* areas, such as Moroccan mountainous regions (Middle Atlas), Serbia and several Spanish regions.

The ongoing analyses based on haplotypes alignment of the ITS region of the rDNA, reveal as preliminary result a pronounced genetic variability among Moroccan *T. aestivum* populations, suggesting a possible phylogeographic differentiation also in these new areas of investigation. Additional analyses are underway to better trace natural populations of *T. aestivum* according to their geographic origin.

These aims could be critical both for truffle industry interest in selecting well-adapted inoculum for the production of mycorrhizal seedlings or traceability of truffles provenance, and for the establishment of programs devoted to biodiversity conservation.

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