

Broadening the investigation area of *Tuber aestivum* genetic diversity.

Beatrice Belfiori¹, Claudia Riccioni¹, Eva Gómez Molina², Sergio Sánchez Durán³, Sergi García Barreda³, Žaklina Marjanovic⁴, Fatima Henkrar⁵, Lahsen Khabar⁵, Luigi Gallo⁶, Andrea Rubini¹

¹Istituto di Bioscienze e Biorisorse (IBBR), Consiglio Nazionale delle Ricerche (CNR), Via della Madonna Alta 130, 06128, Perugia, Italy, beatrice.belfiori@ibbr.cnr.it, claudia.riccioni@ibbr.cnr.it, andrea.rubini@ibbr.cnr.it; ²Centro de Investigación y Experimentación en Truficultura, Partida Fabardo, s/n 22430 Graus (Huesca), España, egomez@dphuesca.es; ³Centro de Investigación y Tecnología Agroalimentaria de Aragón (CITA), Avda. Montañana 930, 50059 Zaragoza, España, ssanchezd@cita-aragon.es, sgarciaba@cita-aragon.es; ⁴University of Belgrade - Institute for Multidisciplinary Research Bulevar despota Stefana 142, 11060 Belgrade, zaklina@yahoo.com; Université Mohammed V, Faculté des Sciences, Département de Biologie, ⁵Centre de Recherche "Biotechnologies Végétale et Microbienne, Biodiversité et Environnement", Avenue Ibn Battouta B.P. 1014, Rabat, Maroc, f.henkrar@um5r.ac.ma, l.khabar@um5r.ac.ma, ⁶Azienda Regionale per lo Sviluppo dell'Agricoltura Calabrese (ARSAC) - Ce.D.A. n.2 - Castrovillari (CS). luigi.gallo@arsac.calabria.it

Tuber aestivum is associated with a wide range of tree species and it is the most widespread edible truffle, being widely distributed not only in Europe, with populations ranging from Sweden to Spain, but also from Turkey to Middle East countries and North Africa (1, 2). Its capability of colonizing many different areas along with a long ripening period, has increased scientific studies and commercial interest in the last decades. 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 (3). 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), southern Italy, and several Spanish and Balkan 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. The possibility of gaining more insight into the extent and distributional patterns of *T. aestivum* genetic diversity over its geographical range could be critical both for truffle industry's interest in selecting well-adapted inocula for the production of mycorrhizal seedlings, and for the establishment of programs devoted to biodiversity conservation.

- 1) G. Chevalier, C. Desmas, H. Frochot, L. Rioussel. (1979). Mushroom ScienceX (Part 1):957–975.
- 2) F. Henkrar, C. Meyad, M. Oikrim, N. Bouhaddou, L. Khabar. (2023). Forests, 14(5), 952.
- 3) C. Riccioni, A. Rubini, A. Türkoğlu, B. Belfiori, F. Paolocci. (2019). Mycologia, 111(1), 26-39.

