

# An Integrated Genomic–Metabolomic Approach to Characterize *Tuber aestivum* Vitt. Diversity Across Ten Italian Regions

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## Background

- The summer truffle (*Tuber aestivum* Vitt.) is an ascomycete belonging to the order Pezizales. It forms ectomycorrhizal associations with a wide variety of plants, it is widely distributed across Europe, and it is appreciated for its distinctive aroma.
- A comprehensive understanding of the genomic structure of summer truffle is instrumental for both the preservation of its natural populations and the optimization of cultivation practices.
- Metabolomics provides a functional perspective for biodiversity analysis by capturing the metabolic phenotype, which is shaped by multiple factors including genetic variation and environmental conditions.



Figure 1 Geographical Distribution of *Tuber aestivum* collected (created with mapchart.net)

## Material and methods

- 96 sample of summer truffles, collected across ten Italian regions (Figure 1): Apulia, Basilicata, Calabria, Campania, Emilia-Romagna, Lazio, Marche, Piedmont, Tuscany and Umbria were analyzed to obtain a genomic and metabolomic profile.
- The ascocarps were collected and cleaned to remove any soil contaminants.
- DNA was extracted from the gleba and sequenced using short-reads shotgun sequencing.
- Metabolomics was conducted using UHPLC-MS-QTDF.

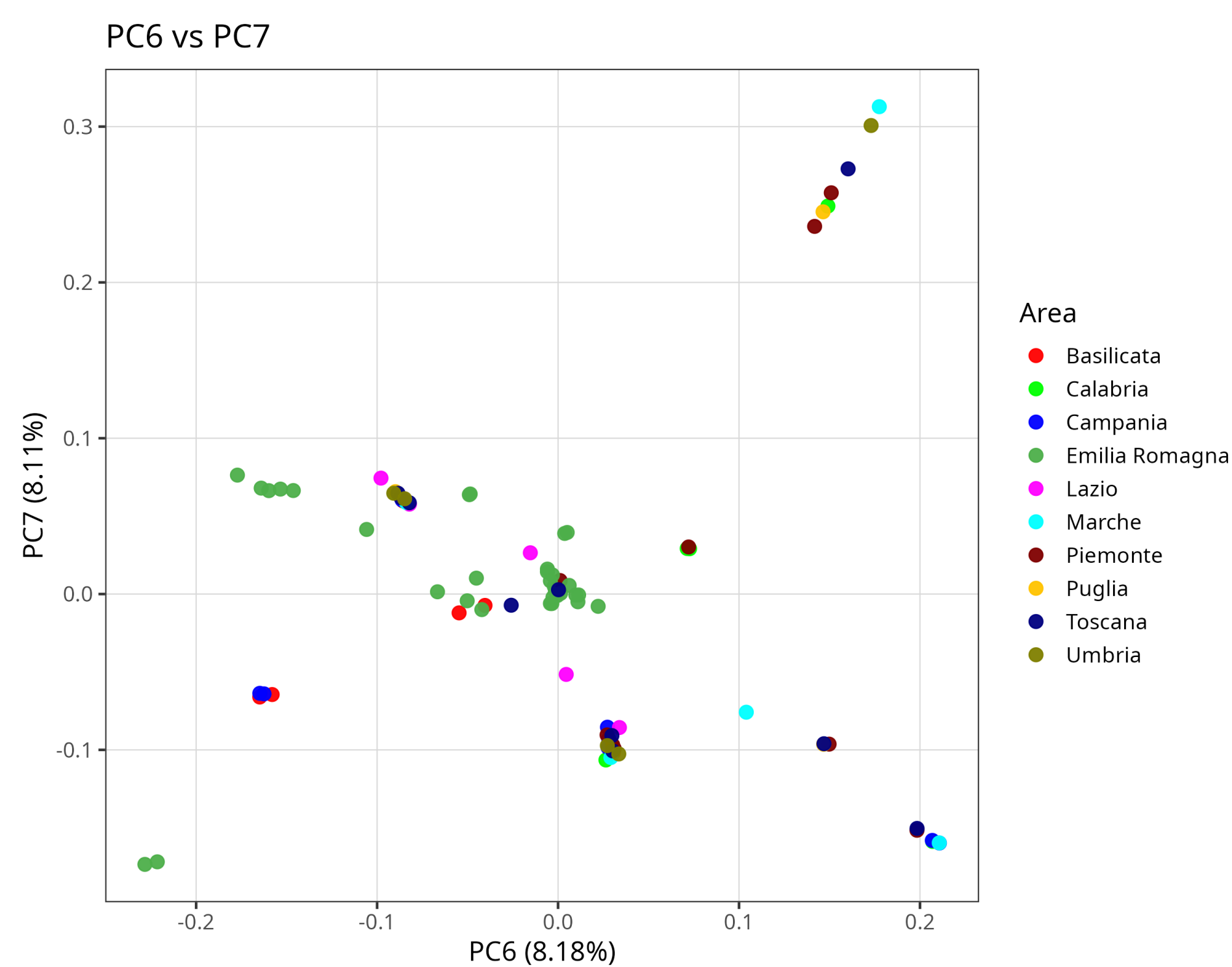


Figure 2. PCA analysis of *Tuber aestivum* samples.

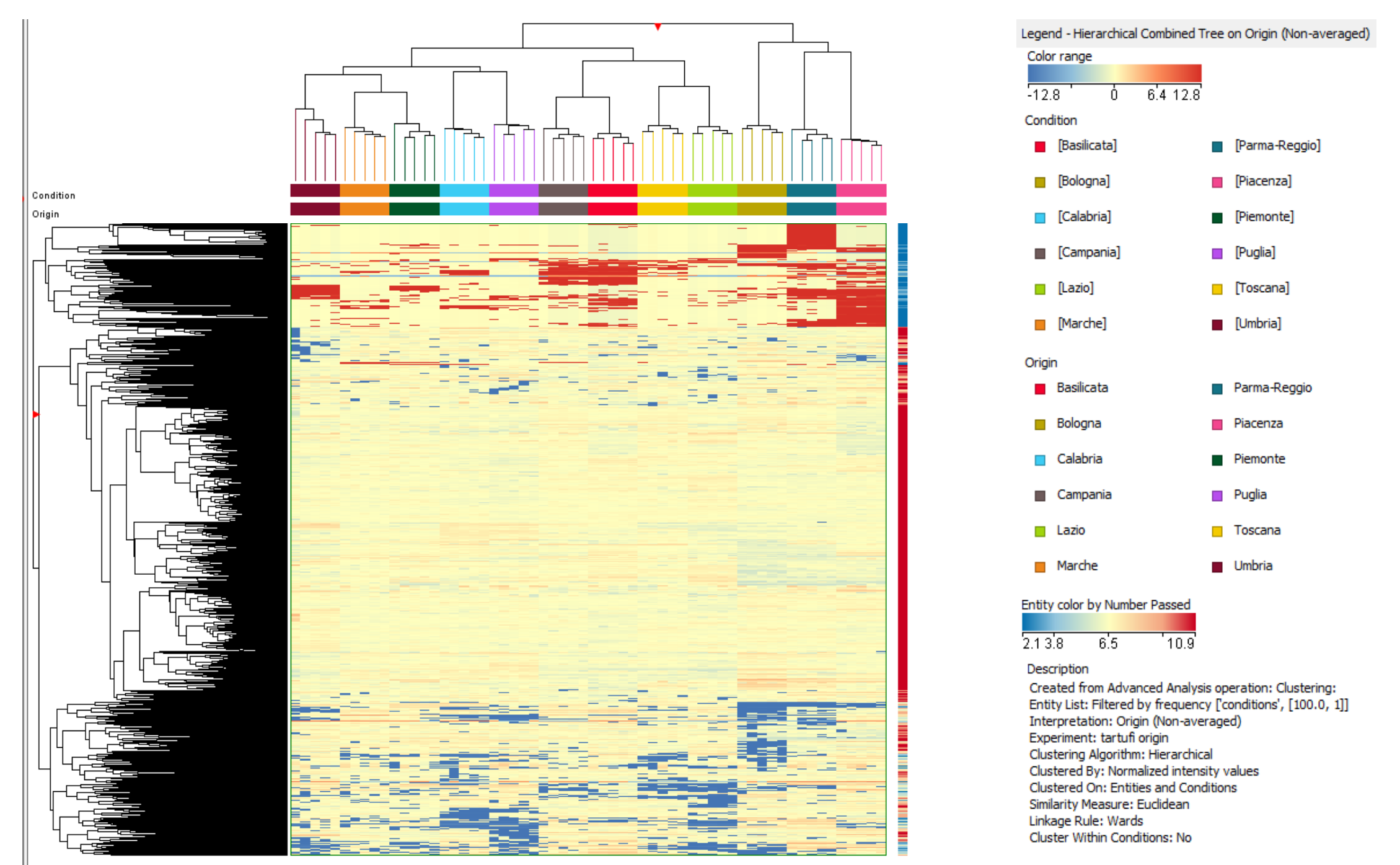


Figure 3. Hierarchical cluster analysis (HCA) of *Tuber aestivum* samples based on untargeted metabolomic data.

## Results

- PCA (Principal Component Analysis) using quality-filtered SNPs (Single Nucleotide Polymorphisms) seem to indicate that the population's genetic variation is structured in a core haplogroup, four smaller group with similar haplotype and some rare/unique haplotypes (Figure 2).
- There is no clear correlation between the grouping of the haplotypes and the geographic origin of the samples, however some samples from neighboring regions cluster together and a nuanced north-south gradient could be hypothesized.
- Hierarchical Cluster Analysis (HCA) showed that the metabolomic profile of the truffle samples seem to be clustered in pairs of neighbouring regions, except for Piedmont, which clusters with Marche and Umbria, and Apulia with Calabria. Samples from the Emilia-Romagna region appear to cluster independently (Figure 3).

## Summary and prospective

- This study provides a preliminary genomic and metabolomic survey of Italian summer truffle.
- The aim of this study is to contribute to the investigation of the current diversity of *T. aestivum* and to explore potential correlations between genetic structure, metabolic profiles, and environmental parameters, to support the conservation of *Tuber aestivum* biodiversity

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