

PROTEOMIC PROFILING OF WHITE TRUFFLE (*TUBER MAGNATUM* PICO) NATURALLY GROWN IN DIFFERENT ITALIAN AREAS

VITA F.*, LUCAROTTI V.*, ALPI E.**, ALESSIO M.**, ALPI A.*

*) Department of Crop Plant Biology, University of Pisa, Via Mariscoglio 34, 56124 Pisa (Italy)

**) Biomolecular Mass Spectrometry Unit, Division of Genetics and Cell Biology, San Raffaele Scientific Institute, Milano (Italy)

Proteomic, truffle, two-dimensional electrophoresis, mass spectrometry

The aim of this work is to verify the origin of the white truffle (*Tuber magnatum* Pico) through protein profiling in which it would be possible to identify one or more proteins related to the area of origin. Truffles are considered an important food resource with a high economic value as high as 300 euros/100 gr. of fresh product. The *Tuber magnatum* variety is particularly appreciated and its demand often outweighs the amount of truffles harvested in its natural habitat.

This species grows almost exclusively in Italy, and its value is related to the area of collection (North, Center or South Italy).

Therefore, it would be crucial to set up a methodology capable of discriminating univocally not only the species analysed, but also its origin, in order to distinguish the more valuable varieties from the less expensive ones.

In order to achieve this goal, samples of *Tuber magnatum* Pico, from selected areas in Tuscany, Piedmont, Umbria and Marches, were collected and then analysed through a proteomic approach. The analyses performed so far using bidimensional electrophoresis have shown a high reproducibility in the protein pattern of *Tuber*.

The preliminary analysis of differentially expressed proteins, by using LC-MS spectrometer, has allowed us to identify specific proteins.