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TRUFFLES IN THE POST-GENOMIC ERA

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Truffles, like other ectomycorrhizal fungi, have a dual lifestyle, living both in the soil as facultative transitory saprotrophs and within the plant roots as symbionts. Thanks to the symbiosis they establish with the roots of woody and shrubby plants, truffles produce prized fruiting bodies. During its life cycle, the mycelium undergoes morphogenetic changes, reflecting the expression of specific genes, which can be influenced by environmental factors. In 2010, the *T. melanosporum* genome sequencing project launched by a French-Italian consortium, was accomplished and the results led to the first information concerning an Ascomycete-symbiotic fungus [1]. The working hypothesis of the further steps was that identification of processes that condition and trigger fruit body and symbiosis formation, ultimately leading to a more efficient production, would be facilitated by a thorough analysis of truffle genomic traits. Starting from the genome data set, several post-genomics activities were developed, in order to focus on specific gene categories (e.g., cell-wall related genes, environmental response genes, etc.) and, among them specific gene families [2, 3, 4]. These results have allowed us to obtain new knowledge on the fungal biology of the black truffle. By contrast, in the absence of the whole genome sequence of the white truffle *T. magnatum*, we have performed a gene expression analysis on specific genes that could be involved in changes during truffle post-harvest storage. In parallel, a metabolite profile has been obtained on fruiting bodies conserved in the same conditions.

Taken together, results coming from both black and white truffles have allowed us to highlight some of the molecular events that take place during truffle development in nature and their conservation for the market.

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