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Studies have shown that the number of bacteria colonizing the intestinal tract in mice reared under conventional conditions of the order of 10^9 CFU/g. The number of bacteria of the genus Lactobacillus-*Enterococcus* was $5{,}0x10^7$ cfu/g, *Clostridium coccoides* $1{,}4x10^8$ cfu/g *Bifidobacterium* sp $1{,}3x10^8$ cfu/g, Bacteroides-Prevotella $8{,}4x10^7$ cfu/g, and the bacteria present in the number of Enterobacterioceae $3{,}7x10^8$ cfu/g. After the addition of probiotics slightly increased the amount of bacteria in the *Lactobacillus* group and at the same time decreasing the amount of bacteria of the genus *Clostridium coccoides* and Enterobacterioceae.
In mice, germ-free quantitative assessment of the total number of bacteria showed that prior to germ-free mice with a probiotic preparation of the digestive tract was sterile. After administration of the probiotic preparation has been observed their gastrointestinal colonization by bacteria of the genus Lactobacillus. This was due to the fact that the probiotics are living micro-organisms are capable of homing and intestinal epithelium.
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Keywords: microbiota; probiotic; mice; germ-free mice

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Truffle genomics and post-genomics to understand the symbiotic life-style

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A special interest in an agronomical and food context is bound to the symbiotic mycorrhizal fungi, and among them to truffles (*Tuber* sp.). Thanks to the symbiosis they establish with the roots of woody and shrubby plants, truffles produce fruiting bodies that are prized and highly requested in all the world markets for their organoleptic properties. The Périgord black truffle (*T. melanosporum*) and the Piedmont white truffle (*T. magnatum*) dominate today's truffle market. In 2007, the *T. melanosporum* genome sequencing project has been launched in Turin as a common project by a French-Italian consortium, and the results were published in Nature in 2010 (Martin et al., 2010). The working hypothesis 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 sequencing project, several post-genomics activities were then 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 (Zampieri et al., 2011; Balestrini et al., 2012; Sillo et al., 2013). These results have allowed us to obtain new knowledge on metabolic processes that happen during the complex life cycle of a symbiotic fungus, giving information on the genes/proteins involved in the symbiosis development as well as in the formation of the precious fruiting bodies. On the other hand, a project for the *T. magnatum* sequencing is still in progress, and it will offer the possibility to understand the biological differences between the two species. In the absence of the whole genome sequence, we have produced an inventory of gene expression in *T. magnatum* by sequencing cDNA from fruiting body. This represents the first step towards the understanding of genome functionality and, thanks to the availability of *T. melanosporum* genome sequence, the identification of genes that could be specific for one truffle species and genes that are common to both species. In addition, starting from the first available sequencing data (genomic and transcript sequences), we have performed gene expression on specific genes putative involved in changes during truffle post-harvest storage, considering that, according to the gastronomy rules, *T. magnatum* is usually consumed raw. In parallel, a metabolite profile has been obtained on fruiting bodies conserved as in the previous analyses. Taken together, the results allowed us to highlight some of the molecular events that take place during truffle conservation. The *Tuber melanosporum* genome sequencing project was a collaborative effort involving the Génoscope and the *Tuber* Genome Consortium.

Keywords: *Tuber* sp.; genome and transcript sequencing; symbiotic fungi; fungal cell wall; RT-qPCR

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