The molecular basis of wheat responses to Trichoderma spp. root colonization

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In this study, the comprehensive framework for the entire phenotypic reaction of wheat to *Trichoderma* was proposed and morpho-physiological, anatomical and at the functional level of the genome (proteins, metabolites, genes) analysis were performed, using the state of the art and high-throughput methodologies.

It was shown that studied *Trichoderma* species are able to colonize the surface of the roots and its internal tissues. It was observed that they significantly affect the growth and development of the root system and above-ground parts of plants as well as yield parameters and basic physiological processes of wheat. Studies at the molecular level have shown that *Trichoderma* fungi also induce significant changes in wheat in terms of gene expression and the production of metabolites and proteins, including those involved in plant immune responses. Moreover, it was found that the type and extent of these changes are strongly dependent both on the species/strain of *Trichoderma* and also plant cultivars, development stage and organ, and growing conditions, which is extremely important in the context of the use of these fungi in biological plant protection or as plant bio-stimulants.

Bearing in mind the global wheat production and its importance in diet, the results of this study may be useful in research aimed at developing innovative strategies for the protection of wheat plants, the production of a new generation targeted bio-fungicides bio-protectants and bio-stimulants, which microbiological components would be consciously selected based on the knowledge of both *Trichoderma* – pathogen and *Trichoderma* – wheat interactions.

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