Pairwise Transcriptomic Analysis of the Interactions Between the Ectomycorrhizal Fungus Laccaria bicolor S238N and Three Beneficial, Neutral and Antagonistic Soil Bacteria

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Résumé en anglais	Ectomycorrhizal fungi are surrounded by bacterial communities with which they interact physically and metabolically during their life cycle. These bacteria can have positive or negative effects on the formation and the functioning of ectomycorrhizae. However, relatively little is known about the mechanisms by which ectomycorrhizal fungi and associated bacteria interact. To understand how ectomycorrhizal fungi perceive their biotic environment and the mechanisms supporting interactions between ectomycorrhizal fungi and soil bacteria, we analysed the pairwise transcriptomic responses of the ectomycorrhizal fungus Laccaria bicolor (Basidiomycota: Agaricales) when confronted with beneficial, neutral or detrimental soil bacteria. Comparative analyses of the three transcriptomes indicated that the fungus reacted differently to each bacterial strain. Similarly, each bacterial strain produced a specific and distinct response to the presence of the fungus. Despite these differences in responses observed at the gene level, we found common classes of genes linked to cell–cell interaction, stress response and metabolic processes to be involved in the interaction of the four microorganisms.
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