
What are the ecological drivers of symbiotic microbiome assemblages? The case of an antic affair between an iconic Mediterranean fruit tree and its symbiotic microbiome

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Abstract

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The root symbiotic microbiome, notably arbuscular mycorrhizal (AM) fungi, is a key factor of plant ecology and agro-ecosystem functioning, but the relative contribution of multiple ecological factors driving their diversity and assemblage are poorly assessed. Moreover, few studies have approached this question with a wide geographical perspective, which is important when dealing with domesticated fruit trees characterised by diverse cultivated, feral or wild populations, and consequently subjected to a wide range of environmental constraints and selection pressures.

In the framework of the international project DYNAMIC (Deciphering sYmbiotic Networks in cArob-based MedIterranean agro-eCosystems), a metabarcoding approach was developed to assess the specificity of tree-symbiotic microbiome associations and to characterise the relative contribution of main ecological drivers of symbiotic microbiome associated with the carob tree in the Mediterranean basin.

The carob tree (*Ceratonia siliqua*) is a multi-use tree of high socio-economical added value with a major place in the traditional rural landscapes of Mediterranean regions. It belongs to the highly diverse family of legumes (Fabaceae) but does not nodulate. However, the carob tree is highly dependent of arbuscular mycorrhizal (AM) symbiosis, and bacterial endophytes were hypothesized as a second major symbiotic partner.

Domestication in the Middle-East around 6,000-4,000 BC may have caused extensive genetic and physiological modifications in carob, conducting to potential changes/adaptations of its associated symbiotic microbiome. These impacts have been investigated for domesticated cereals but rarely for trees.

The results provide new insights into the characterization of a Mediterranean core and accessory "SymbiOme" of the carob tree, highlighting geographical patterns, as well as the contribution of host genetic diversity, habitat and edaphic parameters. The better understanding of ecological rules controlling the specificity of interaction in tree symbiotic associations opens up promising perspectives for the development of more efficient strategies in conservation and agroecology based on plant microbiome symbiosis.