



Proposition d'un sujet de stage au M2 ADAM (2017-2018)

Titre	Study of fungal secreted peptides involved in endomycorrhizal symbiosis
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Equipe(s)	Symbiose endomycorhizienne et Signalisation cellulaire (LRSV)
Résumé	<p><i>Biological context:</i></p> <p>Most plants establish a symbiotic interaction with arbuscular mycorrhizal (AM) fungi. This widespread association involves an exchange of nutrients: Carbon is provided by the plant and the fungus transfers to its host water and minerals, thus improving its nutrition and growth. The study of this ancient symbiosis can lead to promote the use of AM fungi in sustainable agriculture and thus reduce the need for irrigation and chemical inputs.</p> <p>Our main objective is to study the cellular and molecular mechanisms involved in the establishment of the symbiosis. Our group contributed to the discovery of important signals produced by plant roots (the strigolactones) and by the AM fungi (the Myc-LCOs and Cos). These molecules take part to an important molecular dialogue between both organisms. Recent data obtained in the group now strongly suggest that small secreted peptides (< 15 aa) are secreted by the fungal partner to promote symbiosis. The goal of the internship is to understand at the molecular level the role of one of these fungal peptides.</p> <p><i>Training offer:</i></p> <p>We recently discovered that AM fungi secrete peptides with high similarity to CLE peptides, well known hormone peptides in plants. We observed that exogenous application of these peptides on plant roots was modifying root architecture and was promoting the symbiotic interaction. We now focus on the molecular effects of these fungal peptides (plant receptor that are involved, downstream targets). Besides, we plan to study the expression patterns of plant CLE peptide genes with high sequence similarity to fungal peptides. These plant peptides are indeed potentially subverted by the fungal peptides. The student will analyse the symbiotic phenotypes of plant mutants involved in plant CLE modification and perception and will follow plant CLE genes expression patterns through RT-qPCR and with promoter::gus lines. Modulation of plant root architecture in response to peptide treatment will also be characterized in detail, in addition with the analysis of candidate gene expression, highly presumed to be regulated by such peptides.</p>



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