PisolAdapt

Protein synthesis to cell detoxification: could diversification of eEF1Bγ roles in ectomycorrhizal fungi enable adaptation to environmental stress

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Action(s) thématique(s) concernée(s) : WP1 et WP2

Résumé

Fungi have evolved a range of molecular mechanisms that enable them to adapt to environmental constraints and stresses. Comparative genomics is one powerful approach to identify and study the diversity of these molecular systems. By using this approach, we have highlighted an abnormally high diversity among eEF1Bγ (elongation factor of the protein translation-gamma) sequences within the ectomycorrhizal fungal *Pisolithus* genus. eEF1Bγ are ubiquitous to all eukaryotes, typically found as only one or two isoforms per genome. In contrast to fungi studied to date, we have found surprising expansion of full length eEF1Bγ-coding genes in the genomes of certain *Pisolithus* species. In addition, we have found *Pisolithus* may encode novel eEF1Bγ sequences. Canonical proteins involved in this pathway are composed of two domains: a glutathione transferase (GST) domain at the N-terminal of the sequence and an elongation factor G (EFG) domain at the C-terminal part. Certain *Pisolithus* eEF1Bγ-like isoforms were found in our pilot study to lack the EFG domain and thus only encode the GST domain. As classical GSTs are involved in the intracellular detoxification pathway, the presence of such a domain in an elongation factor is intriguing and suggests that these proteins could have a dual role in cells both in translation and detoxification, likely in response to environmental constraints. As most of the *Pisolithus* species analyzed to date have been collected in disturbed soils, and the majority in soils experiencing extreme conditions (e.g. low nutrition, high temperatures), we would hypothesize that the highly duplicated eEF1Bγ and eEF1Bγ-like genes could be functional markers of adaptation to stressful environments. In this project, we propose to focus on the characterization of these atypical proteins from *P. croceorrhizus* ssp. 2 72 (also named *Pisolithus* sp. B) to better understand their involvement in both the cellular processes of protein translation and detoxification, and their evolution pattern that could have resulted in functional specificities. This is a collaborative project between the Partner 1 (Team Stress Response and redox regulation from the Lorraine University), Partner 2 (Hawkesbury Institute for the Environment from the Western Sydney University) and Partner 3 (Team Ecogenomics of interactions, INRAe Nancy), with complementary skills, respectively protein biochemistry, physiology/ecology of fungi and “omics” analysis.