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Exploration of acid-tolerant genes in arbuscular mycorrhizal fungi by comparative transcriptomics

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1. Introduction

Arbuscular mycorrhizal (AM) fungi form symbiotic associations with most land plants. Soil acidity is a major constraint of plant productivity, but acid-tolerant AM fungi can improve plant acid tolerance. The molecular mechanism underlying the acid-tolerance of AM fungi, however, has not yet been elucidated. In my study, a comparative transcriptome approach is applied to identify key genes involved in the acid tolerance, with particular emphasis on transmembrane transporter genes.

2. Materials and Methods

Lotus japonicus was inoculated with the acid tolerant AM fungus *Rhizophagus clarus* CK001 (Indonesian isolate) and grown at pH 3.8, 4.2, and 4.9 in the mesh-bag separated culture system, and extraradical hyphae were collected from the root-free hyphal compartment for RNA sequencing. The sequence reads were *de novo* assembled and mapped on the resultant contigs. Differentially expressed genes among the pH treatments were clustered according to response patterns to pH to identify genes that were upregulated in response to soil acidity. Expression profiles of several orthologous transporter genes that were also upregulated in the different strain (RF1, Hokkaido isolate) of *R. clarus* (Nakanishi, 2017) were compared with those in CK001 to assess similarity in their responsiveness to soil acidity.

3. Results and Discussion

Among the 29,000 genes of *R. clarus*, 617 genes were upregulated in response to soil acidity, including 48 transporter genes. The membrane Mg transporter gene *MMgT* involved in the maintenance of Mg homeostasis in the presence of Al^{3+} and the gene encoding heavy metal-associated (HMA) domain-containing protein involved in heavy-metal detoxification were upregulated with increasing soil acidity in CK001, but not in RF1. Instead, *ALR1* encoding a CorA-like Mg transporter was upregulated in RF1, but not in CK001. Likewise, no transporter gene was commonly upregulated in the two strains, suggesting that their acid-tolerant mechanisms are different, probably due to difference in the environment of original habitats: one is acid sulfate soil and the other is tropical peat soil.