

Identification of Specific Enzymes in the Comparison between *Fusarium oxysporum* and *Arabidopsis thaliana*

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The genus *Fusarium* currently accounts for more than 300 species and is composed of filamentous fungi including many crop pathogens. Species from genus *Fusarium* are fungi widely distributed in soil, plants and in different organic substrates. These mycotoxin-producing fungi cause diseases responsible for significant global economic losses and can even be opportunistic pathogens for humans. The identification of specific enzymes essential to the fungus metabolism might improve the identification of mechanisms for the control of fusariosis. Thus, we performed a comparison of non-redundant enzymatic activities between *Fusarium oxysporum* (879) and *Arabidopsis thaliana* (1044) using the list of Enzyme Commission numbers (ECs) of the Kyoto Database Encyclopedia of Genes and Genomes (KEGG). We recovered the identifiers and protein sequences of the enzymes that are specific to *F. oxysporum*. As the result of this comparison, we found that 248 ECs were only present in the fungus. The list of 248 ECs corresponded to 339 access numbers and 319 non-redundant protein sequences of *F. oxysporum*. The identification of specific enzymes of *F. oxysporum* is important since these enzymes may be participating in key pathways for the fungus survival. The success for parasite control of inhibiting specific enzyme activities in *F. oxysporum* will depend on (i) whether they are involved in essential pathways; (ii) alternative routes exist for these pathways; (iii) the level of disorders of the target inhibition can bring to the fungus survival; and (iv) the consequences of target inhibition to the host plant. Of course, the ideal target candidates to be inhibited are those that will not entail any deleterious effect to the host plant.

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