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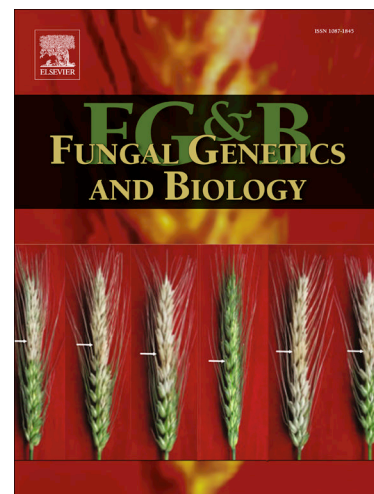
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Comparative analysis of basidiomycete transcriptomes reveals a core set of expressed genes encoding plant biomass degrading enzymes

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Abstract

Basidiomycete fungi can degrade a wide range of plant biomass, including living and dead trees, forest litter, crops, and plant matter in soils. Understanding the process of plant biomass decay by basidiomycetes could facilitate their application in various industrial sectors such as food & feed, detergent, and biofuels, and also provide new insights into their essential biological role in the global carbon cycle. The fast expansion of basidiomycete genomic and functional genomics data (e.g. transcriptomics, proteomics) has facilitated exploration of key genes and regulatory mechanisms of plant biomass degradation. In this study, we comparatively analyzed 22 transcriptome datasets from basidiomycetes related to plant biomass degradation, and identified 328 commonly induced genes and 318 repressed genes, and defined a core set of carbohydrate active enzymes (CAZymes) which was shared by most of the basidiomycete species. High conservation of these CAZymes in genomes and similar regulation pattern in transcriptomics data from lignocellulosic substrates indicate their key role in plant biomass degradation and potential for their further biochemical investigation.

Keywords

Basidiomycete; Plant biomass degradation; Comparative transcriptomics; CAZymes

1. Introduction

Plant biomass is the most abundant renewable carbon source on earth and a substrate for the majority of fungal species. Basidiomycete fungi comprise 32% of the described fungi (Kirk. et al., 2008). Many of them can efficiently use plant biomass as carbon source by degrading plant cell wall polysaccharides via the production of various carbohydrate active enzymes (CAZymes) (Lombard et al., 2014). Wood-decaying basidiomycetes have traditionally been classified as white rot and brown rot species, based on differences in their ability to degrade the major components of plant cell wall.

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