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Genome-Wide Functional Analysis of Phosphatase in Cryptococcus neoformans

Authors : Jae-Hyung Jin, Kyung-Tae Lee, Yee-Seul So, Eunji Jeong, Yeonseon Lee, Dongpil Lee, Dong-Gi Lee, Yong-Sun Bahn

Abstract : Cryptococcus neoformans causes cryptococcal meningoencephalitis mainly in immunocompromised patients as well as immunocompetent people. But therapeutic options are limited to treat cryptococcosis. Some signaling pathways including cyclic AMP pathway, MAPK pathway, and calcineurin pathway play a central role in the regulation of the growth, differentiation, and virulence of C. neoformans. To understand signaling networks regulating the virulence of C. neoformans, we selected the 114 putative phosphatase genes, one of the major components of signaling networks, in the genome of C. neoformans. We identified putative phosphatases based on annotation in C. neoformans var. grubii genome database provided by the Broad Institute and National Center for Biotechnology Information (NCBI) and performed a BLAST search of phosphatases of Saccharomyces cerevisiae, Aspergillus nidulans, Candida albicans and Fusarium graminearum to Cryptococcus neoformans. We classified putative phosphatases into 14 groups based on InterPro phosphatase domain annotation. Here, we constructed 170 signature-tagged gene-deletion strains through homologous recombination methods for 91 putative phosphatases. We examined their phenotypic traits under 30 different in vitro conditions, including growth, differentiation, stress response, antifungal resistance and virulence-factor production.

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