

Members of protein O-mannosyltransferase family in *Aspergillus fumigatus* differentially affect growth, morphogenesis and viability.

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Abstract

O-mannosylation is an essential protein modification in eukaryotes. It is initiated at the endoplasmic reticulum by O-mannosyltransferases (PMT) that are evolutionary conserved from yeast to humans. The PMT family is phylogenetically classified into PMT1, PMT2 and PMT4 subfamilies, which differ in protein substrate specificity and number of genes per subfamily. In this study, we characterized for the first time the whole PMT family of a pathogenic filamentous fungus, *Aspergillus fumigatus*. Genome analysis showed that only one member of each subfamily is present in *A. fumigatus*, PMT1, PMT2 and PMT4. Despite the fact that all PMTs are transmembrane proteins with conserved peptide motifs, the phenotype of each PMT deletion mutant was very different in *A. fumigatus*. If disruption of PMT1 did not reveal any phenotype, deletion of PMT2 was lethal. Disruption of PMT4 resulted in abnormal mycelial growth and highly reduced conidiation associated to significant proteomic changes. The double *pmt1pmt4* mutant

was lethal. The single pmt4 mutant exhibited an exquisite sensitivity to echinocandins that is associated to major changes in the expression of signal transduction cascade genes. These results indicate that the PMT family members play a major role in growth, morphogenesis and viability of *A. fumigatus*.

Beteiligte Forschungseinheiten

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