Functional analysis of the phospholipase C gene CaPLC1 and two unusual phospholipase C genes, CaPLC2 and CaPLC3, of *Candida albicans*.

Kunze D, Melzer I, Bennett D, Sanglard D, MacCallum D, Nörskau J, Coleman DC, Odds FC, Schäfer W, Hube B (2005) Functional analysis of the phospholipase C gene CaPLC1 and two unusual phospholipase C genes, CaPLC2 and CaPLC3, of *Candida albicans*. *Microbiology* 151(Pt 10), 3381-3394.

Abstract

Phospholipases C are known to be important regulators of cellular processes but may also act as virulence factors of pathogenic microbes. At least three genes in the genome of the human-pathogenic fungus Candida albicans encode phospholipases with conserved phospholipase C (Plc) motifs. None of the deduced protein sequences contain N-terminal signal peptides, suggesting that these phospholipases are not secreted. In contrast to its orthologue in Sacharomyces cerevisiae, CaPLC1 seems to be an essential gene. However, a conditional mutant with reduced transcript levels of CaPLC1 had phenotypes similar to Plc1p-deficient mutants in S. cerevisiae, including reduced growth on media causing increased osmotic stress, on media with a non-glucose carbon source, or at elevated or lower temperatures, suggesting that CaPlc1p, like the Plc1p counterpart in S. cerevisiae, may be involved in multiple cellular processes. Furthermore, phenotypic screening of the heterozygous DeltaCaplc1/CaPLC1 mutant showed

additional defects in hyphal formation. The loss of CaPLC1 cannot be compensated by two additional PLC genes of C. albicans (CaPLC2 and CaPLC3) encoding two almost identical phospholipases C with no counterpart in S. cerevisiae but containing structural elements found in bacterial phospholipases C. Although the promoter sequences of CaPLC2 and CaPLC3 differed dramatically, the transcriptional pattern of both genes was similar. In contrast to CaPLC1, CaPLC2 and CaPLC3 are not essential. Although Caplc2/3 mutants had reduced abilities to produce hyphae on solid media, these mutants were as virulent as the wild-type in a model of systemic infection. These data suggest that C. albicans contains two different classes of phospholipases C which are involved in cellular processes but which have no specific functions in pathogenicity.

Beteiligte Forschungseinheiten

Mikrobielle Pathogenitätsmechanismen Bernhard Hube Mehr erfahren

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