Phylogenetic and phenotypic characterisation of the 3-ketoacyl-CoA thiolase gene family from the opportunistic human pathogenic fungus *Candida albicans*.

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Abstract

Gene families are common to all kingdoms of live and most likely derived from gene duplications with subsequent specification for the adaptation to environmental conditions. However, the exact contribution of single members to cellular physiology is difficult to predict. Here, we analysed a family of 3-ketoacyl-CoA thiolases composed of Pot1p, Fox3p and Pot13p from the dimorphic yeast Candida albicans and studied their contribution to fatty acid utilisation and virulence. The presence of three 3-ketoacyl-CoA thiolases in C. albicans contrasts the existence of only one single gene in closely related Saccharomycetales such as Saccharomyces cerevisiae. Phylogenetic analyses revealed that two of the thiolases, Pot1p and Fox3p, were closely related to the S. cerevisiae Pot1p. The third protein clustered with yet uncharacterised thiolases from filamentous fungi. Single, double and triple mutants were generated for phenotypic characterisations. While Pot1p was of general importance for utilisation of fatty acids, Fox3p partially contributed to fatty acid utilisation at elevated temperatures. No phenotype was detectable

for pot13 deletions. When virulence of the different mutants was assessed in an embryonated chicken egg infection model, no significant attenuation was observed for any of the mutants, confirming previous assumptions that β-oxidation is dispensable for C. albicans virulence.

Involved units

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