The novel *Candida albicans* transporter Dur31 Is a multi-stage pathogenicity factor.

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Details

PubMed

Abstract

Candida albicans is the most frequent cause of oral fungal infections. However, the exact pathogenicity mechanisms that this fungus employs are largely unknown and many of the genes expressed during oral infection are uncharacterized. In this study we sought to functionally characterize 12 previously unknown function genes associated with oral candidiasis. We generated homozygous knockout mutants for all 12 genes and analyzed their interaction with human oral epithelium in vitro. Eleven mutants caused significantly less epithelial damage and, of these, deletion of orf19.6656 (DUR31) elicited the strongest reduction in pathogenicity. Interestingly, DUR31 was not only involved in oral epithelial damage, but in multiple stages of candidiasis, including surviving attack by human neutrophils, endothelial damage and virulence in vivo. In silico analysis indicated that DUR31 encodes a sodium/substrate symporter with 13 transmembrane domains and no human homologue. We provide evidence that Dur31 transports histatin 5. This is one of the very first examples of microbial driven import of this highly cytotoxic antimicrobial peptide. Also, in contrast to wild type C. albicans, dur31Δ/Δ was unable to actively increase local environmental pH, suggesting that Dur31 lies in the extracellular alkalinization

hyphal auto-induction pathway; and, indeed, DUR31 was required for morphogenesis. In agreement with this observation, dur31Δ/Δ was unable to assimilate the polyamine spermidine.

Involved units

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Topics

Nutrient acquisition in infections

Awards

Research Award "DGHM FG Eukaryontische Krankheitserreger"; Featured article & front (web)page PLoS Pathogens; picture of the month Lab Journal; best picture DMykG 2013; Cover picture ebook in Front Immunol: Immunity to Human Fungal Pathogens

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