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The Role of Glutamine-Rich Region of Candida Albicans Tec1p in Mediating Morphological Transition and Invasive Growth

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Abstract : Hyphal growth and the transcriptional regulation to the host environment are key issues during the pathogenesis of C. albicans. Tec1p is the C. albicans homolog of a TEA transcription factor family, which share a conserved DNA-binding TEA domain in their N-terminal. In order to define a structure-function relationship of the C. albicans Tec1p protein, we constructed several mutations on the N terminal, C terminal or in the TEA binding domain itself by homologous recombination technology. The modifications in the open reading frame of TEC1 were tested for reconstitution of the morphogenetic development of the tec1/tec1 mutant strain CaAS12. Mutation in the TEA consensus sequence did not confer transition to hyphae whereas the reconstitution of the full-length Tec1p has reconstituted hyphal development. A deletion in one of glutamine-rich regions either in the Tec1p N-terminal or the C-terminal in regions of 53-212 or 637–744 aa, respectively, did not restore morphological development in mutant CaAS12 strain. Whereas, the reconstitution with Tec1p mutants other than the glutamate-rich region has restored the morphogenetic switch. Additionally, the deletion of the glutamine-rich region has attenuated the invasive growth and the heat shock resistance of C. albicans. In conclusion, we show that a glutamine-rich region of Tec1p is essential for the hyphal development and mediating adaptation to the host environment of C. albicans.

Keywords : Candida albicans, morphogenetic development, TEA domain, hyphal formation, TEC1
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