

Immunoproteomic analysis of antibody responses to extracellular proteins of *Candida albicans* revealed the importance of glycosylation for antigen recognition.

Luo T, Krüger T, Knüpfer U, Kasper L, Wielsch N, Hube B, Kortgen A, Bauer M, Giamarellou-Bourboulis EJ, Dimopoulos G, Brakhage AA, Kniemeyer O (2016) Immunoproteomic analysis of antibody responses to extracellular proteins of *Candida albicans* revealed the importance of glycosylation for antigen recognition. *J Proteome Res* 15(8), 2394-2406.

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Abstract

During infection, the human pathogenic fungus *Candida albicans* undergoes a yeast-to-hypha transition, secretes numerous proteins for invasion of host tissues and modulates the host's immune response. Little is known about the interplay of *C. albicans* secreted proteins and the host adaptive immune system. Here, we applied a combined 2D gel- and LC-MS/MS-based approach for the characterization of *C. albicans* extracellular proteins during the yeast-to-hypha transition, which led to a comprehensive *C. albicans* secretome map. The serological responses to *C. albicans* extracellular proteins were investigated by a 2D-immunoblotting approach combined with MS for protein identification. Based on the screening of sera from candidemia and three groups of non-candidemia patients, a core set of 19 immunodominant antibodies against secreted proteins of *C. albicans* was identified, seven of which represent potential diagnostic markers for candidemia (Xog1, Lip4, Asc1, Met6, Tsa1, Tpi1 and Prx1). Intriguingly, some secreted, strongly

glycosylated protein antigens showed high cross-reactivity with sera from non-candidemia control groups. Enzymatic deglycosylation of proteins secreted from hyphae significantly impair sera antibody recognition. Furthermore, deglycosylation of the recombinantly produced, secreted aspartyl protease Sap6 confirmed a significant contribution of glycan epitopes to the recognition of Sap6 by antibodies in patients' sera.

Involved units

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