TITLE: *IN SILICO* IDENTIFICATION OF *TRICHOSPORON ASAHII* ADHESINS AS POTENTIAL VACCINE CANDIDATES BASED ON REVERSE VACCINOLOGY

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ABSTRACT:
Trichosporon asahii is a basidiomycetous yeast which is emerging as agent of invasive infections in immunocompromised patients, with mortality rates up to 80%. This relates to failure in proper treatments and biofilm formation in implanted catheters. Biofilm formation depends upon virulence factors like adhesins expressed on the fungal cell surface, which in *T. asahii*, have never been characterized. Recently, fungal adhesins have shown potential as vaccine candidates to prevent invasive infections. Thus, this work aimed to identify genes encoding putative *T. asahii* adhesins by comparative genomics with potential to be used as vaccine candidate based on reverse vaccinology. Hypothetical adhesin genes were searched in *T. asahii* CBS2479 genome by NCBI-BLAST comparisons with amino acid sequences of known adhesins (*ALS, HWP1, IFF* and *CFL1* families) of *Candida albicans* and *Cryptococcus neoformans*. Aditionally, we used FungalRV and Faapred adhesin prediction websites with default paramethers to survey the complete *T. asahii* proteome (8,300 predicted proteins). To infer vaccinal protective potential, we selected proteins located extracellularly with signal peptide predicted by CELLO and PSORT II programs, followed by NCBI-BLAST analysis against human proteome. The immunostimulatory capability was evaluated by VaxiJen predictor and epitope mapping was performed using Teptool program. After BLAST analysis we found only one protein with 30% identity and 85% similarity to *C. neoformans* adhesin CFL1p. FungalRV predicted 24 proteins with adhesion function and 18 of them were confirmed as adhesins by the Faapred analysis. Excluding the ones without signal peptide and extracellular location, 7 proteins were selected as putative adhesins. Evaluating the vaccinal potential, only one putative adhesin exhibited immunostimulatory capability, possessing 319 amino acids and no significant similarity with human proteins. Predictions showed that it had 49 MHC-I epitopes recognized by 8 alleles, with 32 epitopes with immunogenic potential. Also, it had 46 MHC-II epitopes recognized by 20 alleles, of which 28 had immunogenic potential. Analysis of the epitopes recognized by both MHC-I and II reveled 16 common sequences with immunogenic potential. In conclusion, we successfully identified *in silico* the first adhesin in the surface of *T. asahii* with vaccinal potential to be tested *in vivo* as a candidate to protect patients from invasive fungal infections.

Keywords: *Trichosporon asahii*, adhesin, vaccine candidate, comparative genomics, reverse vaccinology

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