Investigating allelic diversity of the agglutinin-like sequence (ALS) gene family in *Candida albicans*

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The agglutinin-like sequence (ALS) gene family of the fungal pathogen *Candida albicans* contains 8 members that code for cell-surface proteins, which are involved in cell substrate and cell-cell adhesion, which is the first step in the *Candida* infection process. *C. albicans* is a diploid, highly heterozygous organism, and to study allelic diversity genes need to be cloned to obtain the allele-specific sequences. Since allelic sequences were only available for 4 of the 8 ALS genes, the goal of this study was to obtain allelic sequences for the remaining 4 ALS genes, *ALS1, ALS2, ALS4* and *ALS7*. First, the 5-prime and 3-prime regions of these genes were amplified by PCR, ligated into plasmids and transformed into *Escherichia coli*. Correct transformants were checked by restriction digests of plasmids purified from *E. coli*. Multiple clones for each gene were then sequenced and analyzed using Sequencher software. Sequences for both alleles have been successfully obtained for *ALS2* and *ALS4*. All sequences obtained for *ALS1* and *ALS7* have identical sequences. Ongoing experiments include the analysis of additional clones to obtain the sequence information for the second allele. Future experiments will involve the analysis of *C. albicans* isolates that have been passaged through a mouse host.

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