

The dynamic surface proteomes of allergenic fungal conidia

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Abstract

Fungal spores and hyphal fragments play an important role as allergens in respiratory diseases. In this study, we performed trypsin shaving and secretome analyses to identify the surface-exposed proteins and secreted/shed proteins of *Aspergillus fumigatus* conidia, respectively. We investigated the surface proteome under different conditions, including temperature variation and germination. We found that the surface proteome of resting *A. fumigatus* conidia is not static, but instead unexpectedly dynamic, as evidenced by drastically different surface proteomes under different growth conditions. Knockouts of two abundant *A. fumigatus* surface proteins, ScwA and CweA, were found to function only in fine-tuning the cell wall stress response, implying that the conidial surface is very robust against perturbations. We then compared the surface proteome of *A. fumigatus* to other allergy-inducing molds, including *Alternaria alternata*, *Penicillium rubens*, and *Cladosporium herbarum*, and performed comparative proteomics on resting and swollen conidia, as well as secreted proteins from germinating conidia. We detected 125 protein ortholog groups, including 80 with putative catalytic activity, in the extracellular region of all four molds, and 42 nonorthologous proteins produced solely by *A. fumigatus*. Ultimately, this study highlights the dynamic nature of the *A. fumigatus* conidial surface and provides targets for future diagnostics and immunotherapy.

Identifier

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