Proteomic profile of the secretome and biofilm of Aspergillus fumigatus

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Introduction: Fungal diseases are known to affect many individuals around the world, but the exact number of people affected by these diseases is not well established due to the lack of surveillance data that can be used. Aspergillosis is an opportunistic mycosis caused by fungi of the genus Aspergillus, with Aspergillus fumigatus being the main etiological agent. The disease has a variety of clinical presentations, which makes its diagnosis difficult. It is known that during the infection process, this fungus secretes a variety of proteins for its development and that it can form biofilms, which consist of a microbial community surrounded by a self-produced extracellular matrix, which acts as a protective mechanism against hostile environments and antifungal agents. Proteomics is an approach that can help elucidate the proteins of Aspergillus fumigatus that are involved in the infection process and those present in the biofilms it forms. So, the aim of this study was to characterize the protein profile of the secretome and biofilm of Aspergillus fumigatus.Material and Methods: The Aspergillus fumigatus ATCC 46640 strain was reactivated in malt extract agar (MEA) for seven days at 28 °C in a BOD chamber. To obtain the secretome and produce the biofilm, a fungal inoculum was performed at a concentration of 1x106 spores/mL in Czapek (CZ) liquid medium. The fungal culture was incubated in a shaker for 36 hours at temperatures of 28°Cand 37°C, without agitation. Secretome samples were concentrated (Centripep®) with 3.0 kDa cellulose membranes. The biofilm samples were vortexed and sonicated with ultrasound. After this preliminary preparation, secretome and biofilm were prepared for proteomic analysis using a shotgun proteomics approach. The data were analyzed using the PatternLab for proteomics V software and the proteins were identified by PSM and quantification was realized by spectral count. Results and Discussion: Proteomic analysis resulted in the identification of 108 proteins at 28 °C and 175 proteins at 37 °C for the secretome; versus 205 proteins at 28 °C and 172 proteins at 37 °C for the biofilm. Regardless of temperature, both A. fumigatus secretome samples were found to be rich in proteases, peptidases and proteins that have been associated with host allergic response. The Asp-hemolysin, IgE-binding protein and Probable glucan endo-1,3-beta-glucosidase eglC were among the proteins identified in the secretome culture at 37°C. Comparing the two biofilm samples prepared at different temperatures, the proteins fructose-bisphosphate aldolase, inositol-3-phosphate synthase and phosphoglucomutase were more abundant. Conclusion: The proteins identified in this study play important roles in the growth process of Aspergillus fumigatus ATCC 1640, being associated with its metabolism, mainly in obtaining and using nutrients available in the environment. Furthermore, these preliminary results may serve as a basis for the discovery of new targets for the identification of Aspergillus fumigatus when it is acting as a pathogen in the host.

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