

Identification of *Aspergillus fumigatus* Conidium Genes Involved with Mitochondrial Metabolism and Antioxidant Defense by Using Oligonucleotide Microarrays

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Although recent advances in the study of the mitochondrial enzyme system in *A. fumigatus* have been achieved, few are known about its function on the antioxidant processes required for fungus survival in the host organism. The understanding of those functions would help to clarify the mitochondria role in the development of invasive aspergillosis. In order to detect and compare the differential expression of gene associated with the electron transport chain proteins and antioxidant enzymes in *A. fumigatus*, we applied the oligonucleotide microarray technique. The CEA17 strain of the fungus was cultivated at 28°C in PDAY medium. Samples were collected after 20, 24 and more than 25 hours, encompassing the pre-conidiogenesis, early and late conidiogenesis phases, respectively. RNAs were obtained with Trizol reagent. The hybridization protocols developed by JCVI were used in a chip containing 9.926 genes. During different phases of conidiogenesis, microarray analysis allowed the identification of 3.3% of differentially regulated genes in *A. fumigatus*, 14.8% being represented by mitochondrial proteins genes and 4.3% involved with oxidative stress response. Repressed genes totalized 65.1% of the identified ones. Of these, 17.5% encodes mitochondrial proteins and 2.8% is associated with oxidative stress. Among these, catalase gene was down-regulated. On the other hand, thioredoxin gene was up-regulated. The early conidiogenesis represented the phase of higher gene identification. These results allow few comparisons with similar studies due to the low amount of gene identification. However, the application of microarray in the identification of mitochondrial and antioxidant protein genes has shown promising so further tests can improve the significance of those analyses.

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