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Construction and Analysis of Protein-Protein Interaction Network of *Aspergillus fumigatus* Proteins



Authors:

Alper Soylar (*Department of Food Engineering, Middle East Technical University*)

Tolga Can (*Department of Computer Engineering, Middle East Technical University*)

Zumrut B. Ogel (*Department of Food Engineering, Middle East Technical University*)

Short Abstract: This project aims to construct a probabilistic high-coverage *Aspergillus fumigatus* protein-protein interaction network by computational methods with the ultimate goal of integrating multiple data sources such as microarrays, GO annotations, and literature data. This will help to develop new drugs and finding cures for diseases caused by *A.fumigatus*.

Long Abstract:

The increasing availability of genomic, proteomic and other data over the last years made it possible to investigate complex structures of cellular components. It is a central challenge of bioinformatics to use this information in discovering the functional linkages between proteins. New methods have been devised to predict functional links between proteins using genomic information. One of these computational methods is the phylogenetic profiling. A phylogenetic profile describes the pattern of presence or absence of a particular protein across a set of organisms whose genomes have been sequenced. Functional linkages between proteins can also be detected by analyzing fusion patterns of protein domains. A third computational method that reveals functional linkages from genome sequences is the gene neighbor method. Our goal is to construct a probabilistic high-coverage *Aspergillus fumigatus* protein-protein interaction network by computational methods described above with the ultimate goal of integrating multiple data sources such as microarrays, GO annotations, literature data, and high-throughput experimental data.

Aspergillus is a genus of fungi found worldwide; over 180 species are officially recognized, some of which are of medical or industrial importance. *Aspergillus* species are without doubt the most commercially important fungal organisms in the world, being exploited for the production of both primary and secondary metabolites. Some *Aspergillus* species cause serious disease in humans and animals, and can be pathogenic. *A. fumigatus* is opportunistic saprophytic fungus that plays an essential role in recycling environmental carbon and nitrogen. Although this species is not the most prevalent fungus in the world, it is one of the most ubiquitous of those with airborne conidia. Over the past 10 years, *A. fumigatus* has become the most prevalent airborne fungal pathogen, causing severe and usually fatal invasive infections in immunocompromised hosts in developed countries. It is capable of causing a wide spectrum of human diseases, ranging from allergic bronchopulmonary aspergillosis and aspergilloma to invasive aspergillosis and systemic infection due to hematogenous dissemination.

This project will increase understanding of key processes playing role in pathogenicity and will greatly help in development of new drugs and finding cures for diseases caused by *A. fumigatus*.