Fungal Proteomics

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Candida albicans, a normal component of the mammalian gastrointestinal flora, is responsible for most fungal infections in immunosuppressed patients. *Candida* is normally phagocytosed by macrophages and neutrophils, which secrete cytokines and induce hyphal development in this fungus. Neutropenic patients, deficient in these immune cells, are particularly susceptible systemic candidosis. Macrophage and neutrophils represent an important first line and effectors function in the control of *Candida* infections, which kill fungus by cytokine and nitric oxide secretion. However, *Candida albicans* phagocytosed by macrophage are above all re-alive and that mechanism is not yet cleared.

Here, we used proteomic tools to identify host defense mechanisms that are affected by *Candida albicans*. We identified differentially expressed various protein families from mouse monocytic cell lines by 2-D gel analysis. The profiles include genes encoding receptors, signal transduction molecules, anti-inflammatory gene and transcription factors. These results will provide a basis for recognizing *Candida* tactics for evading these responses and thus disease prevention. In addition, topics including development of new antifungal drug, HWY-289 and studies of its mechanism of action using proteomics will also be discussed.