The early transcriptional response of human granulocytes to infection with *Candida albicans* is not essential for killing but reflects cellular communications.

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Abstract

Candida albicans is a polymorphic opportunistic fungus that can cause life-threatening systemic infections following hematogenous dissemination in patients susceptible to nosocomial infection. Neutrophils form part of the innate immune response, which is the first line of defense against microbes and is particularly important in C. albicans infections. To compare the transcriptional response of leukocytes exposed to C. albicans, we investigated the expression of key cytokine genes in polymorphonuclear and mononuclear leukocytes after incubation with C. albicans for 1 h. Isolated mononuclear cells expressed high levels of genes encoding proinflammatory signaling molecules, whereas neutrophils exhibited much lower levels, similar to those observed in whole blood. The global transcriptional profile of neutrophils was examined by using an immunology-biased human microarray to determine whether different morphological forms or the viability of C. albicans altered the transcriptome. Hyphal cells appeared to have the broadest effect, although the

most strongly induced genes were regulated independently of morphology or viability. These genes were involved in proinflammatory cell-cell signaling, cell signal transduction, and cell growth. Generally, genes encoding known components of neutrophil granules showed no upregulation at this time point; however, lactoferrin, a well-known candidacidal peptide, was secreted by neutrophils. Addition to inhibitors of RNA or protein de novo synthesis did not influence the killing activity within 30 min. These results support the general notion that neutrophils do not require gene transcription to mount an immediate and direct attack against microbes. However, neutrophils exposed to C. albicans express genes involved in communication with other immune cells.

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