



Genomic Organization and Expression of Iron Metabolism Genes in the Emerging Pathogenic Mold

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The ubiquitous mold is increasingly recognized as an emerging pathogen, especially among patients with underlying disorders such as immunodeficiency or cystic fibrosis (CF). Indeed, it ranks the second among the filamentous fungi colonizing the respiratory tract of CF patients. However, our knowledge about virulence factors of this fungus is still limited. The role of iron-uptake systems may be critical for establishment of infections, notably in the iron-rich environment of the CF lung. Two main strategies are employed by fungi to efficiently acquire iron from their host or from their ecological niche: siderophore production and reductive iron assimilation (RIA) systems. The aim of this study was to assess the existence of orthologous genes involved in iron metabolism in the recently sequenced genome of . At first, a tBLASTn analysis using iron-related proteins as query revealed orthologs of almost all relevant loci in the genome. Whereas the genes putatively involved in RIA were randomly distributed, siderophore biosynthesis and transport genes were organized in two clusters, each containing a non-ribosomal peptide synthetase (NRPS) whose orthologs in have been described to catalyze hydroxamate siderophore synthesis. Nevertheless, comparative genomic analysis of siderophore-related clusters showed greater similarity between and phylogenetically close molds than with species. The expression level of these genes was then evaluated by exposing conidia to iron starvation and iron excess. The expression of several orthologs of genes involved in siderophore-based iron uptake or RIA was significantly induced during iron starvation, and conversely repressed in iron excess conditions. Altogether, these results indicate that possesses the genetic information required for efficient and competitive iron uptake. They also suggest an important role of the siderophore production system in iron uptake by .

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