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Functional Genomic Analyses of a Human Pathogenic Fungus *Aspergillus fumigatus*

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Recent completion of the genome sequencing of the opportunistic human pathogen *Aspergillus fumigatus* provided a great opportunity to study its biology in greater detail. One of the characteristic phenotypes of *A. fumigatus* is its high adaptability to elevated environmental temperatures not tolerated by other members of the species. These environments, including soil, animal hosts, and compost, requires the fungus to adjust its biochemical constitution and physiology to survive and possibly resume growth after exposure to a temperature as high as 70˚C. We examined genome-wide expression upon temperature shift from low to high and from high to low, within the range of 4˚C to 52˚C. We found that different genes have specific windows of expression over the temperature range and the duration at a given temperature. For example, many heat shock and stress-responsive genes were immediately up-regulated when the culture was shifted to high temperatures (above 48˚C), but some of these were also up at 37˚C after about an hour. On the other hand, many putative virulence genes were readily expressed at 37˚C, as if the fungus were in the host. This suggests that temperature change is an environmental signal by which the fungus adjusts its physiology in an environment appropriate manner. Another finding we made from this study is that many transposases, especially those of the Mariner-4 type, are highly expressed at high temperatures. This suggests that transposition might be activated at high temperatures perhaps as a means to allow improved adaptability to the high temperature stress through genome alterations. We are extending this study relating the temperature-responsive genes to the Comparative Genomic Hybridization (CGH) data with closely related stains.