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## Epigenetic Regulation of Fungal Development and Pathogenesis in the Rice Blast Fungus

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Fungal pathogens have huge impact on health and economic wellbeing of human by causing life-threatening mycoses in immune-compromised patients or by destroying crop plants. A key determinant of fungal pathogenesis is their ability to undergo developmental change in response to host or environmental factors. Genetic pathways that regulate such morphological transitions and adaptation are therefore extensively studied during the last few decades. Given that epigenetic as well as genetic components play pivotal roles in development of plants and mammals, contribution of microbial epigenetic counterparts to this morphogenetic process is intriguing yet nearly unappreciated question to date. To bridge this gap in our knowledge, we set out to investigate histone modifications among epigenetic mechanisms that possibly regulate fungal adaptation and processes involved in pathogenesis of a model plant pathogenic fungus, *Magnaporthe oryzae*. *M. oryzae* is a causal agent of rice blast disease, which destroys 10 to 30% of the rice crop annually. Since the rice is the staple food for more than half of human population, the disease is a major threat to global food security. In addition to the socioeconomic impact of the disease it causes, the fungus is genetically tractable and can undergo well-defined morphological transitions including asexual spore production and appressorium (a specialized infection structure) formation *in vitro*, making it a model to study fungal development and pathogenicity. For functional and comparative analysis of histone modifications, a web-based database (dbHiMo) was constructed to archive and analyze histone modifying enzymes from eukaryotic species whose genome sequences are available. Histone modifying enzymes were identified applying a search pipeline built upon profile hidden Markov model (HMM) to proteomes. The database incorporates 22,169 histone-modifying enzymes identified from 342 species including 214 fungal, 33 plants, and 77 metazoan species. The dbHiMo provides users with web-based personalized data browsing and analysis tools, supporting comparative and evolutionary genomics. Based on the database entries, functional analysis of genes encoding histone acetyltransferases and histone demethylases is under way. Here I provide examples of such analyses that show how histone acetylation and methylation is implicated in regulating important aspects of fungal pathogenesis. Current analysis of histone modifying enzymes will be followed by ChIP-Seq and RNA-seq experiments to pinpoint the genes that are controlled by particular histone modifications. We anticipate that our work will provide not only the significant advances in our understanding of epigenetic mechanisms operating in microbial eukaryotes but also basis to expand our perspective on regulation of development in fungal pathogens.