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"Bridging the gap between increasing knowledge and decreasing resources"

Changes in *Magnaporthe oryzae* Transcriptome During Rice Infection at High Temperature

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Abstract

Future predictions indicate that extreme annual daily maximum temperature will increas by about 1-3 °C by mid-twenty-first century and by about 2-5 °C by the late twentyfirst century. Such changes are predicted to lead to evolution of new pathogen strains, increase pathogen populations, spread of the diseases to new areas and increase susceptibility of plants. Rice blast, caused by *Magnaporthe oryzae* is the most destructive disease of rice worldwide. M. oryzae infects rice by regulating protein secretion, which enables the pathogen to either avoid recognition by the plant resistance proteins or to turn off the plant defenses. It is expected that elevated temperature may affect the biological processes leading to pathogenicity in *M. oryzae*. However, the direction of high temperature effect on pathogen fitness is not well understood. Here, we analysed the effect of temperature on the transcriptome of *M. oryzae* during invasive growth in the rice cultivar Nipponbare at 35 °C and 28 °C. We detected a higher number of putative effectors in plants exposed to 35 °C than in plants infected at 28 °C. The same was found for classical cell wall degrading enzymes. The qPCR relative quantification of in planta fungal biomass did not indicate any difference between 28 °C and 35 °C. However, plants grown and inoculated at 28 °C showed delayed symptom development in contrast to 35 °C, indicating that high temperature hastened biological processes geared towards necrotrophy more than normal temperature. Additionally, elevated temperature induced morphological transitions of *M. oryzae* during growth on the host, which could be related to survival and virulence dynamics.

Keywords: High temperature, Magnaporthe oryzae, pathogenicity, rice

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