ABSTRACT

Rice blast disease caused by *Magnaporthe oryzae* is still a growing threat to the primary staple diet of Indo-Asian world population. Due to high genetic variability of the fungus, it has been difficult to control the pathogen. But the tractable and amenable genome of *M. oryzae* has encouraged the scientific community to develop it as a model pathosystem. We attempted to study the biology of pathogenesis of *M. oryzae* by investigating the role of Histidine phosphotransferase *MoHPT1* in biotic and abiotic stress signalling and pathogenicity. *MoHPT1* in *M. oryzae* produced two different transcripts, of which the longer transcript was expressed only under the influence of light. We observed that MoHPT1 protein is expressed in fungal hyphae, nucleus and appressorium. We characterised *MoHPT1* by knocking down the gene using RNAi technology. The RNAi transformants with the lowest expression of *MoHPT1* showed less pathogenicity. The knock-down of *MoHPT1* rendered the fungus sensitive to osmotic, oxidative and cell wall stress. RNAi transformants were also affected in the expression of TCS components and the downstream HOG1 phosphorylation crucial for stress signalling. *MoHPT1* knock-down affected the expression of PAS Histidine kinases in light induced conditions. Laccase activity was altered in the knock-down transformants. Global differential expression analysis of the *MoHPT1* knock-down transcriptome revealed a majority of the gene classes that might be necessary for pathogenesis during the transition from biotrophy to necrotrophy. Our study gives new insights into the multi-functional role of *MoHPT1* in *M. oryzae*.