

Regulatory pathway modulates infectionrelated morphogenesis and pathogenicity in insecticidal fungus

April 2 2020, by Liu Jia

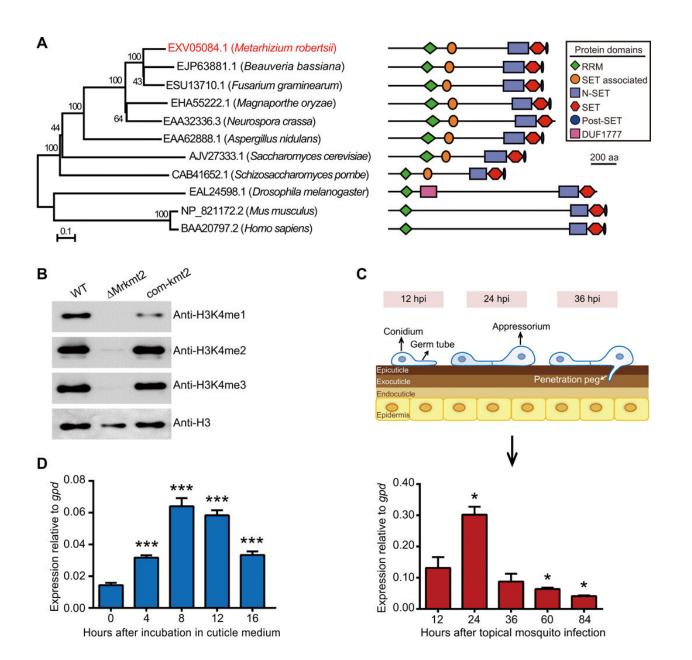




Fig. 1 Characterization of the H3K4 methyltransferase gene Mrkmt2 in M. robertsii ARSEF 2575. *Science Advances* (2020). DOI: 10.1126/sciadv.aaz1659

Prof. WAMG Sibao from Center for Excellence in Molecular Plant Sciences of the Chinese Academy of Sciences (CAS), and Prof. Wei Gang from CAS-MPG Partner Institute for Computational Biology, Shanghai Institute of Nutrition and Health of CAS, and their colleagues, revealed that the KMT2-Cre1-Hyd4 regulatory pathway plays a crucial role in coordinated regulation of the infection-related morphogenesis and fungal pathogenicity against mosquitoes. This study was published online in *Science Advances*.

The entomopathogenic fungi are the only pathogens that can infect the insect host directly through the exoskeletons. During the course of infection in insects, the fungi undergo marked infection-related morphological differentiation on host cuticles. When the spores land on the insect's cuticle, the fungus receives host-specific cues on the cuticle to stimulate spore germination, and then differentiate specialized penetration organ (infection structure), so called appressorium. Through a combination of mechanical pressure and cuticle-degrading enzymes, the fungus penetrates through the cuticle and enter into hemocoel, overwhelms insect defenses and eventually kills the host.

The complex infection-related morphological transitions of the fungus require rapid and fine-tuning regulation of gene expression programs. However, regulatory mechanisms of fungal infection-related morphogenesis are poorly understood.

In this study, the researchers found that a histone lysine



methyltransferase KMT2 in M. robertsii (MrKMT2) was up-regulated upon cuticle induction. MrKMT2 is responsible for methylation at H3K4 and regulates appressorium formation and fungal virulence by upregulating the transcription factor gene Mrcre1 via H3K4 trimethylation (H3K4me3) during mosquito cuticle infection.

Besides, they found that MrCre1 further activates the expression of cuticle-induced genehydrophobin 4(Mrhyd4) to modulate appressorium differentiation and fungal virulence.

The identified MrKMT2-MrCre1-MrHyd4 regulatory pathway allows the fungus to reprogram its gene expression for the appressorium differentiation during cuticle infection.

These findings revealed that the epigenetic regulatory mechanism plays a pivotal role in regulating fungal pathogenesis in insects. This study provides new insights into molecular interactions between pathogenic fungi and insect hosts and the improvement of fungal virulence to control insect pests and mosquito-borne diseases.

The increasing global threat of emerging and reemerging mosquitoborne diseases poses a serious human health problem. Because of the lack of vaccines or effective treatments against these human pathogens, vector control using chemical insecticides remains the major tool for combating mosquito-borne diseases. The growing threat of mosquito insecticide resistance requires the development of more sustainable vector control tools that can overcome insecticide resistance.

Fungal biopesticides are promising environmentally friendly alternatives to chemical insecticides. The entomopathogenic fungi are effective at killing insecticide-resistant and insecticide-susceptible mosquitoes, and have been considered the next-generation control agent for mosquito vectors.



More information: Yiling Lai et al. Coordinated regulation of infection-related morphogenesis by the KMT2-Cre1-Hyd4 regulatory pathway to facilitate fungal infection, *Science Advances* (2020). DOI: 10.1126/sciadv.aaz1659

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