

25-2 - Bewertung einer *Magnaporthe oryzae* MIF-Mutante an der Grasmodellpflanze *Brachypodium distachyon*

Assessment of a *Magnaporthe oryzae* MIF mutant on the grass model plant *Brachypodium distachyon*

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MACROPHAGE MIGRATION INHIBITORY FACTOR (MIF) proteins have been identified in both prokaryotes and mammals to play a key role in a broad range of biological functions, including the ability to modulate innate and adaptive immune responses (Calandra and Roger, 2003; Merk *et al.*, 2012). Consistent with this, recent studies show that MIF-like proteins of plants are involved in biotic stress response pathways, while in aphids and nematodes MIFs promote parasitism by suppressing plant immunity (Dubreuil *et al.*, 2014; Panstruga *et al.*, 2015; Zhao *et al.*, 2019).

Based on sequence information, proteins with conserved MIF motif have also been identified in the fungi kingdom, though details on their functions or mode of action have not yet been published (Michelet *et al.*, 2019). To expand our knowledge on the role in fungi, with a particular focus on the Ascomycota phylum, we analyzed the effect of a genetic knock-out of a *MIF* gene in *Magnaporthe oryzae* (*Mo*), the causal agent of the most important fungal rice disease. The *Mo* genome harbors only one *MIF*, structurally similar to human *MIF*, but different in size. Using the experimental system *Magnaporthe oryzae* - *Brachypodium distachyon* (*Mo* – *Bd*), which is especially suited to study fungal pathogenicity and susceptible interactions, our preliminary results demonstrate that Δ *momif1* is less pathogenic on *Bd* leaves as compared to the wildtype (*wt*) fungus, as revealed by both reduced numbers and reduced sizes of lesions. Unexpectedly, these effects were not detectable in *Bd* roots. Instead, confocal microscopy of root tissue showed that Δ *momif1* undergoes a premature switch to necrotrophy and earlier infection of plant tissue. Taken together, our results provide a first hint that *MoMIF* is required for proper fungal growth and development of infection and substantiates our knowledge on the role of MIF proteins as key regulators immunity.

Literatur

- Calandra, T. and Roger, T., 2003. Macrophage migration inhibitory factor: a regulator of innate immunity. *Nature reviews immunology*, 3(10), pp.791-800.
- Dubreuil, G., Deleury, E., Crochard, D., Simon, J.C. and Coustau, C., 2014. Diversification of MIF immune regulators in aphids: link with agonistic and antagonistic interactions. *BMC genomics*, 15(1), pp.1-12.
- Merk, M., Mitchell, R.A., Endres, S. and Bucala, R., 2012. D-dopachrome tautomerase (D-DT or MIF-2): doubling the MIF cytokine family. *Cytokine*, 59(1), pp.10-17.
- Michelet, C., Danchin, E.G., Jaouannet, M., Bernhagen, J., Panstruga, R., Kogel, K.H., Keller, H. and Coustau, C., 2019. Cross-kingdom analysis of diversity, evolutionary history, and site selection within the eukaryotic macrophage migration inhibitory factor superfamily. *Genes*, 10(10), p.740.
- Panstruga, R., Baumgarten, K. and Bernhagen, J., 2015. Phylogeny and evolution of plant macrophage migration inhibitory factor/D-dopachrome tautomerase-like proteins. *BMC evolutionary biology*, 15(1), p.64.
- Zhao, J., Li, L., Liu, Q., Liu, P., Li, S., Yang, D., Chen, Y., Pagnotta, S., Favery, B., Abad, P. and Jian, H., 2019. A MIF-like effector suppresses plant immunity and facilitates nematode parasitism by interacting with plant annexins. *Journal of experimental botany*, 70(20), pp.5943-5958.

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