

germinate while others formed irregular germ tubes or were stuck at the hooking stage. In the rice sheath assay, only 28% *dam1* Δ mutant appressoria showed normal host penetration and invasion compared to 85% of WT appressoria. Most of the conidia failed to form normal functional appressoria even on the host surface, either failing to show penetration or displaying restricted invasive hyphae.

15. In whole plant infection assay, *dam1* Δ produced smaller and fewer lesions than the WT. Defective development of appressoria and impaired infection in the *dam1* Δ mutant raises the possibility of novel anti-fungal strategies directed towards these fungus-specific Dam1 complex proteins.
16. The length of the mitotic spindle was altered in the absence of Dam1. The nuclear and microtubule organization was affected by the loss of Dam1.
17. In the absence of Dam1, mitosis was prolonged due to delayed anaphase onset, with slow nuclear migration and improper segregation, both during vegetative and pathogenic development. Thus, Dam1 plays a critical role in the poleward segregation of chromosomes during anaphase and in nuclear migration.

Conclusion

The outer kinetochore DASH complex proteins Dam1 and Ask1 display subcellular dynamics different from the inner kinetochore protein Mis12, such that they are associated with the nucleus during mitosis. Further, Dam1 plays a role in proper mitotic progression and chromosome segregation, likely through the establishment of correct spindle structure and KT-MT interactions. Dam1 is important for the development of

conidia, appressoria and host invasion in *M. oryzae*. Thus, the fungus-specific complex can be targeted for development of antifungal treatment of plant pathogens. During interphase, DASH complex proteins associate with cytoplasmic microtubules, accumulate at the tip and play a role in proper vegetative hyphal growth. Thus, in *M. oryzae*, and likely other filamentous fungi, the DASH complex may play additional roles in cell polarity and MT dynamics beyond its role at the mitotic spindle.

Future Directions

What is the role of cytoplasmic DASH complex proteins during interphase?

What are the different oligomeric assemblies of the DASH complex observed *in vivo* in filamentous fungi?

Do different oligomeric DASH assemblies affect MT dynamics differently?

Does DASH interact with other MAPs while regulating MT dynamics?

Are all components of the DASH complex essential in *M. oryzae* and in other filamentous fungi?

Do all components of the DASH complex show similar sub-cellular localisation patterns?

Is there a difference in DASH complex roles in uninucleate and multi-nucleate filamentous fungi?

