

The *Arthroderma benhamiae* hydrophobin HypA mediates hydrophobicity and influences recognition by human immune effector cells.

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ILRS Authors

[Christoph Heddergott](#)

Projects

Secretome analysis/pathogenicity mechanisms of *Arthroderma benhamiae*
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Abstract

Dermatophytes are the most common cause of superficial mycoses in humans and animals. They can coexist with their hosts for many years without causing significant symptoms but also cause highly inflammatory diseases. To identify mechanisms involved in the modulation of the host response during infection caused by the zoophilic dermatophyte *Arthroderma benhamiae*, cell wall-associated surface proteins were studied. By two-dimensional gel electrophoresis, we found that a hydrophobin protein designated HypA was the dominant cell surface protein. HypA was also detected in the supernatant during the growth and conidiation of the fungus. The *A. benhamiae* genome harbors only a single hydrophobin gene, designated hypA. A hypA deletion mutant was generated, as was a complemented hypA mutant strain (hypA(C)). In contrast to the wild type and the complemented strain, the hypA deletion mutant exhibited

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