

Comparative and functional genomics provide insights into the pathogenicity of dermatophytic fungi.

Burmester A, Shelest E, Glöckner G, Heddergott C, Schindler S, Staib P, Heidel A, Felder M, Petzold A, Szafranski K, Feuermann M, Pedruzzi I, Priebe S, Groth M, Winkler R, Li W, Kniemeyer O, Schroeckh V, Hertweck C, Hube B, White TC, Platzer M, Guthke R, Heitman J, Wöstemeyer J, Zipfel PF, Monod M, Brakhage AA (2011) Comparative and functional genomics provide insights into the pathogenicity of dermatophytic fungi. *Genome Biol* 12(1), R7.

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Abstract

Millions of humans and animals suffer from superficial infections caused by a group of highly specialized filamentous fungi, the dermatophytes, which exclusively infect keratinized host structures. To provide broad insights into the molecular basis of the pathogenicity-associated traits, we report the first genome sequences of two closely phylogenetically related dermatophytes, *Arthroderma benhamiae* and *Trichophyton verrucosum*, both of which induce highly inflammatory infections in humans.

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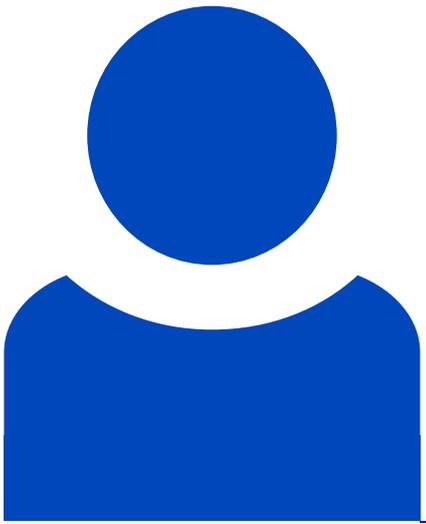
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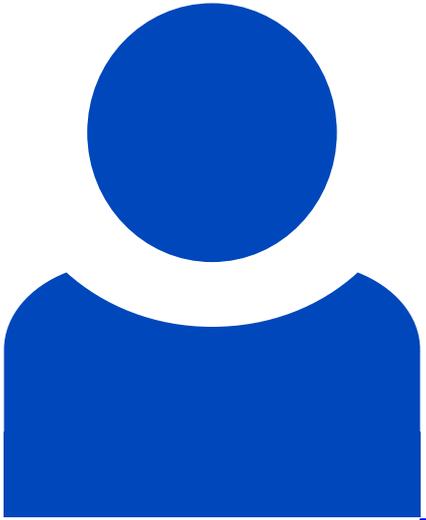
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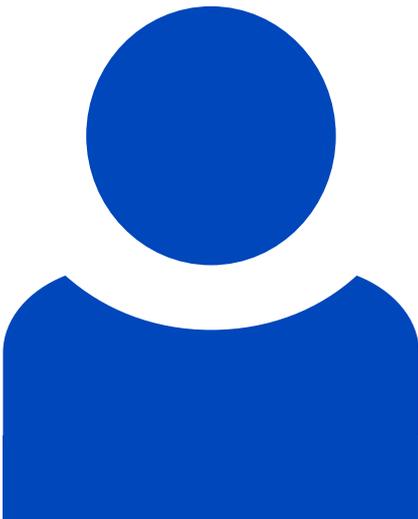
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