Comparative genome analysis of *Trichophyton rubrum* and related dermatophytes reveals candidate genes involved in infection.

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Abstract

The major cause of athlete's foot is Trichophyton rubrum, a dermatophyte or fungal pathogen of human skin. To facilitate molecular analyses of the dermatophytes, we sequenced T. rubrum and four related species, Trichophyton tonsurans, Trichophyton equinum, Microsporum canis, and Microsporum gypseum. These species differ in host range, mating, and disease progression. The dermatophyte genomes are highly colinear yet contain gene family expansions not found in other human-associated fungi. Dermatophyte genomes are enriched for gene families containing the LysM domain, which binds chitin and potentially related carbohydrates. These LysM domains differ in sequence from those in other species in regions of the peptide that could affect substrate binding. The dermatophytes also encode novel sets of fungus-specific kinases with unknown specificity, including nonfunctional pseudokinases, which may inhibit phosphorylation by

competing for kinase sites within substrates, acting as allosteric effectors, or acting as scaffolds for signaling. The dermatophytes are also enriched for a large number of enzymes that synthesize secondary metabolites, including dermatophyte-specific genes that could synthesize novel compounds. Finally, dermatophytes are enriched in several classes of proteases that are necessary for fungal growth and nutrient acquisition on keratinized tissues. Despite differences in mating ability, genes involved in mating and meiosis are conserved across species, suggesting the possibility of cryptic mating in species where it has not been previously detected. These genome analyses identify gene families that are important to our understanding of how dermatophytes cause chronic infections, how they interact with epithelial cells, and how they respond to the host immune response.

Beteiligte Forschungseinheiten

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Vorhersage genregulatorischer Elemente und Gencluster in Pilzen

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