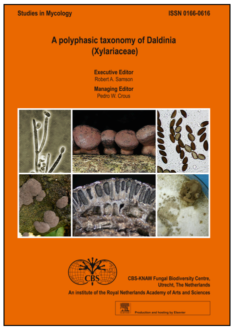

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Phylogeny of dermatophytes with genomic character evaluation of clinically distinct *Trichophyton rubrum* and *T. violaceum*

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Running Title: Dermatophyte phylogeny and genomics

Abstract: *Trichophyton rubrum* and *T. violaceum* are prevalent agents of human dermatophyte infections, the former being found on glabrous skin and nail, while the latter is confined to the scalp. The two species are phenotypically different but are highly similar phylogenetically. The taxonomy of dermatophytes is currently being reconsidered on the basis of molecular phylogeny. Molecular species definitions do not always coincide with existing concepts which are guided by ecological and clinical principles. In this article, we aim to bring phylogenetic and ecological data together in an attempt to develop new species concepts for anthropophilic dermatophytes. Focus is on the *T. rubrum* complex with analysis of rDNA ITS supplemented with LSU, *TUB2, TEF3* and ribosomal protein L10 gene sequences. In order to explore genomic differences between *T. rubrum* and *T. violaceum*, one representative for both species was whole genome sequenced. Draft sequences were compared with currently available dermatophyte genomes. Potential virulence factors of adhesins and secreted proteases were predicted and compared phylogenetically. General phylogeny showed clear gaps between geophilic species of *Arthroderma*, but multilocus distances between species were often very small in the derived anthropophilic and zoophilic genus *Trichophyton*. Significant genome conservation between *T. rubrum* and *T. violaceum* was observed, with a high similarity at the nucleic acid level of 99.38 % identity. *Trichophyton violaceum* contains more paralogs than *T. rubrum*. About 30 adhesion genes were predicted among dermatophytes. Seventeen adhesins were common between *T. rubrum* and *T. violaceum*, while four were specific for the former and eight for the latter. Phylogenetic analysis of secreted proteases reveals considerable expansion and conservation among the analyzed species. Multilocus phylogeny and genome comparison of *T. rubrum* and *T. violaceum* underlined their close affinity. The possibility that they represent a single species exhibiting different phenotypes due to different localizations on the human body is discussed.

Key words: adhesion, *Arthrodermataceae*, character analysis, dermatophytes, genome, phylogeny, protease, *Trichophyton rubrum*, *Trichophyton violaceum*.