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Outbreak of children's dermatophytosis due to highly virulent population of *Trichophyton benhamiae*

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Objectives: Dermatophyte species *Trichophyton benhamiae* is responsible for outbreak of children's dermatophytosis in the Central Europe. Previously almost unknown pathogen with main reservoir host guinea pig is currently one of the most common zoonotic pathogens. What makes this pathogen so successful? Investigation of population structure and virulence factors seems to be a key to answer this question. **Methods:** A total number of 326 *T. benhamiae* strains associated with cases of human and animal dermatophytoses from European countries, Japan and USA were analysed using molecular

markers, and morphological and physiological methods. Identification of virulence factors on the level of secondary metabolites were performed using HPLC and Mass spectrometry.

Results: In Europe, three different population of *T. benhamiae* complex were revealed according to the microsatellite and sequence data. The most common population (78% of all strains) appeared in Europe simultaneously with the beginning of the epidemic (ca in 2000). This outbreak population (with typical yellow strains and clonal population structure) differs from the remaining populations genetically, phenotypically and by production of secondary metabolites. Non-clonal North American population of *T. benhamiae* was identified as closely related to the outbreak European population suggesting that virulent genotype of *T. benhamiae* was introduced to Europe from North America.

Conclusion: High genetic divergence and phenotypic differences between three European populations of *T. benhamiae* indicate that they can be considered independent species. All tentative species can be reliably identified by using molecular genetic data and MALDI-TOF spectra. Majority of isolates can be also recognized by their unique morphology, physiology and secondary metabolite spectra. Correct identification of these species is clinically relevant due to their different host-specificity and further monitoring of the epidemic.

