

Resolving the taxonomy and epidemiology of emerging pathogens in the *Trichophyton benhamiae* complex

Vit Hubka, Adela Cmokova

Czech Academy of Sciences, Czech Republic

Purpose: Species of *T. benhamiae* complex have a worldwide distribution and their host range includes many pet and livestock animals. Nowadays, this complex have become very important due to the epidemic spread of *T. benhamiae* complex species in pets and consequently also in children and pet owners. No causal mechanism has been found that would explain this increase. A considerable genetic and phenotypic variability has been revealed in these emerging pathogens but the species limits are not always clearly defined.

Methods: A total of 352 clinical isolates from *T. benhamiae* complex associated with human and animal dermatophytoses were analysed using molecular markers (DNA sequence data and microsatellites), and morphological and physiological methods.

Results and conclusions: Species boundaries in the *T. benhamiae* clade were resolved by using polyphasic approach. This approach supported recognition of nine species, including three new zoophilic species. *Trichophyton benhamiae* was split into two varieties; *T. benhamiae* var. *luteum* is currently responsible for the European outbreak of zoonotic infections.