# ABSTRACT

*Arthroderma benhamiae* has been almost unknown among clinical mycologists but it is a cause of around 40 % of dermatophytic infections according to current studies in the Czech Republic. The species is primarily transmitted to humans from guinea pigs and other rodents. The epidemiological situation is similar in other countries in Central and Western Europe. The reason of significant increase in the incidence of infections has not been identified yet, and no sufficiently informative molecular markers have been developed for typification of the species that could help to resolve the cause of this problem.

For the purposes of this study, isolates (n=268) from cases of human and animal dermatophytoses from the Czech Republic, Germany, Belgium, Switzerland, Italy, Japan and USA were selected. Ten variable microsatellite markers were developed and sequence analysis of two genetic loci (ITS rDNA and *gpdh* gene) were performed to reveal intraspecific variation. Phenotype was also studied at the level of micro- and macromorphology of the strains and growth parameters at several temperatures and on several cultivation media. Mating type idiomorph of each isolate was determined and mating experiments were performed by crossing pairs of genetically related as well as genetically distant strains.

Sequence analysis revealed six different genotypes (SG1-SG6) among strains of *A. benhamiae*, the majority (99%) of strains belonged to three major subpopulations: Euroamerican (SG1), European (SG2) and the European-Japanese (SG3). Microsatellite analysis revealed 32 different genotypes distributed into four major subpopulations, which were concordant with sequence analysis. However, microsatellites markers were able to distinguish between strains of European and American origin in the Euroamerican subpopulation (SG1). Phenotypic studies also supported distribution of strains into the same four main groups. Disequilibrium was found between ratio of mating types in all four subpopulations (except for SG2), MAT1-1 mating type predominate. All subpopulations (except SG2) were assumed to be clonal. Explanation of recombination within the subpopulation SG2 may be the presence of natural reservoir of infection among wild animals. European isolates of subpopulation SG1 have been identified as a cause of the epidemic in Europe. This isolates were responsible for 78% of all infections in Europe and their morphology was very uniform (yellow-coloured colonies, no production of macroconidia, slow growth parameters). Strongly clonal reproduction was detected between these isolates, all of them were of mating type MAT1-1. The first detection of this genotype in Europe is dated around 2003 and its origin can be in North America where is located the center of genetic variability of *A. benhamiae this* and this population is genetically closely related. This hypothesis, however, should be more thoroughly tested. Microsatelite markers designed in this study represent suitable tool for future precise monitoring of the epidemic's progression, spread of virulent genotypes detection to other geographical areas and changes in the genotype spectrum in specific geographic locations.

Key words: dermatophytes, microsatellites, epidemiology, typization scheme, guinea pig, *Arthroderma benhamiae*