

## SUMMARY

*Malassezia pachydermatis* is a part of the physiological biota of the skin and mucous membranes of most mammals and birds. This opportunistic species causes mainly surface skin infections. However, in extreme cases can also cause fungemia in neonates and patients hospitalized in the intensive care units. Since *M. pachydermatis* is isolated almost equally from diseased animals and those without clinical symptoms of the disease, accurate diagnosis of infections caused by this yeast is a problem of great importance veterinary and medicine. Therefore, the isolation of these fungi from patients is not an equivalent to the identification of the etiologic agent of infection. According to a current state of knowledge, the problem of diseases associated with *M. pachydermatis* is correlated with the metabolic, hormonal and immunological state of the host.

In the light of a literature review, a significant question arises, whether the pathogenicity of *M. pachydermatis* is solely conditioned by host-dependent factors, or pathogenic strains have independent virulence mechanisms and the other factors only trigger their expression. In my work I put forward the following hypothesis: 'The occurrence of features that distinguish *M. pachydermatis* isolates from healthy or diseased animals indicates the presence of typically commensalic and potentially pathogenic strains within the species'.

In order to verify this hypothesis, I created a collection of *M. pachydermatis* strains isolated from dogs with *otitis externa* and dogs without symptoms of the disease. Then I determined and compared the overall genetic diversity and phylogenetic relationships of obtained isolates and, in the next step, I assessed the activities of intracellular and extracellular enzymes, as well as lipid and protein profiles within the studied groups of strains.

By the application of two different techniques, RAPD-PCR fingerprinting and nucleotide sequencing of ITS-1 fragments, I have demonstrated the high level of genetic diversity and an origin-dependent grouping scheme of the strains. These results indicate that *M. pachydermatis*

is a diverse and highly polymorphic species despite adaptations to the occupied ecological niche. In spite of the lack of any speciation signals between strains representing both groups and their high polymorphism, the existence of features differentiating both group of strains cannot be excluded. The separation of clades grouping mostly strains of the same origin supports the hypothesis assuming the existence of a group of potentially pathogenic strains within the species that are endowed with features that facilitate infection.

Results of lipid profiles, phospholipase activities and protein profiles comparison between representatives of both examined groups of *M. pachydermatis* strains also support that hypothesis. In my research, I have shown that the lipid and protein profiles of individual strains correlate to their origin. Particularly noteworthy is the fact that some features (lower content of ergosterol esters and total fatty acids as well as presence of nerve acid) were found only in the case of strains isolated from *otitis externa* irrespective of the culture conditions. In these strains, I also found the presence of specific proteins: the NADP-dependent mannitol dehydrogenase (EC 1.1.1.138) and ketol-acid reductoisomerase (EC 1.1.1.86) which can play an important role in the pathogenesis process. These strains also exhibited significantly higher phospholipase C activity in comparison to strains isolated from dogs without clinical symptoms of disease.

The obtained results do not allow to reject above mentioned hypothesis. The undeniable confirmation of the presence of typically commensalic and potentially pathogenic strains of *M. pachydermatis*. It would require further studies including other *Malassezia* species and additional clinical modeling. Distinctive attributes of the different strains can be used in order to precise diagnose the early steps of infection, prophylactic procedures application or even identification the risk groups prior to onset of clinical symptoms. The identified characteristics (phospholipase activity, presence of characteristic proteins and lipid profile) may become a good marker of strains pathogenicity what is particularly important due to increasing number of opportunistic infections in animals and humans.