

Abstract

The genus *Geosmithia* Pitt (Ascomycota: Hypocreales) belongs to fungi living in symbioses with bark beetles. Its original strategy is association with phloeophagous bark beetles (Coleoptera: Scolytinae). The *Geosmithia* shows strong affiliation to vector (bark beetles) worldwide and the spectrum of host plants is delimited by niche of vector. The genus includes the specialists to family Pinaceae, but also the generalists with wide range of host plants mainly belonging to broad-leaved trees. *G. morbida* changed its ecology from saprotrophic to pathogenic way of life and causes decline of *Junglans nigra* in the USA. Characteristics which allow its pathogenesis are not known. Another derived strategy, which occurred at least twice independently, is association with the ambrosia beetles. The ambrosia beetles create galleries in xylem with low nutritive value, and thus they cultivate ambrosia fungus, on which they are entirely nutritively dependent. The ambrosia fungi share convergent phenotype which leads to large terminal conidia and to ability of yeast growth.

This master thesis is focusing on study of the features, which are important for individual ecological groups: the specialists to family Pinaceae, the pathogene, the ambrosia fungi and the generalists. It is becoming apparent that the most important point in the symbiosis between fungi and bark beetles is nutritive benefit of the beetle, which is acquired through mycetophagy. For that reason I have focused on study of capability of fungi to acquire nutrition, thus make them available to the beetle (enzymatic profile), and on their nutrition potential (quantity of ergosterol and fatty acids). Because the correlation between the genome size and the cell size is found among wide range of organisms, it has been studied whether enlargement of conidia volume of ambrosia fungi is connected to enlargement of their genome sizes.

The enzymatic analysis clearly separated specialists from generalists. The generalists showed much broader enzymatic potential (Biolog method) and affinity with hemicellulose. On the other hand the specialists produced enzymes which decompose lignocellulose. Interesting species was pathogen *G. morbida* with ability to decompose both hemicellulose and lignocellulose. This enzymatic universality apparently bestows pathogenicity on this species. The ambrosia species were considerably distinguished by production of oleic fatty acid. Similar oleic fatty acid production showed sister species of ambrosial *G. microcorthyli*, *G. sp. 8* and *G. sp. CCF4200*. The ambrosia fungi produced conidia with largest volumes and genome sizes in genus (genome size of ambrosial *G. microcorthyli* was approximately double in size than its sister species). This demonstrates the significance of genome size in evolution of ambrosia fungi.

Key words: evolutionary ecology, *Geosmithia*, bark beetles, genome size, enzymatic profile, fatty acids, ergosterol.