ABSTRACT

Aspergillus is a speciose genus encompassing nearly 400 species that has significant economic impacts on human health, the food industry, biotechnology and pharmacology. The research included in this thesis focuses on current issues related to the generic concept, subgeneric classification and species delimitation in *Aspergillus*. It addresses the need for revisions of several sections or species complexes. It provides novel information regarding etiology of aspergillosis as well as the antifungal susceptibilities of several less common opportunistic pathogens.

The taxonomic section of the thesis contributes to the taxonomic stability and the new concept of the genus *Aspergillus*, which changed in response to the discontinuation of dual nomenclature in fungi. Sufficient arguments were collected (e.g., verification of monophyly, unifying phenotypic characters) for maintaining a broad concept of the genus and avoiding splitting it into several genera. All genera typified by sexual morphs and having *Aspergillus* asexual states were synonymized with *Aspergillus* and the appropriate names adopted; new combinations were made for teleomorphic species that lacked *Aspergillus* names. This thesis also contributed to infrageneric taxonomy of the genus via the proposal of four new sections in the subg. *Circumdati*, which were established for previously taxonomically unresolved or ambiguous *Aspergillus* species. In the lower level taxonomic studies, particular emphasis was placed on the species that are medically important or occur in indoor or cave environments. Monographs or definitive taxonomy using a polyphasic approach to species definition were provided for several sections or species complexes, namely, xerophilic members of sects. *Aspergillus* and *Restricti*, predominantly soil-borne and indoor species from sects. *Flavipedes*, *Jani*, *Nidulantes* and *Petersonii*, soil-dwelling opportunistic pathogens from *A. viridinutans* species complex (AVSC, sect. *Fumigati*) and mostly non-pathogenic members of the *A. unilateralis* clade (sect. *Fumigati*). Growth parameters in osmotic-temperature gradients were newly introduced for species differentiation of xerophilic aspergilli and proved to be taxonomically informative. Further taxonomic studies describing new taxa were performed in sects. *Candidi*, *Cremei* and *Usti*. In total, 41 new species were proposed, with contributions of the thesis author representing approximately 10% of overall *Aspergillus* species diversity. In addition, two new names, one new combination, 16 type designations and several dozens of synonymizations were proposed.

The thesis further addresses the definition of species boundaries in *Aspergillus* and specific issues limiting correct species delimitation, such as interspecific hybridization and paralogous genes. Species delimitation in *Aspergillus* was improved by the use of delimitation methods based on a multispecies coalescence model that are more robust and objective than currently used approaches. In contrast, the interpretation of *in vitro* mating experiments (biological species recognition) without a robust phylogeny is controversial, as exemplified by AVSC. Only a relatively minor group of heterothallic AVSC species readily generates sexual states *in vitro*, and interspecific mating assay analysis revealed that five different species combinations were biologically compatible and produced hybrids. Hybrid ascospores showed atypical surface ornamentation and significantly different dimensions compared to parental species, suggesting that species limits in the AVSC are maintained by both pre- and post-zygotic barriers. Consequences of interspecific hybridization are discussed. Reliable tools were provided based on codon usage bias analysis for distinguishing the paralogous β-tubulin genes *benA* and *tubC*, which have caused incongruencies in the phylogenies of black aspergilli, and *benA*-specific primer combinations were provided.

Spectrum of causative agents of systemic infections, otomycosis and superficial infections was elucidated in an epidemiological study comprising clinical samples from four regional institution in the Czech Republic. Almost

40 species were identified in clinical specimens with a high prevalence of cryptic or undescribed species. Their misidentification can influence the prognosis of patients because some of them demonstrate drug resistance to commonly used antifungals. Several clinical cases associated with rare or newly recognized pathogens were detailed. Species descriptions or correct names were provided for several clinically relevant species. *In vitro* antifungal susceptibility data were provided for AVSC and sect. *Candidi* species.