

2. Summary

Hypocreales fungi are the world-wide occurring producers of bioactive secondary metabolites. Among them, *Fusarium* species are common cereal pathogens, causing the most important plant diseases. They significantly reduce the quality of crops and affect the processing of food and feed due to mycotoxins' production, accumulated in plant and animal tissues (including human). Another group of fungi are entomopathogenic species belonging to the *Isaria*, *Beauveria* and *Cordyceps* genera, often used as an alternative to pesticides. The third group are fungi from *Trichoderma* genus, which are not pathogenic, but show a saprotrophic lifestyle and, because of their ability to synthesize various lytic enzymes, can colonize the rhizosphere as opportunistic plant symbionts. It has been shown that these fungi can produce toxic cyclodepsipeptides, mainly beauvericins (BEAs), beauverniatins (BEAEs) and enniatins (ENNs). Structurally, BEAs, BEAEs and ENNs belong to the non-ribosomal cyclic hexadepsipeptides, consisting of alternative three *N*-methyl-L-amino acids residues and three hydroxy acid residues. So far, 37 naturally occurring analogs of BEA, BEAE and ENN have been identified. BEAs, BEAEs and ENNs are synthesized by non-ribosomal peptide synthases (NRPSs). One of them is beauvericin synthase (BEAS), composed of a single, polypeptide chain with a molecular mass of 351 kDa.

The main objectives of this research, as a part of the doctoral dissertation, were to characterize the differences between the sequenced fragments of beauvericin synthase among the analyzed *Hypocreales* fungal isolates and to determine their toxigenic potential through qualitative and quantitative analyses of hexadepsipeptides. The divergence of *BEAS* was determined based on phylogenetic analyses, and the efficiency of mycotoxins' biosynthesis using mass spectrometry.

Molecular analyses showed high variability of sequenced *BEAS* fragments between fungi belonging to *Hypocreales* order, while chemical analyses revealed differences in the biosynthesis of BEAs, BEAEs and ENNs. Qualitative analyses allowed to draw a unique metabolic profile for each tested fungal strain. Varying potential of hexadepsipeptide biosynthesis may result from the adaptation of isolated fungal species to specific ecological niches and could arise independently in the species belonging to *Hypocreales*. The results obtained broaden the knowledge on hexadepsipeptides' biosynthesis concerning the diversified lifestyle and evolutionary specialization of these ecologically divergent taxa. In the future, a better understanding of the mechanisms of mycotoxins biosynthesis could contribute to a wider

use of entomopathogenic fungi as biocontrol agents. It can also help in molecular diagnostics of new depsipeptide toxins as a better and faster method of identification, which would be beneficial for protecting human and animal health. Moreover, possible efficient use of the produced compounds as potential components of new therapeutic substances will be facilitated.