Penicillium digitatum polypeptides detected by MALDI-TOF-mass-spectrometry of cell culture extract

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OBJECTIVES

The aim of this study is to determine the specificity of the polypeptides of the low molecular weight fraction of *P. digitatum* proteome to different fungal taxa that constitute the systematic position of this species.

METHODS

Annotations of mass-spectra of *P. digitatum* strains isolated from hospital air, contaminated spices and damaged architectural materials were included in the study. The original mass-spectra, the composition of the annotation and search for homologous proteins were made as described previously [Riabinin I.A. et al., 6thAdvances Against Aspergillois, 2014; Riabinin I.A., Vasilyeva N.V., 3rdCRICMID, 2016].

RESULTS

As a result of this work it was found that the mass-spectrum of *P. digitatum* cell extract in the Mr range from 2 to 20 kDa contains up to 35 peaks that are formed by up to 33 peptides and light proteins. Among the spectra-forming polypeptides 13 of them (39.4%) are unique to the *P. digitatum*, 10 (30.3%) are specific to the genus *Penicillium*, 4 (12.1%) are specific for members of *Trichocomaceae* family, 5 (15.2%) are found in other ascomycetes, 1 (3%) have homologs in fungi of various taxonomic position. In the latter case 1-family «carbohydrate-binding protein module»are found not only in the Ascomycetes, but also in typical representatives of the basidiomycetes from genera *Sistotremastrum*, *Sphaerobolus* and *Exidia*. Many peptides unique for *P. digitatum* form peaks which were compactly concentrated in the range of m/z 3354 –3780. Among other members of the genus *Penicillium* homologous peptides were found in *P. rubens*, *P. camambertii*, *P. chrysogenum*, *P. italicum*, *P. roqueforti*, *P. freii*, *P. expansum*, *P. nordicum*, *P. brasilianum*, *P. arizonense* *P. griseofulvum* and *P. oxalicum*. Interestingly, homologs for 11 of *P. digitatum* polypeptides that were identified in proteome of other fungi are elements of much larger proteins, but information summaries from UniProt database for original peptides characterized them as separate molecules.

CONCLUSION

P. digitatum is characterized by full accessibility to annotation of the low molecular weight portion of the spectrum, which almost cannot be deciphered in *Aspergillus* spp. Because typical mass-spectra-profiles of *P. digitatum* in the Fungi Library database (Bruker Daltonik GmbH, Germany) have peaks of ions with Mr> 9 kDa, which could not be detected in this study, further research of the low molecular weight fraction of the *P. digitatum* proteome will be continued.

Fig. 1. Peaks of mass-spectrum of the *P. digitatum* cellular extract found in the mass-spectra of other fungi.

Fig. 2. Tertiary structure reconstruction of elected *P. digitatum* spectra-forming polypeptides with using Swiss-Model (<https://swissmodel.expasy.org/>) [Biasini, M. et al. Nucleic Acids Res. 42, W252-W258, 2014].