BOOK OF ABSTRACTS

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COMPLETE GENOME SEQUENCE OF THE GREEN MOULD PATHOGEN TRICHODERMA PLEUROTI

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Trichoderma pleuroti (syn. T. pleurotum S.H. Yu & M.S. Park) is a filamentous ascomycete species belonging to the Harzianum clade of the genus. This species is one of the causal agents of the green mould disease emerging in the cultivation of oyster mushroom (Pleurotus ostreatus). T. pleuroti possesses gliocladium-like conidiophore morphology, which is substantially different from that of the genetically closely related other oyster mushroom green mould agent T. pleuroticola showing pachybasium-like properties. The growth of T. pleuroti is slower or impaired on a series of carbon sources as compared with T. pleuroticola, suggesting that T. pleuroti was accompanied with the loss of the utilisation ability of certain carbon sources. T. pleuroticola is dominant in samples from Italian Pleurotus farms, while the majority of the isolates from Hungary belong to the species T. pleuroti.

The aim of this study was to determine the complete genome sequence of T. pleuroti TPhul, a green mould isolate derived from oyster mushroom cultivation substrate at a mushroom farm in Kecskemét, Hungary. The strain was identified by the sequence analysis of the internal transcribed spacer (ITS) region and a fragment of the translation elongation factor 1α encoding gene tef1, and deposited in the Szeged Microbiology Collection (szmc.com) under the accession number SZMC12454. Fungal genomic DNA was isolated with Qiagen DNeasy® Plant Mini Kit. For the library construction, NEBNext® Fast DNA Library Prep Set for Ion Torrent was used following the 200 and 400 bp protocols with minor modifications. The whole genome sequencing of strain T. pleuroti TPhul was performed on Ion Torrent Next-Generation Sequencing platform both with 200 and 400 bp chemistries on Ion 316 Chip v2. Genome assembly was carried out with SPAdes Genome Assembler 3.6.0 (http://bioinf.spbau.ru/spades). The size of the assembled 2397 contigs was estimated to be 38 Mb with BBMAP (https://sourceforge.net/projects/bbmap). The modular genome annotation pipeline TrichoCODE (http://trichocode.com) – that includes a high quality training set for ab initio gene prediction in Trichoderma – could identify 9928 genes in the genome. Stand-alone BLAST analysis (https://blast.ncbi.nlm.nih.gov/Blast.cgi) of the predicted genes was performed and the results evaluated in tabular format.
The availability of the complete genome sequence of *T. pleurotus* opens a series of new possibilities to study the genetic background of the oyster mushroom green mould disease development.

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