ECCO XXXVI

European Culture Collections' Organisation Annual Meeting



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Brno, Czech Republic 13-15 September, 2017 Prepared by *Czech Collection of Microorganisms* (Department of Experimental Biology, Faculty of Science, Masaryk University, Kamenice 5, Building A25, Brno 625 00, Czech Republic).

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The wording of the abstracts texts were not subjected to revisions and/or corrections; they are presented as provided by individual authors.

Published by: © Tribun EU, s. r. o., Brno, 2017

ISBN 978-80-263-1327-4

Production run: 100 copies

ECCO XXXVI

PO2 Fomes fomentarius lineages in the Mediterranean biogeographical region

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Fomes fomentarius is a common and economically important woodrotting fungus in deciduous forests and prefers different main hosts depending on the region. The fungus often arrives at dead wood relatively early or colonizes already a living tree as a parasite but contrary to other early arriving fungi it exhibits better combative abilities and is not easily replaced (Větrovský et al., 2011). It is distributed within the northern hemisphere in Europe, North Africa, North America, China and Japan. Until recently, F. fomentarius had been considered a homogeneous species but the existence of distinct ITS lineages/sublineages among its strains has been established. Studies were based on ITS rDNA sequence analysis and host preference evaluation. Firstly there were lineages A and B, after more detailed investigation the lineage A was separated into sublineage A1 (consisting of strains isolated from North America) and sublineage A2 (consisting of strains only from Europe). The lineage B consists of strains from Europe and Asia (Gáper et al., 2016). There is little information available about this polypore sequences originating from Portugal so the aim of the present study was to evaluate genetic variability in F. fomentarius in southwestern part of Europe and enrich so far known data in GenBank and biodiversity databases. Results showed that the lineage that occurs in Portugal, and generally in Mediterranean region, is the lineage B. We can conclude that Fomes fomentarius is a non-homogenous medicinal mushroom and its lineages correlate with geographical distribution and host preference.

Větrovský T, Voříšková J, Snajdr J, Gabriel J, Baldrian P., 211. Ecology of coarse wood decomposition by the saprotrophic fungus Fomes fomentarius. Biodegradation, 22(4):709-18

Gáper J., Gáperová S., Pristaš P., Náplavová K. 2016. Medicinal value and taxonomy of the Tinder polypore, Fomes fomentarius (Agaricomycetes): A Review. International Journal of Medicinal Mushrooms 18 (10): 851-859.