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ABSTRACTS

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Akadémiai Kiadó, Budapest
MEMBER OF WOLTERS KLUWER GROUP

GENETIC CHARACTERIZATION OF GRAPE-INFECTING *BOTRYTIS CINEREA* POPULATIONS FROM THE EGER WINE REGION, HUNGARY

ERZSÉBET SÁNDOR[1], KÁLMÁN Z. VÁCZY[2], IRINA DRUZHININA[3], CHRISTIAN P. KUBICEK[3], GYÖRGY J. KÖVICS[1], LEVENTE KARAFFA[4]

[1]Department of Plant Protection, Centre for Agricultural Sciences, Faculty of Agriculture, University of Debrecen, Böszörményi út 138, H-4032 Debrecen, Hungary; [2]Research Institute for Viticulture and Enology Kőlyuktető, Pf. 83, H-3300 Eger, Hungary; [3]Department of Chemical Engineering, Research Area Gene Technology and Applied Biochemistry, TU Wien, Getreidemarkt 9-1665, A-1060 Wien, Austria; [4]Department of Microbiology and Biotechnology, Faculty of Science, University of Debrecen, Egyetem tér 1, H-4100 Debrecen, Hungary

Botrytis cinerea (teleomorph: *Botryotinia fuckeliana*) is a phytopathogen fungus that causes grey mould on a wide range of plants in temperate regions worldwide. *B. cinerea* has been shown to have several variable genetical and physiological traits, and it has developed resistance against most of the fungicides used to control it.

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Modern phytopathology is increasingly taking into account the genetic structure of pathogen populations in order to gain insight into control strategies. In light of recent findings concerning *B. cinerea*, it appears that a major cause of the difficulties in managing plant disease indeed arises from our limited understanding of the genetic structure of *B. cinerea* populations. The complexity and variability of this fungus makes it difficult to control and may actually reflect the existence of several distinct populations of which we were unaware, and which may have different characteristics.

Our aim was to evaluate the genetic diversity of *B. cinerea* in the Eger wine region and to determine whether the three genetically different groups *transposa*, *vacuma* and *boty*, earlier described in France and Chile, were present in this region. *Transposa*, *vacuma* isolates were found and, in addition, isolates containing *Flipper* alone (*flipper* isolates) were also detected. Sequence analysis of MSB1 minisatellite and *tef1* (translation elongation factor 1) revealed a high degree of genetic diversity, with no widespread clonal lineages.

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