



Conference Abstract

Molecular identification and phylogenetic relationships of *Colletotrichum* isolates pathogenic on cultivated plants in Bulgaria

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Abstract

Fungi of the genus *Colletotrichum* are causal agents of plant diseases with constantly growing economic importance. Accurate pathogen identification is a significant prerequisite for effective disease control. The aim of the present investigation was to clarify the species affiliation of *Colletotrichum* isolates obtained from different hosts in Bulgaria and to determine the phylogenetic relationships between them by applying DNA barcoding. Thirty-five fungal isolates obtained from five botanical families (Solanaceae, Rosaceae, Musaceae, Cucurbitaceae and Caryophyllaceae) were morphologically characterized and subjected to molecular analysis based on four fungal barcode markers – the primary ITS barcode and the secondary marker regions ACT, EF-1a and TUB2 (Fig. 1). Three of the barcodes (ITS, ACT and TUB2) showed complete success rate of PCR amplification and sequencing and proved efficient for reliable identification at species level. BLAST analyses identified eleven *Colletotrichum* species assigned to five different complexes – *C. coccodes*, *C. acutatum*, *C. gloeosporioides*, *C. dematium* and *C. spaethianum*. The resolution power of ITS region was not sufficient to discriminate interspecies variations within *C. coccodes*, *C. dematium* and *C. spaethianum* complexes confirming the requirement for secondary barcodes in order to resolve the genetic variability of the *Colletotrichum* isolates. DNA barcoding analyses revealed that the highest species variation was observed among the isolates from pepper (*Capsicum annuum*). Interestingly,

an isolate from the same host identified as *C. truncatum* on the basis of morphological characters appeared to be *C. circinans* when applying DNA barcode markers. According to our knowledge, this species has not been reported as a causal agent of pepper anthracnose. Data obtained in this study improve our understanding of the genetic diversity within the *Colletotrichum* population pathogenic on cultivated plants in Bulgaria.

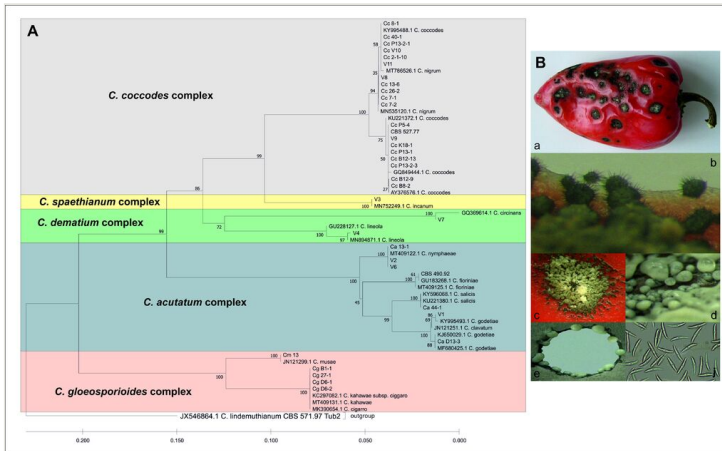


Figure 1. [doi](#)

A. Phylogenetic tree showing the taxonomic assignment of the *Colletotrichum* isolates based on TUB2 barcode marker. B. *Colletotrichum circinans* on pepper fruit (*C. dematium* complex); a. natural infection; b. black acervuli with dark setae; c, d, e. Sporulation of the isolate – in vivo and in vitro on PDA; j. conidia.

Keywords

DNA barcoding, fungi, anthracnose, pathogen identification

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Conflicts of interest

The authors confirm that there is no conflict of interests.