Abstract:

Over 150 isolates of Colletotrichum obtained from olive and various other host plants were separated into two large groups, tentatively identified as C. gloeosporioides and C. acutatum, on the basis of growth rate, optimal growth temperature and sensitivity to benomyl. The electrophoretic analysis of four isozymes revealed considerable genetic variability within each group. The isolates of the causal agent of olive anthracnose from southern Italy were a subgroup with a distinct electrophoretic phenotype within the C. acutatum species complex and were separated into two vegetative compatibility groups (VCGS), one including the isolates from Apulia and the other the isolates from Calabria and Sardinia. Oligonucleotide primers synthetized using DNA sequences from the ITS 1 region of rDNA were used for PCR-amplification of DNA. The isolates of both VCGS produced DNA amplification products with C. acutatum-specific primers Ca Int-1 and Ca Int-2. Conversely, no amplification products were obtained with these isolates using the C. gloeosporioides-specific primer Cg Int. Random amplified polymorphic DNA banding patterns of the isolates, obtained with 16 universal 10-mer primers, indicated that the causal agent of olive anthracnose in southern Italy represents a taxon clearly distinct from both the C. gloeosporioides species complex and other biotypes of C. acutatum, such as those causing olive anthracnose in Portugal and strawberry anthracnose in southern Italy and in California, respectively.