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Development of SNP-based markers for identification of *Colletotrichum gossypii*

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Colletotrichum gossypii, a fungus of phylum Ascomycota, is a causal agent of anthracnose disease in *Gossypii hirsutum* (upland cotton). Previous studies reveal that close genetic similarities of *Colletotrichum gleosporoides* species complex do not let easy development of diagnostic assay. Their spore size and cultural characteristics have recently been reported to vary in different geographical areas. This study was conducted for characterization, evaluation of morphological variance, growth pattern and pathogenicity, and development of molecular diagnostic assay of anthracnose causal agent, *Colletotrichum gossypii*, in cotton plants of different regions of China. To overcome any ambiguity in morphological and pathogenic characteristics, a set of primers targeting the beta-tubulin gene of *Colletotrichum gossypii* was designed. Single nucleotide polymorphisms were used to identify *Colletotrichum gossypii* at species level using DNA sequence of the β -tubulin gene. This set of primers only amplified *Colletotrichum gossypii* of genus *Colletotrichum*. There remained no need for further identification steps like sequencing, BLASTn and alignment.

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