BACKGROUND

Fusarium species have recently emerged as major opportunistic agents in immunocompromised patients. Moreover, Fusarium species are considered the third most common fungal genus after Candida and Aspergillus isolated from systemic infections in bone marrow transplant patients. More than 90% of Fusarium infections are caused by three species: F. solani, F. proliferatum, and F. oxysporum, each responsible for about 30% of clinical cases. The diagnosis of Fusarium infection is based on clinical suspicion and histopathology. The use of rep-PCR (replicase-based PCR) technology and rep-PCR primers is covered by U.S. patents (5,691,136 and 5,523,217) and by international patents for Canada and Europe.

BLAST on NCBI. Rep-PCR was performed using the Diversilab (Applied Biosystems, CA). The products were purified using PERFORMA® DTR Gel and Fus2 oligonucleotides identification was initially determined by 28S rRNA sequencing. A previously published method that utilizes Fus1 differentiation.

A repetitive sequence-based PCR (rep-PCR) method for identification of species level is important for epidemiological purposes and may be absolutely necessary as some new antifungal systemic infections in bone marrow transplant patients. More than 90% of Fusarium infections are caused by three species: F. solani, F. proliferatum, and F. oxysporum, each responsible for about 30% of clinical cases. The diagnosis of Fusarium infection is based on clinical suspicion and histopathology. The use of rep-PCR (replicase-based PCR) technology and rep-PCR primers is covered by U.S. patents (5,691,136 and 5,523,217) and by international patents for Canada and Europe.

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