Molecular identification of *Penicillium* sp. isolated from citrus fruits

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Abstract

Penicillium is one of the most important postharvest pathogens of citrus fruits worldwide. It induces blue or green mold disease, a decay that can lead to significant economic losses during storage. Based on internal transcribed spacer (ITS) sequences, seven *Penicillium* species and one closely related *Talaromyces variabilis* were identified from 30 rotten samples of citrus fruits marketed in Qena. *Penicillium expansum* was the most common species, recovered from 16.7% of the samples, followed by *P. chrysogenum* (10%) and *P. polonicum* (10%). Sixteen isolates were tested through inoculation on healthy citrus fruits; the data exhibited that 68.7% of isolates were highly virulent. A "Specific Gene Random Primer Polymerase Chain Reaction (SGRP-PCR)" marker technique indicated that the genetic similarity among *P. expasum* ranged from 49.4 to 85.7%, and a relatively correlation was found between SGRP band profile and species origin. Patulin was detected in 40% of *P. expansum* isolates. This study provided a useful molecular approach to identify different *Penicillium* species by sequencing ITS region, focus on the pathogenicity, compare between *P. expansum* isolates and their ability in patulin production.