Title Identification of airborne *Penicillium* species in the south African litchi export chain

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## **Abstract**

Penicillium is one of the most common fungal genera encountered in the environment. Being a natural soil inhabitant, it's presence on litchi fruit may indicate cross-contamination. This can cause major losses to the fruit export industry, as postharvest decay of litchi fruit by *Penicillium* species dramatically reduces the shelflife of the fruit. This study was aimed at identifying 58 dominant Penicillium groups throughout the South African litchi export chain. Morphological, as well as molecular methods such as DNA sequencing and Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP) were used in the identification. The Internally Transcribed Spacer (ITS) and beta tubulin (b-tubulin) gene regions were analysed in this study. Eighteen of the most dominant *Penicillium* species isolated during the 2004-2005, 2005-2006 and 2006-2007 seasons were identified as P. glabrum, P. biourgeianum, P. citreonigrum, P. paneum, P. solitum, P. crustosum, P. expansum, P. brevicompactum, P. polonicum, P. citrinum, P. chrysogenum, P. bialowiezense, P. echinulatum, P. corylophilum, P. commune, P. piscarium, P. sumatrense and P. italicum. Fourteen of these 18 species could be differentiated from one another through PCR-RFLP of the b-tubulin gene region. The remaining four groups (P. solitum, P. crustosum, P. commune and P. echinulatum) showed little variation in the banding patterns of the ITS region, while the b-tubulin region appeared to be highly variable. The ITS gene region is highly conserved and serves as a taxonomic indicator for Penicillium species while b-tubulin is more variable and can be used to differentiate between closely related species.