Abstract

The strain L47 of *Aureobasidium pullulans* is an effective biocontrol agent of postharvest diseases. When applied in the field before harvesting it requires a specific monitoring method to evaluate colonization and dispersal in the environment. The randomly amplified polymorphic DNA technique (RAPD) was used for a preliminary screening of *A. pullulans* genetic variability among 205 isolates. This approach allowed the selection of a 1.3-kb fragment (L4) present solely in isolates L47 and 633. In Southern blots, a digoxigenin (DIG)-labeled L4 amplicon specifically recognized the corresponding fragment present in the polymorphic pattern of L47 and 633. The L4 fragment was cloned, sequenced, and used to design two sequence-characterized amplification region (SCAR) primers and a 242-bp riboprobe. Both the SCAR primers and the 242-bp DIG-labeled riboprobe were highly specific for L47. In classical polymerase chain reaction (PCR), with a series of 10-fold dilutions of L47 DNA, the limit of detection was 20 pg/µl. The Ap13 primer was also modified to obtain a Scorpion primer for detecting a 150-bp amplicon by fluorescence emitted from a fluorophore through a self-probing PCR assay. This assay specifically recognized the target sequence of L47 strain over a number of other *A. pullulans* isolates in field-treated grape berry washings. The limit of detection was 105 cells per ml, i.e. 10 times higher than the limit of the CFU method. The method is also proposed as a way to demonstrate the ability of L47 strain to penetrate the epidermis of sweet cherry fruits and to track it in the mesocarp.