A. flavus species have been increasingly recognized as major opportunistic pathogens, especially among HIV, cancer, transplant, and burn patients. There are more than 100 species in the A. flavus group, although three, A. flavus, A. fumigatus and A. terreus account for the majority of invasive aspergillosis (IA). A. flavus, A. fumigatus and A. terreus are rarely encountered as causes of IA. The alarming increase in the reports of these types of infections and their associated mortality rates have created the demand for a fast and accurate method for fungal identification. Traditional methods of identification for A. flavus species include laborious and subjective morphological tests that can take several days to resolve at the species level. These molecular techniques have been extensively used for typing A. flavus isolates. One of these methods, random amplified polymorphic DNA (RAPD) analysis, is difficult to interpret and lacks reproducibility. Strain typing length polymorphisms (RFLP) analysis along with southern hybridization may be tedious and labor intensive. Polymorphic microsatellite markers (PMM) and a RAPD based typing method are less automated and too specific for clinical identification applications. Previous reports describe the application of a repetitive-sequence-based PCR (rep-PCR) method for bacterial strain typing and for characterizing the genetic relatedness among Candida species isolates. These findings support the potential of rep-PCR for use in fungal identification and strain-level discrimination. We present the results of rapid molecular typing of A. flavus species using a commercially available automated rep-PCR assay system, the DiversiLab System™ (Fig. 1).