Genetic structure of *Aspergillus flavus* isolates in hospital environments and their possible public health hazards

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**Introduction:** *Aspergillus flavus* is the second most important *Aspergillus* species causing human infections in tropical countries. Despite an increasing number of infections of *A. flavus* in Iran, the molecular epidemiology of clinical and environmental strains has not been well studied. We used a panel of nine microsatellite markers to analyze the genetic relatedness of clinical and environmental *A. flavus* isolates.

**Materials and Methods:** The environmental and clinical *A. flavus* isolates in two hospitals were evaluated for their genetic relatedness. The *A. flavus* isolates were genotyped by using a panel of nine microsatellite markers that consists of three multiplex PCRs that target each three loci.

**Results:** The STR typing of 143 pure *A. flavus* isolates (n=119 clinical and n=24 environmental) revealed 118 different genotypes could be recognized. Among all genotypes, 102 genotypes were only found once and 21 clusters of related genotypes could be identified differing only at a single locus. A possible outbreak at a pulmonary ward was discovered. Four environmental hospital *A. flavus* isolates with four clinical isolates were of the same genotype.

**Conclusion:** The genetic heterogeneity of *A. flavus* isolates probably reflects the diversity of conidia because they were all collected from different patients either at different wards of hospital, or at different timepoints. High resolution typing method such as microsatellite analysis in the present study yielded better understanding of the molecular epidemiology of *A. flavus*. 