Molecular epidemiology and antifungal susceptibility profiles of *Aspergillus terreus* complex in Iran

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Objectives

Aspergillus terreus is emerging as an etiologic agent of invasive aspergillosis in immunocompromised individuals. Infections caused by *A. terreus* are difficult to treat because of the intrinsic resistance to amphotericin B, and higher mortality compared to infections due to other *Aspergillus* species. The aim of the present study was to determine the in vitro antifungal activity of amphotericin B and 11 comparators against clinical and environmental *A. terreus* isolates and the genetic diversity and population structure of these isolates in Iran.

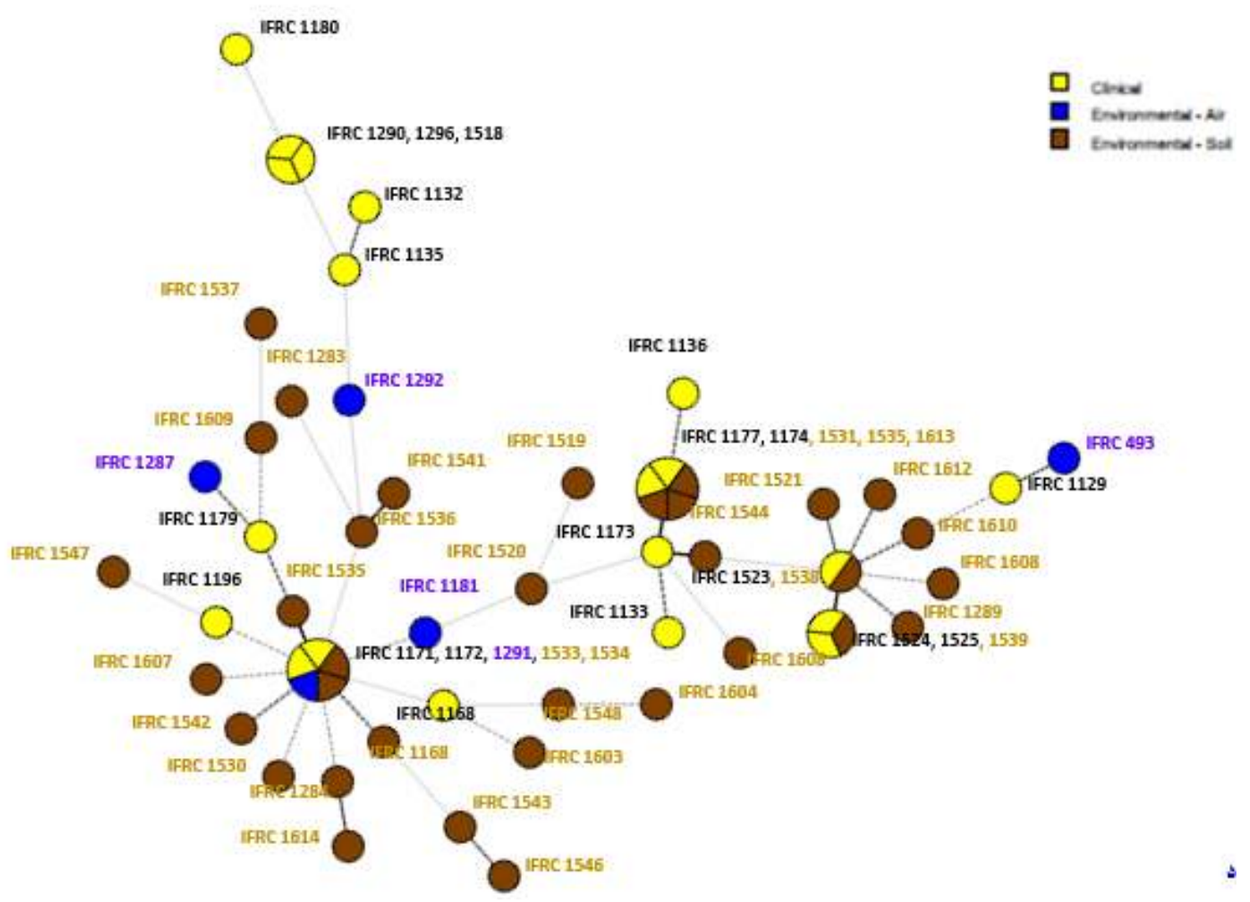
Methods

A panel of 81 *A. terreus* isolates from clinical (n = 36) and environmental (n = 45) sources were collected in five different cities. The population structure of *A. terreus* isolates was determined using microsatellite based typing (STR) technique. Additionally, in vitro antifungal susceptibility was performed using the CLSI M38-A2 procedure.

Results

Molecular identification showed that 66 and 15 isolates were *A. terreus sensu stricto* and *A. citrinoterreus*, respectively. The β-tubulin gene phylogenetic tree yielded 4 distinct clades and clade 1 represented 69.1% of *A. terreus* isolates. All of 81 *A. terreus* isolates were subjected to microsatellite typing using a panel of nine short tandem repeats to evaluate the genetic relatedness between the isolates. Twenty two isolates revealing no amplification at >2 loci and were excluded from the analysis.

The results showed a high genetic diversity revealing 46 distinct genotypes among 59 *A. terreus* isolates. All the nine markers used for STR typing of *A. terreus* species had highly polymorphic. Genetic Diversity Index or Simpson's index (D) in this study was calculated 0.93. The results of susceptibility tests exhibited that amphotericin B had the highest MICs (MIC range, 0.125 to 4 µg/ml; MIC90, 2 µg/ml), followed by terbinafine (MIC range, 0.002 to 1 µg/ml; MIC90, 1 µg/ml). Only one isolate (1/81) showed amphotericin B MIC above the epidemiologic cutoff value (ECV). None of the isolates had a MIC of ≥ ECV for voriconazole, itraconazole and posaconazole.



Conclusion

The reasons for the difference in amphotericin B susceptibility patterns between studies remain unknown. The genetic and species diversity, clinical, environmental and ecological factors in *Terrei* section on various amphotericin B susceptibility profiles in different countries should be considered more as the main reasons associated with these differences.

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