ABSTRACT

The incidence of fungal infections is increasing progressively. *Candida* is a part of normal microflora of body and may act as an opportunistic pathogen. This organism is a leading agent associated with blood stream infections. A total of 72 isolates of *Candida* species obtained from National Culture Collection of Pathogenic Fungi at Post Graduate Institute of Medical Education and Research, Chandigarh, India were characterized. All the isolates were confirmed upto species level by studying their phenotypic and biochemical characteristics. These isolates were further studied for their susceptibility to fluconazole by disc diffusion and micro broth dilution methods. The isolates were distinguishable on the basis of their phenotypic traits. Majority of the isolates (51 out of 72) (70.83%) were sensitive to fluconazole, 6 were sensitive dose dependent (SDD) and 15 exhibited resistance to this drug. Among the resistant species, *C. albicans* and *C. parapsilosis* figured at the top followed by *C. tropicalis*, *C. guillermondii* and *C. glabrata*. The resistant strains (15) and selective sensitive strains (3) were further studied for selective virulence traits such as protease, phospholipase and gelatinase production, hemolytic and biofilm forming abilities, production of hyphae on solid media, adherence ability and agar invasion were studied in vitro. The Protease activity was found in fluconazole resistant isolates, the phospholipase, hemolytic, agar invasion, hyphae formation, biofilm formation and adherence was maximum in *C. albicans* isolates. Variation in the nucleotide sequences and corresponding amino acid sequences of the amplicons of ERG11 gene of different *Candida* species reflected that such variations might be responsible for drug resistance. The variations in amino acid sequences has been observed at positions 150, 154, 157, 158, 161, 217, 235, 255, 265 and 277 when compared with standard published sequences. However, further studies are required in this regard. The present study would be useful in better characterization of *Candida* species from clinical samples and it might help not only in determining the correlation between the virulence and drug resistance but also in better understanding fungal pathogenesis.