

Indian Prevalence of Antifungal Resistant Species of *Candida*

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DESCRIPTION

A consistent estimate of antifungal resistance in immunocompromised and predisposed patients is imperative to determine the spread of life-threatening fungal infections led by species of *Candida*. Conventionally, the Antimicrobial Resistance programs (AMR) neglected antifungals from resistance drugs as fungal pathogens have been widely underplayed as a menace to human health [1,2]. The reason behind the negligence is the biological divergence that obscures the assimilation of antifungals into a presented list of AMR. The concern regarding emerging antifungal resistance has traversed real-world and various equivalents subsist among drug-resistant pathogens [3]. Still, the fungal domain is left to estimate the exact scenario of *Candida* prevalence, distribution and resistance pattern.

In this pursuit, we retrieved the reported data from January 1978 to March 2020 referring to the keywords “*Candida*”, ‘Antifungal Drug Resistance’, (*Candida* and Antifungal Resistance) and India; (Candidemia and Antifungal Resistance) and India; (Candidiasis and Antifungal Resistance) and India”. A systematic PRISMA approach was implemented using the inclusion/exclusion criteria. Subsequently, we squeezed the data to present the exact vision of the distribution, prevalence and antifungal resistance of *Candida* species in India [4]. Consequently, we studied 106 full-text articles that covered the demographic, clinical, quantitative, qualitative, and diagnostic detail of included subjects. The data revealed no relation between disease occurrences with age and gender. A frequent number of studies are reported from the southern zone. A total of 15 antifungals are widely used to treat the infection. Blood is depicted to be the major source of *Candida* infection. Nosocomial diseases are marked as the most predisposing factor for infection. The *C. albicans* is commonly identified isolates among India. In addition, *C. tropicalis*, *C. glabrata*, *C. parapsilosis* and *C. krusei* followed the prevalence of *C. albicans*.

The emergence of antifungal drug resistance in *Candida* species has led to increased morbidity and mortality in immunocompromised patients [5]. The fact enforced the direction of systematic review towards the pattern of resistance

in *Candida* pathogen. Azoles and echinocandins are prescribed on regular basis in India. Among azoles, ketoconazole, miconazole, fluconazole and itraconazole are at the top of the list of resistant drugs for the treatment of infection. *C. albicans*, *C. tropicalis* and *C. glabrata* are observed to be highly resistant to existing drugs. *C. parapsilosis* demonstrated the dose-dependent resistance for voriconazole. The reason behind azole resistance may include i) extensive use, ii) lack of knowledge, iii) poor diagnosis, iv) prescription without diagnosis and v) use in agriculture. In brief, the review illustrated the emergence of drug resistance in all Indian species of *Candida*.

However, the systematic review presents the data that can be the point of reference for reported findings on *Candida* species in India; we didn't perform the meta-analysis due to the paucity of the required data. The search strategy reported in the review is pretty good but modification in inclusion/exclusion criteria could decrease the scarcity of data. Conclusively, we will lose some good studies but allow simple, quick and real set of data that could improve the results with less bias using meta-analysis. Due to the absence of full text, some potential citations were removed without checking their eligibility which could account for selection bias. Finally, the potential effect of gender, age, socioeconomic status, and lifestyle of the included patients on the prevalence of antifungal resistance could not be analyzed because of the unavailability of data in many of the included studies. Moreover, the study is limited to Indian data only. Thus, the worldwide analysis might be helpful in future to reveal the exact country-wise magnitude of antifungal resistance in each species of *Candida*.

REFERENCES

1. Fisher MC, Gurr SJ, Cuomo CA, Blehert DS, Jin H, Stukenbrock EH, et al. Threats posed by the fungal kingdom to humans, wildlife, and agriculture. *MBio*. 2020;11(3):e00449-e0020.
2. Rodrigues ML, Nosanchuk JD. Fungal diseases as neglected pathogens: A wake-up call to public health officials. In *Advances in Clinical Immunology, Medical Microbiology, COVID-19, and Big Data* 2021;399-411.
3. Ksiezopolska E, Gabaldón T. Evolutionary emergence of drug resistance in *Candida* opportunistic pathogens. *Genes*. 2018;9(9):461.

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4. Verma R, Pradhan D, Hasan Z, Singh H, Jain AK, Khan LA. A systematic review on distribution and antifungal resistance pattern of *Candida* species in the Indian population. *Medical mycology*. 2021;59(12):1145-1165.
5. Verma R, Pradhan D, Maseet M, Singh H, Jain AK, Khan LA. Genome-wide screening and in silico gene knockout to predict potential candidates for drug designing against *Candida albicans*. *Infection, Genetics and Evolution*. 2020;80:104196.