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Short tandem repeat genotyping of Indian *Candida tropicalis* isolates reveals intrahospital cross transmission

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Poster session 2, September 22, 2022, 12:30 PM - 1:30 PM

Candida tropicalis is a clinically relevant yeast that causes candidemia in humans with a high mortality rate. The yeast primarily infects immunocompromised patients and causes outbreaks in health care facilities and is the predominant *Candida* species from clinical specimens in India. Antifungal-resistant isolates have been reported. Here, we applied a novel short tandem repeat (STR) *C. tropicalis* typing scheme to a collection of 402 clinical and environmental Indian isolates from New Delhi. Multiple large clusters ($n = 7$) containing more than 2 isolates were detected, and allocated to individual hospitals, except for the largest cluster. This cluster contained 14 isolates from two different hospitals, suggesting cross-transmissions. Two closely related clusters are allocated to the same two hospitals. Altogether, a novel high-resolution STR genotyping for *C. tropicalis* revealed hitherto unrecognized clusters of hospital transmission.

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Development of a multiplex PCR short tandem repeat typing scheme for *Candida tropicalis*

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Candida tropicalis is a clinically relevant yeast that causes candidemia in humans with a high mortality rate. The yeast primarily infects immunocompromised patients and causes outbreaks in health care facilities. Antifungal-resistant isolates have been reported. Here, we report a short tandem repeat (STR) typing scheme, for *C. tropicalis* to enable fast, cost-effective, and high-resolution genotyping. This novel typing approach was applied to 117 clinical isolates. For the development of the typing scheme six novel STR markers were selected, combined into two multiplex PCRs, and used to type 117 *C. tropicalis* isolates, resulting in the identification of 104 different genotypes. The outcome of STR typing of 10 isolates was then compared to single nucleotide polymorphism (SNP) calling from whole genome sequencing (WGS). Isolates with >111 SNPs were also differentiated by the STR assay. Two isolates that were identical according to SNP analysis were separated by STR typing in one marker. To test specificity, STR typing was applied to 15 related yeast species and we found no amplification of these targets. For reproducibility testing, two isolates were typed independently 5-times, which showed identical results in each experiment. In summary, we developed a reliable, rapid, and high-resolution STR genotyping for *C. tropicalis*, which was found to correlate well to SNP calling by WGS.