

In vivo* colonization and pathogenic potential of *C. africana

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Abstract

Candida albicans population displays high genetic diversity illustrated by 18-well differentiated genetic clusters. The most distinctive cluster of its population – Cluster 13, also known as *Candida africana* includes strains first described as atypical *C. albicans* isolates of vaginal origin and showing apparent tropism for the female genital tract. In our study, we explored colonization and pathogenic potential of *C. africana* in four *in vivo* mice models, namely gastrointestinal tract (GIT) colonization, oropharyngeal candidiasis (OPC), vulvovaginal candidiasis (VVC), and systemic candidiasis models. For our study, we selected two *C. africana* strains displaying phenotypic differences (CEC4878 and CEC4854) and compared their interactions with the host to those of reference strain SC5314 and commensal strain 529L. *C. africana* strains displayed significantly decreased ability to colonize the murine GIT compared to strains SC5314 and 529L. Moreover, in the murine model of systemic candidiasis, *C. africana* strains were unable to cause symptoms and mortality in mice, showing significantly decreased fungal burden in kidneys. While there is barely any report of *C. africana* association with the oral cavity our study revealed that *C. africana* strains can colonize the oral cavity, inducing a host immune response. Surprisingly, the VVC model revealed significant differences between the two *C. africana* strains with strain CEC4878 inducing higher host immune response. This study broadens the knowledge about *C. africana* pathogenic potential and may allow us to highlight the specific features of *C. africana* that might contribute to its apparent niche restriction.

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