

Finding needles in a haystack – in silico environmental sampling of emerging pathogenic fungi

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ABSTRACT:

Yeast species in the *Candida haemulonii* complex (*C. haemulonii*, *C. haemulonii* var. *vulnera*, *C. duobushaemulonii*, *C. pseudohaemulonii* and *C. vulturna*) and the closely related species, *C. auris*, *C. heveicola* and *C. ruelliae*, are of significant public health concern worldwide, however, little is known about their natural habitat. To understand the worldwide emergence of fungal pathogens, new approaches to rapidly identify key environmental habitats are needed. Showing the effectiveness of the primary fungal DNA barcode to differentiate the members of the *Candida haemulonii* species complex and related species and reanalysis big data of DNA metabarcodes archived in the SRA database (NCBI) enabled the identification of novel reservoirs over a wide range of geographical areas of those yeasts. Our results infer that climate change is not the main/only driver for the emergence of pathogenic multidrug-resistant yeast species. This approach opens the door for further big data analysis using the fast resources of such databases.

KEYWORDS:

Big data; SRA database searches; DNA metabarcoding, environment; fungal pathogens; *Candida haemulonii* complex; *Candida auris*.