

Exploring the recent evolution of yeast pathogens using the CandidaMine database

Miquel Àngel Schikora-Tamarit^{#1}, Toni Gabaldón[#]

[#]*Comparative genomics lab, Life Sciences Department, BSC*

¹*miquel.schikora@bsc.es*

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EXTENDED ABSTRACT

Background

Advances in medicine (such as chemotherapy or transplants) have extended the life expectancy of patients at the cost of impairing their immune system. This has generated an increasing population of patients highly susceptible to infections. Among them, fungal infections caused by *Candida* species have become a major life-threatening issue, with insufficient diagnostic and therapeutic options. Recent studies have used population genomics in clinical *Candida* isolates to understand their recent evolution, which may also clarify the emergence of phenotypes like drug resistance or virulence. However, there are open questions that hinder our understanding about such evolutionary processes.

Results

We tried to clarify some of these questions by generating variant calling data for ~2,000 isolates from seven major *Candida* pathogens, available at the CandidaMine database. We focused on understanding 1) the role of structural variants (SVs), 2) the genomic determinants of antifungal drug resistance, 3) the role of recombination, 4) the population structure and 5) the similarities among these processes in different *Candida* species. Importantly, our collection represents a higher sample size as compared to previous studies, suggesting that we have unprecedented power.

Interestingly, we found that SVs drive a significant amount of genetic variation, suggesting that their role should not be overlooked. In addition, we found novel clades and recombination events in several species. Finally, our inter-specific comparison analysis revealed important differences between species, which may be relevant to develop species-tailored diagnostics or therapies.

Conclusions

In summary, our work improves the understanding of the recent evolution of the major *Candida* pathogens.

Author biography



Miquel Àngel Schikora-Tamarit was born in Lleida in 1995. In 2017 he obtains a Bachelor Degree in Human Biology by the Universitat Pompeu Fabra (UPF) of Barcelona. He works on several projects focused on understanding single-cell behavior under the supervision of Dr. Lucas Carey in the Department of Experimental and Health Sciences of the UPF between 2014 and 2018. His research, involving experimental molecular biology techniques and computational analysis, yields four publications in the journals *Integrative Biology*, *Transcription*, *Genome Research* and *Cell Reports*. He pursues a Master Degree in Bioinformatics at the UPF between 2017 and 2019. He develops the thesis project in the lab of Dr. Toni Gabaldón of the Center for Genomic Regulation (CRG) understanding the evolution of Complex I from fungal genomes (published in *Open Biology*). He is currently conducting his PhD thesis in Biomedicine at the University of Barcelona (UB), working on the evolution of drug resistance in fungal pathogens under the supervision of Dr. Toni Gabaldón at the Barcelona Supercomputing Center.