



## Proteogenomics of *Candida tropicalis* – an opportunistic pathogen

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### Abstract:

*Candida tropicalis* is an opportunistic pathogen which causes candidiasis in immune-compromised individuals. It is one of the members of the non-albicans group of *Candida* that are known to be azole resistant and is frequently seen in individuals being treated for cancers, HIV-infection and bone-marrow transplant. Although the genome of *C. tropicalis* was sequenced in the year 2009, the genome annotation has not been supported by experimental validation. In the present study, we have carried out in-depth proteomic profiling of *C. tropicalis* using high-resolution Fourier transform mass spectrometry and mapped ~44% of the computationally predicted protein-coding genes with peptide level evidence. In addition to identifying 2,740 proteins in the cell lysate of this yeast, we also analysed the proteome of the conditioned media of *C. tropicalis* culture and identified several unique secreted proteins among a total of 780 proteins. By subjecting the mass spectrometry data derived from cell lysate and conditioned media to proteogenomic analysis, we identified 86 novel genes, 12 novel exons and corrected 49 computationally predicted gene models. To our knowledge, this is the first high-throughput proteomic study to refine the genome annotation of *C. tropicalis*.

### Biography:

Keshava K. Datta is a Ph.D. student at the Institute of Bioinformatics, Bangalore. He has obtained his M.Sc. degree in Biochemistry from Bangalore University.

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