



## HUMAN FUNGAL PATHOGENIC DIVERSITY

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### ABSTRACT :

*Yeast and Molds are the predominate forms of fungal eukaryotic microorganism. The chitin composition of cell wall in kingdom fungi makes organisms distinguished from eukaryotic life kingdoms of animals and plants. As fungi do not photosynthesis, the heterotypic mode of food absorption from environment by secreting the extracellular enzymes outside the cell. These evolutionary relationships generated by comparing a single gene sequence, generally the small subunit ribosomal RNA gene (SSU rRNA). Since then, information from several protein coding genes has revealed diversity and phylogenetic trees of fungus. In present research, elaborating the conserved targets in phylogeny of genus candida with five species for potential drug targets. Hwp1 is significant cell surface protein used as reference have role in C. albicans biofilm formation and thus an opportunistic therapeutic target.*

**Keywords:** Fungi, phylogeny, Candida, conserved sites, drug targets, Hwp1

### 1.INTRODUCTION

Fungi have ancient origins, with evidence from fossil record indicating their first appearance about one billion years ago [1]. They belong one of most diverse groups of living organisms. The oldest plant fossils found fungal hyphae confirming that fungi are an extremely ancient group. However, regardless of fossil record, biochemical characters and molecular level have served as potential tool in tracing the probable evolutionary relationships of fungi [2].

Fungal groups can be related by presence of chitin in cell wall, composition of amino acid tryptophan in enzymes and synthesis of lysine in biochemical pathways. Later on, Molecular phylogenetic analyses that became possible during the 1990s have greatly contributed to the understanding of fungal origins evolution in their diversity.

Initially, these evolutionary relationships generated by comparing a single gene sequence, generally the small subunit ribosomal RNA gene (SSU rRNA). Since then, information from several protein coding genes has revealed diversity and phylogenetic trees of fungi. Now a day, phylogenetic trees built using a wide variety of data and databases. In

present work, we are exploring the conserved sites of five *Candida* species fungal diversity [3]. The five *candida* species are namely, *C. albicans*, *C. Africana*, *C. dubliniensis* CD36, *C. parapsilosis*, *C. tropicalis*. Hwp1 is significant cell surface protein required for *C. albicans* biofilm formation in vivo [4] and is thus an opportunistic therapeutic target.

### 2. METHODS AND METHODOLOGY

#### 2.1NCBI-Protein (<https://www.ncbi.nlm.nih.gov/protein>)

The National center for biotechnology Information facilities the access to genomic information in form of taxonomy, sequences, structure, function etc., the another resource, Protein database is collection

of sequence submitted from different sources. Protein sequences are the fundamental determinants of biological structure to function relationship [5].

**2.2 NCBI-FASTA Format** (<https://www.ncbi.nlm.nih.gov/BLAST/fasta.shtml>)

A single line FASTA format followed by lines of sequence data. A greater-than (>) symbol at the beginning description line (define) is distinguished from the sequence data by. It is recommended that all lines of text be shorter than 80 characters in length [6].

**2.3 Clustal Omega** (<https://www.ebi.ac.uk/Tools/msa/clustalo/>)

A new multiple sequence alignment program that working on seeded guide trees and HMM profile-profile techniques to generate alignments between minimum three **or more** sequences. In case of two sequences pair wise alignment in preferred [7].

**2.4 ProtParam** (<https://web.expasy.org/protparam>)

ProtParam tool allows the analysis of various physical and chemical parameters for a given protein stored in Swiss-prot and user protein sequence. The calculation of parameters includes the mol. weight, theoretical pI, amino acid composition, atomic composition and extinction coefficient etc [8].

**2.5 Uniprot Knowledgebase (UniprotKB)** (<https://www.uniprot.org/uniprot>)

A comprehensive, high-quality and freely available resource of protein sequence and function. Uniprot Knowledgebase (UniprotKB) facilitates the information to biological Function of protein. [9]

**2.6 InterPro** (<https://www.ebi.ac.uk/interpro/>)

InterPro provides families and domains sites for functional analysis of proteins. It produces a powerful integrated database and diagnostic tool [10].

**3. RESULTS**

Significant protein Hwp1 in *Candida* species with FASTA Format has following GenBank accession:

**Table1: Hyphal wall protien1 GenBank ID**

Sr.No.	<i>Candida</i> species	GenBank ID
1	<i>Candida albicans</i>	>ACN63125.1
2	<i>Candida Africana</i>	>ACB11588.1
3	<i>Candida dubliniensis CD36</i>	>XP_002419994.1
4	<i>Candida parapsilosis</i>	>AQY56716.1
5	<i>Candida tropicalis</i>	>ASK40159.1

Source: NCBI-FASTA [www.ncbi.nlm.nih.gov/BLAST/fasta.shtml](http://www.ncbi.nlm.nih.gov/BLAST/fasta.shtml)

Clustal omega results for job clustalo-I20190227-134132-0491-99665060-p1m are in form of phylogenetic tree as shown below:



**Fig 1:** Phylogenetic tree for five *candida* species using Neighbour-joining method.

The phylogenetic tree reveals the *C. tropicalis* and *C. parapsilosis* more similar species with each other and *C. Africana*. Whereas, *C. albicans* and *C. Africana* are more distinct among the comparative species [Fig. 1].

**Function of Hyphal wall protien1 (Gene name: Hwp1):**

- ✓ Plays a role in adhesion and is required for mating, normal hyphal development, and cell-to-cell contact [10].
- ✓ It is also revealed functions necessity in biofilm integrity. The adherence to host and participation in virulence. It promotes effective interactions in colonization [11].
- ✓ Hyphal wall protien1 plays a crucial role in gastrointestinal, mucosal, asymptomatic infections and candidacies, caused by the combined action of fungal virulence factors and host inflammatory responses in immunocompromised individuals.

The physicochemical parameters of hyphal wall protein1 has average 1533 Amino Acids in *Candida* Species having Theoretical pI 7.55 highest in *Candida parapsilosis* with average value. Extinction coefficients (assuming all pairs of Cys residues form cystines) are 3184.4. The Average Estimated half and Instability index is 18hrs and 64.99 the Aliphatic Index has highest value for *Candida parapsilosis* (Table. 2).

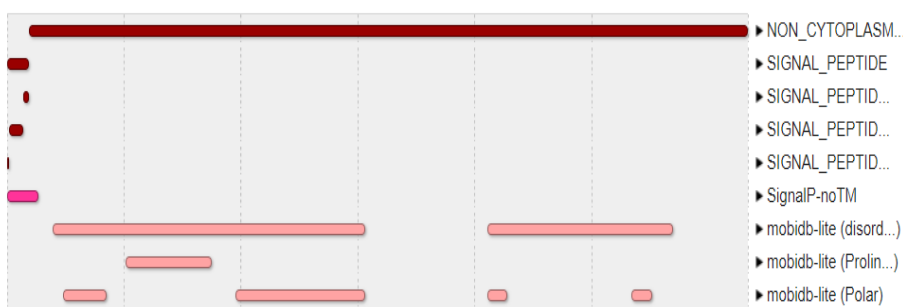
**Table-2: Computation of physicochemical properties of Hwp1 Proteins of Five *Candida* species.**

Parameters/ C.Species	pI	Aa	Ext. coeff	half-life (hrs.)	Insta bility Index	Aliphatic Index
Ca	3.93	264	4845	1.9	68.61	54.70
Caf	3.61	558	3137	30	72.93	53.33
Cd	3.90	421	3074	30	61.34	66.70
Cp	7.55	236	4220	30	39.98	73.56
Ct	3.56	269	3230	1	82.11	57.03

Source: <https://web.expasy.org/cgi-bin/protparam/protparam>

➤ **Domain and repeats:**

The conserved and functional ‘non-cytoplasmic domain’ region of 20-263 aa and four signal peptides at different sites were observed in InterPro results.



**Fig 2: Domain and repeats of hyphal wall protien1 of *C. albicans* (strain SC5314 / ATCC MYA-2876).**

**4. CONCLUSION**

Fungi have ancient origins; belong to one of most diverse groups of living organisms. Presently, the biochemical characters and molecular level have served as potential tool in tracing evolutionary relationships of fungi.

These evolutionary relationships generated by comparing a single and multiple gene as well as protein sequence. Since then, information from several protein coding genes has revealed diversity and phylogenetic trees of genus *Candida*. In our study five species of *Candida* genus were studied with conserved targets in phylogeny for potential drug targets.

Results are showing *Candida* species are having similarity with two distinct species. The physicochemical properties such as half life, stability and aliphatic index signify relevant information about survival and functional environment of protein. Amino acid composition (Positive and Negative) and theoretical pI are related to each other except *C. parapolis*. The

InterPro result shows region of domain and repeats of non-cytoplasmic domain and four sites of signal peptide.

Thus, Hwp1 is significant cell surface protein required for *C. albicans* biofilm formation was considered as opportunistic therapeutic target.

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## 6. REFERENCES

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