# USE OF BIOINFORMATICS TOOLS TO STUDY PHYLOGENETIC ANALYSIS AND SEQUENCE SIMILARITY OF MALASSEZIA SP. A PATHOGEN INVOLVED IN DANDRUFF.

#### Abstract

One of the most prevalent species in the human skin microbiota, Malassezia species, has been linked to skin conditions like dandruff and seborrheic dermatitis. Although Malassezia plays a significant role in common skin diseases, little is understood about its molecular makeup. In this approach, bioinformatics can be quite helpful. Selected genes from Malassezia species can be subjected to BLAST P. It was discovered that M. restrictive shares similarities with the distant human pathogen Candida albicans and the plant pathogen Ustilago mavids by the use of blast, a bioinformatics tool. It is possible to identify the convergent and divergent features of Malassezia species using the bioinformatics tool Culstal W. Researchers must create more potent bioinformatics tools to help manage the growing issue of dandruff and itchiness on the scalp in the human population.

**Keywords**: Bioinformatics, Microbiota, Malassezia Species.

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# IndexTerms—Malassezia,Ustilago, Candidaalbicans,CLUSTALW,BLAST,Dandruff,scalp pruritus.

### I. INTRODUCTION

One of the most important species of skin microbiota is the Malassezia species, which has been linked to a number of skin conditions, including dandruff and seborrheic dermatitis. The molecular makeup of malassezia is largely unknown. There are currently roughly 18 species of Malassezia known, including M.globosa, M.restricta are the most common species found in humans.malassezia is the eukaryotic biota of the human skin. Seborrheic dermatitis and dandruff are common skin conditions that cause itching and skin flaking. While seborrheic dermatitis is characterized by yellow flakes and irritation, dandruff is characterized by loose flakes and lack of inflammation. The proliferation of the commensel malassezia is the cause of dandruff and other diseases that affect about 50% of individuals. Three components seem to be involved in the etiology of D/SD: metabolism by microbiota, secretions from sebaceous glands, and individual vulnerability. (DeAngelis and others, 2005); Ro and Dawson, 2005). This chapter will describe the most common matches of M.globosa sequence and its phylogenetic analysis using bioinformatics tools BLAST and CLUTALW. BLAST is a tool of NCBI. It finds region of similarity between two or more sequences, the sequences can be either protein or nucleotide. BLAST stands for basic local alignment search tool. Blast is basically used to find out evolutionary and functional relationship between two individuals.it is not a single program but a family of programme like BLAST p, BLAST n, BLAST x, tBLASTn etc. it also helps to identify the member of gene families. CLUTALW is a multiple sequence alignment tool for DNA and protein sequence.it is not a tool for pairwise alignment but generally good for comparing three to four sequences. it is tool of European bioinformatics institute.

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SOURCE: https://www.genome.jp/tools-bin/clustalw

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1. Material and Methods: The NCBI GENBANK BLAST server version 2.2.30 (http://blast.ncbi.nlm.nih.gov) was utilized for alignment and homology searches (altschul et al. 1997). The NCBI data base has complete sequence of all the 9 chromosome of Malasseziarestricta as well as the Malasseziarestricta mitochondrion, complete genome. A specific protein synthesized by each chromosome was selected viz lipase protein sequence from chromosome 1 zinc finger domain from chromosome 2, chitin synthetase from chromosome 3 pyruvate synthetase from chromosome 4, carboxyl methyltransferase from chromosome 5, cell division cycle protein 37 of chromosome 6, NADH dehydrogenase (ubiquinone) Fe-S protein 4 of chromosome 7, arginase protein of chromosome 8, DNA repair protein REV1 of chromosome 9 and BLASTp was carried out and homology was identified. The database used for for comparison was non redundant protein databases. Multiple sequence alignment by CLUSTAL W with a K tupule word size of 1 was also carried out between secretory lipase enzymes sequences of Malassezia restricta, Ustilago maydis and Canadida albicans. A questionnaire and random sampling technique were also used on a sample of around 243 respondents, of which 152 were female and the remaining 91 were male.

### **II. RESULT AND CONCLUSION**

Protein BLAST of lipase protein sequence of chromosome 1 revealed similarity with Ustilagosps and most of the smut fungi. The zinc finger domain on chromosome 2 was found to be similar to plant pathogen Ceratobasidiumsp and Mycenasps.

The chitin synthase [Malasseziarestricta] was found to be highly similar to Testiculariasps. andScleroderma sps. andUstilagosps,again all plant pathogen. The pyruvate synthetase gene from chromosome 4 was found to be similar to Violaceomycespalustrisand Ustilagosps.Carboxyl Methyl transferase protein sequence of chromosome 5 was again found to be similar to Ustilagosps.Cell division cycle protein 37 protein sequence of chromosome of chromosome 6 was found to be 98% to Ustilagosps.NADH dehydrogenase (ubiquinone) Fe-S protein 4 of chromosome 7 showed 84% similarity with Ustilagosps.Arginase protein of chromosome 8 was found to be 98% similar to Ustilagomaydis.DNA repair protein REV1of chromosome 9 was found to be 96% to Rhizopussps.and 63% to Ustilagosps.M.restricta was found to more be closely related with the plant fungal pathogen Ustilagomyadis. A MSA between the secretory lipase of C.albicans, M.ristrictaandU.mayadis showed M.restricta and U.mayadis to be more convergent then C.albicans.

A detailed summary of the result is given below in the –

Name	RefSeq	Protein	Functional	SIMILARITY % WITH	
			Protein Selected	Ustilagomyadis	
Chr	Ι	835	lipase protein	85%	
Chr	II	782	zinc finger	Showed similarity	
CIII	11	182	domain	withCeratobasidiumsps	
Chr	III	746	chitin synthase		
Chr	IV	464	pyruvate	84%	
CIII	1 4	+0+	synthetase	0770	
Chr	V	532	carboxyl	64%	
	•	552	methyltransferase		
Chr	VI	410	cell division	98%	
	VI	110	cycle protein 37	2070	
			NADH		
Chr	VII	280	dehydrogenase	84%	
CIII	VII	200	(ubiquinone) Fe-	70	
			S protein 4		
Chr	VIII	233	arginase protein	98%	
Chr	IX	108	DNA repair	63%	
		100	protein REV1	0.5 %	
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name	Keiseq	protein	Protein Selected	Ustilagomyadis	

#### Table 1: summary of BLAST P analysis of M.resticta

#### Futuristic Trends in Biotechnology e-ISBN: 978-93-6252-180-4 IIP Series, Volume 3, Book 6, Part 3, Chapter 1 USE OF BIOINFORMATICS TOOLS TO STUDY PHYLOGENETIC ANALYSIS AND SEQUENCE SIMILARITY OF MALASSEZIA SP. A PATHOGEN INVOLVED IN DANDRUFF.

Chr	Ι	835	lipase protein	85%
Chr	Π	782	zinc finger	Showed similarity
			domain	withCeratobasidiumsps
Chr	III	746	chitin synthase	
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	1 V		synthetase	8470
Chr	V	532	carboxyl	64%
			methyltransferase	0470
Chr	VI	410	cell division	08%
CIII	V I	410	cycle protein 37	2870
			NADH	
Chr	VII	280	dehydrogenase	8406
			(ubiquinone) Fe-	8470
			S protein 4	
Chr	VIII	233	arginase protein	98%
Chr	IX	108	DNA repair	63%
			protein REV1	0570

A questionnaire and random sampling technique were also used on a sample of around 243 respondents, of which 152 were female and the remaining 91 were male.15.9% said they flaked their scalp excessively. Dandruff was shown to be less common as people aged, with a higher incidence in the 25–34 age range. Patients with dandruff were shown to have more severe cases of scalp pruritus than those without dandruff. Among the subjects, antidandruff products of all kinds and home treatments proved to be the least effective.



Figure 1: PhyML of Secretory Lipase

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