Use of bioinformatics tools to study phylogenetic analysis and sequence similarity of *Malassezia sp.* a pathogen involved in Dandruff.

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*Abstract*—:-Malassezia species is one of the most abundant species of human skin micro biota is found to be associated with skin disorders such as seborrheic dermatitis and Dandruff. Despite the importance of Malassezia in common skin disease, little is known at the molecular level. A BLAST P was carried out of selected genes of malassezia species. M.restricta was found to share similarity with plant pathogen Ustilago mayids and distant human pathogen Candida albicans. A Culstal W analysis was also carried out to find the convergent and divergent traits of Malassezia species. A random sampling method and a questionnaire was applied to about 243 subjects out of which 152 were females and remaining 91 were males. Out of these 15.9% reported excessive scalp flaking. The prevalence of dandruff was found to decrease with age, more prevalence was found in the age group 25-34 years. Scalp pruritus was found to be more severe in patients with dandruff then with patients without dandruff. All kinds of antidandruff products and home remedies were found to be least effective among the subjects. The data was collected from beauty salons of Indore division and hair clinics. Scientist needs to devise a method of treatment for this increasing problem of dandruff and scalp pruritus among the human population.

*IndexTerms*—*Malassezia*,*Ustilago, Candidaalbicans,*CLUSTALW,BLAST,Dandruff,scalp pruritus.*\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_*

# **Introduction**

Malassezia species is one of the most abundant species of human skin micro biota is found to be associated with skin disorders such as seborrheic dermatitis and Dandruff.despite the importance of Malassezia in common skin disease, little is known at the molecular level.It is a commensal organism about 18 species of Malassezia has been identified which includes M.globosa,M.restricta are the most common species found in humans. They represent 90% of eukaryotic biota of human skin. Dandruff and seborrheic dermatitis are common skin problems associated with flaking of skin and itch. In dandruff the flakes are loose and inflammation is absent while in seborrheic dermatitis yellow flakes with with inflammation are observed.About 50% of adult these days suffer from these conditions . The global hair care market is projected to grow at a CAGR of 6.6% during the next five years (fortune buissness insights). Both D/SD are not superficial disorders of the skin, the malassezia species are known to alter the epidermis of the skin. ([McOsker and Hannon, 1967](https://www.sciencedirect.com/science/article/pii/S0022202X15526584%22%20%5Cl%20%22bb0100); [Warner et al., 2001](https://www.sciencedirect.com/science/article/pii/S0022202X15526584%22%20%5Cl%20%22bb0165)). They affect the entire scalp and antifungal agents like zinc pyrithione are known as potent treatments of the fungus([Gemmer et al., 2002](https://www.sciencedirect.com/science/article/pii/S0022202X15526584#bb0065); [Batra et al., 2005](https://www.sciencedirect.com/science/article/pii/S0022202X15526584#bb0015). The etiology of D/SD appears to be dependent upon three factors:  sebaceous gland secretions, microflora metabolism and individual susceptibility. ([DeAngelis et al., 2005](https://www.sciencedirect.com/science/article/pii/S0022202X15526584%22%20%5Cl%20%22bb0045); [Ro and Dawson, 2005](https://www.sciencedirect.com/science/article/pii/S0022202X15526584%22%20%5Cl%20%22bb0120)). This paper will describe the most common matches of M.globosa sequence and its phylogeneticanalysis.A survey based study was also carried out between June and July on 243 subjects to find the prevalence of dandruff and scalp pruritus and other associated symptoms. Out of which 56.5% reported dandruff and other skin issues. zinc ,riboflavin and niacin deficiency was also found to be associated with dandruff.

# **Material and methods:**

For alignment and homology searches, NCBI GENBANK BLAST server p 2.2.30 (http://blast.ncbi.nlm.nih.gov) was used (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 Malasseziarestricta,Ustilagomaydis and Canadidaalbicans . A random sampling method and a questionnaire was also applied to about 243 subjects out of which 152 were females and remaining 91 were males.

# **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](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=170446) and *Mycenasps.*

The chitin synthase [*Malasseziarestricta*] was found to be highly similar to *Testiculariasps*. and*Scleroderma sps*. andUstilagosps,again all plant pathogen. The pyruvate synthetase gene from chromosome 4 was found to be similar to *Violaceomycespalustris*and *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 chromososme 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.ristricta*and*U.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 –

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Name | RefSeq | Protein | Functional Protein Selected | SIMILARITY % WITH ***Ustilagomyadis*** |
| Chr | I | 835 | lipase protein | 85% |
| Chr | II | 782 | zinc finger domain | Showed similarity withCeratobasidiumsps |
| Chr | III | 746 | chitin synthase |  |
| Chr | IV | 464 | pyruvate synthetase | 84% |
| Chr | V | 532 | carboxyl methyltransferase | 64% |
| Chr | VI | 410 | cell division cycle protein 37 | 98% |
| Chr | VII | 280 | NADH dehydrogenase (ubiquinone) Fe-S protein 4  | 84% |
| Chr | VIII | 233 | arginase protein | 98% |
| Chr | IX | 108 | DNA repair protein REV1 | 63% |
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Figure 1: PhyML of secretory lipase

# **Acknowledgment**

Acknowledge the almighty for bestowing all humans with the instinct of exploration thankful to Shree ShivajiRaoKadam Institute of Technology and Management for helping a lot in the development of the research. We are also thankful to MAHARAJA BHOJ GOVERNMENT P.G.COLLEGE DHAR (M.P) for providing us the opportunity to do research.

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