

e-ISSN: 2319-8753 | p-ISSN: 2320-6710

EDIA

International Journal of Innovative Research in SCIENCE | ENGINEERING | TECHNOLOGY

INTERNATIONAL JOURNAL OF INNOVATIVE RESEARCH

808

IN SCIENCE | ENGINEERING | TECHNOLOGY

Volume 10, Issue 6, June 2021

INTERNATIONAL STANDARD SERIAL NUMBER INDIA

Impact Factor: 7.512

9940 572 462

6381 907 438

 \odot







| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

Saccharomyces cerevisiae: An Opportunistic Pathogen causing Fungal Infection in Immunocompromised Condition.

Archana Moon^{1*}, V. G. Meshram², Shantanu D. Chilate³, Kanchan K. Thamke⁴, Simran S. Mankar⁵, Shivani S.

Tayde⁶, Priyanka V. Bhade⁷, Vishal K. Kolhe⁸, Pallavi S. Attram⁹, Priti V. Durge¹⁰, Monali Jariya¹¹

Post Graduate Teaching Department of Biochemistry Rashtrasant Tukadoji Maharaj Nagpur University,

Nagpur, India¹⁻¹⁰

Corresponding author: Dr. Archana Moon, Professor, Post Graduate Teaching Department of Biochemistry

Rashtrasant Tukadoji Maharaj Nagpur University, Nagpur, India¹¹

ABSTRACT : Baker's yeast (*Saccharomyces cerevisiae*). It is a well-known yeast for fermentation and a useful research example because of its unicellular nature and fact that having nearly similar mechanism with eukaryotes. Invasive Saccharomyces infections have been documented with multiple risk factors including critical illness and having immunodeficiency. Even some subspecies are most remarkable pathogenic fungi which cause various nosocomial infections annually. As we see, a long time was spent on *S. cerevisiae* isolation clinically. Bloodstream infection due to *S. cerevisiae* have been reported in patients suffering from critical illness and immunosuppression so clinically it was difficult to achieve timely diagnosis of the cause of fungemia. Blood culture of patients shows colonies of *S. cerevisiae* cause fungemia disease which is diagnosed by some molecular techniques. Morbidity rate is more as compared to mortality (due to patients suffering from different critical diseases). We reported the cases through review reading of patients such as having immunocompromised disease, taking episodes of probiotics, and had indwelling vascular catheters. In recent years new clinical syndrome SARS Cov-2 shows severe traces in elements of the immune system show related bloodstream infection risk factor associated with COVID19 patients in ICU.

KEYWORDS: Saccharomyces cerevisiae, yeast, Fungemia, S. boulardii, probiotics & antibiotics, CVC, SARS-COV-2, and COVID-19.

I. INTRODUCTION

The yeast *Saccharomyces cerevisiae* belongs to the *Saccharomyces cerevisiae* genus. Since ancient times, it has been used in winemaking, baking, and brewing. It's thought to have come from grape skin (one can see the yeast as a component of the thin white film on the skins of some dark-coloured fruits such as plums; it exists among the waxes of the cuticle). It is one of the microorganisms behind the most like *Escherichia coli* as the model bacterium. It is the microorganism behind the most common type of fermentation. *S. cerevisiae* are round to ovoid, 5-10µm in diameter. It reproduces by budding, which is a division process. This yeast converts glucose into energy by breakdown of glucose or allowing itself to grow in a container lacking oxygen where it begins to produce ethanol. Yeast is resistance to high sugar and ethanol concentration.



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |



Fig1: Scanning electron microscope of budding yeast, after each bud breaks, scar is left at budding site.

"Saccharomyces" derives from Latinized Greek and means "sugar-mold" or "sugar-fungus", saccharo being the combining form "sugar" and myces being "fungus". Cerevisiae comes from Latin and means "of beer".

1.1. History:

Yeast first observed by Antoni van Leeuwenhoek in 17th century, yeast consist of globules floating in fluid, but he thought its starchy particles of grains from which wort was made. In 1755, Samuel Johnson defines yeast as "the ferment put into drink to make it work, and into bread to make it lighten. In 1857, Louis Pasture discovers the yeast role in alcohol fermentation was conducted by living yeast and by chemical must. In 1859, J. H. van den Broek discovers the role of yeast in fermentation and morphology of yeast [3]. Fleischmann's produces granulated active dry yeast for the US military during the World War II that did not need refrigeration and had a longer shelf life and temperature tolerance then fresh yeast; it is now the standard yeast for us military recipes. The company developed yeast that rises twice as quickly as regular yeast, and allowing bakers to save time. Lesaffre would later create instant yeast in the 1970s, which has gained considerable use and market share at the expense of both fresh and dry yeast in their various applications.

1.2. Ecology:

Yeast is first isolated from grapes skin and then associated with insects during grape harvest season. It isn't airborne, but it does travel with the aid of vectors. The ideal temperature for growth is 30-35°C. Geographical differences in acidic growth environments are important. Most organism get their energy from respiration in the presence of oxygen, but others, like *Saccharomyces cerevisiae*, gets it from the less effective mechanism of fermentation fluxes. The optimization of isolation techniques allowed the detection of new species and targeted metagenomic approaches were able to assess the degree of *Saccharomyces* species. In aerobic condition at high glucose concentration *Saccharomyces cerevisiae* produce ethanol and other two carbon compound via pyruvate with Crabtree-positive. *S. cerevisiae* has resistance to high sugar concentration and they produce number of aromatic, volatile compounds.

1.3. Life cycle:

In life of *Saccharomyces cerevisiae*, cell give rise to two cells is called cell proliferation and undergo period of transition were haploid and diploid cell exist. The transition between haploid and diploid phases of the life cycle is accomplished by mating of two haploids to form a diploid zygote. In meiosis one diploid cell under goes premeiotic s-shape and two meiotic division resulting in four Haploid cells which enclosed in ascosporic wall, haploid cell occur in two mating type. *S. cerevisiae* can stably maintain as either heterothallic or homothallic strain heterothallic strain can be stably maintained as the diploid and haploid whereas homothallic strain is only stable in diploid because the transient haploid cell switches their mating type and mate because the α and γ mating types under control of pair of MAT/MAT heterozygous alleles. Both mating and meiosis are controlled genetically by the mating type locus of two alleles exist to the two sexes. The cell life cycle in yeast consist of G1, S, G2 and M stages. In G1 phase of the cell cycle *S. cerevisiae* cell have option for cell differentiation.



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |



Fig2: Life cycle of heterothallic and homothallic strain of Saccharomyces cerevisiae.



Fig3: Yeast Saccharomyces cerevisiae reproduces sexually and asexually.

Nutritional Requirement:

The yeast *Saccharomyces cerevisiae* a eukaryotic model organism, all strain of *S. cerevisiae* can grow aerobically on glucose maltose, trehalose, galactose and fructose are best fermenting sugar. Glucose, ammonium salt, inorganic ions are help in *S. cerevisiae* growth. Phosphorus and sulphur are assimilated as dehydrogenase phosphate ion and sulphur ion also some metals like magnesium, zinc, iron, calcium are required for growth of the yeast.

1. Yeast is chemoorganotrophic that obtain there carbon and energy by metabolizing organic substrate.

2. Saccharomyces cerevisiae requires supply of organic or inorganic nitrogen e.g. amino acid ammonium salt for growth and fermentation.

3. The sugar and nitrogen source in fermentation media used for fermented beverages production e.g. malt, wort, molasses, wine must, chees contain adequate level of inorganic ion for growth.

4. It requires growth factor at low concentration and these includes vitamins purines, pyrimidines, nucleotides, amino acids, fatty acid and steroids.

Mating:

The yeast *Saccharomyces cerevisiae* is simple single cell eukaryote with both diploid and haploid model existence. Mating of yeast occurs between haploid, which can be either α and γ mating type and thus displays sexual differentiation. Mating leads to genetic recombination i.e. production of navel combination and chromosome. The mating pathway employs a G-protein couple receptor. G– Protein, RGS protein and three-tiered MAPK signalling cascade that is homologous to found in humans. The mating in yeast has two district aspects, Induction and Activation of protein requires for cell fusion in responses to a pheromone signal and other is chemotropism. Pheromone induced polarity during mating is determine by external information. Chemotropism, the ability to reorient cell polarity in response to gradient, has been demonstrated for individual MAT a cell in γ pheromone gradients this receptor of seven trans-membrane segment class that transmit an external signal by interaction with Guanine nucleotide binding protein three sub units: Ga(GPA1),G\beta(STE4) and G γ (STE18). Binding of pheromone to receptor is postulated to exchange of GDP and dissociation of G2 from G $\beta\gamma$.



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

1.4. Cell cycle:

Cell reproduction occurs by elaborate series of event called the cell cycle and it is fundamental to the development and function of all life. Cell cycle regulator derives loss of function and new cell cycle become difficult to regulate and identify to perform genome slow cytometry assay of yeast gene expression cell cycle delay at specific stage. Cyclin dependent kinase regulated by phosphorylation and cyclin degradation before stages of cell cycle that system allows transition between G1|S and G2|M. In cell division divides one cell into two cells containing equal amount of organelle and genetic material. In cell cycle CDK's is central component contents order and timings. There are three checkpoints I.e. G2, CDK's is activated by G1|S and S-phase. Caloric restriction has direct impact on cell cycle progression an influence the life span of cells. In cell cycle control system 19 genes involves.



Fig4: The main event, transition and checkpoint of eukaryotic cell cycle, 'modelling the fission yeast'

Cytokinesis:

Cytokinesis is spatially regulated processed in the cellular constituents of the mother cell are partitions into two daughter cell, that permitting and increasing cell number occurs by actomyosin system and septum formation. Cytokinesis involves a periodic interplay which defects in cell cycle lead to genomic instability which results in reduced fitness, cancer or death. Cytokinesis ensures inheritance of genetic code for maintain species identity during propagation. Cytokinesis is regulated to control the cell in different tissue and organ. Cytokines in fungal cell involved division site powered by contractile actomyosin ring (AMR) and localised membrane and ECM (extra chromosomal matrix) lead to abscission. The AMR timing is same in budding yeast and animal cell but different in myosin at division site. Preparation for budding yeast *S. cerevisiae* begins late G1 about 15 min. At the 15 min time metaphases is visible inside nucleus and diffuse patches of meiosis II over nuclei. By 29 min this patches coalesced into contractile ring form at mitosis.



Fig5: Assembly of execution of key cytokinesis during the cell cycle.



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

Actomyosin Ring and Primary Septum Formations:

1. Actomyosin Ring:

During cytokinesis barbed end actin filaments at cell cortex by unknown protein. This cytoskeleton protein polymerises to form long chain called microfilaments. Actin filaments are thinner and flexible than microtubules.



Fig6: Actin -myosin ring, "The cell cycle : principle of control."

AMR Assembly:

AMR of actin filaments myosin- II heavy chain, light chain, proteins construction with Septum formation. AMR assembly depends on Septin, Rho-GTPase Rho1, formations Bnr1 and Bni1, the IQGAP- homolog Iqg1, tropomyosins, profilin and cell cycle regulated kisses and phosphatase.

Septin:

Septin identified in budding yeast and are GTP binding cytoskeleton protein from yeast to humans and play role in cytokinesis, cell migration and morphogenesis in divers disease including neurodegenerative disease, infertility and cancer. Septins form a ring at bud site in G1 and required for formation of the actin-myosin ring.

Myosin-II:

Myosin-II in budding yeast is a hexamer of heavy chain, Myo1 with an ELC (MC1) and regulated light chain. MIC1 and MIC2 bind to the IQ1 and IQ2 between head and tail of Myo1. The RLC MIC2 displays an identical localization toMyo1 by binding to IQ2 motif of Myo1 cell cycle.

Formins and the actin ring:

Three filamentous actin like Patches, Cables and the ring. The actin patches consist of branched filaments nucleated by ARP complexes for endocytosis. The actin cables and ring consist of linear filaments nucleated by the pair of formins, Bni1 and Bnr1. Linear filaments nucleated by tropomyosins of Tpm1 and Tpm2.

IQGAP:

The IQGAP, Iqg1 in budding yeast play role in AMR assembly. It promotes actin ring formation by binding to actin filaments of Myo1 division site at cytokinesis.

2. Primary septum formation:

It consists of the polymer chitin are integral membrane protein of multiple Trans membrane domain. Budding yeast has three chitin i.e. Chs-1, 2 and 3. CHS1 and CHS3 for cell wall repair and bud scar formation while CH2 prevents packaging into COPII vesicles by CDK1. PS-AMR applies to fission yeast secreted extra chromosomal matrix protein required for preventing cleavage during cytokinesis.



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |



Fig7: Illustration of molecular recognization at the cell division site during mitotic exit. AMR, actomyosin ring, PS, primary septin: secondary septum.

Different form of fission yeast:

A. Division site selection:

In budding yeast division plane is determined in late G1 phase and reflect position of the division site. In budding yeast Septin, actin, Myosin-II, IQGAP, formins, and Men pathway present. In fission yeast the division site is determined in G2 and reflects position of the interphase nucleus and the molecules are Mid1p, actin, formin, Myosin-II, IQGAP, Cdc15p and SIN (Septum Initiation Network) pathway. While in animal cell the division plane is determined during Anaphase that reflects the position of the spindle and molecules are RhoA pathway, actin, Myosin-II, formin, central spindle components.

B. Assembly of Actomyosin Contractile Ring:

The bud neck is smaller than diameter that cytokinesis may not involve an actomyosin ring. The proteins at the bud neck in cell cycle starting from late G1, to cell separation. Assembly at bud neck in late G1 phase, septins by Myosin-II heavy chain Myo1p and light chain MICp in S|G2 phase.

In fission yeast of the actin-myosin ring accumulate the medial cortex from mid G1 to metaphase, in a Mid1p dependent manner. The assembly profilin Cdc3p, light chain myosin Cdc4p, tropomyosin Cdc8p, and IQGAP Chains.

1.5. Biological research:

S. cerevisiae is a model organism, a valuable tool for all aspects of basic research. Unlike other model organisms though, such as *Escherichia coli* or *Caenorhabditis elegans*, and *S. cerevisiae* is concomitantly also a most valuable species for a variety of industrial applications. *S. cerevisiae* can be manipulated genetically allowing for both the addition of new genes or deletion through a plethora of homologous recombination techniques. *Saccharomyces cerevisiae* was the first eukaryotic genome to be completely sequenced. The genome sequence was published in 1996 and has been updated regularly in the Saccharomyces Genome Database. Currently, it is considered that the genome is composed of 12.1 million base pairs and 6275 genes organized on 16 chromosomes. The ability to culture this yeast species as a haploid simplifies the isolation of mutants and haploid diploid hybrid

Aging:

In a normal wild type strain, yeast undergo a spiral form of cellular ageing, with each mother cell appearing at age zero generations and then budding for an average life span of 25-30 generations. The buds appear as zero generation cells in each generation until the end of life; hence, each cell division is asymmetrical in relation to age. The sirtuin route and the TOR (Target of Rapamycim) signalling system are two prominent pathways researched in the context of ageing and age-related disease, and yeast played a key role in their discovery. Replicative and chronological assays for yeast ageing provide a unique opportunity to compare and contrast the ageing processes of both proliferating and non-proliferating cells in a single-celled organism.

Yeast cells are normally cultivated on conditions with high levels of glucose (2%) and plentiful amino acids. Independent investigations have found that decreasing either the glucose or amino acid content of the media (or both) can extend replicative and chronological life span. Calorie restriction (CR) has been used to all of these diverse nutrient restriction paradigms. Yeast ageing genes belong to the protein deacetylase family (sirtuins). It has been intensively



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

researched in a range of taxa, including mammals, for its possible significance as conserved ageing modulators. SIR2 deletion shortens replicative life span whereas overexpression improves replicative life span in yeast, making it the first creature in which this protein is explicitly connected to ageing. Both overexpression of SIR2 and deletion of FOB1 inhibit homologous recombination at rDNA repeats in ribosomal DNA, suggesting that Sir2 is largely a histone deacetylase (rDNA). Sir2 is also involved in Msn2/4 activity and RLS and CLS control. Sir2 does not promote longevity in the chronological ageing paradigm and appears to be antagonistic in the response to DR (Dietary restriction).

Meiosis:

Meiosis occurs with initiation of a/α type of diploid cell with appropriate genotype which gives rise to four haploid meiotic progeny which has been cascade in spore coat. Meiosis requires proper nitrogen and carbon starvation and heterozygosity at mating type locus. a and α cell produce inhibitor so they are not capable for meiosis.



Fig8: The morphogenetic event of spore formation by transcriptional cascade.

The early meiotic specific transcription factor IME1 is needed for the entire major downstream event, including meiosis and sporulation, and is required for the initiation meiosis. Meiosis start with prolong S-phase in which genome is replicate only once. The transcription factor Ndt80p has been involved in meiosis and ascospore formation, Ndt80p target the sporulation specific gene. After meiosis it initiates the spore formation process by slicing out the ascospore.

Recombination and Repair:

In Recombinant DNA, DNA molecules from two different creatures are injected into a host organism to form a novel genetic combination helpful in research, medicine, agriculture, and industry. Researchers can now isolate one gene or any other segment of DNA and establish its nucleotide sequence, study its transcripts, mutate it in extremely specific ways, and reintroduce the modified sequence into living organism using recombinant DNA technology.

Circular DNA elements, particularly tandem repeats, are involved in genome plasticity in the yeast *S. cerevisiae*. However, previously documented amplifications of DNA segments in *Saccharomyces cerevisiae* have used pre-existing repetitive sequences including ribosomal DNA, Ty elements, and Long Terminal Repeats (LTRs). About 1 out of every 5 genes in the yeast Saccharomyces cerevisiae has been discovered as duplication. Furthermore, tandem gene arrays make for almost 2% of the coding sequences in *S. cerevisiae*. Tandem repetitive DNA sequences that include ribosomal DNA (rDNA) and the telomeric loci are very prone to copy number alterations as a consequence of homologous recombination (HR). Such regions play a significant role in the plasticity of the genome. Other repeated elements found throughout the yeast genome, such as Ty elements and solo Long Terminal Repeats (LTRs), are potential substrates for HR between short repeats bordering a DNA segment. Despite the fact that repetitive DNA sequences play a crucial role in increased rates of genome plasticity, segmental amplifications are not limited to repetitive sequences. However, the process of generating tandem gene amplifications from single-copy sequences remains unknown. The circularization of a DNA segment from a chromosome during HR between pre-existing closely positioned homologous sequences such as LTRs, resulting in the excision of the DNA segment, has been related to the production of eccDNA. In the absence of repetitive sequences, there has been scant experimental evidence for the production of eccDNA.

Genome sequence:

The genome of budding *S. cerevisiae* was the first completely form a eukaryote. In 1996, it was released by hundreds of researcher's efforts. The yeast genome used to study the molecular biology and genetics. Maintenances and



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

annotation of genome sequencing have been provided by Saccharomyces genome database and one of the original model organism *Saccharomyces cerevisiae* has a large role in human history, it was the largest genome sequence it contain just over 12 million base pair packed in 16 chromosomes. Yeast have 6000 gene in all 1/3rd this related to human gene. Over one billion year of evaluation due to alteration show separate human and yeast to carry out basic cellular function. The sequencing of first eukaryotic chromosome number 1 was beginning in late 1980 by consortium of yeast researchers completed in 1992. Sequencing of yeast genome number of yeast strain, represent time of *Saccharomyces cerevisiae* genome was almost completed by two intensive yeast sequencing project has already started genome of another model organism *schizosacchoromyces* pombe and important human pathogen *Candida albican*. Phylogenetic relationship it shows the application of gene sequence analysis is systematic released that the phylogenetic relationships based only on phenotypic characters like *Candida albican* and Saccharomyces had the last common ancestor 200 million year ago. Sequencing in yeast genome tells us about the coding potential and regulatory sequencing that are necessary for yeast cell. The present sequence data will be useful for binding of industrial strain and budding yeast pathogen.

Annotating protein coding gene in genome of *Saccharomyces cerevisiae* it has generally been accepted to look open reading frame count (ORF) longer than 100 codon, gene count *Saccharomyces cerevisiae* exceeded 6000 studied suggest that 500 ORF initially annotated, *S. cerevisiae* contain 5700-5800 functional reading frame. The number of protein coding ORF to be low as 5300-5400 proposed that majority of non-coding ORF have arisen by gene duplication followed by mutation, that throw the original duplication copy out of frame, sequence gene 5700- 5800 encoded by *S. cerevisiae* genome. Change in this annotation discover that novel gene, shorter gene, novel intron, ORF extension and fusion of neighbouring ORF; Experiment the novel intron have been verified by 5' rapid amplification cDNA and 84 novel small ORF have been confirmed by transcriptional product. Complete sequence show the origin of model yeast trait; whole genome duplication and horizontal gene transfer are proposed to play important role in evaluation of Saccharomyces complex yeast duplication in biological evaluation by extra genetic material remodel into novel gene products. A variety of datasets are available for searching with BLAST, FASTA and Pattern Matching: the genomic sequence, all GenBank *S. cerevisiae* sequences, a non-redundant set of *S. cerevisiae* protein sequences combined from NCBI's GenPept, PIR and Swiss Prot, the DNA coding sequence of all hypothetical ORFs identified by the systematic sequencing project, the hypothetical translation of all ORF sequences, and the non ORF DNA sequences.

Gene Function and Interaction:

Saccharomyces cerevisiae (baker's or brewer's yeast) is a model eukaryotic organism. It was the first eukaryotic genome sequence to be completed. It is cheap and quick to grow, generally non-pathogenic, and easy to manipulate genetically, and it has been the focus of detailed study over the years. These studies include expression analysis via Northern Blots, SAGE (Salicylic acid gel electrophoresis), microarrays, 2D gel electrophoresis, two-hybrid systems for protein-protein interactions, large scale deletion and mutational analysis and phenotypic analysis. Despite all this biological knowledge and investigation, approximately 40% of the potential genes or Open Reading Frames (ORFs) in yeast remain without clear function or purpose. Many computational methods are used in functional genomics. The most common method of determining the function of a protein is to use a sequence similarity program such as PSI-BLAST to infer function by orthologous homology. It has 16 chromosomes, which contain approximately 6,300 ORFs. 5 different types of data sources are available for yeast.

1. **Sequence data**: This data set consisted of data that can be directly calculated from sequence, such as amino acid ratios, molecular weight, aliphatic index, codon adaption index, sequence length and hydrophobicity.

2. **Phenotype data**: This is data from phenotypic growth experiments, where knockout mutants are grown in a variety of media with the aim of finding growth conditions where the mutant and the wild type (no mutation) differ ('aphenotype').

3. **Expression data:** Many genome-wide microarray experiments have been carried out on yeast. Cell cycle, church, derisi, eisen, gasch1, gasch2, and spo these are the 7 sources of data which measure changes in expression levels under a variety of conditions, such as heat shock, and during the normal lifetime of the cell.

4. **Homology data:** Sequence similarity searches are a standard method of inferring function. The homology data is the result of a PSI-BLAST search for each *S. cerevisiae* ORF against NRDB90. The sequences that are found by PSI-BLAST to have an e-value below the threshold are known as 'hits'.

5. **Predicted secondary structure data:** Data was collected about the predicted secondary structure of the gene products of *S. cerevisiae*. The predictions were expressed as Data log facts representing the lengths and relative positions of the alpha, beta and coil parts of the structure. The predictions also included the distributions of alpha, beta



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

and coil as percentages. The homology and secondary structure datasets are relational in nature, whereas the other data sets are straight forward attribute-value data.

Function classification

The MIPS classification scheme is hierarchical with 19 general classes at the top and more specialised classes at the second level. The hierarchy is four layers deep since these are subdivided and then subdivided again. Since proteins can be involved in more than one role within the cell, an ORF can belong to multiple groups at different level in this hierarchy. Genetic crosses were possible with strain EM93, which is a major breakthrough in yeast genetics. Researchers were able to isolate particular traits and gradually characterise the genes that encoded certain traits. The advent of polymerase chain reaction (PCR), along with the efficiency of homologous recombination in yeast, has led to the development of "designer deletion strains," which, combined with the comprehensively annotated. Saccharomyces Genome database gives yeast geneticists flexibility in experiment design. In 1996, the *S. cerevisiae* genome became the first fully sequenced eukaryotic genome. The sequencing of the *S. cerevisiae* genome has provided a wealth of information on various aspects of genome organization and evolution. In a typical haploid budding yeast cell, the ~12,000 kb of genomic DNA are subdivided into 16 chromosomes, thought to have arisen following an ancient whole-genome duplication event from an ancestral set of 8 distinct chromosomes.

The *S. cerevisiae* genome houses a large number of so- called long terminal repeat (LTR) retro transposons, called Ty elements, scattered across all 16 chromosomes. The active versions of these transposable elements can transpose throughout the genome in a cycle that includes transcription and translation of the element, followed by assembly of viral-like particles, similar to mammalian retroviruses (VLPs). Within the VLPs, reverse transcriptase converts the retro transposons' RNA to complementary DNA (cDNA), which is followed by insertion of the cDNA into the genome. In a recent analysis of the S288C genome, 483 Ty elements were discovered, 427 of which are inactive solo LTRs

Chromosome III in *S. cerevisiae* harbours genetic information that determines the mating type identity of cells. Haploid yeast cells can be either mating type a or α (MATa and MAT α , respectively), which, under the appropriate conditions, can mate with each other to generate MATa/MAT α diploids. These diploid cells can't mate, but they can reproduce by mitosis or meiosis, which produces haploid spores. The MAT locus, which is found on the right arm of chromosome III, controls yeast cell mating behaviour. This locus can harbour one of two non-homologous alleles called MATa and MAT α : MATa cells contain the MATa allele, MAT α cells contain the MAT α allele, and, in most cases, diploid cells contain both alleles (each located on one of the two homologous chromosome IIIs). The two MAT alleles express different sets of proteins, which, through a rather complex mechanism, regulate proper mating-type behaviour of cells. Chromosome III also carries an additional copy of each MAT allele at two additional loci: the HMRa locus located near the end of the right arm of the chromosome contains the MAT α allele. HMRa and HML (also known as silent mating-type cassettes) are embedded in heterochromatin and hence transcriptionally suppressed, but can be exploited by haploid cells to convert from one mating type to the other, unlike the MAT locus.

The budding yeast mating-type system has served as a remarkable model system for understanding a wide array of basic cellular processes, including heterochromatin formation and maintenance, transcriptional silencing, and homologous recombination.

The term genetic interaction (GI) covers a group of functional relationships between genes. Bateson and Mendel were the first to characterise one type of these interactions, called epistasis (1909). The creation of additive, multiplicative, Min, and Log models to determine the predicted phenotype of double mutants was sparked by the advent of systematic and large-scale GI screening, particularly in the yeast *Saccharomyces cerevisiae*.

Genetic interactions have long been studied in model organisms as a means of identifying functional relationships among genes or their corresponding gene products, with the nature of these relationships depending on the types of interactions to theoretical explanations for the selective advantage of sexual reproduction and recombination. The study of genetic interaction has become increasingly systematic and large-scale, especially in the yeast *Saccharomyces cerevisiae*. This allows researchers to investigate the features of various quantitative definitions of genetic interaction and how they affect biological interpretation. There are two parts to a quantitative genetic interaction definition: a phenotypic measure that is quantitative phenotypic measure and a neutrality function that predicts the phenotype of an organism carrying two non-interacting mutations.



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

The difference in phenotype of a double-mutant organism from the expected neutral phenotype is then used to determine interaction. A synergistic (or synthetic) interaction between the related mutations is defined by a double mutant with a more extreme phenotype than expected (synthetic lethality, in the extreme case). When gene products function in concert or in sequence within the same pathway, they often result in alleviating or "diminishing returns" interactions, in which the double-mutant phenotype is less severe than expected. Alleviating interactions occur when a mutation in one gene affects the function of an entire system, concealing the effects of mutations, generally using either a multiplicative or a minimum mathematical function. The multiplicative function, which was first applied to fitness metrics specified in terms of allele frequencies, predicts that double-mutant fitness is the product of single-mutant fitness values. Each of the three fitness measurements above can be paired with the multiplicative function to produce three distinct definitions of genetic interaction.

Constructing a Catalog of Genetic Interactions:

There are two main reasons why mapping GI networks is of biological interest. The first one is to understand the mechanisms underlying the robustness of biological systems. Mapping Genetic Intercoms in Model Organisms Quantitative studies of synthetic sick or lethal (SSL) interactions in the baker's yeast *S. cerevisiae* represent most of the GIs screens done to date. The growth of large-scale GI investigations is attributed to the availability of mutation libraries for both essential and non-essential genes. Non-essential gene mutant libraries contain strains where single gene coding sequences are substituted by a drug-resistance marker while essential genes mutant libraries consist in a collection of conditional alleles. Synthetic genetic array, an automated approach, has made substantial use of these libraries. SGA screening involves constructing double mutants in a high-throughput manner employing single altered yeasts as a query against a full deletion library. In parallel, the epistatic mini array profile (E-MAP) another variant of SGA takes colony size measurements as a basis for the detection of GIs. GIs are then identified through measurement of as lower (SSL, negative GIs) or faster (alleviating positive GIs) growth rate of the double mutants than what is expected from each single mutant growth rate. While SGA was originally set to identify only negative SSL GIs, this allowed for the detection of both positive and negative GIs. E-MAP was also utilised to map GIs in *Schizosaccharomycespombe* and other yeast species.

Among the other high-through put methods to discover GIs in yeast, diploid-based synthetic lethality analysis with micro arrays (dSLAM) uses a library of barcoded mutants and barcode micro arrays to measure the relative abundance of each barcoded double mutants in pooled populations to identify digenic SSL interactions. Optical density measurements, biomass quantification analysis termed flux balance analysis (FBA), quantitative phenotype and gene expression data have also been employed to map GIs in specific biological processes.

Other tools in yeast Research:

In 1996, the genome of baker yeast *S. cerevisiae* has been elucidated the opportunating for the global studding of the expression and function of the eukaryotic genome. International team is working on the synthesised 16 yeast chromosome by synthetic biological tool. The recent development of biological tool and their application to improve production of chemical and fuel in yeast has been widely used for the production of verity of small and large molecule including alcohol, acids, hydrocarbon, and protein. Also availability of genetic tools perturb metabolic pathway, analysis of yeast mutants make yeast an attractive host. In 1898, new approach toward the examination of protein-protein interaction emerged; it was name as the yeast two-hybrid system it allows to detect the interaction of two proteins in the yeast cell. These technique take the advantage of the fact that majority of eukaryotic transcriptional based tool promoter and terminator to design an engineer protein level based on transcript production and stability, we need functional description for promoter and terminator to identify characterise more than 200 synthetic promoters using the *S. cerevisiae* as a part.

Another excellent site of discovery in budding yeast took full advantage of the yeast toolkit is, Randy Schekman's work on eukaryotes vesicle trafficking [24]. This work saves as a foundation of application that allow production and secretion of medically significant molecule such as 'insulin' from yeast and has impacted a wide variety of field changing from neurobiology to virology. Our understanding the other basic cellular process has also taken significant human disorder, such as 'Alzheimer' disease and 'hunting ton's' disease. The conserved nature of this basic cellular process has proven that work in budding yeast is significant in another major area of biomedical research. Regulation of cellular differentiation are well studied using yeast, the amount aging research has been produce from the



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

budding yeast. To study the telomere function budding yeast researchers have related mitochondrial function, oxidative stress, apoptosis, replication stress describing mating type switching event in *S. cerevisiae*.

Synthetic yeast genome project:

The *S. cerevisiae* is showing a technology in synthetic genome, it synthesises a large viral and bacterial genome [23]. The synthetic yeast genome is the large international project is known as 2.0 and 'SC2.0' project. The goal of this SC2.0 project is complete synthesised of genome for systematic study of eukaryotic chromosome is distributed across many location. The main aspect of SC2.0 project is to encourage the study of design and describe both intermediate design chromosome and living strain [21]. In 1996, *S. cerevisiae* is haploid laboratory strain (S288c) become the first eukaryote whose genome was fully sequence. This Sc2.0 project is also known as "blue sky project" because researcher uses this strain as laboratory experiment. The fully sequence genome make the avaibility to fake use for further research the design study of these project is achieved wide variety of thing like property of chromosome, gene contain, genome organization, functional RNA splicing and find which RNA plays important role in yeast study. Aim for design SC2.0 project show the simplify assembly of synthetic chromosome specific base substituted with some of the open frame reading (ORF) to remove or eliminate the inconvenient enzyme organization site [23].

Modified genetic code in which all (TAG) stop codon are change to (TAA). In IoxPsym site is undergoes inducible evaluation system SCRaMbLE and lack repeat element transfer RNA(tRNA) gene.[20] SC2.0 genome is based upon SwAP-In(switching auxotropies progressively for integration). This SwAP-In is replacing the six of yeast native chromosome [23]. The two pairs of IoxPsym site recombine and synthesis this yeast chromosome followed by synII, synV, syn XI, and synX, syn XII. The future aspect of this SC2.0 project is to synthesize the genomic study lead to the industrial based biodiversity, bio–engineering, bio-manufacturing and bio robotics expected for researches and further advance technology.

1.6. Astrobiology:

Astrobiology is the study of life in the universe. If we will searching the life beyond the earth so first we should understanding of life as well as planetary system the astrobiologist can work many plant including like biology oceanography aeronautical engineering. The astrobiological researchers can work with space against like 'NASA' (national aeronautics and space administration) and 'Europe space agency' for current and future research in space mission e.g.-recent mission on focusing the light on 'Mass'. Astrobiology published its last road map in 2004, research in the field has focused link between the 'astro' and 'bio' it make a planetary body habitat. The phobos life (living interplanetary flight experiment) this experiment start with same organism yeast *Saccharomyces cerevisiae* strain 'W303' is used to assist the space flight experiment.

1. The 'LEO' mission is launched by NASA to studies the many biological phenomenon's in various study and variety of model organism. The study was investigating the role of radiation in model organism by interplanetary deep space.

2. Biological cube-sat mission: In 2006 'NASA' Ames research canter launch the Gene-sat1 to study the biology and technology pharma set launch with 3LED optical sensor for study the microbial activity testing yeast cell and their response to fungicide in microgravity.

3. Bio-sentinel mission nano satellite containing the budding yeast *S. cerevisiae* it is the first biological mission beyond 'LEO' this mission is launched by NASA. In this mission Bio sentinel contain two strain of budding yeast wild type strain 'rad51' mission is taken glance our the ionization radiation effect on yeast cell and yeast will save as vigorous from the human study.

1.7. Commercial application:

Due to its excellent conversion of glucose into ethanol with high productivity and great tolerance to numerous inhibiting substances, including ethanol, the yeast *S. cerevisiae* has a long history of industrial application. It, on the other hand, is unable to properly convert D-xylose to ethanol. It dominates in all yeast species for having prolonged influence in the flavour and in around all characteristics of beverages, production of distilled spirits. The optimum condition for fermentation is around 34°c to 38°C at pH 4.0-5.2 using fresh yeast because older yeast required longer formation time. The beans of tropical plants obrama cocoa, basic row material for production of chocolate. To reduce the level of polyphenol and alkaloids, causing bitterness and astringency anti developed flavour are fermented through *S. cerevisiae*.

1.8. Use in Medicines:

Brewer's yeast is used in a protein supplement and rare source of vitamin-B, energy booster, immune enhancer and compounds can be inserted to create a commercialized health product. Modified brewer's yeast-based product



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

(EpiCor) is used to prevent colds and flu symptoms. Yeast-based technology is also being used as a molecular mechanistic model of caloric restriction (CR) with the goal of improving the human life span.

S. cerevisiae is used in probiotic preparation and treatment of various diarrheal disorders, associated with *clostridium diffille* infection. Parenteral is drug in which dried *S. cerevisiae* is used. Along with drugs like florustor, reflarol, Ultra-levure, CNCMT-745 tablets are consists of *S. boulardii* skane. These all drugs are for treatment mostly diarrheal and related disorders, vaginal infections. 'Ulcerative colitis' has been treated with therapeutic regimen including *S. boulardii* and riboximin has seen effective in preventing early flora ups of ulcerative colite. *Anti-Saccharomyces cerevisiae* antibodies (ASCA) are relevant Crohn's disease diagnostic markers. Crohns disease can be treated with *Saccharomyces boulardii* which shows significant reduction in colonic permeability which reduce risk of bacterial translocation. *S. cerevisiae* is capable of adsorbing and degrading mycotoxins and showed that yeast composites were able to bind the nephrotoxic and carcinogenic ochratoxin A (OTA) in liquid media up to 65 %, depending on pH, initial OTA concentration, and yeast strain composition [16]. Raeford drug have composition of *S. boulardii* along with *Receidonil* and *lactobacillus*.

1.9. Human pathogen:

Virulence of different strain

In an examination of a range of laboratory and industrial strains of S. cerevisiae, growth was observed over the range of 37 - 40 °C but only virulent isolates were capable of growth at 42 °C. The ability to develop at this temperature appears to be important for S. cerevisiae pathogenicity and appears to be polygenic. Under some conditions, virulent isolates can grow as psuedohyphae, and psuedohyphae have been shown to pierce agar, which could indicate their role in vivo. Virulent isolates of S. cerevisiae manifest a number of characteristic which are essential for their pathogenicity in the human host, particularly if the host is immunocompromised as a result of therapy or disease and may persist for prolonged periods of time in susceptible hosts. Virulent isolates have also been found to be capable of penetrating tissue and administering from the point of entrance. Virulent cerevisiae are harmful to humans as hosts. Phenotypic switching has been observed in virulent isolates of S. cerevisiae where it occurs at a high frequency and does not require mutagenesis [48]. Exact risk factors are not known but so many risk factors involve for causing it. It is characterized as opportunistic pathogen of low virulence which makes it difficult to study mechanism. The risk factors related to virulence of S. cerevisiae are the secretion of hydrolytic enzyme, Growth of high temperature, pseudo filamentation and phenotypic switching [43, 44]. S. boulardii analysis has revealed moderate virulence levels when tested in murine model of systemic infection. S. cerevisiae can cause a broad range of clinical syndromes including fungemia, liver abscess, superficial infections, vaginitis, pneumonia, esophagitis, asthma and oral infections.

Invasive and systemic infection

Yeast *Saccharomyces cerevisiae* is saprophytic organism widely found in nature and use in everyday life; food supplementary. Maybe that is the reason that fungal infection emerged as an important health problem. Apart from this it is associated with human, as a normal flora of the oral, gastrointestinal, and respiratory tracts and the vaginal mucosa (urinary tract). Among the diarrhoea caused by *S. cerevisiae* fungemia is most severe and verified disease. *S. cerevisiae* has been related to verifies of infections, which range from vaginitis in healthy patients and cutaneous infections to systemic bloodstream infection and infection of essential organs in immunocompromised and critically ill patient's occasion. This opportunistic pathogen attack the patients such as elderly patients, premature children's or patients suffering from immunosuppression due to HIV/AIDS, treatment with immunosuppression agents, or other condition associated with a deficient immune response.

Yeast is resistance to high sugar contain may make patients suffering from invasive bloodstream infection. Overgrowth of yeast *Saccharomyces cerevisiae* can cause infection and attack on organ or system in our body, attack is unceasingly intense until it treated, if it not arrested/taken over control, it will change its form into invasive pathogen cause myriad symptom. Dr. Michael Goldberg state: "Because it is a commensal organism (one that benefits from another organism without damaging or benefiting it) present in virtually all human being from birth, it is ideally positioned to take immediate advantage of any weakness or debility in the host and probably has few equals in the variety and severity of the infections for which it is responsible." [54] *Saccharomyces cerevisiae* is harmless yeast but the overuse of prescription drugs such as antibiotics overtaken of probiotics and other common offenders including diet and even through air surface, in such cases it can overgrowth and turn into opportunistic pathogen. Presence of fungi or yeast in blood or the bloodstream infection of *S. cerevisiae* from throat, stool, urine, and perineum samples. Invasive



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

Saccharomyces infections have been described and are thought to be facilitated by the presence of predisposing factors which are associated with appearance of medical techniques, such as ICU admission/how intensive care units are organized, use of broad spectrum antibiotics, having Intravenous catheters, probiotics, malignancy, increase numbers of organ transplantation, bone marrow transplantation, oral infection and most likely in HIV/AIDS have exponentially increase the number of patients with impair immunity. Most yeast are part of the environment that surrounds us and can even be part of the mucous membranes of the patient, difficult to determine the origin of infections.

Saccharomyces cerevisiae was first reported in 1970 in a patient with a prosthetic mitral valve since then many fungemia cases reported caused by this yeast [55]. Although Saccharomyces cerevisiae is consider as a harmless pathogen but several reports shows this fungus may cause severe invasive infection. S. cerevisiae var. boulardii is the strain of Saccharomyces cerevisiae that is used in probiotic supplements because of its ability to resist the action of gastric acid and bile. It has been recently demonstrated that some of infection are related to S. boulardii therapy were patients with mortality condition shows the colonies of S. boulardii in blood, were there report shows, they have receive probiotics supplements previously or ingestion of probiotic supplement. Sometimes cause of infection, where only by lying in the neighbouring bed received the probiotic supplement. The most frequent risk factors were intravenous catheter use and previous treatment with antibiotics. It can causes invasive infection like pyelonephritis in immune competent patient. Most of hematologic or solid organ malignancies other risk factors include chronic kidney disease, continuous ambulatory peritoneal dialysis, cirrhosis, total parenteral nutrition and solid organ or stem cell transplantation. Infections caused by contamination of medical devices through insertion places of intravenous catheters or presence of an indwelling urinary catheter (urinary tract infection) described as a risk factor of infection. One of the strains of saccharomyces and candida spp. can exploit local or systemic weaknesses in host resistance, to cause disease in virtually any part of the body known as candidiasis. Candida albicans and other candida species are most remarkable pathogenic fungi which cause various nosochemical infections annually. The main characteristic of fungal infection is that it produced as a result of reduce immunity.

Systemic fungal disease due to *S. cerevisiae* has been recorded occasionally and is most frequently found in severely ill patients. Yeast is first colonized the oropharynx of the immunocompromised host and was then aspirated to the lungs where it entered the blood stream and spread hematogenously to spleen and intestine. Under the normal condition these organism is not capable of producing infection but, when the immune response is weakened it attack the host. Another general characteristic is that they are frequently moderate and localized. Fungal pathogen is able to produce fungal disease, systemic infection and even death in the worst science [42]. All this data has changed the status of *S. cerevisiae*, which is now consider as emerging opportunistic pathogen.

II. DISCUSSION

The data searched for our literature revealed that, Saccharomyces invasive infection is rare in all fungal infections, although infection increases after 1990. Fungus is part of flora of soil and plants which is normal but, sometimes it act as enemy for humans they contaminate food which found in gastrointestinal tract. Generally Saccharomyces cerevisiae consider as non-pathogenic and a virulent, it makes colonize in respiratory tract and urinary tract particularly in setting of chronic underlying diseases which are isolates from clinical specimens along with other pathogens and opportunistic organisms. Malnutrition is one of risk factor associated with fungemia, and make direct or indirect impact on immune responses. For understanding Saccharomyces cerevisiae infection European study group in epidemiological markers, found the application of microsatellite polymorphism develop such molecular markers. This technique use non-radioactive method which appear specific for Saccharomyces cerevisiae species. This observes mutations in DNA sequence flanking repeats which lead to negative PCR results. Saccharomyces boulardii is subspecies of Saccharomyces cerevisiae species which obtained by positive PCR result. This suggests strongly towards Saccharomyces boulardii species. Phenotypic Appearance and characteristics of Saccharomyces boulardii are lack of galactose assimilation and lack of alpha-glycosidase activity. Lack of polymorphism of Saccharomyces boulardii isolates result obtained ECORI - generally. Virulence study with animal model determine through RFLP which is significantly different among isolates. This technique is insufficient for accurate identification of closely related species, which highlights pivotal importance of molecular techniques such as Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP), Matrix Assisted Laser Desorption/Ionisation Time-of-Flight mass Spectrometry (MALDI-TOF MS) an DNA sequencing in the clinical laboratory. This idea conflict, that demonstrate the virulence as tested in murine module in clinical isolation and is associated of pattern through RFLP typing method.



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

This literature showed that Saccharomyces cerevisiae invasive fungal infection, fungemia occurs in immunecompetent patients and its make contribution to mortality in immune-compromise patients, enter translocation of ingested micro-organism and CVC (central venous catheter) insertion is main source of bloodstream infection. Literature cases describe and patient's shows fast response, they were immune-compromised, after suspension it can treated by probiotics preparation, CVC removal and antifungal therapies. These observations, takes together, underscore the prognostic importance of rapid diagnosis of fungemia. In paediatric patients invasive fungal infections associated with high mortality and morbidity. Some candida species fungal infection is most common, occurs in blood and recovered. Saccharomyces cerevisiae grown at 42°C which is determine through immune-compromised mice and form pseudohyphae. Important role of virulence of Saccharomyces cerevisiae infection is SSDI which encode protein and affects various cellular processes. Translocation supports the fungemia occur for short periods of time while sometimes it is not, even when they could not exclude After using standard procedures, some biochemical features make it difficult to distinguish between Saccharomyces cerevisiae and Saccharomyces boulardii. Experiments in murine model of invasive infection, Saccharomyces boulardii showers intermediate virulence in both immune competent and immunocompromised mice. Some cases showers that treatment with Saccharomyces boulardii was not safe which is reported classically and enhances physicians to be careful to prescribe probiotics compound, particularly patients suffering with bowel disease such as C. difficile associated colitis. Due to increase in immunocompromised disease patients there is increase in infection through Saccharomyces cerevisiae. Such as vaginitis due to Saccharomyces cerevisiae is extremely rare infection. Saccharomyces cerevisiae sub-species Saccharomyces boulardii consider being dangerous because fungemia is not limited infection only in immunocompromised patients. With increase in population chronic or debilitating diseases, at risk factor increase of immunosuppressed drugs or broad spectrum antibiotics, also parenteral nutrition and use of CVC's. Also for prevention of Antibiotic induced diarrhoea in ICU patients. Freeze-dried preparation labelled of Saccharomyces boulardii is used in several countries as bio therapeutic agents. Majority of Saccharomyces cerevisiae strains are isolates found invasive in nature causing infections. Saccharomyces cerevisiae act as commensals to digestive tracts to contaminate food this shows the epidemiologic characteristics were not fully known. With increase in colonization rates in hospitals patients suffers hematologic disease. Both Candida and Saccharomyces species infection are difficult in differentiation because of in both the cases Chorioretinitis and esophagitis are present but this infection is differentiation due to infection along with micro-organisms, such as endocarditis. Some symptoms shows while infection cause of Saccharomyces cerevisiae in patients developing fever, malaise with nausea, and also night sweat. Bone marrow and urine specimens show isolation of yeast while patients are recovered though/by stop ingesting food containing yeast. Recently pandemic causing COVID-19 virus with patients suffering from immunosuppression which is respiratory deterioration and trigger performance of high resolution CT-Scan (computated tomographyn-scan) and consecutive BAL (Bronchoalveolar lavage). This COVID-19 causing patients are very challenging and performing CT-Scan on a mechanically ventilated and critically ill. X-rays of patient's chest keep bed side and are therefore, standard imaging procedure during COVID-19 patients on ICU (intensive care unit). Due to risk of airborne transmission of SARS-COV-2 regular bronchoscopies are avoid this shows it increase in risk for developing of Saccharomyces cerevisiae infection in COVID-19 patients. Due to availability of new therapies for malignant, inflammatory and debilitating chronic diseases, in addition to increase of diagnostic and therapeutic procedures, increase risk for pathogens, for rare fungal species which change global scenario for clinical mycology. In our literature shows there is no use of intravascular device, like prosthetic valves, aertobifemoral grafts which contaminates during fungemia and potentially increase risk foe fungemia and therapeutic failure. Report suggests risk of fungemia colonization and transmission within the hospital setting if proper hygiene and sterility are not maintained. Invasive Saccharomyces infection due to use of probiotic supplements with risk factor in patient's immunosuppression, CVC antibiotics use, critical illness and ICU hospitalisation can infect blood culture.

The study investigate natural *Saccharomyces cerevisiae* isolates 40 powerful tool to investigating the genotype and phenotype relationship. Evolutionary genome variants are wide phenotypic landscape of this yeast. Our study lays the foundation of Genome Wide Association Studies (GWAS) in *Saccharomyces cerevisiae* and provides population Genomic resources matches of other model organism Single Nucleoside polymorphism (SNP) play role in modulation of phenotypic landscape. GWAS captures genetic variants, SNP's copy number variants and genome contents providing genetic architecture and the source of missing heritability. Antifungal drugs which are effective resistance to *Saccharomyces cerevisiae* infection fungemia is "Fluconazole" and "Voriconazole" reported as good in in vitro against fungal infection, which associate with clinical syndromes like endocarditis, aortic graft infection, and also fever with unknown origin. While "Fluconazole" drugs act as emergency drugs for *Saccharomyces cerevisiae* infection whether, "Voriconazole" exhibits good efficacy. An MIC90 of <0.25 mg/L and MIC (Measuring Drug Susceptibility) value for



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

Amphotericin-B and Fluconazole were 0.19 and 32 mg/L. In switched phenotype Fluconazole developed as cross resistance and multidrug resistance with accumulation of mutations conferring resistance to all antifungal agents have been observed in individual patients. Using of antifungal drugs like Amphotericin-B, Fluconazole, Mycafungin, Clotimazole, Capsofungin and Voriconazole at different dosage level along with CVC's removal found to be effective therapeutic option for patients with *Saccharomyces cerevisiae* invasive infection Fungemia. Amphotericin-B is in vivo resistance to candida fungal infection and also selective gene expression in the adaptive response.

III. CONCLUSION

Through our literature we concluded that, fungal infection by Saccharomyces cerevisiae (yeast) organism is increase in report as agent of invasive infection, especially in immunocopromised or critically ill patients. S. boulardii subtype use in probiotic preparation is also the reason of infection which account for nearly 40% of infectious cases, for which special caution should be taken while use. With the invasive Saccharomyces infection according to our literature acute cholangitis disease, critical illness CVC insertion, ICU admission, Probiotic preparation, Broad-spectrum Antibiotic use and immunosuppression were associated with infection. Patient who has contacted/ associated with bakers or brewer's yeast act as risk factor should consider as a potential cause of infection, appropriately when patient are not responding to antibiotics, surgical debridement and lavages. Supernatant of probiotic S. boulardii helpful in inducing anti proliferative activity, apoptosis and reduction of 'survivin' gene excretion on human gastric adenocarcinoma including EPG and RDB cells, RDB has less effective cytotoxic anticancer activity then SBS cell against EPG gene. Due to complex sketch of glucans and nano protein through the cell wall show anticancer property and make less regulatory expression of surviving gene and so apoptosis and cell death progression in the cancer cell. For these reason probiotic preparation is effective for infection, because SBS (short bowel syndrome) act as prospective drugs or complementary treatment against gastric cancer and chronic diseases. In neutropenia time period is not determine which also an important risk factor for invasive fungal infection. Cause of death in IFI in presence of AML an association of early clinical and laboratory factor. Also bloodstream infection, CRP value (sign of serious infection) < 9mg/dl and pneumonia were aligns with infection. S cerevisiae infection is increase which need more study in rare diseases like virginity. It is challenging and require prolong therapy for treatment. Our case study and discussion substantiate without any doubt high fertility/mortality of candida causing fungal infection Candidemia in patient with immunocopromised critically ill who adequate first line therapy and high adherence.

Study has some outcome that underline allogeneic stem cell transplantation are main factor associated with infection. Although antifungal prophylaxis and use of pre-emptive antifungal therapy in neutropenia patient was initiated three day after symptoms suggest specific strategies (i.e. preventive strategies) kinetic action against infection shown by some antifungal drugs and first option or name of drug come in front to prevent is fluconazole followed by amphotericin B, Voriconazole, Caspofungin, Mycafungin, Anidulafungin etc. But most common and viable dose of fluconazole against *S. cerevisiae* infection is 400mg/day such as amphotericin B has nearly 100mg/day and for other drugs are dissociate according to infection cause in patient. It can also prevent by wearing gloves, removing catheter, less use of probiotic preparation, less antibiotic use, avoiding ICU admission. Another fact of amphotericin B drug is, widely used antimitotic in cell culture because it bind to sterol and form pores in membrane, which cause small molecules come out and stable in cell culture for 3 days at 37°C which effective against *S. cerevisiae* infection while performing experiment. In genome sequencing combined with phenotyping 1011 isolate of *Saccharomyces cerevisiae* variation. The evolutionary history of genome provides relationship of genotype and phenotype. GWAS in *Saccharomyces cerevisiae* provide the population of genomic resources of model organism. In our study GWAS, SNP's, CNV (copy number variation) providing the source of missing heritability SNP's play role in modulating phenotyping landscape.

Among in all fungal infection, antifungal therapies are specific for different underline conditions appropriately, for fungal infection which gives mandatory positive outcome toward patients. We can predict future output that patient receive therapy which get outcome of become better cure or condition become worst. These invasive infection associate with high mortality of COVID-19 patient; proper diagnosis and treatment is important for clinical sources. The epidemiology are needed to define the invasive among the patient with COVID-19 studies include that the systematic blood and biological sample collection enhance future research in invasive fungal infection.



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

REFERENCES

- 1. Alba-Lois, L. and Segal Kischinevzky, C., Beer and Wine Maker. Nature Education, 2010; 3(9):17.
- 2. Gianni Liti, The Natural History of Model Organisms: The fascinating and secret Wild life of the budding yeast *Saccharomyces cerevisiae*, 2015;69.
- 3. P. Jauhten, O. Ponomarova et.al. Saccharomyces cerevisiae metabolism in ecological context. 2016; 16(7).
- 4. J. Boynton, Duncan Greig, The ecology and evolution of non-domesticated Saccharomyces species L 2014 ;(34).
- 5. H. Alexander, Flor of yeast *Saccharomyces cerevisiae* Their ecology, genetics and metabolism. International J. of food technology, 2013; 167:269-275.
- 6. Roger Schneiter, Genetics, Molecular and Cell Biology of Yeast. Uni of fribourz susse, 2004.
- 7. ^{1*}Montes de Oca, R., ¹Salem A Z M , ²Kholif, A E , ¹Monroy H, ¹Perez L S, ¹Zamora, J L And ¹Gutierez, A, Yeast: Description and structure, Jan2006.
- 8. Michael Hanscho¹, David E. Ruckerbauer², Neha Chauhan³, Harald F Hofbauer, Stefan Krahulec et.al, Nutritional requirements of the BY series of *Saccharomyces cerevisiae* strains for optimum growth, Institute of biosciences, 12,796-808,2012.
- 9. Matt Kaeberlein*, Christopher R. Burtner, Brian K. Kennedy*, Recent Developments in Yeast Aging", plos genetics2007; vol3(5):655-660.
- 10. Valter D. Longo^{1*}. Gerald S. Shadel², Matt Kaeberlein^{3,4} and Brian Kennedy^{4,5,*}, Replicative and Chronological Aging in *Saccharomyces cerevisiae*, R. cell metabolism, 16: 2012.
- 11. Ramamurthy Mani, Robert P. St. Onge, John L. Hartman IV, Guri Giaever, and Frederick P. Roth, Defining genetic interaction, The National Academy of Sciences of the USA,2008;vol.105(9):3461-3466.
- 12. Neil R. Adames¹, Jenna E. Gallegos², Jean Peccoud³, Yeast genetic interaction screens in the age of CRISPR/Cas, Current Genetics, 2009;65:307–327.
- 13. Benjamin Boucher, Saragh jenna, Genetic Interaction Network: better understanding to better predict. 2003; 4(290):1-16.
- 14. David Botstein, Gerald R. Fink, Yeast: An Experimental Organism for 21st Century Biology. Genetics, Vol. 189, 695–704, Nov2011.
- 15. Mark A. Mayad, Brewer's/Baker's yeast (*Saccharomyces cerevisiae*) and preventive medicine: part II. 2008; vol28 (1):75-5.
- 16. C. Gottchalk, B. Biermaier, et al., Ochratoxin A in brewer's yeast used as food supplement.2006;vol.32:1-5.
- 17. Guslandi, M., Saccharomyces boulardii plus refavinin in masalamine involvment ulcerative colitis.
- 18. Akon H. Enyenihi and William S. Saunders, Large-Scale Functional Genomic Analysis of Sporulation and Meiosis in *Saccharomyces cerevisiae*. Genetics Society of America, Jan 2003; 163:47–54.
- 19. Aaron M. Neiman, Sporulation in the budding yeast Saccharomyces cerevisiae, Genetics, Nov2011; vol.189: 737-765.
- 20. Michael K. Jensen *et.al.* Recent application of synthetic biology tools for yeast metabolic engineering, J. invest, FEMSyeast Res. 2015; 15(1): 1-10.
- 21. Richardson S. Mitchell,L.A., Stracquadanio G., Yang K. et.al., Design of synthetic yeast genome. Science 2017; 355:1040-1044.
- 22. Annaluru N., Muller H., Mitchell L.A., Ramalingam S., Stracquadanio G. *et.al.*, Total synthesis of functional designer eukaryotic chromosomes. Science 2014; 344:55-58.
- 23. I.S. Pretorious and J.D Boeke, Yeast 2.0-connecting the dots in the construction of the world are first functional synthetic eukaryotic genome, FEMS yeast research 2018; vol.1:18(4).
- 24. Andria A. Dunia,* Mary E. Miller,¹ and Jill B. Keeney,¹ Budding yeast for Budding Geneticists: A primer as the *Saccharomyces cerevisiae* model system; Genetics May2014; vol.197:page no.133-48.
- 25. Angoulvant A.E. and Hannequin C. *et.al*, Invasive Saccharomyces Infection: A Comprehensive Review, CID 2005; 41:1059-68.
- 26. John N. Aucott, John fayen, Hans Grossnicklas, Anne Marrissey, Micheal M. Lederman and Robert A. Salata, Invasive Infection with *Saccharomyces cerevisiae* Report of Three Cases and Review, R. of infectious Disease, 1989; vol.12:406-411.
- 27. Maria Fernanda Landaburua, b, Gabriela A Lopez Daneria, Silvia Rellosoa, Leandro Jorge Zarlengab, Monica Alejandra Vinateb, Maria Teresa Mujicaa,*, Methaemoglobinaemia with concurrent blood isolation of Saccharomyces and Candida. Arch. Dis. Child. Fetal Neonatal Ed. 2003;88: F444-F446.
- 28. Hengyao Nilu¹, Woo-Hyun Chung², Zhu Zhu², Youngho Kwon¹, Weixing Zhao¹, Peter Chi¹, Rohit Prakash¹, Changhuyn Seong¹, Dongqing Liu¹, Licy Lu¹, Gregory Ira^{2,3}, & Patrick Sung^{1,3}, Mechanism of the ATP-dependent DNA End Reaction Machinery from *S. cerevisiae*. PMC 2011; 467(7311):108-111.
- 29. I Karaa, F. Yidirima, O. Ozgenb, S. Erganisc, M Aydogdud, M. Dizbayb, *et.al, Saccharomyces cerevisiae* fungemia after probiotic treatment in an invasive care unit patient. Mycmed 2017; 730:1-4.
- 30. Landaburu M F, Gabriela A. Lopez daneri, Silvia Relloso, et. al., Fungemia following *Saccharomyces cerevisiae var. boulardii* probiotic treatment in an elderly patient. Rev Agent Microbiaol.2020; 52(1):27-30.



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| <u>www.ijirset.com</u> | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

- 31. Serkan Atici, Ahmet Soysala, Kivilcim Karadeniz Cerit, Yilmaz, AKsuc B, Kiyan G, Bakir M. Catheter-related *Saccharomyces cerevisiae* fungemia following *Saccharomyces boulardii* probiotic treatment: in a child in intensive care unit and review of the literature. Med Mycol Case Rep.2007; 15:33-5.
- 32. Patricia Munoz¹, Emilio Bouza¹, Manuel Cuenca-Estrella³, Jose Maria Eiros¹, Maria Jesus Perez², Mar Sanchez-Somolinos¹, Cristina Rincon², Javier Hortal², & Teresa Pelaez¹, *Saccharomyces cerevisiae* fungemia: an emerging infectious disease. Clin Infect Dis. 2005; 40:1625-34.
- 33. Mariappa Premanathan^{1,2,3}, Fathi Abdullah Shakurfow¹, Ahmad Alii Ismail³, Mohamad Ayad Berfad⁴, Adel Tawfik Ebrahim⁵ and Moussa Malid Awaj⁶, Treatment of Oral Candidiasis (thrush) by *Saccharomyces cerevisiae*. Int. J. Med. Med. Sci.2011; vol.3(3):83-86.
- 34. Ludo A.H. Muller* and John H. McCusker, Microsatellite analysis of genetic diversity among clinical and nonclinical *Saccharomyces cerevisiae* isolates suggests heterozygote advantage in clinical environments. Mol Ecol.2009;18(13):2779-2786.
- 35. Dimas Alexander Kliemann1, Vicente Sperb Antonello2, Luis Carlos Severo1,3,4, Alessandro Comaru Pasqualotto1,5, *Saccharomyces cerevisiae* oesophagitis in a patient with oesophageal carcinoma. J. Infect Dev Ctries 2011;5(6): 493-495.
- 36. Lynne V McFarland, Systematic review and meta- analysis of *Saccharomyces boulardii* in adult patients. World J. of Gastroenterology 2010; 16(18):2202-2222.
- 37. Rosa de Llanosa, Amparo Querola, Javier Pemanb, Miguel Gobernadob, et al. Food and Probiotics strain from the *Saccharomyces cerevisiae* species as a possible origin of human systemic infections. Int J. of food Micro 2006;110: 286-290.
- 38. R. de Llanos, M T Fernandez- Espinar, A Querol, A comparison of clinical and food *Saccharomyces cerevisiae* isolates on the basis of potential virulence factors. 2006;90:221-231.
- 39. S. Henry, L D Hondt, M Andre, X. Holemans and J. L. Canon, *Saccharomyces cerevisiae* fungemia in a head and neck cancer patient: a case report and review of the literature. Acta Clinica Belgica, 2004; 59-3.
- 40. Piseth Seng^{a,b,c,*}, Alexandre Cerlier^d, Carole Cassagne^{e,f}, Mathieu Coulange^g, Regis Legre^d, Andreas Stein^{a,b,c}, *Saccharomyces cerevisiae* osteomyelitis in an immunocompetent baker. IdCase 2006; 5:1-3.
- 41. Roberto Perez-Torrado, Amparo Querol, *Saccharomyces cerevisiae* show low levels of traversal across human endothelial barrier in vitro [verson2, referees:2 approved] F1000Research 2017;6944.
- 42. Roberto Perez-Torrado, Amparo Querol, Opportunistic Strain of *Saccharomyces cerevisiae*: A potential Risk Sold in Food Products. Frontiers in Microbiology,2016;vol.6:1-5.
- 43. John H. McCuske, et.al. Genetic Characterisation of Pathogenic *Saccharomyces cerevisiae* Isolates. Genetics soc. of America, 1994; 136:1261-1269.
- 44. Mc Cusker J H, Clemons K V, Steven D A, Devis RW, *Saccharomyces cerevisiae* virulence phenotype as determined with CD-1 mice is associate with the ability to grow at 42°C and form pseudo hyphae Infect Immune 1994;
- 45. Roberto P. T., Llopis S., P. Benedetta et.al, Comparative Genomic analysis reveals a critical role of De Nova nucleotide biosynthesis for Saccharomyces cerevisiae virulence. Plos one, 2015; 10(3):1-16.
- 46. Ossama W. Tawfik¹, Christopher J. Papasian^{2*}, Anita Y Dixon^{1,3}, and Lonna M. Potter³, *Saccharomyces cerevisiae* Pneumonia in a patient with acquired immune deficiency syndrome. J. of clin. microbiol, 1989; 27(7):1689-1691.
- 47. J D Sobel, J Vazquez, M Lynch, C Meriwether, and M J Zervos, Vaginitis due to *Saccharomyces cerevisiae:* Epidemiology, clinical aspects and therapy. CID 1993; 16:93-9.
- 48. K V Clemons, L C hanson, D A Stevens, Colony Phenotype switching in clinical and non-clinical isolates of *Saccharomyces cerevisiae*, J. of Med and veterinary mycology; 1996; 34:259-264.
- 49. Christopher J Shoff and Jhon R Perfect, Uncommon yeast and mold causing Human disease, Encyclopaedia of mycology, 2020; 1-14.
- 50. Alan Murphy, Kevin Kavanogh, Emergence of *Saccharomyces cerevisiae* as human pathogen Implications for biotechnology, 1999.
- 51. Radu Agrosoaie^{1*}, Adrin Streinu-Cercel^{2,3}, Doina Azoicai , Codrina Bejan¹, Olga Dorobat³, Alexandru Mihai, et.al, Epidemiological data and antifungal susceptibility in invasive fungal infection-a Romanian infectious diseases tertiary hospital's experience. Preliminary report, Revista Romana de Medicina De Leborator, 2017; vol.25 (4)345-352.
- 52. Horn R, Wong B., Kiehn T. E. et.al, Fungemia in a cancer Hospital: Changing frequency, earliar onset, and results of therapy. R. of Infectious disease, 1985; vol.7 (5):646-655.
- 53. Maiken Cavling Arendrup,^{1*} Sofia Sulim,² Anette Holm,³ Lene Nielson,⁴ Susanne Dam Nielsen,⁵ et.al, Diagnostic issue, clinical characteristics and outcomes for patients with fungemia. J. of clin microbial, 2011; vol.49: 3300-3308.
- 54. David Perlmutter, MD, The candida cure: Yeast, Fungus & Your Health, 2014.
- 55. M. Fadhel *et al.*, *Saccharomyces cerevisiae* fungemia in critically ill patient with acute cholangitis and long term probiotic use, Medi mycology care report,2019;vol.23: 23-25.
- 56. Leslie K. Derr. The Involvement of Cellular Recombination and Repair Genes in RNA-Mediated Recombination in *Saccharomyces cerevisiae*, Genetics 148: 937–945.



| e-ISSN: 2319-8753, p-ISSN: 2320-6710| www.ijirset.com | Impact Factor: 7.512|

|| Volume 10, Issue 6, June 2021 ||

| DOI:10.15680/IJIRSET.2021.1006372 |

- 57. Tsukamoto Y, Jun-ichi Karto, Silencing factors participate in DNA repair and recombination in *Saccharomyces cerevisiae*, nature, 1997; vol.388.
- 58. Flona E. Benson, Peter Baumann et.al, Synergistic action of Rad51 and Rad52 in recombination and repair, nature, 1998; vol.39.
- 59. Cantero A P, Thomson P et.al, Antifungal susceptibility of *Saccharomyces cerevisiae* and therapy in a murine model of disseminated infection. Rev Iberoam Microl. 2019;36(1):37-40..
- 60. Z. Salvdo, F N Arroyo-Lopez, Temperature adaptation markedly determines evoluation within the genus Saccharomyces, App and Envir microl, 2011; vol.77:2292-2302.
- 61. Irene Stefanini^{a,1}, Leonardo Dapporto^{b,c,1}, Jean-Luc Legras^{d,e,f,} Antonio Calabretta^{a,b}, Monica Di Paola^g, Carlotta De Felippo^h, Roberto Violac, Paolo Capretti, Mario Polsinelli, Stefaon Turillazzi, and Duccio Cavalieri Role of social wasps in *Saccharomyces cerevisiae* ecology and evaluation, PNAS, 2012; vol.109:13398-13403.
- 62. Stacia R Engel,*1 Fred S Dietrich, Dianna G Fisk,* Gail Binkley*, Rama Balakrishnan, Maria C Costanzo, Selina S Dwight, Benjamin C Hitz, Kalpana Karra, Rober S Nash, et.al, The reference genome of *Saccharomyces cerevisiae*: then and now, genetics, 2014;vol.4: 389-397.
- 63. Marco Cassone,^{1*} Pietro Serra,1 Francersca Mondello² Antonietta Girolamo,² Sandro Scafetti,³ Eleonora Pistella,1 and Mario Venditti1 Outbreak of *Saccharomyces cerevisiae* Subtype boulardii Fungemia in Patients Neighboring Those Treated with a Probiotic Preparation of the Organism. J. of clin microl, Nov. 2003; vol.43: p. 5340–5343.
- 64. C. Hannequin,^{1,2}* A. Thierry,² G. F. Richard,² G. Lecointre,³ H. V. Nguyen,⁴ C. Gallardin,⁴ and B. Dujon, Microsatellite typing as a new tool for identification of *Saccharomyces cerevisiae* strains. J. of medi microl. 2001; vol.39: 551-559.
- 65. Cezar V W Riche, Renato Cassole., et.al, (2020) Is the frequency of candidemia Increasing in COVID-19 patients receiving corticosteroids, J. Fundi, 2020; 286(6):1-4.
- 66. Abdullah M S, AI-Hatmi, COVID-19 associated invasive candidiasis, J of Infection, 2020; e45-e46.
- 67. Ioannis ventoulis¹, Theopisti Sarmourli², Pinelopi Amoiridou¹, Paraskevi Mantzana³, Maria Exindari Georgia Gioula, and Timoleon-Achilleas Vyzantiadis²,* Bloodstream infection by *Saccharomyces cerevisiae* in two COVID-19 patients after receiving supplement of Saccharomyces in the ICU, J. Fundi 2020; 98(6):1-7.
- 68. Babak pakbin, et.al, Probiotic *Saccharomyces cerevisiae var. boulardii* supernatant inhabits surviving gene expression and induces apoptosis in human gastric cancer cells, Food sei Nutr. 2020; 9:692-700.
- 69. Ujjwayini Roy¹, Laxman G. Jessani², Shivapkash M. Rudramuthy³ Ram Gopalakrishnan², et.al, Seven cases of Saccharomyces fungemia related to use of probiotics, Mycosses 2017; 1-6.
- 70. Ewa Zymanczyk-Duda, Malgorzata B R, et.al, Yeast as a versatile tool in biotechnology. Yeast-industrial applications, 1017.
- 71. S. Cherifi, J. Robberecht, Y. Miendje, *Saccharomyces cerevisiae* fungemia in an elderly patient with clostridium difficile colitis. Acta clin Belgica, 2004; 59-3.
- 72. Adela Enacha-Angoulvant¹ and Chritophe Hannequin², Invasive Saccharomyces infection a comprehensive Review, CID, 2005;41:1555-68.
- 73. Jumanah N. Algazaq¹, Kevan Akrami², Fernando Martinez³, Allen mcCutchan², and Ajay R. Bharti², *Saccharomyces cerevisiae* Laryngitis and Oral Lesion in a Patient with Laryngeal Carcinoma, infectious disease, 2017;1-5.
- 74. Heather E. Hallen-Adam and Mallory J. Suhr, Fungi in the all human gastrointestinal track, virulence2017; vol.8:352-358.
- 75. J. Michael Cherry, Caroline Adler, Catherine Ball, Stephan A Chervitz, Selina S Dwight, Erich T Hester, Yankai Jia, Gail Juvik, et.al, SDS: Saccharomyces genome database, Nucleic acid research, 1998;vol.26: 73-88.
- 76. Karen R Christie, Shuai Weng, Rama Balakrishna, Maria C Costanzo, Kara Dolinski1, Selina S Dwight, Stacia R Engel, et.al, Saccharomyces genome database (SDS) provides tools to identify and analyse sequences from *Saccharomyces cerevisiae* and related sequences from other organism. NAR, 2004, vol.32: D311-D314.



Impact Factor: 7.512





INTERNATIONAL JOURNAL OF INNOVATIVE RESEARCH

IN SCIENCE | ENGINEERING | TECHNOLOGY





www.ijirset.com