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Yeast species of diverse functionality in health sciences: A concise report

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Abstract

The health of a living being is of paramount importance in productivity, which may be human productivity, animal productivity, crop plant productivity, or aquaculture productivity. Among the several pathogenic entities responsible to affect health, yeast is emerging as an important pathogen, while on the other hand; it is also being used as a probiotic agent in treating certain diseases of human and animals. These single-cell budding microorganisms are inhabitant of soil, water, and environment, and are associated with decomposing and fermenting material, living being, and agricultural crops and produce. These are specific in their association, activities, and role and belong to different genera/species.

The most common yeast species that act as agents of human disease are species of *Candida particularly Candida albicans, Candida tropicalis, Candida glabrata, Candida parapsilosis, and Cryptococcus neoformans*. Similarly, the most evident emerging yeast pathogens are *Malassezia furfur, Trichosporon beigelii, Rhodotorula species, Hansenula anomala, Candida lusitaniae,* and *Candida krusei*. The yeast responsible for animal infection and diseases mostly belongs to *Candida* species, the most important being *C. albicans, C. glabrata, C. parapsilosis, C. tropicalis,* and *C.krusei* besides some other candida species to cause various types of infectious diseases in animals. *Cryptococcus neoformis* and *Cryptococcus gattii* are other two important yeast of the *Cryptococcus* genus implicated in animal diseases. Other cryptococcus species like *C. laurentii* and *C. albidus* affect immunocompromised animals. The yeast *Malassezia* is also reported to cause disease in animals. Bird's infections are mostly reported to cause by species of *Candida.*

The yeast species useful as probiotics in the treatment of human health ailments includes *Saccharomyces boulardii*, while in the use of animal and poultry health is *Saccharomyces cerevisiae.*

The yeast species known to cause disease infection in Marine animals include the ascomycetous yeasts which comprise 9 known species from four genera (viz. *Candida, Meyerozyma, Kodamaea*, and *Wickerhamomyces*), and the basidiomycetous yeasts comprises 10 known species from eight genera (viz. *Vishniacozyma, Filobasidium, Naganishia, Papiliotrema, Sterigmatomyces, Cystobasidium, Rhodotorula*, and *Rhodosporidiobolus*). The species with the highest occurrence is *Rhodotorula mucilaginosa.*

The yeast species involved in plant growth-promoting activities directly or indirectly includes the species of *Candida, Rhodotorula, Saccharomyces, Geotrichum, Williopsis, Hanseniaspora, Meyerozyma, Torulaspora, Trichosporon, Pichia, Debaryomyces, Lachanceae and Rhodosporidiu ;* While the yeast species implicated in plant disease control activities includes *Candida tropicals, Candida valida, Candida saitoana, Saccharomyces cerevisiae, Saccharomyces kudriavzevii, Rhodotorula glutinis, Rhodotorula mucilaginosa, Zygosaccharomyces bailli, Aureobasidium sp, Pichia caribaea, Geotrichum candidum, Trichosporon asahii and Eremothecium cymbalariae.* The diverse functionality of these yeasts is discussed in this paper.

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1. Introduction

The yeasts constitute a large and heterogeneous group of microorganisms that are currently attracting increased attention from scientists and industry. Numerous and diverse biological activities make them promising candidates for a wide range of applications not limited to the food sector. In addition to their major contribution to flavor development in fermented foods, their antagonistic activities toward undesirable bacteria, and fungi are now widely known. These activities are associated with their competitiveness for nutrients, acidification of their growth medium, their tolerance to high concentrations of ethanol, and the release of antimicrobial compounds such as antifungal killer toxins or "mycocins" and antibacterial compounds. While the design of foods containing probiotics (microorganisms that confer health benefits) has focused primarily on *Lactobacillus* and *Bifidobacterium, the yeast Saccharomyces cerevisiae var. boulardii* has long been known as effective for treating gastroenteritis. In this report, the yeast pathogen which affects human health, animal and bird's health, aquaculture health, and plant health along with their beneficial antimicrobial activities are discussed.

2. Review

2.1. Yeast species implicated in human disease infection

The most common yeast species that act as agents of human disease are *Candida albicans, Candida tropicalis, Candida glabrata, Candida parapsilosis,* and *Cryptococcus neoformans*. The incidence of infections by other yeasts has increased during the past decade. The most evident emerging yeast pathogens are *Malassezia furfur, Trichosporon beigelii, Rhodotorula species, Hansenula anomala, Candida lusitaniae,* and *Candida krusei*. Organisms once considered environmental contaminants or only industrially important, such as *Candida utilis* and *Candida lipolytica*, have now been implicated as agents of fungemia, onychomycosis, and systemic disease.

The unusual yeasts primarily infect immunocompromised patients, newborns, and the elderly. Yeasts of the genus *Malassezia* are unique among the fungal kingdom as the only species to form part of the normal human cutaneous commensal flora. In addition, *Malassezia* species are able to cause several cutaneous diseases, systemic diseases in suitably predisposed humans, and dermatitis in a wide range of animals. Thus, they exist at the very interface between commensal and pathogen and, as such, their interaction with the human immune system is of great interest

Most yeast infections in humans are caused by species of *Candida* and *Cryptococcus*. However, there are other genera that have emerged as pathogens paralleling the increases in immunocompromised populations. The genera most likely to cause infections include *Malassezia*, *Trichosporon, Pichia, Rhodotorula, Saccharomyces, Sporobolomyces, and Blastoschizomyces. Trichosporon* and *Malassezia* species are frequently involved in superficial infections, but members of the other six genera cause fungemia with or without organ invasion in compromised patients and often are resistant to antifungals thereby a challenge to treat the infection.

Current routine methods for yeast identification may be insufficient to identify the unusual yeasts within 2 days after isolation. The recognition of unusual yeasts as agents of sometimes life-threatening infection and their unpredictable antifungal susceptibilities increase the burden on the clinical mycology laboratory to pursue complete species identification and MIC determinations. Given the current and evolving medical practices for the management of seriously ill patients, further evaluations of the clinically important data about these yeasts are needed. *Trichosporon, Malassezia, Rhodotorula,* and *Sporobolomyces* are basidiomycetous yeasts characterized by their urease activity, diazonium blue B (DBB) staining reactions, guanine/cytosine (G/C) content, DNA association rates, and RNA sequencing. 7 species of these genera are often anamorphs (asexual states), *Sporobolomyces* spp. being the anamorph of the sexual stage in the genus *Sporidiobolus* and *Rhodotorula* being the anamorph of the sexual stage in the genus *Rhodosporidium.*

Saccharomyces, Pichia, and *Blastoschizomyces* are ascomycetous yeasts characterized by a lack of urease production and the formation of ascoconidia. *Saccharomyces* has a sexual cycle, some species of the teleomorphic genus *Pichia* have *Candida* anamorphs, while *Blastoschizomyces* has no known teleomorph. Although they are not recovered from clinical specimens as frequently as many *Candida spp*., they can be important pathogens. *Saccharomyces* is the most frequently encountered in clinical specimens, often as a colonizer, whereas *Pichia* and *Blastoschizomyces* are uncommon but important causes of opportunistic infections. The serious concern of yeast infection can be observed from the case of *Candida auris*. *Candida auris* was first seen as an agent of human disease in 2009, when it had been isolated from the

ear canal of a patient in Japan (Satoh et al 2009). It has subsequently spread rapidly around the world and is now a major health threat on a global scale having been associated with potentially lethal infections in patients in ICUs in Eastern and South Asia, South Africa, Europe, the USA, and South America. Sequence-based analyses have grouped *C. auris* isolates from around the world into at least four different clades, represented by clonal populations (Lockhart et al. 2017). More than 90% of isolates are fluconazole resistant and many isolates are cross-resistant to more than one of the three major classes of antifungals – azoles, echinocandins and polyenes (Lockhart et al. 2017). A few strains of this fungus are resistant to all of the major classes of antifungals used by doctors to treat fungal infections. The species has a propensity to colonize skin, and it has proven to be difficult to eradicate from ICUs. Worldwide mortality rates for disease cases with *C. auris* infections of the bloodstream approach 50%. Concern about the emergence and spread of *C. auris* has resulted in alerts being posted by the CDC (Centers for Disease Control and Prevention, USA), the ECDC (European Centre for Disease Prevention and Control, Sweden), and PHE (Public Health England, UK) . *C. auris* colonizes the skin of patients and can be transmitted via contact with patients or contaminated hospital fixtures, which has already resulted in several health care associated outbreaks. The horizontal transmission potential of *C. auris* demands strict decontamination methods and infection prevention protocols, since mortality rates in patients with systemic infections can be up to 50% (Kean et al 2018).

Necrotrophic mycoparasitism describes the ability of one fungal species to kill other fungal species. Active mycoparasitism in yeast was discovered in 1997, when species of the genus *Saccharomycopsis* were first described as necrotrophic predacious yeasts (Lachance and Pang, 1997). It has not been studied whether *Saccharomycopsis* species attack *Candida* species other than *Candida albicans* (Lachance and Pang, 1997). Predacious behavior depends on solid structural support, presumably to allow for stable cell-cell contact and has been suggested to be starvation induced. Specifically, a lack of organic sulfur-containing organic compounds such as methionine has been suggested as a trigger for predation, as all *Saccharomycopsis* yeasts share (for microorganisms) the rare feature of being unable to assimilate sulfate as their sole source of sulfur. Recently, it is reported the lack of eight genes in the sulfate assimilation pathway in draft genomes of *Saccharomycopsis fodiens* and *Saccharomycopsis fermentans.* Here it has been shown that *S. schoenii* efficiently attacks and kills a range of pathogenic *Candida* species, including the newly emerged human pathogenic yeast fungus *C. auris*. This follows the predation process using time lapse microscopy in combination with fluorescent dyes. Efficient predation as shown here could be useful for biocontrol purposes in either clinical settings for skin clearance or in agricultural settings for combatting plant pathogens.

Candidemia is a life-threatening infection caused by yeast species within the *Candida* genus, which can result in high morbidity, mortality, and extra hospital costs in the healthcare settings. Five species of *Candida* viz., *C. albicans, C. glabrata, C. tropicalis, C. parapsilosis,* and *C. krusei,* account for the vast majority of the candidemia cases. *Candida albicans* is considered as the leading cause of nosocomial candidemia in most clinical settings; however, non-*Candida albicans* species, as well as several rare yeast species have been increasingly reported in clinical settings. The normal habitat of *Candida albicans* is the mucosal membranes of humans and other warm-blooded animals, where it grows as a yeast and causes little or no damage. In fact, it can be isolated from the mucosa of up to 50% of humans - from the mouth, the gut, the vagina or, less often, from the surface of the skin. In some circumstances, however, the same strains of *C. albicans* that grow as harmless commensals can become pathogenic, invading the mucosa and causing significant damage. This usually happens when a variety of predisposing factors cause the yeast population to multiply, escaping the normal competition from resident bacteria which keep the yeast population in check. Then the yeast cells sprout a hyphal outgrowth which locally penetrates the mucosal membrane, causing irritation and shedding of the tissues.

Candidiasis is an infection caused by yeast called *Candida*. *Candida* normally lives on the skin and inside the body, in places such as the mouth, throat, gut, and vagina, without causing any problems. Sometimes, *Candida* can multiply and cause an infection if the environment inside the mouth, throat, or esophagus changes in a way that encourages fungal growth. Candidiasis in the mouth and throat is also called thrush or oropharyngeal candidiasis. Candidiasis in the esophagus (the tube that connects the throat to the stomach) is called esophageal candidiasis or Candida esophagitis. Esophageal candidiasis is one of the most common infections in people living with HIV/AIDS (Georgopapadakou & Walsh, 1994). The symptomatology of thrush includes a white speckling of the tongue and the back of the throat, resembling the speckling on the bird's chest. This is common in newborn babies, perhaps resulting from passage through an infected birth canal. It is also common in AIDS patients and people who have had a prolonged course of antibacterial therapy, reducing the normal resident bacterial population. *C. albicans* also causes vaginitis i.e. inflammation and invasion of the vaginal mucosa, especially during the third trimester of pregnancy and in women who take the pill. The predisposing factors seem to be hormonal, associated with changes in the balance of cell types in the lining epithelium of the vagina. A similar condition termed stomatitis is common in people who wear dentures. *Candida* can adhere to denture resin, and high sugar levels in the diet can also increase the adhesion by enhancing the production of a mannoprotein adhesive on the yeast cell surface. Systemic candidosis is a more serious condition, when yeast cells proliferate in the circulatory system. This can occur after invasive surgical techniques,

including the insertion of intravenous catheters to which the yeast cells adhere, providing a base from which the cells can bud and be disseminated.

Candida glabrata has been considered a relatively nonpathogenic saprophyte of the normal flora of healthy individuals, rarely causing serious infection in humans. However, following the widespread and increased use of immunosuppressive therapy together with broad-spectrum antimycotic therapy, the frequency of mucosal and systemic infections caused by *C. glabrata* has increased significantly. In fact, depending on the site of infection, *C. glabrata* is often the second or third most common cause of candidiasis after *C. albicans. C. glabrata* infections can be mucosal or systemic and are common in abnormal hosts (e.g., immunocompromised persons or those with diabetes mellitus). In contrast to other *Candida* species, *C. glabrata* is not dimorphic; consequently, it is found as blastoconidia both as a commensal and as a pathogen. *C. glabrata* infections are difficult to treat and are often resistant to many azole-antifungal agents, especially fluconazole. Consequently *C. glabrata* infections have a high mortality rate in compromised, at-risk hospitalized patients.

Unfortunately, there have been relatively few investigations of *C. glabrata* compared to other *Candida* species. Although this infection is second or third in frequency after *C. albicans*, difficult to treat, and associated with a high mortality rate, publications to date on *C. glabrata* account for only a small percentage of published studies on medically important fungal infections. Very little is known about the virulence of *C. glabrata*, and virtually nothing is known about the host defenses directed against the organism. There are only two established animal models of experimental *C. glabrata* infections (systemic and vaginal). Therefore, studies to understand the pathogenesis of *C. glabrata* infections are urgently needed.

Candida parapsilosis is an emerging major human pathogen that has dramatically increased in significance and prevalence over the past 2 decades *in neonatal and intensive care units, where patients are at the highest risk for infection,* in such a way that *C. parapsilosis* is now one of the leading causes of invasive candidiasis disease. *C. parapsilosis* infections are especially associated with hyperalimentation solutions, prosthetic devices, and indwelling catheters, as well as the nosocomial spread of disease through the hands of health care workers. Factors involved in disease pathogenesis include the secretion of hydrolytic enzymes, adhesion to prosthetics, and biofilm formation. (Trofa et al 2008). *The* environmental survival and persistence properties have been documented for Candida parapsilosis (Trofa et al 2008). Similar to *C. auris, C. parapsilosis* has been documented in nosocomial infections from environmental sources and is also known to survive for weeks on plastics, fabrics, and nonporous surfaces. The modes and mechanisms of survival and transmission of *C. parapsilosis* in hospitals can occur via horizontal transfer through medical devices or other external sources, even without prior colonization (Trofa et al 2008). Both *C. auris* and *C. parapsilosis* can survive and persist outside their host on dry, nonporous surfaces for weeks, emphasizing the importance of infection control for preventing nosocomial transmission (Welsh et al.2017*)*. Colonization of skin cells by *C. auris* or *C. parapsilosis* could contribute to prolonged outbreaks with high transmissibility in health care settings. Although, *C. parapsilosis* currently tends to display lower levels of pathogenicity and antifungal resistance than the emerging multidrug-resistant *C. auris*, the rise of antifungal resistance among *C. parapsilosis* is concerning.

Candida. kruse is an emerging yeast nosocomial pathogen. It has been considered to be a facultative saprophyte and is widely distributed in nature. *C. kruse* has been isolated from a wide variety of natural habitats including the atmosphere, soil, silage, sewage, foods, fruits, beer, and wines. The infection of *C. kruse* is primarily found in the immunocompromised people, the patients with hematological malignancies, and organ transplant recipients. Mortality rate caused by *C. krusei* fungemia is much higher than the more common *C. albicans*, which is reported to be 30–60%. *Candida* spp. has been reported to have several virulence attributes, including the production of phospholipases and proteinases, adherence to host surfaces, and hyphae formation, which help the fungus escape from the host immune defences. *C. krusei* grew with both the yeast and mycelial phases, in the infected tissues. However, the fungus typically showed less invasiveness than *C. albicans* or *C. tropicalis. C. krusei* did not penetrate the stratum corneum, while *C. albicans* generate extensive epithelial invasion and penetrated all the layers of the epithelium. (Samaranayake and Samaranayake, 1994).

The pathogenic role of *Malassezia* yeasts in skin diseases has always been a matter of controversy. Commensal *Malassezia* yeasts are clearly implicated in human skin diseases without the presence of inflammation but with heavy fungal load, such as in pityriasis versicolor. They are also associated with other skin disorders with characteristic inflammation, such as seborrheic dermatitis, atopic dermatitis, folliculitis, and psoriasis, where their role in the pathogenesis is less clear and, in some cases, speculative. Emerging evidence demonstrates that the interaction of *Malassezia* yeasts with the skin is multifaceted and entails constituents of the fungal wall, enzymes, and metabolic products, as well as the cellular components of the epidermis. Some skin disorders can be exacerbated by the interactions between *Malassezia* yeasts and the host immune system (Saunders et al., 2012). Although *Malassezia*

globosa was initially reported to be the main species associated with pityriasis versicolor, subsequent studies have shown that the distribution of other *Malassezia* species from healthy and diseased skin is equivalent. *M. globosa* and *M. restricta* are the most commonly found species on healthy and diseased human skin (Gaitanis et.al, 2013). However, other species such as *M. sympodialis* or *M. furfur* have been also associated with various human skin disorders. *M. furfur* and *M. pachydermatis* have been reported to be the cause of a low percentage of yeast systemic infections. Skin colonization by *Malassezia* species of healthy human neonates does not include *M. pachydermatis*, whereas the occurrence of other species such as *M. sympodialis* and *M. globosa* begins at birth and increases in the first weeks of life. This fact corroborates the animal origin of *M. pachydermatis* in human infections. Furthermore, it should be noted that zoonotic transfer of *M. pachydermatis* has been documented from dogs to neonates by healthcare workers who own dogs (Chang, 1998). However, fungemia produced by these yeasts may be under-diagnosed by modern automated blood systems for fungal detection if culture media with lipids are not included in the diagnostic protocol. The majority of published case reports and mini-epidemics have involved infants, children, and adults with profound immunosuppression, serious concurrent health problems, and the infusion of total parenteral nutrition with lipid supplementation through central vascular catheters. The main ingredients of this nutrition system (i.e., linoleic, oleic, and palmitic acids) are potent growth stimulants for *Malassezia* species.

The yeast genus *Cryptococcus* (teleomorph *Filobasidiella*) responsible for cryptococcosis comprises basidiomycetous yeast species, most of which are environmental saprophytes that do not cause infections in human or animal. The pathogenic agents of cryptococcosis are classified into two species, *C. neoformans* and *C. gattii* . Diseases caused by other *Cryptococcus* species, such as *Cryptococcus laurentii* and *Cryptococcus albidus*, have been reported infrequently and generally in immunocompromised hosts (Harris et al., 2012). The two species differ ecologically: *C. neoformans* was isolated primarily from bird droppings, whereas *C. gattii* was associated with trees, primarily *Eucalyptus* species, initially in Australia, where the importance of koalas feeding on these trees in perpetuating the yeast's persistence in the environment was suggested. Subsequently, infections with *C. gatti* were reported in other regions as well. In addition, differences are found in the population at risk: while *C. neoformans* infects primarily immune-compromised patients, *C. gattii* may affect people with intact immune systems (de Abreu et al, 2017). A large outbreak of human and animal *C. gattii* infections that started in 2000 in Vancouver Island have been seen during the following years.

Kodamaea (*Pichia*) *ohmeri*, previously known as *Yamadazyma ohmeri*, is an ascomycetous yeast that belongs to the *Saccharomycetaceae* family (Yamada et al, 1995). It is the teleomorphic state of *Candida guilliermondii* var. *membranaefaciens* and is widely used in the food industry for fermentation of fruits, pickles and rinds (Yamada et al, 1995). The first clinical isolation of *K. ohmeri* was made in 1984 from pleural fluid of a patient from Java, but this isolate was regarded as a contaminant. To the best of our knowledge, the first authentic case of *K. ohmeri* fungemia was described in 1998 in a 48-year-old diabetic female who had multiple underlying complications and died despite treatment with high-dose amphotericin B (Bergman et al, 1998). Since then, this species has emerged as an important opportunistic agent of fungemia in immunocompromised patients.

Trichosporon species are yeast-like anamorphic organisms that belong to the basidiomycetes yeasts. *Trichosporon* species are broadly spread in nature but mostly found in areas where warm and tropical temperatures prevail. These organisms are usually found in substrates like soil; water areas like rivers, lakes, and even seawater; decomposing wood; air; foods like cheese; scarab beetles, and faeces from birds, pigeons, bats, and cattle. In humans, they are occasionally found as part of gastrointestinal and oral cavity microbiota and can transiently colonize the respiratory tract, skin, and vagina (Galligan et al.,2019). Beigel first described the genus *Trichosporon* in 1865 upon discovering that it can cause a benign hair shaft infection. The absence of simple methods to distinguish among the species in the clinical microbiology laboratory led to multiple members of the genus *Trichosporon* being categorized together under the name *T. beigelii*. However, modern molecular techniques led to the discovery of several strains that are part of other fungi groups and the strain categorization of *Trichosporon* spp. Currently, more than 50 different subspecies and around 16 different strains cause human disease. Geographical distribution of infections due to *Trichosporon* species varies, but data collected between 1997 and 2005 during the ARTEMIS DISK Surveillance Study found that infections with *Trichosporon* are predominantly found with equal frequencies in tropical and temperate areas such as South America, the Middle East, India, Southeast Asia, Africa, Europe, Japan, and parts of south-eastern USA. *Trichosporon* spp. causing an invasive infection develops into the disease known as *Trichosporon*osis. This infection has a mortality rate between 50% and 80%, and it is the second or third cause of fungemia in immunocompromised patients just after *Candida spp. Trichosporon*osis is considered an endogenous disease because the microorganism is commonly found as a part of the flora in the gastrointestinal tract, lungs, and skin. These opportunistic systemic infections have gained clinical importance due to their growing prevalence in certain groups of patients. Neutropenia is the main risk factor. A relationship between *Trichosporon*osis and having undergone an invasive clinical procedure (e.g., probes and catheters) has been established as well.

The genus *Trichosporon* represents a group of imperfect filamentous yeast fungi of the family Cryptococcaceae, order Monilialis, which are normal flora of the respiratory and digestive tracts of humans and animals. As part of the normal flora of the human skin, *Trichosporon* spp. may cause benign cutaneous infections, known as white piedra, when the organisms penetrate the cells of the cuticle, forming whithish-yellow nodules on the hair follicles especially of the beard, axillary, and genital regions (Zaror and Moreno, 1996). Other superficial infections due to *T. beigelii* include onychomycosis, and possibly otomycosis. Torssander et al. (1984) described anal colonization by *T. beigelii* in homosexual men, and white piedra of scrotal hair folicles. In the environment, *T. beigelii* has been implicated as the cause of hypersensitivity pneumonitis. *T. beigelii* is a common pathogen in humans and one of the causative agents of white piedra, as well as potentially life-threatening localized visceral or disseminated Trichosporonosis in immunocompromised hosts. In addition, *Trichosporon* spp. have been diagnosed in endocarditis, endophthalmitis, and endometritis in immunocompetent hosts. Bottari et al. (1997) presented an unusual case of esophageal stenosis complicated by gastrointestinal reflux due to *T. beigelii* in the absence of a pathologic predisposition or immunodeficiency. *T. beigelii* was also reported to cause disseminated infection in neonates with associated high mortality. There have been reports of Trichosporonosis in HIV-positive individuals. In two of these cases the patients had a bloodstream infection with *T. beigelii*. In a third case, the patient, who had chronic renal failure, developed peritonitis (with no evidence of disseminated disease) while on CAPD. Trichosporonosis is rapidly emerging as an opportunistic invasive fungal disease, with frequently fatal outcome up to 64%. Some non-neutropenic patients with Trichosporonosis have been reported to experience mortality rates as high as 78% (Hoy, 1986). Immunocompromised patients, such as those with neoplastic disease (acute and chronic leukemia, multiple myeloma, solid tumors, aplastic anemia, and non-Hodgkin's lymphoma) have been at high risk for developing invasive Trichosporonosis (Ujiie et al 1998). Other immunosuppressed conditions like solid organ and bone-marrow transplantation, prosthetic valve surgery, chronic active hepatitis, intravenous drug abuse, and cataract extractions have also been reported to be predisposing factors for Trichosporonosis. Studies by Wong et al. (1982) demonstrated that Trichosporonosis has been common among non-neutropenic patients with iron overload and hemochromatosis. Small clusters of infection have also been observed in low birth-weight neonates. The most likely portals of entry for *Trichosporon* spp. are the alimentary tract and the lungs (Hoy, 1986). Indwelling catheters (Hickman catheters, central venous catheters, and peripheral venous cannulae), and intravenous injections can be other potential portals of entry. Trichosporonosis has been characterized by the presence of cutaneous lesions i.e. discrete maculopapular erythematous skin rash, pulmonary and renal involvement, peritonitis, and chorioretinitis. Disseminated Trichosporonosis in granulocytopenic patients usually has a rapid onset of fever, fungemia, funguria, azotemia, pulmonary infiltrates, and cutaneous lesions with invasion of the kidney, lungs, skin, and other tissues.

Most cases of white piedra have been reported in children and young adults, particularly females. Different studies have come to a mutual consensus, where colonization from *Trichosporon* spp in admitted patients to the hospital wards can be from 1% to 3%. In the outpatient setting, asymptomatic volunteers had skin colonization at higher rates of 12.4%. The mode of transmission of superficial *Trichosporon* spp. infections is not clear, but the main reported risk factors include close contact, poor hygienic habits such as bathing in stagnant waters, long hair, and humidity. Sexual transmission has been reported in cases of pubic white piedra, a report from a clinic in Houston, Texas, and is reported as more common in black men. The disease presented with genital symptoms in young men are 40% of the time. A Danish study reported rectal colonization rates of 13% among men who have sex with men and 2.5% among heterosexual men who attended a sexually transmitted diseases clinic. In invasive infection, and epidemiology is quite different. Most cases are seen in patients with neutropenia plus malignancies, either hematological or from a solid organ. Actually, disseminated Trichosporonosis has been reported, right after candida, as the second most common yeast infection in patients with hematological malignancies, reaching a mortality rate of 80% despite antifungal therapy. Another group that is at increased risk are neonates with low birth weight, premature neonates with AIDS, patients on steroids or with intravascular catheters, patients who had heart valve surgery or liver transplant, and patients with kidney failure who are on dialysis.

In the last few years, cases of onychomycosis associated with infections caused by *Trichosporon spp*. have increased. Around the world, this genus is the agent responsible for 1.3% to 10% of onychomycosis cases, being *T. asahii, T. mucoides, and T. inkin,* the most frequently involved yeast species. There have been discrepancies between cases reported in Mexico and other countries. In a study performed in pediatric patients from a rural area, Archer-Dubon et al. (2003) isolated *T. cutaneum* in 42% of the patients with onychomycosis and athlete's foot, a percentage higher than the estimated for infections by dermatophytes and *Candida spp*. yeast typically responsible for foot infections.

Hansenula anomala is known as opportunistic yeast found in soil, fruits, and other organic substrates. Fungus has been reported to cause human diseases. Although infection with this yeast is rare in humans, it can be a dangerous pathogen, especially in immunocompromised hosts . *Hansenula anomala* was also described as an emerging fungal pathogen in hematologic–oncologic patients, preterm infants, and other severely ill patients hospitalized in a surgical intensive care

unit (Kalenic et al., 2001). Moreover, *H. anomala* fungemia was described in an infant with gastric and cardiac complications and in patients after bone marrow transplantation. The case of fungal arthritis due to *H. anomala* in a diabetic patient also was reported.

Wickerhamomyces anomalus is environmental yeast, mainly found in soil, plants, and fruit juices, and has been rarely isolated from clinical samples (Ratcliffe et al., 2011). New lines of studies, however, have revealed its clinical importance and have implicated this species in a wide range of fungal infections, such as keratitis, meningitis, and candidemia, in immunocompromised and neonatal patients (Ratcliffe et al., 2011). Moreover, this species has been associated with a relatively high mortality rate of 41.2%, and numerous studies have found this species as a cause of outbreaks, especially among neonates (Yang et al., 2021). While molecular tools failed to be identified from the hands of healthcare workers, they have revealed that *W. anomalus* isolates obtained from the outbreaks are genetically related, and importantly, the application of strict infection control and hand hygiene practices has resulted in eradication of such infections in hospitals with ongoing outbreaks due to *W. anomalus* . Moreover, *W. anomalus* isolates have an intrinsic high minimum inhibitory concentration (MIC) value to fluconazole, which is regarded as the most widely used antifungal drug used in developing countries.

Rhodotorula is common environmental yeast that is found in air, soil, lakes, ocean water, milk, and fruit juice. *Rhodotorula* species, part of the Basidiomycota phylum, colonise plants, humans, and other mammals. The genus *Rhodotorula* includes eight species, of which *R. mucilaginosa, R. glutinis, and R. minuta* are known to cause disease in humans. Previously considered non-pathogenic, *Rhodotorula* species have emerged as opportunistic pathogens with the ability to colonise and infect susceptible patients. Recent studies have demonstrated that the incidence of fungemia caused by *Rhodotorula* was between 0.5% and 2.3% in the USA and Europe (Duboc de Almeida et al 2008). Most cases of infection with *Rhodotorula* fungemia are associated with central catheters in patients with haematologic malignancies. Considering that *Rhodotorula* is an ubiquitous and saprophytic fungus, the isolation of *Rhodotorula* from nonsterile human sites, especially from the mucous membranes, has often been of questionable clinical significance. Localised infections without fungemia including endophthalmitis, onychomycosis, meningitis, prosthetic joint infections, and peritonitis (usually associated with continuous peritoneal dialysis) have been reported in immunocompromised and immunocompetent patients

Sporobolomyces species are recovered from various environmental sites. In contrast, case reports of infections caused by *Sporobolomyces spp*. include one mycetoma in which *S. roseus* was isolated, and one patient with dermatitis due to *S. holsaticus* is reported (Bergman et al 1984) while in several instances *S. salmonicolor* was isolated from clinical specimens. *S. salmonicolor* has been associated with a nasal polyp, lymphadenitis and bone marrow involvement in AIDS patients, a prosthetic cranioplasty infection, a case of endogenous endophthalmitis in a previously healthy woman and a case of extrinsic allergic alveolitis.

Saccharomyces (baker's yeast) is a yeast genus represented by *S. cerevisiae*. It is often associated with fruits, vegetables, and other foods. Humans may become colonized, although this is often transient in nature. Human infections with *S. cerevisiae* do occur, (Enache-Angoulvant and Hennequin 2005) and 80% of all cases have been diagnosed since 1990. Approximately 40% (51% of fungemias) were due to *S. cerevisiae subtype boulardii*, a probiotic used for prophylaxis and treatment of diarrheal disorders such as *Clostridium difficile* infection (Munoz et al 2005). *Saccharomyces cerevisiae* is a colonizer of mucosal surfaces and part of the normal flora of the gastrointestinal tract, the respiratory tract, and the vagina. It is not known, however, whether *S. cerevisiae* is a persistent commensal of the digestive tract or whether it is transiently present after food ingestion. It is isolated from clinical specimens worldwide and accounts for 57% of clinical isolates of non-*Candida*, non-*Cryptococcus* yeasts in Europe but is uncommon in the Asia-Pacific and Latin American regions (8–9%). Since the 1980s, *S. cerevisiae* has also been isolated from individuals with pathogenic conditions and has been a cause of invasive fungal infections ((Enache-Angoulvant and Hennequin 2005,). Clinical syndromes such as pneumonia, empyema, liver abscess, peritonitis, vaginitis, esophagitis, urinary tract infection, cellulitis, unexplained fever, and septic shock have been reported. Its presence in sterile sites has been ascribed to rupture of local barriers or to very high fungal loads. Portals of entry include translocation of organisms from the enteral or oral mucosa and contamination of intravenous catheter insertion sites (Hennequin et al 2000). The most important syndrome caused by *S. cerevisiae* is fungemia. It occurs in immunosuppressed patients and critically ill patients, but also in relatively healthy hosts (Enache-Angoulvant and Hennequin 2005). Population-based studies suggest that *S. cerevisiae* accounts for 0.1–3.6% of all episodes of fungemia and the crude mortality rate is 28% (Munoz et al 2005). It is important to note that 80% of the reports of *S. cerevisiae* causing serious invasive fungal infection have been published since 1990 and 40% of those have implicated *S. cerevisiae subtype boulardii* (Munoz et al 2005). Risk factors associated with invasive *Saccharomyces* infections are similar to those reported for invasive candidiasis, except for treatment with a probiotic containing *S. cerevisiae subtype boulardii* (Enache-Angoulvant and Hennequin 2005).

Pichia is an ascomycetous yeast found in plants, fruits, soil, and other organic material. Human infections are generally sporadic, but outbreaks have been reported (Chakrabarti et al 2001, Paula et.al 2006). The two species associated with human infection are *P. anomala* (formerly *Hansenula anomala*; anamorph, *Candida pelliculosa*) and *P. (Kodomaea) ohmeri* (anamorph *Candida guilliermondii var. membranaefaciens*); *P. anomala* is encountered more often than *P. (Kodomaea) ohmeri. Pichia anomala* is found in soil, plants, and fruit juices and has also been described as a contributor to the microbial flora of the skin, throat and alimentary tract. It is a rare pathogen, but has been recognized as an emerging opportunistic pathogen causing serious infections in immunocompromised patients and in infants in neonatal intensive care units (Paula et.al 2006). The first report of human infection involving *P. anomala* was in an infant who died of interstitial pneumonia in 1953. Subsequently, *P. anomala* has been implicated as a pathogen in sporadic cases of pneumonia, endocarditis, fungemia, ventriculitis, urinary tract infection, and oral mucosal infection. *Pichia anomala* has been the cause of outbreaks in neonatal, pediatric and adult intensive care units (Paula et.al 2006). The most extensive outbreak of *P. anomala* fungemia occurred over 23 months (April 1996 to February 1998) and involved 379 neonates and children (4.2% of all admissions) in a pediatric service in India (Chakrabarti et al 2001). Infants with *P. anomala* fungemia had a lower mean birth weight, a younger mean gestational age, and a longer hospital stay than controls without fungemia. Colonization was detected in 28% of neonates admitted to the unit and 20% of them subsequently developed fungemia. Molecular epidemiologic studies suggested a common source. Among neonates with *P. anomala* fungemia, the most common site of colonization was the umbilicus (80%), followed by the mouth (60%), the rectum (30%), and the groin (20%). *P. anomala* was isolated from one post-infusion drip set, a wash basin, and the hands of two healthcare workers. It was hypothesized that cross-contamination occurred via the hands of the healthcare personnel, with a possible role of the inanimate hospital environment and colonized infants as a reservoir of *P. anomala* (Chakrabarti et al 2001). An additional seven outbreaks of *P. anomala* fungemia, ranging from 2 to 24 patients, in either neonatal or pediatric intensive care units and two outbreaks involving adult four and eight patients, respectively have been reported (Kalenic et al 2001). In several of these outbreaks, analysis of the epidemic curve and molecular epidemiologic markers suggested a common exogenous source for *P. anomala* fungemia. Risk factors include central venous catheters, previous antibiotic therapy, parenteral nutrition, long duration of hospitalization and, in infants low birth weight and prematurity. Crude mortality rates as high as 41% have been reported (Chakrabarti et al 2001) underscoring the severely compromised nature of the infected patients. These findings support *P. anomala* as an emerging nosocomial pathogen.

Yeast of *Blastoschizomyces* genus have many similarities to *Trichosporon* species. There is only one species i. e. *B. capitatus* (teleomorph: *Dipodascus capitatus*). Former names for this organism were *Trichosporon capitatum, Geotrichum capitatum*, and *Blastoschizomyces pseudotrichosporon. B. capitatus* is commonly found in the environment and may be recovered from the skin, gastrointestinal tract, and respiratory tract of healthy humans. Invasive disease has been documented in immunocompromised patients. *Blastoschizomyces capitatus* (a.k.a. *Magnusiomyces capitatus*, *Trichosporon capitatum*, *Geotrichum capitatum* and *Saprochaete capitata*) is known to cause disseminated opportunistic infections particularly in neutropaenic patients with haematologic malignancies. Infections can range in severity, affecting the lungs, liver, brain, spleen, kidney and endocardium (Groll and Walsh, 2001). *B. capitatus* is a frequent constituent of the normal skin, gastrointestinal and upper respiratory tract flora and is more frequently reported as causing invasive infections in neutropaenic patients usually with haematologic malignancies (Arendrup et al 2013). Their clinical presentation is similar to that of the more common fungal infections. Over 90% of all *Blastoschizomyces* cases in immunocompromised patients have been reported from Europe, with significant numbers from Italy, Spain or France (Arendrup et al 2013). A large survey of almost 3000 cases of fungaemia in a tertiary cancer centre in Houston, USA, found that 3·1% were secondary infections due to non-*Candida* spp. Of these, 5% corresponded to *G. capitatum*, which was associated with a high mortality overall. In another series of 88 cases of *Blastoschizomyces* infection, all had an underlying malignancy with acute myeloid leukaemia being the most common. A positive blood culture with *Blastoschizomyces* was seen in 77·3% of cases and 46% had disseminated infection reaching almost every organ, causing meningitis, osteomyelitis, endocarditis, hepatitis, gastroenteritis, nephritis and onychomycosis. Localised infection was seen most commonly in lung parenchyma (19·3%). The organism has also been isolated from wood and soil, as well as catheters, intravenous fluids and environmental samples. A nosocomial outbreak in a haematological unit was associated with milk contaminated by yeasts (Gurgui et al 2011).

2.2. Yeast species implicated in Animal and Bird's disease infection

The genus *Candida* currently comprises over 200 species of which 15 have been isolated from infections in humans and animals. Most prominent as causes of disease are *C. albicans, C. glabrata, C. parapsilosis, C. tropicalis*, and *C. krusei.* These species are also frequently found as part of the microbiota of healthy humans and animals (Al-Yasiri et al. 2016) and are thus considered as commensal and facultatively pathogenic. While *C. albicans* and *C. glabrata* appear to occur only in association with warm-blooded hosts, other infectious *Candida* species are also known from the environment. Infections are usually caused by strains that commensally pre-colonized the host rather than by vertical or longitudinal

transfer, and the zoonotic potential can thus be considered to be low. Although *C. albicans* is the most virulent *Candida* species, others might be more prominent in specific animals depending on the site of infection (Table 1).

Table 1 Important candida species implicated in Animal disease Infection

Animals	***Candida species involved***	***Diseases caused***
Ruminant Animals		
1.Cattles.	*C. albicans*	Gastrointestinal infection, Disseminated candidiasis.
	Candida spp.	Disseminated candidiasis, Otitis externa.
	C. glabrata	Gastrointestinal infection.
	C. krusei	Bronchopneumonia.
	C. parapsilosis and C. tropicalis.	Abortion.
	C. albicans, C. catenulata, C. guilliermondii, C. kefyr, C. krusei, C. maltosa and C. rugosa.	Mastitis.
2.Goats, Sheeps, Camels.	*C. albicans*	Dermatitis.
	Candida spp.	Disseminated candidiasis.
3. Horses.	*Candida spp.*	Keratitis, Arthritis.
	C. albicans	Systemic candidiasis.
	C. parapsilosis	Endocarditis
4. Alpacas, Lamas, Guanaco.	*C. albicans* *Candida spp.*	Disseminated candidiasis.
Non-Ruminant Animals		
1. Dogs	*C. guilliermondii*	Joint infection
	C. albicans, C. glabrata	Peritonitis
	C. albicans, C. guilliermondii, C. parapsilosis, C. tropicalis.	Dermititis, Otitis externa.
	C. albicans, C. parapsilosis,	Urinary tract infection.
	C. tropicalis.	Candidura, Cystitis.
	Candida spp.	Pneumonia.
	C. albicans	Keratitis.
	C. albicans, Candida spp.	Disseminated candidiasis (incl. endophtalmitis, pericarditis, spondylitis).
2. Cats	*C. parapsilosis*	Granulomatous rhinitis
	C. albicans	Urinary tract infection, intestinal granuloma, pyothorax
	Candida spp.	Disseminated candidiasis (incl. ocular involvement).
3. Pigs	*Candida spp.*	Oral candidiasis, Gastroesophageal candidiasis.
	C.guilliermondii, C.pseudotropicalis.	Abortion
	C. albicans	Mucocutaneous candidiasis.

Table 2 Important *Candida* spp. implicated in Bird infection

Birds	***Candida* spp. involved**	**Diseases caused**
Pigeon, parrot, Gilliformes, passeriformes	*Candida spp.*	Oral & Gastrointestinal candidiasis
Sun conure, raptors	*C. albicans, C. krusei*	Pulmonary candidiasis
Passeriformes, Chicken.	*C. albicans*	Cutaneous candidiasis

(Source: Seyedmousavi et.al. 2018).

Besides *Candida* species, the yeasts of the genus *Cryptococcus* cause disease known as cryptococcosis in birds. The genus *Cryptococcus* (teleomorph: *Filobasidiella*) comprises basidiomycetous yeast species, The pathogenic agents of cryptococcosis are classified into two species, *C. neoformans* and *C. gattii.* The species *C. neoformans* comprises two varieties, *C. neoformans* var. *grubii* and *C. neoformans* var. *neoformans.* The species *C. neoformans* consists of the VNI-VNIV and VNB molecular genotypes, comprising var. *grubii* (serotype A or VNI, VNII, and VNB strains), var. *neoformans* (serotype D or VN IV strains), and serotype AD strains (VNIII), which represents hybrids of the two varieties (Know-Chung and Verma,2006). The species *C. gattii* is subdivided into two serotypes (B and C), and four molecular types VGI, VGII, VGIII, and VGIV varying in virulence, geographic distribution, and possibly susceptibility to antimycotic drugs (Kwon-Chung et.al, 2017). Diseases caused by other *Cryptococcus* species, such as *Cryptococcus laurentii* and *Cryptococcus albidus*, have been reported infrequently and generally in immunocompromised hosts.

Cryptococcus neoformans infections have been reported in a large variety of animals from lower invertebrates such as soil dwelling amoebae, nematodes, cockroaches, and mites, to higher mammals (Voelz et.al, 2014). Cats are the most frequently infected animals with the involvement of the upper and or lower respiratory tract, subcutaneous granulomata, and disseminated infections. Dogs may present with similar symptoms but central nervous system (CNS) involvement is more common. Moreover, cryptococcosis has been reported causing mastitis in dairy animals (Emmon et.al, 1947) and respiratory infections in horses (Secombe et.al, 2017). Another Cryptococcus species i. e. *Cryptococcus gattii* was isolated from different animal species, including cats, dogs, marine mammals, ferrets, and llamas in the regions affected by the outbreak that started in Vancouver Island and subsequently spread to the Pacific Northwest regions of the United States. The upper respiratory tract infections and subcutaneous masses were the most frequent primary lesions, but in several cases the CNS, lymphatic tissue, lungs, oral cavity, and eyes were affected. Among pets, a higher number of CNS involvement in dogs was found, whereas subcutaneous masses were shown more frequently in cats (Headley et.al, 2016). CNS involvement was associated with higher mortality rates. In addition, gastrointestinal infections in dogs have been reported (de Abreu et.al, 2017). Moreover, a disseminated canine infection with C. *neoformans* var. *grubii* was reported. Surveys have shown that incidence of cryptococcosis does not increase in environment contaminated with bird dropping, including immunocompromised patients (Hajjeh et.al, 1999). Nevertheless, molecular analysis indicated in some cases that human and environmental isolates were identical (Elad 2013).

About eight decades ago, Sangiorgi (1922) described the presence of *Cryptococcus* in the large mononuclear cells of liver and spleen of a rat (*Rattus norvegicus*). Further, during the investigation about histoplasmosis, Emmons et al. (1947) isolated *Cryptococcus* from mice and rats. After a long gap, naturally acquired cryptococcosis was again reported, but this time in the greater bandicoot rat (*Bandicota indica*) (Singh et al, 2007). Pathological lesions were observed only in liver and lungs but other organs like kidneys, spleen, and brain were found positive for *Cryptococcus neoformans* var. *grubii*. Singh et.al. (2007) also isolated *C. n. grubii* from animal's burrow and surrounding bamboo debris, thus suggesting *B. indica* as a sentinel animal, which potentially amplified the pathogen in the environment. Recently, a case cluster of cryptococcosis has been observed in a synanthropic South-eastern Asian murid (*Mus musculus castaneus*) (Singh et al, 2007). Unlike bandicoot rats, no lesions were recorded in any organ of the animals, however, *C. n*. var. *grubii* was recovered from cultures of tissue homogenates of brain, lungs, liver, and kidneys. The habitat soil and fresh faeces of the animals were also positive for the yeast fungus. It is interesting to note that, despite the presence of *Cryptococcus* in the central vein, neither liver nor any other organ exhibited pathological signs. Since the pathogen passes through the animal host without affecting it and all isolates recovered from *M. musculus* were weakly pathogenic to experimental mice, which define the status of *M. musculus* as passenger host for *C. n*. var. *grubii* in a more appropriate manner. It is noteworthy that in most of the cases, *Cryptococcus* yeasts have been isolated from apparently healthy rodents. The household rodents are nuisance animals and may serve as a continuous source of infection for humans and their pets. On one hand, rodents especially rats and mice have expanded their geographic range dramatically and also have significantly extended the territory of harbored pathogens and may play a role in acting as sentinel for the presence of *Cryptococcus* in the environment. On the basis of degree of interaction between host and harbored pathogens, rodents may be termed as natural reservoirs, alternate hosts, sentinel animals, carriers, and passenger hosts.

2.3. Yeast species implicated in Marine animal's disease infection

Yeasts have been shown to be present in various marine invertebrates including oysters, clams, mussels, shrimp, and crabs; and the most frequently isolated yeasts from these organisms are generally those which are prevalent in the water of their habitats. Counts of yeast cells can be much higher in marine invertebrates than in the water of their habitats as a result of their feeding activities and concentration of nutrients in their digestive tracts. Yeasts may be of nutritional importance to their invertebrate hosts. Cowley & Chranowski (1980) noted an association of *Rhodotorula glutinis* with the crab *Uca pugilator* and that this yeast is probably ingested rather than multiplying in the digestive tract. Opportunistic pathogenic yeasts including *C. parapsilosis, Candida tropicalis, Candida glabrata, Candida guilliermondii, Candida krusei* and *Candida albicans* were found to be present in bivalve shellfish from Long Island Sound demonstrating their presence in a valuable marine resource (Buck et al. 1977).

It has been well known that many diseases in marine animals can be caused by many species of marine bacteria and marine viruses. However, in recent years, many evidences have shown that some marine yeasts are pathogenic to some marine animals. Like bacterial and virus disease, the yeast disease has caused big economic losses in maricultural industry in some regions of China (Xu, 2005). For example, an explosive epidemic disease which is called milky disease occurred in cultured Crab (*Portunus trituberculatus*) since 2001 in Zhoushan, Zhejiang Province, China, leading to high mortality of these crabs and great economic loss in this area. The pathogenic agent for the milky disease was found to be a yeast strain. The purified yeast strain from the diseased parts of the marine animal can develop the same symptom in the muscle, heart and hepatopancreas of the infected marine animals in the challenging test. It was found that nystatin, benzalkonium bromide and extract of goldthread root and garlic are active against the pathogenic yeast; however, the compounds with minimum inhibitory concentration (MIC) are toxic to the crab and it was impossible to apply the expensive antibiotics to the open sea.

Another yeast species i. e. *Torulopsis mogii* is pathogenic to some shrimp in China. The yeast *Metschnikowia bicuspidate var. bicuspidate*, a pathogenic yeast of aquatic invertebrates was capable of infecting aquaculture-reared, disease-free Artemia (Moore and Strom, 2003). A new species of marine yeast *Kluyveromycs penaeid* was isolated from the heart tissue of subadult shrimp (*Penaeus chinensis*) during tissue culture. The yeast grew well in seawater supplemented with 2% shrimp extract, but did not grow in YPD and Malt extract medium in which most of yeast cells grow well.

Corals and zoanthids are known to harbour diverse consortiums of microorganisms, including bacteria, archaea, fungi, viruses, and algae. Microorganisms associated with corals, including yeasts, are suspected of playing a key role in coral biology by contributing to the nutrition, defence, immunity, and development of corals (Orlić 2019). The associations between bacteria and corals have received more attention than research on yeasts associated with corals and zoanthids, on which information is scarce worldwide. The few articles have reported investigations of culturable yeasts associated with corals at deep-sea hydrothermal sites in the Mid-Atlantic Ridge, the South Pacific Basin, and the East Pacific Rise (found during oceanographic cruises) and of zoanthids on a Brazilian reef (Paulino et.al 2017).

Diversity of yeasts associated with corals and zoanthids in the Gulf of Thailand was studied by Kaewkrajay et al. (2020). Fifty yeast strains were isolated from 25 of the 40 samples collected. Identification based on sequence analyses of the D1/D2 domain of the large subunit rRNA gene revealed a higher number of strains in the phylum *Basidiomycota* (68%) than in the phylum *Ascomycota*. The ascomycetous yeasts comprised nine known species from four genera (*Candida, Meyerozyma, Kodamaea*, and *Wickerhamomyces*), whereas the basidiomycetous yeasts comprised 10 known species from eight genera (*Vishniacozyma, Filobasidium, Naganishia, Papiliotrema, Sterigmatomyces, Cystobasidium, Rhodotorula*, and *Rhodosporidiobolus*) and one potentially new species. The species with the highest occurrence was *Rhodotorula mucilaginosa*

A new species of marine yeast *Kluyveromycs penaeid* was isolated from the heart tissue of subadult shrimp *Peaaeus chinensis* during tissue culture. Another yeast sp**.** *Metschnikowia bicuspidata var. bicuspidata* was associated with live adult brine shrimp (Artemia franciscana). The live adult Artemia are one of the best foods for culturing fish fry and post-larval crustaceans (Soundarapandian et al., 1998). The nutritional value of adult Artemia is superior to that of freshly hatched nauplii. Lobster farming relies on adult Artemia, and the best results are obtained using live Artemia, compared with frozen or freeze-dried. Live adult Artemia have also been shown to be an excellent food for salmon fry. Coho salmon fed adult Artemia from first-feeding grew significantly faster than coho fed Artemia nauplii or commercial feed. Rearing adult Artemia from cysts is time consuming and labour intensive. The least expensive source of adult Artemia is commercial harvest from natural and man-controlled salt-pond systems. A major aquaculture industry in the state of California is the production, harvesting, and sale of Artemia for the aquarium industry and as feed for larval fish and shellfish aquaculture. These Artemia are produced in managed, hypersaline evaporation salt ponds at a number of sites located in the San Francisco Bay Area and desert areas of southern California. However, mortalities associated with

feeding live Artemia have caused concern that they may be vectors for pathogenic organisms, though no major bacterial pathogens have been isolated including viruses. However, it was reported as a case of disease transmission through Artemia where a fungal yeast *Metschnikowia bicuspidata var. bicuspidata* is implicated as the causative agent (Moore and Strom, 2003). Microscopic examination of the Artemia shipments revealed that the yeast was present in the transport water and within the Artemia. Infected Artemia had high numbers of yeast cells throughout the body.

2.4. Yeast species Associated with insects Pests

Planthoppers have sucking mouthparts designed for acquiring phloem sap from plants, a diet that may be poor in nutrients without microbial supplements. The yeast-like symbionts (YLSs) of hemipterans have never been found free living in nature, and the host and microbial organisms cannot be grown separately, characteristics of obligate interactions. The most studied YLS is that of the brown planthopper *Nilaparvata lugens,* where the yeast species called *Entomomyces delphacidicola* was detected, but apparently the taxon has not been described formally according to the rules of nomenclature. The YLSs are intracellular (endosymbiotic), located within specialized cells (mycetocytes) in the fat body, a differentiated cluster of cells connected to the gut of planthoppers, aphids, and leafhoppers. The YLSs are present in all stages of the insect life history from egg to adult, and vertical transmission from one generation to another is ensured by transmission from the female parent to the egg by transovarial infection. Various researchers helped to develop the planthopper–YLS interaction as a model system in which the YLS provides essential functions for the insect, allowing for survival on a low nutrient diet. *Symbiotaphrina buchneri* and *Symbiotaphrina kochii* have long been known (van der Walt 1961) as YLSs associated with *Stegobium paniceum*, the drugstore beetle, and *Lasioderma serricorne*, the cigarette beetle (Anobiidae), respectively. The beetles eat processed plant material that often contains toxic secondary metabolites, and they have been found living in sacks of flour, cigarette tobacco shreds in packs, and other harsh, arid environments. The females pass yeast cells to their offspring by smearing them on the surface of the eggs. As the larvae chew out the egg shell, they ingest some of the cells from the shell that will eventually populate the midgut caeca. Some of the yeast cells reproduce in the larval gut, but most of them never move from the gut into the caeca, so that part of the population is not passed on to the offspring vertically, an important observation that is mentioned again. Uninfected beetles are reported to die prematurely, while symbiont-infected beetle hosts survive. The beetles obtain amino acids and B-complex vitamins from the YLS. The beetles also obtain ergosterol and 5-dihydroergosterol from the YLSs that they convert to 7-dehydrocholesterol (Nasir and Noda 2003). Species of beetles from families *Passalidae, Cerambycidae*, *Buprestidae*, and *Tenebrionidae* ingest wood as they tunnel through several year-old white-rotted logs. The most common yeasts associated with wood-ingesting beetles are members of the *Scheffersomyces* and *Spathaspora* clades.

Many of the yeasts are marked by a rare attribute, xylose fermentation, among other properties. Xylose-fermenting yeasts are consistently present in termites, wood roaches, and other animals that feed in dead wood. In addition, several other clades of xylose-assimilating yeasts have also been present, including species of *Lodderomyces* and basidiomycetous species of *Trichosporon* and *Tremellomycetes* genera previously included within Cryptococcus. Comparisons of gut yeasts from fungus-feeding beetles with those of wood-ingesting beetles show that very different communities are associated with each group of yeasts, in part due to physiological adaptations for use of nutrients and survival of the gut physical conditions. *Odontotaenius disjunctus* (Passalidae) harbors the xylose-fermenting species, *Scheffersomyces stipitis*, in the hindgut. The yeast has a holdfast by which it attaches to the hindgut wall (Nardi et al. 2006). A holdfast, rarely observed as a yeast adaptation, may indicate that selection has been in favor of the yeast that benefits from an advantageous position to acquire nutrients in a dynamic gut region (Nardi et al. 2006). All attempts to cure the beetles of yeasts failed. The species *Scheffersomyces cryptocercus* has been isolated several times in association with a wood roach, *Cryptocercus* sp. and apparently free living from the bark of forest trees. Different xylose-fermenting yeast, *Spathaspora passalidarum*, also has been isolated from the gut of *O. disjunctus*. The list of xylose-fermenting yeasts from rotted wood, beetles, and termites grows longer and now includes species of *Sugiyamaella* and other plant cell wall-degrading yeasts of biotechnological potential (Riley et al. 2016).

Wickerhamomyces anomalus, a mosquito gut yeast, produces an inhibitor of the β-1,3-glucans in the spore walls of several protistan parasites, including an agent of malaria, *Plasmodium berghei*. Inhibition of the protistan spores occurs in vitro but also in the mosquito gut where inhibition is up to 90% greater than in the controls (Valzano et al. 2016).

2.5. Yeast in Plant Health management

Yeasts occur naturally in soil and on plants, but in a lower proportion compared to bacteria and filamentous fungi. The role played by yeasts in agricultural ecosystems is not completely understood and research on these microorganisms as PGP agents is scarce (de Souza et al., 2019). However, a diversity of studies indicates that plant growth may be directly or indirectly enhanced by yeasts, being described as potential biofertilizers. The promoting effect of yeasts could be due to the active substances produced (phytohormones, amino acids, vitamins or NH3), solubilization of inorganic phosphate or zinc, iron capture through siderophores and restriction of pathogen colonization (de Souza et al., 2019).

For example, some species of Candida, Rhodotorula, Saccharomyces, Geotrichum and Williopsis are able to nitrify ammonium to nitrate (Al-Falih, 2006). *Candida spp*., *Hanseniaspora uvarum*, *Meyerozyma caribbica*, Saccharomyces cerevisiae or *Torulaspora* spp. among others, have been described as producing IAA and some of them also synthesize siderophores, catalase, NH3 and cell wall-degrading enzymes (de Souza et al., 2019). Although most studies on yeast growth-enhancing capacity to date have been conducted in vitro, the effectiveness of field applications has also been demonstrated. Nakayan et al. (2013) reported that *Meyerozyma guilliermondii* CC1 increased the seed vigour index in maize and Chinese cabbage, and applications combined with a half dose of chemical fertilizer significantly improved the dry weight and nutrient uptake of maize and lettuce under greenhouse conditions. Similarly Candida tropicalis CtHY inoculated on rice seedlings rapidly colonized the roots, increasing plant dry weight up to 35% compared to non-inoculated control seedlings. These results validated the inclusion of this strain in the commercial biofertilizer product BioGro.

Besides their plant growth promoting activities, the use of yeast is also reported in plant diseases control and therefore can be employed in agricultural crop production system. Kamel and Hossam (2013) reported the yeast species *Candida tropicalis, Pichia caribaea* and *Geotrichum candidum* for their potential to act as plant growth promoter in tomato crop and similarly to act as antagonist biocontrol agents against root rot diseases in tomato caused by *Fusarium solani, Rhizoctonia solani* and *Pythium aphanidermatum*. Khaled A El-Tarabily (2004) reported root colonization ability of 3 yeast species viz. *Candid valida, Rhodotorula glutinis* and *Trichosporon asahii* in sugar-beet crop using root colonization plate assay and sand tube method. *C.valida* and *T. asahii* colonized 95 % of root after 6 days while *Rhodotorula glutinis* colonized 90 % of root after 8 days. These 3 yeast species individually or in combination promoted plant growth and reduced damping off, crown and root rot of sugar-beet in glasshouse trials. El-Ghaouth et.al, (1998) reported the yeast *Candida saitoana* to restrict the proliferation of *Botrytis cinera* in wounded apple tissues This yeast species multiplied at wounded site and suppressed disease caused by *B. cinera* and *Penicillium expansum* in apple. The ultrastructural and cytochemical studies indicated that the hyphae of the pathogen in close proximity of antagonistic yeast exhibited severe cytological injury, such as cell wall swelling and protoplasm degeneration. Colonization of wound site by *C. saitoana* cells did not cause degradation of host cell walls. In addition to restricting fungal colonization, *C.saitoana* induced formation of structural defense responses in apple tissues. The ability of *C. saitoana* to prevent the necrotrophic growth of the pathogen and stimulate structural defense responses may be the basis of its biocontrol activity. Sali et.al (2016) reported the presence of new yeast *Eremothecium cymbalariae* in soils of Maharashtra, India which was found effective as biocontrol agent against the soil dwelling damping off pathogen *Pythium spp.*

Soil may be a warehouse of many yeast species. Ignatova et.al (2015) isolated 538 yeast strains from dark chestnut soil collected from under the plants of the legume family (*Fabaceae*). The greatest number of microorganisms is found at soil depth 10–20 cm. Among the 538 strains of yeast 77 (14.3%) strains demonstrated the ability to synthesize IAA. 15 strains were attributed to high IAA-producing yeasts (above 10 μg/ml). The most active strains were YA05 with 51.7 ± 2.1 μg/ml of IAA and YR07 with 45.3 ± 1.5 μg/ml. 10 strains demonstrated the ability to inhibit the growth and development of phytopathogenic fungi. YA05 and YR07 strains formed the largest zones of inhibition compared to the other strains – from 21.6 ± 0.3 to 30.6 ± 0.5 mm. Maximum zone of inhibition was observed for YA05 against *Phytophtora infestans* and YR07 strains against *Fusarium graminearum*. YA05 and YR07 strains were identified as *Aureobasidium pullulans* YA05 (GenBank accession No JF160955) and *Rhodotorula mucilaginosa* YR07 (GenBank accession No JF160956).

Fernandez-San Millan et.al, (2020) characterized a collection of 69 yeast strains isolated from Spanish vineyards. Phyto-beneficial attributes such as solubilization of nutrients, synthesis of active biomolecules and cell wall-degrading enzyme production were analyzed and strains with multiple growth-promoting characteristics were identified. The *in vitro* co-culture of *Nicotiana benthamiana* with yeast isolates showed enhancement of plant growth in 10 strains (up to 5-fold higher shoot dry weight in the case of *Hyphopichia pseudoburtonii* Hp-54), indicating a beneficial direct yeast-plant interaction. In addition, 18 out of the 69 strains increased dry weight and the number of roots per seedling when tobacco seeds were inoculated. Two of these, *Pichia dianae* Pd-2 and *Meyerozyma guilliermondii* Mg-11, also increased the chlorophyll content. The results in tobacco were mostly reproduced in lettuce with these two strains, which demonstrates that the effect of the yeast-plant interaction is not species-specific. In addition, the yeast collection was evaluated in maize seedlings grown in soil in a phytotron. Three isolates (*Debaryomyces hansenii* Dh-67, *Lachancea thermotolerans* Lt-69 and *Saccharomyces cerevisiae* Sc-6) promoted seedling development (increases of 10 % in dry weight and chlorophyll content). In conclusion, the authors confirm that several yeast strains can promote plant growth and could be considered for the development of biological fertilizer treatments. Chen et.al. (2023) reported that yeast isolate *Rhodosporidium paludigenum* JYC100 exhibited good performance for solubilizing calcium phosphate. They found that it can be regulated by the amount of soluble phosphate. Furthermore, *R. paludigenum* JYC100 promotes plant growth under specific conditions (P deficiency, but with insoluble phosphate) in different media and soil pots. In contrast, the yeast *Aureobasidium pullulans* JYC104 exhibited weak phosphate-solubilizing capacities and no plant

growth-promoting ability. Compared to control plants, the biomass, shoot height, and cellular inorganic P content of plants increased in plants co-cultivated with *R. paludigenum* JYC100. In addition, histochemical GUS and qRT-PCR assays of phosphate starvation-induced (PSI) genes showed that the transcript levels of these PSI genes are decreased in the plants co-cultured with *R. paludigenum* JYC100. These findings reflect the unique ability of *R. paludigenum* JYC100 to convert insoluble P compounds to plant-available P, thereby leading to growth promotion. Their study results highlight the use of yeasts as potential substitutes for inorganic phosphate fertilizers to meet the P demands of plants, which may eventually improve yields in sustainable agricultures.

Petkova et.al (2022) reported the biosynthetic and biocontrol potential of endophytic yeast to improve the growth and development of tobacco. Three yeast strains were enriched and isolated from different plant tissues. Partial sequence analysis of ITS5-5.8-ITS4 region of the nuclear ribosomal DNA with universal primers identified YD5, YE1, and YSW1 as *Saccharomyces cerevisiae* (*S. cerevisiae*), *Zygosaccharomyces bailii* (*Z. bailii*), and *Saccharomyces kudriavzevii* (*S. kudriavzevii*), respectively. When cultivated in a medium supplemented with 0.1% L-tryptophan, isolated yeast strains produced indole-3-acetic acid (IAA). The capacities of those strains to improve the mobility of phosphorus and synthesize siderophores has been proven. Their antimicrobial activities against several Solanaceae plant pathogenic fungi (*Alternaria solani pathovar. tobacco, Rhizoctonia solani,* and *Fusarium solani pathovar. phaseoli*) were determined. *S. cerevisiae* YD5, *Z. bailii* YE1, and *S. kudriavzevii* YSW1 inhibited the growth of all tested pathogens. Yeast strains were tested for endophytic colonization of tobacco by two different inoculation methods: soil drench (SD) and leaf spraying (LS). Both techniques of inoculation showed a high frequency of colonization from 83.33% to 100%. To determine the effectiveness of the microbial endophytes, their effect on some physiological processes in the plant were analyzed, such as photosynthesis, stomatal conductivity, and transpiration intensity. The most significant stimulating effect was recorded in tobacco plants treated by foliar spraying with *Z. bailii* YE1 and *S. cerevisiae* YD5. In contrast, *S. kudriavzevii* YSW1 had a better effect when applied as a soil drench. Thus, *S. cerevisiae* YD5, *Z. bailii* YE1, and *S. kudriavzevii* YSW1 have a high potential to be used as a biocontrol agent in organic agriculture.

3. Yeast species useful in management of disease pathogens and ailments

3.1. Useful in treating Human ailments

First isolated from litchi fruit in Indochina and described in 1984 as saprophytic yeast, *S. cerevisiae* var. *boulardii* has emerged as a probiotic species for human consumption (Van der Aa Kühle et al., 2005). This strain has also been recommended for the prevention and treatment of several types of gastroenteritis in children and adults (Htwe et al., 2008). Nowadays, probiotic yeasts can be delivered either in fermented foods or as lyophilized cultures administered orally, for example, to patients who have been hospitalized as a consequence of severe diarrhea. Several yeast species, including *D. hansenii*, *Torulaspora delbrueckii* , *Kluyveromyces lactis*, *Yarrowia lipolytica* , *K. marxianus*, *K. lodderae* have been found strongly antagonistic to pathogenic bacteria and to tolerate passage through the gastrointestinal tract. In a recent *in vitro* study, Etienne-Mesmin et al. (2011) investigated the probiotic effect of *S. cerevisiae* CNCM I-3856 against *E. coli* O157:H7. The results showed that the probiotic yeast exert the antagonistic effects in the distal part of the small intestine and that might be due to ethanol production. However, only *S. boulardii* is considered as a probiotic. As probiotic, these yeast species are useful in the control of diseases like antibiotic associated diarrhea (AAD), Clostridium difficile associated diarrhea, Traveler's diarrhea, Acute diarrhea in adults and children, Tube-feeding-associated diarrhea, Inflammatory bowel disorders, and Chronic diarrhea in human immunodeficiency virus and others.

Antibiotic therapy is well known to destroy the normal bacterial population of the digestive tract, which allows harmful bacteria to colonize and irritate the host gut and cause antibiotic associated diarrhea. Numerous placebo-controlled clinical studies have shown the beneficial effects of *S. boulardii* in preventing antibiotic associated diarrhea. In a double-blind study, a significant reduction in AAD symptoms in the group that received 200 mg of *S. boulardii* (10^9 CFU/day) for 7 days has been shown.

The effects of *S. boulardii* on *C. difficile* have also been studied. *C. difficile* is responsible for 20% of antibiotic associated diarrhea cases and causes pseudomembranous colitis, an infection of the colon. There are only two standard antibiotics for *C. difficile* infection, viz. vancomycin and metronidazole, and the response rate to the later has been declining (McFarland, 2007). *S. boulardii* in combination with antibiotics has been shown effective for treating *C. difficile* associated diarrhea and colitis.

Each year millions of people worldwide develop traveler's diarrhea. *S. boulardii* activities in the prevention of traveler's diarrhea have been widely investigated. In 1016 travelers visiting various countries in the world reported a significant reduction in diarrhea among patients receiving 5 billion CFU of *S. boulardii*/day (34% versus 40% in patients receiving placebo $P = 0.019$). Based on analysis of 12 studies on the use of probiotics to prevent traveler's diarrhea, McFarland

(2007) reported a significant benefit of two probiotics, viz. *S. boulardii* and a mixture of *Lactobacillus acidophilus* and *Bifidobacterium bifidum*.

Every year, an estimated 2 million deaths occur worldwide as a result of acute diarrhea (Billoo et al., 2006). Several studies have shown the beneficial effects of *S. boulardii* in preventing acute diarrhea. In a group of 50 children (aged 2 months to 2 years) receiving 10 billion CFU of *S. boulardii*/day or a placebo in combination with oral rehydration salt and nutritional support prevent acute diarrhea. Billoo et al. (2006) showed significant reductions in stool frequency and duration of diarrhea in the *S. boulardii* group compared to the placebo group. In a double-blind randomized study a significant reduction in the number of days with diarrhea and hospitalization among 200 children treated with *S. boulardii* has been shown.

DeMeo et al. (1998) estimated that approximately 68% of tube-fed patients develop diarrhea. Several studies suggest the beneficial effects of *S. boulardii* in restoring normal intestinal microflora and preventing tube-feeding-associated diarrhea. In a double-blind placebo-controlled trial involving 40 tube-fed patients, a 50% reduction in days with diarrhea was observed among patients given *S. boulardii* compared to the placebo group. Another double-blind placebo-controlled study following 128 critically ill tube-fed patients (Bleichner et al., 1997) showed a significant but small reduction in days with diarrhea among patients given 40 billion CFU of *S. boulardii* four times/day (14.2 versus 18.9% in patients receiving placebo).

Inflammatory bowel diseases (IBD), Crohn's disease, ulcerative colitis and Irritable Bowel Syndrome are chronic inflammatory disorders of the gastrointestinal tract. Numerous studies showed that *S. boulardii* hold promise for the treatment of inflammatory bowel disorders. In a double-blind study of 20 patients suffering from Crohn's disease showed a significant reduction in the bowel movement among patients receiving *S. boulardii* in addition to their conventional therapy. In a single-blind study of 32 patients with Crohn's disease (Guslandi et al., 2000) similar results were reported for patients receiving *S. boulardii* (20×10^9 CFU/day) compared to patients receiving 500 mg of mesalazine three times daily.

In a randomized double-blind study of 35 patients with AIDS-related diarrhea, Saint-Marc et al. (1995) reported a reduction in diarrhea among patients receiving *S. boulardii* (3 g/day for 7 days). Finally, other studies revealed the efficacy of *S. boulardii* to reduce diarrhea in people suffering from giardiasis, amebiasis where S. boulardii reduces the number of red cells adhering to amoeba and the number of amoebae bearing red cells, and Helicobacter pylori gastritis. It was reported that *S. boulardii* had improved the post-treatment dyspepsia symptoms of H. pyloris infection without having a significant effect on the rate of H. pylori eradication.

Blanquet et al. (2001) defined bio-drugs as orally administered living recombinant microorganisms that express disease-fighting proteins. The application of non-recombinant yeast as antimycotics for therapeutic treatment of human and animal fungal infection has also received considerable attention. The killer toxin of *L. mrakii* has been proposed as an antifungal compound against *Candida* spp., due to its similarity to aculeacin and stability to pH and temperature changes. Weiler and Schmitt (2003) found that the zygocin, produced by *Zygosaccharomyces bailii*, has a rapid killing effect against a wide range of pathogenic yeasts including *Candida albicans*, *Candida glabrata* and *Candida krusei*, and *Sporothrix schenckii* based on disruption of membrane ion gradients. However, it is important to note that killer toxins are large glycoprotein compounds and hence capable of inducing an immune response in the host. To deal with this potential challenge, several strategies have been proposed. For example, Magliani et al. (1997) synthesized small non-antigenic peptides with killer activity. The same group suggested the utilization of an anti-idiotypic antibodies from killer toxin secreted by *W. anomalus* . These "antibodies" (i.e., immunoglobulin molecules acting directly to provide passive immunity without involvement of other immune system factors) showed a significant microbicidal activity against wide range of pathogenic agents through the interaction with specific killer toxin receptors composed by beta-glucans. A novel antifungal vaccine derivative of *W. anomalus* killer toxin (PaKT) has been described recently by Polonelli et al. (2011).

3.2. Useful in treating Animal ailments

Supplementing animal feed with yeast fractions is being shown to decrease pathogen pressures in the gut, while promoting pathogen removal from animals by preventing the first steps of infection (namely pathogen attachment to intestinal cells). Recent peer reviewed scientific articles have demonstrated that adding Safmannan, a premium quality Selected Yeast Fraction (SYF), to animal diets can help enhance resilience against several important bacterial diseases, especially the ones caused by *E. coli, Salmonella* or *Clostridium perfringens*. Adding SYF to animals' diet has been proven to promote the animals' natural defences and zootechnical performance, while also reducing mortalities.

3.3. Useful in treating Aquaculture ailments:

Pathogenic yeasts have recently caused immense losses in marine aquaculture. For example, the pathogen that causes the 'emulsification disease' in the crab *Portunus trituberculatus* is the yeast *Metschnikowia bicuspidata*. However, given the similarity of the structures and functions of yeast cells with those of human and animal cells, controlling yeast diseases is challenging. *The marine yeast strain Metschnikowia saccharicola DD21-2, isolated from sediments in the Yalu River, produces a killer toxin with a lethal effect on Metschnikowia bicuspidate strain WCY, a pathogenic yeast strain that infects crabs.*

A variety of yeasts isolated from different marine environments have been recently shown to be capable of producing toxins that antagonize *M. bicuspidata WCY*, a yeast strain that is lethal to crabs. Killer yeasts and their produced killer toxins have a relatively wide range of adaptability and can specifically act on the cell wall of a target yeast, so the killer yeasts could be applied to aquaculture. yeast strain *M. saccharicola DD21-2*, which kills the emulsification disease-causing *WCY* strain, and determined that its killer toxin has high killing activity and a relatively wide antibiogram. The toxin specifically acts on the cell walls of sensitive yeasts, thereby avoiding damage to the cells of the marine host animal. These characteristics render this killer yeast a potential candidate for preventing and treating pathogenic yeast infections in marine aquaculture. This is also the first to report killer activity of *M. saccharicola* against marine pathogenic yeast *M. bicuspidata WCY*.

Killer toxin produced by some yeast strains is a low molecular mass protein or glycoprotein toxin which kills sensitive cells of the same or related yeast genera without direct cell–cell contact (Schmitt and Breinig, 2002). The killer strains themselves are immune to their own toxin, but remain susceptible to the toxins secreted by other killer yeasts. The killer phenotype is very common in occurrence and can be found both in natural yeast isolates and in laboratory yeast strain collections. Up to now, toxin-producing killer yeasts have been identified in genera *Candida, Cryptococcus, Debaryomyces, Hanseniaspora, Hansenula, Kluyveromyces, Metschnikowia, Pichia, Saccharomyces, Torulopsis, Williopsis and Zygosaccharomyces,* indicating that the killer phenomenon is indeed widespread among yeasts (Magliani et al., 1997). Killer determinants are either cytoplasmically inherited encapsulated dsRNA viruses, linear dsDNA plasmids or nuclear genes (Schmitt and Breinig, 2002). The analysis in mechanisms of killer toxin can also provide important information for combating yeast infections caused by certain human pathogenic strains of the yeasts particularly *Candida albicans and/or Sporothrix schenkii*. Regular antibiotics are not effective against pathogenic yeasts, and long-term use of these antibiotics results in drug resistance, which ultimately puts human health at risk. Studies have shown that killer yeasts and the killer toxins they produce have antimicrobial activity and can be used to control the growth of pathogenic yeasts in humans, animals and plants.

Kurtzman and Robnett (1998) developed methods not only to identify yeasts rapidly but also to begin to arrange them phylogenetically which can be used for proper identification of yeast implicated in health sciences.

4. Conclusion

Yeasts are single celled microbes with diverse functionality which have an important role in the wellbeing of the living beings. These can be either harmful or beneficial entities. These are known to cause diseases in all living beings vis-a-vis are known as bio-pharmaceutical to act as probiotics, bio-control agents besides their use in the wine industry, fermentation process, dairy industry, baking industry and bio-preservative etc. In this concise report, all the yeast genera and species with their role is discussed which will pave way for further research on identification and report on new yeast species around the world.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

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