Aquatic yeasts: diversity, characteristics and potential health implications
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ABSTRACT
There has been a rising interest in the levels, diversity and potential impacts of yeasts in aquatic environments. Some of the species isolated from such niches are known pathogens or have pathogenic and antifungal resistance features. This deems it necessary to understand the characteristics and potential health implications of such environmental yeasts species. Studies on these subjects are limited. Most studies on aquatic yeasts have linked them to water pollution. However, the current gold standards to determine microbial pollution of water use bacteria as the main indicator organisms. Including yeasts in water quality standards may provide a different dimension on the quality of water when determining its fit-for-use properties. Pathogenic yeasts cause superficial infections or life-threatening infections, especially in immunocompromised people. Some of the yeast species isolated in recent studies were resistant to commonly used antifungal agents of clinical and veterinary relevance. With the high prevalence rate of HIV in sub-Saharan Africa, particularly in South Africa, antifungal resistance is a public concern as it poses serious medical and economic challenges. Most available studies are concerned with clinical environments only. There is, thus, a need to review the literature that also focuses on aquatic environments.

Key words | aquatic yeasts, diversity, health implications, microbial pollution, resistance, water quality

INTRODUCTION
Yeasts are eukaryotic microorganisms classified in the kingdom fungi and are divided into two phylogenetic groups, i.e. ascomycetes and basidiomycetes. Yeasts commonly occur in water, animals, plants, soil and insects (Montes de Oca et al. 2016). Cases where yeasts were identified as the primary agent that caused infections increased, which, in turn, increased interest in the specific species and characteristics of that particular yeast. Interest was further fuelled by the advent of human immunodeficiency virus (HIV) co-infectious or opportunistic infections by some yeasts species infecting immunocompromised individuals (Moges et al. 2016; Mnge et al. 2017). Most of these patients that are compromised are those in therapeutic technology including organ transplants and anticancer therapies or have certain disease conditions such as malignancy and HIV (Pincus et al. 2007; Richardson & Lass-Florl 2008). The latter presents a global challenge, especially in South Africa with its high HIV epidemic of 37.9 million and a further 7.1 million people that are currently living with HIV (UNAIDS 2019).

Initially, the identification of yeast was based on its morphological and physiological traits (van Uden & Ahearn 1965; Woollett & Hendrik 1970; Hagler & Medonca-Hagler 1981;
such as bacteria and protozoans has not been largely studied has received little attention. Furthermore, the occurrence indoors, the presence of yeasts in aquatic environments Compared with other environments such as soils and environments. Yeasts identiﬁcation was strenuous and in many cases, inconclusive (Kurtzman & Robnett 1998). Various studies showed that molecular analyses are more reliable when identifying yeasts to species level (Brandão et al. 2010, 2011, 2017; Brilhante et al. 2016; Novak Babič et al. 2016; Monapathi et al. 2017, 2018; Pires et al. 2017; Moubasher et al. 2018; Maciel et al. 2019). Recent studies conducted in different environments furthermore applied next generation sequencing (NGS) methods to determine yeasts community structures and dynamics (Aguilar et al. 2016; Okuno et al. 2016; Romão et al. 2017).

Although yeasts constitute the aquatic environments microbial community, their biodiversity and distribution have been ignored (Yurkov & Pozo 2017). The present study explores the occurrence of yeasts in natural water resources with emphasis on freshwater systems. A structured review was conducted to determine the extent of current knowledge of yeasts in freshwater systems using the literature relevant to the characteristics, diversity and health implications of aquatic yeasts. The following databases were used during this research: EBSCOhost, Google scholar, Sabinet and Science Direct. The literature that included one or more keywords, such as yeasts, identiﬁcation, uses, aquatic environments, microbial pollution, yeast infections, antifungal resistance and resistance mechanisms, were used as references.

YEAST DIVERSITY IN AQUATIC ENVIRONMENTS

Compared with other environments such as soils and indoors, the presence of yeasts in aquatic environments has received little attention. Furthermore, the occurrence of yeasts in water as compared with other microorganisms such as bacteria and protozoans has not been largely studied (Pereira et al. 2010). With limited studies on aquatic yeasts, most of them are concentrating on polluted water (Nagahama 2006). Few yeast species exclusively associated with aquatic environments (Libkind et al. 2017). The section below addresses the diversity of yeasts in different aquatic environments.

Freshwater

The diversity and ecology of yeasts in freshwater environments (temperate and tropical rivers, lakes and lagoons) has been reviewed in a study by Libkind et al. (2017). The review conforms to the present review with respect to yeast identiﬁcation. Identiﬁcation of yeasts was primarily based on morphological and physiological characteristics. However, the identiﬁcation was strenuous and in many cases, inconclusive (Kurtzman & Robnett 1998). As stipulated in Table 1, most of the conducted studies before 2001 relied on morphology and physiological tests for identiﬁcation. The use of more reliable molecular data in yeasts identiﬁcation followed in most studies thereafter. From a review by Libkind et al. (2017) and studies summarized in the current study (Table 1), yeast isolates associated with tropical and temperate lakes, rivers and lagoons comprise species of Candida, Clavispora, Cryptococcus, Debaryomyces, Hanseniaspora, Kluyveromyces, Metschnikowia, Meyerozyma, Pichia, Rhodotorula, Saccharomyces, Torulaspora, Trichosporon and Yarrowia. Studies on yeasts in tropical rivers and lakes have been linked to freshwater pollution. Tropical ecosystems are surrounded by forests and located near urban areas. Rich yeasts species reﬂect inputs from terrestrial sources such as soil and plant debris and anthropogenic activities (Medeiros et al. 2008; Brandão et al. 2011; Libkind et al. 2017). Furthermore, some of the yeast species isolated from these freshwater environments have been implicated as opportunistic pathogens (Medeiros et al. 2008, 2012; Brandão et al. 2011; Van Wyk et al. 2012; Monapathi et al. 2017, 2018).

Drinking water

Surface water and groundwater are primary sources of drinking water (Katsanou & Karapanagioti 2017). Regular detection of emerging opportunistic yeast pathogens in taps suggests that it might be a vector for human infections (Novak Babič et al. 2017). From studies conducted (Table 1), the following yeast genera have been isolated from water distribution systems and tap water: Candida, Clavispora, Cryptococcus, Debaromyces, Meyerozyma, Pichia, Rhodotorula, Trichosporon and Yarrowia. Yamaguchi et al. (2007) isolated the following Candida species, namely C. albicans,
Table 1 | Some of the aquatic environment studies conducted on yeasts (✓ – done; nd – not done)

| Authors                        | Background to study | Resource type           | Country   | Mode of identification                                    | Asco/ Basidiomycota activity | Resistance mechanisms | Virulence tests |
|--------------------------------|---------------------|-------------------------|-----------|------------------------------------------------------------|-----------------------------|----------------------|------------------|
| **Freshwater environments**    |                     |                         |           |                                                           |                             |                      |                  |
| van Uden & Ahearn (1963)       | Diversity           | Surface and deep water  | USA       | Morphology and physiological tests                        | Both                         | nd                   | nd               |
| Woollett & Hendrik (1970)      | Pollution           | Lakes and rivers        | USA       | Morphology and physiological tests                        | Both                         | nd                   | nd               |
| Hagler & Medonca-Hagler (1981) | Pollution           | Estuarine waters        | Brazil    | Morphology and physiological tests                        | Both                         | nd                   | nd               |
| Sláviková et al. (1992)        | Diversity           | Artificial fresh lakes  |           | Morphology and physiological tests                        | Both                         | nd                   | nd               |
| Rosa et al. (1995)             | Pollution           | Lake                    | Brazil    | Morphology and physiological tests                        | Both                         | nd                   | nd               |
| Sláviková & Vadkertiová (1997)| Pollution           | River                   | Slovakia  | Morphology and physiological tests                        | Both                         | nd                   | nd               |
| Dynowska (1997)                | Pollution           | River                   | Poland    | Physiological tests                                        | Both                         | nd                   | nd               |
| Boguslawska-Was & Dabrowski (2001) | Pollution           | Lagoon                  | Poland    | Morphology and physiological tests                        | Both                         | nd                   | nd               |
| Gadanho & Sampaio (2004)       | Diversity           | River                   | Portugal  | Sanger sequencing                                         | Both                         | nd                   | nd               |
| Medeiros et al. (2008)         | Diversity           | Natural lakes and rivers| Brazil    | Physiological tests and Sanger sequencing                 | Both ✓                      | nd                   | nd               |
| Brandão et al. (2010)          | Diversity           | Lakes                   | Lakes     | Physiological tests and Sanger sequencing                 | Ascomycota ✓                 | nd                   | nd               |
| Biedunkiewicz & Baranowska (2011) | Diversity           | Lake                    | Poland    | Morphology and physiological tests                        | Ascomycota                   | nd                   | nd               |
| Brandão et al. (2011)          | Diversity           | Lakes                   | Brazil    | Morphology, physiological tests and molecular tests       | Both                         | nd                   | nd               |
| Medeiros et al. (2012)         | Diversity           | Lakes                   | Brazil    | Molecular techniques                                       | Both                         | nd                   | nd               |
| Van Wyk et al. (2012)          | Diversity           | Rivers                  | South Africa | Morphology and physiological tests                       | Both                         | nd                   | nd               |
| Biedunkiewicz et al. (2015)    | Diversity           | Lakes                   | Poland    | Morphology and physiological tests                        | Ascomycota                   | nd                   | nd               |
| Silva-Bedoya et al. (2014)     | Diversity           | Artificial lakes        | Colombia  | Morphology and molecular tests                            | Both                         | nd                   | nd               |
| Aguilar et al. (2016)          | Diversity           | Surface water, tailing ponds and sediments | Canada | Molecular techniques                                       | Both                         | nd                   | nd               |

(continued)
| Authors                  | Background to study | Resource type                          | Country       | Mode of identification                                                                 | Asco/ Basidiomycota | Antimicrobial activity | Resistance mechanisms | Virulence tests |
|-------------------------|---------------------|----------------------------------------|---------------|----------------------------------------------------------------------------------------|---------------------|------------------------|----------------------|------------------|
| Brillhante et al. (2016)| Resistant mechanisms| Lake                                   | Brazil        | Morphology and physiological tests                                                      | Both                | √                      | √                    | nd               |
| Brandão et al. (2017)   | Diversity           | Lake                                   | Brazil        | Morphology, physiological tests and molecular tests                                      | Both                | nd                     | nd                   | nd               |
| Monapathi et al. (2017) | Diversity           | Rivers                                 | South Africa  | Physiological tests and molecular tests                                                  | Ascomycota          | √                      | nd                   | nd               |
| Monapathi et al. (2018) | Resistant mechanisms| Rivers                                 | South Africa  | Physiological tests and molecular tests                                                  | Ascomycota          | √                      | √                    | nd               |
| Moubasher et al. (2018) | Diversity           | Mud from hypersaline and freshwater bodies | Egypt         | Physiological tests and molecular techniques                                            | Both                | nd                     | nd                   | nd               |
| **Drinking water environments** |                     |                                        |               |                                                                                         |                     |                        |                      |                  |
| Yamaguchi et al. (2007) | Diversity           | Bottled and tap water                  | Brazil        | Physiological and molecular tests                                                        | Ascomycota          | nd                     | nd                   | nd               |
| Kanzler et al. (2008)   | Diversity           | Wells, water tanks, tap water and groundwater | Austria    | Morphology and physiological tests                                                      | Both                | nd                     | nd                   | nd               |
| Ayanbimpe et al. (2012) | Diversity           | Taps, wells, boreholes and streams      | Nigeria       | Morphology and physiological tests                                                      | Both                | nd                     | nd                   | nd               |
| Biedunkiewicz et al. (2014)| Diversity         | Bottled and tap water                  | Poland        | Morphology and physiological tests                                                      | Both                | nd                     | nd                   | nd               |
| Novak Babič et al. (2016)| Diversity        | Tap and groundwater                    | Slovenia      | Physiological and molecular tests                                                      | Both                | nd                     | nd                   | nd               |
| Zupančič et al. (2016)  | Diversity           | Dishwashers                            | Slovenia      | Molecular techniques                                                                   | Both                | nd                     | nd                   | nd               |
| **Wastewater environments** |                     |                                        |               |                                                                                         |                     |                        |                      |                  |
| Yang et al. (2011)      | Diversity           | Activated sludge                       | China         | Morphology and molecular techniques                                                      | Both                | nd                     | nd                   | nd               |
| Liébana et al. (2015)   | Diversity           | Activated sludge                       | Spain         | Morphology and molecular techniques                                                      | Both                | nd                     | nd                   | nd               |
| Karimi & Hassanshahian (2016)| Diversity       | Soil and wastewater                    | Iran          | Molecular techniques                                                                   | Ascomycota          | nd                     | nd                   | nd               |
| Rajendran et al. (2016) | Diversity           | Sewage water and sludge                | Taiwan        | Morphology and molecular techniques                                                      | Ascomycota          | nd                     | nd                   | nd               |
| Mahgoub et al. (2016)   | Diversity           | Activated sludge                       | Egypt         | Morphology and molecular techniques                                                      | Ascomycota          | nd                     | nd                   | nd               |
| Pires et al. (2017)     | Diversity           | Wastewater                             | Brazil        | Morphology and molecular techniques                                                      | Both                | nd                     | nd                   | nd               |
| Authors          | Diversity | Environment                      | Country     | Methods                                | Both | nd | nd | nd |
|------------------|-----------|----------------------------------|-------------|---------------------------------------|------|----|----|----|
| Assress et al. (2019) | Diversity | Wastewater                       | South Africa | Molecular techniques                  | Both | nd | nd | nd |
| Kanzler et al. (2008) | Diversity | Wells, water tanks, tap water and groundwater | Austria     | Morphology and molecular techniques   | Both | nd | nd | nd |
| Pereira et al. (2009) | Diversity | Groundwater, surface and spring water | Portugal    | Morphology and physiological tests    | Both | nd | nd | nd |
| Pereira et al. (2010) | Diversity | Groundwater, surface and springs  | Portugal    | Molecular techniques                  | Both | nd | nd | nd |
| Branda et al. (2010) | Diversity | Superficial and deep sediments, ice cores and meltwaters | Italy       | Molecular techniques                  | Both | nd | nd | nd |
| Samah et al. (2014)  | Diversity | Groundwater wells                 | Egypt       | Morphology and physiological tests    | Ascomycota | nd | nd | nd |
| Novak Babič et al. (2016) | Diversity | Tap and groundwater               | Slovenia    | Physiological and molecular tests     | Both | nd | nd | nd |
| Rédou et al. (2015)  | Diversity | Deep subseafloor sediment         | New Zealand | Molecular techniques                  | Both | nd | nd | nd |
| Chang et al. (2015)  | Diversity | Sea surface microlayer and underlying water | Taiwan     | Molecular techniques                  | Both | nd | nd | nd |
| Zuza-Alves et al. (2016) | Pathogenesis | Beaches                          | Brazil      | Physiological tests                  | Ascomycota | √  | nd | √  |
| Francis et al. (2016) | Diversity | Seaweeds                          | New Zealand | Molecular techniques                  | Both | nd | nd | nd |
| Abreu et al. (2016)  | Diversity | Beach sands                       | Portugal    | Physiological tests                  | nd | nd | nd | nd |
| Zaky et al. (2016)   | Diversity | Seashore                          | UK, Egypt and USA | Morphology, physiological and molecular techniques | Ascomycota | nd | nd | nd |
| Romão et al. (2017)  | Diversity | Beach sands                       | Portugal    | Molecular techniques                  | Both | nd | nd | nd |
| Maciel et al. (2019) | Antifungal susceptibility | Sand and seawater            | Brazil      | Morphology, physiological and molecular techniques | Both | √  | nd | √  |
*C. glabrata* and *C. parapsilosis* from bottled mineral and tap water from municipal supplies. In a study conducted by Ayanbimpe et al. (2012), yeasts species such as *Candida tropicalis*, *Yarrowia lipolytica* and *Rhodotorula* sp. were isolated from tap water. Novak Babić et al. (2016) and Zupančič et al. (2016) isolated ubiquitous opportunistic pathogenic yeasts *Candida parapsilosis* and *Rhodotula mucilaginosa* from tap water and hot aerosols from dishwashers.

**Groundwater**

Freshwater from groundwater represents the raw water that is used to produce drinking tap water (Libkind et al. 2017). The diversity of yeasts in groundwater is comparable to that of surface water (Novak Babić et al. 2016) and comprise of genera *Candida, Clavispora, Cryptococcus, Geotrichum, Pichia, Rhodotorula, Saccharomyces, Trichosporon* and *Yarrowia* (Kanzler et al. 2008; Pereira et al. 2009, 2010; Brandão et al. 2010; Ayanbimpe et al. 2012; Samah et al. 2014; Novak Babić et al. 2016; Libkind et al. 2017). However, groundwater is dominated by black yeasts (Kanzler et al. 2008; Novak Babić et al. 2016). With groundwater systems as drinking water and freshwater resources, it could be expected and it is not surprising to observe similar genera in these water systems.

**Marine**

Marine environments are treated by pollution from municipal sewage/wastewater and industrial discharges, surface and agricultural run-off and domestic effluent. This is a public health risk to coastal residents and tourists in direct contact with the water (Maciel et al. 2019). Yeasts have been studied from marine environments, including oceans, marine sediments, seawater, seaweeds and digestive tracts of marine organisms (Zaky et al. 2014). Some yeast species isolated from marine environments are opportunistic pathogens (Maciel et al. 2019). The following yeast genera have been isolated from the studies stipulated in Table 1: *Bullera, Candida, Clavispora, Cryptococcus, Debaryomyces, Hanseniaspora, Kluyveromyces, Meyerozyma, Metschnikowia, Pichia, Rhodotula, Saccharomyces, Yarrowia* and *Wickerhamomyces*. Yeasts in marine environments are vital in the food web (Zaky et al. 2014). They might be sources of food for some marine invertebrates and zooplanktons (Naghahama 2006). Moreover, marine yeasts are important for their application in the production of biofuel, enzyme production, single-cell protein, single cell oil and nanoparticles (Zaky et al. 2014; Sarkar & Rao 2016).

**Wastewater**

Microorganisms (including pathogenic) are required for treatment processes in waste water treatment plants (WWTPs) (Kowalski et al. 2017). Yeast species belonging to the genera *Candida, Cryptococcus, Debaryomyces, Pichia, Rhodotorula, Torulaspora, Trichosporon, Saccharomyces, Yarrowia* and *Wickerhamomyces* (Yang et al. 2011; Liébana et al. 2015; Karimi & Hassanshahian 2016; Mahgoub et al. 2016; Rajendran et al. 2016; Pires et al. 2017; Assress et al. 2019) have been isolated from WWTPs. Some yeast species have the potential to act as a biological treatment in the WWTP (Pires et al. 2017). They can treat high concentrations of organic wastewater, heavy metal ion wastewater and domestic sewage (Wang et al. 2018). Their importance in wastewater treatment stems from their ability to degrade phenol compounds (Karimi & Hassanshahian 2016).

**SURVIVAL OF YEASTS IN FRESHWATER ENVIRONMENTS**

Existing environmental conditions maintain the survival of yeasts in the ecosystem. Most yeasts are mesophilic and grow best at temperatures between 20 and 30°C (Deak 2006). Human pathogens grow well at 37°C, the normal internal temperature of the human body (Gabaldón & Carreté 2016). Yeasts species that grow at this particular temperature may have pathogenic potential as opportunistic species for humans. Yeasts prefer a slightly acidic medium with optimum pH between 4.5 and 5.5 (Deak 2006). Furthermore, yeasts can grow aerobically on particular carbon compounds such as alcohols, organic acids and amino acids as their sole energy source (Rodrigues et al. 2006). Deak (2006) stipulated that increased dissolved oxygen and dissolved organic matter in aquatic environments favour yeast growth. Yeasts can also utilize a wide range...
of nitrogen compounds as nitrogen sources. Some nitrogen-containing compounds such as amino acids and ammonia can also be used by yeasts as carbon sources (Messenguy et al. 2006).

YEASTS- POLLUTION MONITORING TOOL

Recent microbial water pollution has been determined by standard faecal indicator bacteria (SFIB) such as *Escherichia coli* and intestinal enterococci (Kirschner et al. 2017). However, some studies have demonstrated that yeast counts can be potential microbial monitoring tools. From studies conducted by Van Wyk et al. (2012) and Monapathi et al. (2017) in North West Rivers, South Africa, yeast levels ranged up to 8,680 and 2,573 CFU/l, respectively. In a study conducted by Medeiros et al. (2012) in the Doce River basin in Brazil, the highest yeasts count was 4,660 CFU/l. A study done in Brazil at Lago Rico River reported on 721.6 CFU/l yeast counts (Brandão et al. 2011). However, some studies have demonstrated that yeast counts can be potential microbial monitoring tools. From studies conducted by Van Wyk et al. (2012) and Monapathi et al. (2017) in North West Rivers, South Africa, yeast levels ranged up to 8,680 and 2,573 CFU/l, respectively. In a study conducted by Medeiros et al. (2012) in the Doce River basin in Brazil, the highest yeasts count was 4,660 CFU/l. A study done in Brazil at Lago Rico River reported on 721.6 CFU/l yeast counts (Brandão et al. 2017). Total yeast counts up to 1,720 CFU/l in water and 4,085 CFU/l in sands were enumerated in a study by Maciel et al. (2019). Aquatic environments in the aforementioned studies were associated with anthropogenic activities, eutrophication and high influx of domestic and industrial waste. A rapid response of yeasts to organic contamination makes yeasts important indicators of nutrient enrichment since these convert easily accessible carbon sources into energy for reproduction (Brandão et al. 2010). Yeasts could potentially be informative water quality indicators. They can be utilized as complements and/or alternatives to faecal indicator bacteria.

OPPORTUNISTIC PATHOGENIC YEASTS

Some of the yeasts species mentioned in the section ‘Yeast diversity in aquatic environments’ are opportunistic pathogens and may cause mild to severe infections in humans. Most invasive yeast infections are frequently caused by pathogens from the genera *Candida* and *Cryptococcus* (Bajpai et al. 2019). Candidiasis is one of the common opportunistic infections caused by *Candida* species. *C. albicans* is the most prevalent causal species (Friedman & Schwartz 2019). The following non-*Candida albicans* species are also to cause candidiasis: *C. glabrata*, *C. parapsilosis*, *C. tropicalis*, *C. krusei* and *C. auris* (Kullberg & Arendrup 2015; Zupančič et al. 2016; Friedman & Schwartz 2019). Human cryptococcal infections are primarily caused by *Cryptococcus neoformans* and *C. gattii* (Mada et al. 2017). Cryptococcosis is one of the leading causes of mortality in adults living with HIV in sub-Saharan Africa (Hurtado et al. 2019).

Rare non-*Candida* and non-*Cryptococcus* species are also associated with yeast infections. *Trichosporon* species (*Trichosporon asahii*, *T. faecale*) cause invasive trichosporonosis in patients with haematological malignancies and other medical conditions associated with immunocompromised people (Castano & Mada 2018; Maciel et al. 2019; Ruosta et al. 2019). Opportunistic pathogenic *Rhodotorula* species (*R. mucilaginosa*, *R. glutinis* and *R. minuta*) cause infections with high mortality rates in haematologic patients particularly on central venous catheters (Potenza et al. 2018). The above-uncommon clinical yeast species have also been reported as opportunistic pathogens: *Clavispora lusitania*, *Cyberlindnera fabianii*, *Debaryomyces hansenii*, *Kluyveromyces marxianus*, *Meyerozyma guilliermondii*, *Pichia kudriavzevii*, *Saccharomyces cerevisiae*, *Torulaspora delbrueckii* and *Yarrowia lipolytica* (Chitasombat et al. 2012; Al-Sweih et al. 2018; Ruosta et al. 2019). The above-mentioned pathogenic yeast species have been isolated from freshwater water environments (Medeiros et al. 2008, 2012; Brandão et al. 2010, 2011, 2017; Van Wyk et al. 2012; Monapathi et al. 2017; Moubasher et al. 2018; Maciel et al. 2019). There is a lack of studies that link these isolates/strains from the environment to those from clinical settings.

Virulence factors in pathogenic yeasts

The expression of virulence factors in pathogenic/opportunistic pathogenic yeasts enable them to cause diseases (Polvi et al. 2015). Detailed knowledge about these factors in yeasts is limited. Some of the virulent traits in pathogenic yeasts are high-temperature growth, adaptation to pH, overexpression of melanin, nutrient limitation, morphological transition, secretion of extracellular enzymes, induction of capsule formation and formation of biofilms (Polvi et al. 2015). Virulence factors have been detected in
some studies in pathogenic environmental yeasts (Zuza-Alves et al. 2016; Maciel et al. 2019). Virulence factors allow pathogenic yeast species to invade hosts, to resist their immune system defence mechanisms and to cause infections, especially in immunocompromised people (Abulreesh et al. 2019).

Antifungal resistance in pathogenic yeasts

Antifungal drugs are available to treat yeasts infectious (Perfect 2017). There has been a concerted effort to monitor and report on resistance development among clinical yeasts isolates to commonly used antifungal agents. Antifungal susceptibility studies have been conducted on pathogenic environmental yeasts (Medeiros et al. 2008; Brandão et al. 2010; Brilhante et al. 2016; Monapathi et al. 2017, 2018; Maciel et al. 2019) and antimicrobial resistance has been observed. Resistance to antifungal agents develops from continuous exposure of yeasts to antifungal agents (Morschlhäuser 2016). Prolonged contact of pathogenic yeasts in water to antifungal agents could result from subtherapeutic levels of antifungal agents that constantly land into aquatic environments (Singer et al. 2016; Meade et al. 2017). This is linked to prevailing therapy regimes (infection control or prophylactic treatment), disposal routes, waste (wastewater) treatment options and agricultural run-off. The presence of antifungal agents in any environment affects the diversity and selection of antifungal resistant pathogens/opportunistic pathogens (Cowen et al. 2015).

PUBLIC HEALTH CONCERN OF FINDING PATHOGENIC YEASTS IN ENVIRONMENTAL WATER

The occurrence of opportunistic yeast species in environmental water suggests a potential risk to direct water users. This public health threat is worsened by poor susceptibility to commonly used antifungal drugs (Maciel et al. 2019). People at peril are communities that use water for domestic and agricultural purposes as well as activities where direct exposure is common such as recreation and religious cleansing or baptism (Zenani & Mistri 2005). Direct contact with water polluted with pathogenic yeasts could cause diseases/infections in healthy and immunocompromised individuals (Monapathi et al. 2017; Maciel et al. 2019). This is a public and health concern and needs more research to highlight this aspect but also to generate sufficient data to evaluate if policy changes are required for including yeasts in water quality guidelines.

POSSIBLE ROUTES OF YEAST INFECTIONS: AQUATIC INTERVENTION

Some of the yeast species in water resources are pathogenic and infectious diseases may be transmitted through contaminated water (Ayanbimpe et al. 2012). Figure 1 shows possible routes of yeast infections via water resources. Drinking water is the direct route of yeasts to humans (DEFRA 2011). Drinking water can be a reservoir for opportunistic pathogenic yeasts, which can cause infections in immunosuppressed patients (Kanzler et al. 2008). Yeasts species of Candida, Cryptococcus, Debaryomyces, Saccharomyces and Trichosporon have been detected from gut microbiota in human (Hallen-Adams & Suhr 2017). Microorganisms in the gut constitute human sewage microbiome. These are from different human body sources, including skin, respiratory tract, oral cavity, gastrointestinal tract and urogenital tract. The sewage is taken to the WWTPs for treatment (Cai et al. 2014). These are the same WWTPs that are known to harbour pathogenic yeasts (Chu et al. 2018). Subsequently, treated and/or untreated wastewater will end up in surface water (Edokpayi et al. 2017).

Drinking water from surface and groundwater resources is purified through various processes and disinfected before it is distributed to consumers. If water is inefficiently treated, yeasts from the aforementioned resources could end up in drinking water (DEFRA 2011). Yeasts in drinking water distribution systems are known to act as pathogens (Oliveira et al. 2016). Their occurrence in drinking water can pose a health threat to consumers with direct daily contact such as drinking and showering (Novak Babić et al. 2016). The possible pathway of yeast infections from drinking to surface water is confirmed by the presence of similar genera of species in the gut, WWTPs and surface water. Furthermore, studies by Götlitch et al. (2002) and Oliveira et al. (2016) suggest groundwater as a yeast vehicle to drinking water. Plants
may be the other route of yeast infections in humans. Faeces of animals and humans used as fertilizers in agriculture contain pathogenic bacteria and yeasts. The use of fertilizers could contaminate the soil and field crops, and ultimately infect consumers (Scheinemann et al. 2015; Al-Sadi 2017; Lamastra et al. 2018).

The human population exploits a large number of aquatic animal species for food (Ogden 2017). Some of these animals require surface and marine water for survival. If the water is contaminated with pathogenic yeasts, human beings are likely to be infected through consumption of these animals. There have been some reports on marine water contamination from oil spills, pharmaceuticals and personal care products and microplastics (Arpin-Pont et al. 2016; Brennecke et al. 2016). These reports are bothersome as marine environments are used for recreational activities such as swimming, fishing, surfing and boating (Sumaila & Cisneros-Montemayor 2010; Beaumont et al. 2019). From another public health view, in direct contact with the water, this association could serve as an additional route of pathogenic yeasts to humans.

**MICROBIOLOGICAL RISK ASSESSMENTS**

Microbiological risk assessment (MRA) is an estimate of the possibility of illness from a pathogen in a given population (Rocourt et al. 2003). It is vital in risk management and communication thereof to minimize negative impacts on human health (Brown & McClure 2006). MRA assists in policy development, public health decision-making and establishment of microbial pathogen regulations and research planning (Sherif et al. 2009). Most of the pathogenic yeasts isolated until now have been from clinical samples where known infections occurred (Shokohi et al. 2018; Consortium OPATHY & Gabaldón 2019; Friedman & Schwartz 2019). Finding similar species in environmental water is thus cumbersome. For aquatic yeasts, contact transmission is
normally the route of infection (Eames et al. 2009). In determining MRA in aquatic pathogenic yeasts, a qualitative exposure assessment would be ideal.

There are direct and indirect possible contact ways between yeasts and humans through aquatic pathways (Figure 1). Surface and groundwater are drinking water resources. Furthermore, they are also used in agricultural, industrial and/or domestic sectors (Wada et al. 2014; Katsanou & Karapanagioti 2017; Libkind et al. 2017). Drinking water or consuming plants and/or animals contaminated with pathogenic yeasts may also be an important direct exposure to humans. According to a study by Hageskal et al. (2009), drinking contaminated water has not caused acute diseases in healthy individuals. However, there is a risk of superficial or localized infections in these healthy individuals and more severe and invasive infection in immunocompromised persons. As mentioned in the previous section on marine environments, recreational activities also expose humans to possibly contaminated water.

A quantitative risk characterization would assist in determining the severity of known and potential adverse health effects (Rocourt et al. 2003). From clinical tests, for microorganisms to cause an infection, the number of colony-forming units (CFU)/ml in the bloodstream should be defined. In bloodstream infection, Candida CFU/ml in the first 50% positive blood culture had <1 CFU/ml of circulating organisms (Pfeiffer et al. 2011). For candidemia, classified as high-grade and low-grade candidemia, 25 CFU or more per 10 ml and 10 CFU or fewer per 10 ml of blood, respectively, were defined (Telenti et al. 1993). According to Perlin & Wiederhold (2017), a low initial concentration (often <10 CFU/ml) of the pathogen within the collected specimen can grow to cause an infection. This suggests that low levels of yeasts in direct exposure to humans could cause an infection. Similar quantitative risk data for environmental exposures are not available, and there is a necessity to generate such information.

**CONCLUSION**

The number of peer-reviewed articles about yeast diversity in water has increased and some have originated in South Africa. The present review largely focused on freshwater environments. Most of the studies on yeasts in aquatic environments address water pollution aspects. Yet, bacterial indicator species are mainly the microbes that are used in water quality assessments. Declining water quality is a global concern, and in these systems, the chemical and physical conditions are such that yeast species could survive. Some of these are known as pathogenic or opportunistic pathogens. Future studies are needed to generate data to determine whether it is necessary to include yeasts in water quality guidelines. This may be necessary if one considers the large sections of populations in developing countries that are immunocompromised, particularly those living with HIV. Studies on health implications have mostly been addressed on pathogenic clinical isolates. This creates a gap in research as similar isolates have been isolated from aquatic environments. The same resistance patterns to antifungal agents and resistance mechanisms associated with clinical isolates were also found to exist among environmental isolates. Molecular methods to study antifungal resistance mechanisms should be extended to environmental isolates. Direct exposure to polluted water is a health threat. Studies in the clinical settings have shown that to cause an infection, yeast level as low 1 CFU/ml is sufficient. Similar data for environmental water levels are needed. More studies are required in South Africa and globally to address the possible implications of antifungal resistant pathogenic yeasts in water.

**ACKNOWLEDGEMENTS**

This work is based on the research supported in part by the National Research Foundation of South Africa for Grant No. 93621 and the Water Research Commission of South Africa (Contract: K5/2547). Financial support of NWU and Nation Manpower Development Secretariat (Lesotho Bursary) grant to Mzimkhulu Monapathi is also acknowledged. The views expressed are those of the authors and not of the funding agency.

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First received 3 December 2019; accepted in revised form 3 March 2020. Available online 13 March 2020