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Diversity of yeasts and filamentous fungi in mud from hypersaline and freshwater bodies in Egypt

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The diversity of yeasts and filamentous fungi in muds from hypersaline alkaline lakes of Wadi El-Natrun and fresh water of the Nile River and Ibrahimia Canal was evaluated. The mean pH of saline water mud was 9.21, but fresh water mud registered 8.07.

A total of 193 species (two varieties were distinguished in two of them) belonging to 67 genera were recovered from both muds investigated on DRBC (55 genera, 164 species), DG18 (36 genera, 117 species) and MY50G (23 genera, 76 species) media. From these, 17 species assigned to 12 genera were yeasts and 176 species and 2 varieties assigned to 55 genera were filamentous fungi. The highest numbers of fungal propagules were recovered on DRBC from freshwater mud, while the lowest on MY50G from saline water mud.

Yeasts constituted a small proportion of all propagules from the two mud types on all three media, whereas filamentous fungi were the major component. However, freshwater mud samples yielded higher numbers of yeast genera and species using all three media. *Candida* was common in freshwater mud and rare in saline water mud, while *Meyerozyma* and *Rhodotorula* were infrequent in both muds. The remaining yeast species were recovered from freshwater mud only.

Aspergillus (46 species) was the most common genus of filamentous fungi encountered in all samples, ranging in frequency from 39.82% to 96.62%; *A. terreus*, *A. flavipes* and *A. niger* dominated in both types of mud. *Cladosporium* (9 species), *Fusarium* (8 species), *Penicillium* (18 species) and *Scopulariopsis* (7 species) were encountered in both types of mud. Notably, 47 filamentous species were isolated only on the media with lower water activity (DG18, MY50G).

Key words: fungal diversity, alkalinity, Wadi El-Natrun, lakes, Ibrahimia Canal, River Nile, molecular characterisation, ITS.

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Diverzita kvasinek a vláknitých hub byla hodnocena ve vzorcích bahen z hypersalinních jezer ve vádí El-Natrun a sladkých vod Nilu a kanálu Ibrahimia. Průměrné pH bahna ze slaných vod bylo 9,21, zatímco ve sladkovodním bylo zaznamenáno 8,07.

Celkem byly zaznamenány 193 druhy (ve dvou případech byly rozlišeny dvě variety od jednoho druhu) ze 67 rodů, a to na různých médiích – na DRBC 164 druhy z 55 rodů, na DG18 bylo 117 druhů z 36 rodů a na MY50G 76 druhů z 23 rodů. Z toho kvasinky představovaly 17 druhů ze 12 rodů a vláknité houby 176 druhů (plus dvě odlišené variety) z 55 rodů. Nejvyšší počet houbových propagulí byl zaznamenán na DRBC ze sladkovodního bahna, nejnižší naopak na MY50G ze slaného bahna.

Ve všech případech dominovaly vláknité houby, jen drobný podíl ze všech propagulí (z obou typů bahen) představovaly kvasinky. Na všech médiích byl zaznamenán vyšší počet druhů kvasinek ze sladkovodních vzorků. Zde byly vcelku běžné druhy rodu *Candida* (vzácné ve slaných bahnech), zatímco zástupci rodů *Meyerozyma* a *Rhodotorula* byly nehojné v obou typech bahen a ostatní druhy kvasinek se vyskytovaly pouze ve sladkých vodách.

Mezi vláknitými houbami byly jednoznačně nejběžnější druhy rodu *Aspergillus*, jejichž zastoupení dosáhlo od 39,82 % až po 96,62 %; jako dominující druhy byly zaznamenány *A. terreus*, *A. flavipes* a *A. niger*. Dalšími druhy zjištěnými v obou typech bahen jsou *Cladosporium* (9 druhů), *Fusarium* (8 druhů), *Penicillium* (18 druhů) a *Scopulariopsis* (7 druhů). Za zaznamenání stojí, že 47 druhů vláknitých hub bylo izolováno jen na médiích s nižší vodní aktivitou (DG18, MY50G).

INTRODUCTION

Yeasts are widespread in terrestrial, aquatic and aerial environments and their distribution, frequency and metabolic characteristics have been found to be governed by existing environmental conditions (Spencer & Spencer 1997). In freshwater habitats, yeasts are commonly found in the sediments of running waters (Palmer et al. 1997). Microorganisms of the sediments, including yeasts, substantially contribute to the biogeochemical processes of aquatic ecosystems (Rastogi et al. 2011, Sanchez-Andrea et al. 2011), such as leaf litter decomposition, nutrient transformations, energy flow, and self-purification (Bärlocher 1992, Gessner et al. 1999, Gulis & Suberkropp 2004, Gerbersdorf et al. 2011, Green et al. 2011, Song et al. 2011, Yang et al. 2013, Maini & Shukla 2015).

Yeasts and yeast-like organisms can be potentially found everywhere in an aquatic ecosystem. They are ecologically flexible, which allows them to tolerate a wide range of salinities, environmental temperatures, oxygen saturation levels, and acidities in the surrounding medium (Bogusławska-Wąs & Dąbrowski 2001). They have been isolated from lake and sea sediments (MacGillivray & Shiaris 1993, Bogusławska-Wąs & Dąbrowski 2001) and at various depths from the water (Wurzbacher et al. 2010). Furthermore, a large variety of yeasts have been isolated from lakes with different organic loads. They have been found in mesotrophic lakes of the United States (van Uden & Ahearn 1963), oligotrophic lakes of Patagonia, Argentina (Brandão et al. 2011), in lakes receiving sewage discharges (Meyers et al. 1970), and in lakes for recreational tourism in Brazil (Medeiros et al. 2008). In most cases, the dominant species were from the *Rhodotorula*, *Candida* and *Cryptococcus* genera. Pathogenic species of these genera were found in lakes contaminated by human activities and can be used as biological indicators to establish the contamination levels of these water bodies

(Hagler 2006). *Hortaea werneckii* was found in slope sediments of the Bay of Bengal on the east coast of the Indian peninsula, India (Kutty et al. 2013b). Also, species of *Candida*, *Cryptococcus*, *Williopsis*, *Hanseniaspora*, *Rhodotorula*, *Saccharomyces*, *Torulaspora*, *Trichosporon* and *Yarrowia lipolytica* were recovered from sediment and water samples from two artificial lakes in Universidad del Valle (Cali, Colombia) (Silva-Bedoya et al. 2014).

In aquatic environments, filamentous fungi also belong to the microbial communities important for organic decomposition, nutrient cycling and energy fluxes (Kirchman 2008, Song et al. 2011, Yang et al. 2013, Fabian et al. 2016). *Aspergillus*, *Penicillium*, *Curvularia*, *Alternaria*, *Cladosporium*, *Drechslera*, *Fusarium*, *Phoma* and *Rhizopus* were found to be dominant members of sediments in a marine ecosystem off the east coast of Tamil Nadu, India (Saravanan & Sivakumar 2013) and at four stations in the Suq-Alshuyukh marshes in the Thi-Qar Governorate, Iraq (Al-Jawhari 2015). *Aspergillus*, *Eupenicillium* and *Penicillium* were also common in sediments of the Gulf of Aqaba, Jordan (Jaber et al. 2012).

In freshwater environments, the most common fungi were species of *Aspergillus* and *Penicillium* in submerged mud of Aswan High Dam Lake, Egypt (El-Hissy et al. 1990), *Acremonium*, *Alternaria*, *Aspergillus*, *Fusarium*, *Mucor*, *Penicillium*, *Rhizopus* and *Ulocladium* in mud-flats of Tigris Edges in Baghdad (Abdulla 2008), *Penicillium*, *Fusarium*, *Aspergillus*, *Trichoderma* and *Talaromyces* in wetland sediments along the Changjiang River, China (Wu et al. 2013), and *Penicillium* and *Mucor* in sandy loam soil samples collected from a freshwater swamp area in Obrikom, Ogba Egbema Ndoni Local Government Area of Rivers State, Nigeria (Dirisu 2015).

In some locations, temperature, ion content and pH may deviate from those of most habitats, resulting in the formation of specific zones termed 'extreme habitats', restricting growth of most organisms. Saline or alkaline habitats with high pH values (> 8) represent an example of such extreme habitats. Salt concentrations in these habitats may vary from low to saturation (Jones et al. 1998, Grum-Grzhimaylo et al. 2016).

This study aims to describe and compare the biodiversity of yeasts and filamentous fungi in mud collected from hypersaline alkaline (extreme habitat) and fresh waters (normal habitat). Molecular identification was used to confirm the phenotypic characteristics of yeasts and some filamentous isolates.

MATERIAL AND METHODS

Sampling sites. Wadi El-Natrun depression is an extreme habitat located on the western side of the Nile Delta of Egypt and includes some water bodies characterised by high salinity and alkalinity. It is located approximately

110 km northwest of Cairo and 90 km south of Alexandria. Wadi El-Natrun depression is about 50 km long, narrow at both ends and wider in the middle (Zahran & Willis 1992). It lies 23 m below sea level and 38 m below the water-level of the Rosetta branch of the Nile (Abdel-Malek & Rizk 1963). It is characterised by a series of twenty small separate lakes in the bottom of the Wadi. Ten of these lakes are relatively larger and have a permanent water layer in all or some of their parts. Inland saline lakes and salt crusts occupy the lowest part of the depression encircled by the zero contour line (Abu Zeid 1984). The principal lakes of Wadi El-Natrun are Fasida, Umm-Risha, Al-Razoniya (Rosetta), Hamra, El-Zugm (Zaagig), Al-Beida, Khadra and Al-Gaar (Zahran & Willis 1992, Taher 1999).

Wadi El-Natrun depression gets its water from two sources: springs in the bottom (e.g. in Lake Hamra), and from groundwater flowing from the Rosetta branch and its satellite branches into the lakes (Pavlov 1962, Shata & El Fayoumi 1967). Shallow saline pools shrink in volume by > 60% following evaporation in summer. The water of Wadi El-Natrun's saline lakes is enriched with dissolved minerals which have accumulated in the brines following evaporation. Detailed chemical analysis of the lakes of Wadi El-Natrun depression in Egypt have revealed a high pH level (> 11.5) and a high concentration of carbonate, chloride, phosphate, sodium, potassium and silicon oxide (Grant 2006).

The Nile River, 6,650 km in length, runs from East and East-Central Africa to the Mediterranean Sea and has its watershed in 11 countries (Tanzania, Burundi, Rwanda, Democratic Republic of Congo, Kenya, Uganda, Ethiopia, Eritrea, South Sudan, Sudan and Egypt; Abtew & Melessa 2014). In Egypt, many large (Ibrahimia) and small irrigation canals have been created on the Nile.

Ibrahimia Canal is one of the longest (316.3 km) irrigation canals in Egypt. It starts at 400 m upstream of the Assiut barrages and ends in the Giza Irrigation General Directorate. The canal is bounded by a railway line on the right bank and the Cairo-Aswan Agriculture Road on the left bank. The canal runs through many cities and residential areas, and is affected negatively by crossing roads and railway lines. Waste dumps and deposits cause the canal to contract (Abdelmoaty 2013).

Collection of mud samples. A total of 36 mud samples were collected: 24 samples from the largest eight hypersaline lakes of Wadi El-Natrun (in March 2012) and 12 samples from fresh water of the Nile River and Ibrahimia Canal in the Assiut area (from September 2012 to June 2013). At least five samples were taken at random from each location, and made into one composite sample which was mixed thoroughly several times. Each mixed mud sample was put directly into a clean container or plastic bag. Samples were taken to the laboratory and kept in a refrigerator (5 °C) until analysed.

Determination of moisture content and pH. The moisture of the mud was determined by drying replicates of freshly collected samples in an oven at 105 °C until constant weight was reached. The loss of weight was determined, and the mean percentage of moisture content was calculated.

To determine the pH of the mud samples, their extracts were prepared by mixing the sample with distilled water in a ratio of 1 : 5 (w/v), shaking for about 30 min and letting it settle overnight. The extracts were then filtered, centrifuged at 4000 rpm for 15 min. To determine the pH of the mud samples, the electrode of the pH meter (Orior Research Model GOHL Digital Ionalyzer, Cambridge, Massachusetts, USA) was immersed directly in the mud suspension (Jackson 1958).

Isolation of fungi. The dilution-plate method was used for the determination of fungal species frequencies, as described by Johnson & Curl (1972). The plates (5 plates for each type of medium) were incubated at 28 °C for 1–2 weeks, after which the developing fungi were counted and isolated, and the number of colony forming units (CFU) was calculated per gram of fresh sample. Isolates were maintained on yeast extract malt extract agar (YM, for yeasts), Czapek yeast extract agar (CYA), malt extract agar slants (for filamentous fungi) and stored at 5 °C until the identification was confirmed.

The total number of CFU was calculated for all fungal taxa per gram of fresh mud in all samples for each type of mud. The CFU percentage was calculated for each taxon per total number of CFU in all samples.

Media used for isolation of fungi.

1. Dichloran rose Bengal chloramphenicol agar (DRBC; King et al. 1979). Dichloran (20 µg/ml) was added to restrict growth of mucoraceous fungi without affecting other species, rose Bengal (25 µg/ml) and chloramphenicol (100 µg/ml) were used as bacteriostatic agents.
2. Dichloran glycerol agar (DG18; Hocking & Pitt 1980), which is recommended for enumeration and isolation of yeasts and filamentous fungi in samples with low water activity ($a_w < 0.95$). A low water activity of this medium hampers outgrowth by bacteria and fast-growing fungi.
3. Malt extract yeast extract 50% glucose agar (MY50G; Pitt & Hocking 1985).

Our previous experience (Abdel-Sater et al. 2016, Moubasher et al. 2017) revealed that zygomycetes prevailed on most of the isolation media used, therefore the first two media were finally chosen since both contained dichloran, which restricts mucoraceous growth without affecting other species (King et al. 1979, Hocking & Pitt 1980). The first medium ($a_w = 1.0$) was used as a general isolation medium (King et al. 1979), the second ($a_w = 0.95$) for xerotolerant fungi and the third ($a_w = 0.89$) for xerophilic ones (Gunde-Cimerman et al. 2000, Butinar et al. 2005).

Phenotypic identification of fungi. The fungi were identified based on their macro- and microscopic features, according to the keys by Raper & Fennell (1965), Pitt (1979), Sivanesan (1987), Moubasher (1993), de Hoog et al. (2000), Zare & Gams (2004), Leslie & Summerell (2006), Domsch et al. (2007), Samson & Varga (2007), Seifert et al. (2011) and Samson et al. (2011, 2014) for filamentous fungi, and Barnett et al. (2000) for yeasts.

Physiological characterisation of yeast strains. Fermentation of sugars and oxidative utilisation of carbon compounds were performed according to Barnett et al. (2000). Assimilation of nine nitrogen compounds (potassium nitrate, sodium nitrite, ethylamine, L-lysine, creatine, creatinine, D-glucosamine, imidazole and D-tryptophan) was determined as in Suh et al. (2008). Growth at high osmotic pressure, growth in the presence of cycloheximide, production of extracellular starch-like compounds and formation of a dark red colour on diazonium blue B were also tested following Suh et al. (2008). Identification keys by Barnett et al. (2000) were used to assign each isolate to the species level. Confirmation of these identifications was carried out using DNA-based information.

Genotypic identification of fungal strains. For a number of isolates, molecular identification using ITS rDNA sequence was employed as follows. The fungi were grown at 25 °C on CYA plates for 7 days (for filamentous fungi) and on YM plates for 2 days (for yeast isolates). A small amount of fungal biomass was scraped off and resuspended in 100 µl of distilled water and boiled at 100 °C for 15 minutes following the manufacturer's protocol (SolGent Company, Daejeon, South Korea). The fungal samples were sent to Korea for DNA extraction, amplification (using the universal primers ITS1 and ITS4), PCR and sequencing. Fungal DNA was extracted using SolGent purification beads at this company. Internal transcribed spacer (ITS rDNA) sequences of nuclear ribosomal DNA were amplified using the universal primers ITS1 (5'- TCC GTA GGT GAA CCT GCG G -3') and ITS4 (5'- TCC TCC GCT TAT TGA TAT GC -3') (White et al. 1990). Then amplification was performed using the polymerase chain reaction (PCR) (The GeneAmp® PCR System 9700 thermal cycler, Applied Biosystems, Foster City, California, USA). The PCR reaction mixtures were prepared using SolGent EF-Taq as follows: 10X EF-Taq buffer 2.5 µl, 10 mM dNTP (T) 0.5 µl, primer (F-10p) 1.0 µl, primer (R-10p) 1.0 µl, EF-Taq (2.5 U) 0.25 µl, template 1.0 µl, DW to 25 µl. Then the amplification was carried out using the following PCR reaction conditions: one round of amplification consisting of denaturation at 95 °C for 15 min followed by 30 cycles of denaturation at 95 °C for 20 s, annealing at 50 °C for 40 s and extension at 72 °C for 1 min, with a final extension step of 72 °C for 5 min. The PCR products were then purified with the SolGent PCR Purification Kit-Ultra (SolGent, Daejeon, South Korea) prior to sequencing. Then the purified PCR products were reconfirmed (using a size marker) by electrophoreses

of the PCR products on 1% agarose gel. Then these bands were eluted and sequenced. Each sample was sequenced in both directions (Abdel-Sater et al. 2016). Raw sequences were assembled in contigs with the CLCBio Main Workbench program. The sequence obtained from each isolate was further analysed with BLAST at the National Center of Biotechnology Information (NCBI) website.

The recovered yeast isolates were characterised using phenotypic, physiological and molecular criteria (Tabs. 1, 2), while most of the filamentous fungi were identified by phenotypic characteristics based on macro- and microscopic features. Representative strains of the species recovered are deposited at the Assiut University Mycological Centre (AUMC) culture collection and the ITS rDNA sequences of the filamentous and yeast strains were deposited at National Center for Biotechnological Information (NCBI) with accession numbers given in Tab. 1.

RESULTS AND DISCUSSION

OVERALL ASSESSMENT

pH and moisture content of muds

pH of mud samples collected from freshwater bodies of River Nile and Ibrahimia Canal ranged from 7.72 to 8.36 with a mean of 8.07, while those from hypersaline habitats of Wadi El-Natrun lakes were highly alkaline and ranged from 8.00 to 10.15 with a mean value of 9.21 (Tab. 3). In agreement with the current results, the pH of mud samples collected from Wadi El-Natrun lakes ranged from 8.78 to 10.24 (Ismail et al. 2017), while those from Mono Lake (California) ranged from 8.6 to 9.45 (Steiman et al. 2004), whereas it ranged from 6.0 to 8.3 in freshwater mud collected at the Nile margin, 500 m upstream of the Assiut Barrage (El-Hissy & El-Nagdy 1983).

Mean moisture content was 72.46% in hypersaline water mud and 65.22% in the freshwater mud (Tab. 3). Somewhat lower values of moisture content (17.56–58.5%) were obtained recently from mud of Wadi El-Natrun lakes (Ismail et al. 2017).

Fungi recovered from muds

In general, the total amount of CFU and the number of yeast species was much lower than those of filamentous species on all three isolation media we tested. The numbers of CFU and filamentous fungal taxa reported from freshwater mud were higher than those reported from saline mud except when cultivated on MY50G medium. The general isolation medium DRBC recovered more fungal propagules than media with low water activity, such as DG18 and MY50G (Tab. 3).

Tab. 1. Assiut University Mycological Centre accession numbers (AUMC) of filamentous fungi and yeasts isolated from mud samples with GenBank accession numbers together with the closest match in the GenBank database and sequence similarity (%) to the match as inferred from BLASTn searches of ITS sequences.

AUMC number	Isolation source (mud origin)	GenBank accession number	Length (bp)	Closest GenBank match # ITS	Culture collection code	Sequencing similarity (%)	Species	Reference
Filamentous strains								
10269	Saline water (Khadra Lake)	KX373703	569	AJ557830 NR_130684	NRRL 20420 MUCL 9724^{T}	566/569 (99.47) 531/533 (99.62)	*Corallomycetella repens* *Sarocladium kiliense*	Rossman et al. 2016 Perdomo et al. 2011
10270	Saline water (Zugm Lake)	KX233858	550	JN997370 NR_145338	Hw6 CBS 107.67^{T}	536/539 (99.44) 467/473 (98.73)	*Hortaea werneckii*	de Hoog et al. 1999
Yeast strains								
10271	Saline water (Khadra Lake)	KX218253	598	KP132411 EU568913	PMM08-431L CBS 2022	597/597 (100) 596/596 (100)	*Meyerozyma caribbica* (anamorph: *Candida fermentati*)	Desnos-Ollivier et al. 2008
10272	Saline water (Rosetta Lake)	KX218252	603	EF197814 NR_111247	HK53 CBS 2030^{T}	596/598 (99.67) 565/565 (100)	*Meyerozyma guiliermondii* (≡ *Pichia guilliermondii*)	Serena et al. 2011
10273	Fresh water	KX218265	538	HQ876043 NR_125332	ATCC 18804^{T} CBS 562^{T}	522/526 (99.24) 494/495 (99.79)	*Candida albicans*	Suh et al. 2013
10274	Fresh water	KX233863	409	KY102346	CBS 2063^{T}	368/411 (89.54)	*Candida pseudolambica**	Vu et al. 2016
10275	Fresh water	KX218254	513	KY102470	CBS 94^{T}	436/511 (85.32)	*Candida tropicalis**	Vu et al. 2016
10276	Fresh water	KX218264	530	KT832461 NR_111250	L1 CBS 94^{T}	525/531 (98.87) 492/493 (99.79)	*Candida tropicalis*	Vu et al. 2016
10277	Fresh water	KX218267	534	KT832461 NR_111250	L1 CBS 94^{T}	527/531 (99.25) 492/493 (99.79)	*Candida tropicalis*	Vu et al. 2016
10278	Fresh water	KX233860	492	KP675687 NR_111250	n110a CBS 94^{T}	473/492 (96.14) 444/471 (94.27)	*Candida tropicalis*	Vu et al. 2016
10279	Fresh water	KX218257	570	KP131996 NR_111211	CNRMA10.725 CBS 1600^{T}	553/554 (99.82) 515/525 (98.09)	*Cyberlindnera jadinii* (anamorph: *Candida utilis*)	Playford et al. 2006
10280	Fresh water	KX218258	567	KP131996 NR_111211	CNRMA10.725 CBS 1600^{T}	563/565 (99.64) 515/525 (98.10)	*Cyberlindnera jadinii* (anamorph: *Candida utilis*)	Playford et al. 2006
10281	Fresh water	KX233862	528	NR_111211	CBS 1600^{T}	486/505 (96.24)	*Cyberlindnera jadinii*	Playford et al. 2006

AUMC number	Isolation source (mud origin)	GenBank accession number	Length (bp)	Closest GenBank match # ITS	Culture collection code	Sequencing similarity (%)	Species	Reference
10282	Fresh water	KX218260	647	KY103281 NR_120016	CBS 5921^T JCM 1990^T	623/625 (99.68) 616/625 (98.56)	*Debaryomyces nepalensis* *Debaryomyces hansenii*	Vu et al. 2016 Schoch et al. 2012
10283	Fresh water	KX218269	375	KF112070 NR_077071	TOM_YEAST CBS 9194	371/374 (99.20) 326/342 (95.32)	*Galactomyces candidus*	Groenewald et al. 2012
10284	Fresh water	KX233856	375	KJ817904 NR_077071	WLL1 CBS 9194	374/376 (99.47) 332/341 (97.36)	*Galactomyces candidus*	Groenewald et al. 2012
10285	Fresh water	KX218268	335	NR_077071	CBS 9194	302/326 (92.64)	*Galactomyces candidus*	Groenewald et al. 2012
10286	Fresh water	KX218256	380	JN974292 JN974291	CBS 10073 CBS 626.83	377/379 (99.47) 372/379 (98.15)	*Galactomyces pseudocandidus*	Groenewald et al. 2012
10287	Fresh water	KX218266	598	KY104225 KX011598	CBS 5241 AUMC 10242	585/585 (100) 585/585 (100)	*Meyerozyma caribbica* (anamorph: *Candida fermentati*)	Vu et al. 2016
10288	Fresh water	KX218263	511	KP132509 AY939808	PMM09-2886L ATCC 24210^T	509/511 (99.61) 507/510 (99.41)	*Pichia kudriavzevii* (= *Issatchenkia orientalis*)	Leinberger et al. 2005
10289	Fresh water	KX218255	621	NR_073296	CBS 316^T	614/617 (99.51)	*Rhodotorula mucilaginosa*	Scorzetti et al. 2002
10290	Fresh water	KX233857	621	NR_073296	CBS 316^T	611/619 (98.71)	*Rhodotorula mucilaginosa*	Scorzetti et al. 2002
10291	Fresh water	KX218259	849	NR_111007	CBS 1171^T	749/754 (99.37)	*Saccharomyces cerevisiae*	Sugita et al. 1999
10292	Fresh water	KX218261	789	KY105650 KF300901	CBS 2926^T CBS 2187^T	773/776 (99.61) 741/745 (99.46)	*Torulaspora franciscae* *Torulaspora pretoriensis*	Vu et al. 2016 Wu & Hao 2014
10293	Fresh water	KX421107	503	NR_073341	CBS 2479^T	501/502 (99.80)	*Trichosporon asahii*	Scorzetti et al. 2002
10294	Fresh water	KX218270	546	NR_073341	CBS 2479^T	540/541 (99.82)	*Trichosporon asahii*	Scorzetti et al. 2002
10295	Fresh water	KX233855	546	NR_073341	CBS 2479^T	540/541 (99.82)	*Trichosporon asahii*	Scorzetti et al. 2002
10296	Fresh water	KX233859	546	NR_073341	CBS 2479^T	540/541 (99.82)	*Trichosporon asahii*	Scorzetti et al. 2002
10297	Fresh water	KX218262	541	JN943751 NR_077066	CBS 4375 CBS 5601^T	536/538 (99.63) 519/540 (96.11)	*Apiotrichum scarabaeorum* (≡ *Trichosporon scarabaeorum*)	Schoch et al. 2012
10298	Fresh water	KX233861	577	NR_111210	CBS 5759^T	465/524 (88.74)	*Wickerhamomyces anomalus**	Playford et al. 2006

* The strains probably represent species of the genera *Candida* (AUMC 10274, AUMC 10275) and *Wickerhamomyces* (AUMC 10298), but the exact identification is somewhat doubtful due to rather low sequencing similarity.

Tab. 2. Physiological comparison of the tested strains of the recorded yeast species from mud.
Ascomycetous species: 1 = *Candida albicans* AUMC 10273, 2 = *C. pseudolambica* AUMC 10274, 3 = *C. tropicalis* AUMC 10275, 4 = *C. tropicalis* AUMC 10277, 5 = *C. tropicalis* AUMC 10278, 6 = *Cyberlindnera jadinii* AUMC 10279, 7 = *C. jadinii* AUMC 10281, 8 = *Debaryomyces nepalensis* AUMC 10282, 9 = *Galactomyces candidus* AUMC 10283, 10 = *G. candidus* AUMC 10285, 11 = *G. pseudocandidus* AUMC 10286, 12 = *Meyerozyma caribbica* AUMC 10271, 13 = *M. caribbica* AUMC 13203, 14 = *M. guilliermondii* AUMC 10272, 15 = *Pichia kudriavzevii* AUMC 10288, 16 = *Saccharomyces cerevisiae* AUMC 10291, 17 = *Torulaspora franciscae* AUMC 10292, 18 = *Wickerhamomyces anomalus* (≡ *Pichia anomala*) AUMC 10298.
Basidiomycetous species: 19 = *Rhodotorula mucilaginosa* AUMC 10289, 20 = *R. mucilaginosa* AUMC 10290, 21 = *Trichosporon asahii* AUMC 10294, 22 = *Apiotrichum scarabaeorum* (≡ *Trichosporon scarabaeorum*) AUMC 10297, 23 = *Prototheca zopfii* var. *hydrocarbonea* AUMC 13204.
Symbols: + = growth, ++ = growth with large amount of gas, w = weak growth, d = delayed growth, – = no growth.

Species no.	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20**	**21**	**22**	**23**
Fermentation of sugars																							
D-glucose	+	+	+	++	+	++	+	–	–	–	–	++	+	++	+	+	++	++	–	–	–	+	–
D-galactose	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Maltose	–	–	+	+	+	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Methyl-α-D-glucoside	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	+	+	–	–	–	–	–	–
Sucrose	–	–	+	+	–	+	+	–	–	–	–	+	+	–	–	+	+	+	–	–	–	–	–
Lactose	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Raffinose	–	+	–	–	–	+	+	–	–	–	–	+	w	–	–	+	+	+	–	–	–	–	–
Inulin	–	–	–	–	–	–	–	–	–	–	–	+	+	–	–	–	–	–	–	–	–	–	–
Starch	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
D-xylose	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Assimilation of carbon compounds																							
D-glucose	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
D-galactose	+	–	+	+	+	+	+	+	+	+	+	+	+	+	–	+	+	+	+	+	+	+	+
L-sorbose	–	–	+	+	+	+	+	+	+	+	+	+	+	+	–	–	+	+	+	+	+	+	–
D-glucosamine	+	w	w	+	w	+	+	+	–	–	–	+	+	+	–	–	–	+	–	–	+	w	–
D-ribose	–	–	–	–	–	+	w	+	–	–	+	+	+	+	–	–	–	+	+	+	+	–	–
D-xylose	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	–	+	+	+	+	+	+	–
L-arabinose	+	–	w	+	w	+	+	+	+	+	w	+	+	+	–	–	–	–	+	+	+	–	–

Species no.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
L-rhamnose	–	–	–	–	–	–	–	+	–	–	–	+	+	+	–	–	–	–	+	+	+	–	–
Sucrose	+	+	+	+	+	+	+	+	–	–	w	+	+	+	–	+	+	+	+	+	+	+	+
Maltose	+	w	+	+	+	+	+	+	w	w	–	+	+	+	–	+	+	+	+	+	+	–	w
α,α-trehalose	+	–	+	+	+	+	+	+	–	–	–	+	+	+	–	+	+	+	+	+	+	+	+
Methyl-α-D-glucoside	+	–	+	+	+	+	+	+	–	–	w	+	+	+	–	+	+	+	+	+	+	–	–
Cellobiose	–	–	+	+	+	+	+	+	–	–	–	+	+	+	–	–	–	+	+	+	+	+	–
Salicin	–	w	–	+	–	+	+	+	–	–	w–	+	+	+	–	+	+	+	+	+	+	–	–
Arbutin	–	–	–	+	–	+	+	+	–	–	w–	+	+	+	–	–	+	+	+	+	+	w	–
Lactose	–	+	–	–	–	–	–	+	–	–	–	–	–	–	–	–	–	–	–	–	+	+	–
Raffinose	–	–	–	–	–	+	+	+	–	–	–	+	+	+	–	+	+	+	+	+	–	–	–
Melezitose	+	–	+	+	+	+	+	+	–	–	–	+	+	+	–	+	+	+	+	+	+	–	–
Inulin	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	w
Soluble starch	+	+	+	+	+	+	+	+	–	–	wd	–	–	w	+	–	w	+	–	–	+	w	w
Glycerol	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Meso-erythritol	–	–	–	–	–	–	–	+	–	–	w	–	–	–	–	–	+	+	w	w	+	–	–
Ribitol	+	w	+	+	+	+	+	+	+	+	w	+	+	+	–	+	+	+	+	+	+	+	–
Xylitol	+	–	–	+	–	+	+	+	–	–	+	+	+	+	–	–	+	+	+	+	+	+	–
D-glucitol	+	–	+	+	+	+	+	+	+	+	+	+	+	+	–	d	+	+	+	+	+	+	–
D-mannitol	+	–	+	+	+	+	+	+	+	+	+	+	+	+	w	+	+	+	+	+	+	+	–
Galactitol	–	–	–	–	–	–	–	+	–	–	–	+	+	+	–	–	+	w	–	–	+	w	w
Myo-inositol	–	–	–	–	–	–	–	–	–	–	–	–	w	–	–	–	–	w	–	–	–	+	–
Glucono-D-lactone	+	w	+	+	+	+	+	+	+	+	+	+	+	+	+	–	+	+	+	+	–	–	–
2-keto-D-gluconate	+	–	+	+	+	+	+	+	+	+	+	+	+	+	–	+	+	+	+	+	+	+	w
D-gluconate	+	–	+	+	+	+	+	+	+	+	+	+	+	+	+	–	+	+	+	+	+	+	–
D-glucuronate	–	–	–	+	–	–	–	–	–	–	+	+	–	–	–	–	–	w	–	–	+	+	–
D-galacturonate	–	–	–	–	–	–	–	+	+	+	+	–	–	–	–	–	–	–	w	w	–	–	–
DL-lactate	+	+	–	+	–	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+

Species no.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
Succinate	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Citrate	+	–	+	+	+	+	+	+	+	+	–	+	+	+	+	–	+	+	+	+	+	–	–
Methanol	–	–	–	–	–	–	–	w	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Ethanol	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Propane-1,2-diol	–	–	–	+	–	+	+	w	w	w	–	w	w	–	+	–	–	–	–	–	–	–	–
Butane-2,3-diol	+	–	–	–	–	+	+	–	+	+	+	–	–	–	–	–	–	+	+	+	+	+	+
Quinic acid	–	–	w	–	w	–	–	+	–	–	–	–	–	–	–	–	–	+	+	+	–	–	–
Utilisation of nitrogen sources																							
Nitrate	–	–	–	–	–	+	+	–	–	–	–	–	–	–	–	–	–	+	–	–	–	–	–
Nitrite	–	–	–	–	+	+	+	+	–	–	–	–	–	–	–	–	–	+	–	–	–	–	–
Ethylamine	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	–	–	+	+	+	+	–	+
L-lysine	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	–	+	+	+	+	+	+	+
Creatine	–	–	–	–	–	–	–	+	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Creatinine	–	–	–	–	–	–	–	+	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
D-glucosamine	+	+	+	+	+	+	+	+	w	+	+	+	+	+	+	w	+	+	+	+	+	+	+
Imidazole	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
D-tryptophane	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	–	w	+	+	+	+	+	+
Miscellaneous tests																							
0.01% Cycloheximide	+	–	+	+	+	–	–	+	+	+	+	+	+	+	+	–	–	+	–	–	+	+	–
0.1% Cycloheximide	+	–	+	+	+	–	–	+	+	+	+	+	+	+	+	–	–	+	–	–	+	–	–
50% D-glucose	+	–	+	+	+	–	–	+	+	–	–	+	+	+	–	–	+	+	+	+	+	–	–
60% D-glucose	–	–	–	–	–	–	–	+	–	–	–	–	–	–	–	–	–	+	–	–	–	–	–
10% NaCl	+	–	+	+	+	–	–	+	–	–	–	+	+	+	–	–	+	+	+	+	+	–	–
16% NaCl	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Starch formation	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Urease	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	+	+	+	+	–
Diazonium blue B	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	+	+	+	+	–

A total of 193 species (two varieties being distinguished in two of them) belonging to 67 genera were recovered from both types of mud on the three isolation media. Freshwater mud harboured more species (49 genera / 132 taxa in total) than mud from hypersaline lakes (43 / 125).

The most dominant filamentous fungi were species of the genus *Aspergillus* followed by *Cladosporium*, *Fusarium*, *Penicillium* and *Scopulariopsis*. *Candida* was the most dominant yeast in freshwater mud and rare in saline mud, while *Meyerozyma* and *Rhodotorula* were infrequent in both muds.

Tab. 3. Mean values of moisture contents and pH, mean amounts of colony forming units (CFU) per one sample, and total numbers of yeast and filamentous taxa recovered from mud samples.

Parameters	Hypersaline water mud (n = 24)	Freshwater mud (n = 12)
Mean moisture content	72.46	65.22
Mean pH	9.21	8.07
Mean amount of all CFU/g on DRBC	2186.54	98133.33
Mean amount of all CFU/g on DG18	1844.54	102441.67
Mean amount of all CFU/g on MY50G	1312.46	68258.33
Mean amount of filamentous CFU/g on DRBC	2133.63	85883.33
Mean amount of filamentous CFU/g on DG18	1833.71	97408.33
Mean amount of filamentous CFU/g on MY50G	1312.46	68066.67
Mean amount of yeast CFU/g on DRBC	52.92	12250.00
Mean amount of yeast CFU/g on DG18	10.83	5033.33
Mean amount of yeast CFU/g on MY50G	0.00	191.67
Number of filamentous taxa* on DRBC	65	81
Number of filamentous taxa* on DG18	53	66
Number of filamentous taxa* on MY50G	50	40
Number of yeast species on DRBC	4	17
Number of yeast species on DG18	2	8
Number of yeast species on MY50G	0	2
Number of filamentous taxa* on all media (178)	121	115
Number of yeast species on all media (17)	4	17
Total number of all taxa* on all media (195)	125	132

* Varieties of two species (distinguished apart from the type varieties) are calculated separately.

FUNGI FROM HYPERSALINE MUD

Yeast fungi

Yeasts obtained from saline mud were represented by only 4 species (*Candida tropicalis*, *Meyerozyma caribbica*, *M. guilliermondii* and *Rhodotorula mucilaginosa*) (Tab. 4).

Tab. 4. Colony forming units (CFU/g mud in all samples), percentage CFU and frequency of fungal genera and species recovered from mud samples collected from Wadi El-Natrun Lakes (hypersaline), Ibrahimia and the Nile River canals (freshwater) on the three isolation media.
F = Frequency of occurrence out of 24 samples in the case of saline mud and out of 12 samples in the case of freshwater mud.
O = Occurrence remarks: H = high, 18–24; M = moderate, 12–17; L = Low, 6–11; R = rare, 1–5 samples in the case of saline mud; H = 9–12; M = 6–8; L = 3–5; R = 1–2 in the case of freshwater mud.

Source	**Hypersaline mud**						**Freshwater mud**					
Medium	**DRBC**		**DG18**		**MY50G**		**DRBC**		**DG18**		**MY50G**	
Taxa	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**
Yeast fungi	2.42	4 R	0.59	2 R			12.48	10 H	4.91	6 M	0.28	5 L
Candida Berkhout	0.05	1 R					4.16	8 M	1.77	4 L	0.16	3 L
C. albicans Boidin, Pignal & Besson							0.21	2 R				
C. pseudolambica M.T. Sm. & Poot							0.04	1 R				
C. tropicalis Berkhout	0.05	1 R					3.91	7 M	1.77	4 L	0.16	3 L
Cyberlindnera jadinii (Sartory, R. Sartory, Weill & J. Mey.) Minter							0.24	1 R	0.23	1 R		
Debaryomyces nepalensis Goto & Sugiyama							0.03	1 R	0.10	1 R		
Galactomyces Redhead & Malloch							1.24	3 L	0.94	1 R		
G. candidus de Hoog & M.T. Sm.							0.64	2 R				
G. pseudocandidus de Hoog & M.T. Sm.							0.60	2 R	0.94	1 R		
Meyerozyma Kurtzman & M. Suzuki	2.32	3 R	0.59	2 R			0.21	2 R				
M. caribbica (Vaughan-Mart., Kurtzman, S.A. Mey. & E.B. O'Neill) Kurtzman & M. Suzuki	0.11	2 R	0.14	1 R			0.18	2 R				
M. guilliermondii (Wick.) Kurtzman & M. Suzuki	2.21	2 R	0.45	2 R			0.03	1 R				
Pichia kudriavzevii Boidin, Pignal & Besson							0.34	1 R	0.10	1 R		
Prototheca zopfii var. *hydrocarbonea* Pore							0.17	1 R				
Rhodotorula mucilaginosa (Jorgensen) Harrison	0.05	1 R					0.13	1 R	0.03	1 R		
Saccharomyces cerevisiae Meyen ex E.C. Hansen							0.14	1 R				
Torulaspora franciscae Capr.							2.58	5 L	0.20	1 R		
Trichosporon Behrend							3.20	5 L	1.55	3 L	0.12	2 R

Source	Hypersaline mud						Freshwater mud					
Medium	**DRBC**		**DG18**		**MY50G**		**DRBC**		**DG18**		**MY50G**	
Taxa	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**
T. asahii Akagi ex Sugita, Nishikawa & Shinoda							2.69	5 L	1.55	3 L	0.12	2 R
T. scarabaeorum Middelhoven, Scorzetti & Fell							0.51	1 R				
Wickerhamomyces anomalus (E.C. Hansen) Kurtzman, Robnett & Basehoar-Powers							0.03	1 R				
Filamentous fungi	97.58	24 H	99.41	24 H	100.00	24 H	87.52	12 H	95.09	12 H	99.72	12 H
Absidia glauca Hagem	0.04	1 R	0.05	1 R	0.06	1 R	0.13	2 R	0.16	1 R	0.10	1 R
Acremonium W. Gams	1.39	13 M	0.86	6 L	0.95	6 L	0.19	3 L				
A. furcatum Moreau & F. Moreau ex Gams	0.33	4 R					0.07	1 R				
A. hyalinulum Moreau & F. Moreau ex Gams	0.31	7 L			0.06	1 R						
A. potronii Vuill.	0.09	2 R					0.04	1 R				
A. rutilum W. Gams	0.02	1 R	0.01	1 R	0.01	1 R						
A. spinosum (Negroni) W. Gams	0.04	1 R	0.05	1 R	0.06	1 R	0.08	2 R				
A. zonatum (Sawada) W. Gams	0.29	2 R	0.73	1 R	0.81	3 R						
Acremonium sp.	0.27	4 R	0.07	2 R								
Alternaria Nees: Fr.	0.13	4 R	0.07	2 R	0.08		0.13	1 R	0.12	2 R	0.24	1 R
A. alternata (Fr.) Keissl.	0.02	1 R					0.13	1 R			0.24	1 R
A. chlamydospora Mouch.	0.11	3 R	0.07	2 R	0.08	2 R			0.04	1 R		
Aspergillus P. Micheli ex Haller	39.82	23 H	49.80	20 H	54.26	18 H	62.82	12 H	72.74	12 H	96.62	12 H
A. aculeatinus Noonim, Frisvad, Varga & Samson			0.02	1 R			0.07	1 R				
A. aculeatus Iizuka	0.05	1 R					0.04	1 R				
A. aegyptiacus Moub. & Moustafa							0.25	3 L	0.19	3 L	0.38	3 L
A. aureoterreus Samson, S.W.Peterson, Frisvad & Varga							0.04	1 R			0.12	1 R
A. brasiliensis Varga, Frisvad & Samson			0.56	1 R			13.77	6 M	10.22	5 L	15.69	3 L
A. carneus Blochwitz							0.25	3 L	0.24	2 R	0.48	2 R
A. chevalieri Thom & Church	0.08	2 R	0.01	1 R	0.06	1 R			0.08	2 R	1.40	3 L

Source	Hypersaline mud						Freshwater mud					
Medium	DRBC		DG18		MY50G		DRBC		DG18		MY50G	
Taxa	%CFU	F&O	%CFU	F&O	%CFU	F&O	%CFU	F&O	%CFU	F&O	%CFU	F&O
A. cristatus Raper & Fennell									0.03	1 R	0.15	1 R
A. flavipes (Bainier & Sartory) Thom & Church	9.71	7 L	16.56	6 L	5.65	4 R	0.04	1 R	0.12	2 R	0.35	2 R
A. flavofurcatus Bat. & H. Maia	0.15	3 R	0.05	1 R			0.51	2 R	0.49	2 R	0.20	2 R
A. flavus Link var. *flavus*	0.55	3 R	0.27	2 R	0.13	1 R	0.74	6 M	1.55	5 L	0.18	2 R
A. flavus var. *columnaris* Raper & Fennell	0.04	1 R	1.60	4 R	0.19	1 R	0.47	4 L	1.62	7 M	2.93	2 R
A. fumigatus Fresen. var. *fumigatus*	1.07	8 L	2.37	6 L	0.95	1 R	0.08	2 R	0.04	1 R	0.24	2 R
A. fumigatus var. *ellipticus* Raper & Fennell	0.26	4 R			0.06	1 R						
A. insulicola Montem. & A.R. Santiago	9.39	2 R	12.90	5 R	11.16	3 R						
A. lacticoffeatus Frisvad & Samson							0.04	1 R			0.06	1 R
A. leucocarpus Hadlok & Stolk											0.76	6 M
A. montevidensis Talice & J.A. Mackinnon	0.05	1 R			0.54	6 L			0.73	3 L	1.72	10 H
A. nidulans (Eidam) G. Winter							4.99	3 L	1.23	2 R	5.07	5 L
A. niger Tiegh.	0.17	5 R	0.55	6 L	0.30	5 R	12.63	10 H	11.59	10 H	14.17	9 H
A. ochraceus K. Wilh.					0.16	2 R	1.21	5 L	6.23	6 M	6.96	6 M
A. parasiticus Speare	0.33	3 R	0.17	4 R	0.22	3 R	5.15	5 L	3.15	5 L	0.90	3 L
A. petrakii Vörös-Felkai	0.99	3 R	0.36	4 R	0.95	2 R			0.20	1 R		
A. proliferans G. Sm.			0.07	2 R	0.19	1 R						
A. pseudoglaucus Blochwitz									0.08	1 R	0.12	1 R
A. quadrilineatus Thom & Raper							0.23	3 L				
A. ruber Thom & Church			0.05	1 R	0.13	2 R						
A. sydowii (Bainier & Sartory) Thom & Church					0.30	2 R	4.25	6 M	12.12	8 M	25.55	9 H
A. tamarii Kita	0.02	1 R							0.10	1 R		
A. terreus Thom	16.93	8 L	14.23	8 L	33.26	10 L	16.69	9 H	13.67	10 H	18.11	9 H
A. tubengensis Mosseray							0.17	1 R	0.16	2 R		
A. ustus (Bainier) Thom & Church							0.34	2 R	0.16	3 L	0.12	2 R

Source	Hypersaline mud						Freshwater mud					
Medium	**DRBC**		**DG18**		**MY50G**		**DRBC**		**DG18**		**MY50G**	
Taxa	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**
A. versicolor (Vuill.) Tirab.			0.03	2 R			0.17	2 R	0.08	1 R	0.17	2 R
A. westerdijkiae Frisvad & Samson	0.04	2 R										
Aspergillus sp. (section *Nidulantes*)									7.20	3 L		
Bipolaris clavata Alcorn									0.12	2 R		
Chaetomium Kunze	0.02	1 R			0.08	1 R	0.63	3 L				
C. piluliferum J. Daniel	0.02	1 R					0.59	2 R				
Cladosporium Link	1.30	16 M	7.03	17 M	5.31	18 H	0.26	4 L	0.30	4 L		
C. cladosporioides (Fresen.) G.A. de Vries	0.34	7 L	1.75	13 M	0.84	8 L	0.19	3 L	0.10	1 R		
C. fusiforme Zalar, de Hoog & Gunde-Cim.	0.04	1 R	0.24	4 R	0.25	1 R			0.13	1 R		
C. herbarum (Pers.) Link	0.14	4 R	3.75	4 R	2.56	7 L			0.07	2 R		
C. macrocarpum Preuss	0.09	2 R	0.09	1 R								
C. oxysporum Berk. & M.A. Curtis	0.19	2 R	0.01	1 R	0.08	1 R	0.08	2 R				
C. ramotenellum K. Schub., Zalar, Crous & U. Braun	0.34	6 L	0.14	3 R	0.01	1 R						
C. sphaerospermum Penz.	0.04	1 R	0.96	6 L	1.27	7 L						
C. subtilissimum K. Schub., Dugan, Crous & U. Braun	0.08	1 R	0.09	1 R	0.29	2 R						
Clonostachys rosea (Link) Schroers, Samuels, Seifert & W. Gams	0.23	2 R										
Corallomycetella repens (Berk. & Broome) Rossman & Samuels	8.04	3 R										
Curvularia Boedijn	0.13	2 R	0.18	3 R					0.08	2 R		
C. lunata (Wakker) Boedijn			0.09	1 R					0.08	2 R		
C. tuberculata B.L. Jain	0.08	1 R	0.05	1 R								
Epicoccum nigrum Link	0.01	1 R	0.05	1 R								
Exserohilum rostratum (Drechsler) K.J. Leonard & Suggs	0.05	1 R			0.01	1 R	0.04	1 R				
Fusarium Link	7.32	4 R	5.48	5 R			4.01	11 H	3.96	8 M	0.06	1 R
F. incarnatum (Roberge) Sacc.	0.27	1 R	0.68	1 R			0.24	3 L	0.72	3 L		
F. solani (Mart.) Sacc.	3.49	1 R	3.84	2 R			3.18	9 H	2.96	7 M	0.06	1 R

Source	Hypersaline mud						Freshwater mud					
Medium	DRBC		DG18		MY50G		DRBC		DG18		MY50G	
Taxa	%CFU	F&O	%CFU	F&O	%CFU	F&O	%CFU	F&O	%CFU	F&O	%CFU	F&O
F. verticillioides (Sacc.) Nirenberg	3.56	4 R	0.96	2 R			0.25	3 L	0.12	1 R		
Graphiopsis chlorocephala Trail	0.04	1 R	0.05	1 R								
Haplotrichum croceum (Mont.) Partr. & Morgan-Jones	0.07	2 R										
Humicola Traaen							1.05	7 M	0.28	2 R		
H. fuscoatra Traaen							0.29	5 L	0.28	2 R		
H. grisea Traaen							0.76	4 L				
Microascus Zukal	0.67	7 L	0.35	5 R	0.17	3 R	0.14	1 R	4.19	5 L	0.12	2 R
M. brevicaulis S.P. Abbott	0.07	2 R			0.09	2 R	0.14	1 R	2.40	4 L		
M. chartarum (G. Sm.) Sandoval-Denis, Gené & Guarro	0.59	4 R	0.23	4 R					1.79	1 R	0.06	1 R
M. paisii (Pollacci) M. Sandoval-Denis, Gené & Guarro	0.01	2 R	0.11	1 R								
Mucor Fresen.	0.25	3 R	0.32	3 R	0.38	2 R	1.42	3 L	5.30	4 L	0.73	1 R
M. circinelloides Tiegh.	0.25	3 R	0.09	2 R	0.19	1 R	0.74	3 L	2.33	4 L	0.73	1 R
M. hiemalis Wehmer							0.68	1 R	2.97	1 R		
M. racemosus Fresen.			0.23	1 R	0.19	1 R						
Paraboeremia putaminum (Speg.) Q. Chen & L. Cai							1.78	1 R	0.04	1 R		
Penicillium Link	24.00	20 H	33.15	19 H	36.48	13 M	2.28	6 M	5.70	10 H	1.60	3 L
P. brevicompactum Dierckx	0.02	1 R	0.05	1 R								
P. chrysogenum Thom	19.37	17 M	31.39	18 H	36.10	13 M	1.14	4 L	2.66	9 H	0.43	2 R
P. corylophilum Dierckx	3.54	2 R	0.09	1 R			0.13	2 R				
P. expansum Link	0.08	2 R									0.68	1 R
P. griseofulvum Dierckx	0.42	2 R	1.13	2 R	0.25	3 R						
P. oxalicum Currie & Thom	0.19	1 R	0.05	1 R			1.02	2 R	0.33	1 R	0.39	1 R
P. restrictum J.C. Gilman & E.V. Abbott	0.04	1 R	0.05	1 R								
P. rolfsii Thom					0.06	1 R			0.03	1 R	0.10	1 R
P. simplicissimum (Oudem.) Thom	0.11	1 R	0.01	1 R	0.01	1 R						

Source	Hypersaline mud						Freshwater mud					
Medium	**DRBC**		**DG18**		**MY50G**		**DRBC**		**DG18**		**MY50G**	
Taxa	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**
P. solitum Westling	0.20	3 R	0.25	2 R	0.06	1 R						
P. viridicatum Westling	0.02	1 R	0.05	1 R								
Phialophora Medlar					0.08	1 R	0.08	1 R				
Phoma levellii Boerema & G.J. Bollen							6.11	2 R	1.18	1 R		
Plectosphaerella cucumerina (Lindf.) W. Gams	0.17	2 R										
Pseudallescheria boydii (Shear) McGinnis, A.A. Padhye & Ajello	0.12	2 R					0.10	2 R				
Rhizopus arrhizus A. Fisch.					0.06	1 R	0.04	1 R			0.12	1 R
Sarocladium W. Gams & D. Hawksw.	9.61	9 L	0.46	3 R	1.03	3 R	0.76	2 R	0.04	1 R		
S. kiliense (Grütz) Summerbell	0.64	4 R					0.08	1 R	0.04	1 R		
S. strictum (W. Gams) Summerbell	8.97	6 L	0.46	3 R	1.03	3 R	0.68	1 R				
Scopulariopsis Bainier	0.48	5 R	0.21	4 R	0.03	1 R	0.29	2 R	0.40	2 R	0.06	1 R
S. asperula (Sacc.) S. Hughes			0.05	1 R	0.03	1 R	0.21	1 R	0.04	1 R		
S. brumptii Salv.-Duval	0.32	2 R	0.14	2 R								
S. candidus Vuill.	0.10	1 R	0.01	1 R					0.12	1 R		
S. fusca Zach	0.05	1 R							0.24	1 R		
S. koningii (Oudem.) Vuill.	0.01	1 R	0.01	1 R			0.08	1 R			0.06	1 R
Stachybotrys Corda	0.02	1 R					0.30	1 R				
S. chartarum (Ehrenb.) S. Hughes	0.02	1 R					0.13	1 R				
Stemphylium Wallr.	0.02	1 R					0.25	1 R				
Syncephalastrum racemosum Cohn ex J. Schröt.	0.23	1 R	0.72	1 R	0.32	1 R	0.04	1 R	0.04	1 R		
Talaromyces C.R. Benj.	1.17	6 L	0.85	6 L			3.32	6 M				
T. dendriticus (Pitt) Samson, Yilmaz, Frisvad & Seifert	0.95	3 R										
T. duclauxii (Delacr.) Samson, Yilmaz, Frisvad & Seifert			0.17	1 R			1.38	2 R				
T. pinophilus (Hedgc.) Samson, Yilmaz, Frisvad & Seifert	0.05	1 R	0.06	1 R			1.40	3 L				

Source	Hypersaline mud						Freshwater mud					
Medium	**DRBC**		**DG18**		**MY50G**		**DRBC**		**DG18**		**MY50G**	
Taxa	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**	**%CFU**	**F&O**
T. purpureogenus (Stoll) Samson, Yilmaz, Houbraken, Spierenburg, Seifert, Peterson, Varga & Frisvad	0.17	3 R	0.12	3 R			0.17	2 R				
Thermoascus aurantiacus Miehe	0.05	1 R					0.13	2 R				
Torula sp.							0.47	3 L				
Trichoderma Pers.	1.99	6 L	0.06	1 R			0.42	5 L				
T. atroviride P. Karst.	0.80	3 R	0.06	1 R			0.04	1 R	0.04	1 R		
T. harzianum Rifai	1.15	5 R					0.13	2 R	0.04	1 R		
T. koningii Oudem.	0.04	1 R					0.21	4 L	0.12	2 R		
Wallemia sebi (Fr.) Arx			0.06	1 R	0.22	3 R						
Total amount of CFU	**52477**		**44269**		**31499**		**1177600**		**1229300**		**819100**	
Number of genera (total 67)	**35**		**23**		**19**		**42**		**28**		**12**	
Number of taxa* (total 193 species + 2 non-type varieties)	**88+2***		**74+1***		**48+2***		**96+1***		**71+1***		**41+1***	

* Taxa = species except two *Aspergillus* species (*A. flavus* and *A. fumigatus*), where different varieties within one species are calculated as separate taxa.

Filamentous fungi isolated once on one medium from one mud type only are listed below:
From saline water mud on DRBC: *Acremonium blochii*, *Cladosporium antarcticum*, *Curvularia pallescens*, *Gymnoascus* sp., *Lecanicillium acerosum*, *Penicillium miczynskii*, *Preussia aemulans*, *Scytalidium lignicola*, *Stemphylium sarciniforme*, *Wardomyces ovalis*;
— on DG18: *Acremonium sclerotigenum*, *Beauveria bassiana*, *Curvularia hawaiiensis*, *Emericellopsis* sp., *Fusarium proliferatum*, *Gliomastix luzulae*, *Microascus croci*, *Penicillium aurantiogriseum*, *P. digitatum*, *P. spinulosum*, *Sarcinomyces* sp., *Talaromyces variabilis*;
— on M50G: *Acremonium fusidioides*, *Chaetomium globososporum*, *Cladophialophora devriesii*, *Cosmospora butyri*, *Hortaea werneckii*, *Microascus cirrosus*, *Phialophora* sp.
From freshwater mud on DRBC: *Aspergillus candidus*, *A. costaricaensis*, *A. dentatus*, *A. pulvinus*, *A. unguis*, *Cephaliophora tropica*, *Chaetomium globosum*, *Didymella pomorum*, *Fusarium lateritium*, *F. oxysporum*, Oomycete sp., *Phialophora cyclaminis*, *Rhinocladiella* sp., *Stachybotrys lunzinensis*, *S. kampalensis*, *Stemphylium botryosum*, *Talaromyces diversus*, *T. islandicus*, *T. piceae*, *Trichoderma aureoviride*;
— on DG18: *Alternaria tenuissima*, *Aspergillus latus*, *A. niveus*, *A. varians*, *Cunninghamella echinulata*, *Fusarium equiseti*, *F. nygamai*, *Penicillium citrinum*, *P. hirsutum*, *P. vinaceum*, *Pestalotiopsis guepinii*, *Pochonia* sp.;
— on M50G: *Aspergillus aureolatus*, *A. dimorphicus*, *A. neocarnoyi*, *A. ostianus*, *Byssochlamys laguncularia*e, *Microascus cinereus*.

In similar studies, *Candida* and *Pichia* were the most commonly isolated genera from sediments of estuaries at Rio de Janeiro, Brazil, and were also frequently recovered from aquatic environments including mangrove substrates (Hagler et al. 1982, Araujo et al. 1995, Soares et al. 1997). *Candida* was the predominant genus identified from slope sediments of both the Arabian Sea and the Bay of Bengal (Kutty et al. 2013a). *Rhodotorula glutinis* and *R. mucilaginosa* were isolated from sediments collected from the deep-sea floor in various areas of the northwest Pacific Ocean (Nagahama et al. 2001). *Rhodotorula*, *Debaryomyces*, *Torulopsis*, *Cryptococcus*, *Candida*, *Trichosporon*, *Hansenula*, *Saccharomyces*, *Pichia*, *Kluyveromyces*, *Sporobolomyces* and *Lachancea* yeasts were reported from marine sediments (Kutty & Philip 2008). *Pichia guilliermondii*, *Debaryomyces hansenii*, *Yarrowia lipolytica*, *Metschnikowia bicuspidata*, *Candida parapsilosis*, *Rhodosporidium sphaerocarpum*, *R. babjevae*, *Rhodotorula laryngis* and *Trichosporon mucoides* were identified in hypersaline waters from eight different salterns on the North Adriatic coast, between Slovenia and Croatia, as well as from the Dead Sea, Enriquillo Lake (Dominican Republic) and the Great Salt Lake (Utah) (Butinar et al. 2005). *Cryptococcus liquefaciens*, *Kondoa aeria*, *Rhodosporidium dibovatum*, *R. sphaerocarpum*, *Rhodotorula mucilaginosa*, *R. dairenensis*, *R. slooffiae*, *Aureobasidium pullulans*, *Candida zeylanoides*, *Kluyveromyces neofermentans*, *Metschnikowia bicuspidata* and *Williopsis saturnus* were isolated from mud samples collected from Sagami Bay and the Japan Trench (Minegishi et al. 2006). *Candida tropicalis* was among the most frequently isolated yeasts from coastal waters of northeastern Taiwan (Chen et al. 2009). *Meyerozyma guilliermondii*, *Rhodotorula mucilaginosa*, *Cryptococcus victoriae* and *Candida glaebosa* were the most common yeasts recovered from marine and terrestrial samples collected in Antarctica (Duarte et al. 2013). *Meyerozyma* was also recorded in the salt crust of Huama Lake, China (Liu et al. 2014).

Filamentous fungi

Filamentous fungi (121 taxa in 40 genera) were recovered from all hypersaline mud samples on the three isolation media, constituting 97.6% (on DRBC) – 100% (on MY50G) of the total amount of fungal CFU. Most commonly encountered genera across all three media were *Aspergillus* (24 species), *Cladosporium* (9) and *Penicillium* (15), while less frequent genera included *Absidia* (1), *Acremonium* (10), *Alternaria* (2), *Microascus* (5), *Mucor* (2), *Sarocladium* (2), *Scopulariopsis* (5) and *Syncephalastrum* (1). The genera *Curvularia* (4 species), *Fusarium* (4), *Talaromyces* (5) and *Trichoderma* (3) were moderately frequent on DRBC and DG18. Sixty-three species of the genera mentioned above were encountered on one or two media, whereas 29 species were encountered on

all three media. Some species were reported only on the low water activity media but not on DRBC (Tab. 4).

In accordance with our finding, filamentous fungi were recovered from salterns at higher frequencies (Butinar et al. 2011) than yeasts (Butinar et al. 2005). *Aspergillus*, *Eurotium* and/or *Penicillium* were the predominant genera in hypersaline soils (Moubasher et al. 1990, Hujslová et al. 2010, Al-Musallam et al. 2011), in the Great Salt Plains of Oklahoma, USA (Evans et al. 2013), while *Fusarium* and *Ulocladium* were less frequent in arid hypersaline soils in Egypt (Moubasher et al. 1990), in the Great Salt Plains of Oklahoma, USA (Evans et al. 2013). Species of *Cladosporium* are widespread and have been found in the Sabkha area, Kuwait (Al-Musallam et al. 2011), and in solar salterns (Cantrell et al. 2006). *Alternaria*, *Aspergillus*, *Penicillium*, and *Fusarium* were recovered from underwater sediments in the alkaline salt Huama Lake, China (Liu et al. 2014). *Aspergillus sydowii*, *Eupenicillium javanicum*, and *Penicillium expansum* were isolated from sediments of the Gulf of Aqaba, Jordan (Jaber et al. 2012). *Acremonium kiliense*, *A. rutilum*, *Alternaria chlamydospora*, *Aspergillus alliaceus*, *A. cremeus*, *A. oryzae*, *A. tamarii*, *A. terreus*, *Chaetomium* sp., *Cladosporium cladosporioides*, *C. elatum*, *C. herbarum*, *C. oxysporum*, *Cladosporium* sp., *Embellisia chlamydospora*, *Emericella nidulans* (≡ *Aspergillus nidulans*), *Epicoccum nigrum*, *Eurotium amstelodami* (= *Aspergillus montevidensis*), *Gymnoascus* sp., *Penicillium expansum* and *P. megasporum* were dominant species in saline depressions in the Sabkha area, Kuwait (Al-Musallam et al. 2011). The halophilic mycobiota in water and sediments from the Mandovi estuary which flows into the Arabian Sea, on the west coast of the Indian Peninsula, was dominated by species of *Aspergillus* and *Penicillium*, whereas *Cladosporium* and *Eurotium* were found in smaller numbers (Gonsalves et al. 2012). Moderate alkalitolerants (which at a high pH have a growth rate half of that at a neutral pH), including *Scopulariopsis*, *Fusarium*, *Cladosporium* and many asexual *Acremonium*-like species from *Bionectriaceae*, and weak alkalitolerants (often neutrophiles which can barely cope with a high ambient pH, showing highly reduced growth), represented by sporadic isolates of *Penicillium* species, *Purpureocillium lilacinum* and *Alternaria alternata*, were reported from soils around the basin of soda lakes in Asia and Africa (Grum-Grzhimaylo et al. 2016). *Aspergillus niger*, *A. fumigatus*, *A. flavus*, *A. versicolor*, *A. candidus*, *A. nidulans*, *A. ustus*, *A. wentii*, *A. kanagawaensis*, *A. restrictus*, *Alternaria alternata*, *Fusarium solani*, *Penicillium funiculosum*, *P. brevicompactum*, *P. raistrickii*, *P. bilaiae*, *Phoma* sp. and *Rhizopus stolonifer* were isolated from the upper surface of sediments at four stations in the Suq-Alshuyukh marshes in Thi-Qar Governorate, Iraq (Al-Jawhari 2015).

Similar to the results obtained in the current work, *Aspergillus* was the predominant genus recovered from the mud of hypersaline, alkaline lakes of Wadi

El-Natrun, Egypt, followed by *Penicillium*, while *Acremonium*, *Cladosporium*, *Fusarium*, *Scopulariopsis* and *Trichoderma* were isolated in low frequencies (Gouda 2009, Ismail et al. 2017). *Hortaea werneckii* (on MY50G) and *Wallemia sebi* (on DG18 and MY50G) are reported here for the first time from mud of Wadi El-Natrun, but the former was reported from Egypt for the first time from offshore salt marshes of Gamasa on Damietta Road (Elsayed et al. 2016) and the latter species from different sources (Ismail et al. 2015). *Hortaea werneckii* was found very seldom in slope sediments of the Bay of Bengal (Kutty et al. 2013b); *H. werneckii* (Gunde-Cimerman et al. 2000, Fettich et al. 2011, Nayak et al. 2012, Kutty et al. 2013b) and *Wallemia ichthyophaga* (Zalar et al. 2005, Gunde-Cimerman & Zalar 2014) have also been repeatedly observed from natural hypersaline environments.

FUNGI FROM FRESHWATER MUD

A relatively high number of fungal propagules were recovered from freshwater mud (approximately 1.2×10^6, 1.2×10^6 and 0.8×10^6 of total amount of CFU on DRBC, DG18 and MY50G, respectively) compared to those from saline water mud (5.2×10^4, 4.4×10^4 and 3.1×10^4).

Yeast fungi

Yeast diversity was constituted by 17 species (relating to 12 genera). Only two of them (*Candida tropicalis* and *Trichosporon asahii*) were recovered on the three isolation media, and these were the most commonly encountered yeast species. In addition, *Torulaspora franciscae* (from 5 out of 12 mud samples), *Candida albicans*, *Galactomyces candidus*, *G. pseudocandidus*, *Meyerozyma caribbica* (2 samples each) were also common on DRBC, while the remaining 10 species were reported once from mud samples (Tab. 4).

Similar to the present finding, *Candida albicans*, *C. pseudolambica*, *Rhodotorula mucilaginosa*, *Saccharomyces cerevisiae*, but differently *Candida diversa*, *C. glabrata*, *Cryptococcus podzolicus*, *C. rajasthanensis*, *C. laurentii*, *Williopsis saturnus*, *Hanseniaspora thailandica*, *H. uvarum*, *Torulaspora delbrueckii*, *T. pretoriensis*, *Trichosporon jirovecii*, *T. laibachii* and *Yarrowia lipolytica* were recovered from sediment and water samples from two artificial lakes in Universidad del Valle (Cali, Colombia) (Silva-Bedoya et al. 2014).

The current results are in accordance with the previous reports that yeast populations are sparser in marine water than in fresh water (van Uden & Fell 1968, Butinar et al. 2005). Also Hagler & Ahearn (1987) stated that yeast populations are less frequent in marine environments than in fresh ones.

Filamentous fungi

Filamentous fungi were recovered in all freshwater mud samples on the three isolation media, constituting 87.52% (on DRBC) – 99.72% (on MY50G) of the total amount of fungal CFU.

The most commonly encountered genera on all three isolation media were *Aspergillus* (42 species), *Fusarium* (7 species) and *Penicillium* (8 species); less frequent genera included *Absidia* (1 species), *Alternaria* (3 species), *Microascus* (3 species), *Mucor* (2 species) and *Scopulariopsis* (4 species), which were encountered on all three media. Less frequent species were reported only on the low water activity media but not on DRBC (22 species on DG18, 8 species on MY50G, 3 species on both media). The remaining species were recovered less frequently on only DRBC or both DRBC and MY50G (Tab. 4).

Most of the above species were reported in previous studies: *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus* and *Penicillium funiculosum* were the most common species in submerged mud of Aswan High Dam Lake, Egypt (El-Hissy et al. 1990), *Acremonium strictum*, *Alternaria alternata*, *Aspergillus ochraceus*, *A. niger*, *A. fumigatus*, *A. sydowii*, *A. flavus*, *A. terreus*, *A. oryzae*, *Fusarium oxysporum*, *Mucor circinelloides*, *Penicillium chrysogenum*, *P. cyclopium*, *P. frequentans*, *Rhizopus oryzae* and *Ulocladium consortiale* were isolated from mud-flats of Tigris banks in Baghdad (Abdulla 2008). *Penicillium*, *Fusarium*, *Aspergillus*, *Trichoderma* and *Talaromyces* were the dominant genera in wetland sediments at 10 locations along the Changjiang River and at 10 other locations in China (Wu et al. 2013). *Mucor* sp. and *Penicillium* sp. were isolated from freshwater swamp forest soil area in Obrikom, Ogba Egbema Ndoni Local Government Area of Rivers State, Nigeria (Dirisu 2015), while *Aspergillus niger*, *A. flavipes*, *Botrytis cinerea*, *Cladosporium* sp., *Fusarium solani*, *F. culmorum*, *Mucor hiemalis*, *Penicillium chrysogenum*, *P. expansum*, *Pythium proliferum*, *Phoma* sp., *Saprolegnia ferax*, *Rhizopus nigricans* and *Alternaria* sp. were recovered from the mud and water of Hanna Lake in Quetta, Pakistan (Leghari et al. 2016).

SUMMARY

Usefulness of isolation media

The DRBC medium supported the highest total number of fungal propagules from hypersaline mud (52,477 CFU), while the lowest count was recorded on MY50G (31,499 CFU). The highest diversity of genera and species (35 genera and 90 species) was observed on DRBC and the lowest (19 and 50) on MY50G. The total number of yeast propagules constituted a minor proportion of the total amount of all CFU on DRBC (2.42 %) and on DG18 (0.59 %), while yeasts were

absent on MY50G (all four yeast species from saline mud were recovered on DRBC, while 2 on DG18, see Tab. 4). The number of filamentous fungal taxa registered on DRBC (35 genera + 69 species) was higher than that registered on DG18 (23 + 53) or on MY50G (19 + 50).

However, in a previous study on spices, the number of CFU from Oregano was significantly higher on MY50G compared to that recovered on the general isolation medium Sabouraud malt agar (SMA, a_w 0.98–0.99), while SMA was more appropriate than MY50G for qualitative and quantitative determination of moulds, which relates to the fact that media with a limited amount of free water suppress the growth of moulds which are not extremely xerophilic in nature (Skrinjar et al. 2012).

In freshwater mud, forty-nine genera represented by 132 taxa were recovered from 12 samples on the three media. The highest total amount of fungal CFU was recovered on DG18 (1,229,300 CFU), while the lowest count was recorded on MY50G (819,100 CFU).

All 17 yeast species were recovered on DRBC, 8 on DG18, while only 2 on MY50G. The total amount of yeast propagules comprises a minor proportion of the total amount of CFU of all fungi, ranging from 0.28% on MY50G to 12.48% on DRBC. The number of filamentous fungi taxa observed on DRBC (42 genera + 98 species) was higher than that seen on DG18 (27 + 72) with the lowest number recorded on MY50G (12 + 42).

Overview on the diversity of fungi from hypersaline and freshwater muds

The frequency of yeasts ranged from 0 in saline mud on MY50G agar to 12.48% of the total amount of CFU in freshwater mud on DRBC. They represented 12 genera with 17 species and were encountered more commonly in freshwater sediments than in saline mud. Only *Candida tropicalis*, *Meyerozyma caribbica*, *M. guilliermondii* and *Rhodotorula mucilaginosa* were encountered in saline mud, while in addition to these 4 species, another 13 yeast species were recovered from freshwater mud.

Filamentous fungi comprised the majority of the total amount of CFU on all media from both types of mud. *Aspergillus* (44 taxa), *Penicillium* (18), *Microascus* (6), *Scopulariopsis* (5), *Alternaria* (3), *Mucor* (3) and *Absidia* (1) were encountered in both mud types on all three isolation media. *Aspergillus* was the most common fungus in both muds, accounting for 40% of the total amount of CFU in saline mud on DRBC to 96.6% in freshwater mud on MY50G agar (Tab. 4). The genus was represented by 44 taxa with *A. flavipes*, *A. flavus* var. *flavus*, *A. flavus* var. *columnaris*, *A. fumigatus* var. *fumigatus*, *A. niger*, *A. parasiticus* and *A. terreus* recovered from both saline and fresh muds on the three types of media.

Some other species were encountered in both muds (57 taxa) but on one or two media, while representatives of a third group were isolated only from saline (60 taxa), but not from freshwater mud and vice versa (56 taxa).

The diversity of species in some genera was more pronounced depending on the type of mud, e.g. in *Acremonium* (10 species from saline mud versus 3 species from fresh mud), *Cladosporium* (9 versus 4) and *Aspergillus* (42 in freshwater mud versus 23 in saline mud). Even though mud from both waters shared many fungi, some other species were confined only to one mud type and not to the other. For example, *Clonostachys rosea*, *Corallomycetella repens*, *Curvularia tuberculata*, *Epicoccum nigrum*, *Graphiopsis chlorocephala*, *Haplotrichum croceum*, *Microascus paisii*, *Penicillium brevicompactum*, *P. griseofulvum*, *P. restrictum*, *P. simplicissimum*, *P. viridicatum*, *Plectosphaerella cucumerina*, *Talaromyces dendriticus* and *Wallemia sebi*, in addition to those mentioned below Tab. 4 were found in saline mud only, while other species were confined to freshwater mud only, e.g. *Bipolaris clavata*, *Humicola fuscoatra*, *H. grisea*, *Mucor hiemalis*, *Paraboeremia putaminum*, *Phoma levellii* and *Torula* sp., in addition to those below Tab. 4.

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