



## Diversity of floricolous yeasts and filamentous fungi of some ornamental and edible fruit plants in Assiut area, Egypt

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### Abstract

The floricolous yeasts and filamentous fungi of 44 samples of flowers from both ornamental (20 samples) and edible fruit plants (24 samples) were evaluated. The general isolation medium DRBC supported more fungal species diversity in both flowers, than the xerophilic media (DG18 and MY50G). The highest numbers of fungal propagules were recovered on DG18 from flowers of ornamental plants, while the lowest on MY50G from flowers of edible plants. Yeasts constituted small proportion of propagules from the two flower types on the three media. Yeasts were represented by 18 genera and 26 species. *Metschnikowia* (3 species, from which *M. reukaufii* and *M. viticola*), *Candida* (4 species, from which *C. riodecensis* and *C. vaccinia*), *Cryptococcus* (*C. albidus* var. *kuetzingii*), *Meyerozyma* (*M. guilliermondii*), *Naganishia* (*N. diffluens*), *Rhodotorula* (2 spp., *R. mucilaginosa*), and *Vishniacozyma* (2 spp., *V. carnescens*) were infrequently encountered on the three media, beside *Filobasidium* (2 species), *Galactomyces* (*G. candidus*), *Papiliotrema* (*P. flavescens*), *Pichia* (*P. kluyveri*), and *Sporidiobolus* (*S. metaroseus*) which were recorded on two media. Some other yeast species were recovered only from one flower type but not from the other. *Cladosporium* (10 species) was the most common genus (100 % of samples from both types of flowers), accounting from 66.45 % to 87.25 % of total fungi. *C. herbarum*, *C. cladosporioides*, *C. oxysporum*, and *C. sphaerospermum* were recovered in high frequency from both types of flowers, but *C. herbarum* yielded the major proportion (61.23 % to 75.77 % of total fungi). Other filamentous fungi e.g. *Alternaria* (19 species, from which *A. alternata* and *A. chlamydospora*), *Aspergillus* (47 species, from which *A. flavus*, *A. niger*, and *A. terreus*), *Penicillium* (29 spp., *P. chrysogenum* and *P. olsonii*), *Fusarium* (12 spp., *F. incarnatum*, *F. solani*, and *F. verticillioides*), and *Stemphylium* (3 species, *S. botryosum* and *S. sarcciniforme*) were found contaminating all flowers on almost all isolation media.

**Key words** – Camel's foot tree – Candelabra – Chamomile – Fungi – Guava – ITS – Khella – Lemon – Mango – Phenotypic and genotypic characterization – Pomegranate – Snapdragon

### Introduction

Flowers usually harbour yeast communities which are thought to be vectored by flower-associated insects (Lachance et al. 2001a, b, Pozo et al. 2011). The yeasts in the flowers are either active colonists of the flower nectar (Brysch-Herzberg 2004, Herrera et al. 2009, 2010, Pozo et al. 2011, 2012) or passive contaminants (Sipiczki 2013). Many of them are osmotolerant (Tokuoka et

al. 1987, Pozo et al. 2011) and can also occur in other substrates with high sugar content (Rosa et al. 2003). Within flowers, nectar is a substrate suitable for yeast colonization (Pozo et al. 2011, 2012). Nectar is the most frequent form of floral reward that animal-pollinated plants provide for their mutualistic counterparts (Simpson & Neff 1983). Despite the huge number of publications on nectar properties appearing in the last few decades, there is still one peculiar feature of floral nectar that remains largely unexplored to date from an ecological perspective, namely its role as a natural habitat for many kinds of microorganisms and, more specifically, yeasts. That yeasts are frequent inhabitants of floral nectar was already familiar to microbiologists more than a century (Boutroux 1884, Schoellhorn 1919, Nadson & Krassilnikov 1927, Capriotti 1953, Baker & Baker 1975, Gilliam et al. 1983, Ehlers & Olesen 1997, Lachance et al. 2001a, b, c, Brysch-Herzberg 2004, Sipiczki 2010, Misra et al. 2012, Han et al. 2014, 2015). Over the last decade it has become gradually more apparent that yeast metabolism alters the physicochemical properties of nectar, including the sugar concentration and composition (Canto et al. 2007, 2008, Herrera et al. 2008, de Vega et al. 2009, de Vega & Herrera 2013), amino acid profile (Peay et al. 2012) and even flower temperature (Herrera & Pozo 2010). Some of these changes occur due to the density-dependent action of a species-poor yeast community. Understanding the patterns of yeast prevalence and distribution in natural habitats has, therefore, become a topic of broad ecological interest (de Vega et al. 2009, Pozo et al. 2009, Belisle et al. 2012, Jacquemyn et al. 2013).

Investigations on a few bumble-bee-pollinated plants from southeastern Spain have recently revealed that (a) yeasts are quite frequent and can reach extraordinarily high densities in the floral nectar of some species; (b) yeast populations degrade floral nectar by reducing the sugar concentration and drastically altering the sugar composition profile; and (c) very small-scale patchiness in nectar yeast densities generates small-scale, intraspecific patchiness in nectar characteristics that can influence pollinator behaviour (Canto et al. 2007, 2008, Herrera et al. 2008). In the flowers of some bumble bee-pollinated plants, dense populations of specialized nectarivorous yeasts deplete the sugar content of nectar, which reduces the reward available to the plants' mutualistic pollinators (Herrera et al. 2008, de Vega et al. 2009).

Sipiczki (2012) isolated *Pichia bruneiensis* from *Hibiscus* flowers in Brunei. *Pseudozyma* spp. including 17 strains of *Pseudozyma rugulosa*, 6 strains of *Pseudozyma aphidis*, and three strains of *Pseudozyma tsukubaensis* were the dominant species and *Bullera coprosmaensis* was isolated from wild flowers around Jangseong Lake in Jeollanam-do, Republic of Korea (Han et al. 2015). *Starmerella syriaca*, an osmotolerant yeast species was also isolated from *Malva* sp. flowers in Syria (Sipiczki 2015).

Kim & Kim (2015) found that *Aureobasidium pullulans*, *Candida* spp. and *Rhodosporidium* spp. dominated the yeast composition of the wild fleabane (*Erigeron annuus*) flower, representing 49 %, 21 %, and 18 % of the isolates, respectively. The least abundant yeasts were *Cryptococcus* spp. (8%) and *Rhodotorula* spp. (4%). Among the isolates were several species, including *Candida tropicalis* (11 isolates), *C. parapsilosis* (6), *Rhodosporidium azoricum* (13), and *R. fluviale* (1).

The aim of this work is to identify and evaluate the diversity of flower-dwelling yeasts and filamentous fungi of some ornamental and edible plant species in Assiut city. The identification was based on phenotypic characteristics in case of filamentous fungi, and genotypically in case of yeasts.

## Materials & Methods

### Collection of flower samples

A total of 48 samples of flowers, 24 from edible plants and 20 from ornamental plants, were collected from Assiut region, Egypt during the period from March 2012 to September 2012 (Table 1). As soon as the composite flower samples were collected, they were put in sterilized paper bags and transferred into the mycological laboratory for fungal analysis.

### **Isolation of flower-dwelling fungi**

The dilution-plate method was used for enumeration of different fungal species as described by Johnson & Curl (1972) and employed in this laboratory by Moubasher and his collaborators as follows: Ten g of whole flowers were placed in a sterile 250 ml Erlenmeyer flask containing 90 ml of sterile distilled water. The flask containing the suspension was shaken on a mechanical orbital shaker for 30 minutes. A serial dilution was repeated until the desired final dilution was (1:1000) reached which supports a total of about 25-40 colonies per plate. One ml of the desired dilution was transferred aseptically into each of several Petri-dishes and ~20 ml / plate of an appropriate agar medium were added. Five plates for each medium type were incubated at 28°C for 1-2 weeks during which the developing fungi were counted and isolated for further identification and the number of colony forming units (CFUs) was calculated per g flower sample. Isolates of different fungi were maintained on YM (for yeasts), Czapek's agar and malt extract agar slants (for filamentous fungi) and stored at 5°C till confirming the identification.

### **Media used for isolation of fungi from different sources**

#### **Dichloran rose bengal chloramphenicol agar (DRBC)**

King et al. (1979) of the following composition was used: (g/l): peptone 5, potassium dihydrogen phosphate 1, magnesium sulphate 0.5, glucose 10, agar 15. Dichloran at 2 µg/ml was used to limit the growth of mucoraceous fungi, and Rose bengal (25 µg/ml) and chloramphenicol (100 µg/ml) were used as bacteriostatic agents.

#### **Dichloran 18% Glycerol Agar Base (DG18)**

Hocking & Pitt (1980) of the following composition was employed: (g/l): glucose 10, peptone 5, potassium phosphate monobasic 1, magnesium sulfate heptahydrate 0.5, dichloran (0.2 % in ethanol, w/v) 1 ml, agar 15, chloramphenicol 0.1, glycerol 220, Distilled water 1000 ml. This medium is recommended for enumeration and isolation of yeasts and moulds. The low water activity of this medium reduces interference by bacteria and fast-growing fungi.

#### **Malt Extract Yeast Extract 50% Glucose Agar (MY50G)**

Pitt & Hocking (1985) of the following composition was employed: (g/l): malt extract 10, yeast extract 2.5, agar 10, glucose 500, distilled water 500 ml. Agar, yeast extract, and malt extract are added to water and boiled to dissolve agar. Glucose is slowly added while stirring to avoid lumps. The medium is dispensed as required and autoclaved at 121 °C for 30 minutes.

### **Phenotypic identification of fungi**

The filamentous fungi were identified based on their macro- and microscopical features following the keys of Raper & Fennell (1965), Ellis (1971), Pitt (1979), Sutton (1980), Moubasher (1993), De Hoog et al. (2000), Zare & Gams (2004), Leslie & Summerell (2006), Samson & Varga (2007), Domsch et al. (2007), Crous et al. (2007), Simmons (1967, 2007), Seifert et al. (2011) for filamentous fungi and Barnett et al. (2000) for yeasts.

### **Physiological characters of yeast strains**

Biochemical characteristics were performed for yeasts (Table 2). A fermentation test of sugars was performed and oxidative utilization of carbon compounds was tested according to Barnett et al. (2000). The growth of yeast strains on nine nitrogen compounds (potassium nitrate, sodium nitrite, ethylamine-HCl, L-lysine-HCl, creatine, creatinine, D-glucosamine, imidazole, D-tryptophan) was also determined (Suh et al. 2008). Hydrolysis of urea, growth at high osmotic pressure, growth at different temperatures, growth in the presence of cycloheximide, diazonium blue B (DBB) and production of extracellular starch-like compounds were also performed. Identification keys of Barnett et al. (2000) were employed to assign each isolate to species level. Confirmations of these identifications were carried out using molecular techniques.

## Genotypic identification of yeast strains

The fungus was grown at 25 °C on CYA plates for 7 days (for filamentous isolates) and on YM plates for 2 days (for yeast isolates). A small amount of fungal biomass was scraped off and suspended 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 samples were directly sent to Korea for extraction and sequencing. Fungal DNA was extracted and isolated using SolGent purification beads at this company. Internal transcribed spacer (ITS) 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'). 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 and the PCR product was then purified with the SolGent PCR Purification Kit-Ultra prior to sequencing in sense and antisense direction (Refer to Moubasher et al. 2016, 2017). Contigs were created from the sequence data using the CLCBio Main Workbench program. The sequence obtained from each isolate was further analysed using BLAST from the National Center of Biotechnology Information (NCBI) website. Sequences obtained together with those retrieved from the GenBank database were subjected to the Clustal W analysis using MegAlign software version 5.05 (DNASTAR Inc., Madison, Wisconsin, USA) for the phylogenetic analysis (Thompson et al. 1994). Sequence data were deposited in GenBank and accession numbers are given for them.

## Results & Discussion

The yeast isolates were characterized using phenotypic, physiological and molecular methods while filamentous fungi were identified using only phenotypic characteristics based on macro- and microscopic features. Representative strains of the species recovered are deposited at Assiut University Mycological Center Culture Collection (AUMC) and ITS gene sequences of the yeast strains were deposited at the National Center for Biotechnological Information (NCBI) and accession numbers are given for them (Tables 2, 3).

### A. Fungi recovered from flowers of ornamental plants

Sixty-three genera represented by 192 species and 2 varieties were recovered from 20 samples of flowers of ornamental plants on the three media. The highest total number of CFUs was recovered on DG18 (94084 CFUs) while the lowest count on MY50G (67355 CFUs). The broadest spectrum of genera and species (59 genera and 162 species) was collected on DRBC and the narrowest (19 and 66) on MY50G (Table 4).

Yeasts represented a small proportion of CFUs ranging from 0.18 % on MY50G to 2.03 % on DRBC, 16 out of 20 samples on DG18 and 4 samples only on MY50G. Eighteen species of yeasts belonging to 13 genera were isolated. *Cryptococcus* (*C. albidus* var. *kuetzingii*), *Metschnikowia* (2 species), *Naganishia* (*N. diffluens*), and *Rhodotorula* (2 species) were recovered on the three isolation media, and these were the most commonly encountered yeast species. *Candida* (2 species), *Filobasidium* (2 species), *Galactomyces* (*G. candidus*), *Meyerozyma* (*M. guilliermondii*), *Papiliotrema* (*P. flavescens*), *Sporidiobolus* (*S. metaroseus*), and *Vishniacozyma* (2 species) were recovered infrequently on DRBC and DG18, while *Hannaella zae* and *Pichia kluyveri* were recovered on DRBC only (Table 4). Results revealed that, some yeast species were commonly isolated from most types of flowers, however others were characteristic of only flowers from one plant species (Table 5).

Nectar-inhabiting microfungi in Europe, South Africa, and elsewhere seem to be characterized by a similarly low level of species diversity, with *Metschnikowia reukaufii* being one of the dominant species (Brysch-Herzberg 2004, de Vega et al. 2009, Herrera et al. 2010, Lachance et al. 2011, Schmitt 2014). *Auerobasidium pullulans*, *Candida rancensis*, *Cryptococcus* sp., *Hanseniaspora valbyensis*, *Metschnikowia gruessii*, *M. koreensis*, *M. reukaufii* and *Starmerella bombicola* were isolated from flowers of *Mimulus aurantiacus*, a hummingbird-pollinated shrub

(Belisle et al. 2012). Nectars of hummingbird-pollinated *Mimulus aurantiacus* are dominated by specialized ascomycetes, such as *M. reukaufii* and *Candida rancensis* (Belisle et al. 2012). *Saccharomyces cerevisiae* together with *Candida lambica* (teleomorph *Pichia fermentans*), *Candida tropicalis*, *Debaryomyces hansenii*, and *Candida guilliermondii* (teleomorph *Meyerozyma guilliermondii*) were detected in the nectar of *Hibiscus rosa-sinensis* (Misra et al. 2012). *Cryptococcus adeliensis* and *Cryptococcus uzbekistanensis* were isolated from wild flowers in Yokjido, Gyeongsangnam-do, Korea (Hyun & Lee 2014). *Starmerella syriaca* was member of the *Starmerella* clade, it is closely relative to *Candida vaccinia*, isolated from *Malva* sp. flowers in Syria (Sipiczki 2015). Species of the genera *Candida*, *Rhodosporidium*, *Cryptococcus*, and *Rhodotorula* were recovered from fleabane flowers *Erigeron annuus* (L.) Pers. in Uljin, Korea (Kim & Kim 2015). *Metschnikowia reukaufii* was the most frequent yeast species followed by *Metschnikowia gruessii* and *Cryptococcus carnescens* from flowers in Canary Islands (Mittelbach et al. 2015).

Filamentous fungi were recovered from all flower samples on the three isolation media, constituting 97.97 % (on DRBC) – 99.82 % (on MY50G) of the total fungal CFUs. The number of filamentous taxa registered on DRBC (46 genera and 144 species) was higher than those registered on DG18 (32 and 97) or on MY50G (15 and 62). *Aspergillus* (43 species, basically *A. brasiliensis*, *A. flavus*, *A. niger*, *A. sydowii*, and *A. terreus*), *Cladosporium* (9, basically *C. cladosporioides*, *C. herbarum*, *C. oxysporum*, and *C. sphaerospermum*), and *Penicillium* (23, basically *P. chrysogenum* and *P. solitum*) were the most common genera encountered from all samples on the three isolation media followed by *Alternaria* (16, basically *A. alternata* and *A. chlamydospora*), *Epicoccum* (*E. nigrum*), *Stemphylium* (3, basically *S. botryosum* and *S. vesicarium*), *Rhizopus* (2, *R. arrhizus*), *Talaromyces* (6, *T. variabilis*), *Didymella* (*D. pomorum*), *Acremonium* (5), *Lasiodiplodia* (*L. theobromae*), and *Wallemia* (*W. sebi*) were infrequently isolated on the three isolation media (Table 4).

Some species were reported only on the low water activity media (DG18 and MY50G) but not on DRBC and these were: *Absidia cylindrospora*, *Aspergillus costaricaensis*, *A. oryzae*, *A. proliferans*, *Chaetomium* sp., *Chrysosporium merdarium*, *Cladophialophora bantiana*, *Fusarium scripi*, *Haplobasidium lelebae*, *Microascus croci*, *Penicillium fennelliae*, *P. oxalicum*, *P. phoeniceum*, and *Periconia minutissima* were isolated on DG18 only. However, *Acremonium curvulum*, *Arthrimum saccharicola*, *Aspergillus aculeatinus*, *A. thecius*, *A. dimorphicus*, *A. niveus*, *A. ruber*, *Cladosporium subtilissimum*, *Merimbla ingelheimensis*, and *Penicillium madriti* were recovered on MY50G only (Table 4).

In South Africa, *Chaetomium globosum*, *C. indicum*, *Gibberella* sp., *Gondwanamyces proteae*, *Ophiostoma africanum*, *O. protearum*, *O. splendens*, *Acremonium* spp., *Alternaria alternata*, *Cladosporium cladosporioides*, *C. sphaerospermum*, *C. tenuissimum*, *Cladosporium* spp., *Drechslera erythrospila*, *Penicillium canescens*, *P. chrysogenum*, *P. dendriticum*, *P. funiculosum*, *P. glabrum*, *P. minioluteum*, *P. novae-zealandiae*, *P. purpurescens*, *Phoma* sp., *Pithomyces valparadisiacus* and *Torula herbarum* were recovered from *Protea* species flowerheads (Wingfield et al. 1988, Wingfield & Van Wyk 1993, Marais & Wingfield 1994, 1997, 2001, Marais et al. 1998, Lee & Crous 2003, Lee et al. 2003, 2005).

### **Fungi recovered from flowers of edible fruit plants**

Seventy-one genera represented by 176 species and 3 varieties were recovered from 24 samples of flowers of edible fruit plants on the three media. The highest total number of CFUs was recovered on DG18 (90574 CFUs/g) while the lowest count on MY50G (42188 CFUs). The broadest spectrum of genera and species (64 genera and 153 species) was collected on DRBC and the narrowest (22 and 72) on MY50G (Table 4).

Yeast counts contributed a small proportion of total CFUs ranging from 0.38 % on MY50G to 7.55 % on DRBC, 20 out of 24 samples on DG18 and 10 samples only on MY50G. Twenty-four species assigned to 17 genera were yeasts. *Candida* (4 species, mainly *C. riodecensis* and *C. vaccinii*), *Metschnikowia* (2 species, *M. sinensis* and *M. viticola*), *Meyerozyma* (*M. guilliermondii*),

and *Vishniacozyma* (*V. carnescens*) were the most commonly encountered yeast species, recovered on the three isolation media. *Cryptococcus* (*C. albidus* var. *kuetzingii*), *Filobasidium* (2), *Galactomyces* (*G. candidus*), *Naganishia* (*N. diffluens*), *Papiliotrema* (*P. flavescens*), *Pichia* (*P. kluyveri*), *Rhodotorula* (2), and *Sporidiobolus* (*S. metaroseus*) were recovered infrequently on DRBC and DG18, while *Schwanniomyces vanrijiae* var. *vanrijiae* and *Trichosporon asahii* were recovered on DRBC, *Lodderomyces elongisporus* on DG18, and *Debaryomyces nepalensis* on MY50G only (Table 4). Results presented in Table (5) revealed that, some yeast species were common and isolated from the four types of flowers, however others were characteristic of only flowers from one plant species.

In Colombia, Gaviria & Osorio (2012) found that *Cryptococcus laurentii*, *C. flavescens*, *C. nemorosus*, *C. heveanensis*, *Pichia kluyveri*, *Pseudozyma tsukubaensis* and *Candida asparagi* were presented in the inflorescences of mango (*Mangifera indica*), while *Candida leandrae*, *Cryptococcus laurentii*, *Candida parazyza*, *Aureobasidium pullulans* and *Pseudozyma tsukubaensis* were predominant species in flowers of Lulo 'Arboreo' (*Solanum wrightii*). *Candida kunwiensis*, phylogenetically related to the genus *Metschnikowia*, was isolated from sweet potato (*Ipomoea batatas*) flowers in Korea (Hong et al. 2003). In southwest Slovakia, *Metschnikowia pulcherrima* and *Aureobasidium pullulans* were the most frequently isolated species from blossoms of apple (*Malus domestica* Borkh.), pear (*Pyrus communis* L.), and plum trees (*Prunus domestica* L.), while *Barnettozyma californica*, *Candida boidinii*, *C. catenulata*, *C. tropicalis*, *Cryptococcus albidus*, *Debaryomyces hansenii*, *Meyerozyma guilliermondii*, *Pichia kudriavzevii*, *Saccharomyces cerevisiae*, and *Wickerhamomyces anomalus* were less frequent (Vadkertiová et al. 2012). *Cryptococcus flavescens*, *C. victoriae*, *C. tephrensensis*, *C. heimaeyensis*, *C. oeiensis* and *C. stepposus* were the most abundant detected from strawberry flowers in Lamezia Terme, Southern Italy (Abdelfattah et al. 2016).

Filamentous fungi were recovered from all flower samples on the three isolation media (54 genera and 155 species), constituting 92.45 % (on DRBC) – 99.62 % (on MY50G) of the total fungal CFUs. The number of filamentous taxa registered on DRBC (50 genera + 132 species) was higher than those registered on DG18 (30 + 103) or on MY0G (16 + 64). *Aspergillus* (34 species, mainly *A. flavus*, *A. niger*, *A. ochraceus* and *A. terreus*), *Cladosporium* (6 spp., mainly *C. cladosporioides*, *C. herbarum*, *C. oxysporum* and *C. sphaerospermum*), and *Penicillium* (21 spp., mainly *P. chrysogenum*, *P. olsonii* and *P. solitum*) were the most prevalent genera encountered from all samples on the three isolation media followed by *Alternaria* (14 spp., mainly *A. alternata* and *A. chlamydospora*), *Stemphylium* (3 spp., *S. botryosum* and *S. sarciniforme*), *Epicoccum* (*E. nigrum*), and *Fusarium* (10 spp., *F. incarnatum* and *F. verticillioides*) while *Lasioidiplodia* (*L. theobromae*), *Talaromyces* (6 spp., mainly *T. pinophilus* and *T. variabilis*), *Rhizopus* (2, mainly *R. arrhizus*), *Pleospora* (*P. herbarum*), *Pyrenophora* (*P. biseptata*) and *Quambalaria* (*Q. cyansensis*) were infrequently isolated on the three isolation media (Table 4).

Some species were reported only on the low water activity media but not on DRBC and these were: *Aspergillus oryzae*, *A. wentii*, *Chaetomium* sp., *Cladosporium ramotenellum*, *Penicillium sclerotiorum*, *P. vinaceum*, *Phialaphora cyclaminis*, and *Scytalidium japonicum* were isolated on DG18 only. However, *Aspergillus niveus* was recovered on MY50G only.

In Pretoria, South Africa, the most prevalent filamentous fungal species in mango flowers were *Alternaria alternata*, *Cladosporium cladosporioides*, and the yeast-like *Aureobasidium pullulans* (De Jager 1999). *Cladosporium cladosporioides* and *C. tenuissimum* were identified as the pathogens causing blossom blight in strawberries in Korea (Nam et al. 2015). In Lamezia Terme, Southern Italy, *Botrytis* spp. (basically *B. cinerea*) and *Cladosporium* spp. (basically *C. sphaerospermum*) were the most dominant genera in the strawberry flowers while *Alternaria alternata*, *Aureobasidium pullulans* were less abundant (Abdelfattah et al. 2016).

**Table 1** English, Latin and family names, collection date and number of flowers samples of different plant species investigated.

English name	Scientific (latin) name	Family (all Angiosperms)	Collection date	No. of samples
<b>Flowers from edible plants</b>				24
Pomegranate	<i>Punica granatum</i> L.	Lythraceae	May-2012	9
Mango	<i>Mangifera indica</i> L.	Anacardiaceae	June-2012	5
Guava	<i>Psidium guajava</i> L.	Myrtaceae	Sept-2012	5
Lemon	<i>Citrus limon</i> (L.) Burm. f.	Rutaceae	17-Mar-2012 (1 sample) 18-July-2012 (2 samples) 25-Aug-2012 (2 samples)	5
<b>Flowers from ornamental/crop plants</b>				20
Callistemon	<i>Melaleuca citrina</i> (Curtis) Dum.Cours. ≡ <i>Callistemon citrinus</i> (Curtis) Skeels	Myrtaceae	April-2012	3
Camel's foot tree	<i>Phanera variegata</i> (L.) Benth. ≡ <i>Bauhinia variegata</i> L.	Fabaceae	28-March-2012 25-April-2012	2
Candelabra	<i>Euphorbia ingens</i> E.Mey. ex Boiss.	Euphorbiaceae	April-2012	2
Khella	<i>Ammi visnaga</i> (L.) Lam.	Apiaceae	April-2012	2
Chamomile	<i>Matricaria chamomilla</i> L.	Asteraceae	28-March-2012	1
Snapdragon	<i>Antirrhinum majus</i> L.	Plantaginaceae/Veronicaceae	27-March-2012	1
Eucalyptus (river red gum)	<i>Eucalyptus camaldulensis</i> Dehnh.	Myrtaceae	29-May-2012	1
Cotton	<i>Gossypium barbadense</i> L.	Malvaceae	28-March-2012	1
Adhatoda (Malabar nut=Vasa)	<i>Justicia adhatoda</i> L. (≡ <i>Adhatoda vasica</i> Nees)	Acanthaceae	27-March-2012	1
Mexican petunia	<i>Ruellia brittoniana</i> Leonard	Acanthaceae	April-2012	2
Dwarf rose		Rosaceae	April-2012	2
Chinese hibiscus, China rose	<i>Hibiscus rosa-sinensis</i> L.	Malvaceae	2-May-2012	2

**Table 2** Physiological comparison of the yeast species strains isolated from flowers.

Ascomyceteous species: 1 *Candida albicans* AUMC 11215. 2 *C. rancensis* AUMC 11245. 3 *C. rancensis* AUMC 11246. 4 *C. riodecensis* AUMC 11239. 5 *C. vaccinii* AUMC 11247. 6 *Debaryomyces nepalensis* AUMC 11240. 7 *Galactomyces candidus* AUMC 11229. 8 *Lodderomyces elongisporus* AUMC 11243. 9 *Metschnikowia reukaufii* AUMC 11217. 10 *M. sinensis* AUMC 11232. 11 *M. viticola* (= *C. kofuensis*) AUMC 11224. 12 *M. viticola* AUMC 11244. 13 *Meyerozyma guilliermondii* AUMC 11230. 14 *Pichia kluyveri* AUMC 11231. 15 *Schwanniomyces vanriijiae* AUMC 11237. Basidiomyceteous yeasts. 16 *Cryptococcus albidus* var. *kuetzingii* AUMC 11222. 17 *Filobasidium floriforme* AUMC 11211. 18 *F. magnum* AUMC 11228. 19 Yeast sp. (red) AUMC 13201. 20 *Hannaella zaeae* AUMC 11216. 21 *Moniliella* sp. AUMC 13202. 22 *Naganishia diffluens* AUMC 11219. 23 *Papiliotrema flavescens* AUMC 11212. 24 *Rhodotorula glutinis* AUMC 11223. 25 *R. mucilaginosa* AUMC 11221. 26 *Sporodiobolus metaroseus* AUMC 11213. 27 *S. metaroseus* AUMC 11220. 28 *Trichosporon asahii* AUMC 11242. 29 *Vishniacozyma carnescens* AUMC 11226. 30 *V. peneaus* AUMC 11227.

Test /species strain number	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	
<b>Fermentation</b>																															
D-glucose	+	++	++	-	++	-	-	-	++	++	++	++	++	+	-	-	-	-	-	-	-	++	-	-	-	-	+	-	-	-	-
D-galactose	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Maltose	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Me- $\alpha$ -D-glucoside	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Sucrose	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	
Lactose	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Raffinose	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Inulin	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Starch	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
D-xylose	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
<b>Assimilation of carbon sources</b>																															
D-glucose	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
G-galactose	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	w	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
L-sorbose	-	+	+	+	+	+	+	-	+	+	+	+	+	w	-	+	+	+	+	-	+	+	+	+	+	+	+	w	+		
D-glucosamine	+	-	-	-	+	+	-	w	-	-	-	w	+	-	w	-	+	+	+	-	-	w	-	-	-	-	-	+	+		
D-ribose	-	-	-	-	+	+	-	-	+	-	-	-	+	w	+	+	w	+	-	+	+	+	+	+	+	w	w	+	+		
D-xylose	+	+	+	w	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+		
L-arabinose	+	-	-	-	-	+	+	w	-	-	-w	-	+	+	-	+	+	+	+	-	-	+	+	-	+	-	-	+	+		
L-rhamnose	-	-	-	-	-	+	-	-	-	-	-	-	+	+	-	-	+	+	+	-	-	+	+	-	+	-	-	+	+		
Sucrose	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+		
Maltose	+	+	+	w	+	+	w	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+		
$\alpha$ , $\alpha$ -trehalose	+	+	+	w	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+		
Methyl- $\alpha$ -d-glucoside	+	+	+	-	+	+	-	+	+	+	+	+	+	+	-	-	+	+	+	+	+	-	+	+	+	+	-	-	+		
Cellobiose	-	+	+	-	+	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+		



**Table 2** Continued.

Test /species strain number	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	
salicin	-	+	+	-	+	+	-	-	+	+	+	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+		
Arbutin	-	+	+	-	+	+	-	-	+	+	+	+	+	+	-	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	
Lactose	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	+	+	+	+	-	-	+	+	-	-	-	-	+	+	+	
Raffinose	-	-	-	+	+	+	-	-	-	-	-	-	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	-	+	+	
Melezitose	+	+	+	-	+	+	-	+	+	+	+	+	+	+	-	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	
Inulin	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
Soluble starch	+	-	+	-	w	+	-	-	-	-	+	+	w	-	-	+	+	+	+	+	w	+	+	+	-	+	+	+	-	+	
Glycerol	+	+	+	+	+	+	+	+	+	+	+	+	\+	+	-	-	+	+	+	+	+	+	+	+	+	+	+	+	w	+	
Meso-erythritol	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-	w	-	-	+	+	+	-	w	-	-	+	-	+	
Ribitol	+	+	+	w	+	+	+	+	+	+	+	+	+	w	+	-	w	+	+	+	w	+	+	+	+	+	+	+	+	+	
Xylitol	+	+	+	+	+	+	-	+	+	+	+	+	+	w	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	
D-glucitol	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	
D-mannitol	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
Galactitol	-	-	+	w	+	+	-	-	+	-	w	w	-	+	w	-	+	+	+	+	w	+	+	+	-	w	w	+	+	+	
Myo-inositol	-	-	-	-	+	-	-	-	-	-	-	-	-	w	-	+	+	+	+	-	-	+	+	-	-	+	+	-	+	+	
Glucono-d-lactone	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+	-	+	+	+w	+	+	+	+	+	-	-	+	
2-keto-d-gluconate	+	+	+	+	+	+	+	+	+	+	+	+	+	+	w	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
D-gluconate	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	w	+	+	+	+	+	+	+	+	+	
D-glucuronate	-	-	-	-	+	-	-	-	-	-	-	+	-	+	-	+	+	+	+	-	-	+	+	-	-	-	-	+	+	+	
D-galacturonate	-	w	-	-	+	+	+	-	-	-	-	w	-	w	-	-	-	+	+	-	-	+	+	-	w	-	-	-	-	+	
DL-lactate	+	w	+	-	+	+	+	w	+	+	w	+	+	+	-	+	w	+	-	w	w	+	+	+	+	+	+	+	+	w	+
Succinate	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	w	+	+	+	+	+	+	+	+	+	
Citrate	+	+	+	+	+	+	+	+	w	+	+	+	+	+	+	+	-	+	+	+	w	+	+	+	+	+	+	+	+	w	+
Methanol	-	-	-	-	-	w	-	-	-	-	w	-	-	w	-	-	-	w	-	-	-	+w	-	-	-	-	-	-	-	-	
Ethanol	+	+	+	w	+	+	+	+	+	+	+	w	+	+	+	+	-	+	+	+	+	+	+	+	+	w	w	+	-	-	
Propane 1,2 diol	-	-	-	-	-	w	w	-	-	-	+	-	-	+	-	w	-	w	-	-	w	+	w	-	-	-	-	-	-	+	
Butane 2,3 diol	+	-	-	-	-	-	+	-	-	-	-	-	w	+	-	w	-	w	+	-	w	+	+	w	+	-	-	+	-	+	
Quinic acid	-	-	-	-	-	+	-	-	-	+	-	w	-	w	-	-	-	-	+	+	-	-	w	+	+	+	+	-	-	-	
<b>Nitrogen sources</b>																															
Nitrate	-	-	-	-	+	-	-	+	-	-	+	-	-	-	-	+	+	+	+	+	+	+	-	+	-	+	-	-	+	-	
Nitrite	-	-	-	-	+	-	-	+	-	-	w	-	+	-	-	+	+	+	+	+	+	+	+	+	-	w	+	+	+	+	
Ethylamine	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+	+	+	+	+	-	-	+	-	+	
L-lysine	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	+	+	+	+	+	-	-	+	w	+	
Creatine	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Creatinine	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
D-glucosamine	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	w	+	+	+	+	+	+	+	+	+	
Imidazole	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	w	-	-	-	-	-	-	-	-	-	

**Table 2** Continued.

Test /species strain number	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
D-tryptophane	+	-	-	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-	-	-	-	+	+	+	+	+	+	+	w	+
<b>Miscellaneous</b>																														
0.01%	+	-	-	-	-	+	+	+	-	-	-	-	+	-	+	-	-	-	+	-	-	-	-	+	-	+	+	+	-	-
Cycloheximide																														
0.1 %	+	-	-	-	-	+	+	+	-	-	-	-	+	-	+	-	-	-	+	-	-	-	-	-	-	-	-	+	-	-
Cycloheximide																														
50% d-glucose	+	+	+	+	+	+	-	+	+	+	+	+	+	+	-	-	-	+	-	+	-	-	+	+	-	+	+	-	-	
60% d-glucose	-	+	+	+	+	+	-	+	+	+	w	-	+	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	
10% NaCl	+	+	+	+	+	+	-	+	+	+	+	+	+	-	+	+	w	+	+	+	-	+	+	+	+	+	w	+	+	+
16% NaCl	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Starch formation	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	-	+	-	+	-	-	-	-	-	-	+	+
Urease	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Diazonium blue B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+

+: growth; -: no growth; w: weak growth.

**Table 3** Assiut University Mycological Centre accession number (AUMC) of filamentous and yeast strains isolated from flowers of some plant species with accession GenBank numbers given together with the closest match in the GenBank database and sequence similarity in percent to the match as inferred from Blastn searches of ITS sequences.

AUMC number	Flower origin	Accession GenBank number	Length (bp)	Closest Genbank match # ITS		Sequencing similarity (%)	Species
				Culture Collection Code	Accession no.		
<b>Filamentous fungi</b>							
11214	Snapdragon	KY611819	560	CBS 892.70 <sup>T</sup>	DQ825985	459/464(99)	<i>Gibellulopsis piscis</i>
11234	Pomegranate	KY611835	623	CBS 237.32 <sup>T</sup>	AF484462	611/623(98)	<i>Sporothrix stenoceras</i>
<b>Yeasts</b>							
11211	Lemon	KY611817	655	CBS 140 <sup>T</sup>	NR_130655N	557/558(99)	<i>Filobasidium magnum</i>
				CBS 6241 <sup>T</sup>	R_119429	555/557(99)	<i>Filobasidium floriforme</i>
11212	Adhatoda	KY940306	531	CBS 942 <sup>T</sup>	NR_130696	502/506(99)	<i>Papiliotrema flavescens</i>
11213	Chamomile	KY611818	609	CBS 486 <sup>T</sup>	AY015438	601/608(99)	<i>Sporidiobolus metaroseus</i>
11215	Snapdragon	KY611820	542	ATCC 18804 <sup>T</sup>	HQ876043	527/531(99)	<i>Candida albicans</i>
11216	Snapdragon	KY611821	482	CBS 10801 <sup>T</sup>	NR_144771	456/459(99)	<i>Hannaella zaeae</i>
11217	Camel's foot tree	KY611822	392	CBS 5834 <sup>T</sup>	KY104208	380/393(97)	<i>Metschnikowia reukaufii</i>

**Table 3** Continued.

AUMC number	Flower origin	Accession GenBank number	Length (bp)	Closest Genbank match # ITS		Sequencing similarity (%)	Species
				Culture Collection Code	Accession no.		
11218	Dwarf rose	MF071283	602	CBS 486 <sup>T</sup>	AY015438	594/602(99)	<i>Sporidiobolus metaroseus</i>
11219	Dwarf rose	MF071284	625	CBS 160 <sup>T</sup>	NR_111051	620/623(99)	<i>Naganishia diffluens</i>
11220	Candelabra	KY611823	571	CBS 101075 <sup>T</sup>	KY105523	201/232(87)	<i>Sporidiobolus metaroseus</i>
11221	Callistemon	KY611824	620	CBS 316 <sup>T</sup>	NR_073296	617/618(99)	<i>Rhodotorula mucilaginosa</i>
11222	Khella	KY611825	618	ZA-18	HQ327002	616/619(99)	<i>Cryptococcus albidus</i> var. <i>kuetzingii</i>
11223	Candelabra	KY611826	612	CBS 20 <sup>T</sup>	NR_073294	606/610(99)	<i>Rhodotorula glutinis</i>
11224	Khella	KY611827	311	CBS 9950 <sup>T</sup>	NR_077083	302/305(99)	<i>Metschnikowia viticola</i>
11225	Khella	KY611828	624	CBS 160 <sup>T</sup>	NR_111051	620/621(99)	<i>Naganishia diffluens</i>
11226	Camel's foot tree	KY611829	526	CBS:973 <sup>T</sup>	KY105817	514/515(99)	<i>Vishniacozyma carnescens</i>
11227	Mexican petunia	KY888876	504	CBS 2409 <sup>T</sup>	KY105826	497/498(99)	<i>Vishniacozyma peneaus</i>
11228	Chinese hibiscus	KY888877	628	CBS 140 <sup>T</sup>	NR_130655	627/627(100)	<i>Filobasidium magnum</i>
11229	Pomegranate	KY611830	298	NBYeast2013A03	KM115152	297/298(99)	<i>Galactomyces candidum</i>
11250	Pomegranate	MF114305	628	CBS 140 <sup>T</sup>	NR_130655	627/628(99)	<i>Filobasidium magnum</i>
11230	Mango	KY611831	598	CBS 2030 <sup>T</sup>	KY104252	572/572(100)	<i>Meyerozyma guilliermondii</i>
11231	Mango	KY611832	446	CBS 188 <sup>T</sup>	KY104559	428/434(99)	<i>Pichia kluyveri</i>
11232	Mango	KY611833	380	CBS10357 <sup>T</sup>	KY104211	368/377(98)	<i>Metschnikowia sinensis</i>
11233	Mango	KY611834	607	CBS 486 <sup>T</sup>	AY015438	600/606(99)	<i>Sporidiobolus metaroseus</i>
11235	Pomegranate	KY611836	525	CBS 973 <sup>T</sup>	KY105817	514/515(99)	<i>Vishniacozyma carnescens</i>
11236	Eucalyptus	KY611837	526	CBS 973 <sup>T</sup>	KY105817	513/515(99)	<i>Vishniacozyma carnescens</i>
11237	Lemon	KY611838	642	CBS 3024 <sup>T</sup>	KY105408	539/660(82)	<i>Schwanniomyces vanrijiae</i> var. <i>vanrijiae</i>
11238	Lemon	KY611839	445	CBS 188 <sup>T</sup>	KY104559	429/434(99)	<i>Pichia kluyveri</i>
11239	Lemon	KY611840	473	CBS 10087 <sup>T</sup>	NR_137870	442/473(93)	<i>Candida riococensis</i>
11240	Lemon	KY611841	633	CBS 5921 <sup>T</sup>	KY103281	618/618(100)	<i>Debaryomyces nepalensis</i>
11241	Pomegranate	KY611842	621	CBS 316 <sup>T</sup>	NR_073296	616/619(99)	<i>Rhodotorula mucilaginosa</i>
11242	Guava	KY611843	545	CBS 2479 <sup>T</sup>	FJ943429	542/543(99)	<i>Trichosporon asahii</i>
11243	Guava	KY611844	558	ATCC 11503 <sup>T</sup>	NR_111593	535/536(99)	<i>Lodderomyces elongisporus</i>

**Table 3** Continued.

AUMC number	Flower origin	Accession GenBank number	Length (bp)	Closest Genbank match # ITS		Sequencing similarity (%)	Species
				Culture Collection Code	Accession no.		
11244	Lemon	KY611845	364	CBS 8058 <sup>T</sup>	KY102172	245/256(96)	<i>Metschnikowia viticola</i>
				CBS 9950 <sup>T</sup>	NR_077083	245/256(96)	(= <i>Candida kofuensis</i> )
11245	Guava	KY611846	327	CBS 8174 <sup>T</sup>	KP027649	244/295(83)	<i>Candida rancensis</i>
11246	Guava	KY611847	331	CBS 8174 <sup>T</sup>	KP027649	244/299(82)	<i>Candida rancensis</i>
11247	Guava	KY611848	412	CBS 7318 <sup>T</sup>	KJ630498	359/426(84)	<i>Candida vaccinii</i>

**Table 4** Comparison between the percentage counts of CFUs (%CFU) and frequency of occurrence (O) of fungal taxa recovered from the flowers of ornamental and edible plant species on DRBC, DG18 and MY50G at 25° C.

Medium	DRBC				DG18				MY50G			
	Ornamental		Edible		Ornamental		Edible		Ornamental		Edible	
Source of flowers	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
<b>Taxa</b>												
<b>Yeast fungi</b>	2.03	20	7.55	24	1.05	16	1.72	20	0.18	4	0.38	10
<i>Candida</i>	0.11	6	0.53	12	0.015	2	0.19	8			0.19	4
<i>C. albicans</i>	0.02	1	0.01	1	0.01	1	0.00	1				
<i>C. kofuensis</i>	0.06	3	0.12	2	0.005	1	0.04	2			0.08	2
<i>C. rancensis</i>			0.01	1			0.01	1				
<i>C. riodecensis</i>	0.03	2	0.26	7			0.04	2			0.05	1
<i>C. vaccinii</i>			0.14	5			0.10	5			0.06	2
<i>Cryptococcus albidus</i> var. <i>kuetzingii</i>	0.31	13	1.05	4	0.07	5	0.06	3	0.01	1		
<i>Debaryomyces nepalensis</i>											0.01	1
<i>Filobasidium</i>	0.38	10	0.27	8	0.10	4	0.15	4				
<i>F. floriforme</i>	0.23	7	0.15	7	0.03	2	0.13	4				
<i>F. magnum</i>	0.15	7	0.12	4	0.07	4	0.02	1				
<i>Galactomyces candidus</i>	0.01	1	0.44	2	0.04	2	0.005	1				
<i>Hannaella zeae</i>	0.01	1										
<i>Lodderomyces elongisporus</i>							0.03	1				
<i>Metschnikowia</i>	0.12	3	0.18	5	0.10	3	0.07	4	0.11	2	0.08	2
<i>M. reukaufii</i>	0.07	1	0.06	2	0.10	3	0.005	1	0.11	2		

**Table 4** Continued.

Medium	DRBC				DG18				MY50G			
	Ornamental		Edible		Ornamental		Edible		Ornamental		Edible	
Source of flowers	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
Taxa	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
<i>M. sinensis</i>			0.12	3			0.04	2			0.08	2
<i>M. viticola</i>	0.05	2					0.03	1				
<i>Meyerozyma guilliermondii</i>	0.02	2	0.64	13	0.03	2	0.18	8			0.08	5
<i>Moniliella</i> sp.							0.01	1			0.02	1
<i>Naganishia diffluens</i>	0.47	10	2.55	14	0.18	5	0.22	8	0.06	1		
<i>Papiliotrema flavescens</i>	0.01	1	0.02	2	0.03	1	0.04	2				
<i>Pichia kluyveri</i>	0.02	1	0.19	5			0.16	2				
<i>Rhodotorula</i>	0.11	4	0.27	9	0.14	5	0.09	4	0.00	1		
<i>R. glutinis</i>	0.01	1	0.16	5	0.03	2	0.01	2				
<i>R. mucilaginosa</i>	0.10	3	0.11	6	0.11	4	0.08	2	0.00	1		
<i>Schwanniomyces vanrijiae</i> var. <i>vanrijiae</i>			0.01	1								
<i>Sporidiobolus metaroseus</i>	0.11	7	0.31	7	0.08	5	0.27	7				
<i>Trichosporon asahii</i>			0.04	1								
<i>Vishniacozyma</i>	0.36	10	1.07	15	0.25	5	0.24	4			0.02	1
<i>V. carnescens</i>	0.22	10	1.07	15	0.25	5	0.24	4			0.02	1
<i>V. peneaus</i>	0.14	2										
<b>Filamentous fungi</b>	97.97	20	92.45	24	98.95	20	98.28	24	99.82	20	99.62	24
<i>Absidia cylindrospora</i>					0.005	1						
<i>Acremonium</i>	0.33	8	0.46	16	0.02	1	0.03	2	0.01	1		
<i>A. blochii</i>	0.09	3	0.07	3	0.02	1						
<i>A. curvulum</i>									0.01	1		
<i>A. fusidioides</i>			0.02	2			0.02	1				
<i>A. hyalinulum</i>	0.23	6	0.29	13			0.01	1				
<i>A. rutilum</i>			0.07	2								
<i>Acremonium</i> sp.	0.01	1										
<i>Alternaria</i>	4.87	20	2.45	24	2.29	19	1.42	24	0.33	9	0.81	13
<i>A. atra</i>	0.07	4	0.17	8	0.04	1	0.04	3			0.15	2
<i>A. alternata</i>	2.00	18	0.88	22	0.30	8	0.55	21	0.03	2	0.32	7
<i>A. botrytis</i>	0.05	5	0.03	2	0.06	4	0.04	3			0.06	1

**Table 4** Continued.

Medium Source of flowers Taxa	DRBC				DG18				MY50G			
	Ornamental		Edible		Ornamental		Edible		Ornamental		Edible	
	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
<i>A. brassicicola</i>	0.34	2	0.11	3	0.27	1	0.14	6	0.05	1		
<i>A. chartarum</i>	0.02	2	0.06	4	0.005	1	0.01	1	0.01	1	0.04	1
<i>A. chlamydospora</i>	1.24	16	0.62	20	1.56	18	0.47	16	0.03	2	0.22	8
<i>A. chlamydosporigena</i>	0.04	1										
<i>A. citri</i>	0.01	1	0.27	6			0.09	1				
<i>A. consortiale</i>	0.01	1										
<i>A. dianthi</i>	0.01	1										
<i>A. dianthicola</i>	0.01	1										
<i>A. didymospora</i>			0.02	1	0.01	1	0.01	1				
<i>A. phragmaspora</i>	0.20	2							0.10	2		
<i>A. longipes</i>					0.02	1			0.10	3	0.00	1
<i>A. raphani</i>			0.01	1								
<i>A. tenuissima</i>			0.07	1			0.02	1				
<i>A. tuberculata</i>	0.01	1	0.04	2								
<i>A. yaliinficienns</i>			0.02	2								
<i>Alternaria</i> sp.	0.36	3	0.15	4	0.03	1	0.05	3	0.02	1	0.02	1
<i>Arthrimum</i>	0.08	2	0.01	1					0.01	1		
<i>A. phaeospermum</i>	0.08	2										
<i>A. saccharicola</i>									0.01	1		
<i>A. sphaerospermum</i>			0.01	1								
<i>Aspergillus</i>	6.55	20	5.98	24	4.79	20	4.12	24	6.44	20	6.97	24
<i>A. aculeatinus</i>			0.04	2			0.05	1	0.05	1	0.21	2
<i>A. aculeatus</i>	0.01	1	0.17	4			0.07	3			0.14	3
<i>A. aegyptiacus</i>			0.03	2								
<i>A. thecius</i>									0.01	1		
<i>A. aureolatus</i>	0.10	5			0.10	2	0.01	1				
<i>A. aureoterreus</i>			0.01	1								
<i>A. auricomus</i>			0.01	1								
<i>A. brasiliensis</i>	0.98	10	0.27	8	0.07	3	0.16	6	1.32	9	0.42	8

**Table 4** Continued.

Medium Source of flowers Taxa	DRBC				DG18				MY50G			
	Ornamental		Edible		Ornamental		Edible		Ornamental		Edible	
	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
<i>A. campestris</i>	0.00	1										
<i>A. candidus</i>	0.08	1	0.02	1	0.01	1	0.05	2			0.02	1
<i>A. carneus</i>			0.02	1	0.00	1	0.01	1				
<i>A. chevalieri</i>	0.05	1			0.04	2	0.06	3	0.11	6	0.04	2
<i>A. clavatus</i>	0.01	1										
<i>A. costaricaensis</i>					0.02	1						
<i>A. dimorphicus</i>									0.05	2		
<i>A. flavipes</i>	0.05	4			0.05	4	0.06	3			0.02	1
<i>A. flavus</i>	0.43	14	0.96	21	0.25	11	0.81	19	0.51	14	0.69	17
<i>A. flavus</i> var. <i>columnaris</i>	0.12	3	0.29	4	0.01	2	0.07	3	0.01	1	0.04	1
<i>A. fumigatus</i>	0.02	2	0.21	12	0.01	2	0.01	2	0.21	7	0.38	6
<i>A. japonicus</i>	0.02	2					0.03	1	0.01	1	0.09	1
<i>A. lacticoffeatus</i>	0.05	2										
<i>A. leucocarpus</i>	0.01	1			0.04	3			0.17	8		
<i>A. mangini</i>					0.06	4			0.15	5		
<i>A. melleus</i>	0.02	2			0.00	1	0.00	1				
<i>A. montivedensis</i>	0.01	1	0.01	1	0.11	6	0.09	4	0.07	4	0.07	3
<i>A. nidulans</i>	0.09	6	0.14	6			0.03	3	0.23	7	0.12	1
<i>A. niger</i>	3.10	18	2.47	23	3.32	20	1.62	20	2.68	20	3.15	21
<i>A. niveus</i>									0.01	1		
<i>A. ochraceus</i>	0.23	9	0.32	11	0.18	10	0.18	9	0.17	7	0.22	8
<i>A. oryzae</i>					0.01	1	0.00	1				
<i>A. parasiticus</i>	0.22	5	0.16	7	0.01	1	0.12	3	0.11	5	0.41	6
<i>A. proliferans</i>					0.01	1						
<i>A. pseudoglaucus</i>					0.07	6	0.10	6	0.10	6	0.21	9
<i>A. quadrilineatus</i>	0.05	2			0.03	2	0.01	1	0.12	3	0.02	1
<i>A. ruber</i>							0.10	5	0.01	1	0.07	3
<i>A. rugulosus</i>	0.02	1										
<i>A. stella-maris</i>	0.04	2	0.05	2	0.00	1	0.03	1			0.11	1

**Table 4** Continued.

Medium Source of flowers Taxa	DRBC				DG18				MY50G			
	Ornamental		Edible		Ornamental		Edible		Ornamental		Edible	
	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
<i>A. stellatus</i>	0.01	1	0.01	1	0.04	2	0.01	1				
<i>A. sydowii</i>	0.47	14	0.05	6	0.07	3	0.04	4	0.17	8	0.32	6
<i>A. tamaritii</i>	0.01	1	0.07	3	0.03	2						
<i>A. terreus</i>	0.30	12	0.60	12	0.18	10	0.15	6	0.15	7	0.08	4
<i>A. tubengensis</i>	0.01	1	0.02	1	0.02	1	0.21	6			0.15	3
<i>A. unguis</i>	0.01	1							0.01	1		
<i>A. ustus</i>	0.01	1	0.01	1			0.01	1				
<i>A. versicolor</i>	0.02	2	0.03	1	0.05	2	0.03	2	0.02	2		
<i>A. wentii</i>							0.00	1				
<i>Aspergillus</i> sp. (section <i>Nidulantes</i> )	0.01	1			0.005	1						
<i>Bartalinia</i> sp.							0.03	1				
Basidiomycete sp.			0.01	1								
<i>Bipolaris</i>	0.07	4			0.00	1						
<i>B. clavata</i>	0.06	3			0.00	1						
<i>B. iridis</i>	0.01	1										
<i>Botrytis</i>	0.21	6	0.02	2	0.03	1						
<i>B. aclada</i>	0.11	2										
<i>B. cinerea</i>	0.05	2	0.02	2								
<i>Botrytis</i> sp.	0.05	3			0.03	1						
<i>Chaetomium</i>	0.05	4	0.04	3	0.06	2						
<i>C. globosum</i>	0.02	1										
<i>C. murorum</i>			0.01	1								
<i>C. nozdrenkoae</i>			0.02	1								
<i>C. piluliferum</i>	0.03	3	0.01	1								
<i>Chaetomium</i> sp.					0.06	2						
<i>Chalara</i> sp.			0.01	1								
<i>Chrysosporium merdarium</i>					0.03	1						
<i>Chuppia</i> sp.			0.13	1								
<i>Cladophialophora</i>	0.06	2	0.11	1	0.01	2						



**Table 4** Continued.

Medium Source of flowers Taxa	DRBC				DG18				MY50G			
	Ornamental		Edible		Ornamental		Edible		Ornamental		Edible	
	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
<i>C. bantiana</i>					0.01	2						
<i>C. carrionii</i>			0.11	1								
<i>Cladophialophora</i> sp.	0.06	2										
<i>Cladosporium</i>	73.98	20	66.45	24	84.06	20	79.18	24	87.25	20	73.50	02
<i>C. cladosporioides</i>	1.64	18	1.45	22	0.98	13	2.18	19	0.50	10	1.35	8
<i>C. fusiforme</i>	0.01	1										
<i>C. herbarum</i>	61.23	18	61.59	23	65.18	16	74.00	24	75.77	14	68.97	20
<i>C. macrocarpum</i>			0.01	1	0.01	1	0.02	1	0.005	1		
<i>C. oxysporum</i>	1.57	15	0.32	13	1.39	14	0.67	17	0.56	5	1.38	8
<i>C. ramotenellum</i>							0.01	1				
<i>C. sphaerospermum</i>	9.44	14	3.08	12	16.49	16	2.31	19	10.35	12	1.80	9
<i>C. spongiosum</i>	0.01	1			0.02	1			0.05	1		
<i>C. subtilissimum</i>									0.01	1		
<i>C. variabile</i>	0.08	1							0.005	1		
<i>Cochliobolus</i>	0.04	5			0.29	3						
<i>C. bicolor</i>	0.01	1										
<i>C. nodulosus</i>	0.01	1										
<i>C. spicifer</i>	0.02	3			0.29	3						
<i>Cosmospora butyri</i>	0.01	1	0.04	1								
<i>Curvularia</i>	0.52	6	0.04	4	0.26	11						
<i>C. lunata</i>	0.01	1	0.01	1	0.03	2						
<i>C. pallescens</i>	0.01	1										
<i>C. papendorfii</i>	0.02	1			0.005	1						
<i>C. subpapendorfii</i>	0.02	2			0.03	2						
<i>C. tsudae</i>	0.46	5	0.03	3	0.20	8	0.00	1				
<i>Cylindrocarpon</i> sp.	0.01	1	0.02	2								
<i>Didymella pomorum</i>	0.01	1	0.07	3	0.06	3			0.06	1		
<i>Dothiorella dulcispinae</i>	0.15	1										
<i>Drechslera biseptata</i>	0.03	1	0.07	3			0.23	1			0.02	1

**Table 4** Continued.

Medium Source of flowers Taxa	DRBC				DG18				MY50G			
	Ornamental		Edible		Ornamental		Edible		Ornamental		Edible	
	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
<i>Epiccocum nigrum</i>	0.94	17	0.52	19	0.48	12	0.46	21	0.01	1	0.16	6
<i>Exserohilum rostrata</i>	0.06	1	0.06	3			0.01	1				
<i>Fusarium</i>	0.92	12	1.00	19	0.57	7	0.62	18			0.19	4
<i>F. camptoceras</i>			0.02	1			0.02	1				
<i>F. chlamydosporum</i>			0.03	2								
<i>F. culmorum</i>							0.05	2				
<i>F. equiseti</i>	0.08	2			0.01	1	0.01	1				
<i>F. incarnatum</i>	0.48	7	0.06	5	0.49	3	0.15	10			0.08	3
<i>F. nygamai</i>	0.03	2	0.07	4			0.04	2			0.02	1
<i>F. oxysporum</i>			0.02	1								
<i>F. proliferatum</i>	0.01	1	0.22	8			0.05	4				
<i>F. pseudonygami</i>	0.04	1										
<i>F. scripi</i>					0.04	1						
<i>F. solani</i>	0.13	6	0.30	7	0.01	2	0.15	5				
<i>F. verticillioides</i>	0.15	6	0.28	6	0.03	2	0.16	8			0.09	2
<i>Fuscoannellis carbonaria</i>	0.01	1										
<i>Gibellulopsis</i>	0.01	1	0.01	1								
<i>G. nigricans</i>			0.01	1								
<i>G. piscis</i>	0.01	1										
<i>Graphiopsis chlorocephala</i>	0.80	5	0.03	1	0.09	3						
<i>Hamigera insecticola</i>	0.03	1			0.05	2						
<i>Haplobasidion lelebae</i>					0.01	1						
<i>Hypomyces chrysospermus</i>	0.01	1										
<i>Lasiodiplodia theobromae</i>	0.11	5	0.21	9	0.08	3	0.19	7	0.04	1	0.11	1
<i>Melanopsama pomiformis</i>			0.04	3								
<i>Merimbla ingelheimensis</i>									0.01	1		
<i>Microascus</i>	0.13	4	0.10	4	0.02		0.02	3				
<i>M. brevicaulis</i>	0.05	2	0.10	4			0.02	2				
<i>M. chartarum</i>	0.08	2					0.03	1				

**Table 4** Continued.

Medium	DRBC				DG18				MY50G			
	Ornamental		Edible		Ornamental		Edible		Ornamental		Edible	
Source of flowers	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
Taxa	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
<i>M. croci</i>					0.02	2						
<i>Monodictys levis</i>	0.01	1										
<i>Mucor</i>	0.03	4	0.11	4	0.01	1					0.02	1
<i>M. circinelloides</i>	0.01	2	0.11	4	0.01	1						
<i>M. hiemalis</i>	0.01	1										
<i>M. racemosus</i>	0.01	1									0.02	1
<i>Myrothecium</i> sp.			0.06	3			0.01	1				
<i>Neurospora crassa</i>	0.06	2	0.03	1	0.04	3	0.01	1				
<i>Nigrospora</i>	0.04	3	0.02	1	0.02	2	0.04	2				
<i>N. oryzae</i>	0.02	3	0.02	1			0.04	2				
<i>N. sphaerica</i>	0.02	1			0.02	2						
<i>Paecilomyces variotii</i>	0.02	1	0.03	2								
<i>Papulospora immersa</i>			0.02	1			0.01	1				
<i>Penicillium</i>	3.91	20	10.99	24	4.36	20	10.39	24	5.27	20	16.90	24
<i>P. adametzoides</i>			0.01	1			0.01	1				
<i>P. aurantiogriseum</i>	0.08	2	0.84	3	0.13	4	1.19	4			2.83	4
<i>P. brevicompactum</i>	0.10	5	0.26	5								
<i>P. camemberti</i>	0.05	1			0.03	2						
<i>P. chrysogenum</i>	2.16	19	0.73	16	2.62	20	1.28	19	3.64	19	1.65	20
<i>P. citrinum</i>	0.08	3	0.09	5	0.02	2	0.15	5	0.01	1	0.15	2
<i>P. corylophilum</i>	0.14	3	0.11	2	0.01	2	0.02	1	0.08	3	0.10	2
<i>P. digitatum</i>	0.02	1										
<i>P. expansum</i>	0.02	3							0.02	1	0.04	2
<i>P. fennelliae</i>					0.01	1						
<i>P. glabrum</i>			0.11	5	0.03	1	0.07	5	0.14	1	0.27	4
<i>P. granulatum</i>			0.08	1								
<i>P. griseofulvum</i>	0.03	3	0.05	3	0.03	1	0.06	1			0.03	2
<i>P. implicatum</i>	0.02	1	0.05	3			0.04	3			0.21	2
<i>P. italicum</i>	0.01	1										

**Table 4** Continued.

Medium	DRBC				DG18				MY50G			
	Ornamental		Edible		Ornamental		Edible		Ornamental		Edible	
Source of flowers	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
Taxa	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
<i>P. madriti</i>									0.03	1		
<i>P. melinii</i>	0.01	1										
<i>P. olsonii</i>	0.51	5	6.96	14	0.49	3	5.87	11	0.20	5	10.11	10
<i>P. oxalicum</i>			0.18	3	0.09	1	0.09	3			0.02	1
<i>P. phoeniceum</i>					0.03	1						
<i>P. purpurascens</i>			0.01	1								
<i>P. raistrickii</i>	0.02	1	0.30	4			0.22	2			0.09	1
<i>P. sclerotiorum</i>							0.03	1				
<i>P. solitum</i>	0.25	8	0.97	10	0.70	14	0.96	13	1.09	4	1.05	3
<i>P. spinulosum</i>	0.01	1										
<i>P. vinaceum</i>							0.02	1				
<i>P. viridicatum</i>	0.31	5	0.03	2	0.12	3	0.02	2	0.02	1		
<i>P. waksmanii</i>			0.02	1								
<i>Penicillium</i> sp.	0.08	1	0.19	4	0.07	1	0.38	6	0.04	1	0.34	3
<i>Periconia minutissima</i>			0.03	1	0.01	1						
<i>Phialaphora cyclaminis</i>							0.01	1				
<i>Pithomyces cynodontis</i>	0.01	1										
<i>Pleospora herbarum</i>			0.13	3			0.03	1			0.08	1
<i>Pochonia chlamydosporia</i>	0.03	1	0.05	2								
<i>Purpureocillium lilacinum</i>	0.05	2										
<i>Quambalaria cyanescens</i>			0.01	1			0.02	1			0.05	3
<i>Rhinochadiella</i> sp.			0.01	1			0.01	1				
<i>Rhizopus</i>	0.04	3	0.07	6	0.31	15	0.02	2	0.18	10	0.11	5
<i>R. arrhizus</i>	0.04	2	0.06	6	0.21	11	0.01	2	0.13	7	0.07	4
<i>R. stolonifer</i>	0.01	1	0.01	1	0.10	4	0.005	1	0.05	4	0.04	2
<i>Sagonemella diversispora</i>	0.06	3	0.03	2								
<i>Sarocladium</i>	0.48	4	0.36	10	0.07	3	0.05	3				
<i>S. kiliens</i>			0.03	1			0.005	1				
<i>S. strictum</i>	0.48	4	0.33	10	0.07	3	0.05	2				

**Table 4** Continued.

Medium	DRBC				DG18				MY50G			
	Ornamental		Edible		Ornamental		Edible		Ornamental		Edible	
Source of flowers	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
Taxa	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
<i>Ochroconis tshawytschae</i>			0.03	1								
<i>Scopulariopsis</i>	0.01	1	0.07	2					0.01	1		
<i>S. candidus</i>	0.01	1	0.005	1					0.01	1		
<i>S. fusca</i>			0.02	1								
<i>Scytalidium</i>	0.09	3	0.23	3			0.01	1				
<i>S. infestans</i>	0.09	3	0.09	2								
<i>S. japonicum</i>							0.01	1				
<i>S. lignicola</i>			0.14	1								
<i>Sporothrix stenoceras</i> (= <i>Ophiostoma stenoceras</i> )	0.05	2	0.12	6							0.01	1
<i>Stachybotrys chartarum</i>			0.13	5			0.01	1				
<i>Stemphylium</i>	2.89	15	1.07	12	0.82	11	1.20	12	0.15	5	0.54	9
<i>S. botryosum</i>	0.86	13	0.41	14	0.44	9	0.82	19	0.14	4	0.48	8
<i>S. sarciniforme</i>	1.62	11	0.54	15	0.02	1	0.26	6			0.02	1
<i>S. vesicarium</i>	0.41	8	0.12	7	0.36	5	0.12	7	0.01	1	0.04	2
<i>Stenella araguata</i>			0.02	1								
<i>Talaromyces</i>	0.49	18	0.84	9	0.03	3	0.15	6	0.02	1	0.05	2
<i>T. dauclauxii</i>	0.15	8	0.03	2			0.01	2				
<i>T. dendriticus</i>	0.01	1	0.02	1								
<i>T. islandicus</i>	0.09	4	0.01	1								
<i>T. pinophilus</i>	0.02	2	0.28	3			0.01	1			0.01	1
<i>T. purpureogenus</i>	0.10	7	0.10	3	0.01	2	0.04	1				
<i>T. variabilis</i>	0.12	7	0.40	2	0.02	1	0.10	2	0.02	1	0.04	1
<i>Torula</i> sp.			0.01	1								
<i>Toxicocladosporium irritans</i>			0.01	1								
<i>Trichoderma</i>	0.08	3	0.09	3	0.01	1						
<i>T. atroviride</i>	0.01	1										
<i>T. aureoviride</i>			0.04	2								
<i>T. harzianum</i>	0.07	3	0.05	2	0.01	1						

**Table 4** Continued.

Medium	DRBC				DG18				MY50G			
	Ornamental		Edible		Ornamental		Edible		Ornamental		Edible	
Source of flowers	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O	%CFU	O
<i>Trichothecium roseum</i>	0.09	6	0.04	3	0.05	5	0.00	1				
<i>Wallemia sebi</i>	0.02	2			0.02	2	0.01	1	0.03	3	0.11	1
Total	100	20	100	24	100	20	100	24	100	20	100	24
Total CFUs	76980		75986		94084		90574		67355		42188	
No. of genera (84)	59		64		43		44		19		22	
No. of species (244+3 varieies)	160+2		150+3		109+2		122+2		64+2		71+1	

\*%CFU: percentage counts of CFUs (calculated per total CFUs) and O: frequency of occurrence out of 20 samples of ornamental flowers and from 24 samples of edible plants.

**Table 5** Flowers of edible and ornamental plants and their characteristic yeast species from which they were isolated.

Edible	
Pomegranate	<i>Candida albicans</i> , <i>C. riodocensis</i> , <i>Cryptococcus albidus</i> var. <i>kuetzingii</i> , <i>Filobasidium floriforme</i> , <i>F. magnum</i> , <i>Galactomyces candidus</i> , <i>Metschnikowia reukaufii</i> , <i>M. sinensis</i> , <i>M. viticola</i> , <i>Meyerozyma guilliermondii</i> , <i>Naganishia diffluens</i> , <i>Papiliotrema flavescens</i> , <i>Pichia kluyveri</i> , <i>Rhodotorula glutinis</i> , <i>R. mucilaginosa</i> , <i>Sporidiobolus metaroseus</i> , <i>Vishniacozyma carnescens</i>
Mango	<i>Cryptococcus albidus</i> var. <i>kuetzingii</i> , <i>Filobasidium floriforme</i> , <i>F. magnum</i> , <i>Galactomyces candidus</i> , <i>Metschnikowia sinensis</i> , <i>Meyerozyma guilliermondii</i> , <i>Naganishia diffluens</i> , <i>Pichia kluyveri</i> , <i>Rhodotorula glutinis</i> , <i>R. mucilaginosa</i> , <i>Sporidiobolus metaroseus</i> , <i>Vishniacozyma carnescens</i>
Guava	<i>Candida rancensis</i> , <i>C. riodocensis</i> , <i>C. vaccinii</i> , <i>Cryptococcus albidus</i> var. <i>kuetzingii</i> , <i>Filobasidium floriforme</i> , <i>F. magnum</i> , <i>Lodderomyces elongisporus</i> , <i>Meyerozyma guilliermondii</i> , <i>Metschnikowia viticola</i> , <i>Moniliella</i> sp., <i>Naganishia diffluens</i> , <i>Papiliotrema flavescens</i> , <i>Pichia kluyveri</i> , <i>Rhodotorula mucilaginosa</i> , <i>Sporidiobolus metaroseus</i> , <i>Trichosporon asahii</i> , <i>Vishniacozyma carnescens</i>
Lemon	<i>Candida albicans</i> , <i>C. riodocensis</i> , <i>C. vaccinii</i> , <i>Cryptococcus albidus</i> var. <i>kuetzingii</i> , <i>Debaryomyces nepalensis</i> , <i>F. floriforme</i> , <i>Galactomyces candidus</i> , <i>Metschnikowia reukaufii</i> , <i>M. sinensis</i> , <i>M. viticola</i> , <i>Meyerozyma guilliermondii</i> , <i>Naganishia diffluens</i> , <i>Pichia kluyveri</i> , <i>R. mucilaginosa</i> , <i>Sporidiobolus metaroseus</i> , <i>Schwanniomyces vanrijiae</i> var. <i>vanrijiae</i> , <i>Vishniacozyma carnescens</i>

**Table 5** Continued.

<b>Ornamental</b>	
Camel's foot tree	<i>Candida albicans</i> , <i>Cryptococcus albidus</i> var. <i>kuetzingii</i> , <i>Filobasidium floriforme</i> , <i>F. magnum</i> , <i>Galacomycetes candidus</i> , <i>Metschnikowia reukaufii</i> , <i>M. viticola</i> , <i>Naganishia diffluens</i> , <i>Sporidiobolus metaroseus</i> , <i>Vishniacozyma carnescens</i> ,
Candelabra	<i>Cryptococcus albidus</i> var. <i>kuetzingii</i> , <i>Filobasidium magnum</i> , <i>Metschnikowia viticola</i> , <i>Naganishia diffluens</i> , <i>Rhodotorula glutinis</i> , <i>R. mucilaginosa</i> , <i>Sporidiobolus metaroseus</i> , <i>Vishniacozyma carnescens</i>
Khella	<i>Candida riodocensis</i> , <i>Cryptococcus albidus</i> var. <i>kuetzingii</i> , <i>Filobasidium floriforme</i> , <i>Metschnikowia viticola</i> , <i>Naganishia diffluens</i> , <i>Sporidiobolus metaroseus</i> , <i>Vishniacozyma carnescens</i>
Chamomile	<i>Cryptococcus albidus</i> var. <i>kuetzingii</i> , <i>Sporidiobolus metaroseus</i>
Snapdragon	<i>Candida albicans</i> , <i>Cryptococcus albidus</i> var. <i>kuetzingii</i> , <i>Hannaella zaeae</i> , <i>Filobasidium floriforme</i> , <i>F. magnum</i> , <i>Metschnikowia reukaufii</i> , <i>Naganishia diffluens</i> , <i>Sporidiobolus metaroseus</i> , <i>Vishniacozyma carnescens</i>
Callistemon	<i>Cryptococcus albidus</i> var. <i>kuetzingii</i> , <i>Filobasidium floriforme</i> , <i>F. magnum</i> , <i>Metschnikowia reukaufii</i> , <i>M. viticola</i> , <i>Meyerozyma guilliermondii</i> , <i>Naganishia diffluens</i> , <i>Pichia kluyveri</i> , <i>Rhodotorula mucilaginosa</i> , <i>Sporidiobolus metaroseus</i> , <i>Vishniacozyma carnescens</i> , <i>V. peneaus</i>
Eucalyptus	<i>Filobasidium floriforme</i> , <i>Meyerozyma guilliermondii</i> , <i>Naganishia diffluens</i> , <i>Vishniacozyma carnescens</i>
Cotton	<i>Candida riodocensis</i> , <i>Cryptococcus albidus</i> var. <i>kuetzingii</i>
Chinese hibiscus	<i>Cryptococcus albidus</i> var. <i>kuetzingii</i> , <i>Filobasidium floriforme</i> , <i>F. magnum</i> , <i>Metschnikowia viticola</i> , <i>Naganishia diffluens</i> , <i>Rhodotorula glutinis</i> , <i>R. mucilaginosa</i> , <i>Sporidiobolus metaroseus</i> , <i>Vishniacozyma carnescens</i>
Adhatoda	<i>Papiliotrema flavescens</i> , <i>Vishniacozyma carnescens</i>
Mexican petunia	<i>Cryptococcus albidus</i> var. <i>kuetzingii</i> , <i>Filobasidium magnum</i> , <i>Galacomycetes candidum</i> , <i>Metschnikowia viticola</i> , <i>Meyerozyma guilliermondii</i> , <i>Naganishia diffluens</i> , <i>Rhodotorula mucilaginosa</i> , <i>Sporidiobolus metaroseus</i> , <i>Vishniacozyma carnescens</i> , <i>V. peneaus</i>
Dwarf rose	<i>Cryptococcus albidus</i> var. <i>kuetzingii</i> , <i>F. floriforme</i> , <i>F. magnum</i> , <i>Naganishia diffluens</i> , <i>Sporidiobolus metaroseus</i> , <i>Vishniacozyma carnescens</i>

## Overview on the mycobiota inhabiting flowers of ornamental and edible fruit plants

A total of 244 species and 3 varieties belonging to 84 genera were recovered from 44 samples of flowers of both ornamental plants (20 samples) and edible fruit plants (24) collected randomly during the period from March to September 2012. From these, 24 species + 2 varieties assigned to 18 genera were yeasts and 220 species and 1 variety belonging to 66 genera were filamentous fungi. Two hundred and eleven species belonging to 76 genera were recorded on DRBC, 155 species appertaining to 58 genera on DG18, and 95 species assigned to 30 genera on MY50G. The highest numbers of fungal propagules were recovered on DG18 from flowers of ornamental plants while the lowest on MY50G medium from flowers of edible fruit plants. Yeasts constituted a small proportion of propagules from the two flower types on the three media. From yeasts, *Vishniacozyma carnescens* was recovered from all flowers of edible and ornamental flowers except those of cotton and Chamomile; and *Cryptococcus albidus* var. *kuetzingii* from all except *Adhatoda* and *Eucalyptus*, while others were characteristic of one flower type. Of filamentous fungi, *Cladosporium* percentage counts were clearly dominant (66 – 87 %) over those of all other genera. This dominance pattern of *Cladosporium* on the flower leaves is similar to its pattern in the air and phyllosphere of foliage leaves in many plants and in many parts of the world.

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