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Changes in urban soil yeast communities after a reduction in household waste during the COVID-19 pandemic

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ARTICLE INFO

Keywords:
Soil basidiomycetous yeasts
COVID-19 pandemic
Urban soils
Household waste
Opportunistic yeasts

ABSTRACT

The soils of streets, urban parks and suburban areas were examined for yeasts in the summer of 2020 on the territory of the southern cities of Russia and the Republic of Crimea: Krasnodar, Maykop, Sochi and Simferopol. The results of this study are compared with the results of a previous study carried out in these cities in 2019. This study was conducted three months after the lockdown due to the COVID-19 pandemic, which led to a sustained decline in household waste deposition in these areas. The number of tourists visiting these southern cities decreased significantly, and the number of walkers and visitors to urban parks fell sharply. In 2020, after the decline of household waste loads, the yeast abundance was slightly but reliably higher than in 2019. A total of 30 yeast species were observed - 11 ascomycetes and 19 basidiomycetes. This was more than in 2019 and was caused by twice as many autochthonous basidiomycetous yeast species (natural core community), which were found in urban soils only after the reduction in household waste in the environment - Apiotrichum dulcitum, A. laibachii, Saitozyma podzolica Solicoccozyma terricola. And at the same time, the proportion of clinically significant (opportunistic) yeasts, Candida sake and Meyerozyma guilliermondii, was much lower in 2020 than in 2019. Thus, the observed changes in yeast communities in urban soils could be a short-time response of the microbial community to a reduction in household waste.

1. Introduction

The current pace of urbanization is leading to a significant increase in the generation of household waste, which is seriously affecting the ecology of urban areas. In general, the situation is fairly considered very negative in many places, as it represents a true burden for human health, biodiversity, and the environment (Breuste et al., 2021).

Soil is an essential component of all ecosystems, regulating the surrounding environment (Mishra et al., 2020). Its pollution from anthropogenic activities, especially urbanization, alters soil organic matter and its biodiversity (Singh and Singh, 2020). During the COVID-19 pandemic lockdown and restrictions, there were reports of a significant reduction in household waste (Fan et al., 2020; Ouhsine et al., 2020), municipal, industrial, commercial, and gray water waste (Qarani, 2020). Recovering green areas and reduced soil erosion, both were observed during the period (Qarani, 2020). Waste generated by tourists was significantly reduced, leading to a temporary improvement in environmental conditions (Zambrano-Monserrate et al., 2020). Improved air and water quality resulted in lower acid contamination of the soil and thereby causing a drop in soil acidification. Taken together, these factors substantially improved soil quality during the pandemic (Loh et al., 2021).

Due to the COVID-19 pandemic and the introduction of internal restrictive measures and lockdowns, an exceptional situation arose in many countries. From the beginning of spring 2020 until almost autumn, various restrictive and prohibitive measures related to the pandemic were announced in all regions of Russia: people over 65 were not allowed to go out, students switched to distance learning, hotels were closed, tourist flows decreased by more than 90 %, urban parks were closed to visitors. This exceptional situation, thus, provided a unique opportunity to study how a sharp decline in household waste can affect soil microbial communities.
In this study, we compared the abundance, species diversity, and proportion of opportunistic species in urban soil yeast complexes in the southern tourist cities of Russia and the Republic of Crimea before and after the ongoing restrictive measures and the lockdown due to the COVID-19 pandemic. We evaluated impact of reduction in household waste on soil yeast communities.

2. Materials and methods

2.1. Study location and sampling

We have studied soil samples collected on the territory of the southern cities of Russia and the Republic of Crimea: Krasnodar, Maykop, Sochi and Simferopol in July 2020, three months after the announcement of self-isolation and lockdown, which was accompanied by a sharp decrease in household waste in urban areas. The main characteristics of the studied localities are listed in Table 1.

The studied urban street soils had inclusions in soil profiles of household and constructional materials, while showing signs of natural zonality and specificity of the sediments on which these soils were formed. All urban street soils with a significant degree of anthropogenic influence had the diagnostic horizon urbic in their profile (Prokof'eva et al., 2014). Soils in urban parks and suburban soils surrounding cities were selected as controls for comparison. Modern botanical gardens, the specially protected natural green areas of the city, were defined as urban parks. Suburban areas were defined as areas with minimal pollution from household wastes and no agricultural activity.

The names of the soils according to the World Reference Base (WRB) for soil resources and their locations are listed in Table 2 (IUSS Working Group, 2015). Sampling was done from the topsoil (0–20 cm layer) of each studied soil.

Mixed samples were collected from the topsoils. Each mixed soil sample consisted of 20 point samples: 4 samples from different sides and other samples from two diagonal transects with 10–15 cm grid. The mixed samples were packed in a sterile zip bag and provided with an accompanying label. The samples were packed in special refrigerated bags at a temperature of 10 °C and delivered to the laboratory within 48 h for microbiological examinations. In the laboratory, the mixed samples were stored in a refrigerated chamber at a temperature not exceeding 4 °C for a maximum of four days. Four mixed samples were taken from each of the 10 soils tested. A total of 40 mixed samples were analyzed. From each mixed sample, 10 subsamples were then taken and analyzed.

2.2. Microbiological analyses and species identification

The abundance and taxonomic structure of yeasts were studied using a surface plating method on solid media. Ten subsamples were taken from each mixed soil sample and poured with sterile water to obtain a 1:10 dilution. The suspensions were vortexed on a Multi Reax Vortexer (Heidolph Instruments, Germany) for 15 min at 2000 rpm without further dilution. Thus, 400 prepared suspensions were plated in six replicates on glucose-peptone-yeast extract (GPY) agar (20 g/L glucose, 10 g/L peptone, 5 g/L yeast extract, 20 g/L agar) supplemented with chloramphenicol (500 mg/L) to prevent bacterial growth. A total of 2400 plates were incubated at 22 °C for 5–7 days. The grown yeast colonies were classified into morphological types using a dissecting microscope and the number of colonies of each type was counted. From each morphotype, 5–7 colonies were isolated into a pure culture.

Identification of yeast species was based on the ITS rDNA nucleotide sequence. DNA isolation and PCR were performed according to the previously described procedure (Glushakova and Kachalkin, 2017). DNA sequencing was performed using the Big Dye Terminator V3.1 Cycle Sequencing Kit (Applied Biosystems, USA) with subsequent analysis of the reaction products on an Applied Biosystems 3130xl Genetic Analyzer at the facilities of Evrogen (Moscow, Russia). For sequencing, the ITS primer (5′- GGA AGT AAA AGT CGT AAC AAG G) -33 % 24 March –

Average seasonal tourist traffic, min

Decline in tourist traffic in 2020

Severe restrictions period in 2020

The differences in the beginning and end between the cities were 2–3 days.
performed by plating on Endo agar media. Identification was based on the 16 S rDNA nucleotide sequence data using the BLAST NCBI. DNA isolation from pure bacterial cultures was performed using the PrepMan Ultra Sample Preparation Reagent (Applied Biosystems, USA) kit according to the manufacturer’s recommendations. Sequencing of the PCR product of variable v3 and v4 regions of the 16 S rRNA gene was performed according to the standard MicroSeq 500 16 S rDNA Bacterial Identification Kit’s protocol (Thermo Fisher, USA) using standard ID1/rd1 primers as described before (Manucharova et al., 2008). DNA sequencing was performed on an ABI Prism 3130 genetic analyzer. For analysis of the obtained electrophoretograms and nucleotide sequences, we used the MicroSeq ID v.2.0 (Applied Biosystems, USA) software and the validated MicroSeq ID 16 S rDNA 500 Library v2.0. Analysis of the 16 S rRNA sequences was performed at Syntol (Moscow, Russia).

### Table 3

The average relative abundance (%) of yeasts isolated in 2020 from urban street soils and control soils in Sochi, Simferopol, Maykop, Krasnodar.

| Yeast species                  | Urban street soils | Soils of urban parks | Suburban soils |
|-------------------------------|--------------------|----------------------|---------------|
|                               | 1| 2 | 3 | 4 | 1 | 2 | 3 | 4 | 1 | 2 | 3 | 4 |
| Acycomyces                    |        |        |        | 5.60 3.62 1.17 | 1.22 – – 3.14 | – – 2.45 |
| Barnetosyza                    |        |        |        | Candida fluviatilis | – – – – 4.82 | – – – – |
| Candida membranifera          | 2.10 | – – 2.20 | – – – – | Candida sp. | – – 2.14 7.21 | – – 5.16 | – – | – – 3.51 |
| C. sake                       | 7.66 | – – 7.12 | – – – – | Cyberlinkinera misamensis | – – – – | – – – – | – – 1.09 |
| Debaryomyces                  | 1.08 | 1.44 | 2.03 1.14 14.16 20.8 2.00 | – – 0.23 |
| D. fabryi                     | – – | 66.15 40.07 | – – | Meyerozyma guillermondii | 1.10 3.30 18.25 19.51 18.33 | 14.80 |
| Meyerozyma                    | 2.09 | – – | 9.74 | 1.02 | – – | – – | – – | – – 2.72 |
| Schuvannomyces                 | 1.73 | – – | – – | Sch. occidentalis | 1.25 1.22 | – – | – – | – – 7.02 |
| Basidiomycota                 |        |        |        | – – | – – | – – | – – | – – | – – | – – | – – | – – |
| Apiotrihum dulcitum           | 1.15 | 1.63 | 2.14 | 1.67 | 4.14 | 3.06 | – – 11.02 | 5.11 |
| A. laibachii                  | 2.74 | 4.68 | 5.02 | 1.09 | 2.01 | 0.59 | 5.02 | 1.15 | 2.20 | 1.67 | 4.14 | 3.06 | 2.72 |
| A. porosum                    | 2.74 | 4.68 | 5.02 | 1.09 | 2.01 | 0.59 | 5.02 | 1.15 | 2.20 | 1.67 | 4.14 | 3.06 | 2.72 |
| Pediococcus                   | 1.33 | 0.68 | 1.17 | 4.45 | 0.20 | 3.17 | 0.16 | 0.54 |
| Pediococcus                   | 1.33 | 0.68 | 1.17 | 4.45 | 0.20 | 3.17 | 0.16 | 0.54 |
| Rhodotorula                   | 1.10 | 5.61 | – – | – – | 1.15 | 2.20 | – – | – – |
| Rh. glutinis                  | 0.78 | 8.52 | – – | – – | 2.08 | 2.86 | – – | 1.10 |
| Rh. graminis                  | 2.45 | – – | – – | – – | 1.11 | 1.04 | – – | – – |
| Rh. mucilagrosa               | 1.17 | 16.86 | 3.80 | 3.87 | 5.24 | 6.02 | 5.78 | 5.08 | 8.13 |
| Rhodospiridiobolus            | 8.12 | – – | – – | – – | 4.16 | 3.94 | 7.56 | 4.24 | – – |
| Saintoxys                  | 0.71 | 0.09 | 1.27 | 4.16 | 3.94 | 7.56 | 4.24 | – – |
| Solicscoecysa                  | 3.27 | – – | 2.15 | 10.22 | 6.67 | 2.45 | 2.19 | 5.16 | 7.12 |
| S. terrae                   | 10.16 | 24.89 | 4.12 | 3.00 | 9.73 | 3.18 | 1.10 | 16.82 | 4.19 |
| S. tericola                  | 13.12 | 5.39 | 4.75 | 2.00 | 5.96 | 6.90 | 2.05 | 4.55 | 2.18 | 6.21 |
| Sporeobolomyces              | – – | – – | – – | – – | 0.28 | – – | – – | – – |
| Tausonia pullulans           | 4.07 | 0.39 | 9.22 | 4.11 | – – 11.26 | 5.18 | 2.48 |

†1, Sochi; 2, Simferopol; 3, Maykop; 4, Krasnodar. “—” not found.

#### 2.3. Data analyses

In 2019, a similar scheme of sampling, microbial analysis, and species identification was conducted. The results obtained in 2019 (Glushakova et al., 2020, 2021) were used for comparison with the data of the current study. The number of yeast colonies was used to calculate the number of yeast cells (CFU) in each type of sample per dry weight. The relative abundances of the species were calculated as the proportion (%) of colonies that appeared on the plates.

Statistical data processing and graphical representation of the obtained results were performed using Excel 2010 (Microsoft, USA), Statistica 8.0 (StatSoft, USA) and PAST 4.09 (Hammer et al., 2001) programs. After application of the Shapiro-Wilk test, the analysis of variance (ANOVA) was carried out using average yeast numbers to identify significant difference in each type of soil (urban street soil, urban park soil and suburban soil) between studied towns (Krasnodar, Maykop, Sochi and Simferopol) for both years (2019 and 2020). Effects were considered to be statistically significant at the level $p \leq 0.05$. Pairwise yeast comparison was calculated using the Sorensen similarity index. Principal component analysis was conducted for ordination yeast structure by relative abundance and values for yeast similarity by Sorensen index between plots and years.

### 3. Results

#### 3.1. Studied results

Yeasts were found in all soil samples examined. For the cities of Krasnodar and Simferopol, we were able to obtain a complete data set for all three soil groups (urban street soil - urban park soil - suburban soil) in both 2019 and 2020. For Sochi, we obtained data for urban street soils and for urban park soils in 2019 and 2020. The lack of data for

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**Fig. 1.** Abundance of soil yeasts (mean with standard deviation) in Sochi, Simferopol, Maykop and Krasnodar by current research and 2019 data (Glushakova et al., 2020). The arrow shows a statistically significant increase in yeast abundance.
suburban soils is due to the fact that there are hardly any areas and soil in the Sochi agglomeration that have never been exposed to anthropogenic activities. Intensive development of the urban area has been taking place since the 1950s. At present, Sochi is a tourist center in the south of Russia. In Maykop, we obtained data on yeasts in urban street soil in both 2019 and 2020; for suburban soil in 2019; for soil in urban parks in 2020. In 2020, unfortunately, the suburban area sampled in 2019 fell under the urban expansion program and was left to development.

3.2. Yeast abundance

In the tourist city of Simferopol, the average abundance of soil yeasts decreased in a range of urban street soil - urban park soil - suburban soil in both 2019 and 2020. However, in 2020, the average abundance of soil yeasts in urban park soil was an order of magnitude higher compared to that of 2019 (Fig. 1). In Krasnodar, the trend of change in yeast abundance in 2019 was the same as in Simferopol, but in 2020, the abundance of yeasts in the urban park soil was slightly higher than in urban street soil (Fig. 1).

The largest number of yeasts was detected in urban street soils of the tourist cities of Sochi and Simferopol. The abundance of yeasts in urban street soils was higher than in control soils in the urban park in Sochi, which were examined in both 2019 and 2020. There were no significant differences between yeast numbers in urban street soils. But in the control soils, yeast abundance was significantly higher in 2020. In Maykop, yeast abundance was only slightly higher in urban street soils and control soils in 2020 compared to 2019 (Fig. 1).

The three-way ANOVA using 2019 (Glushakova et al., 2020) and 2020 data showed that soil yeast abundance was most dependent on year of sampling ($F=291.25, p<0.01$), soil group ($F=65.54, p<0.01$), and to a lesser extent location ($F=24.61, p<0.01$).

In most of the studied soils, yeast numbers increased in 2020 compared to 2019 (Fig. 1).

3.3. Yeast diversity

A total of 162 yeast strains were isolated from all soils in this study. These isolates were identified to 30 species (Table 3), 11 ascomycetes and 19 basidiomycetes belonging to three subphyla of Fungi: Agaricomycotina (13), Pucciniomycotina (6), and Saccharomycotina (11). The majority of yeast genera were represented by only one species; yeasts of the genera Cystofilobasidium, Debaryomyces, and Schwanniomyces were represented by two species, and genera Apiotrichum and Solticoccospora by three species. Only two yeast genera, Candida and Rhodotorula, were represented by four species.

During the two years of research, a total of 17 yeast genera were observed in the soils. The number of yeast genera in 2020 was 15; the number of yeast genera in 2019 (Glushakova et al., 2020) was 14. Yeasts from the genera Bullera and Cyberlindnera were not found in 2020; yeasts from the genera Filobasidium, Papillotrema, and Saitozyma were not found in 2019 (Glushakova et al., 2020).

The highest species richness was observed in urban street soils in Sochi (8 species) and in urban park soils and suburban soils in Krasnodar (7 and 6 species, respectively). The average number of yeast species per studied soil sample was 3.6.

Soils in which most yeast species were detected included: urban park soils in Krasnodar (24 species, predominantly Debaryomyces fabryi and Saitozyma podzolica); urban street soils in Sochi (21 species, predominantly Rhodotorula mucilaginosa and Solticoccospora terricola); and suburban soils in Krasnodar (20 species, predominantly D. fabryi and Apiotrichum dulcitum). In 2019 (Glushakova et al., 2020), the soils in which the most yeast species were found included only soils from Krasnodar: urban park soils (14 species, predominantly Schwanniomyces occidentalis and A. porosum); suburban soils (11 species, predominantly Barnettozyma californica and A. porosum); and urban street soils (10 species, predominantly Sch. occidentalis and Tausonia pullulans).

Detection of strains of clinically important (opportunistic) yeasts Candida sake and Meyerozyma guilliermondii distinguished urban soils of Sochi and Simferopol from urban soils of Krasnodar and Maykop. In 2020, the relative abundances of C. sake and Mey. guilliermondii in urban soils of Sochi and Simferopol were significantly lower than in 2019 (Glushakova et al., 2020). The relative abundance of C. sake was 24.47 % and 18.67 %, respectively, compared to 7.66 % in the urban street soil of Simferopol in 2020 (Table 3). The proportion of Mey. guilliermondii in Sochi in 2019 was 15.33 %, in 2020–7.14 %, in Simferopol in 2019–12.74 %, in 2020 only 2.09 %.

Comparison of the studied soils using principal component analysis of relative abundance of yeast species showed that all studied soil yeast complexes differ significantly in 2019 and 2020 (Fig. 2). The data show that the cities are divided into two types: moderately tourist (Maykop and Krasnodar) and tourist (Sochi and Simferopol). The similarity of the yeast species assemblages for Sochi and Simferopol and the differences in the species between 2019 and 2020 data sets are also confirmed by the ordination of data based on the Sørensen index (Fig. 3).
3.4. Sanitary bacteria

Urban soils exposed to significant household waste usually show a marked increase in the abundance of sanitary indicator bacteria in the topsoil (Rhodes and Kator, 1988; van Donsel et al., 1967). In 2020, testing of urban street soils for the presence of clinically significant sanitary microorganisms from Enterobacteriaceae did not reveal an excess of more than 10 CFU/g in any of the soils (Table 4).

4. Discussion

The restructuring of yeast complexes in various components of the urban environment (especially in urban soils) has long been the focus of our research, both taxonomic and ecological alterations.

It is well known and has been demonstrated in numerous studies of soil yeasts in natural biotopes in different geographical zones that autochthonous basidiomycetous yeasts of the genera Apiotrichum, Bullera, Cystofibasidium, Cystobasidium, Filobasidium, Papiliotrema, Rhodotorula, Urban environment (especially in urban soils) has long been the focus of our research, both taxonomic and ecological alterations.

Table 4

| Soil type and city | Number of yeast species | Ascomycota | Basidiomycota | Autochthonous basidiomycetes | E. coli, CFU/g | Ent. faecalis, CFU/g |
|--------------------|-------------------------|------------|---------------|----------------------------|----------------|---------------------|
|                    | 2019  | 2020  | 2019  | 2020  | 2019  | 2020  | 2019  | 2020  | 2019  | 2020  | 2019  | 2020  |
| Urban areas        |       |       |       |       |       |       |       |       |       |       |       |       |
| Sochi              | 7     | 21    | 5     | 4     | 2     | 17    | 2     | 8     | 96 ± 0.37 | 7 ± 0.17 | 38 ± 0.22 | 2 ± 0.26 |
| Simferopol         | 5     | 17    | 4     | 4     | 1     | 13    | 1     | 6     | 68 ± 0.37 | 8 ± 0.32 | 16 ± 0.76 | —         |
| Maykop             | 3     | 9     | 2     | 2     | 1     | 7     | 1     | 5     | 3 ± 0.19 | —         | —         | —         |
| Krasnodar          | 10    | 17    | 5     | 2     | 12    | 3     | 7     | 34 ± 0.19 | 3 ± 0.09 | 14 ± 0.11 | —         |
| Soils of urban parks |       |       |       |       |       |       |       |       |       |       |       |       |
| Sochi              | 4     | 15    | 2     | 5     | 2     | 10    | 2     | 4     | 2 ± 0.11 | —         | —         | —         |
| Simferopol         | 4     | 18    | 2     | 5     | 2     | 13    | 2     | 7     | 6 ± 0.13 | —         | —         | —         |
| Maykop             | ns    | 18    | ns    | 2     | ns    | 16    | ns    | 6     | ns     | —         | ns        | —         |
| Krasnodar          | 14    | 24    | 6     | 5     | 8     | 19    | 3     | 7     | —       | —         | —         | —         |
| Suburban soils      |       |       |       |       |       |       |       |       |       |       |       |       |
| Simferopol         | 2     | 15    | 0     | 3     | 2     | 12    | 2     | 6     | —       | —         | —         | —         |
| Maykop             | 2     | ns    | 0     | ns    | 2     | 2     | ns    | 2     | ns     | ns        | —         | ns        |
| Krasnodar          | 11    | 20    | 3     | 6     | 8     | 14    | 4     | 8     | —       | —         | —         | —         |

“ns” – not studied. “—” – not found.

During a detailed study of urban street and park soils in the southern cities in 2019, we observed four autochthonous basidiomycetous yeast species: A. porosum, S. aeria, S. terrea, and T. pullulans (Glushakova et al., 2020). However, species richness of the core basidiomycetous yeasts in southern urban soils was twice higher after a long period of decline in household waste deposition during the COVID-19 pandemic lockdown (Tables 3 and 4). In addition to the species isolated in 2019, pedobiotic autochthonous yeasts A. dulcita, A. laibachii, S. terricola, and Sait. podzolica were also observed in 2020 (Table 3).

Meanwhile, the number of ascomycetous yeast species observed in 2019 and 2020 did not change or changed insignificantly (Table 4).

Certains Candida species are present in healthy humans but can cause systemic infections in immunocompromised individuals due to ability to adapt to diverse host niches (Eggimann et al., 2003; Sardi et al., 2013). Although C. albicans, C. glabrata and C. parapsilosis are the most common species involved in invasive fungal infections, the incidence of infections due to non-albicans species, including Candida sake (Aggarwal et al., 2008; Arend et al., 2006; Bhattacharjee, 2016; Guclu et al., 2009; Juneja et al., 2011; Palmisano et al., 2011) and Meyerozyma guilliermondii (Farmakiotis and Kontoyiannis, 2017; Parvu et al., 2019; Sardi et al., 2013), are increasing. Recently, it has been shown that environmental strains of Candida sake and Meyerozyma guilliermondii isolated from the Moscow agglomeration can be resistant to widely used antymycotics (Akhapkin et al., 2020a, 2020b; Glushakova et al., 2017). Therefore, decreased proportion of these yeasts in soils should be considered to be a positive development leading to decontamination of soils.

It has been demonstrated that Enterobacteriaceae substantially contributed to soil bacterial communities in urban street soils (Glushakova et al., 2021). The highest abundance of E. coli and Ent. faecalis, which pose major threat to human health, was found in the urban soils of Sochi. Decreased abundances of E. coli and Ent. faecalis in soils sampled in 2020 additionally highlight the resilience of soil communities under reduced pollution by household waste. It cannot be said with certainty whether the lockdown and drop in household waste caused the increase of the soil-borne core species and simultaneous decline of opportunistic ascomycetous species. But previous studies on soil yeasts suggest this possibility (Slavikova and Vadrkertiov, 2003; Vadrkertiov et al., 2017; Yurkov, 2018; Yurkov et al., 2015).

The core community of yeast complexes in various unmanaged soils in Russia is exposed to extremely low anthropogenic impact, for example soddy-podzolic soil in the Central Forest State Nature Biosphere...
Reserve (56°30′N. 32°29′E); dark gray forest soil (Haplic Luvisol (Humic)) in the Kaluzhskie Zaseki Reserve (53°35′N. 35°47′E); and chernozem in Privolzhskaya Forest-Steppe Reserve (53°20′N. 46°51′E) (Glushakova et al., 2017; Maksimova and Chernov, 2004; Yurkov, 2018; Yurkov et al., 2015). These soil communities composed of typical autochthonous basidiomycetous yeast species Saitozyma podzolica, Solicoccyma terricola, S. terrea, S. aeria, Tassonia pullulans, etc. Clinically-relevant yeast species were observed only in dark gray forest soil in the Kaluzhskie Zaseki Reserve in low abundance, 2.1 % for Candida sake and 5.9 % for Meyerozyma guilliermondii.

Thus, an increase in the species diversity of soil core yeast community (mainly basidiomycetes) and a decline in the proportion of clinically-relevant species observed in this study indicated resilience of soil yeast communities in response to reduced deposition of household waste in urban areas. It cannot be excluded that soil yeast communities under different anthropogenic stress predominantly harbor arcomaicytous yeasts and the proportion of basidiomycetous species decreases (Vadkertiov et al., 2017; Yurkov, 2018; Yurkov et al., 2012).

### 5. Conclusion

Clinically significant bacteria are known to respond to household waste (Rhodes and Kator, 1988; van Donsel et al., 1967). The number of these bacteria and the amount of household waste are positively correlated (Ouattara et al., 2014; Pickering et al., 2018). Our data on opportunistic yeast species in urban soils are consistent with those obtained for clinically important bacteria. Of course, we should not yet discount biodiversity resilience, which appears to be sufficiently high at present. Signs of this may yet emerge after the negative effects have receded. We also observed that autochthonous basidiomycetous yeasts can quickly restore their diversity and numbers in soils following environmental stress relief exemplified here by the recent COVID – 19 pandemic lockdown.

### CRediT authorship contribution statement

A.M. Glushakova: Conceptualization, Data curation, Formal analysis, Methodology, Visualization, Writing – original draft. A.V. Kachalnik: Conceptualization, Data curation, Visualization, Writing – original draft. A.B. Umarnova: Funding acquisition, Resources, Supervision. A.E. Ivanov: Resources, Data curation. T.V. Prokof’eva: Resources, Conceptualization, Data curation.

### Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

### Acknowledgements

This research was carried out as a part of the Scientific Project to Lomonosov Moscow State University (No. 121040800174-4).

### Appendix

See Table A1.

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