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CULTURAL STUDY OF MICROMYCETES
FROM DEEP-SEA BOTTOM SEDIMENTS OF THE ADRIATIC SEA

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For the first time, taxonomic composition of fungi and features of structure of their complexes were identified for horizons down to 30 cm below the water–bottom boundary in deep-sea bottom sediments of the Adriatic Sea. A 0–30-cm core of bottom sediments was sampled on 18.10.2007 from aboard the RV "Palagruža" (Croatia) with a column sampler of a QUEST 4000 remotely operated vehicle at a 1,020-m depth (41°43′13″N, 17°34′19″E). The sample of gray silt was cut into 30 sections, each 1 cm thick. Fungi were isolated on Czapek agar and Sabouraud agar, two replicates on each medium, under aerobic conditions, at +18 °C, with chloramphenicol 3% alcohol solution added (1 mL *per* 1 L of a medium). Abundance of fungal colony-forming units (CFU) was calculated *per* 1 g of dry sediment. Sixteen taxa were found; 12 were identified down to the species level, and 4, to the genus level. The taxa were assigned to 13 genera, 8 families, 7 orders, and 5 classes of the phyla Ascomycota and Basidiomycota; sterile mycelium was identified as well. Fungi were not recorded in a horizon of 0–1 cm. Maximum abundance of fungi was 4,300 CFU·g^{-1} dry sediment (a horizon of 6–7 cm). Maximum number of taxa, 6, was revealed for a horizon of 14–15 cm. In the sample studied, 87.5% of fungal species belonged to Ascomycota. Based on literature data, we compiled a list of fungal species known for various sediment horizons of the Atlantic, Indian, and Pacific oceans and the Black Sea. This list was used to calculate two indices, Δ^+ (average taxonomic distinctness index, AvTD) and Λ^+ (variation in taxonomic distinctness index, VarTD), and to plot graphs. The analysis showed the similarity of mycobiota structure of the water basins as evidenced by values of the indices within the 95% confidence interval. Close values of the indices are due to the prevalence of fungal species representing the classes Dothideomycetes, Eurotiomycetes, Sordariomycetes, and Saccharomycetes; those account for 73.13% (the Indian Ocean) to 87.50% (the Black and Adriatic seas) of the species composition.

Keywords: deep-sea bottom sediments, underlying horizons, marine fungi, taxonomic distinctness indices

Micromycetes inhabit various environments – marine, freshwater, and terrestrial ones – and maintain viability under extreme conditions. In a number of works, fungal diversity in deep-sea bottom sediments at depths from several centimeters to 1,884 m below the seabed was studied using culture-dependent and molecular methods [Florio Furno et al., 2022; Jebaraj et al., 2010; Rojas-Jimenez et al., 2020; Rédou et al., 2015; Xu et al., 2018]. As a rule, fungi isolated from different horizons of bottom sediments are well-known cosmopolitans capable of adapting to conditions of deep-sea habitats [Damare et al., 2006; Rédou et al., 2015; Wang et al., 2019; Zhang et al., 2014]. For example, a yeast *Rhodotorula mucilaginosa* (A. Jörgensen) F. C. Harrison, 1927 contains an antifreeze protein that plays a key role in deep-sea adaptation [Rédou et al., 2015; Zhang et al., 2015].

Due to their structural and functional diversity, deep-sea fungi inhabiting marine sediments at depths of more than 1,000 m from the bottom surface have become an important source of industrial, agricultural, and nutraceutical compounds. To date, over 180 biologically active secondary metabolites obtained from deep-sea fungi have been described in literature. These include compounds with antitumor, antimicrobial, antifungal, antiprotozoal, and antiviral activities [Wang et al., 2015].

In sediments of the Mediterranean submarine canyons (Tricase and Crotone) at depths of 200–1,000 m, 1,742 fungal OUT (operational taxonomic units) were found belonging to all currently known fungal phyla. Out of them, representatives of the phylum Ascomycota dominated, with known genera accounting for only 36% [Barone et al., 2018].

The Adriatic Sea is a part of the Mediterranean Sea. This semi-enclosed sea with an area of 138,600 km^2 is located between the Apennine and Balkan peninsulas. The mean depth is 252 m, and the maximum one is 1,230 m. The marine biodiversity of the Adriatic Sea is determined by many biogeographical, ecological, geological, and anthropogenic factors. Over a long period of time, it has undergone significant changes both due to enrichment with endogenous substances and due to anthropogenic load: hydrocarbon production, heavy shipping traffic, intensive fishing and aquaculture, and pollution with plastic and other economic waste [Lipej et al., 2022].

We did not find available data on mycobiota of bottom sediments of the South Adriatic Basin of the Adriatic Sea; so, our studies are relevant. The aim of this work is to identify the taxonomic composition and structural features of mycocomplexes from different horizons of the Adriatic Sea sediments.

MATERIAL AND METHODS

A 0–30-cm core of bottom sediments was sampled on 18.10.2007 from aboard the RV "Palagruža" (Croatia) at a 1,020-m depth (41°43′13″N, 17°34′19″E). Water salinity at this site was 34‰. The sampling was carried out by D. Sc., Prof. S. Gulin. The bottom sediments were sampled in the South Adriatic Basin area with a column sampler of a QUEST 4000 remotely operated vehicle. The sample of gray silt was cut into 30 sections, each 1 cm thick (0–1, 1–2, 2–3… 29–30 cm). These sediment samples were placed in sterile Petri dishes and stored in a freezer at −18 °C for a month until laboratory processing.

Fungi were isolated by sediment suspension seeding on Czapek agar and Sabouraud agar prepared with artificial seawater, two replicates on each medium. Specifically, 1 mL of sediment suspension in a 1 : 10 dilution was added to a Petri dish and filled with molten medium cooled to approximately +45 °C, with chloramphenicol 3% alcohol solution added (1 mL *per* 1 L of a medium) to suppress bacterial growth. Dishes with the material were incubated in a thermostat at +18 °C under aerobic conditions for a month. Pure cultures were isolated from grown colonies and used to identify the fungi; some isolates were identified down to the genus level.

The number of fungal embryos was calculated *per* 1 g of dry sediment by the formula:

$$A = a \times b \times c/d \, ,$$

where A is the mean abundance of fungal colony-forming units *per* 1 g of dry sediment (CFU·g^{-1});

a is the mean number of fungal colonies in Petri dishes (CFU);

b is the dilution from which the inoculation was made;

c is the weight of wet sediment, g;

d is the weight of dry sediment, g [Metody, 1982].

From the sediment sample, two identical samples were made. One of them was dried to a constant weight at +105 °C in a drying oven.

Micromycetes were identified by morphological and cultural features according to [Atlas of Clinical Fungi, 2000; Bilai, Koval, 1988]. All fungal names were checked in the electronic database Index Fungorum [2024].

The data were processed using MS Office Excel and a software package PRIMER 5.2.8. The species similarity of mycocomplexes was calculated using the Bray–Curtis coefficient based on the presence/absence of a taxon according to its frequency of occurrence relative to the total number of samples (Similarity function). The Shannon index of mycocomplexes by sediment horizons was determined based on the number of taxa and their abundance (DIVERSE).

Based on literature data, the authors compiled a list of marine micromycete species isolated from different horizons of bottom sediments of the Indian Ocean (down to 4.7 m) [Damare et al., 2006; Raghukumar, Raghukumar, 1998; Raghukumar et al., 2010; Xu et al., 2018; Zhang et al., 2014], the Pacific Ocean (down to 1,884 m) [Keeler, 2021; Rédou et al., 2015; Xu et al., 2014], the Atlantic Ocean (down to 5 m) [Keeler, 2021], and the Black Sea (down to 0.40 m) [Kopytina et al., 2024; Zaitsev, Polikarpov, 2008]. In the absence of species identification, but the genus of a micromycete indicated by other author, the name of the genus was included in the list with a designation sp. 1. The list consists of 182 names of taxa isolated by seeding or identified by genetic analysis techniques (accuracy is up to 98%).

The list was used to calculate indices of the taxonomic composition of fungal complexes in order to plot graphs of taxonomic indices for each considered area. The indices were determined based on data on the presence or absence of a species taking into account family relationships between species (from species to phylum) and the number of species in each community. Δ^+ is the average taxonomic distinctness index, AvTD; Λ^+ is the variation in taxonomic distinctness index, VarTD. Those show the similarity/dissimilarity in the species structure of mycocomplexes (TAXDTEST). The graphs of these indices provide a statistical justification for the structure relationship within the community. Specifically, Δ^+ is the average length of links in a series of species of the taxonomic tree, and this index reflects vertical links (number of families, orders, *etc.*). Λ^+ is the dispersion of paired lengths of related links, and this index reproduces the horizontal proportion of the community (the number of taxa at each level of the hierarchical tree) [Clarke et al., 2014].

The percentage of the abundance of fungi from different phyla was calculated as the ratio of the total abundance of taxa within the phylum to the total abundance of sediments isolated from samples. The frequency of occurrence of taxa was determined by taking the number of samples (30) as 100%.

RESULTS

For the first time, deep-sea bottom sediments below the water–bottom boundary down to 30 cm were studied layer by layer in the Adriatic Sea. Twelve fungal taxa were identified down to the species level, and four, down to the genus level. Micromycetes were assigned to the phyla Ascomycota and Basidiomycota. Sterile mycelium was also isolated. Most species were grouped in the phylum Ascomycota; in terms of the number of representatives, its classes Sordariomycetes (5 species), Dothideomycetes (4), and Eurotiomycetes (4) were the prevailing ones.

In the sediments studied, all species of micromycetes were represented by terrestrial cosmopolitan species.

The frequency of occurrence of taxa varied from 3.3% (*Alternaria tenuissima* and *Cladosporium sphaerospermum*) to 56.7% (*Metschnikowia* sp. 1). In 18 sediment horizons, 1–2 taxa were identified. Information on the systematic affiliation of micromycetes, their distribution in sediment horizons, and abundance is provided in Table 1.

Table 1. Species composition, abundance, and distribution of fungi in sediments of the Adriatic Sea (0–30-cm layers)

Species	Sediment horizon, cm	Abundance, CFU·g^{-1} dry sediment (min–max)
Phylum Ascomycota, class Dothideomycetes		
Alternaria chartarum Preuss, 1851	8–9, 11–12, 14–15, 24–25	30–180
Al. tenuissima (Kunze) Wiltshire, 1933	18–19	90
Cladosporium sphaerospermum Penzig, 1882	11–12	30
Stemphylium sarciniforme (Cavara) Wiltshire, 1938	4–5, 11–12, 13–14, 14–15, 20–21, 24–25	35–100
Class Eurotiomycetes		
Aspergillus flavus Link, 1809	17–18, 27–28	40–100
As. fumigatus Fresenius, 1863	16–17, 19–20	40–80
Penicillium chrysogenum Thom, 1910	9–10, 14–15, 15–16, 17–18, 24–25	30–90
Penicillium sp. 1	5–6, 6–7, 17–18, 27–28	30–440
Class Sordariomycetes		
Acremonium sp. 1	20–21, 21–22, 28–29, 29–30	16–96
Amesia atrobrunnea (L. M. Ames) X. Wei Wang et Samson, 2016	6–7, 13–14, 15–16	30–487
Botryotrichum murorum (Corda) X. Wei Wang et Samson, 2016	4–5, 5–6, 6–7, 13–14	30–792
Chaetomium elongatum Czerepanova, 1962	6–7, 13–14	80–860
Stachybotrys chartarum (Ehrenberg) S. Hughes, 1958	1–2, 14–15, 20–21	30–41
Class Saccharomycetes		
Metschnikowia sp. 1	2–3, 3–4, 6–7, 8–9, 10–11, 11–12, 12–13, 14–15, 17–18, 18–19, 19–20, 20–21, 22–23, 23–24, 25–26, 27–28, 29–30	90–1,720
Phylum Basidiomycota, class Tremellomycetes		
Trichosporon asteroides (Rischin) M. Ota, 1926	9–10, 26–27	60–90
Class Malasseziomycetes		
Malassezia sp. 1	1–2, 5–6, 16–17, 21–22, 28–29	150–300
Unidentified taxa		
Mycelia sterilia 1	2–3, 7–8, 14–15	30–70
Mycelia sterilia 2	25–26	240

Fungi were not found in a horizon of 0–1 cm. The maximum number of taxa, 6, was revealed in a layer of 14–15 cm. Only sterile mycelium was recorded in a layer of 7–8 cm. The similarity of the fungal species composition by horizons varied from 0.0 (no common taxa were registered) to 100.0% (1 species was identified, *Metschnikowia* sp. 1) (sediment horizons of 3–4, 10–11, 12–13, 22–23, and 23–24 cm).

The abundance of fungi fluctuated from 0 (a layer of 0–1 cm) to 4,300 CFU·g^{-1} dry sediment (a layer of 6–7 cm). The Shannon diversity index value was 0 to 1.55. H'(log$_e$) = 0 in case of isolation of 1 species or absence of species (7 sediment horizons) (Table 2).

Table 2. Indicators of fungi abundance and taxonomic diversity in deep-sea sediment horizons of the Adriatic Sea (0–30 cm)

Sediment horizon, cm	Number of taxa	Abundance, CFU·g^{-1} dry sediment	Shannon index, H'(log$_e$)
0–1	0	0	0.000
1–2	2	330	0.305
2–3	2	240	0.604
3–4	1	160	0.000
4–5	2	200	0.693
5–6	3	420	0.759
6–7	5	4,300	1.480
7–8	1	30	0.000
8–9	2	300	0.637
9–10	2	90	0.637
10–11	1	400	0.000
11–12	4	570	1.094
12–13	1	100	0.000
13–14	4	240	1.330
14–15	6	380	1.550
15–16	2	120	0.562
16–17	2	220	0.474
17–18	4	400	1.321
18–19	2	220	0.677
19–20	2	420	0.451
20–21	4	574	0.895
21–22	2	178	0.416
22–23	1	480	0.000
23–24	1	360	0.000
24–25	3	120	1.040
25–26	2	640	0.662
26–27	2	160	0.685
27–28	3	190	0.910
28–29	2	250	0.673
29–30	2	176	0.305

In sediment samples, representatives of the phylum Ascomycota dominated in terms of the number of species and abundance: 88.9 and 89.64%, respectively.

No pattern was revealed in distribution of the number of fungal taxa and abundance across sediment horizons. This can be explained by the small number of samples studied and certain limitations in isolating microscopic fungi with culture-dependent methods applied.

DISCUSSION

Many studies on deep-sea sediments of the World Ocean provide taxonomic ranks at the level of families, orders, classes, and phyla; in some cases, only a genus of fungi is indicated. This creates difficulties when comparing the species composition in water bodies. We compiled a list of 182 fungal species assigned to 93 genera, 56 families, 31 orders, and 13 classes from the phyla Ascomycota, Basidiomycota, and Mucoromycota. The indicators of taxonomic richness and diversity of fungal complexes in underlying sediment horizons of the Adriatic and Black seas and the Atlantic, Indian, and Pacific oceans are presented in Table 3.

Table 3. Indices of taxonomic richness and diversity of fungal complexes from deep-sea sediments of the Adriatic and Black seas and Atlantic, Indian, and Pacific oceans (g, genus; f, family; s, species)

Water body	Number of taxa					Proportions		
	species	genus	family	order	class	g/f	s/f	s/g
Phylum Ascomycota								
The Adriatic Sea	15	12	8	6	4	1.50	1.76	1.25
The Black Sea	21	10	8	7	4	1.25	2.62	2.1
The Atlantic Ocean	34	15	12	11	5	1.25	2.83	2.27
The Indian Ocean	68	37	23	12	6	1.61	2.96	1.84
The Pacific Ocean	63	39	24	15	6	1.63	2.63	1.62
Phylum Basidiomycota								
The Adriatic Sea	2	2	2	2	2	1.00	1.00	1.00
The Black Sea	2	2	2	2	2	1.00	1.00	1.00
The Atlantic Ocean	4	4	3	3	4	1.33	1.33	1.00
The Indian Ocean	18	15	10	8	6	1.50	1.80	1.20
The Pacific Ocean	16	12	8	7	3	1.50	2.00	1.33
Phylum Mucoromycota								
The Adriatic Sea	0	0	0	0	0	0	0	0
The Black Sea	1	1	1	1	1	1.00	1.00	1.00
The Atlantic Ocean	0	0	0	0	0	0	0	0
The Indian Ocean	0	0	0	0	0	0	0	0
The Pacific Ocean	1	1	1	1	1	1.00	1.00	1.00

The similarity of the species composition of fungi isolated from sediments of the Adriatic Sea and the Indian Ocean is 5.8% (common taxa are *Penicillium chrysogenum*, *Cladosporium sphaerospermum*, and yeasts of the genus *Malassezia*); the Atlantic Ocean, 10.9% (*Alternaria tenuissima*, *C. sphaerospermum*, and *P. chrysogenum*); the Pacific Ocean, 18.56% (*Aspergillus fumigatus*, *As. flavus*, *C. sphaerospermum*, *P. chrysogenum*, *Stachybotrys chartarum*, and species of the genera *Acremonium*, *Metschnikowia*, and *Meyerozyma*); and the Black Sea, 34.2% (*Al. tenuissima*, *As. fumigatus*, *Botryotrichum murorum*, *C. sphaerospermum*, *S. chartarum*, and yeasts of the genera *Metschnikowia* and *Malassezia*). Seven species of micromycetes and representatives of four genera isolated from bottom sediment samples of the Adriatic Sea were found in other areas of the World Ocean as well [Edgcomb et al., 2002; Kiel Reese et al., 2021; Kopytina et al., 2024; Pachiadaki et al., 2016; Rojas-Jimenez et al., 2020; Rédou et al., 2014, 2015; Xu et al., 2018, 2019; Zhang et al., 2014; Zhou et al., 2021].

Deep-sea sediments of the Black Sea are contaminated with hydrogen sulfide. However, some species of yeast and mycelial fungi easily adapt to permanent or temporary anoxia using oxygen from the material they have contaminated, as they are facultative anaerobes [Kurakov et al., 2008, 2011].

The graphs of the taxonomic indices Δ^+ and Λ^+ reflect the general pattern of the vertical and horizontal distribution of lower taxa (species and genus) by higher taxonomic ranks in five water basins (Fig. 1A, B).
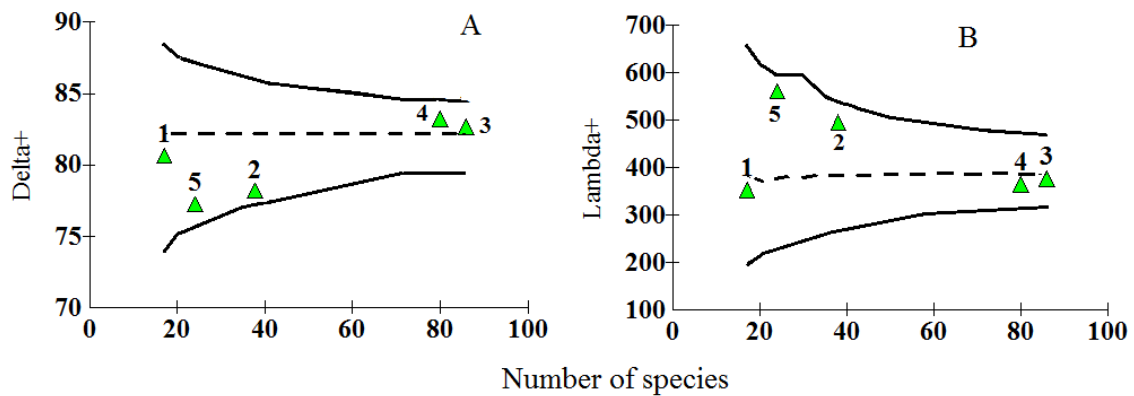
Fig. 1. Values of taxonomic indices Δ^+ (A) and Λ^+ (B) for fungal complexes in underlying sediment horizons in different water bodies calculated according to the general list of species from these water bodies (1, the Adriatic Sea; 2, the Atlantic Ocean; 3, the Indian Ocean; 4, the Pacific Ocean; 5, the Black Sea). Solid lines denote the 95% probability funnel; dashed line denotes the mean calculated value of the index

In Fig. 1A, the values of Δ^+ are included in the probability funnel. Therefore, the structures of mycocomplexes are similar and do not differ statistically significantly. Distribution of lower taxa by higher ranks corresponds to an average one, as evidenced by the index values (77.23–82.66). Despite the fact that in the water basins analyzed, different numbers of higher taxa were found (2–3 phyla and 7–12 classes), the overall structure remained proportional, and similar index values were governed by the presence of fungal species of the classes Dothideomycetes, Eurotiomycetes, Sordariomycetes, Saccharomycetes, and Malasseziomycetes. Those accounted for 71.25% (the Pacific Ocean) to 94.12% (the Adriatic Sea) of the species composition.

In Fig. 1B, the values of Λ^+ are within the confidence funnel of the calculated average expected value. Consequently, in complexes of underlying layers of deep-sea bottom sediments of the Adriatic and Black seas, as well as the Atlantic, Pacific, and Indian oceans, a high similarity of the taxonomic structure was revealed (with species distribution by higher taxonomic ranks taken into account). This fact is confirmed by s/g proportions (see Table 3): the values vary within 1.21–2.00.

Studies carried out using culture-dependent and transcriptomic methods have shown as follows. In underlying sediments of the World Ocean, fungi from the phyla Ascomycota and Basidiomycota dominate: 43–80 and 3–20%, respectively. Unidentified fungal species account for 2.4–64%; representatives of the phylum Zygomycota, 0.55–1.5%; and representatives of the phylum Chytridiomycota, 0.8% [Barone et al., 2018; Florio Furno et al., 2022; Jebaraj et al., 2010; Rojas-Jimenez et al., 2020; Vargas-Gastélum, Riquelme, 2020; Xu et al., 2018, 2019; Zhang et al., 2016]. Taxa from the classes Eurotiomycetes, Sordariomycetes, Dothideomycetes, and Saccharomycetes (Ascomycota), as well as Tremellomycetes and Malasseziomycetes (Basidiomycota), often occur in various horizons of deep-sea sediments. Representatives of the above-listed classes were isolated in sediment samples from the Adriatic Sea. In this study, 87.5% of the species belonged to the phylum Ascomycota, and 12.5%, to the phylum Basidiomycota. The similarity of mycocomplexes is confirmed by the graphs of the taxonomic indices.

Species of the genera *Penicillium* and *Aspergillus* prevail in water and bottom sediments of the Adriatic Sea; *Cladosporium*, *Alternaria*, and *Chaetomium* representatives are found there as well [Muntañola-Cvetković, Ristanović, 1980; Ristanović et al., 1975]. It suggests that fungi of these genera are typical inhabitants of the Adriatic Sea.

Conclusion. In the Adriatic Sea sediment core sampled down to 30 cm, 16 fungal taxa from the phyla Ascomycota and Basidiomycota were identified; Mycelia sterilia was also found. In terms of the number of representatives, three classes of the phylum Ascomycota dominated: Sordariomycetes (5 species), Dothideomycetes (4), and Eurotiomycetes (4). The results obtained are consistent with literature data on micromycetes from deep-sea sediments, *inter alia* from underlying horizons of other areas of the World Ocean. Analysis of the taxonomic structure of mycocomplexes from underlying layers of deep-sea sediments of the Adriatic and Black seas, as well as the Atlantic, Pacific, and Indian oceans, was performed applying the taxonomic indices Δ^+ and Λ^+. It showed the similarity of their structure, as evidenced by the values of the indices included in the 95% confidence funnel. Similar values of the indices are governed by the dominance of fungal species from the classes Dothideomycetes, Eurotiomycetes, Sordariomycetes, and Saccharomycetes accounting for 73.13% (the Indian Ocean) to 87.50% of the species composition (the Black and Adriatic seas).

Deep-sea micromycetes are not investigated properly. So, further detailed and coordinated studies of their biological diversity, quantitative characteristics, ecological role, and adaptive mechanisms to different habitat conditions in various areas of the World Ocean are required.

REFERENCES

1. Bilai V. I., Koval' E. Z. *Aspergilly* : opredelitel'. Kyiv : Naukova dumka, 1988, 204 p. (in Russ.)

2. Kopytina N., Bocharova E., Gulina L. New findings of cultured micromycetes in the deep-sea sediments of the Black Sea. *Trudy Instituta biologii vnutrennikh vod im. I. D. Papanina RAN*, 2024, no. 105 (108), pp. 45–53. (in Russ.). https://doi.org/10.47021/0320-3557-2024-45-53

3. Kurakov A. V., Lavrent'ev R. B., Nechitailo T. Yu., Golyshin P. N., Zvyagintsev D. G. Diversity of facultatively anaerobic microscopic mycelial fungi in soils. *Mikrobiologiya*, 2008, vol. 77, no. 1, pp. 103–112. (in Russ.)

4. Kurakov A. V., Khidirov K. S., Sadykova V. S., Zvyagintsev D. G. Anaerobic growth ability and alcohol fermentation activity of microscopic fungi.

Prikladnaya biokhimiya i mikrobiologiya, 2011, vol. 47, no. 2, pp. 187–193. (in Russ.)

5. *Metody eksperimental'noi mikologii* : spravochnik. Kyiv : Naukova dumka, 1982, 550 p. (in Russ.)

6. *Atlas of Clinical Fungi.* 2nd ed. / G. S. de Hoog, J. Guarro, J. Gene, M. J. Figueras (Eds). Utrecht : Centraalbureau voor Schimmelcultures, 2000, 1126 p.

7. Barone G., Rastelli E., Corinaldesi C., Tangherlini M., Danovaro R., Dell'Anno A. Benthic deep-sea fungi in submarine canyons of the Mediterranean Sea. *Progress in Oceanography*, 2018, vol. 168, pp. 57–64. https://doi.org/10.1016/j.pocean.2018.09.011

8. Clarke K. R., Gorley R. N., Somerfield P. J., Warwick R. M. *Change in Marine Communities: An Approach to Statistical Analysis and Interpretation.* 3rd ed. Plymouth : PRIMER-E, 2014, 260 p.

9. Damare S., Raghukumar C., Raghukumar S. Fungi in deep-sea sediments of the Central Indian Basin. *Deep Sea Research Part I: Oceanographic Research Papers*, 2006, vol. 53, iss. 1, pp. 14–27. https://doi.org/10.1016/j.dsr.2005.09.005

10. Edgcomb V. P., Kysela D. T., Teske A., de Vera Gomez A., Sogin M. L. Benthic eukaryotic diversity in the Guaymas Basin hydrothermal vent environment. *Proceedings of the National Academy of Sciences*, 2002, vol. 99, no. 11, pp. 7658–7662. https://doi.org/10.1073/pnas.062186399

11. Florio Furno M., Poli A., Ferrero D., Tardelli F., Manzini C., Oliva M., Pretti C., Campani T., Casini S., Fossi M. C., Varese G. C., Prigione V. The culturable mycobiota of sediments and associated microplastics: From a harbor to a marine protected area, a comparative study. *Journal of Fungi*, 2022, vol. 8, iss. 9, art. no. 927 (18 p.). https://doi.org/10.3390/jof8090927

12. *Index Fungorum* / Royal Botanic Gardens, Kew : [site]. URL: https://www.kew.org/science [accessed: 23.04.2024].

13. Jebaraj C. S., Raghukumar C., Behnke A., Stoeck T. Fungal diversity in oxygen-depleted regions of the Arabian Sea revealed by targeted environmental sequencing combined with cultivation. *FEMS Microbiology Ecology*, 2010, vol. 71, iss. 3,

pp. 399–412. https://doi.org/10.1111/j.1574-6941.2009.00804.x

14. Keeler E., Burgaud G., Teske A., Beaudoin D., Mehiri M., Dayras M., Cassand J., Edgcomb V. Deep-sea hydrothermal vent sediments reveal diverse fungi with antibacterial activities. *FEMS Microbiology Ecology*, 2021, vol. 97, iss. 8, art. no. fiab103 (20 p.). https://doi.org/10.1093/femsec/fiab103

15. Kiel Reese B., Sobol M. S., Bowles M. W., Hinrichs K.-U. Redefining the subsurface biosphere: Characterization of fungi isolated from energy-limited marine deep subsurface sediment. *Frontiers in Fungal Biology*, 2021, vol. 2, art. no. 727543 (19 p.). https://doi.org/10.3389/ffunb.2021.727543

16. Lipej L., Kovačić M., Dulčić J. An analysis of Adriatic ichthyofauna–ecology, zoogeography, and conservation status. *Fishes*, 2022, vol. 7, iss. 2, art. no. 58 (29 p.). https://doi.org/10.3390/fishes7020058

17. Muntañola-Cvetković M., Ristanović B. A mycological survey of the South Adriatic Sea. *Journal of Experimental Marine Biology and Ecology*, 1980, vol. 43, iss. 3, pp. 193–206. https://doi.org/10.1016/0022-0981(80)90047-7

18. Pachiadaki M. G., Rédou V., Beaudoin D. J., Burgaud G., Edgcomb V. P. Fungal and prokaryotic activities in the marine subsurface biosphere at Peru Margin and Canterbury Basin inferred from RNA-based analyses and microscopy. *Frontiers in Microbiology*, 2016, vol. 7, art. no. 846 (16 p.). https://doi.org/10.3389/fmicb.2016.00846

19. Raghukumar C., Damare S. R., Singh P. A review on deep-sea fungi: Occurrence, diversity and adaptations. *Botanica Marina*, 2010, vol. 53, no. 6, pp. 479–492. https://doi.org/10.1515/bot.2010.076

20. Raghukumar C., Raghukumar S. Barotolerance of fungi isolated from deep-sea sediments of the Indian Ocean. *Aquatic Microbial Ecology*, 1998, vol. 15, no. 2, pp. 153–163. https://doi.org/10.3354/ame015153

21. Ristanović B., Muntañola-Cvetković M., Munjko I. Phenoldegrading fungi from South Adriatic Sea and Lake Skadar. *European*

Journal of Applied Microbiology and Biotechnology, 1975, vol. 1, iss. 4, pp. 313–322. https://doi.org/10.1007/BF01382690

22. Rojas-Jimenez K., Grossart H.-P., Cordes E., Cortés J. Fungal communities in sediments along a depth gradient in the Eastern Tropical Pacific. *Frontiers in Microbiology*, 2020, vol. 11, art. no. 575207 (9 p.). https://doi.org/10.3389/fmicb.2020.575207

23. Rédou V., Ciobanu M. C., Pachiadaki M. G., Edgcomb V., Alain K., Barbier G., Burgaud G. In-depth analyses of deep subsurface sediments using 454-pyrosequencing reveals a reservoir of buried fungal communities at record-breaking depths. *FEMS Microbiology Ecology*, 2014, vol. 90, iss. 3, pp. 908–921. https://doi.org/10.1111/1574-6941.12447

24. Rédou V., Navarri M., Meslet-Cladière L., Barbier G., Burgaud G. Species richness and adaptation of marine fungi from deep-subseafloor sediments. *Applied and Environmental Microbiology*, 2015, vol. 81, no. 10, pp. 3571–3583. https://doi.org/10.1128/AEM.04064-14

25. Vargas-Gastélum L., Riquelme M. The mycobiota of the deep sea: What omics can offer. *Life*, 2020, vol. 10, iss. 11, art. no. 292 (18 p.). https://doi.org/10.3390/life10110292

26. Wang Y. T., Xue Y. R., Liu C. H. A brief review of bioactive metabolites derived from deep-sea fungi. *Marine Drugs*, 2015, vol. 13, iss. 8, pp. 4594–4616. https://doi.org/10.3390/md13084594

27. Wang Z.-P., Liu Z.-Z., Wang Y.-L., Bi W.-H., Liu L., Wang H.-Y., Zheng Y., Zhang L.-L., Hu S.-G., Xu S.-S., Zhang P. Fungal community analysis in seawater of the Mariana Trench as estimated by Illumina HiSeq. *RSC Advances*, 2019, vol. 9, no. 12, pp. 6956–6964. https://doi.org/10.1039/c8ra10142f

28. Xu W., Gao Y., Gong L., Li M., Pang K.-L., Luo Z.-H. Fungal diversity in the deep-sea hadal sediments of the Yap Trench by cultivation and high throughput sequencing methods based on ITS rRNA gene. *Deep Sea Research Part I: Oceanographic*

Research Papers, 2019, vol. 145, pp. 125–136. https://doi.org/10.1016/j.dsr.2019.02.001

29. Xu W., Gong L., Pang K.-L., Luo Z.-H. Fungal diversity in deep-sea sediments of a hydrothermal vent system in the Southwest Indian Ridge. *Deep Sea Research Part I: Oceanographic Research Papers*, 2018, vol. 131, pp. 16–26. https://doi.org/10.1016/j.dsr.2017.11.001

30. Xu W., Pang K.-L., Luo Z.-H. High fungal diversity and abundance recovered in the deep-sea sediments of the Pacific Ocean. *Microbial Ecology*, 2014, vol. 68, pp. 688–698. https://doi.org/10.1007/s00248-014-0448-8

31. Zaitsev Y. P., Polikarpov G. G. Recently discovered new biospheric pelocontour function in the Black Sea reductive bathyal zone. *Journal of the Black Sea / Mediterranean Environment*, 2008, vol. 14, no. 3, pp. 151–165.

32. Zhang T., Wang N. F., Zhang Y. Q., Liu H. Y., Yu L. Y. Diversity and distribution of fungal communities in the marine sediments of Kongsfjorden, Svalbard (High Arctic). *Scientific Reports*, 2015, vol. 5, art. no. 14524 (11 p.). https://doi.org/10.1038/srep14524

33. Zhang X., Tang G., Xu X., Nong X., Qi S.-H. Insights into deep-sea sediment fungal communities from the East Indian Ocean using targeted environmental sequencing combined with traditional cultivation. *PLoS One*, 2014, vol. 9, iss. 10, art. no. e109118 (11 p.). https://doi.org/10.1371/journal.pone.0109118

34. Zhang X.-Y., Wang G.-H., Xu X.-Y., Nong X.-H., Wang J., Amin M., Qi S.-H. Exploring fungal diversity in deep-sea sediments from Okinawa Trough using high-throughput Illumina sequencing. *Deep Sea Research Part I: Oceanographic Research Papers*, 2016, vol. 116, pp. 99–105. https://doi.org/10.1016/j.dsr.2016.08.004

35. Zhou Y., Gao X., Shi C., Li M., Jia W., Shao Z., Yan P. Diversity and antiaflatoxigenic activities of culturable filamentous fungi from deep-sea sediments of the South Atlantic Ocean. *Mycobiology*, 2021, vol. 49, iss. 2, pp. 151–160. https://doi.org/10.1080/12298093.2020.1871175

КУЛЬТУРАЛЬНОЕ ИССЛЕДОВАНИЕ МИКРОМИЦЕТОВ ИЗ ГЛУБОКОВОДНЫХ ДОННЫХ ОТЛОЖЕНИЙ АДРИАТИЧЕСКОГО МОРЯ

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Впервые выявлены таксономический состав и особенности структуры комплексов грибов с горизонтов до 30 см ниже границы вода — дно в глубоководных донных отложениях Адриатического моря. Керн донных отложений 0–30 см был взят 18.10.2007 с борта НИС Palagruža (Хорватия) с помощью колончатого пробоотборника подводного телеробота QUEST 4000 на глубине 1020 м в точке с координатами 41°43′13″N, 17°34′19″E. Пробу серого ила разрезали на 30 частей толщиной в 1 см. Грибы выделяли на агаризованные среды Чапека и Сабуро, по две повторности на каждой среде, в аэробных условиях, при температуре +18 °C, с добавлением 3%-ного спиртового раствора хлорамфеникола (1 мл·л$^{-1}$ среды). Количество грибных колониеобразующих единиц (КОЕ) рассчитывали на 1 г сухого осадка. Обнаружили 16 таксонов; 12 определили до вида, 4 — до рода. Таксоны отнесены к 13 родам, 8 семействам, 7 порядкам, 5 классам отделов Ascomycota и Basidiomycota; также выделен стерильный мицелий. В горизонте осадка 0–1 см грибы не выявлены. Максимальная численность грибов составляла 4300 КОЕ·г$^{-1}$ сухого осадка (горизонт 6–7 см). Максимальное количество таксонов, 6, обнаружено в горизонте 14–15 см. В этом исследовании к отделу Ascomycota относились 87,5 % видов. По литературным данным составлены списки видов грибов из подстилающих горизонтов осадков Атлантического, Индийского и Тихого океанов и Чёрного моря, на основании которых вычислены значения таксономических индексов Δ^+ (average taxonomic distinctness index, AvTD) и Λ^+ (variation in taxonomic distinctness index, VarTD) и построены их графики. Анализ показал общую структуру микобиот водоёмов, о чём свидетельствуют значения индексов, входящие в 95%-ную доверительную воронку. Близкие значения индексов обусловлены доминированием видов грибов из классов Dothideomycetes, Eurotiomycetes, Sordariomycetes и Saccharomycetes, составляющих от 73,13 % (Индийский океан) до 87,50 (Чёрное и Адриатическое моря) от видового состава.

Ключевые слова: глубоководные донные отложения, подстилающие слои, морские грибы, таксономические индексы