

SUPPLEMENTARY MATERIAL

Microbial life in nutrient depleted aquatic habitats - results of cultivation and molecular studies

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Table S1. Archaeal species richness and diversity indices calculated from 16S rRNA gene amplicon sequencing data.

Sample	nseqs	sobs	ace	ace_lci	ace_hci	chao	chao_lci
Ciprián	2242	275	282.2016	277.9844	292.3784	276.663	275.3581
Dandár_1	2242	37	44.96296	39.34455	64.04514	52	40.50249
Dandár_2	2242	44	104.0403	76.60437	154.5631	82.5	57.06271
Dandár_3	2242	60	74.04633	65.53356	95.65509	81.85714	66.98085
Dandár_4	2242	68	75.88787	70.84288	89.88569	74.06667	69.68132
Szentendre_1	2242	872	1583.405	1451.704	1745.026	1408.361	1292.972
Szentendre_2	2242	814	1956.697	1808.565	2126.891	1394.603	1266.37
Szentendre_3	2242	790	2176.337	2003.755	2373.458	1502.796	1344.547
Szent Flórián_1	2242	194	248.6622	226.0897	287.1127	240.6667	217.9046
Szent Flórián_2	2242	191	251.9538	227.258	293.4701	256.3571	225.1055
Szent_Flórián_3	2242	189	246.731	223.4361	285.7843	240.6563	215.7164
Tatabánya	2242	685	1585.752	1458.691	1733.679	1147.697	1035.679

Sample	chao_hci	invsimpson	invsimpson_lci	invsimpson_hci	shannon	shannon_lci
Ciprián	282.7237	32.03878	28.85436	36.01328	4.562843	4.494772
Dandár_1	101.2401	2.32628	2.20938	2.456241	1.477513	1.411318
Dandár_2	157.4718	2.994928	2.881867	3.117223	1.481256	1.425879
Dandár_3	128.435	2.768636	2.656855	2.890237	1.594868	1.524744
Dandár_4	89.89016	3.022236	2.908833	3.144839	1.670845	1.600057
Szentendre_1	1555.38	217.2022	188.615	256.003	6.184313	6.128952
Szentendre_2	1559.187	113.8012	97.74928	136.1608	5.940844	5.876292
Szentendre_3	1706.204	58.00284	50.50723	68.11096	5.668637	5.591798
Szent_Flórián_1	285.103	36.46891	34.00308	39.32034	4.202421	4.146212
Szent_Flórián_2	316.2455	29.56005	27.39909	32.09107	4.073393	4.013766
Szent_Flórián_3	288.8776	30.3057	28.46131	32.40571	4.019129	3.960142
Tatabánya	1295.498	53.55963	46.40783	63.31731	5.525372	5.450833

Table S2. Bacterial species richness and diversity indices calculated from 16S rRNA gene amplicon sequencing.

Sample	nseqs	sobs	ace	ace_lci	ace_hci	chao	chao_lci
Ciprián	6670	424	1827.383	1586.973	2117.491	994.8571	835.9699
Dandár_1	6670	256	258.0841	256.4938	264.7962	256.1389	256.0075
Dandár_2	6670	306	352.4726	334.5715	381.5892	353.0426	331.489
Dandár_3	6670	400	437.9379	423.2789	461.8279	426.3919	413.7966
Dandár_4	6670	338	378.0644	362.405	403.7717	373.5091	356.8245
Szentendre_1	6670	3985	6489.51	6232.384	6776.055	5841.957	5650.409
Szentendre_2	6670	3674	7771.324	7366.765	8220.205	6558.875	6255.696
Szentendre_3	6670	3145	5910.811	5620.837	6234.748	5182.722	4944.693
Szent_Flórián_1	6670	836	1213.576	1136.461	1310.484	1117.783	1047.51
Szent_Flórián_2	6670	1331	3263.716	3066.964	3482.769	2233.4	2070.2
Szent_Flórián_3	6670	780	1076.424	1012.773	1157.481	1015.291	953.8627
Tatabánya	6670	866	3324.817	3049.071	3635.393	1834.085	1633.085

Sample	chao_hci	invsimpson	invsimpson_lci	invsimpson_hci	shannon	shannon_lci	shannon_hci
Ciprián	1215.023	2.439123	2.360241	2.52346	1.95568	1.898044	2.013316
Dandár_1	258.5795	8.232099	7.784089	8.734828	3.555161	3.504287	3.606036
Dandár_2	392.8217	12.20819	11.61044	12.87084	3.699926	3.65208	3.747773
Dandár_3	450.4859	28.68855	26.71251	30.98031	4.590216	4.548374	4.632059
Dandár_4	404.9816	15.59544	14.73188	16.56656	4.012899	3.965906	4.059891
Szentendre_1	6055.536	3708.089	3344.482	4160.4	8.111344	8.090392	8.132296
Szentendre_2	6897.658	1879.425	1706.747	2090.977	7.886787	7.860847	7.912728
Szentendre_3	5452.232	637.9576	559.6759	741.6988	7.57154	7.539546	7.603533
Szent_Flórián_1	1211.404	73.96619	69.7471	78.72857	5.344894	5.303592	5.386195
Szent_Flórián_2	2432.632	69.23972	63.95926	75.47056	5.717254	5.670162	5.764346
Szent_Flórián_3	1098.422	31.57442	29.47941	33.98997	4.925548	4.876343	4.974753

Tatabánya	2087.755	9.023826	8.704551	9.367415	3.556589	3.494184	3.618995
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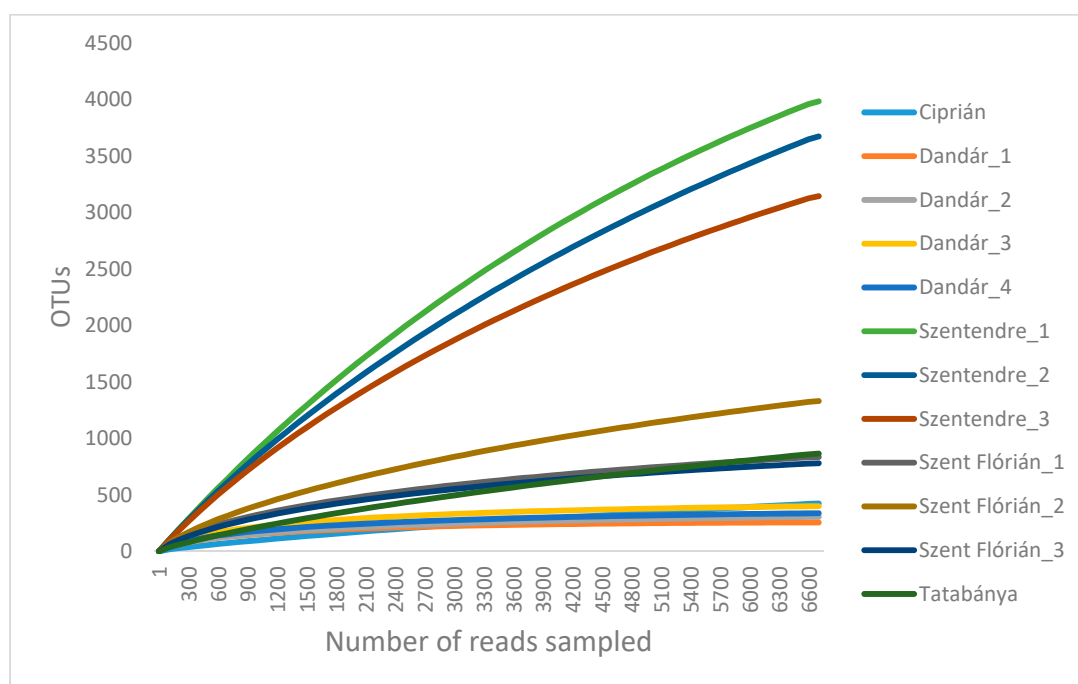


Figure S1. Rarefaction curves of bacterial OTUs of the samples based on 16S rRNA gene amplicon sequencing

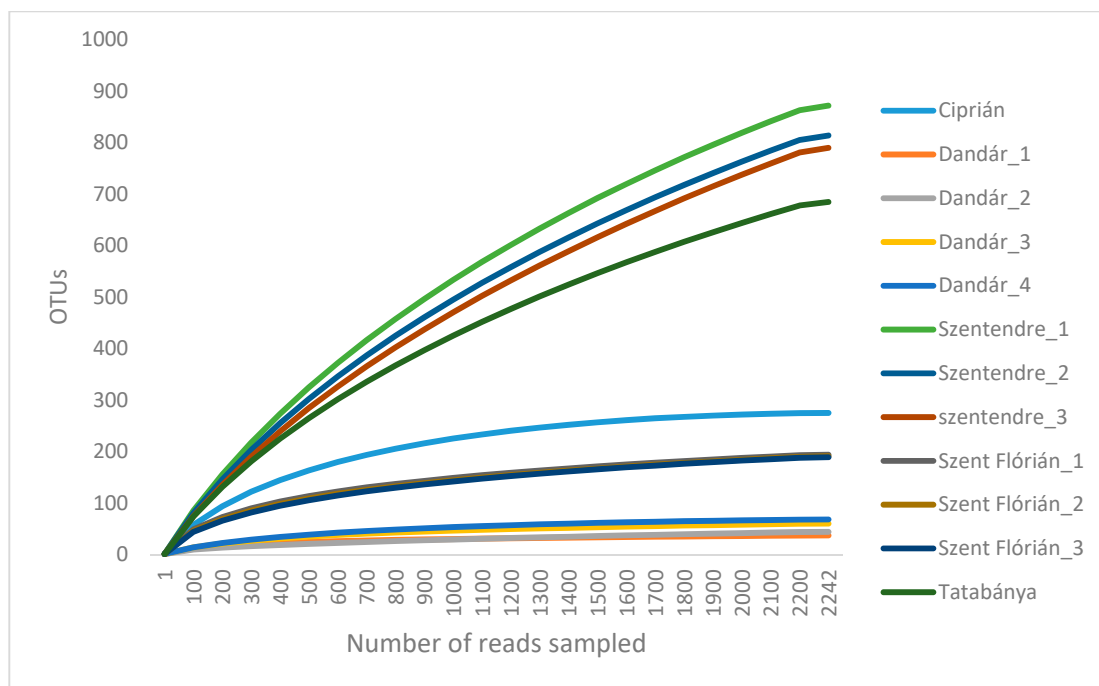


Figure S2. Rarefaction curves of archaeal OTUs of the samples based on 16S rRNA gene amplicon sequencing

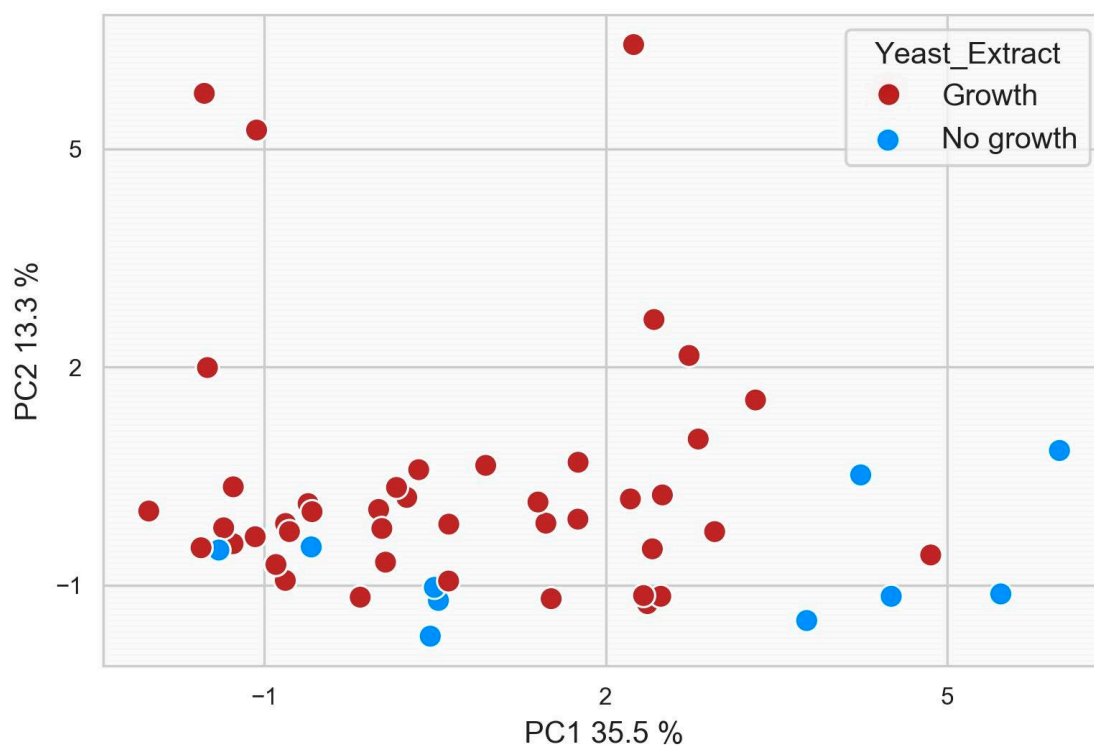


Figure S3. PCA ordination of the bacterial strains growth in 100% yeast extract medium

Table S3. Results of taxonomic identification of group representative bacterial strains using 16S rRNA gene sequencing.

Name	Closest related type strain (EZbiocloud)	Similarity (%)	Phylum	Number of isolates
SG_E_30_P1*	<i>Salinibacterium hongtaonis</i>	96.33	<i>Actinobacteria</i>	3
SG_E_28_P3*	<i>Paenibacillus sinopodophylli</i>	97.97	<i>Firmicutes</i>	9
SG_E_25_P2*	<i>Rhizobium alvei</i>	96.44	<i>Proteobacteria</i>	1
SG_23_I_P2_1_T	<i>Moraxella osloensis</i>	99.1	<i>Proteobacteria</i>	1
SG_18_I_P	<i>Pararhizobium herbae</i>	99.33	<i>Proteobacteria</i>	1
SG_16_I_P3	<i>Streptomyces tateyamensis</i>	98.86	<i>Actinobacteria</i>	2
SG_6_I	<i>Microbacterium tumbae</i>	98.45	<i>Actinobacteria</i>	1

SA_E_32_P2_2	<i>Brevibacillus nitrificans</i>	96.61	Firmicutes	4
SA_E_31_P2	<i>Prostheco bacter algae</i>	99.62	Verrucomicrobia	2
SA_E_8_P3	<i>Microbacterium keratanolyticum</i>	99.46	Actinobacteria	2
SA_E_7_P1	<i>Ancylobacter rudongensis</i>	99.81	Proteobacteria	2
SA_E_5_P2	<i>Paenibacillus tundrae</i>	99.72	Firmicutes	1
SA_E_2_P2	<i>Flectobacillus roseus</i>	99.27	Bacteroidetes	15
SA_19_I*	<i>Sphingobium aquiterrae</i>	97.74	Proteobacteria	2
SA_3_I_P1	<i>Streptomyces rhizosphaerihabitans</i>	99.08	Actinobacteria	1
SG_E_30_P3	<i>Variovorax boronicumulans</i>	99.41	Proteobacteria	1
SG_E_25_P3	<i>Pedobacter miscanthi</i>	97.9	Bacteroidetes	1
SG_E_24	<i>Verrucomicrobium spinosum</i>	99.81	Verrucomicrobia	1
SG_25_I_P1	<i>Massilia lutea</i>	99.03	Proteobacteria	2
SG_24_I	<i>Sphingomonas aerolata</i>	100	Proteobacteria	1
SG_17_I_P1	<i>Bacillus simplex</i>	100	Firmicutes	1
SG_8_I	<i>Streptomyces scabiei</i>	99.87	Actinobacteria	1
SG_5_I	<i>Variovorax paradoxus</i>	99.63	Proteobacteria	3
SA_E_40	<i>Ferro vibrio soli</i>	99.15	Proteobacteria	1
SA_E_39	<i>Lysinibacillus fusiformis</i>	100	Firmicutes	1
SA_E_34_P2	<i>Bacillus mycoides</i>	100	Firmicutes	1
SA_E_34_P1	<i>Azospirillum largimobile</i>	98.76	Proteobacteria	1
SA_E_32_P3	<i>Caulobacter mirabilis</i>	99.12	Proteobacteria	1
SA_E_15_P1	<i>Brevundimonas terrae</i>	99.48	Proteobacteria	1
SA_E_12	<i>Paenibacillus typhae</i>	99.71	Firmicutes	1
SA_E_4_P1	<i>Pararhizobium giardinii</i>	98.25	Proteobacteria	2
SA_E_3	<i>Taonella mepensis</i>	99.81	Proteobacteria	1
SA_20_I_P	<i>Bacillus timonensis</i>	99.45	Firmicutes	1
SA_16_I_P	<i>Pseudomonas lini</i>	99.89	Proteobacteria	1
SA_6_I	<i>Streptomyces umbrinus</i>	99.04	Actinobacteria	1
SA_1_I_P1*	<i>Flavobacterium granuli</i>	97.53	Bacteroidetes	1
SG_15_I	<i>Agromyces fucosus</i>	99.9	Actinobacteria	1
SA_15_I	<i>Ensifer adhaerens</i>	99.31	Proteobacteria	1
SA_9_I	<i>Pigmentiphaga aceris</i>	99.51	Proteobacteria	1

FG_E_46	<i>Microbacterium paraoxydans</i>	99.27	<i>Actinobacteria</i>	9
FG_E_32_P2	<i>Microbacterium oxydans</i>	99.64	<i>Actinobacteria</i>	5
FG_E_20	<i>Pseudoxanthomonas mexicana</i>	99.17	<i>Proteobacteria</i>	1
FA_E_42_P2*	<i>Paracoccus acridae</i>	97.75	<i>Proteobacteria</i>	4
FA_E_40	<i>Aurantimonas altamirensis</i>	99.55	<i>Proteobacteria</i>	9
FA_E_13	<i>Novosphingobium lindaniclasticum</i>	98.83	<i>Proteobacteria</i>	4
FG_E_32_P1	<i>Flavobacterium mizutaii</i>	99.62	<i>Bacteroidetes</i>	11
FA_E_42_P2	<i>Paracoccus haematequi</i>	100	<i>Proteobacteria</i>	1
FA_E_3_P2	<i>Bosea robiniae</i>	99.43	<i>Proteobacteria</i>	1
CG_E_11_P2	<i>Achromobacter deleyi</i>	99.56	<i>Proteobacteria</i>	2
CG_E_6_P1	<i>Bacillus idriensis</i>	99.55	<i>Firmicutes</i>	2
CG_22_I	<i>Rhodobacter azotoformans</i>	96.91	<i>Proteobacteria</i>	2
CG_19_I	<i>Curvibacter delicatus</i>	99.53	<i>Proteobacteria</i>	5
CG_14_I*	<i>Rheinheimera mesophila</i>	97.9	<i>Proteobacteria</i>	2
CA_E_2*	<i>Dyadobacter hamtensis</i>	97.89	<i>Bacteroidetes</i>	1
CA_18_I_P	<i>Rhodoferrax antarcticus</i>	98.55	<i>Proteobacteria</i>	1
CA_3_I_P1	<i>Hydrogenophaga taeniospiralis</i>	98.61	<i>Proteobacteria</i>	3
CG_E_16_P	<i>Pseudomonas wadenswilerensis</i>	98.95	<i>Proteobacteria</i>	1
CG_E_11_P1	<i>Devosia riboflavina</i>	100	<i>Proteobacteria</i>	1
CG_E_5	<i>Paenibacillus tritici</i>	100	<i>Firmicutes</i>	1
CG_E_1	<i>Paenibacillus populi</i>	99.43	<i>Firmicutes</i>	7
CG_20_I	<i>Flavobacterium sasangense</i>	98.47	<i>Bacteroidetes</i>	1
CG_17_I	<i>Rhodoluna limnophila</i>	100	<i>Actinobacteria</i>	1
CG_14_I*	<i>Rheinheimera aquatica</i>	97.97	<i>Proteobacteria</i>	1
CG_11_I	<i>Brevundimonas denitrificans</i>	99.51	<i>Proteobacteria</i>	1
CG_8_I	<i>Devosia insulae</i>	100	<i>Proteobacteria</i>	1
CG_2_I	<i>Fictibacillus barbaricus</i>	99.82	<i>Firmicutes</i>	1
CG_1_I_P1	<i>Bacillus butanolivorans</i>	98.49	<i>Firmicutes</i>	1
CA_E_10	<i>Yonghaparkia alkaliphila</i>	98.95	<i>Actinobacteria</i>	1
CA_E_9*	<i>Devosia submarina</i>	97.85	<i>Proteobacteria</i>	1

CA_E_2	<i>Dyadobacter koreensis</i>	98.41	<i>Bacteroidetes</i>	1
CA_23_I	<i>Pseudorhodobacter sinensis</i>	97.12	<i>Proteobacteria</i>	11
CA_20_I	<i>Aurantimicrobium minutum</i>	98.86	<i>Actinobacteria</i>	1
CA_12_I_P1	<i>Cellulomonas oligotrophica</i>	99.91	<i>Actinobacteria</i>	1
CA_10_I*	<i>Aquabacterium commune</i>	97.19	<i>Proteobacteria</i>	1
CA_8_I	<i>Acidovorax temperans</i>	99.28	<i>Proteobacteria</i>	1
CA_1_I_P2	<i>Arenimonas aquaticum</i>	99.03	<i>Proteobacteria</i>	1
CG_E_13*	<i>Dyadobacter sediminis</i>	97.23	<i>Bacteroidetes</i>	3
CG_13_I	<i>Malikia spinosa</i>	99.81	<i>Proteobacteria</i>	2
CG_9_I_P1	<i>Aquabacterium citratiphilum</i>	99.53	<i>Proteobacteria</i>	1
CA_E_6_P2_L	<i>Bosea eneeae</i>	99.7	<i>Proteobacteria</i>	7
CA_9_I_P2	<i>Altererythrobacter troitsensis</i>	99.15	<i>Proteobacteria</i>	1
CA_1_I_P1	<i>Jeotgalibacillus campisalis</i>	99.91	<i>Firmicutes</i>	1
B_15	<i>Sphingomonas koreensis</i>	99.5	<i>Proteobacteria</i>	13
B_13	<i>Microbacterium album</i>	98.48	<i>Actinobacteria</i>	27
AG_66_I	<i>Kineococcus radiotolerans</i>	98.71	<i>Actinobacteria</i>	2
AG_57	<i>Methylobacterium pseudosasaie</i>	99.59	<i>Proteobacteria</i>	2
AG_56_I	<i>Nevskia ramosa</i>	99.56	<i>Proteobacteria</i>	2
AG_45_E	<i>Pseudoxanthomonas mexicana</i>	99.83	<i>Proteobacteria</i>	19
AG_9_E	<i>Sphingopyxis chilensis</i>	99.34	<i>Proteobacteria</i>	3
AA_11_I	<i>Sphingopyxis solisilvae</i>	100	<i>Proteobacteria</i>	1
AA_10_I	<i>Sphingomonas hunanensis</i>	99.74	<i>Proteobacteria</i>	6
AA_6_I	<i>Sphingopyxis fribergensis</i>	98.89	<i>Proteobacteria</i>	3
AA_66_E_P2	<i>Pseudomonas psychrotolerans</i>	100	<i>Proteobacteria</i>	1
AG_11_E_P2	<i>Methylobacterium pseudosasaie</i>	99.64	<i>Proteobacteria</i>	2
AW_35_I	<i>Acinetobacter pittii</i>	99.91	<i>Proteobacteria</i>	1
AW_39_I	<i>Paracoccus yeei</i>	99.56	<i>Proteobacteria</i>	2
AW_40_I	<i>Micrococcus yunnanensis</i>	99.35	<i>Actinobacteria</i>	3

GW_2_I	<i>Pseudomonas zeshuii</i>	99.74	<i>Proteobacteria</i>	15
WA_10_E	<i>Bacillus licheniformis</i>	99.34	<i>Firmicutes</i>	13
WA_63_E	<i>Roseomonas mucosa</i>	99.82	<i>Proteobacteria</i>	1
WG_2_E	<i>Bacillus circulans</i>	100	<i>Firmicutes</i>	6
SG_E_43	<i>Skermanella rosea</i>	98.4	<i>Proteobacteria</i>	1
SA_1_I_P2	<i>Parasegetibacter terrae</i>	99.2	<i>Bacteroidetes</i>	1
CA_X_I_P1	<i>Cellulomonas aerilata</i>	100	<i>Actinobacteria</i>	1

*Novel bacterial taxo