

# Diversity and metagenome analysis of a hydrocarbon-degrading bacterial consortium from asphalt lakes located in Wietze, Germany

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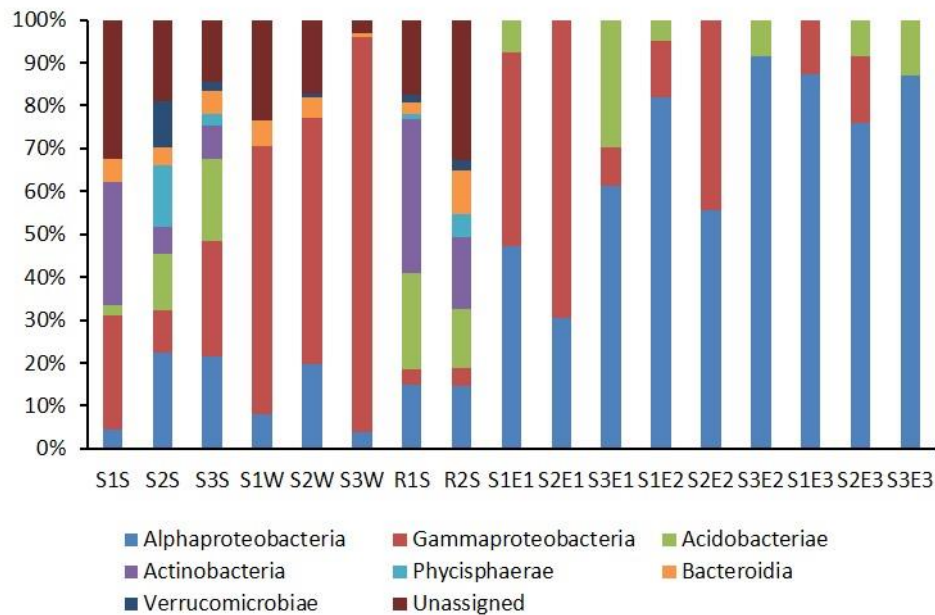
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## Supplementary Materials



**Supplementary Figure S1.** Bacterial taxonomic distribution of all samples based on 16S rRNA gene amplicon data.

**Supplementary Table S2.** Richness, diversity and evenness obtained from the 16S rRNA sequencing of sampling sites and enrichment cultures

Sample ID	Name	Richness	Chao1	Chao1 (%)	Shannon Diversity	Pielou's Evenness
X20200114.BEWE.a.2136_S261	S1S	381.99	475.51	80.33	4.140482857	0.696418531
X20200114.BEWE.a.2137_S262	S2S	958.43	1166.75	82.15	5.927652696	0.863422675
X20200114.BEWE.a.2138_S263	S3S	885.54	1076.78	82.24	5.625668073	0.828986773
X20200114.BEWE.a.2139_S264	S1W	731.44	971.95	75.25	4.491982504	0.68111784
X20200114.BEWE.a.2140_S265	S2W	666.94	848.21	78.63	3.840835511	0.590652415
X20200114.BEWE.a.2141_S266	S3W	389	581.5	66.9	2.409478261	0.40403223
X20200114.BEWE.a.2142_S267	R1S	629.32	806.44	78.04	4.89315041	0.759258936
X20200114.BEWE.a.2143_S268	R2S	1168.08	1274.35	91.66	6.322569919	0.89515298
X20200114.BEWE.a.2144_S269	S1E1	62.34	67.76	92	2.684138231	0.649503002
X20200114.BEWE.a.2145_S270	S2E1	44.91	50.35	89.2	2.228003222	0.585598434
X20200114.BEWE.a.2146_S271	S3E1	38.41	40.95	93.8	1.755745383	0.481247923
X20200114.BEWE.a.2147_S272	S1E2	45.09	56.52	79.78	1.896011697	0.497815886
X20200114.BEWE.a.2148_S273	S2E2	31.88	35.16	90.68	1.921605494	0.555059859
X20200114.BEWE.a.2149_S274	S3E2	14.05	14.66	95.82	0.829529079	0.313903749
X20200114.BEWE.a.2150_S275	S1E3	23.26	30.09	77.3	1.761694985	0.55984851
X20200114.BEWE.a.2151_S276	S2E3	27.44	40.95	67	1.257543211	0.379692792
X20200114.BEWE.a.2152_S277	S3E3	15.28	19.03	80.3	0.962736927	0.353097786

**Supplementary Table S2.** Metagenome-assembled genomes (MAGs) from both the soil and the enrichment metagenomes.

User_genome	Source metagenome	classification	closest_placement_taxonomy	closest_placement_ani	aa_percent
BEWE_m_45_metabat2.1	Soil sample	f__Acidobacteriaceae;g__Terracidiphilus;s__	s__Terracidiphilus sp002314435	80.06	73.89
BEWE_m_45_metabat2.11	Soil sample	f__Mycobacteriaceae;g__Williamsia_A;s__	s__Williamsia_A herbipolensis	80.27	89.46
BEWE_m_45_metabat2.15	Soil sample	f__Acetobacteraceae;g__Acidocella;s__	N/A	N/A	74.21
BEWE_m_45_metabat2.18	Soil sample	f__Steroidobacteraceae;g__;s__	N/A	N/A	71.59
BEWE_m_45_metabat2.19	Soil sample	f__Koribacteraceae;g__Koribacter;s__	s__Koribacter sp003151155	89.00	70.85
BEWE_m_45_metabat2.21	Soil sample	f__Rhodanobacteraceae;g__Rudaea;s__	s__Rudaea cellulositytica	78.03	68.95
BEWE_m_45_metabat2.22	Soil sample	f__UBA5335;g__UBA5335;s__	s__UBA5335 sp002862435	94.10	61.21
BEWE_m_45_metabat2.25	Soil sample	f__UBA5335;g__;s__	N/A	N/A	94.40
BEWE_m_45_metabat2.26	Soil sample	f__Nevskiaceae;g__Solimonas;s__	N/A	N/A	65.24
BEWE_m_45_metabat2.27	Soil sample	f__Burkholderiaceae;g__BOG-994;s__	N/A	N/A	86.96
BEWE_m_45_metabat2.28	Soil sample	f__UBA4822;g__UBA4822;s__	N/A	N/A	73.71
BEWE_m_45_metabat2.33	Soil sample	f__Actinomycetaceae;g__Pauljensenia;s__	N/A	N/A	81.75
BEWE_m_45_metabat2.35	Soil sample	f__UBA5335;g__;s__	N/A	N/A	87.62
BEWE_m_45_metabat2.41	Soil sample	f__Acetobacteraceae;g__;s__	N/A	N/A	66.59
BEWE_m_45_metabat2.6	Soil sample	f__Burkholderiaceae;g__Caballeronia;s__	N/A	N/A	93.91
BEWE_m_46_metabat2.2	Enrichment culture	f__Acetobacteraceae;g__Acidocella;s__	s__Acidocella aminolytica	82.29	82.02
BEWE_m_46_metabat2.4	Enrichment culture	f__Acidobacteriaceae;g__Acidobacterium;s__	s__Acidobacterium capsulatum	85.13	97.02
BEWE_m_46_metabat2.5	Enrichment culture	f__Acetobacteraceae;g__Acidocella;s__	N/A	N/A	96.83

**Supplementary Table S3.** Quality check for the MAGs

Bin.Id	Marker.lineage	X..genomes	X..markers	X..marker.sets	X0	X1	X2	X3	X4	X5.	Completeness	Contamination	Strain. Heterogeneity
BEWE_m_45_metabat2.1	k__Bacteria (UID3187)	2258	187	116	54	125	8	0	0	0	82.75	6.47	12.5
BEWE_m_45_metabat2.11	o__Actinomycetales (UID1814)	148	572	276	25	547	0	0	0	0	97.53	0	0
BEWE_m_45_metabat2.15	o__Rhodospirillales (UID3754)	63	336	201	48	284	4	0	0	0	93.75	1.49	25
BEWE_m_45_metabat2.18	c__Gammaproteobacteria (UID4202)	67	481	276	110	329	41	0	1	0	77.26	8.06	0
BEWE_m_45_metabat2.19	k__Bacteria (UID3187)	2258	188	117	55	132	1	0	0	0	87.39	0.85	0
BEWE_m_45_metabat2.21	f__Xanthomonadaceae (UID4214)	55	659	290	103	536	20	0	0	0	91.72	3.88	30
BEWE_m_45_metabat2.22	c__Gammaproteobacteria (UID4201)	1164	275	174	93	179	3	0	0	0	64.27	1.72	66.67
BEWE_m_45_metabat2.25	c__Gammaproteobacteria (UID4267)	119	544	284	28	513	3	0	0	0	94.55	0.82	0
BEWE_m_45_metabat2.26	k__Bacteria (UID203)	5449	104	58	48	52	4	0	0	0	66.07	6.03	50
BEWE_m_45_metabat2.27	c__Betaproteobacteria (UID3888)	323	387	234	41	340	5	1	0	0	89.01	0.88	25
BEWE_m_45_metabat2.28	k__Bacteria (UID203)	5449	102	56	13	89	0	0	0	0	80.36	0	0
BEWE_m_45_metabat2.33	f__Actinomycetaceae (UID1531)	42	420	211	58	358	2	2	0	0	87.1	2.37	25
BEWE_m_45_metabat2.35	c__Gammaproteobacteria (UID4267)	119	544	284	44	493	7	0	0	0	90.77	1.88	14.29
BEWE_m_45_metabat2.41	o__Rhodospirillales (UID3754)	63	336	201	114	219	3	0	0	0	65.49	0.76	66.67
BEWE_m_45_metabat2.6	g__Burkholderia (UID4006)	64	769	248	51	692	26	0	0	0	94.03	1.51	38.46
BEWE_m_46_metabat2.2	o__Rhodospirillales (UID3754)	63	336	201	80	256	0	0	0	0	72.39	0	0
BEWE_m_46_metabat2.4	k__Bacteria (UID3187)	2258	188	117	1	186	1	0	0	0	99.79	0.85	0
BEWE_m_46_metabat2.5	o__Rhodospirillales (UID3754)	63	336	201	0	335	1	0	0	0	100	0.08	0