

Microbial diversity in deep subsurface hot brines of the North West Poland: from a community structure to isolate characteristics

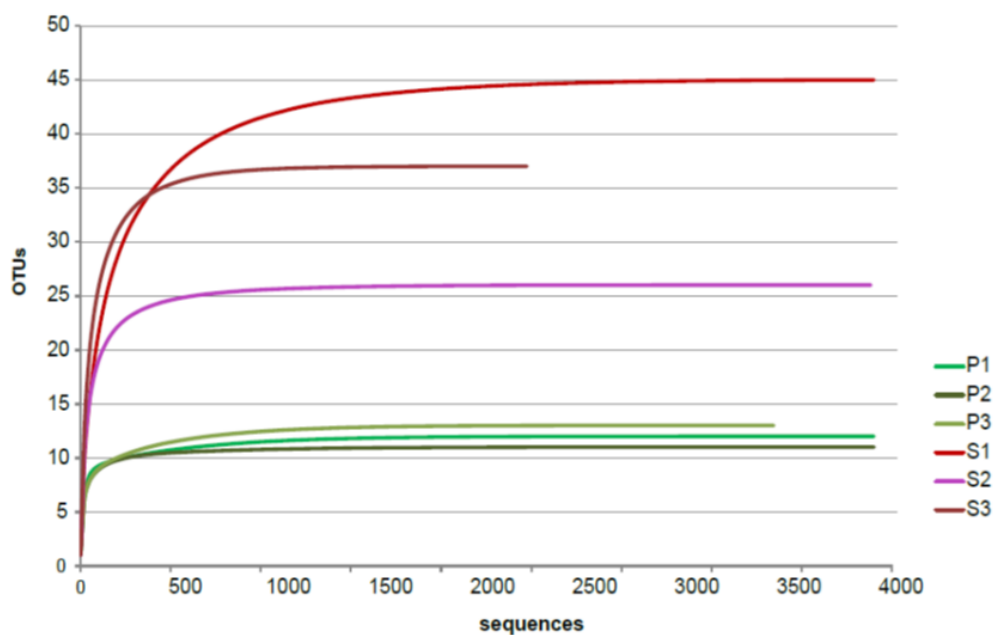


Fig. S1 Rarefaction analysis of sequences from Pyrzyce (P1-P3) and Stargard (S1-S3) applying 97% similarity threshold of the 16S rRNA gene

TABLE S1 The list of the contaminating genera present in the negative controls and in environmental samples

	DNA-extraction blank	No-template amplification
<i>Acinetobacter</i>	-	+
<i>Candidatus Solibacter</i>	-	+
<i>Corynebacterium_1</i>	+	-
<i>Desulfovibrio</i>	+	-
<i>Escherichia-Shigella</i>	+	-
<i>Granulicella</i>	-	+
<i>Massilia</i>	+	-
<i>Pelomonas</i>	+	-
<i>Reyranella</i>	-	+
<i>Rhodanobacter</i>	-	+
<i>Sediminibacterium</i>	+	+
<i>Shewanella</i>	+	+
<i>Sphingomonas</i>	+	-
<i>Xanthobacteraceae_unclassified</i>	-	+

TABLE S2 Identification of bacterial isolates obtained from thermal waters from Pyrzyce and Stargard based on 16S rRNA gene sequence

Name	Top-hit taxon	Top-hit strain	Similarity (%)	Completeness* (%)
TP1	<i>Bacillus paralicheniformis</i>	KJ-16 (T)	99.93	100.0
TP4	<i>Bacillus paralicheniformis</i>	KJ-16 (T)	98.79	100.0
TP6	<i>Bacillus paralicheniformis</i>	KJ-16 (T)	99.79	100.0
TP7	<i>Bacillus paralicheniformis</i>	KJ-16 (T)	98.82	83.2
TP8	<i>Bacillus oryzaecorticis</i>	R1	93.59	100.0
TS4	<i>Bacillus paralicheniformis</i>	KJ-16 (T)	99.93	97.1
TS5	<i>Bacillus paralicheniformis</i>	KJ-16 (T)	100.00	96.9
TS6	<i>Bacillus paralicheniformis</i>	KJ-16 (T)	100.00	100.0
TS7	<i>Bacillus paralicheniformis</i>	KJ-16 (T)	99.93	100.0
TS10	<i>Bacillus paralicheniformis</i>	KJ-16 (T)	99.44	96.7

*degree of coverage of a query 16S rRNA gene sequence with respect to the full-length, complete 16S rRNA gene sequence

TABLE S3 General features and characteristics of *Bacillus paralicheniformis* genomes used for comparative genomics analysis

Strain	TS6	14DA11	KJ-16
BioSample	SAMN10888088	SAMN07594137	SAMN03573918
Bioproject	PRJNA476244	PRJNA401080	PRJNA282685
Assembly	GCA_004282815.1	GCA_002393225.1	GCA_001042485.2
Level	Contig	Genome	Contig
Size Mb	4.35	4.53	4.52
GC%	4.35	45.8	45.8
WGS	SHMY01	-	LBMN02
Scaffolds	52	-	39
Gene	4424	4675	4616
Protein	4179	4337	4375