Supplementary materials for the article:

Muccee F. et al. Whole Genome Shotgun Sequencing-Based Insights into the Benzene and Xylene Degrading Potentials of Bacteria.
Pol J Microbiol. 2025, Vol. 74, No 2, 244-261

Table SI
Characterization of benzene and xylene-degrading bacteria based on ribotyping, growth phases, biochemical characteristics, and organic compound removal efficiencies and GC-MS based analysis.

No.	Isolate identified (NCBI accession number)	Growth phases				Biochemical characteristics	Benzene/xylene removal efficiency	Pathways identified
		Lag	Log	Static	Death			
Benzene degrading bacteria								
1	*Paracoccus aestuarii* PUB1 (OR272055)	0–23	24–47	48–48	49 – onwards	ADH, ODC, LDC, TET, LIP, KSF, SBL, PRO, GGT, PYR, ADON	31 mg/l per 47 hour	Benzene methylation pathway, benzene degradation via benzaldehyde and via carboxylation, meta and ortho cleavage pathways, benzene degradation via phenol
2	*Bacillus tropicus* PUB2 (OR272056)	0–10	10–23	24–40	41 – onwards	ODC, LDC, LIP, KSF, SBL, GUR, PRO, GGT, PYR, ADON	30 mg/l per 23 hour	
3	*Bacillus albus* PUB3 (OR272059)	0–23	23–47	48–49	50 – onwards	ADH, ODC, LDC, TET, LIP, KSF, SBL, PRO, GGT, PYR, ADON	34 mg/l per 47 hour	
4	*Bacillus subtilis* PUB4 (OR272058)	0–23	23–47	48–48	49 – onwards	TET, LIP, KSF, SBL, PYR, ADON	32 mg/l per 47 hour	
5	*Bacillus thuringiensis* PUB5 (OR272061)	0–23	23–47	48–49	50 – onwards	ADH, ODC, LDC, LIP, PRO, GGT, PYR	30 mg/l for 47 hour	

No.	Isolate identified (NCBI accession number)	Growth phases				Biochemical characteristics	Benzene/xylene removal efficiency	Pathways identified
		Lag	Log	Static	Death			
6	*Bacillus cereus* PUB6 (OR272060)	0–23	23–47	48–49	50 – onwards	ADH, ODC, LDC, TET, LIP, KSF, SBL, PRO, GGT, PYR, ADON	31 mg/l per 47 hour	
Xylene degrading bacteria								
1	*Bacillus cereus* PUX1(OR272064)	0–11	12–48	49–50	51 – onwards	TRD, EST, URE, PRO, PYR, NO_3	65 mg/l per 48 hour	xylene degradation via benzoate formation and anaerobic oxidation pathway
2	*Bacillus thuringiensis* PUX2 (OR272063)	0–11	12–48	49–50	51 – onwards	TRD, EST, URE, PRO, PYR, NO_3, GLU	40 mg/l per 48 hour	
3	*Bacillus cereus* PUX3 (OR272072)	0–23	24–48	49–50	51 – onwards	TRD, URE, PRO, PYR, NO_3	30 mg/l per 48 hour	
4	*Bacillus mycoides* PUX4 (OR272071)	0–11	12–48	49–50	51 – onwards	TRD, URE, PRO, PYR, NO_3	50 mg/l per 48 hour	
5	*Bacillus cereus* PUX5 (OR272073)	0–23	24–48	49–50	51 – onwards	TRD, EST, URE, PRO, PYR, NO_3	35 mg/l per 48 hour	

ADH – Arginine dihydrolase, ADON – adonitol fermentation test, EST – triglyceride test, GGT – hydrolysis of *γ*-glutamyl-*β*-naphthylamide hydrolysis test, GLU – glucose test, GUR – β-glucuronidase test, KSF – sugar aldehyde utilization test, LDC – lysine decarboxylase test, LIP – lipase detection test, NO_3 – sodium nitrate test, ODC – ornithine decarboxylase test, PRO – proline- β-naphthylamide test, PYR – pyrrolidonyl-*β*-naphthylamide, SBL – sorbitol fermentation test, TET – aliphatic thiol utilization test, TRD – aliphatic diol test, URE – urea test

Table II
Raw data statistics calculated for present study the bacterial DNA consortium during whole genome sequencing analysis

Sample ID	Total bases (bp)	Total reads	GC (%)	AT (%)	Q20 (%)	Q30 (%)
Bacterial DNA	2,232,222,732	14,782,932	54.9	45.1	93.9	86.2

Fig. S1. Quality control analysis of the DNA consortium sample by running on agarose gel electrophoresis.