

Evaluating the aerobic xylene-degrading potential of the intrinsic microbial community of a legacy BTEX-contaminated aquifer by enrichment culturing coupled with multi-omics analysis: uncovering the role of *Hydrogenophaga* strains in xylene degradation

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Table S1:

Year	BTEX compounds (µg/L)					Physicochemical parameters							
	Well code	Xylene	Benzene	Toluene	Ethyl-benzene	Temperature (°C)	pH	DO (mg/L)	NO ₃ ⁻ (mg/L)	Fe ₂ ⁺ (mg/ L)	SO ₄ ²⁻ (mg/L)	CH ₄ (mg/L)	Redox potential (mV)†
2011*	SKV	<2	<0.2	<1	<1	14.2	6.7	3.3	61	<0.02	71	<0.04	369
	ST2	6700	340	64	966	14.3	8.0	0.6	2	4	24	1.9	148
2019	SKV	<2	<0.2	<1	<1	14.5	6.8	2.1	40	0.13	60	<0.04	14
	ST2	2760	227	15	862	14.2	7.6	1.2	<5	8.2	<30	2.19	-42

†measured with a standard hydrogen reference electrode.

*Data source: Táncsics et al 2012

Table S2: Alpha diversity index of enrichment samples (M= *m*-xylene-degrading enrichments, P= *p*-xylene-degrading enrichments , O= *o*-xylene-degrading enrichments)

	M1	M2	P1	P2	O1	O2
Simpson_1-D	0.4684	0.5013	0.7699	0.7507	0.7669	0.7841
Shannon_H	1.22	1.297	1.818	1.757	1.999	2.065
Chao-1	12	12	10	10	15	15



Figure S1: Rarefaction curves were assembled showing the number of OTUs, defined at the 97% sequence similarity cut-off in Mothur, relative to the number of total sequences

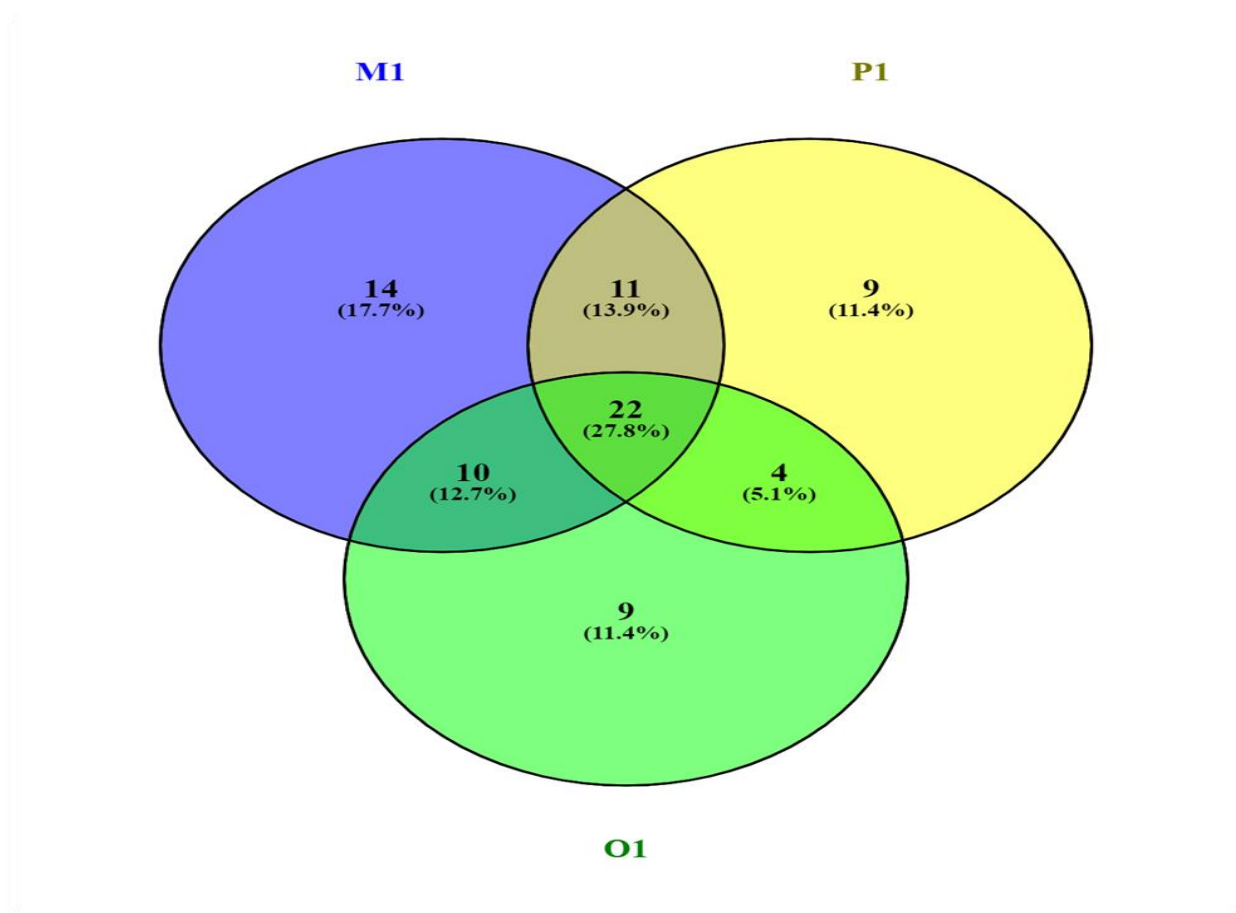


Figure S2: Venn diagram showing shared and unique genera at 97% identity among the three groups M1 (*m*-xylene-degrading enrichment), P1 (*p*-xylene-degrading enrichment) and O1 (*o*-xylene-degrading enrichment). Based on Genus with relative abundance more than 1%.