

Microbial Profile of the Leachate from Mexico City's "Bordo Poniente" Composting Plant: an Inoculum to Digest Organic Waste

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Table S1. 16S rDNA primers for high throughput sequencing for Bacteria and Archaea.

BACTERIA				
Primer	Ion Torrent linker	Golay barcode	Spacer	16S rDNA
V3-341 F23	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TTGGGTACACGT	GT	CCTACGGGAGGCAGCAG
V3-341 F24	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AAGGCGCTCCTT	GT	CCTACGGGAGGCAGCAG
V3-341 F25	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TAATACGGATCG	GT	CCTACGGGAGGCAGCAG
V3-341 F26	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCGGAATTAGAC	GT	CCTACGGGAGGCAGCAG
V3-341 F27	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGTGAATTCGGA	GT	CCTACGGGAGGCAGCAG
V3-341 F28	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CATTCGTGGCGT	GT	CCTACGGGAGGCAGCAG
V3-341 F31	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ACCAGACGATGC	GT	CCTACGGGAGGCAGCAG
V3-341 F32	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ACGCTCATGGAT	GT	CCTACGGGAGGCAGCAG

16S rDNA is complementary sequence for the forward primer V3-341F (positions 340-356) and the reverse V3-518 (positions 517-533) of *Escherichia coli* GenBank J01859.1

ARCHAEA				
Primer	Ion Torrent linker	Golay barcode	Spacer	16S rDNA
ArcF3	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CAAACAACAGCT	GT	ATTAGATACCCSBGTAGTCC
ArcF4	CCATCTCATCCCTGCGTGTCTCCGACTCAG	GCAACACCATCC	GT	ATTAGATACCCSBGTAGTCC
ArcF5	CCATCTCATCCCTGCGTGTCTCCGACTCAG	GCGATATATCGC	GT	ATTAGATACCCSBGTAGTCC
ArcF7	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGTCGTGCACAT	GT	ATTAGATACCCSBGTAGTCC
ArcF9	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGAGGGAAAGTC	GT	ATTAGATACCCSBGTAGTCC
ArcF11	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGATTGACCAAC	GT	ATTAGATACCCSBGTAGTCC
ArcF12	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGTTACGAGCTA	GT	ATTAGATACCCSBGTAGTCC
ArcF13	CCATCTCATCCCTGCGTGTCTCCGACTCAG	GCATATGCACTG	GT	ATTAGATACCCSBGTAGTCC

16S rDNA is complementary sequence for the forward primer Arc787F (positions 716-735) and the reverse Arc1059R (positions 971-986) of *Methanoculleus horonobensis* GenBank AB436897.2

Table S2. Alpha diversity of Bacteria and Archaea.

Group	Sample	Observed		Chao1		Shannon		Simpson	
		Bacteria	Archaea	Bacteria	Archaea	Bacteria	Archaea	Bacteria	Archaea
	LCP	1300	960	1446.6	974.95	4.48	1.76	0.94	0.72
	INCB	1024	1263	1435.7	1565.4	3.95	1.17	0.92	0.44
Negative Control	NC17	1582	1003	2114.5	1541.7	4.77	0.85	0.96	0.27
	NC30	1169	1535	1743.8	2136.7	4.19	1.62	0.93	0.58
Positive Control	PC17	678	356	1017.9	707.92	3.42	2.23	0.85	0.77
	PC30	892	1472	1118.7	1819.9	4.79	2.24	0.97	0.73
Substrate	SB17	1062	770	1604.6	1265.4	4.53	2.23	0.96	0.47
	SB30	1463	1483	1876.1	2090.7	4.75	2.16	0.97	0.79

LCP: leachate composting plant; INCP: Inoculum composting plant; NC17: Negative control at 17th day; NC30: Negative control at 30th day; PC17: Positive control at 17th day; PC30: Positive control at 30th day; SB17: Substrate at 17th day; SB30: Substrate at 30th day.

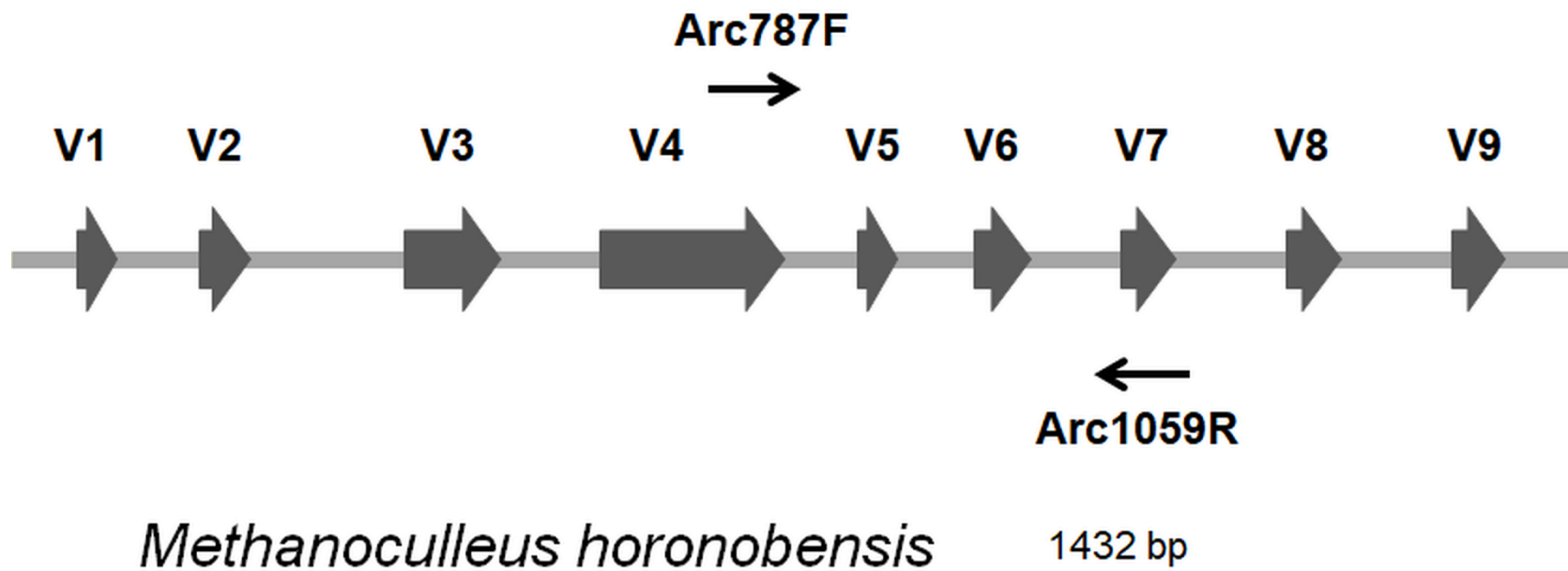


Figure S1. Map of the 16S rDNA gene and primer's positions of the *Methanoculleus horonobensis* GenBank AB436897.2. The primer Arc787F shows the sequence of forward primer (positions 716-735) and reverse Arc1059R primer (971-986).

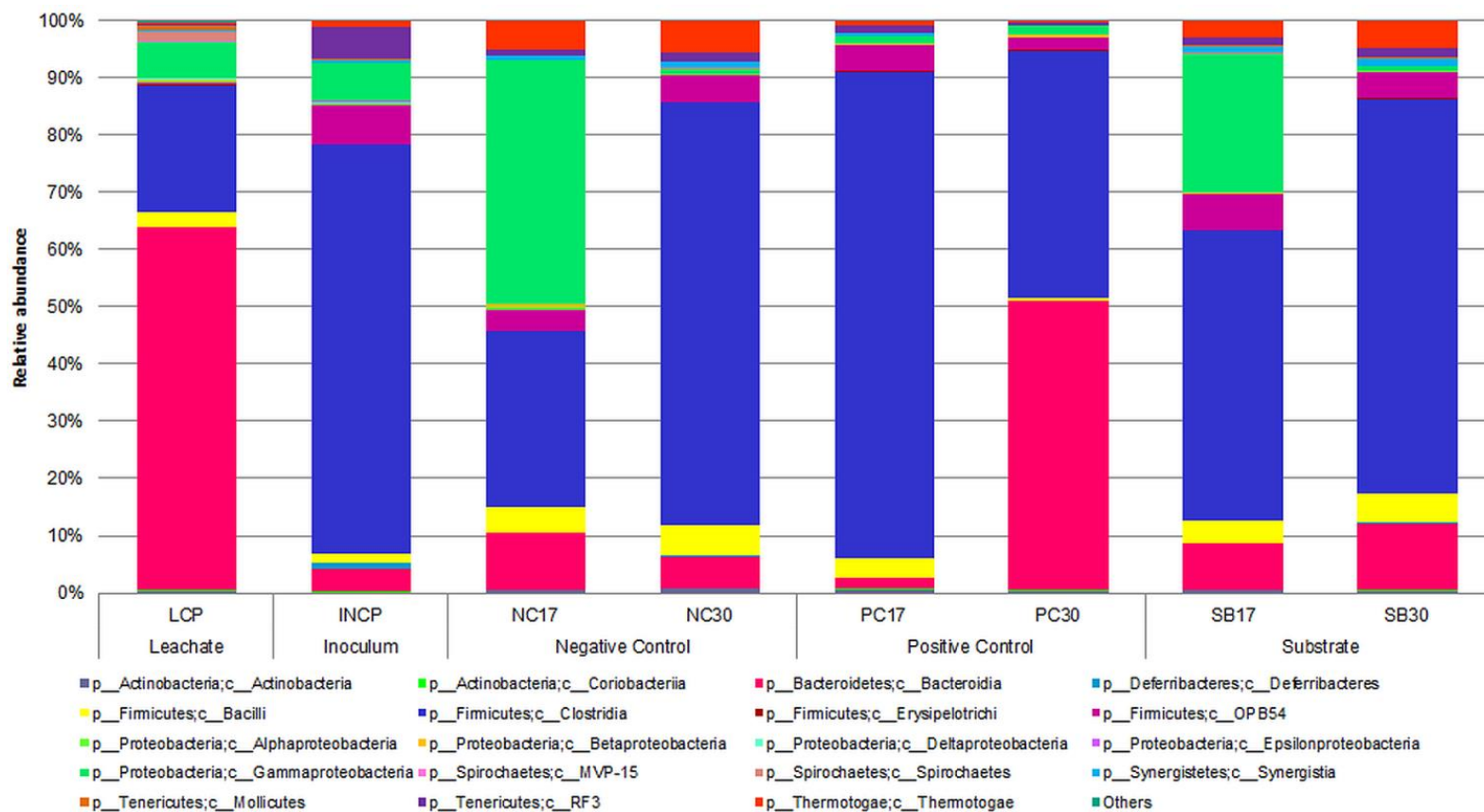


Figure S2: Relative abundance (%) of bacterial class in the leachate (LCP), inoculum (INCP; day 1), and treatment groups (NC-negative control; PC-positive control; SB-substrate; 17-on 17 days; 30-on 30 days).

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