

Table S1 Kinetic parameters of DEHP degradation

DEHP (mg/L)	Kinetic equations	$t_{1/2}$ (d)	R^2
2000	$\ln C = -0.01934t + 7.6001$	1.49334	0.9107
1000	$\ln C = -0.03281t + 6.9013$	0.88025	0.9274
500	$\ln C = -0.06471t + 6.1809$	0.44632	0.9076
200	$\ln C = -0.06411t + 5.3237$	0.45049	0.8906

C: The concentration of DEHP at time t; $t_{1/2}$: half-life

Table S2 The whole genome sequencing and assembly related information of *Gordonia* sp. GZ-YC7

Platform	Insert Size	Reads Length	Raw Data	Adapter	Duplication	Total Reads	Filtered Reads	Low Quality Filtered	Clean Data
	(bp)	(bp)	(Mb)	(%)	(%)		(%)	Reads (%)	(Mb)
DNBSEQ	350	(150:150)	1,314	0	0.02	8,764,210	0.07	0	1,308

Platform	Valid Zero-Mode	Subreads Number	Subreads Total	Subreads Mean	Subreads	Subreads	Subreads Max	Subreads Min
	Waveguides Number		Bases (bp)	Length (bp)	N50 (bp)	N90 (bp)	Length (bp)	Length (bp)
PacBio	34,772	248,485	2,525,005,289	10,161	11,060	6,917	150,259	2,000

Table S3 Gene numbers of each category

Category	Gene number
tRNA	51 (1.10 %)
5s rRNA	4 (0.09 %)
16s rRNA	4 (0.09 %)
23s rRNA	4 (0.09 %)
sRNA	9 (0.19 %)
VFDB	223 (4.79 %)
ARDB	7 (0.15 %)
TREMBL	4,476 (96.17 %)
CAZY	126 (2.70%)
IPR	3,870 (83.15 %)
Swiss-Prot	1,758 (37.77 %)
COG	3,463 (74.4 %)
CARD	1 (0.02 %)
GO	2,670 (57.37 %)
KEGG	2,400 (51.56 %)
NR	4,481 (96.28 %)
T3SS	1,026 (22.04 %)

Table S4 Esterase genes in previous publications

Type	Ester	Strains	Reference
I	<i>dph</i>	<i>Acinetobacter</i> sp. M673	[50]
I	<i>EstS1</i>	<i>Sulfobacillus acidophilus</i> DSM10332	[2]
I	<i>EstSP1</i>	<i>Sphingomonas glacialis</i> PAMC 26605	[45]
II	<i>mehpH</i>	<i>Gordonia alkanivorans</i> YC-RL2	[31]
II	<i>mehpH</i>	<i>Gordonia</i> sp. P8219	[44]
II	<i>patE</i>	<i>Rhodococcus jostii</i> RHA1	[46]
III	<i>EstG</i>	<i>Sphingobium</i> sp. SM42	[47]
III	<i>CarEW</i>	<i>Bacillus</i> sp. K91	[48]
III	<i>pehA</i>	<i>Arthrobacter</i> sp. ZJUTW	[30]