

Supplementary material

**Bioplastic (poly-3-hydroxybutyrate) producing
Massilia endophytica sp. nov., isolated from
Cannabis sativa L. ‘Cheungsam’**

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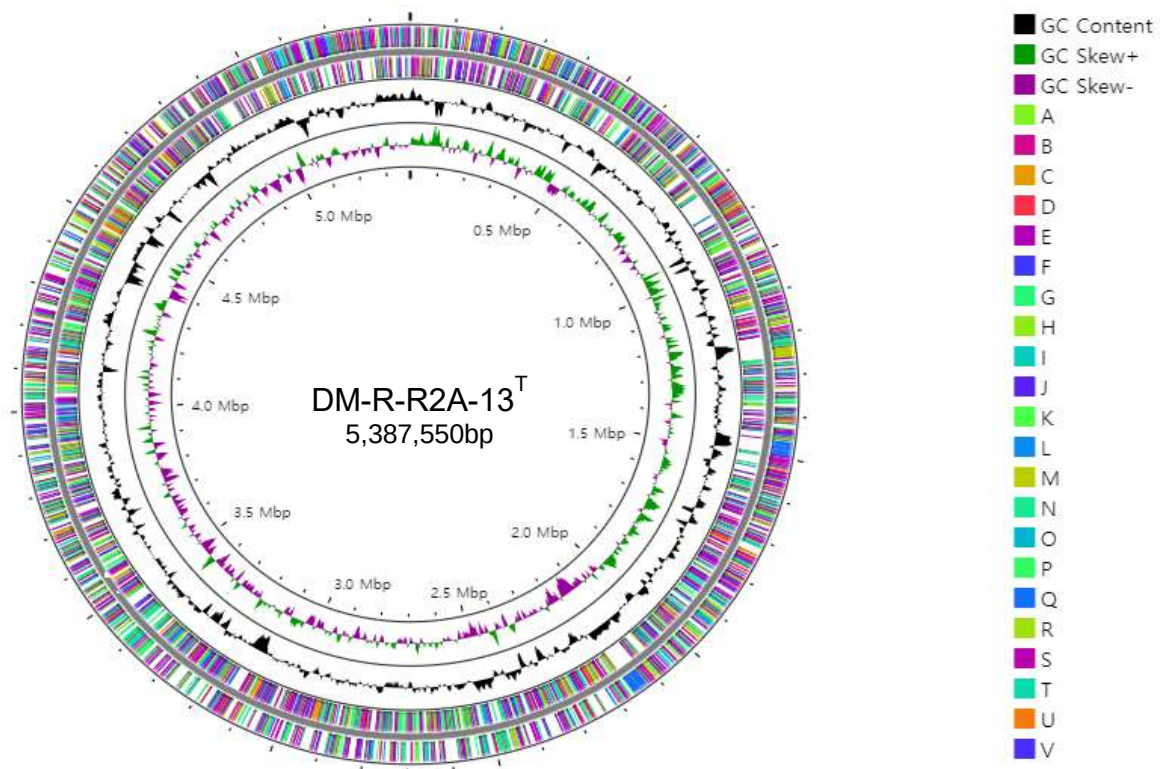


Fig. S1. Genome map of the DM-R-R2A-13^T generated using CGView. Distinctive features illustrated from out to inner rings. Ring 1 and ring 2 depict forward and reverse Cluster Orthologous Group (COG) annotation, respectively. Ring 3 illustrates the G+C % content plot, while ring 4 depicts the GC skew. The COG categories are: A, RNA processing and modification; B, chromatin structure and dynamics; C, energy production and conversion; D, cell cycle control, cell division, chromosome partitioning; E, amino acid transport and metabolism; F, nucleotide transport and metabolism; G, carbohydrate transport and metabolism; H, coenzyme transport and metabolism; I, lipid transport and metabolism; J, translation, ribosomal structure and biogenesis; K, transcription; L, replication, recombination and repair; M, cell wall/membrane/envelope biogenesis; N, cell motility; O, posttranslational modification, protein turnover, chaperones; P, inorganic ion transport and metabolism; Q, secondary metabolites biosynthesis, transport and catabolism; R, general function prediction only; S, function unknown; T, signal transduction mechanisms; U, intracellular trafficking, secretion, and vesicular transport; V, defense mechanisms.

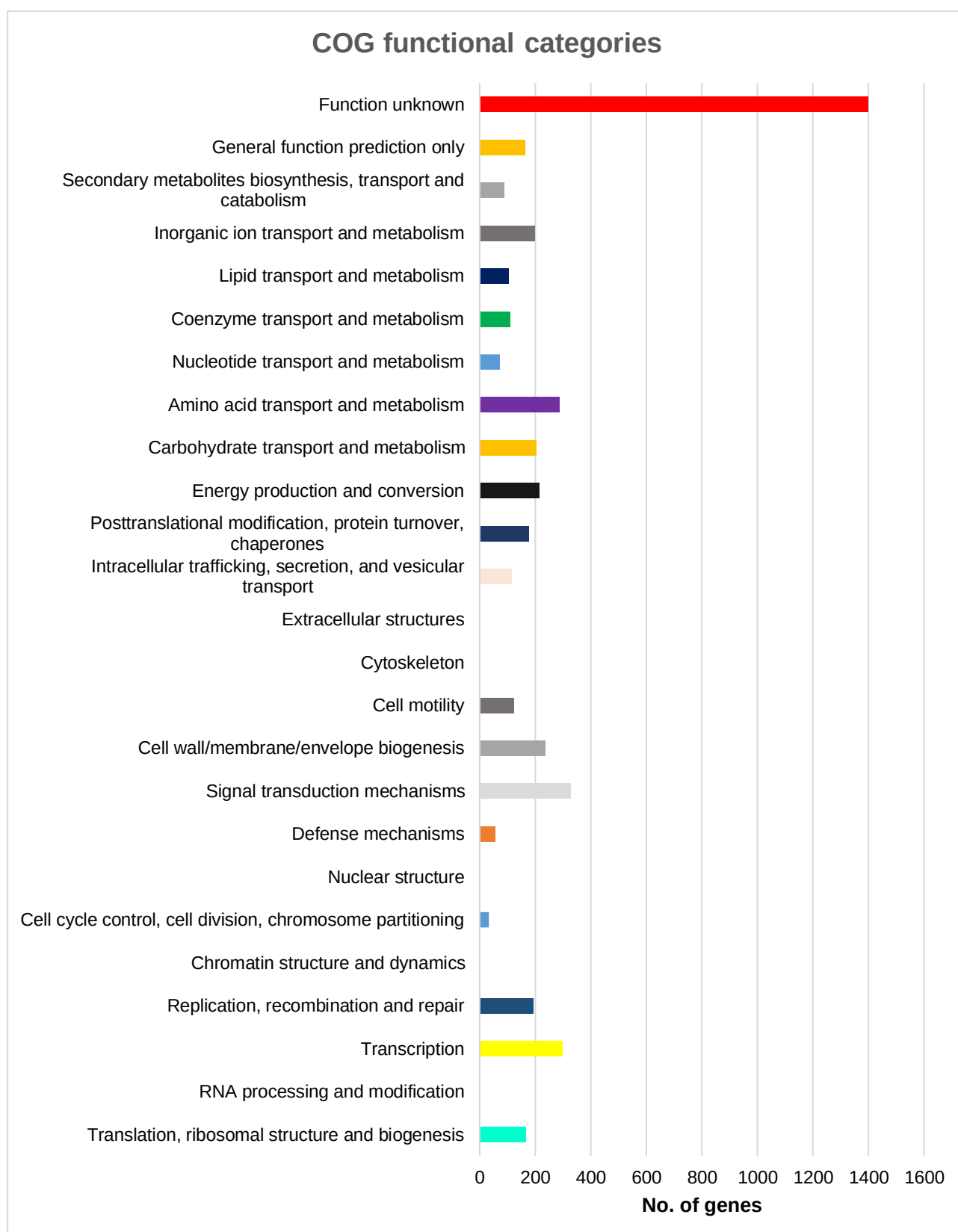


Fig. S2. COG classification of strain DM-R-R2A-13^T genome. Of the 4,569 transcripts identified using the eggNOG database, 3,170 were categorized into 25 COG clusters.

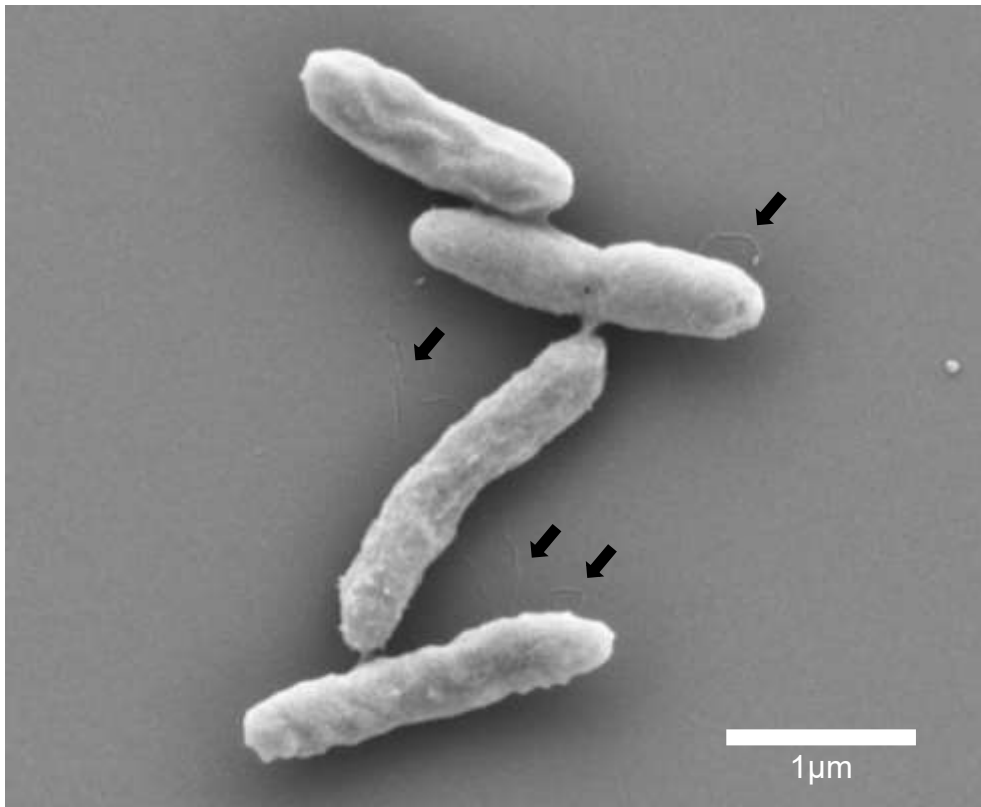


Fig. S3. Scanning electron microscopy (SEM) image of DM-R-R2A-13^T grown in R2A medium at 30°C. Scale bar, 1 µm.

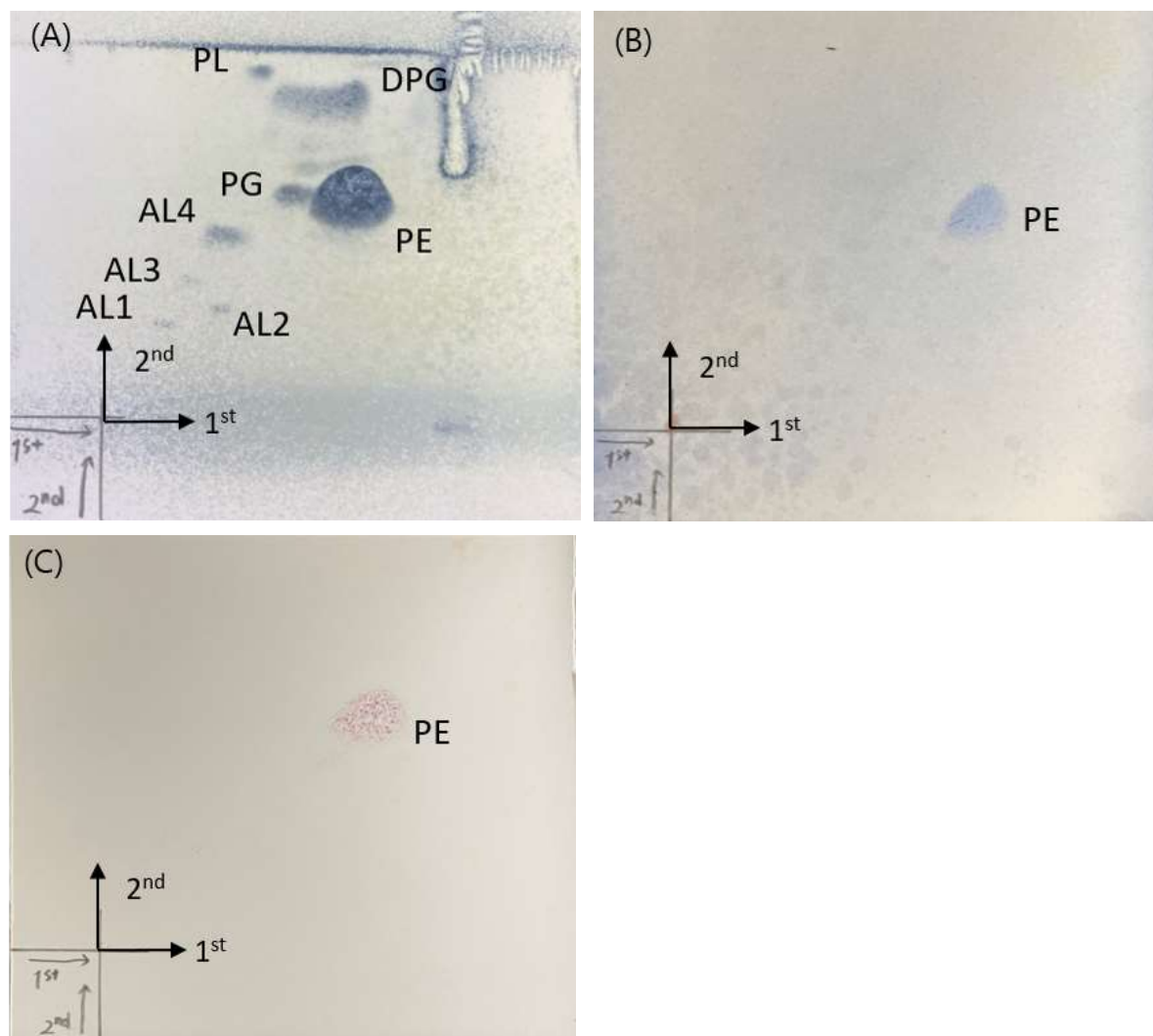


Fig. S4. Two-dimensional thin-layer chromatography of polar lipids of strain DM-R-R2A-13^T. (A) Total lipids were detected by spraying with phosphomolybdic acid. (B) Phospholipids (PL) were detected by spraying with molybdenum blue. (C) Aminolipids (AL) were detected by spraying with ninhydrin. Diphosphatidylglycerol (DPG), phosphatidylethanolamine (PE), phosphatidylglycerol (PG), one unidentified PL, and four unidentified AL were observed.

Table S1. Comparative analysis of PHA synthesis genes in strain DM-R-R2A-13^T and other bacterial proteins. The protein sequences were obtained from the National Center for Biotechnology Information (NCBI), and the percentage identity was calculated using Cluster Omega multiple sequence alignments (Clustal v.2.1).

Organism	PhaC		PhaR	
	GeneBank no.	Identity (%)	GeneBank no.	Identity (%)
<i>R. eutropha</i> H16 ^a	QCC00456.1	60.88	QCC00459.1	72.53
<i>B. megaterium</i> ATCC 14581 ^b	QSF29105.1	27.81	QSF29103.1	18.80
<i>A. vinosum</i> DSM 180 ^c	ADC61033.1	25.00	ADC61036.1	44.90

^a *R. eutropha* (= *Raltonia eutropha*, = *Cupriavidus necator*)

^b *B. megaterium* (= *Bacillus megaterium*, = *Priestia megaterium*)

^c *A. vinosum* (= *Allochromatium vinosum*)