

# **Biosynthesis of poly(3-hydroxybutyrate-*co*-3-hydroxyhexanoate) from glucose by *Escherichia coli* through butyryl-CoA formation driven by Ccr-Emd combination**

Shu Saito<sup>1</sup>, Ryu Imai<sup>1</sup>, Yuki Miyahara<sup>2</sup>, Mari Nakagawa<sup>1</sup>, Izumi Orita<sup>1</sup>,  
Takeharu Tsuge<sup>2</sup>, and Toshiaki Fukui<sup>1,\*</sup>

1) School of Life Science and Technology, 2) School of Materials and Chemical Technology, Tokyo Institute of Technology, Yokohama, Japan

\*Corresponding author

Toshiaki Fukui

School of Life Science and Technology  
Tokyo Institute of Technology  
Tel/Fax: +81-45-924-5766  
e-mail: [tfukui@bio.titech.ac.jp](mailto:tfukui@bio.titech.ac.jp)

Table S1

Table S2

Table S3

Table S4

Table S5

Supplementary Table S1. Strains and plasmids used in this study.

Strain or plasmid	Relevant marker	Source or reference
<b><i>Escherichia coli</i></b>		
DH5 $\alpha$	F <sup>-</sup> , $\varphi 80lacZ\Delta M15$ , $\Delta(lacZYA-argF)$ U169, <i>deoR</i> , <i>recA1</i> , <i>endA1</i> , <i>hsdR17(rK<sup>-</sup>, mK<sup>+</sup>)</i> , <i>phoA</i> , <i>supE44</i> , $\lambda^{-}$ , <i>thi-1</i> , <i>gyrA96</i> , <i>relA1</i>	Lab stock
JM109	<i>endA1</i> , <i>recA1</i> , <i>gyrA96</i> , <i>thi-1</i> , <i>hsdR17(rK<sup>-</sup> mK<sup>+</sup>)</i> , <i>relA1</i> , <i>supE44</i> , $\Delta(lac-proAB)$ , F'[ <i>traD36</i> , <i>proAB</i> , <i>lacI<sup>q</sup></i> , <i>lacZ\Delta M15</i> ]	Lab stock
BW25113	<i>rrnB</i> , $\Delta lacZ4787$ , <i>hsdR514</i> , $\Delta araBAD567$ , $\Delta rhabAD568$ , <i>rph-1</i>	Datsenko and Wanner (2000)
JW $\Delta$ cra	JW0078-KC (BW25113 <i>\Delta cra::Km<sup>r</sup></i> ) derivative, <i>\Delta cra::FRT</i>	This study
JW $\Delta$ pdhR	JW0109-KC (BW25113 <i>\Delta pdhR::Km<sup>r</sup></i> ) derivative, <i>\Delta pdhR::FRT</i>	This study
JW $\Delta$ rng	JW3216-KC (BW25113 <i>\Delta rng::Km<sup>r</sup></i> ) derivative, <i>\Delta rng::FRT</i>	This study
JW $\Delta$ cra $\Delta$ rng	JW $\Delta$ cra derivative, <i>\Delta rng::FRT</i>	This study
JW $\Delta$ pgi	JW3985-KC (BW25113 <i>\Delta pgi::Km<sup>r</sup></i> ) derivative, <i>\Delta pgi::FRT</i>	This study
JW $\Delta$ pgi $\Delta$ rng	JW $\Delta$ pgi derivative, <i>\Delta rng::FRT</i>	This study
JW $\Delta$ pta	JW2294-KC (BW25113 <i>\Delta pta::Km<sup>r</sup></i> ) derivative, <i>\Delta pta::FRT</i>	This study
JW $\Delta$ pta $\Delta$ poxB	JW $\Delta$ pta derivative, <i>\Delta poxB::FRT</i>	This study
<b>Plasmids</b>		
pBKS-PCJAB	pBluescript II KS(+) derivative; <i>P<sub>lac</sub>-P<sub>Ac</sub>-phaP<sub>D4N</sub>C<sub>NSDG</sub>J<sub>Ac</sub></i> , <i>P<sub>Re</sub>-phaABI<sub>Re</sub></i>	This study
pBKS-PCJA	pBluescript II KS(+) derivative; <i>P<sub>lac</sub>-P<sub>Ac</sub>-phaP<sub>D4N</sub>C<sub>NSDG</sub>J<sub>Ac</sub></i> , <i>P<sub>Re</sub>-phaA<sub>Re</sub></i>	This study
pBBRtac	pBBR1-MCS2 derivative; <i>P<sub>tac</sub></i>	Fukui et al. 2009
pBtac-CJ <sub>Re</sub> E	pBBRtac derivative, <i>P<sub>tac</sub>-ccr<sub>Me</sub>-phaJ4a<sub>Re</sub>-emd<sub>Mm</sub></i>	This study
pBtac-CJ <sub>Re</sub> EB	pBBRtac derivative, <i>P<sub>tac</sub>-ccr<sub>Me</sub>-phaJ4a<sub>Re</sub>-emd<sub>Mm</sub>-bktB<sub>Re</sub></i>	This study
pBtac-CJ4 <sub>Pa</sub> E	pBBRtac derivative, <i>P<sub>tac</sub>-ccr<sub>Me</sub>-phaJ4<sub>Pa</sub>-emd<sub>Mm</sub>-bktB<sub>Re</sub></i>	This study
pSTV-HC	pSTV28 derivative; <i>P<sub>tac</sub>-had<sub>Re</sub>-crt2<sub>Re</sub></i>	This study
pSTV-HCB	pSTV28 derivative; <i>P<sub>tac</sub>-had<sub>Re</sub>-crt2<sub>Re</sub>-bktB<sub>Re</sub></i>	This study
pSTV-PCB	pSTV28 derivative; <i>P<sub>tac</sub>-paaH1<sub>Re</sub>-crt2<sub>Re</sub>-bktB<sub>Re</sub></i>	This study
pMW-Gm-ptxD <sub>EAAR</sub> ABC	pMW218 derivative, $\Delta \text{Km}^r::\text{Gm}^r$ , <i>ptxD<sub>EAAR</sub>-ptxABC</i>	This study

FRT, FLP recombinase target; *Ac*, *Aeromonas caviae*; *Me*, *Methylobacter extorquens*; *Mm*, *Mus musculus*; *Re*, *Ralstonia eutropha*.

Supplementary Table S2. The sequences of primers used in this study.

Primer	Sequence (5'-3')	Note
Construction of plasmids		
del-phaB1-inv5	CCTGCCGGCCTGGTTCAACCAAGTCG	For construction of pBKS-PCJA
del-phaB1-inv3	GTCCACTCCTGATTGGCTTCGTTA	
del-PphaP-inv5	AAAGAGGAGAAATTAACATGGCTGCAAGCGCAGCA	For construction of pBtac-CJ <sub>Re</sub> E
del-PphaP-inv3	CCGGCCT GGGGGTGGGCGAAGAACTCCAGCAT	
tac-5	TTGAATTGAGCTCAATATTCTGAAATGAGCTGTTGA	
tac-Rv	GGTCAATTCTGTTCTGTG	
bktB-Fw1	CGCTTCGAATCTAGAAAGGAGGC	For construction of pBtac-CJ <sub>Re</sub> EB
bktB-Rv1	ATCCACCCCTCCTCAGATACGC	
phaJ4a-Inv1	GTCGATAGTCTCCTCTTGACGATAAAC	For construction of pBtac-CJ4 <sub>Pa</sub> E
phaJ4a-Inv2	GGATCCGTTTTTGGGCTAGCAGGAGGA	
phaJ4Pa_N	ATGCCATTCTGACCGTAGCA	
phaJ4Pa_C	TCAGACGAAGCAGAGGCTGA	
A0602-F	ATGCAAATCCAAGGCAACGTATTCA	For construction of pSTV-HC
A0602-R-Fus	ATGTATTGCCTTACTTGGGCTGCATCCGA	
A3307-R	GCCTTAGCGATGCTGGAAATT	
A3307-F-Fus	CCAAGTAAAGGCAAATACATAGGAGAAGACA	
pSTV-inv5	TATCGATGATAAGCTGTCACAAACA	
pSTV-inv3	CATTAATGAATCGGCCAACGCGC	
pSTV-inv5_2	GGCTTAAGCCAGCCCCGACACC	For construction of pSTV-HCB
pSTV-inv3_2	TTAGCGATGCTGGAAATTGGGG	
Ptac-rrnB-Inv3	ATGATAATCCTCCTGAATTCAATTGTTATCCGCTCAC	For construction of pSTV-PCB
AATTCCACACATT		
pSTV-AA-Inv_3307N	GGCAAATACATAGGAGAAGACAT	
A0282_N	ATGAGCATCAGGACAGTGGGCA	
A0282_C	TTACTTGCTATAGACGTACACG	
Construction of double-knockout strains of <i>E. coli</i>		
rng-KC-Fw	TGAATTATTAAGTAATTAAACGCAC	For construction of JWΔcraΔrng and JWΔpgiΔrng
rng-KC-Rv	GCG	
poxB-KC-Fw	CCTTATTATGACGGAAATGCCACCC	For construction of JWΔptaΔpoxB
poxB-KC-Rv	GATGAACCTAAACTGTTACCGTTATC	

Supplementary Table S3. P(3HB-*co*-3HHx) biosynthesis from glucose by *E. coli* JM109-derived recombinant strains.

Entry	Plasmid 1	Plasmid 2	Plasmid 3	Dry cell mass (g/L)	PHA [g/L]	Residual cell mass (g/L)	PHA content [wt%]	3HHx [mol%]	Monomer amount in PHA [mmol/L-culture]	
									3HB	3HHx
1	pBKS-PCJAB			9.86 ± 0.05	5.64 ± 0.18	4.22 ± 0.19	57.2 ± 1.8	0	65.6 ± 2.0	0
2	pBKS-PCJAB	pBtac-CJ <sub>Re</sub> E		6.29 ± 0.59	2.37 ± 0.41	3.92 ± 0.27	37.5 ± 3.4	0	27.6 ± 4.8	0
3	pBKS-PCJAB	pBtac-CJ <sub>Re</sub> E	pSTV-HCB	6.87 ± 0.26	2.82 ± 0.30	4.05 ± 0.05	41.0 ± 2.8	14.0 ± 0.3	27.0 ± 2.9	4.4 ± 0.5
4	pBKS-PCJA	pBtac-CJ <sub>Re</sub> E	pSTV-HCB	3.51 ± 0.04	0.14 ± 0.02	3.38 ± 0.03	3.9 ± 0.52	21.5 ± 0.8	1.2 ± 0.2	0.32 ± 0.05
5	pBKS-PCJAB	pBtac-CJ <sub>Re</sub> E	pSTV-HC	4.49 ± 0.05	0.59 ± 0.08	3.91 ± 0.12	13.0 ± 1.8	0	6.8 ± 0.9	0
6	pBKS-PCJAB	pBtac-CJ <sub>Re</sub> EB		8.06 ± 0.15	3.39 ± 0.13	4.66 ± 0.17	42.1 ± 1.7	1.2 ± 0.1	38.8 ± 1.4	0.49 ± 0.06

The cells were cultivated in a 100 ml LB medium containing 2% (w/v) glucose and 1 mM IPTG for 48 h at 30°C (*n*=3).

pBKS-PCJAB (*phaP*<sub>D4N</sub>*C*<sub>NSDG</sub>*J*<sub>Ac</sub>-*phaAB*<sub>Re</sub>), pBKS-PCJA (*phaP*<sub>D4N</sub>*C*<sub>NSDG</sub>*J*<sub>Ac</sub>-*phaA*<sub>Re</sub>)

pBtac-CJ<sub>Re</sub>E (*ccr*<sub>Me</sub>-*phaJ4a*<sub>Re</sub>-*emd*<sub>Mm</sub>), pBtac-CJ<sub>Re</sub>EB (*ccr*<sub>Me</sub>-*phaJ4a*<sub>Re</sub>-*emd*<sub>Mm</sub>-*bktB*<sub>Re</sub>)

pSTV-HCB (*had*<sub>Re</sub>-*crt2*<sub>Re</sub>-*bktB*<sub>Re</sub>), pSTV-HC, (*had*<sub>Re</sub>-*crt2*<sub>Re</sub>)

Supplementary Table S4. Effects of replacements of (*R*)-hydratase gene and/or 3HB-CoA dehydrogenase gene on P(3HB-*co*-3HHx) biosynthesis from glucose by *E. coli* JM109-derived recombinant strains.

Plasmid 1	Plasmid 2 ( <i>R</i> -hydratase gene)	Plasmid 3 (3HB-CoA DH gene)	Dry cell mass (g/L)	PHA [g/L]	Residual cell mass (g/L)	PHA content [wt%]	3HHx comp. [mol%]	Monomer amount in PHA [mmol/L-culture]	
								3HB	3HHx
pBtac-CJ <sub>Re</sub> E ( <i>phaJ4aRe</i> )	pSTV-HCB ( <i>hadRe</i> )		6.55 ±0.18	2.06 ±0.19	4.48 ±0.04	31.5 ±2.0	15.4 ±1.5	19.4 ±1.4	3.5 ±0.1
	pSTV-PCB ( <i>paaHIRe</i> )		6.68 ±0.13	2.05 ±0.14	4.63 ±0.05	30.7 ±1.5	14.2 ±0.4	19.6 ±1.4	3.2 ±0.2
pBKS-PCJAB	pSTV-HCB ( <i>hadRe</i> )		6.58 ±0.04	1.93 ±0.03	4.66 ±0.06	29.3 ±0.5	16.1 ±0.2	17.9 ±0.3	3.4 ±0.04
		pBtac-CJ4 <sub>Pa</sub> E ( <i>phaJ4Pa</i> )	pSTV-PCB ( <i>paaHIRe</i> )	6.78 ±0.05	2.09 ±0.22	4.69 ±0.21	30.8 ±3.2	14.3 ±1.0	19.9 ±1.8

The cells were cultivated in a 100 ml LB medium containing 2% (w/v) glucose and 1 mM IPTG for 48 h at 30°C (*n*=3).

pBKS-PCJAB (*phaP<sub>D4N</sub>C<sub>NSDG</sub>J<sub>Ac</sub>-phaAB<sub>Re</sub>*)

pBtac-CJ<sub>Re</sub>E (*ccr<sub>Me</sub>-phaJ4aRe-emd<sub>Mm</sub>*), pBtac-CJ4<sub>Pa</sub>EB (*ccr<sub>Me</sub>-phaJ4Pa-emd<sub>Mm</sub>-bktB<sub>Re</sub>*)

pSTV-HCB (*hadRe-crt2Re-bktB<sub>Re</sub>*), pSTV-PCB (*paaHIRe-crt2Re-bktB<sub>Re</sub>*)

Supplementary Table S5. Effects of mutation(s) in sugar metabolism-regulating genes and acetate formation on P(3HB-*co*-3HHx) biosynthesis from glucose by *E. coli* BW25113-derived recombinant strains harboring pBKS-PCJAB/pBtac-cJ<sub>Ree</sub>/pSTV-HCB.

Entry	Host strain	Dry cell mass	PHA	Residual cell mass	PHA content	3HHx comp.	Monomer amount in PHA [mmol/L-culture]		Glucose consumption [g/L]	Acetate formation [g/L]
		(g/L)	[g/L]	(g/L)	[wt%]	[mol%]	3HB	3HHx		
7	BW25113 (control)	6.10 ± 0.17	1.97 ± 0.14	4.13 ± 0.03	32.2 ± 1.4	15.7 ± 0.24	18.3 ± 1.4	3.42 ± 0.21	17.0 ± 0.5	0.73 ± 0.11
<b>Sugar metabolisms</b>										
8	JWΔcra	1.60 ± 0.01	0.07 ± 0.00	1.53 ± 0.01	4.5 ± 0.1	3.1 ± 0.2	0.80 ± 0.02	0.03 ± 0.01	6.8 ± 0.5	2.1 ± 0.2
9	JWΔpdhR	3.02 ± 0.18	0.36 ± 0.01	2.66 ± 0.17	11.8 ± 0.4	trace	4.1 ± 0.1	trace	9.8 ± 0.3	0.56 ± 0.14
10	JWΔrng	8.45 ± 0.24	3.63 ± 0.33	4.82 ± 0.13	42.9 ± 2.8	trace	42.2 ± 3.9	trace	19.9 ± 0.1	0.17 ± 0.02
11	JWΔcraΔrng	8.23 ± 0.12	3.28 ± 0.08	4.95 ± 0.08	39.8 ± 0.6	trace	38.1 ± 0.9	trace	19.9 ± 0.1	0.16 ± 0.02
12	JWΔpgi	4.01 ± 0.18	0.75 ± 0.06	3.27 ± 0.12	18.6 ± 0.7	22.2 ± 1.1	6.3 ± 0.4	1.8 ± 0.2	12.9 ± 0.6	1.3 ± 0.1
13	JWΔpgiΔrng	3.82 ± 0.06	0.66 ± 0.05	3.10 ± 0.02	18.8 ± 0.7	6.5 ± 0.1	7.6 ± 0.5	0.54 ± 0.03	11.2 ± 0.2	1.2 ± 0.1
<b>Acetate formation</b>										
14	JWΔpta	5.29 ± 0.09	2.19 ± 0.06	3.10 ± 0.03	41.4 ± 0.5	1.9 ± 0.2	24.9 ± 0.6	0.47 ± 0.1	14.2 ± 0.3	0.51 ± 0.03
15	JWΔptaΔpoxB	1.65 ± 0.12	trace	1.65 ± 0.12	trace	0	trace	0	6.9 ± 0.1	1.4 ± 0.1 (pyruvate)

The cells were cultivated in a 100 ml LB medium containing 2% (w/v) glucose and 1mM IPTG for 48 h at 30°C (*n*=3).

pBKS-PCJAB (*phaP*<sub>D4N</sub>*C*<sub>NSDG</sub>*J*<sub>Ac</sub>-*phaAB*<sub>Re</sub>), pBtac-CJ<sub>Re</sub>E (*ccr*<sub>Me</sub>-*phaJ4a*<sub>Re</sub>-*emd*<sub>Mm</sub>), pSTV-HCB (*had*<sub>Re</sub>-*crt2*<sub>Re</sub>-*bktB*<sub>Re</sub>)