

[Back to article](#)**Table S1.** Contig size of folate biosynthetic genes from six folate-producing lactic acid bacteria (LAB) isolates

Isolate	<i>folE</i>	<i>folQ</i>	<i>folB</i>	<i>folK</i>	<i>folP</i>	<i>folC₁</i>	<i>folA</i>	<i>folC₂</i>
R23	273	123	265	131	163	333	273	478
4C261	271	128	265	142	194	332	364	470
JK13	209	115	257	215	185	333	248	478
BG7	274	124	265	206	185	333	260	487
S2SR08	274	216	265	208	194	333	364	488
NG64	273	105	257	209	233	331	272	487

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Table S2. Percent identity of folate biosynthetic genes from six folate-producing lactic acid bacteria (LAB) with nucleotide sequences from various LAB species in the NCBI databases (29)

Gene	Isolate	NCBI blastn	
		Identity/%	Description
<i>folE</i>	4C261	100	<i>L. plantarum</i> strain SKO-001 chromosome, complete genome; ID: CP040374.1
	R23	100	<i>L. plantarum</i> strain TCI507 chromosome, complete genome; ID: CP054259.1
	JK13	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	BG7	100	<i>L. plantarum</i> strain TCI507 chromosome, complete genome; ID: CP054259.1
	NG64	100	<i>L. plantarum</i> strain TCI507 chromosome, complete genome; ID: CP054259.1
	S2SR08	100	<i>L. plantarum</i> strain TCI507 chromosome, complete genome; ID: CP054259.1
<i>folQ</i>	4C261	100	<i>L. plantarum</i> strain SRCM102737 chromosome, complete genome; ID: CP028261.1
	R23	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	JK13	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	BG7	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	NG64	100	<i>L. plantarum</i> strain SRCM103418 chromosome, complete genome; ID: CP035168.1
	S2SR08	100	<i>L. plantarum</i> strain SRCM103418 chromosome, complete genome; ID: CP035168.1
<i>folB</i>	4C261	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	R23	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	JK13	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	BG7	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	NG64	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	S2SR08	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
<i>folK</i>	4C261	100	<i>L. fermentum</i> strain LfQi6 chromosome; ID: CP025592.1
	R23	100	<i>L. fermentum</i> strain LfQi6 chromosome; ID: CP025592.1
	JK13	100	<i>L. fermentum</i> strain LfQi6 chromosome; ID: CP025592.1
	BG7	100	<i>L. fermentum</i> strain LfQi6 chromosome; ID: CP025592.1
	NG64	100	<i>L. fermentum</i> strain LfQi6 chromosome; ID: CP025592.1
	S2SR08	100	<i>L. fermentum</i> strain LfQi6 chromosome; ID: CP025592.1
<i>folP</i>	4C261	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	R23	100	<i>L. fermentum</i> strain HFD1 chromosome, complete genome; ID: CP050919.1
	JK13	100	<i>L. fermentum</i> strain HFD1 chromosome, complete genome; ID: CP050919.1
	BG7	100	<i>L. fermentum</i> strain HFD1 chromosome, complete genome; ID: CP050919.1
	NG64	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	S2SR08	100	<i>L. fermentum</i> strain HFD1 chromosome, complete genome; ID: CP050919.1
<i>folC₁</i>	4C261	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	R23	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	JK13	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	BG7	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	NG64	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	S2SR08	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
<i>folA</i>	4C261	100	<i>L. plantarum</i> strain TCI507 chromosome, complete genome; ID: CP054259.1
	R23	100	<i>L. plantarum</i> strain TCI507 chromosome, complete genome; ID: CP054259.1
	JK13	100	<i>L. plantarum</i> strain TCI507 chromosome, complete genome; ID: CP054259.1
	BG7	100	<i>L. plantarum</i> strain TCI507 chromosome, complete genome; ID: CP054259.1
	NG64	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	S2SR08	100	<i>L. plantarum</i> strain NCIMB8826 (WCFS1) chromosome, complete genome; ID: CP037961.1
<i>folC₂</i>	4C261	100	<i>L. plantarum</i> strain LLY-606 chromosome, complete genome; ID: CP023306.1
	R23	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	JK13	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	BG7	100	<i>L. plantarum</i> strain Heal19 chromosome, complete genome; ID: CP055123.1
	NG64	100	<i>L. plantarum</i> strain SRCM100442 chromosome, complete genome; ID: CP028221.1
	S2SR08	100	<i>L. plantarum</i> strain SRCM100442 chromosome, complete genome; ID: CP028221.1

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Table S3. The comparison of the number of conserved sites (C) and variable sites (V) of eight folate biosynthetic genes between six folate-producing lactic acid bacteria (LAB) isolates and the reference strain (*Lactiplantibacillus plantarum* WCFS1)

Isolate	Reference strain (WCFS1)															
	<i>folE</i>		<i>folQ</i>		<i>folB</i>		<i>folK</i>		<i>folP</i>		<i>folC₁</i>		<i>folA</i>		<i>folC₂</i>	
	C	V	C	V	C	V	C	V	C	V	C	V	C	V	C	V
R23	271/314	2/314	123/221	0/221	263/268	2/268	72/257	59/257	92/302	68/302	327/345	6/345	272/374	1/374	478/509	0/509
4C261	269/314	2/314	127/221	1/221	263/268	2/268	53/257	84/257	59/302	134/302	327/345	5/345	361/374	3/374	469/509	1/509
JK13	209/314	0/314	115/221	0/221	256/268	1/268	76/257	134/257	65/302	119/302	327/345	6/345	247/374	1/374	478/509	0/509
BG7	271/314	3/314	124/221	0/221	263/268	2/268	73/257	128/257	65/302	119/302	327/345	6/345	259/374	1/374	487/509	0/509
S2SR08	271/314	3/314	212/221	4/221	263/268	2/268	73/257	130/257	67/302	126/302	327/345	6/345	362/374	2/374	484/509	4/509
NG64	271/314	2/314	104/221	1/221	256/268	1/268	74/257	130/257	70/302	162/302	327/345	4/345	272/374	0/374	483/509	4/509