



Figure S1. Length-density distribution diagram of effective sequences from culturable endophytic bacteria in pea embryos.

Table S1. Colony morphology of the 27 putative nitrogen-fixing bacterial (NFB) strains identified from pea embryos.

Strain No.	Size	Shape	Edge	Texture	Color	Raised/Flat	Transparency
S18P01-1	Small	Round	Smooth	Dry	White	Flat	Opaque
S18P01-2	Medium	Round	Smooth	Wet	None	Raised	Transparent
S18P02-1	Small	Round	Smooth	Wet	White	Raised	Translucent
S18P02-2	Medium	Round	Smooth	Wet	Yellowish	Raised	Transparent
S18P02-3	Large	Round	Smooth	Wet	Milky	Raised	Translucent
S18P03-1	Medium	Round	Smooth	Wet	Milky	Raised	Translucent
S18P03-2	Medium	Round	Smooth	Wet	Light yellow	Raised	Translucent
S18P04-1	Medium	Round	Smooth	Wet	Light yellow	Raised	Transparent
S18P04-2	Large	Round	Smooth	Wet	Yellow	Raised	Translucent
S18P04-3	Medium	Round	Smooth	Wet	Light yellow	Raised	Translucent
S18P05-1	Small	Round	Smooth	Dry	White	Raised	Opaque
S18P05-2	Small	Round	Smooth	Wet	None	Raised	Transparent
S18P06-1	Small	Round	Smooth	Wet	Light yellow	Raised	Translucent
S18P06-2	Small	Round	Smooth	Wet	Light yellow	Raised	Opaque
S18P06-3	Small	Round	Smooth	Wet	Light yellow	Raised	Transparent
S18P07-1	Large	Round	Smooth	Wet	Light yellow	Raised	Translucent
S18P07-2	Small	Round	Smooth	Wet	White	Raised	Translucent
S18P07-3	Medium	Round	Smooth	Wet	Light yellow	Raised	Translucent
S18P08-1	Medium	Round	Smooth	Wet	Light yellow	Raised	Opaque
S18P08-2	Medium	Round	Smooth	Wet	Milky	Raised	Opaque
S18P08-3	Small	Round	Smooth	Wet	White	Raised	Translucent
S18P09	Small	Round	Smooth	Wet	Milky	Raised	Translucent
S18P10	Medium	Round	Smooth	Wet	Light yellow	Raised	Transparent
S18P11-1	Medium	Round	Smooth	Wet	Milky	Raised	Opaque
S18P11-2	Medium	Round	Smooth	Wet	Light yellow	Raised	Translucent
S18P12-1	Medium	Round	Smooth	Wet	Milky	Raised	Translucent
S18P12-2	Medium	Round	Smooth	Wet	Milky	Raised	Translucent

Table S2. Summary of effective DNA sequencing reads from endophytic bacteria in pea embryos and derived operational taxonomic units (OTUs).

Sample No.	Effective reads	OTUs	Sample No.	Effective reads	OTUs
S18P01.1	25236	690	S18P11.1	34886	301
S18P01.2	36987	362	S18P11.2	36418	283
S18P02.1	33292	271	S18P12.1	31574	311
S18P02.2	33984	334	S18P12.2	33842	310
S18P03.1	36059	360	S18P13.1	31849	406
S18P03.2	33734	379	S18P13.2	35615	418
S18P04.1	33225	433	S18P14.1	36546	514
S18P04.2	34204	483	S18P14.2	33946	488
S18P05.1	32964	332	S18P15.1	35856	399
S18P05.2	35107	341	S18P15.2	36085	423
S18P06.1	31884	358	S18P16.1	32335	338
S18P06.2	23449	323	S18P16.2	34855	446
S18P07.1	33543	460	S18P17.1	36774	374
S18P07.2	33656	604	S18P17.2	37104	354
S18P08.1	34236	367	S18P18.1	35905	604
S18P08.2	36669	335	S18P18.2	27585	452
S18P09.1	35348	453	S18P19.1	35176	297
S18P09.2	35535	329	S18P19.2	34399	395
S18P10.1	35810	343	S18P20.1	34660	342
S18P10.2	34477	278	S18P20.2	35954	387

Table S3. Sequencing depths and diversity indexes of endophytic bacterial samples in pea embryos.

Sample No.	Sequencing depth	Diversity index		
		Chao1	Shannon	Simpson
S18P02.1	0.9993	239.39	6.91	0.98
S18P02.2	0.9990	300.41	6.45	0.94
S18P03.1	0.9988	300.93	7.13	0.98
S18P03.2	0.9992	302.72	7.14	0.98
S18P04.1	0.9987	346.90	7.31	0.99
S18P04.2	0.9985	394.01	7.42	0.99
S18P05.1	0.9991	284.61	7.21	0.99
S18P05.2	0.9983	312.30	6.62	0.96
S18P06.1	0.9986	305.09	7.01	0.98
S18P06.2	0.9992	268.86	6.68	0.97
S18P08.1	0.9990	305.40	7.05	0.98
S18P08.2	0.9990	301.90	6.49	0.95
S18P10.1	0.9993	288.42	5.89	0.88
S18P10.2	0.9991	239.01	5.61	0.89
S18P11.1	0.9989	262.95	6.34	0.94
S18P11.2	0.9982	226.26	1.20	0.20
S18P12.1	0.9989	276.76	7.20	0.99
S18P12.2	0.9991	245.85	7.19	0.99

Table S4. The long 16S rDNA sequences of four selected nitrogen-fixing bacterial (NFB) strains.

> S18P02-2 (GenBank Accession No. PP082614)

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> S18P08-2 (GenBank Accession No. PP082615)

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> S18P08-3 (GenBank Accession No. PP082616)

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> S18P12-1 (GenBank Accession No. PP082617)

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LOCUS PP082614 1364 bp DNA linear BCT 04-JAN-2024

DEFINITION *Klebsiella oxytoca* strain 02-2 16S ribosomal RNA gene, partial
sequence.

ACCESSION PP082614

VERSION PP082614

KEYWORDS .

SOURCE Klebsiella oxytoca

ORGANISM Klebsiella oxytoca

Bacteria; Pseudomonadota; Gammaproteobacteria; Enterobacterales;
Enterobacteriaceae; Klebsiella/Raoultella group; Klebsiella.

REFERENCE 1 (bases 1 to 1364)

AUTHORS Hao,J., Zhang,X., Qiu,S., Song,F., Lyu,X., Ma,Y. and Peng,H.

TITLE Species Diversity, Nitrogen Fixation and Nutrient Solubilization
Activities of Endophytic Bacteria in Pea Embryos

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1364)

AUTHORS Hao,J., Zhang,X., Qiu,S., Song,F., Lyu,X., Ma,Y. and Peng,H.

TITLE Direct Submission

JOURNAL Submitted (04-JAN-2024) Qingdao Academy of Agricultural Sciences,
Qingdao Academy of Agricultural Sciences, Qingdao, Qingdao,
Shandong 266100, China

COMMENT Sequences were screened for chimeras by the submitter using SeqMan7.1.

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

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DEFINITION *Enterobacter rogenkampii* strain 08-2 16S ribosomal RNA gene,
partial sequence.

ACCESSION PP082615

VERSION PP082615

KEYWORDS .

SOURCE Enterobacter roggenkampii

ORGANISM Enterobacter roggenkampii

Bacteria; Pseudomonadota; Gammaproteobacteria; Enterobacterales;
Enterobacteriaceae; Enterobacter; Enterobacter cloacae complex.

REFERENCE 1 (bases 1 to 1430)

AUTHORS Hao,J., Zhang,X., Qiu,S., Song,F., Lyu,X., Ma,Y. and Peng,H.

TITLE Species Diversity, Nitrogen Fixation and Nutrient Solubilization
Activities of Endophytic Bacteria in Pea Embryos

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1430)

AUTHORS Hao,J., Zhang,X., Qiu,S., Song,F., Lyu,X., Ma,Y. and Peng,H.

TITLE Direct Submission

JOURNAL Submitted (04-JAN-2024) Qingdao Academy of Agricultural Sciences,
Qingdao Academy of Agricultural Sciences, Qingdao, Qingdao,
Shandong 266100, China

COMMENT Sequences were screened for chimeras by the submitter using SeqMan7.1.

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

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LOCUS PP082616 929 bp DNA linear BCT 04-JAN-2024

DEFINITION *Enterobacter soli* strain 08-3 16S ribosomal RNA gene, partial sequence.

ACCESSION PP082616

VERSION PP082616

KEYWORDS .

SOURCE Enterobacter soli

ORGANISM Enterobacter soli

Bacteria; Pseudomonadota; Gammaproteobacteria; Enterobacterales;
Enterobacteriaceae; Enterobacter.

REFERENCE 1 (bases 1 to 929)

AUTHORS Hao,J., Zhang,X., Qiu,S., Song,F., Lyu,X., Ma,Y. and Peng,H.

TITLE Species Diversity, Nitrogen Fixation and Nutrient Solubilization
Activities of Endophytic Bacteria in Pea Embryos

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 929)

AUTHORS Hao,J., Zhang,X., Qiu,S., Song,F., Lyu,X., Ma,Y. and Peng,H.

TITLE Direct Submission

JOURNAL Submitted (04-JAN-2024) Qingdao Academy of Agricultural Sciences,
Qingdao Academy of Agricultural Sciences, Qingdao, Qingdao,
Shandong 266100, China

COMMENT Sequences were screened for chimeras by the submitter using SeqMan
7.1.

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

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/organism="Enterobacter soli"

/mol_type="genomic DNA"

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LOCUS PP082617 1333 bp DNA linear BCT 04-JAN-2024

DEFINITION *Enterobacter roggenkampii* strain 12-1 16S ribosomal RNA gene,
partial sequence.

ACCESSION PP082617

VERSION PP082617

KEYWORDS .

SOURCE *Enterobacter roggenkampii*

ORGANISM *Enterobacter roggenkampii*

Bacteria; Pseudomonadota; Gammaproteobacteria; Enterobacterales;
Enterobacteriaceae; *Enterobacter*; *Enterobacter cloacae* complex.

REFERENCE 1 (bases 1 to 1333)

AUTHORS Hao,J., Zhang,X., Qiu,S., Song,F., Lyu,X., Ma,Y. and Peng,H.

TITLE Species Diversity, Nitrogen Fixation and Nutrient Solubilization
Activities of Endophytic Bacteria in Pea Embryos

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1333)

AUTHORS Hao,J., Zhang,X., Qiu,S., Song,F., Lyu,X., Ma,Y. and Peng,H.

TITLE Direct Submission

JOURNAL Submitted (04-JAN-2024) Qingdao Academy of Agricultural Sciences,
Qingdao Academy of Agricultural Sciences, Qingdao, Qingdao,
Shandong 266100, China

COMMENT Sequences were screened for chimeras by the submitter using SeqMan 7.1.

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..1333
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/clone="16s DNA"
/collection_date="Oct-2023"

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/product="16S ribosomal RNA"

ORIGIN

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121 aaagaggggg accttcgggc ctcttgccat cagatgtgcc cagatgggat tagctagtag
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241 actggaactg agacacggtc cagactccta cgggaggcag cagtggggaa tattgcacaa
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