

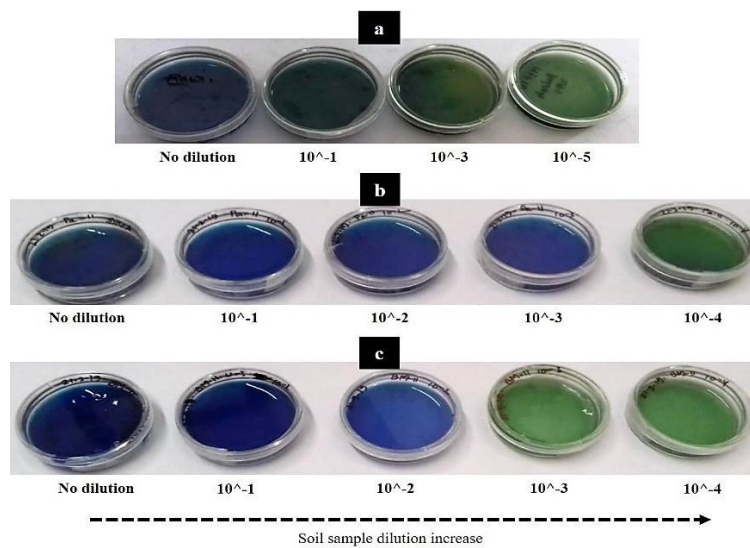
Screening and isolation of potential nitrogen-fixing *Enterobacter* sp. GG1 from mangrove soil with its accelerated impact on green chili plant (*Capsicum frutescens* L.) growth amelioration

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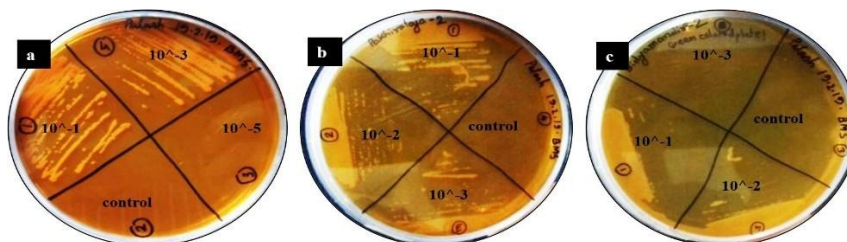
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doi: <https://doi.org/10.7324/JABB.2023.139674>

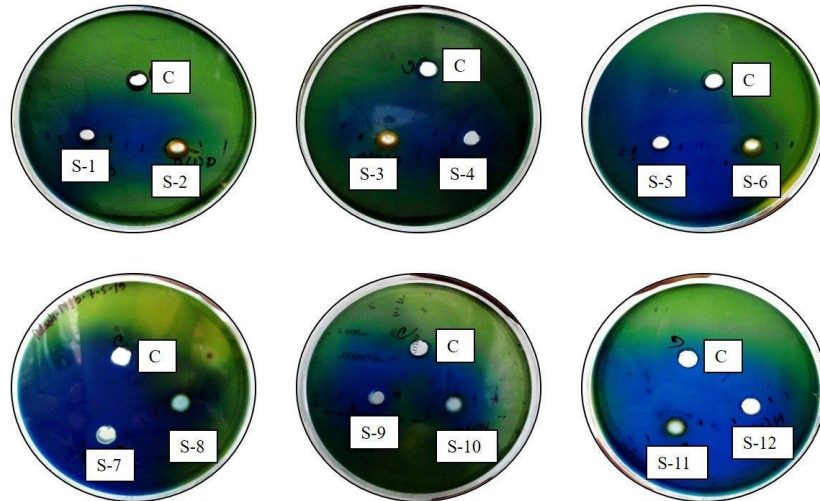
Supplementary Figures:



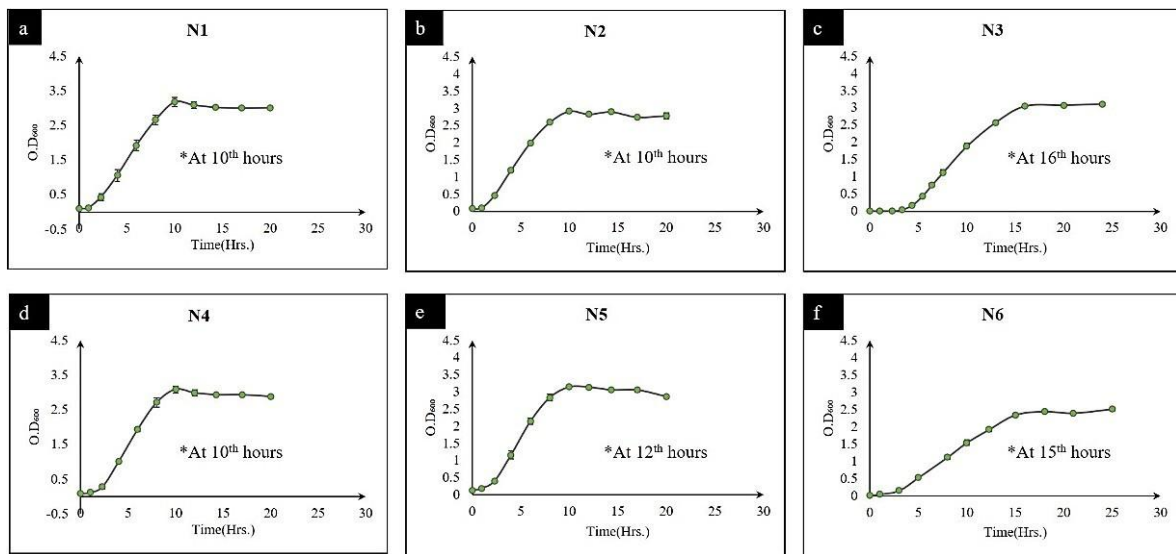
Supplementary Figure S1: Isolation of N-fixing bacteria in Nfb semi-solid medium (a: Dobanki sample; b: Pakhiralay sample; c: Mathurakhanda sample)



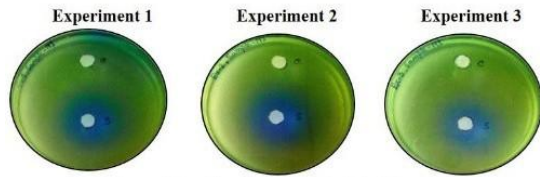
Supplementary Figure S2: Streak in BMS medium for N-fixing bacterial single colony isolation (a: Dobanki sample; b: Pakhiralay sample; c: Mathurakhanda sample)



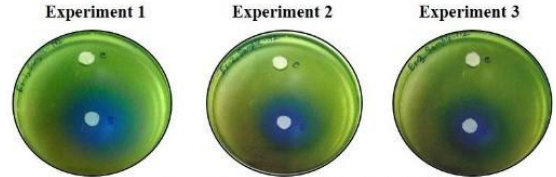
Supplementary Figure S3: Preliminary study of primary screening by well diffusion method in Nfb agar plate (C=control; S=sample).



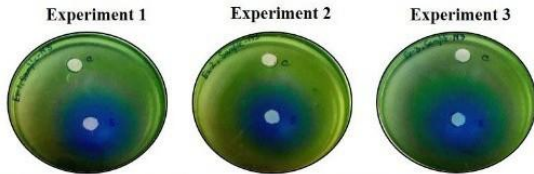
Supplementary Figure S4. Exponential phase study of nitrogen-fixing bacteria in Nfb media.



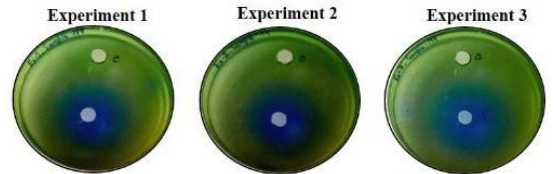
a: N1 isolate bacterial N_2 -fixation ability check by blue zone measure after 72 hours treatment in Nfb solid media plate (n=3)



b: N2 isolate bacterial N_2 -fixation ability check by blue zone measure after 72 hours treatment in Nfb solid media plate (n=3)



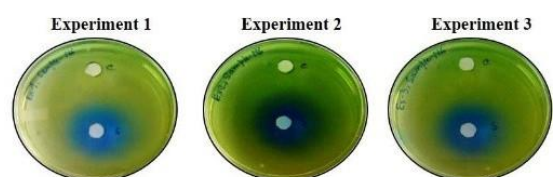
c: N3 isolate bacterial N_2 -fixation ability check by blue zone measure after 72 hours treatment in Nfb solid media plate (n=3)



d: N4 isolate bacterial N_2 -fixation ability check by blue zone measure after 72 hours treatment in Nfb solid media plate (n=3)

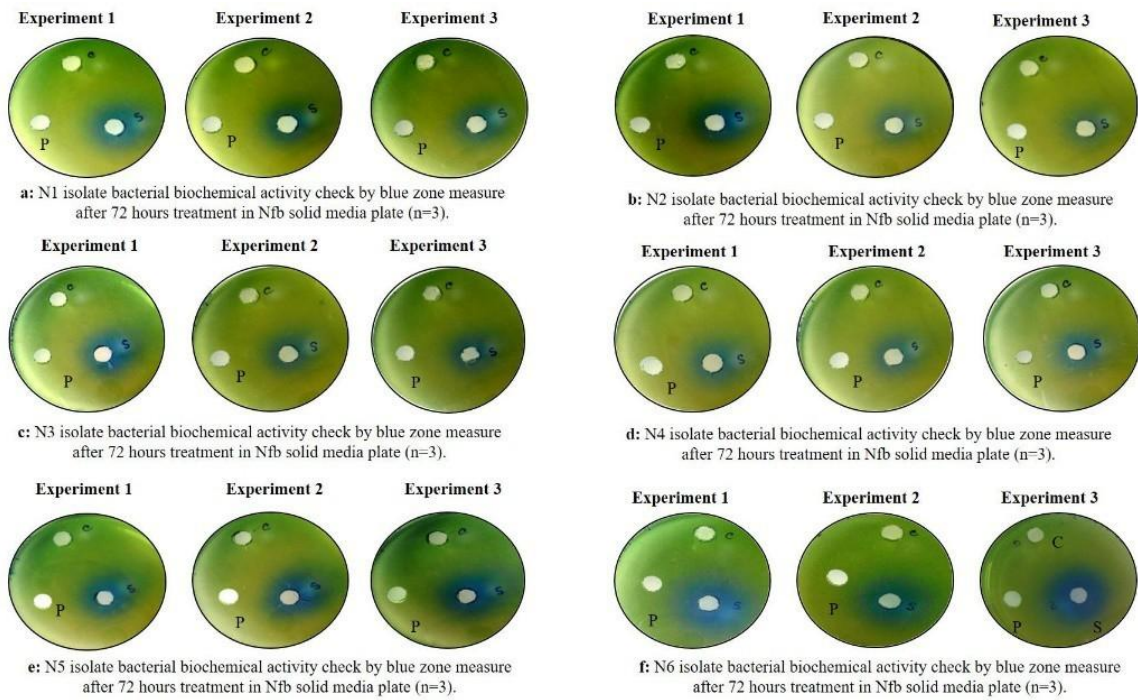


e: N5 isolate bacterial N_2 -fixation ability check by blue zone measure after 72 hours treatment in Nfb solid media plate (n=3)

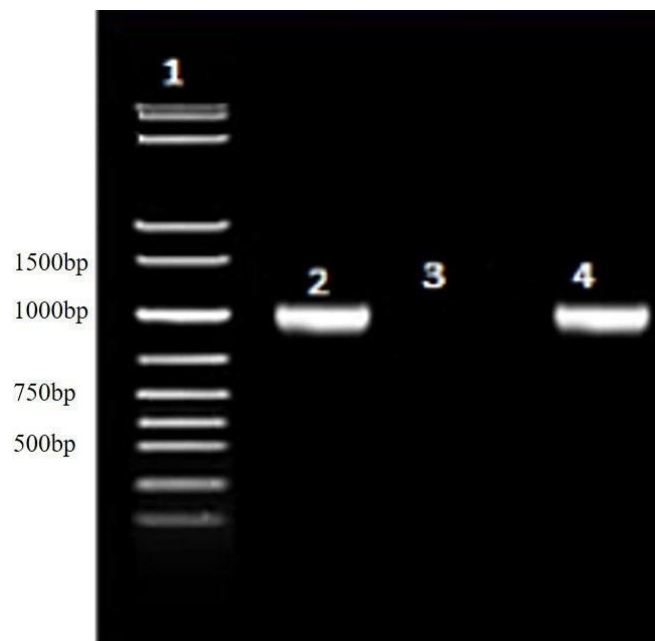


f: N6 isolate bacterial N_2 -fixation ability check by blue zone measure after 72 hours treatment in Nfb solid media plate (n=3)

Supplementary Figure S5: Exponential phase study of nitrogen-fixing bacteria in Nfb media (C= control; S= isolated culture).



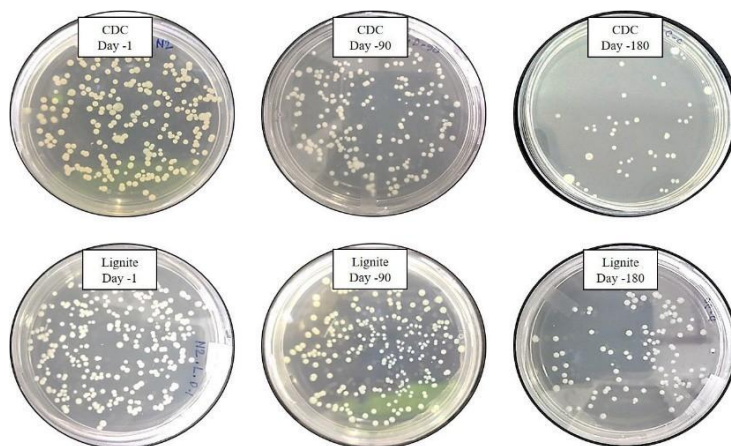
Supplementary Figure S6: Determine the extracellular or intracellular response for N-fixation in Nfb media; when, C= PBS buffer as a control, P= crude extract of N-fixing bacterial isolate (for intracellular response investigation), S= N-fixing bacterial alive cell (for extracellular response investigation).



Supplementary Figure S7: Shows a single 1Kb PCR product of 16S rRNA gene on 2% agarose gel (Lane 1: 1KB DNA ladder, Lane 2: 16S amplicon (Positive Control: *E. coli*), Lane 3: Negative Control, Lane 4: Sample).

Description	Max Score	Total Score	Query Cover	E value	Per. Ident
Enterobacter sp. FF16 16S ribosomal RNA gene, partial sequence	2346	2346	100%	0.0	98.93%
Enterobacter cloacae strain ACD1 16S ribosomal RNA gene, partial sequence	2340	2340	100%	0.0	98.86%
Enterobacter mori strain AS5 16S ribosomal RNA gene, partial sequence	2340	2340	100%	0.0	98.86%
Enterobacter ludwigii strain AA1 16S ribosomal RNA gene, partial sequence	2340	2340	100%	0.0	98.86%
Enterobacter tabaci strain NAC74 16S ribosomal RNA gene, partial sequence	2340	2340	100%	0.0	98.86%
Enterobacter sp. strain LSB19 16S ribosomal RNA gene, partial sequence	2340	2340	100%	0.0	98.86%
Enterobacter sp. strain LSB10 16S ribosomal RNA gene, partial sequence	2340	2340	100%	0.0	98.86%
Enterobacter roggenkampii CCI9 gene for 16S ribosomal RNA, partial sequence	2340	2340	100%	0.0	98.86%
Enterobacter asburiae strain TY175-13 16S ribosomal RNA gene, partial sequence	2340	2340	100%	0.0	98.86%
Enterobacter ludwigii strain TY175-12 16S ribosomal RNA gene, partial sequence	2340	2340	100%	0.0	98.86%

Supplementary Figure S8: 16S rRNA sequence of N4 bacterial isolates was generated BLAST analysis to compare with the sequences in the NCBI GenBank database. The N4 isolate has been higher similar to *Enterobacter* sp. bacterial strain.



Supplementary Figure S9: Best plat show of viability study at 180 days of *Enterobacter* sp. GG1 in carriers (CDC and lignite).

Supplementary Data file SD1

Enterobacter sp. GG1_16s rRNA gene => Enterobacter sp. GG1

TGTGTACAAGCCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGATTACTAGCGATTCCGACT
TCATGGAGTCGAGTTGTCAGACTCCAATCCGGACTACGACGCATTTTATGAGGTCCGCTTGCTCTCG
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AAGTCCCCCTCTTTGGTCTTGCAGCTTATGCGGTATTAGCTACCGTTCCAGTAGTTATCCCCCT CC
ATCAGGCAGTTTCCAGACATTACTACCAATGCGCCGCTCGCCGGCAAAGTAG

Azotobacter chroococcum YSC6 => AB696769.1:798-1494 Azotobacter chroococcum gene for 16S ribosomal RNA, partial sequence, strain: NTUIOB YSC6

ACGCCGTAACGATGTCGACTAGCCGTTGGGCTCCTTGAGAGCTTGGTGGCGCAGCTAACGCATTA
AGTCGACCGCCTGGGGAGTACGGCCGAAGGTTAAAACCTCAAATGAATTGACGGGGGCCCGCAC
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CGCGAGGTGGAGCTAATCCAGAAAACCGATCGTAGTCCGGATCGCAGTCTGCAACTCGACTGCG
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ACACCGCCGTCACACCATGGGAGTGGGTTGCTCCAGAAGTAGCTAGTCTAACCTTCGGGGGGAC
GGTTACCACGGAGTGATTATGACTGGGGTGAAGTCGTAACAA

Azospirillum lipoferum B7=> AY685925.1:1-281 Azospirillum lipoferum clone B7 16S-23S intergenic spacer, complete sequence

CTAAGGAAGCCGACCCTGGTGGGTCCGGCACCTTCAAGTCCAGATGGCGCATCTCTGCCGCCGCCG
GCGCATCCCTTCTCGACGATCCGGAACACCCGCTGACAGTGCATCCGCACTGTCTCGGCCGGATTG
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GTTTTAAGTGACCGAGGATGCATCTCATGAGCGTCCACGAGGCAGGAGCGGTTGCCCTGTGCG
TGACGTTCCGGAATAGAG

Beijerinckia sp. strain 37L => MG904942.1:1-1317 Beijerinckia sp. strain 37L 16S ribosomal RNA gene, partial sequence

TAAACGAGTGGGGCAGGTTAACACATGCAAGTCGAACGCCCGCAAGGGGAGTGGCAGACGGGT
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Burkholderia sp. strain OKR4-1 => OP872624.1:1-1502 Burkholderia sp. strain OKR4-1 16S ribosomal RNA gene, partial sequence

TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTGTTTTTTTTTGCTCTATGAGCTGCGCATGCTTACACATGCAA
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GTGGCTAGTCTAACCGCAAGGAGGACGGTACCACGGTAGGATTCTGACTGGGTGAGCAAAAA

Clostridium sp. M98449 => M98449.1:1-137 Clostridium sp. 16S ribosomal RNA (16S rRNA) gene, partial sequence

GAGATTAGGAAGAACCCAGTGGCGAAGGCGGCTTTCTGGACTGTAACCTGACGCTGAGGCCCGAA
AGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTACTAGGTG TAGGAGG

Enterobacter cloacae strain OsEp_A&N_15A7=> MT367840.1:12-1397 Enterobacter cloacae strain OsEp_A&N_15A7 16S ribosomal RNA gene, partial sequence

GAACGGTAGCACAGAGAGCTTGTCTCGGGTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGAA
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Gluconacetobacter sp. 0w26 => OK641906.1:1-579 Gluconacetobacter sp. strain 0w26 16S ribosomal RNA gene, partial sequence GTAACGCGTAGGAATCTATCTTTGGGTGGGGGATAACTGTGGGAAACTACAGCTAATACCGCATG
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Herbaspirillum sp. Ah5_2.5 => GQ181144.1:13-488 Herbaspirillum sp. enrichment culture clone Ah5_2.5 16S ribosomal RNA gene, partial sequence
TAGGAGCTTGCTCCTGATGGCGAGTGGCGAACGGGTGAGTAATATATCGGAACGTGCCCTAGAGT
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TGAGTGAAGAAGGCCTTCGGGTTGTAAGCTTTTGTTCAGGGAAGAAACGGTTCCAGCTAATATC
TGGAGCTAATGACGGTACCTGAAGAATAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATA
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Ideonella sp. URA-8=> LC505027.1:1-1471 Ideonella sp. URA-8 gene for 16S ribosomal RNA, partial sequence
TGGCTCAGATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGTAACGCGGGCAACC
TGGCGACGAGTGGCGAACGGGTGAGTAATGCATCGGAACGTGCCAGTAGTGGGGGATAGCCCGG
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CCGTACACCATGGGAGCGGGTCTGCCAGAAGTAGTTAGCCTAACCGCAAGGAGGGCGATTACC
ACGGCAGGGTTTCGTGACTGGGGTGAAGTCGTAACAA

Klebsiella sp. SXW12 => OP648246.1:1-1418 Klebsiella sp. strain SXW12 16S ribosomal RNA gene, partial sequence
AGCTACACATGCAGTCGAGCGGTAGCACAGAGAGCTTGCTCTCGGGTGACGAGCGGCGGACGGGT
GAGTAATGCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCA
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TGGGTTGCAAAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTACCA

Methanosarcina sp. T40UC2 => MG008506.1:1-1135 Methanosarcina sp. strain T40UC2 16S ribosomal RNA gene, partial sequence

TGCTGGAATGCTTTATGCGTCAAATGGATTTCGTCTGCCCAAGGATGGGTCTGCGGCCTATCAGGTA
GTAGTGGGTGTAATGTACCTACTAGCCGACAACGGGTACGGGTTGTGAGAGCAAGAGCCCGGAGA
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ACTGTGAAGCATCTGTTAAGTCAAGCAACGAGCGAGACCCGTGCCACTGTTACCAGCATATTCT
CCGGAATGATGGGTACTCTGTGGGGACCGCTATGTTAAATAGGAGGAAGGTGCGGGCCACGGTA
GGTCAGTATGCCCCGAATCTCCCGGGCTACACGCGGGCTACAATGGATGGGACAATGGGTCCCTC
CCCCGAAAGGGCTGGTAATCTCACAACCCATTTCGTAGTTCGGATCGAGGGCTGTAACCTCGCCCT
CGTGAAGCTGGAATCCGTAGTAATCGC

Pseudomonas sp. strain S'23 => MW578905.1:26-1387 Pseudomonas sp. strain S'23 16S ribosomal RNA gene, partial sequence

GTCGAGCGGATGAGAGGAGCTTGCTCCTTGATTTAGCGGCGGACGGGTGAGTAATGCCTAGGAAT
CTGCCTGGTAGTGGGGGATAACGTTCCGAAAGGAACGCTAATACCGCGTACGTCTACGGGAGAA
AGCAGGGGACCTTCGGGCCTTGCCTATCAGATGAGCCTAGGTCCGATTAGCTAGTTGGTGAGGT
AATGGCTCACCAAGGCGACGATCCGTAACCTGGTCTGAGAGGATGATCAGTCACACTGGAAGTGA
ACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATC
CAGCAATGCCCGTGTGTGAAGAAGGTCTTCGGATTGTAAGCACTTTAAGTTGGGAGGAAGGGC
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AGAGTACGGTAGAGGGTGGTGGAATTTCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAAC
ACCAGTGGCGAAGGCGACCACTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGGAGCAA
ACAGGATTAGATACCTGGTAGTCCACGCCGTAACGATGTCAACTAGCCGTTGGAATCCTTGAGA
TTTTAGTGGCGCAGCTAACGCATTAAGTTGACCGCTGGGAGTACGGCCGCAAGGTTAAACACTC
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AACCTTGTCTTATGTTACCAGCACCTCGGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGG
AGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCAGGGCTACACACGTGCTACAAT
GGTCCGTACAAAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCATAAAAACCGATCGTAGTCCGG
ATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGTGAATCAGAATGTCACG
GTGAATACGTTCCCGGGCCTTGTACACACCCGCGTACACCATGGGAGTGGGTTGCT

Paenibacillus chibensis SK4-3.2 => MN421117.1:179-1267 Paenibacillus chibensis strain SK4-3.2 16S ribosomal RNA gene, partial sequence

CGGAGCAACGCCGCTGAGTGATGAAGGTTTTCCGGATCGTAAAGCTCTGTTGCCAGGGAAGAACG
TCCGGTAGAGTAACTGCTACCGGAGTGACGGTACCTGAGAAGAAAGCCCCGGCTAATTACGTGCC
AGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAG
GCGGTCACTTAAGTCTGGTGTTTAAGGCCAAGGCTCAACCTTGGTTGCACTGGAAACTGGGTGAC
TTGAGTGCAGAAGAGGAGAGTGAATTCACGTGTAGCGGTGAAATGCGTAGATATGTGGAGGAA
CACCAGTGGCGAAGGCGACTCTCTGGGCTGTAACCTGACGCTGAGGCGCGAAAGCGTGGGGAGCAA
ACAGGATTAGATACCTGGTAGTCCACGCCGTAACGATGAATGCTAGGTGTTAGGGGTTTCGATA
CCCTTGGTGGCGAAGTTAACACATTAAGCATTCCGCTGGGGAGTACGGTCCGAAGACTGAAACTC
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ACCTTACCAAGTCTTGACATCCCTCTGAATCCCTAGAGATAGAGGCGGCCCTTCGGGACAGAGGTG
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GGCCAGTACAACGGGAAGCGAAGTCGCGAGATGGAGCCAATCCTATCAAAGCTGGTCTCAGTTCG
GATTGCAGGTGCAACCCGCTGCATGAAGTCGGAATTGCTAGTAATCGCGGATCAGCATGCCGC
GGTGAATACGTTCCCGGTCTTGTACACACCCGCGTACACCACGAGAGTTTACAACACCCGAAG
TCGGTGGGTAACCCGCAAGGGAGCCAGCCGCGAAGGTGGG

Supplementary Data file SD2: Multiple sequence alignment of N-fixing free living bacterial based on 16s rRNA gene sequences



Consensus CA0AG0ACATGGACTGAGA0ACGGC0AA0T0C -TACGGGAGGCAGCAGTGGGG-

Azospirillum lipoferum B7 21
B akh odriasp.OKR4+a 367
Enterobacter *doacae* OsEp_AN_15A7 297
Glucosacetobacter sp. Dw26 312
Ideonella sp. URA-8 335
Klebsiella sp. SXW12 312
Pseudomonas sp. S23 298

A T T C A T A C T T C A C C C T T C

Durkholderia sp.OKR4-1 430
Glucosacetobacter sp. Dw26 297
Ideonella sp. URA-8 398
Methanosarcina sp.T40UC2 558
Pseudomonas sp. S23 30
Paenibacillus chibensis SK4-3.2

A A A C T T T A C A A T G C G G A A A C C G T A T A A C G G A C A C C G A T T G T C A - - - - - 0 C A T C A T A T G C T H G C T G C C A G 0 T

Enterobacter sp. GG1 450
B akh rodens sp.OKR4-a 510
Enterobacter *doacae* OsEp_AN_15A7 440
Glucosacetobacter sp. Dw26 352
Ideonella sp. URA-8 470
Klebsiella sp. SXW12 498
Paenibacillus chibensis SK4-3.2 116

C A C T C C C C C T A T C C A T T C A T A T C T A A C

Enterobacter sp. GG1 520
Azospirillum lipoferum B7 87
B akh rodens sp.OKR4+a 509
Enterobacter *doacae* OsEp_AN_15A7 537
Glucosacetobacter sp. Dw26 478
Herbaspirillum sp. RhS_2.5 557
Ideonella sp. URA-8 525
Klebsiella sp. SXW12 510
Pseudomonas sp. S23

Consensus
 Enterobacter sp.GG1
 Azobacter chrooocum Y5G5
 Azospirillum lipoferum B7
 Beijerinckia sp. 37L
 Burkholderia sp.OKR4-1
 Clostridium sp.M98449
 Enterobacter doacae OsEp_AN_15A7
 Gluconacetobacter sp. 0w26
 Herbaspirillum sp.Ah5_2.5
 Ideonella sp. URA-8
 Klebsiella sp.SXW12
 Methanosarcina sp.T40UC2
 Pseudomonas sp.S23
 Paenibacillus chibensis SK4-3.2



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 Enterobacter sp.GG1
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 Herbaspirillum sp.Ah5_2.5
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 Klebsiella sp.SXW12
 Methanosarcina sp.T40UC2
 Pseudomonas sp.S23
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 Klebsiella sp.SXW12
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 Pseudomonas sp.S23
 Paenibacillus chibensis SK4-3.2



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 Paenibacillus chibensis SK4-3.2



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 Ideonella sp. URA-8
 Klebsiella sp.SXW12
 Methanosarcina sp.T40UC2
 Pseudomonas sp.S23
 Paenibacillus chibensis SK4-3.2

Consensus A...CGGCOTGGGGAGFA065 0G0AA...GTTAAA0F0AAA...GAATW6ACGGGG...004G0-A0AAGGG

Azotobacter chroococcum T5Cb
Azospirillum lipoferum B7
Beijerinckia sp. 37L
Burkholderia sp. OKR4-1

Enterobacter doecae OsEp_AN_15A7

Ideonella sp. URA-8
Klebsiella sp. SXW12
Methanosarcina sp. T4OUC2
Pseudomonas sp. S23

G ACCGCCTGGCTGCCTTTACGCCAGTAATTCGGATTAAACGCTAGCACCCCTCGTATTACCGCGG--CTGCTGGCACGG
 AGTCGACCGCCTGGGGAGTACGGCCGCCAA-----GGTTAAAACCTAAA-----TGAATTGACGGGGGCCCGC-ACAAAGCG 12s
 A ACATTCCGCCTGGGGAGTACGGTCCGCAA-----GATTAAAACCTAAA-----GGAATTGACGGGGGCCCGC-ACAAAGCG ia7
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A ATCGA CCGCCTGGGGAGTACGGCCGCCAA-----GGTTAAAACCTAAA-----TGAATTGACGGGGGCCCGC-ACAAAGCG 876

A GTTGA CCGCCTGGGGAGTACGGCCGCCAA-----GGTTAAAACCTAAA-----GGAATTGACGGGGGCCCGC-ACAAAGCG 9y2
 A ATCGA CCGCCTGGGGAGTACGGCCGCCAA-----GGTTAAAACCTAAA-----TGAATTGACGGGGGCCCGC-ACAAAGCG 892
 A GCGAGCCACCTGGGAAGTACGGCCGCCAA-----GGCTGAAACTAAA-----GGAATTGCGGGGGAGCACAAACAGCG 721
 A GTTGA CCGCCTGGGGAGTACGGCCGCCAA-----GGTTAAAACCTAAA-----TGAATTGACGGGGGCCCGC-ACAAAGCG 8y2

GTGGAGCATGTGGTTAATTCGAAAGCAACGCCGAA
 AACVITACCTGGCT TGA

Enterobacter sp. GG1
Azotobacter chroococcum Y5Cb

Beijerinckia sp. 37L
Burkholderia sp. OKR4-1

Pseudomonas sp. S23
Paenibacillus chibensis SK4-3.2

eGZPAGCCGGTGCFSPYI CTGCGGGI AACGvCé *YcGcvGAs GFIAI Y^h ACCTSCAa Ca CCYrc-----YC 952
 GYGGGGcEY GYGGGL YAWY CGAA CAACGCGAA-----sAAeCTYA^c CzseccY-----?GA 10a

GTGGAGCATGTGGTTAATTCGAAAGCAACGCCGCA-----GAACCTTACCAGCTCT-----TGA 902
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 GTGGAGCATGTGGTTAATTCGAAAGCAACGCCGAA-----GAACCTTACCAGCTCT-----TGA 928
 GTGGAGTATGTGGTTAATTCGAAAGCAACGCCGAA-----GAACCTTACCAGCTCT-----TGA 633

Enterobacter sp. GG1
 As e bacter chiooi horn
 As @iFlum lipoferum W

Burkholderia sp. OKR4-1

Ideonella sp. URA-8
Klebsiella sp. SXW12

Pseudomonas sp. S23
Paenibacillus chibensis SK4-3.2

CCC-GCTGAAAGT--ACTTTACAACCCGAAGCCCTTCTC--AT-----ACACGGGCATGGGTGCATCAGGC lajs
 CAT-CCCTGCGAAC--CTTCCAGAGATGAGAGGCTGCTTC--GGAACTGTGAGACAGGTGCTGCATGGCTGTCCGTCAGC 20j
 CAT-TCGGGATAGGGCATTGGAGACGATGCTCTCAGTTAGGCTGGCCCAAGACAGGTGCTGCATGGCTGTCCGTCAGC i7q
 CAT-GGTCGGAAT--CCGCTGAGAGGTGGAGTGTCTCGAAAAGAAACCGCGCACAGGTGCTGCATGGCTGTCCGTCAGC loss

CAT-GCCTGGAAT--CCTGCAGAGATGTTGGAGTGTCTCGAAAAGAGGCCAGGACACAGGTGCTGCATGGCTGTCCGTCAGC 104j
 CAT-CCACAGAAC--TTTCCAGAGATGGATTGTGCTTTC--GGAACTGTGAGACAGGTGCTGCATGGCTGTCCGTCAGC 1020
 CAA-GCTGAAGAC--TTTCCCTGAATCGCTGAG-----AGGAGGTGCATGGCTGTCCGTCAGC
 CAT-GCTGAGAAC--TTTCCAGAGATGGATTGTGCTTTC--GGAACTGTGAGACAGGTGCTGCATGGCTGTCCGTCAGC i0os
 CATCCCTCTGAAT--CCTCTAGAGATAGAGGCTGCTTTC--GGACAGAGGTGACAGGTGCTGCATGGTGTCCGTCAGC 690

Consensus TGGTG...TGTGAATG7*...GGGFFAAGT000G0A0GAG0G0A000TTG:GTF:GFT'00AG

Enterobacter sp. GG1
 As e bacter chiooi horn
 As @iFlum lipoferum W
Beijerinckia sp. 37L

Enterobacter doecae OsEp_AN_15A7

Ideonella sp. URA-8
Klebsiella sp. SXW12
Methanosarcina sp. T4OUC2
Pseudomonas sp. S23

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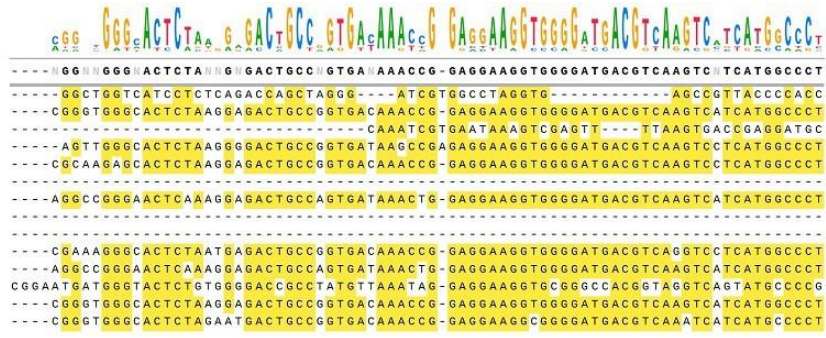
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 TGGCG---TTTTGAAATTTT-----CAAACCGCGGATCTTT----- 178
 TCCTG---TCGTGAGATGTT-----GGGTTAAGTCCCCTAACGAGCGCAACCCCTGCTTATGTTCCAGCATTT---- 1048

TCCTG---TCGTGAAATGTT-----GGGTTAAGTCCCCTAACGAGCGCAACCCCTATGCTTGTGTGCACGGGTT---- 1071

TCCTG---TCGTGAGATGTT-----GGGTTAAGTCCCCTAACGAGCGCAACCCCTGTGATTAGTGTCTA----- 1104
 TCCTG---TCGTGAAATGTT-----GGGTTAAGTCCCCTAACGAGCGCAACCCCTTATGCTTGTGTGCACGGGTT---- 1087
 TCCTA---CTGTGAAGCATC-----CTGTTAAGTCCGCAACGAGCGGACCCCTGCCACTGTTACAGCATATTTCTC 913
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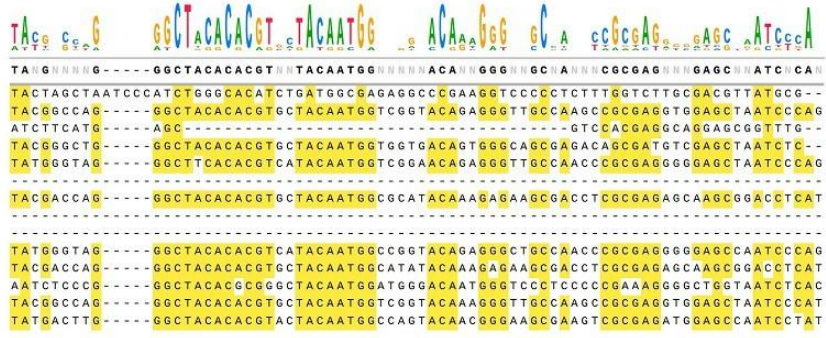
Consensus

Enterobacter sp.GG1
 Azobacter chrooocum Y5G5
 Azospirillum lipoferum B7
 Beijerinckia sp. 37L
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 Klebsiella sp.SXW12
 Methanosarcina sp.T40UC2
 Pseudomonas sp.S23
 Paenibacillus chibensis SK4-3.2



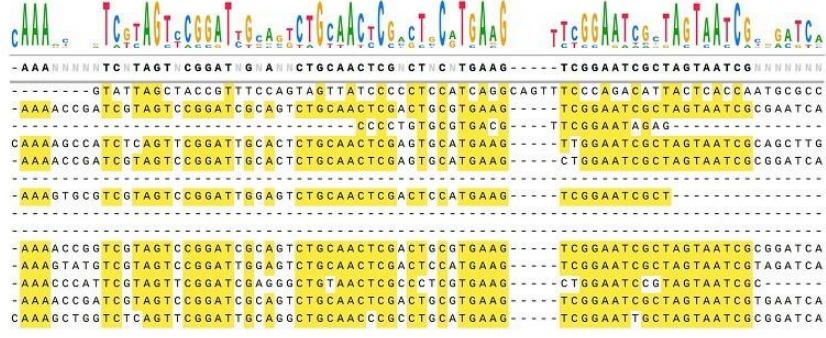
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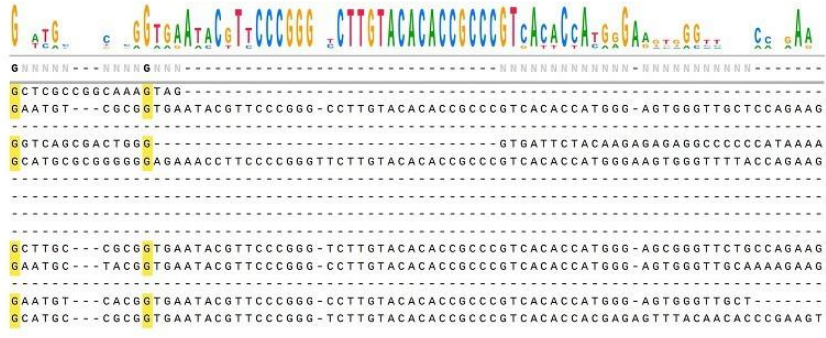
Consensus

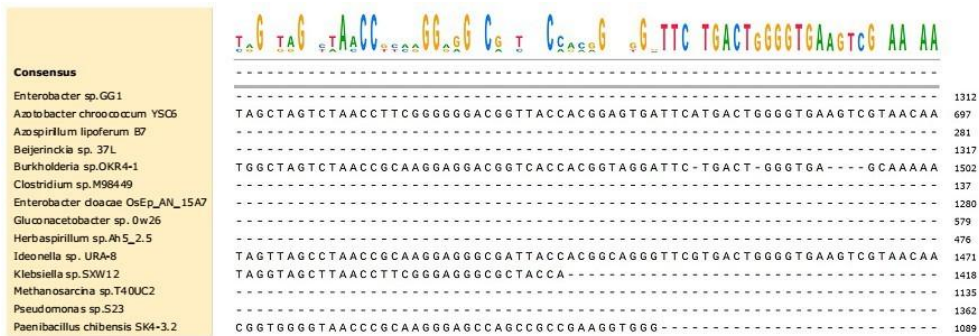
Enterobacter sp.GG1
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Supplementary Table 1: Comparative data analysis of nitrogen fixing microbes with newly isolates *Enterobacter* sp. GG1

Name of organism	Comparative features	Reference
<i>Enterobacter</i> sp. GG1	Effective nitrogen fixation, growth rate, variability very high, non-pathogenic, effective efficacy result show in saline soil	Current study
<i>Pseudomonas aeruginosa</i>	Nitrogen fixation rate high but pathogenicity very high	[28]
<i>Frankia</i> sp.	Nitrogen fixation rate high but that become infected the actinorhizal plants	[52]
<i>Corynebacterium</i> sp.	Nitrogenase activity and viability little bet low	[53]
<i>Clostridium botulinum</i>	Nitrogen fixation rate high but pathogenicity very high, growth rates declined with and increasing saline stress condition	[29]
<i>Azotobacter</i> sp.	Nitrogen fixation rate very high but high salt concentration and temperature	[54]
<i>Anabaena</i> sp.	Nitrogen fixation rate very high but growth rate is very low compare to bacterial growth	[55]