CHAPTER – 4

Results

4. RESULTS

4.1. Isolation from Rhizosphere

Several bacterial strains were isolated from the rhizosphere of the five (5) selected legume plants. However, a total of twenty-six isolates (26) were selected for further study in the current work. The selected isolates viz., *Crotalaria juncea*: CJS.T-1, CJS.IE-1A, CJS.IE-2, CJS.B-1 and CJS.IW-1, *Crotalaria pallida*: CPS.B-1, CPS.B-2, CPS.T-1, CPS.IW-3, CPS.IE-2A and CPS.IE-3, *Sesbania sesban*: SS.T-1, SS.IE-1, SS.B-1, SS.IW-1 and SS.IW-3, *Leucaena leucocephala*: LLS.IE(B)-1, LLS.IE(B)-2, LLS.B-1, LLS.T-1 and LLS.IW-2 and *Parkia roxburghii*: PS.T(A)-2, PS.T(B)-2, PS.B-3, PS.IW-1 and PS.IE-2 were isolated by using the nitrogen free Burk's media as described by Wilson and Knight (1952). Pure colonies of the isolates were obtained through repeated streaking of the isolates on the same medium.

4.1.1 Morphological characteristics

Colony characteristics were done for preliminary characterization of the bacterial isolates by examining the growth of the isolates on solid media in petri plates. The colony characteristics like size, forms, margins, elevations and colony colour were taken into account as per the accepted methods described by Annon, (1957). For observation colony characteristics, bacterial isolates are streak plated in Nutrient Agar medium and the examination was done after 48 hours of incubation. The largest single colony was observed to be upto 8mm in size, however majority of the single colony of the isolates range in size between 2-3mm. Motility test of the isolates were also done by Hanging Drop Mount Method**.** A total of seventeen (17) isolates were found to motile, six (6) were non-motile and 3 (three) were variable meaning they could not be ascertained. The details of Colony characteristics as well as motility of the bacterial isolates are given in Table no. 1. Out of the twenty-six bacterial strains, fourteen strains were found to be gram negative rod shaped and five were found out to be gram positive rod shaped bacteria. The remaining seven bacterial are found to be gram negative spherical shaped bacteria.

Table. 1: Colony Morphology and Motility of isolates from Rhizosphere.

Isolates	Features					
	Colony Size	**Forms**	**Margins**	**Elevations**	**Colour**	**Motility**
LLS.IE(B)-1	2-3mm	Circular	Entire	Convex	White	Motile
LLS.IE(B)-2	1-7mm	Circular and Wrinkled	Smooth	Hilly	Off white	Motile
LLS.T-1	2-3mm	Round	Curled	Flat	Yellow	Motile
LLS.IW-2	<1mm	Punctiform	Smooth	Convex	Off-white	Non-motile
LLS.B-1	4-6mm	Irregular and spreading	Lobate	Umbonate	Pink	Motile
PS.IW-1	2-4mm	Irregular	Undulate	Umbonate	White	Motile
PS.IE-2	3-6mm	Irregular and spreading	Lobate	Raised	Off-white	Non-motile
PS.T(A)-2	4-5mm	Round	Smooth	Raised	Off-white	Non-motile
PS.T(B)-2	2-5mm	Irregular and spreading	Lobate	Crateriform	White	Motile
PS.B-3	2-5mm	Round	Smooth	Raised	White	Motile
CPS.B-1	1-3mm	Irregular and slimy	Undulate	Flat	Light brown	Variable
CPS.B-2	2-3mm	Circular	Lobate	Flat	Colorless	Motile
CPS.T-1	2-3mm	Circular	Lobate	Flat	Colorless	Motile
CPS.IW-3	2-4mm	Irregular	Undulate	Umbonate	White	Motile
CPS.IE-2(A)	2-5mm	Wrinkled	Smooth	Hilly	Off white	Motile
CPS.IE-3	3-5mm	Round with raised margin	Wavy	Crateriform	Off white	Non-motile
CJS.IE-1	1.5mm	Irregular	Undulate	Flat	Colorless	Motile
CJS.IE-2	2-8mm	Irregular and spreading	Undulate	Flat	Creamy	Non-motile
CJS.T-1	1-3mm	Irregular	Lobate	Crateriform	Off-white	Variable
CJS.IW-1	2-3mm	Round	Smooth	Convex	Yellowish	Motile
CJS.B-1	<1mm	Punctiform	Smooth	Convex	White	Non-motile
SS.IE-1	2-5mm	Wrinkled	Smooth	Raised	Off white	Motile
SS.T-1	2-3mm	Circular	Lobate	Raised	Colorless	Motile
SS.IW-1	2-5mm	Round	Smooth	Raised	White	Variable
SS.IW-3	1.5mm	Irregular	Undulate	Flat	Colorless	Motile
SS.B-1	1.5mm	Irregular	Undulate	Flat	Colorless	Motile

4.2. Isolation from Root Nodules

Here, isolation of bacteria from *Parkia roxburghii* was omitted as there are no nodules present in the root. Therefore isolation was done from the four legumes viz., *Crotalaria juncea, Crotalaria pallida, Sesbania sesban* and *Leucaena leucocephala*. Several numbers of bacterial strains were isolated from the root nodules of the four (4) selected legume plants. However, a total of twenty (20) bacterial samples were selected for further study. The selected isolates viz., *Crotalaria juncea*: CJN.IE-1, CJN.IE-2 CJN.IW-1, CJN.B-1 and CJN.T-1, *Crotalaria pallida*: CPN.IE, CPN.B, CPN.IW-1, CPN.IW-2, CPN.T-1 and CPN.T-4, *Sesbania sesban*: SN.IE, SN.IW, SN.B-1 and SN.T and *Leucaena leucocephala*: LLN.T-1, LLN.IE-1, LLN.IW-1, LLN.B-1 and LLN.B-2 were isolated by using the nitrogen free YEMA media. Pure colonies of the isolates were again obtained through repeated streaking of the isolates on the same medium.

4.2.1. Morphological characteristics

Again colony characteristics were done for preliminary characterization of the bacterial isolates by examining the growth of the isolates on solid media in petri plates. Colony characteristics like size, forms, margins, elevations and colony colour were taken into account as per the accepted methods described by Annon, (1957). For observation colony characteristics, bacterial isolates are streak plated in Nutrient Agar medium and the examination was done after 48 hours of incubation. The largest single colony was observed to be upto 6mm in size, however majority of the single colony of the isolates range in size between 2-5mm. After performing Motility test, seventeen isolates out of twenty were found to be motile and the remaining three isolates were non-motile**.** The details of Colony characteristics as well as motility of the bacterial isolates are given in Table no. 2. Out of the twenty bacterial isolates fifteen were detected to be gram negative rod, three were gram negative sphere and two isolates were gram positive rod.

Table. 2: Colony Morphology and Motility of isolates from Root nodules.

Isolates	**Features**					
	Size	**Forms**	**Margins**	**Elevations**	**Colour**	**Motility**
CPN.IW-1	2-5mm	Round	Undulate	Raised	Greenish	Motile
CPN.IW-2	2-5mm	Round	Undulate	Raised	Greenish	Motile
CPN.T-1	2-5mm	Circular	Entire	Convex	Yellow	Motile
CPN.T-4	1.5mm	Irregular	Undulate	Flat	Colorless	Motile
CPN.B	2-3mm	Round	Curled	Flat	Yellow	Motile
CPN.IE	2-3mm	Round	Curled	Flat	Yellow	Motile
LLN.T-1	2-6mm	Wrinkled	Smooth	Hilly	Greenish	Motile
LLN.IE-1	1-2mm	Round	Entire	Convex	White	Motile
LLN.IW-1	2mm	Circular	Smooth	Raised	Creamy	Non-motile
LLN.B-1	2-3mm	Round	Entire	Flat	Creamy	Motile
LLN.B-2	2-6mm	Irregular and spreading	Serrate	Flat	Off-white	Non-motile
CJN.T-1	2-5mm	Circular	Entire	Convex	Yellow	Motile
CJN.B-1	2-5mm	Circular	Entire	Convex	Yellow	Motile
CJN.IW-1	2-4mm	Irregular	Undulate	Umbonate	White	Motile
CJN.IE-1	2-4mm	Irregular	Undulate	Umbonate	White	Motile
CJN.IE-2	<1mm	Punctiform	Smooth	Convex	White	Motile
SN.IE-1	2-4mm	Circular	Lobate	Flat	Greenish	Motile
SN.B-1	1-6mm	Circular and Slimy	Smooth	Raised	Creamy	Motile
SN.IW	1-2mm	Round	Smooth	Droplike	White	Non-motile
SN.T	2-4mm	Circular and Slimy	Entire	Convex	Colorless	Motile

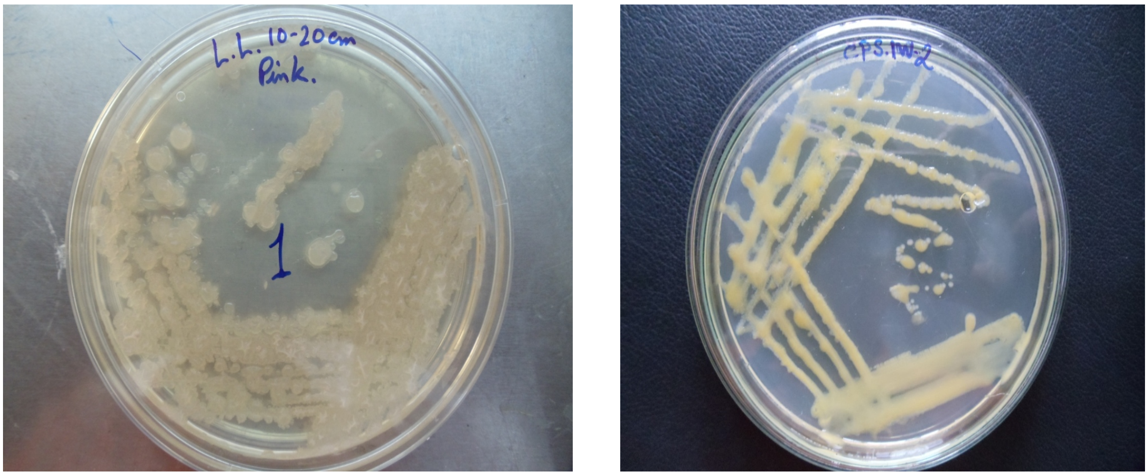
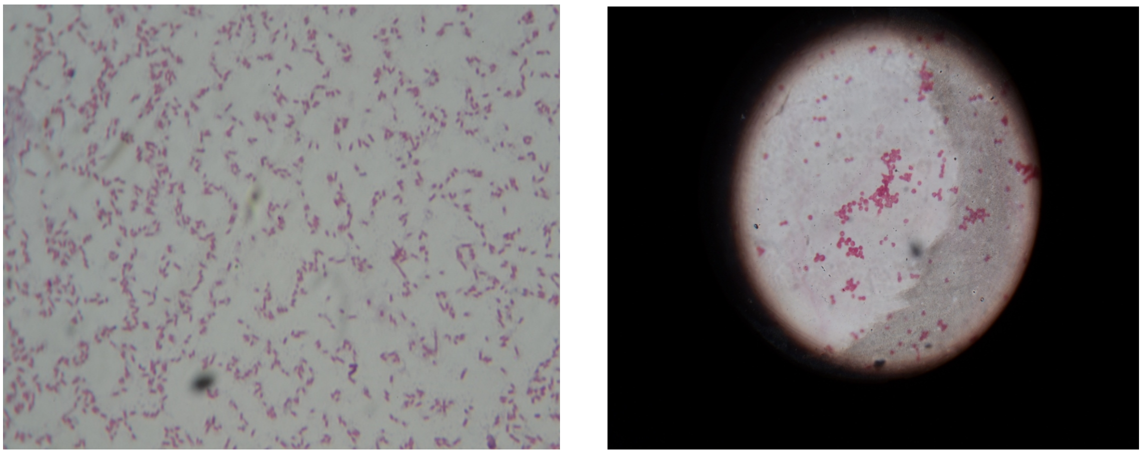
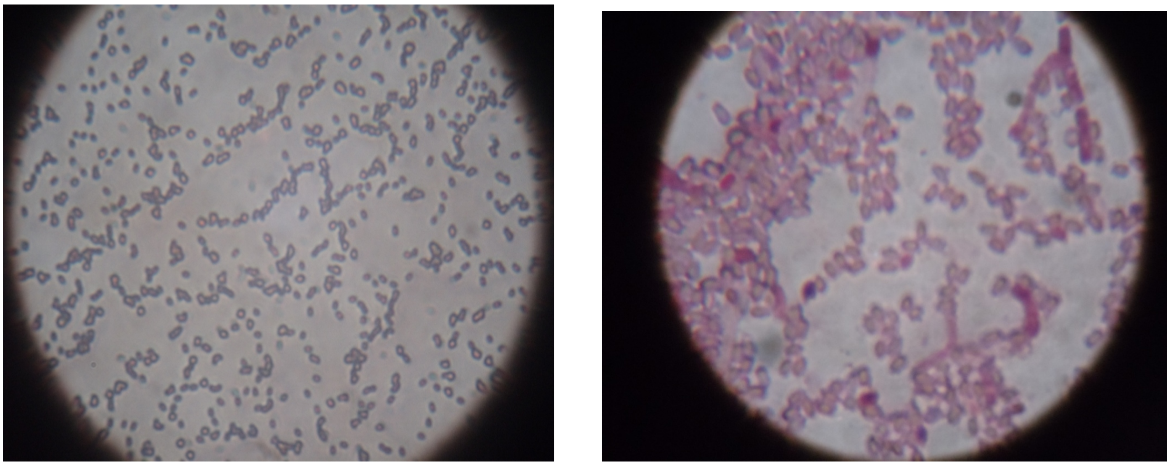


Fig. 7: Bacterial culture streak plated on agar media.



Gram –ve isolate

Gram –ve isolate (under oil emmersion)



Gram +ve isolate

Gram –ve isolate, oil emmersion (zoomed)

Fig. 8: Gram Staining images of some Bacterial isolates.

4.3. Biochemical Test

4.3.1. Isolates from Rhizosphere:

All the twenty-six bacterial samples isolated from the rhizosphere soil of legume plants showed positive result for Catalase test. All the samples isolated from the rhizosphere soil of *Crotalaria pallida* are found to show positive result for Starch hydrolysis test whereas those isolated from *Crotalaria juncea* were found to be negative for the same test. All the isolates from both the plant source as well as those from *Sesbania sesban* are found to be positive for Nitrate reduction test. Only the two isolates, LLS.IE(B)-2 and PS.IE-2 shows negative result for Nitrate reduction test. Majority of the samples shows negative result for Urease test and only five samples shows positive result. Every bacterial sample isolated from the rhizosphere soil of *Parkia roxburghii* tested positive for Oxidase test. Seventeen out of twenty-six samples turns out to be Citrate test positive and the remaining nine isolates shows negative result. Overall number of positive and negative results for the biochemical tests of the isolates are given in Fig.9.

Table.3: Biochemical characteristics of the samples isolated from Leucaena leucocephala. (Soil)

Isolate	Location	Gram stain	Catalase test	Starch hydrolysis	Nitrate Reduction	Urease test	Oxidase test	Citrate test
LLS.IE(B)-1	Imphal (E)	+ve	+ve	+ve	+ve	+ve	+ve	−ve
LLS.IE(B)-2	Imphal (E)	−ve	+ve	−ve	−ve	−ve	+ve	+ve
LLS.T-1	Thoubal	−ve	+ve	−ve	+ve	−ve	−ve	+ve
LLS.IW-2	Imphal West	-ve	+ve	+ve	+ve	−ve	+ve	+ve
LLS.B-1	Bishnupur	+ve	+ve	+ve	+ve	−ve	+ve	−ve

Table.4: Biochemical characteristics of the samples isolated from Parkia roxburghii. (Soil)

Isolate	Location	Gram stain	Catalase test	Starch hydrolysis	Nitrate Reduction	Urease test	Oxidase test	Citrate test
PS.IW-1	Kwa-keithel	−ve	+ve	+ve	+ve	−ve	+ve	+ve
PS.IE-2	Khurai	−ve	+ve	−ve	−ve	+ve	+ve	+ve
PS.T(A)-2	Khangabok	−ve	+ve	−ve	+ve	−ve	+ve	+ve
PS.T(B)-2	Khangabok	−ve	+ve	+ve	+ve	−ve	+ve	+ve
PS.B-3	Moirang	+ve	+ve	+ve	+ve	−ve	+ve	−ve

Table.5: Biochemical characteristics of the samples isolated from Crotalaria pallida. (Soil)

Isolate	Location	Gram stain	Catalase test	Starch hydrolysis	Nitrate Reduction	Urease test	Oxidase test	Citrate test
CPS.B-1	Bishnupur	-ve	+ve	+ve	+ve	+ve	+ve	+ve
CPS.B-2	Bishnupur	−ve	+ve	+ve	+ve	−ve	−ve	+ve
CPS.T-1	Thoubal	−ve	+ve	+ve	+ve	−ve	−ve	+ve
CPS.IW-3	Imphal West	+ve	+ve	+ve	+ve	−ve	+ve	−ve
CPS.IE-2(A)	Imphal East	−ve	+ve	+ve	+ve	−ve	+ve	−ve
CPS.IE-3	Imphal East	−ve	+ve	+ve	+ve	−ve	+ve	−ve

Table.6: Biochemical characteristics of the samples isolated from Crotalaria juncea. (Soil)

Isolate	Location	Gram stain	Catalase test	Starch hydrolysis	Nitrate Reduction	Urease test	Oxidase test	Citrate test
CJS.IE-1(A)	Imphal East	−ve	+ve	−ve	+ve	−ve	+ve	+ve
CJS.IE-2	Imphal East	−ve	+ve	−ve	+ve	−ve	+ve	−ve
CJS.T-1	Thoubal	−ve	+ve	−ve	+ve	+ve	+ve	+ve
CJS.IW-1	Imphal West	−ve	+ve	−ve	+ve	−ve	+ve	−ve
CJS.B-1	Bishnupur	−ve	+ve	−ve	+ve	+ve	−ve	+ve

Table.7: Biochemical characteristics of the samples isolated from Sesbania sesban. (Soil)

Isolate	Location	Gram stain	Catalase test	Starch hydrolysis	Nitrate Reduction	Urease test	Oxidase test	Citrate test
SS.IE-1	Imphal East	−ve	+ve	+ve	+ve	−ve	+ve	+ve
SS.T-1	Thoubal	−ve	+ve	+ve	+ve	−ve	−ve	+ve
SS.IW-1	Imphal West	-ve	+ve	+ve	+ve	−ve	+ve	−ve
SS.IW-3	Imphal West	−ve	+ve	−ve	+ve	+ve	+ve	+ve
SS.B-1	Bishnupur	−ve	+ve	+ve	+ve	−ve	+ve	+ve

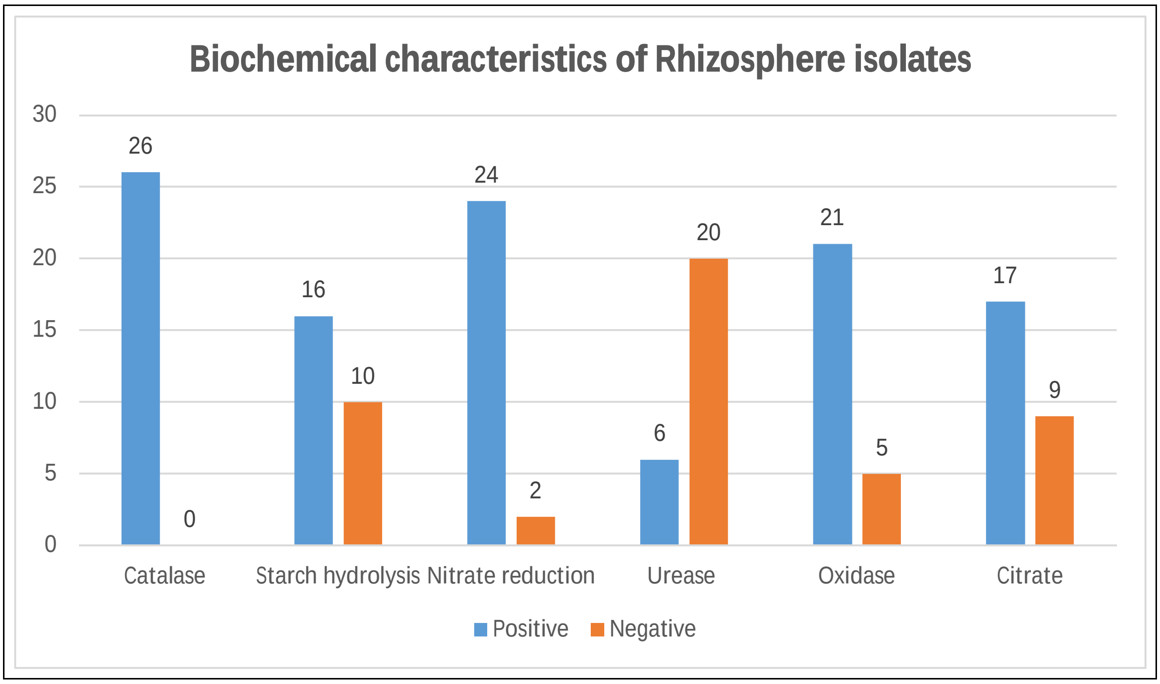


Fig.9: Biochemical characteristics of different isolates obtained from Rhizosphere.

4.3.2. Isolates from Root nodules:

All the twenty bacterial samples isolated from the root nodules of the four legume plants showed positive result for Catalase test. Four isolates out of five from the root nodules of *Crotalaria juncea* are found to be positive for Starch hydrolysis test. Again two isolates from the same plant tested positive for oxidase test. All the isolates from *Sesbania sesban* are found to be positive for Nitrate reduction test as well as oxidase test. The isolate SN.B-1 from the same plant was detected to be negative for Urease test. Only one isolate from Leucaena leucocephala gives negative result for Oxidase test whereas only one isolate gives positive result for Citrate Test. Overall number of positive and negative results for the biochemical tests of the isolates are given in Fig.10.

Table.8: Biochemical characteristics of the samples isolated from Leucaena leucocephala. (Nodules)

Isolate	Location	Gram stain	Catalase test	Starch hydrolysis	Nitrate Reduction	Urease test	Oxidase test	Citrate test
LLN.T-1	Khangabok	−ve	+ve	+ve	+ve	−ve	+ve	−ve
LLN.IE-1	Khurai	−ve	+ve	+ve	+ve	+ve	+ve	−ve
LLN.IW-1	Kwa-keithel	−ve	+ve	+ve	−ve	+ve	+ve	+ve
LLN.B-1	Moirang	+ve	+ve	−ve	−ve	−ve	−ve	−ve
LLN.B-2	Moirang	−ve	+ve	+ve	+ve	−ve	+ve	−ve

Table.9: Biochemical characteristics of the samples isolated from Crotalaria pallida. (Nodules)

Isolate	**Location**	**Gram stain**	**Catalase test**	**Starch hydrolysis**	**Nitrate Reduction**	**Urease test**	**Oxidase test**	**Citrate test**
CPN.IE	Imphal East	−ve	+ve	−ve	−ve	+ve	+ve	+ve
CPN.B	Bishnupur	−ve	+ve	+ve	+ve	+ve	+ve	+ve
CPN.IW-1	Imphal Est	−ve	+ve	+ve	+ve	−ve	+ve	−ve
CPN.IW-2	Imphal East	−ve	+ve	−ve	−ve	−ve	+ve	−ve
CPN.T-1	Thoubal	-ve	+ve	+ve	+ve	+ve	+ve	+ve
CPN.T-4	Thoubal	−ve	+ve	+ve	+ve	−ve	−ve	+ve

Table. 10: Biochemical characteristics of the samples isolated from Crotalaria juncea. (Nodules)

Isolate	**Location**	**Gram stain**	**Catalase test**	**Starch hydrolysis**	**Nitrate Reduction**	**Urease test**	**Oxidase test**	**Citrate test**
CJN.IE-1	Imphal East	−ve	+ve	+ve	−ve	+ve	−ve	−ve
CJN.IE-2	Imphal East	−ve	+ve	−ve	+ve	+ve	+ve	+ve
CJN.IW-1	Imphal West	−ve	+ve	+ve	+ve	−ve	+ve	+ve
CJN.B-1	Bishnupur	−ve	+ve	+ve	+ve	+ve	−ve	+ve
CJN.T-1	Thoubal	−ve	+ve	+ve	+ve	−ve	−ve	+ve

Table. 11: Biochemical characteristics of the samples isolated from Sesbania sesban. (Nodules)

Isolate	**Location**	**Gram stain**	**Catalase test**	**Starch hydrolysis**	**Nitrate Reduction**	**Urease test**	**Oxidase test**	**Citrate test**
SN.IE-1	Imphal East	−ve	+ve	−ve	+ve	+ve	+ve	+ve
SN.IW	Imphal West	−ve	+ve	−ve	+ve	+ve	+ve	+ve
SN.B-1	Bishnupur	+ve	+ve	+ve	+ve	−ve	+ve	−ve
SN.T	Thoubal	-ve	+ve	+ve	+ve	+ve	+ve	−ve

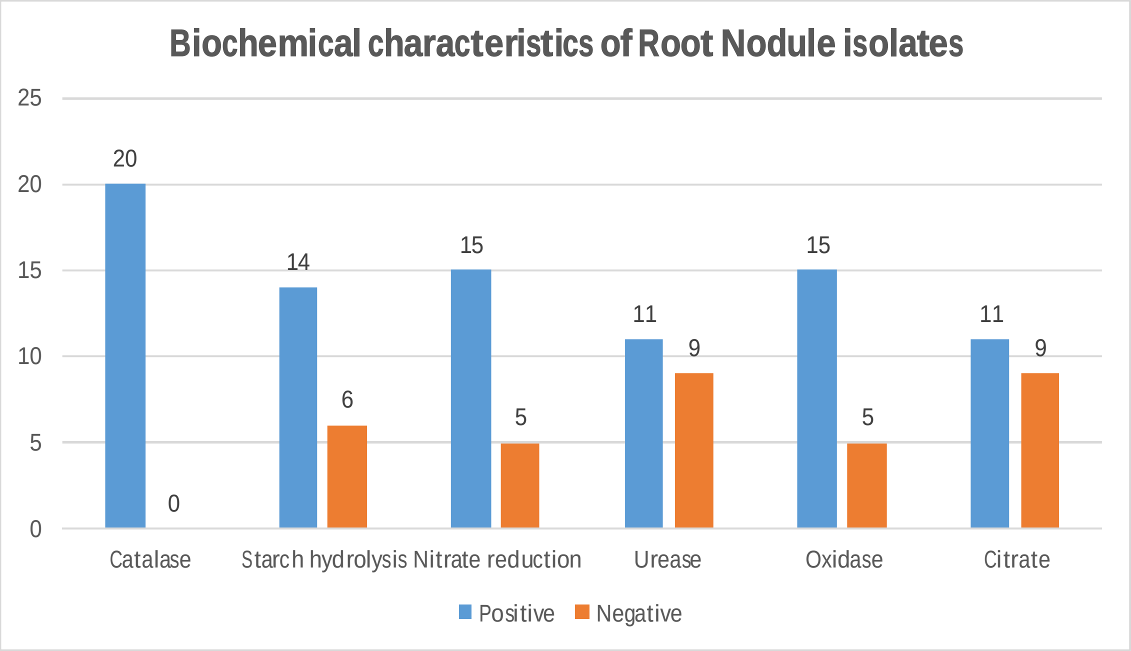


Fig.10: Biochemical characteristics of different isolates obtained from Root Nodules.

Fig. 11: Photographs of Catalase test positive isolates.

Fig. 12: Photographs of Starch Hydrolysis test.

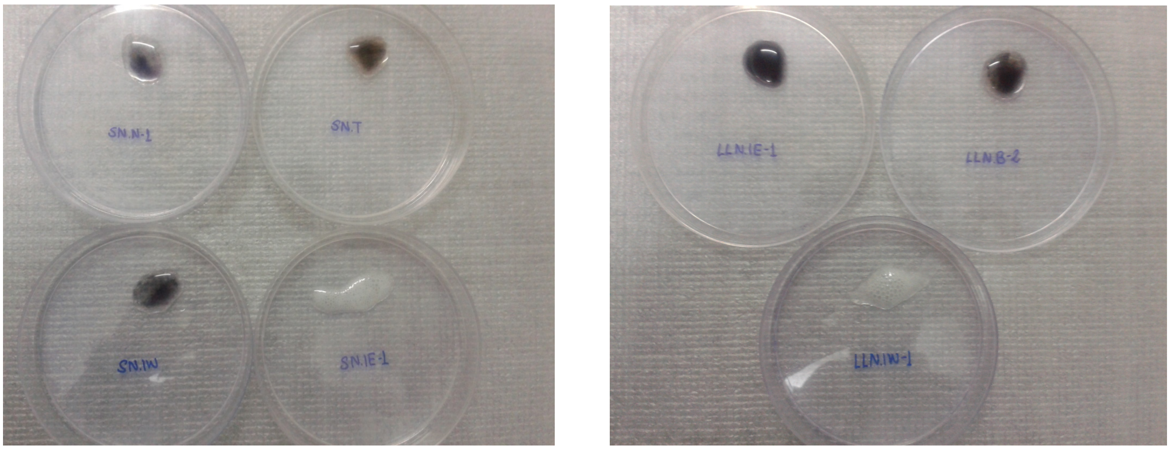


Fig. 13: Isolates showing both Positive and Negative result for Nitrate Reduction test.

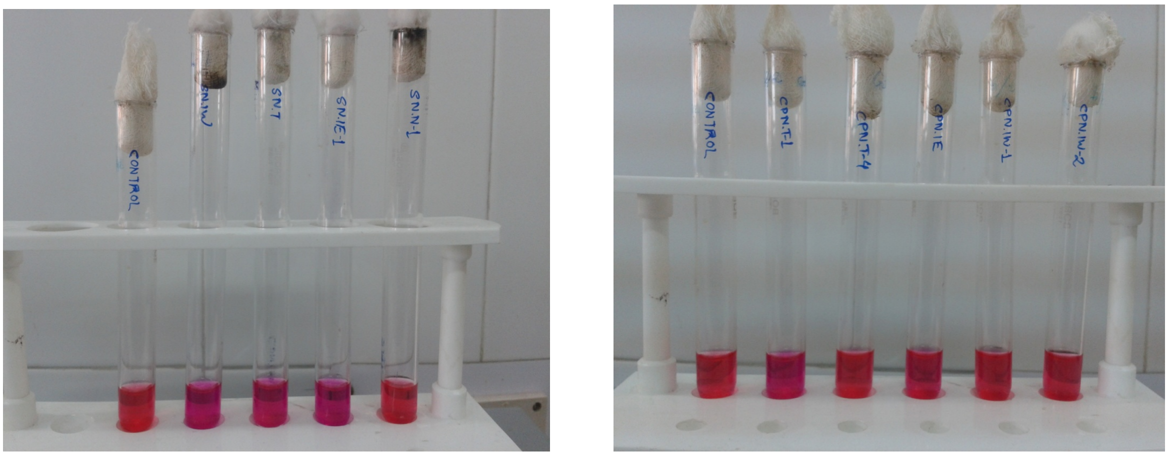


Fig. 14: Photographs of Urease test for different isolates.

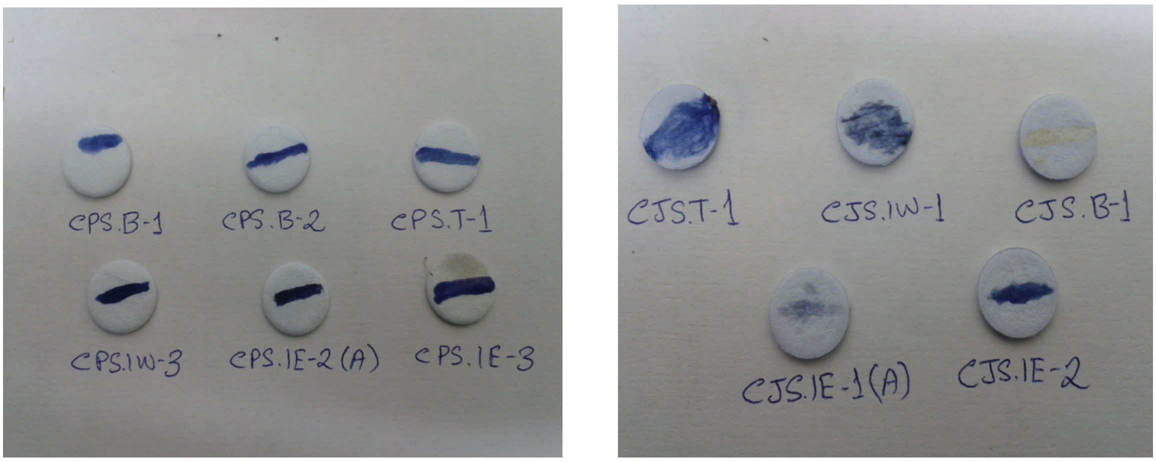


Fig. 15: Photographs of Oxidase test for different isolates.

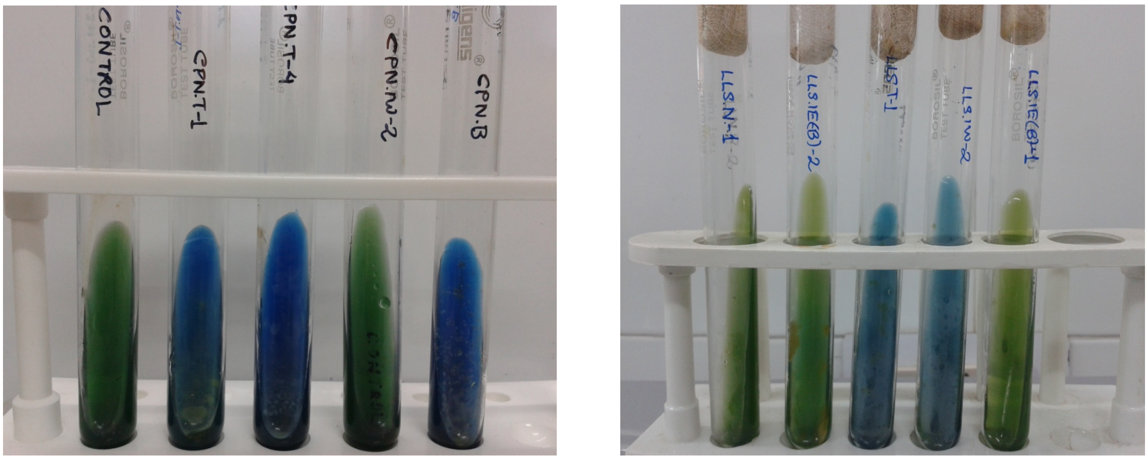


Fig. 16: Different isolates showing both Positive and negative result for Citrate test.

4.4. Antibiotic Sensitivity test:

For determining the sensitivity of antibiotics by the bacterial isolates, HIMedia Susceptibility discs were used. In the present work susceptibility towards antibiotics of all the isolates were tested against six antibiotics *viz.* Imipenem (IPM), oxacilin (OX), chloramphenicol (C), novobiocin (NV), ciproflocacin (CIP) and amoxyclav (AMC). All the bacterial isolates were found to be susceptible against CIP, C and IPM. All the details about susceptibility and tolerance of all the bacterial isolates isolates are given in table.12 (isolates from rhizosphere) and table. 13 (isolates from root nodules). Zone of Inhibition (ZOI) of the antibiotics are given in centimetre inside bracket. It has been inferred that any zone above 1.1cm is susceptible and below it will be considered resistant as per the standard results given by researchers.

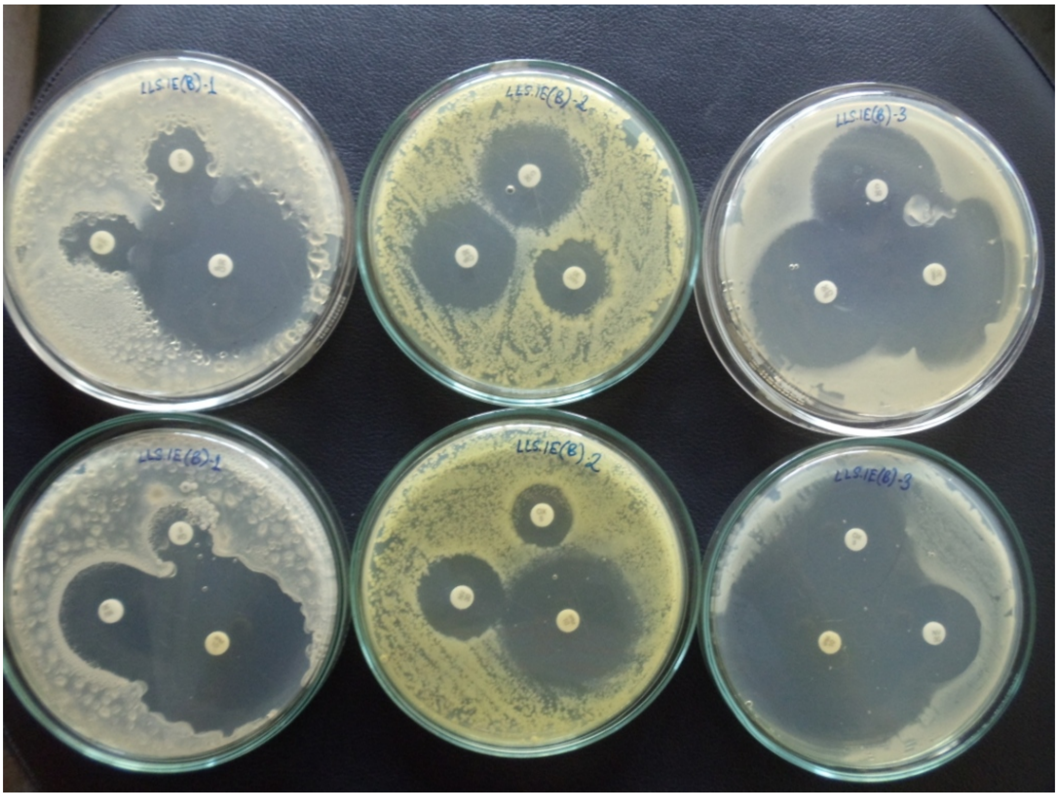


Fig. 17: Zone of inhibition shown by Isolates against different Antibiotic discs.

Table.12: Antibiotic sensitivity test for samples isolated from rhizosphere soil (ZOI is given in centimetre inside bracket).

ISOLATES	NV	OX	CIP	AMC	C	IPM
LLS.IE(B)-1	+ve(2.9)	+ve(1.8)	+ve(4.9)	+ve(1.4)	+ve(1.6)	+ve(4.6)
LLS.IE(B)-2	+ve(2.3)	+ve(1.7)	+ve(3.0)	+ve(2.0)	+ve(2.9)	+ve(3.6)
LLS.T-1	-ve	-ve	+ve(4.0)	-ve	+ve(3.4)	+ve(1.1)
LLS.IW-2	+ve(4.0)	+ve(1.5)	+ve(3.9)	+ve(3.1)	+ve(3.0)	+ve(4.5)
LLS.B-1	+ve(1.6)	-ve	+ve(2.5)	-ve	+ve(2.5)	+ve(2.8)
PS.IW-1	+ve(2.7)	+ve(3.3)	+ve(3.9)	+ve(3.9)	+ve(3.8)	+ve(4.9)
PS.IE-2	+ve(1.5)	-ve	+ve(2.8)	-ve	+ve(2.5)	+ve(2.8)
PS.T(A)-2	+ve(2.1)	-ve	+ve(2.6)	-ve	+ve(2.8)	+ve(3.7)
PS.T(B)-2	+ve(1.5)	-ve	+ve(3.7)	+ve(0.9)	+ve(1.8)	+ve(3.6)
PS.B-3	+ve(2.0)	+ve(0.8)	+ve(2.7)	-ve	+ve(2.5)	+ve(3.2)
CPS.B-1	+ve(1.5)	-ve	+ve(3.7)	+ve(0.9)	+ve(1.8)	+ve(3.6)
CPS.B-2	+ve(2.9)	-ve	+ve(2.9)	-ve	+ve(3.0)	+ve(1.8)
CPS.T-1	+ve(1.7)	+ve(2.4)	+ve(4.0)	+ve(4.0)	+ve(4.5)	+ve(5.7)
CPS.IW-3	+ve(2.5)	+ve(2.6)	+ve(3.8)	+ve(3.6)	+ve(3.5)	+ve(4.6)
CPS.IE-2(A)	+ve(2.0)	-ve	+ve(2.4)	+ve(0.7)	+ve(1.9)	+ve(3.4)
CPS.IE-3	+ve(1.0)	-ve	+ve(4.7)	-ve	+ve(2.4)	+ve(4.8)
CJS.IE-1(A)	+ve(1.0)	-ve	+ve(3.0)	-ve	+ve(2.4)	+ve(1.9)
CJS.IE-2	+ve(2.4)	-ve	+ve(2.9)	+ve(0.8)	+ve(2.9)	+ve(3.8)
CJS.T-1	-ve	-ve	+ve(3.8)	-ve	+ve(3.5)	+ve(1.5)
CJS.IW-1	+ve(2.5)	+ve(2.6)	+ve(3.5)	+ve(2.1)	+ve(3.6)	+ve(4.5)
CJS.B-1	+ve(1.3)	-ve	+ve(2.5)	-ve	+ve(2.7)	+ve(3.5)
SS.IE-1	+ve(1.7)	-ve	+ve(2.5)	-ve	+ve(2.5)	+ve(2.0)
SS.T-1	-ve	-ve	+ve(3.0)	-ve	+ve(2.7)	+ve(1.0)
SS.IW-1	+ve(3.0)	+ve(2.1)	+ve(3.8)	+ve(2.8)	+ve(3.8)	+ve(4.9)
SS.IW-3	+ve(2.2)	-ve	+ve(5.5)	+ve(2.8)	+ve(1.5)	+ve(5.9)
SS.B-1	+ve(3.0)	+ve(2.1)	+ve(3.8)	+ve(2.8)	+ve(3.8)	+ve(4.9)

Table.13: Antibiotic sensitivity test for samples isolated from root nodules (ZOI is given in centimetre inside bracket).

ISOLATES	NV	OX	CIP	AMC	C	IPM
CPN.IW-1	+ve(2.1)	-ve	+ve(2.4)	-ve	+ve(2.5)	+ve(3.6)
CPN.IW-2	+ve(2)	+ve(2.2)	+ve(3.1)	+ve(1.9)	+ve(2.9)	+ve(4.1)
CPN.T-1	+ve(1.9)	-ve	+ve(2.7)	-ve	+ve(2.4)	+ve(3.2)
CPN.T-4	-ve	-ve	+ve(2.9)	-ve	+ve(2)	+ve(1.8)
CPN.B	+ve(2)	-ve	+ve(3.4)	-ve	+ve(3)	+ve(2.9)
CPN.IE	+ve(3.0)	-ve	+ve(3.2)	+ve(1.3)	+ve(1.0)	+ve(5.6)
LLN.T-1	+ve(2.4)	+ve(2.4)	+ve(4)	+ve(2.4)	+ve(3.7)	+ve(4.9)
LLN.IE-1	+ve(2.3)	-ve	+ve(3.5)	+ve(1.1)	+ve(3)	+ve(2.7)
LLN.IW-1	+ve(2)	-ve	+ve(2.8)	-ve	+ve(2.2)	+ve(2.8)
LLN.B-1	+ve(2.9)	+ve(2.7)	+ve(3.5)	+ve(3.1)	+ve(3.7)	+ve(4.4)
LLN.B-2	+ve(2.5)	+ve(2.6)	+ve(3.6)	+ve(2.1)	+ve(3.5)	+ve(4.5)
CJN.T-1	+ve(2.0)	-ve	+ve(2.9)	-ve	+ve(2.8)	+ve(3.8)
CJN.B-1	+ve(1.9)	-ve	+ve(2.5)	-ve	+ve(2.7)	+ve(3.8)
CJN.IW-1	+ve(2.3)	+ve(2)	+ve(4.5)	+ve(2.4)	+ve(3.2)	+ve(6.0)
CJN.IE-1	+ve(2.0)	+ve(2.8)	+ve(3.6)	+ve(3.7)	+ve(3.2)	+ve(6.0)
CJN.IE-2	-ve	+ve(2.4)	+ve(3.3)	–ve	+ve(2.8)	+ve(5.4)
SN.IE-1	+ve(2.1)	–ve	+ve(2.7)	–ve	+ve(2.4)	+ve(3.9)
SN.B-1	+ve(2.1)	–ve	+ve(2.8)	–ve	+ve(2.2)	+ve(4)
SN.IW	+ve(1.8)	+ve(1.6)	+ve(2.2)	+(1.8)	+ve(2.7)	+ve(3.2)
SN.T	+ve(2.3)	+ve(2)	+ve(4.5)	+ve(2.4)	+ve(3.2)	+ve(6.0)

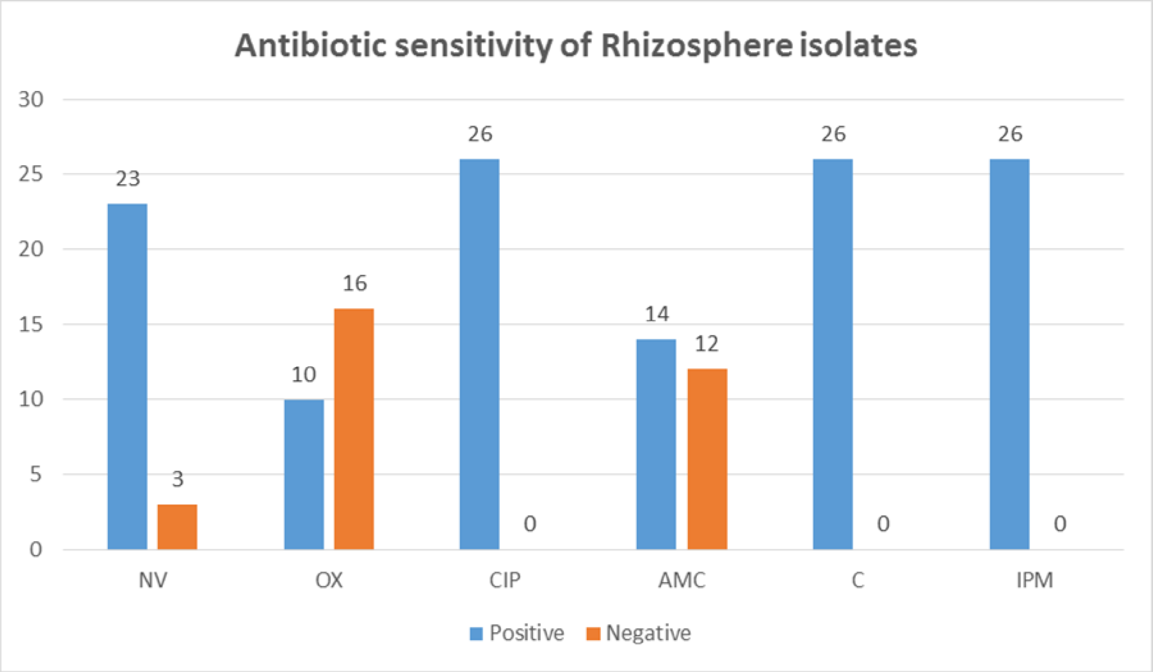


Fig.18: Antibiotic sensitivity of different isolates from Rhizosphere (NV- Novobiocin, OX- Oxacilin, CIP- Ciproflocacin, AMC- Amoxyclav, C- Chloramphenecol and IPM- Imipenem).

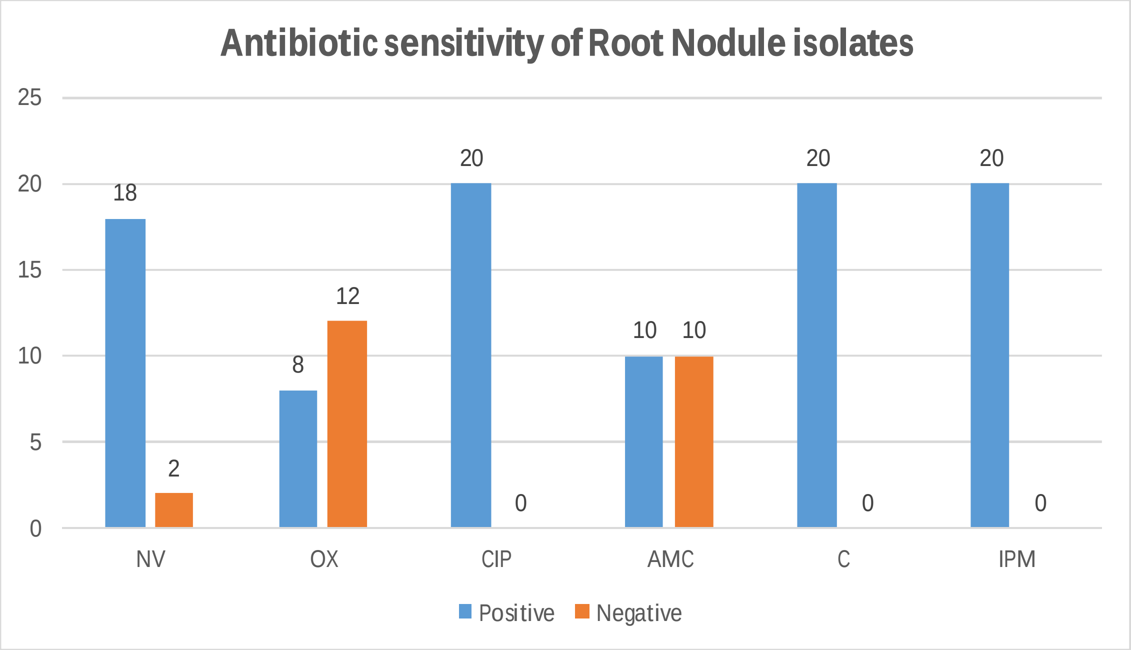


Fig.19: Antibiotic sensitivity of different isolates from Root nodule (NV- Novobiocin, OX- Oxacilin, CIP- Ciproflocacin, AMC- Amoxyclav, C- Chloramphenecol and IPM- Imipenem).

4.5. Acetylene Reduction Assay (ARA)

ARA was performed for all the twenty-six bacterial isolates obtained from the Rhizosphere and chosen for the study. Nineteen isolates were found to show some ability for fixing Nitrogen (nitrogenase activity), whereas the remaining seven isolates showed negligible or no nitrogenase activity at all. The bacterial samples isolated from the rhizosphere of *Crotalaria juncea* particularly failed to show any significant amount of reducing Acetylene to Ethylene, thus it could be considered that it may not have the capacity of fixing nitrogen. However the bacterial isolate CJS.IE-1 isolated from the rhizosphere of *Crotalaria juncea* and isolate SS.IW-3 from the rhizosphere of *Sesbania sesban* were selected for 16S rDNA sequencing considering their morphology, biochemical characteristics and nifH gene amplification along with other isolates. The ability of nitrogen fixation even though the amount were in small quantity, is visible from the following Table. 14.

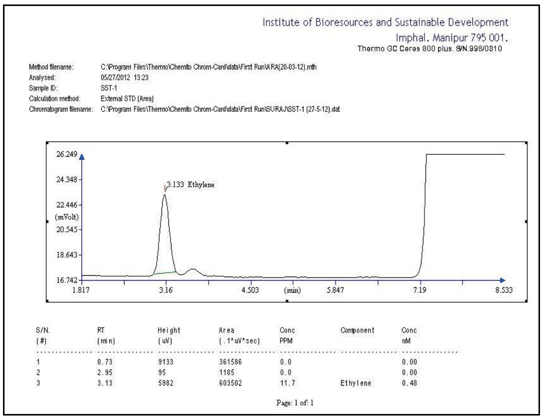
Table.14: Amount of Acetylene reduced to Ethylene (nM/hr/5ml) by Rhizosphere isolates.

SL.No.	Bacterial Isolates	Amount of Ethylene in nM/hr/5ml
1.	SS.T-1	0.72 nM/hr/5ml.
2.	SS.IW-1	0.195 nM/hr/5ml.
3.	SS.IW-3	0.0 nM/hr/5ml.
4.	SS.IE-1	0.165 nM/hr/5ml.
5.	SS.B-1	0.045 nM/hr/5ml.
6.	CPS.B-1	2.7 nM/hr/5ml.
7.	CPS.B-2	0.12 nM/hr/5ml.
8.	CPS.T-1	1.38 nM/hr/5ml.
9.	CPS.IW-3	2.49 nM/hr/5ml.
10.	CPS.IE-2(A)	2.04 nM/hr/5ml.
11.	CPS.IE-3	2.415 nM/hr/5ml.
12.	CJS.IE-1	0.06 nM/hr/5ml.
13.	CJS.IE-2	0.03 nM/hr/5ml.
14.	CJS.T-1	0.045 nM/hr/5ml.
15.	CJS.IW-1	0.075 nM/hr/5ml.
16.	CJS.B-1	0.045 nM/hr/5ml.
17.	LLS.IE(B)-1	0.735 nM/hr/5ml.
18.	LLS.IE(B)-2	0.735 nM/hr/5ml.
19.	LLS.T-1	0.75 nM/hr/5ml.
20.	LLS.IW-2	0.405 nM/hr/5ml.
21.	LLS.B-1	0.42 nM/hr/5ml.
22.	PS.IW-1	2.325 nM/hr/5ml.
23.	PS.IE-2	1.8 nM/hr/5ml.
24.	PS.T(A)-2	0.9 nM/hr/5ml.
25.	PS.T(B)-2	2.4 nM/hr/5ml.
26.	PS.B-3	2.235 nM/hr/5ml.

ARA was also performed for all the twenty bacterial isolates obtained from the Root Nodules of the selected legume plants. Seventeen isolates were found to show some ability for fixing Nitrogen (nitrogenase activity), whereas the remaining three isolates showed negligible or no nitrogenase activity at all. Bacterial isolate SN.IW obtained from the nodules of *Sesbania sesban,* and two isolates obtained from the *Leucaena leucocephala viz.*, LLN.T-1 and LLN.IW-1 failed to show any significant amount of reducing Acetylene to Ethylene, indicating that they may not have the capacity of fixing nitrogen. However, the isolates LLN.T-1 isolated from the rhizosphere of *Crotalaria juncea* and isolate SS.IW-3 from the rhizosphere of *Leucaena leucocephala* was selected for 16S rDNA sequencing considering their morphology, biochemical characteristics and nifH gene amplification along with other isolates. The ability of nitrogen fixation even though the amount were in small quantity, is visible from the following Table. 15.

Table.15: Amount of Acetylene reduced to Ethylene (nM/hr/5ml) by Root Nodule isolates.

SL.No.	Bacterial Isolates	Amount of Ethylene in nM/hr/5ml
1.	SN.IE-1	0.18 nM/hr/5ml
2.	SN.IW	0.0 nM/hr/5ml
3.	SN.B-1	2.04 nM/hr/5ml
4.	SN.T	2.415 nM/hr/5ml
5.	CPN.IE	0.105 nM/hr/5ml
6.	CPN.B	1.59 nM/hr/5ml
7.	CPN.IW-1	0.99 nM/hr/5ml
8.	CPN.IW-2	0.93 nM/hr/5ml
9.	CPN.T-1	2.16 nM/hr/5ml
10.	CPN.T-4	1.32 nM/hr/5ml
11.	CJN.IE-1	0.135 nM/hr/5ml
12.	CJN.IE-2	2.235 nM/hr/5ml
13.	CJN.IW-1	0.285 nM/hr/5ml
14.	CJN.B-1	1.065 nM/hr/5ml
15.	CJN.T-1	0.135 nM/hr/5ml
16.	LLN.T-1	0.03 nM/hr/5ml
17.	LLN.IE-1	1.215 nM/hr/5ml
18.	LLN.IW-1	0.045 nM/hr/5ml
19.	LLN.B-1	2.13 nM/hr/5ml
20.	LLN.B-2	0.18 nM/hr/5ml



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Imphal. Manipur 795 001.
Thermo GC Ceres 800 plus. S/N.998/0310

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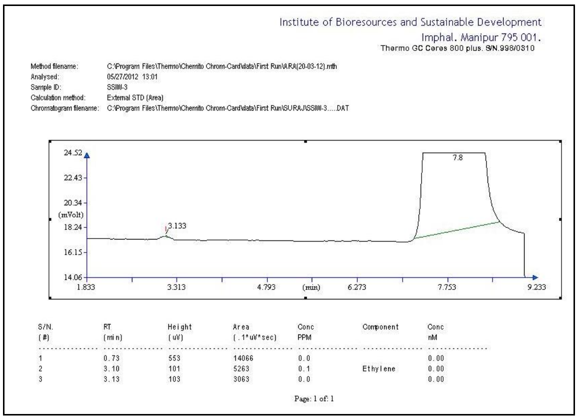
Sample ID: SST-1
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\SST-1 (27-5-12).dat

S/N. (#)	RT (min)	Height (uV)	Area (.1*uV*sec)	Conc PPM	Component	Conc nM
1	0.73	9133	361586	0.0		0.00
2	2.95	95	1185	0.0		0.00
3	3.13	5982	603502	11.7	Ethylene	0.48

Page: 1 of: 1

SS.T-1



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Thermo GC Ceres 800 plus. S/N.998/0310

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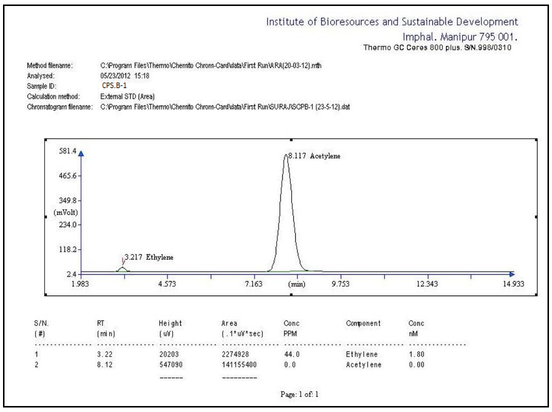
Analysed: 05/27/2012 13:01
Sample ID: SSIW-3
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\SSIW-3.....DAT

S/N. (#)	RT (min)	Height (uV)	Area (.1*uV*sec)	Conc PPM	Component	Conc nM
1	0.73	553	14066	0.0		0.00
2	3.10	101	5263	0.1	Ethylene	0.00
3	3.13	103	3063	0.0		0.00

Page: 1 of: 1

SS.IW-3



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Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/23/2012 15:18
Sample ID: CPS.B-1
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\SCPB-1 (23-5-12).dat

S/N. (#)	RT (min)	Height (uV)	Area (.1*uV*sec)	Conc PPM	Component	Conc nM
1	3.22	20203	2274928	44.0	Ethylene	1.80
2	8.12	547090	141155400	0.0	Acetylene	0.00
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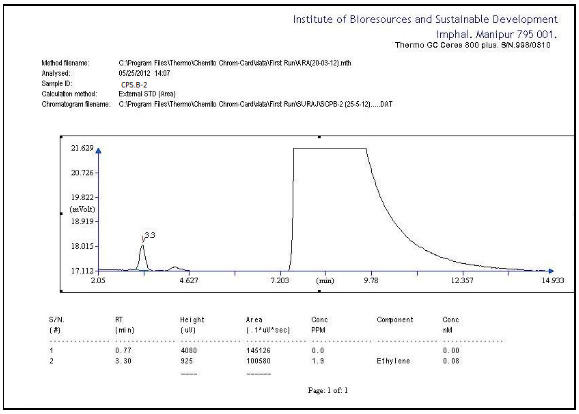
Page: 1 of: 1

CPS.B-1



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Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/25/2012 14:07
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Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\SCPB-2 (25-5-12).....DAT

S/N. (#)	RT (min)	Height (uV)	Area (.1*uV*sec)	Conc PPM	Component	Conc nM
1	0.77	4080	145126	0.0		0.00
2	3.30	925	100580	1.9	Ethylene	0.08
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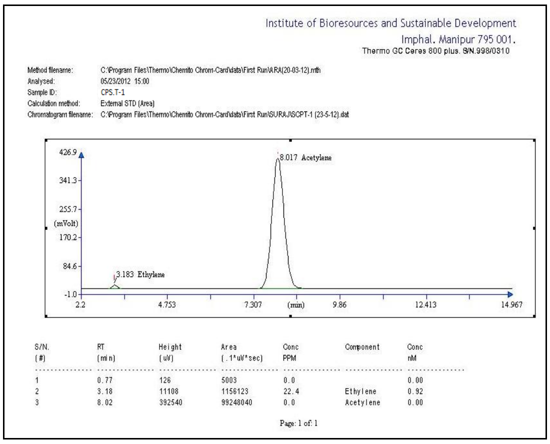
Page: 1 of: 1

CPS.B-2



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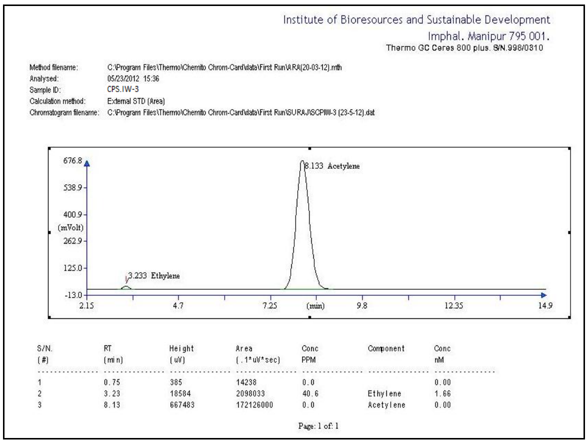
Thermo GC Ceres 800 plus. S/N.998/0310

Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/23/2012 15:00
Sample ID: CPS.T-1
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\SCPT-1 (23-5-12).dat

S/N. (#)	RT (min)	Height (uV)	Area (.1*uV*sec)	Conc PPM	Component	Conc nM
1	0.77	126	5003	0.0		0.00
2	3.18	11108	1156123	22.4	Ethylene	0.92
3	8.02	392540	99248040	0.0	Acetylene	0.00

Page: 1 of: 1

CPS.T-1



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Thermo GC Ceres 800 plus. S/N.998/0310

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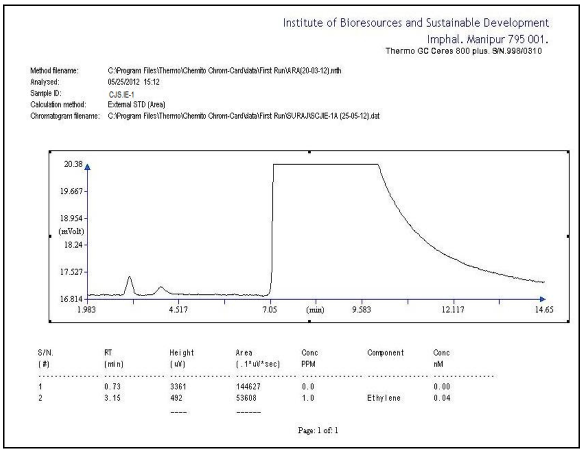
Analysed: 05/23/2012 15:36
Sample ID: CPS.IW-3
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\SCPIW-3 (23-5-12).dat

S/N. (#)	RT (min)	Height (uV)	Area (.1*uV*sec)	Conc PPM	Component	Conc nM
1	0.75	385	14238	0.0		0.00
2	3.23	18584	2098033	40.6	Ethylene	1.66
3	8.13	667483	172126000	0.0	Acetylene	0.00

Page: 1 of: 1

CPS.IW-3

Fig. 20: Acetylene reduction curve of six different Isolates (Selected for 16S rDNA analysis).



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                                                Thermo GC Ceres 800 plus. S/N.998/0310

Method filename:        C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed:               05/25/2012  15:12
Sample ID:              CJS.IE-1
Calculation method:     External STD (Area)
Chromatogram filename:  C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\SCJIE-1A (25-05-12).dat

S/N.      RT        Height    Area          Conc      Component   Conc
(#)       (min)     (uV)      (.1*uV*sec)   PPM                   nM
--------- --------- --------- ------------- --------- ----------- ---------
1         0.73      3361      144627        0.0                   0.00
2         3.15      492       53608         1.0       Ethylene    0.04
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                          Page: 1 of: 1
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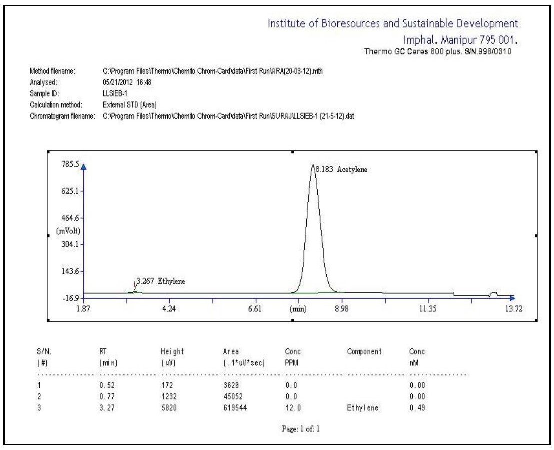
CJS.IE-1



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Analysed:               05/21/2012  16:48
Sample ID:              LLSIEB-1
Calculation method:     External STD (Area)
Chromatogram filename:  C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\LLSIEB-1 (21-5-12).dat

S/N.      RT        Height    Area          Conc      Component   Conc
(#)       (min)     (uV)      (.1*uV*sec)   PPM                   nM
--------- --------- --------- ------------- --------- ----------- ---------
1         0.52      172       3629          0.0                   0.00
2         0.77      1232      45052         0.0                   0.00
3         3.27      5820      619544        12.0      Ethylene    0.49

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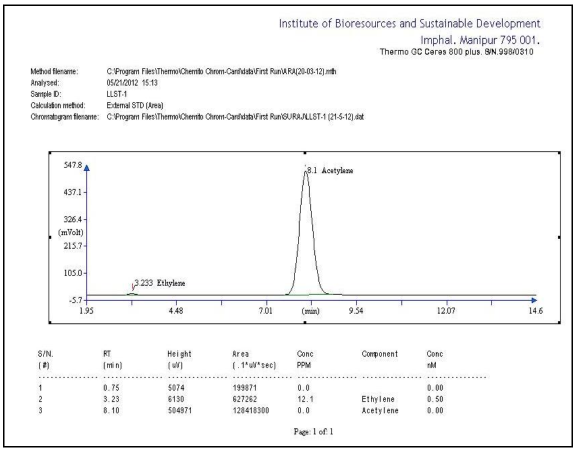
LLS.IE(B)-1



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                                                Thermo GC Ceres 800 plus. S/N.998/0310

Method filename:        C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed:               05/21/2012  15:13
Sample ID:              LLST-1
Calculation method:     External STD (Area)
Chromatogram filename:  C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\LLST-1 (21-5-12).dat

S/N.      RT        Height    Area          Conc      Component   Conc
(#)       (min)     (uV)      (.1*uV*sec)   PPM                   nM
--------- --------- --------- ------------- --------- ----------- ---------
1         0.75      5074      199871        0.0                   0.00
2         3.23      6130      627262        12.1      Ethylene    0.50
3         8.10      504971    128418300     0.0       Acetylene   0.00

                          Page: 1 of: 1
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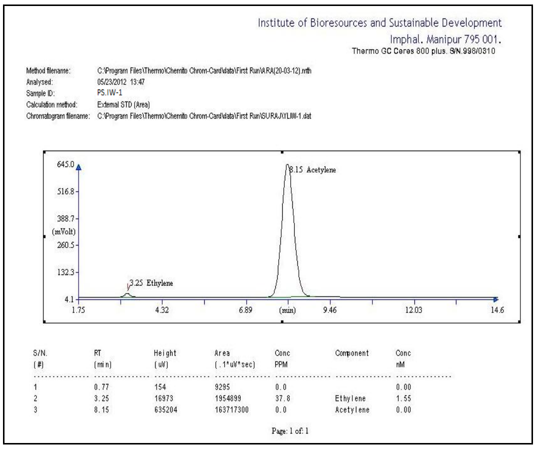
LLS.T-1



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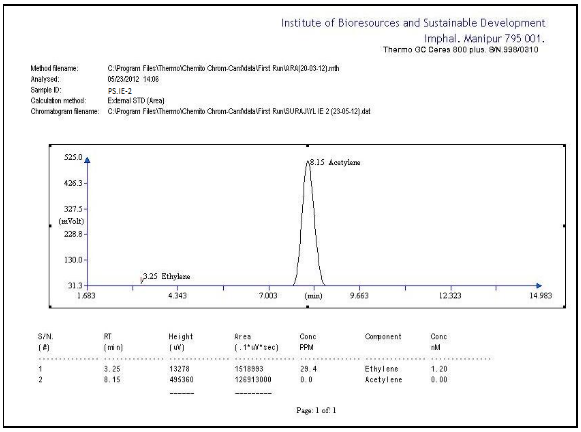
Method filename:        C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed:               05/23/2012  13:47
Sample ID:              PS.IW-1
Calculation method:     External STD (Area)
Chromatogram filename:  C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\YLIW-1.dat

S/N.      RT        Height    Area          Conc      Component   Conc
(#)       (min)     (uV)      (.1*uV*sec)   PPM                   nM
--------- --------- --------- ------------- --------- ----------- ---------
1         0.77      154       9295          0.0                   0.00
2         3.25      16973     1954899       37.8      Ethylene    1.55
3         8.15      635204    163717300     0.0       Acetylene   0.00

                          Page: 1 of: 1
```

PS.IW-1



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                                  Institute of Bioresources and Sustainable Development
                                                              Imphal. Manipur 795 001.
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Method filename:        C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed:               05/23/2012  14:06
Sample ID:              PS.IE-2
Calculation method:     External STD (Area)
Chromatogram filename:  C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\YL IE 2 (23-05-12).dat

S/N.      RT        Height    Area          Conc      Component   Conc
(#)       (min)     (uV)      (.1*uV*sec)   PPM                   nM
--------- --------- --------- ------------- --------- ----------- ---------
1         3.25      13278     1518993       29.4      Ethylene    1.20
2         8.15      495360    126913000     0.0       Acetylene   0.00
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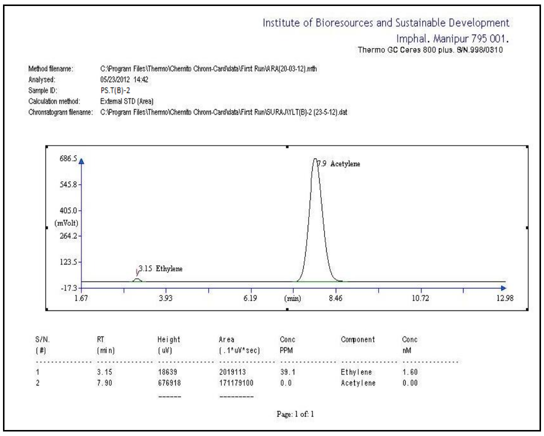
                          Page: 1 of: 1
```

PS.IE-2



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                                  Institute of Bioresources and Sustainable Development
                                                              Imphal. Manipur 795 001.
                                                Thermo GC Ceres 800 plus. S/N.998/0310

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Analysed:               05/23/2012  14:42
Sample ID:              PS.T(B)-2
Calculation method:     External STD (Area)
Chromatogram filename:  C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\YLT(B)-2 (23-5-12).dat

S/N.      RT        Height    Area          Conc      Component   Conc
(#)       (min)     (uV)      (.1*uV*sec)   PPM                   nM
--------- --------- --------- ------------- --------- ----------- ---------
1         3.15      18639     2019113       39.1      Ethylene    1.60
2         7.90      676918    171179100     0.0       Acetylene   0.00
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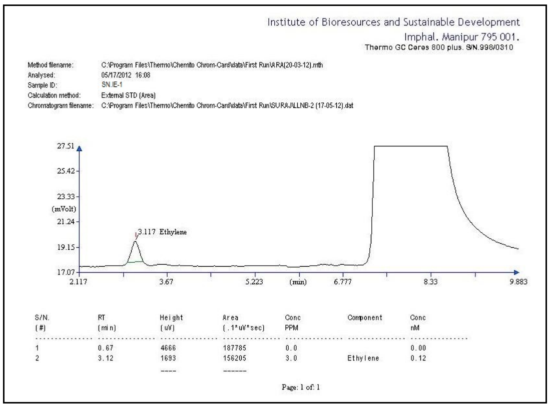
PS.T(B)-2

Fig. 21: Acetylene reduction curve of six different Isolates (Selected for 16S rDNA analysis).



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Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/17/2012 16:08
Sample ID: SN.IE-1
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\LLNB-2 (17-05-12).dat

S/N. (#)	RT (min)	Height (uV)	Area (.1*uV*sec)	Conc PPM	Component	Conc nM
1	0.67	4666	187785	0.0		0.00
2	3.12	1693	156205	3.0	Ethylene	0.12
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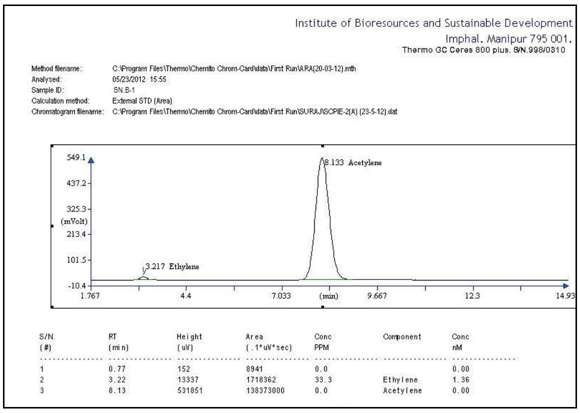
Page: 1 of: 1



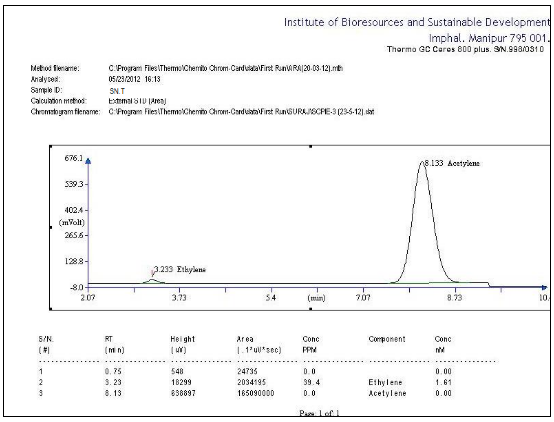
Institute of Bioresources and Sustainable Development
Imphal. Manipur 795 001.
Thermo GC Ceres 800 plus. S/N.998/0310

Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/23/2012 15:55
Sample ID: SN.B-1
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\SCPIE-2(A) (23-5-12).dat

S/N. (#)	RT (min)	Height (uV)	Area (.1*uV*sec)	Conc PPM	Component	Conc nM
1	0.77	152	8941	0.0		0.00
2	3.22	13337	1718362	33.3	Ethylene	1.36
3	8.13	531851	138373000	0.0	Acetylene	0.00

SN.IE-1

SN.B-1

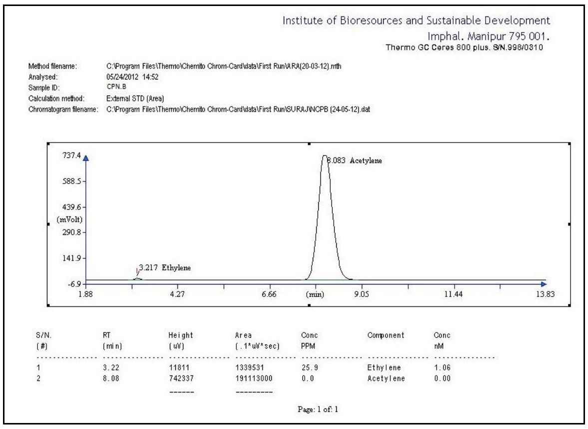


Institute of Bioresources and Sustainable Development
Imphal. Manipur 795 001.
Thermo GC Ceres 800 plus. S/N.998/0310

Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/23/2012 16:13
Sample ID: SN.T
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\SCPIE-3 (23-5-12).dat

S/N. (#)	RT (min)	Height (uV)	Area (.1*uV*sec)	Conc PPM	Component	Conc nM
1	0.75	548	24735	0.0		0.00
2	3.23	18299	2034195	39.4	Ethylene	1.61
3	8.13	638897	165090000	0.0	Acetylene	0.00

Page: 1 of: 1



Institute of Bioresources and Sustainable Development
Imphal. Manipur 795 001.
Thermo GC Ceres 800 plus. S/N.998/0310

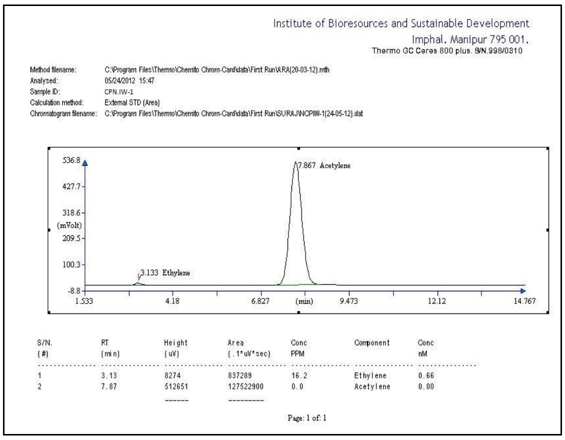
Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/24/2012 14:52
Sample ID: CPN.B
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\NCPB (24-05-12).dat

S/N. (#)	RT (min)	Height (uV)	Area (.1*uV*sec)	Conc PPM	Component	Conc nM
1	3.22	11811	1339531	25.9	Ethylene	1.06
2	8.08	742337	191113000	0.0	Acetylene	0.00
		------	---------			

Page: 1 of: 1

SN.T

CPN.B

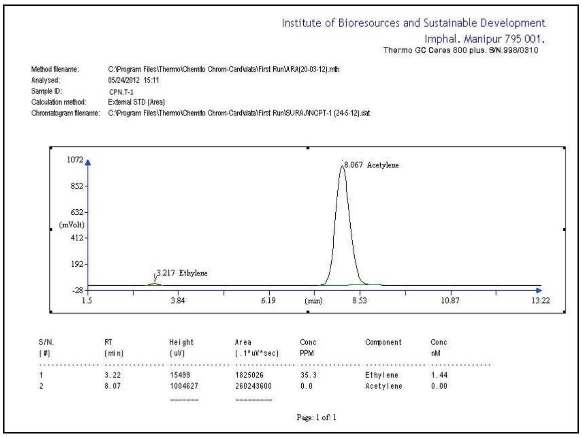


Institute of Bioresources and Sustainable Development
Imphal. Manipur 795 001.
Thermo GC Ceres 800 plus. S/N.998/0310

Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/24/2012 15:47
Sample ID: CPN.IW-1
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\NCPIW-1(24-05-12).dat

S/N. (#)	RT (min)	Height (uV)	Area (.1*uV*sec)	Conc PPM	Component	Conc nM
1	3.13	8274	837289	16.2	Ethylene	0.66
2	7.87	512651	127522900	0.0	Acetylene	0.00
		------	---------			

Page: 1 of: 1



Institute of Bioresources and Sustainable Development
Imphal. Manipur 795 001.
Thermo GC Ceres 800 plus. S/N.998/0310

Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/24/2012 15:11
Sample ID: CPN.T-1
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\NCPT-1 (24-5-12).dat

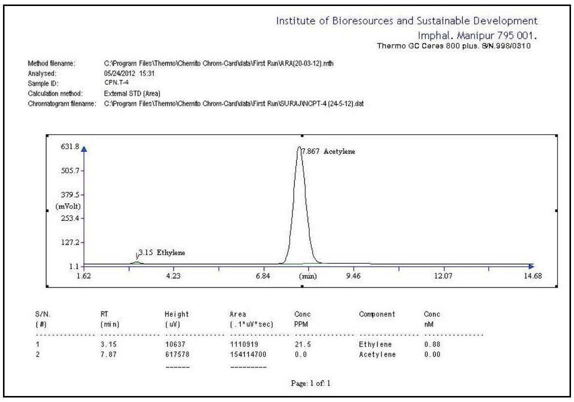
S/N. (#)	RT (min)	Height (uV)	Area (.1*uV*sec)	Conc PPM	Component	Conc nM
1	3.22	15499	1825026	35.3	Ethylene	1.44
2	8.07	1004627	260243600	0.0	Acetylene	0.00
		-------	---------			

Page: 1 of: 1

CPN.IW-1

CPN.T-1

Fig. 22: Acetylene reduction curve of six different Isolates (Selected for 16S rDNA analysis).



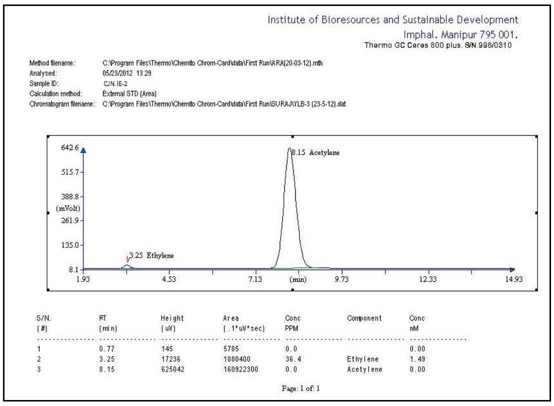
Institute of Bioresources and Sustainable Development
Imphal. Manipur 795 001.
Thermo GC Ceres 800 plus. S/N.998/0310

Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/24/2012 15:31
Sample ID: CPN.T-4
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\NCPT-4 (24-5-12).dat

```
S/N.            RT              Height          Area            Conc            Component       Conc
(#)             (min)           (uV)            (.1*uV*sec)     PPM                             nM
--------------- --------------- --------------- --------------- --------------- --------------- ---------------
1               3.15            10637           1110919         21.5            Ethylene        0.88
2               7.87            617578          154114700       0.0             Acetylene       0.00
                                ------          ---------
```

Page: 1 of: 1

CPN.T-4



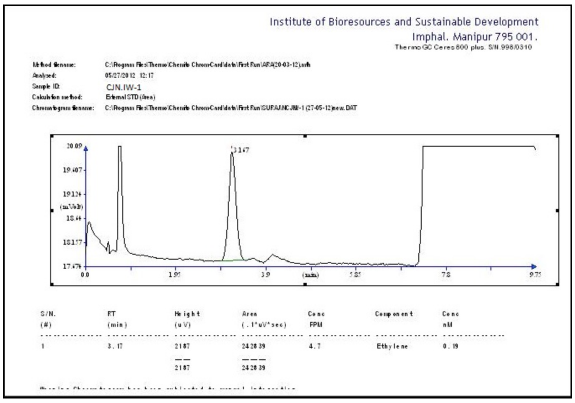
Institute of Bioresources and Sustainable Development
Imphal. Manipur 795 001.
Thermo GC Ceres 800 plus. S/N.998/0310

Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/23/2012 13:29
Sample ID: CJN.IE-2
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\YLB-3 (23-5-12).dat

```
S/N.            RT              Height          Area            Conc            Component       Conc
(#)             (min)           (uV)            (.1*uV*sec)     PPM                             nM
--------------- --------------- --------------- --------------- --------------- --------------- ---------------
1               0.77            145             5785            0.0                             0.00
2               3.25            17236           1880400         36.4            Ethylene        1.49
3               8.15            625042          160922300       0.0             Acetylene       0.00
```

Page: 1 of: 1

CJN.IE-2

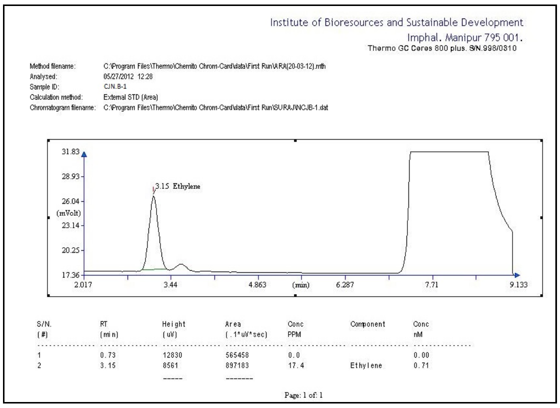


Institute of Bioresources and Sustainable Development
Imphal. Manipur 795 001.
Thermo GC Ceres 800 plus. S/N.998/0310

Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/27/2012 12:17
Sample ID: CJN.IW-1
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\NCJIW-1 (27-05-12)new.DAT

```
S/N.            RT              Height          Area            Conc            Component       Conc
(#)             (min)           (uV)            (.1*uV*sec)     PPM                             nM
--------------- --------------- --------------- --------------- --------------- --------------- ---------------
1               3.17            2187            242839          4.7             Ethylene        0.19
                                ----            ------
                                2187            242839
```

CJN.IW-1



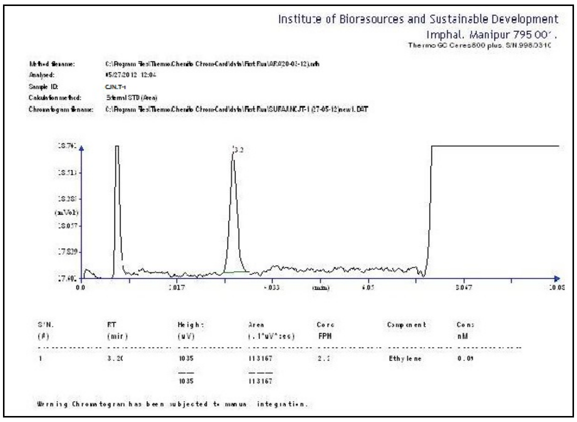
Institute of Bioresources and Sustainable Development
Imphal. Manipur 795 001.
Thermo GC Ceres 800 plus. S/N.998/0310

Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/27/2012 12:28
Sample ID: CJN.B-1
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\NCJB-1.dat

```
S/N.            RT              Height          Area            Conc            Component       Conc
(#)             (min)           (uV)            (.1*uV*sec)     PPM                             nM
--------------- --------------- --------------- --------------- --------------- --------------- ---------------
1               0.73            12830           565458          0.0                             0.00
2               3.15            8561            897183          17.4            Ethylene        0.71
                                -----           -------
```

Page: 1 of: 1

CJN.B-1



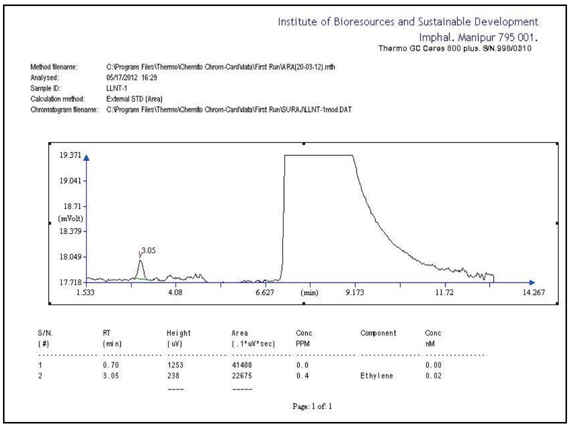
Institute of Bioresources and Sustainable Development
Imphal. Manipur 795 001.
Thermo GC Ceres 800 plus. S/N.998/0310

Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/27/2012 12:04
Sample ID: CJN.T-1
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\NCJT-1 (27-05-12)new1.DAT

```
S/N.            RT              Height          Area            Conc            Component       Conc
(#)             (min)           (uV)            (.1*uV*sec)     PPM                             nM
--------------- --------------- --------------- --------------- --------------- --------------- ---------------
1               3.20            1035            113167          2.[illegible]   Ethylene        0.09
                                ----            ------
                                1035            113167
```

Warning Chromatogram has been subjected to manual integration.

CJN.T-1



Institute of Bioresources and Sustainable Development
Imphal. Manipur 795 001.
Thermo GC Ceres 800 plus. S/N.998/0310

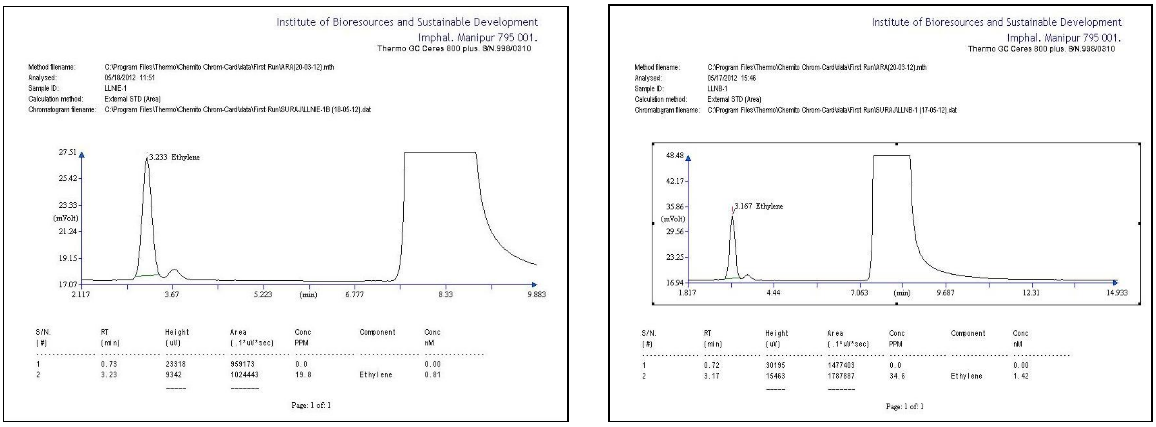
Method filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed: 05/17/2012 16:29
Sample ID: LLNT-1
Calculation method: External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\LLNT-1mod.DAT

```
S/N.            RT              Height          Area            Conc            Component       Conc
(#)             (min)           (uV)            (.1*uV*sec)     PPM                             nM
--------------- --------------- --------------- --------------- --------------- --------------- ---------------
1               0.70            1253            41488           0.0                             0.00
2               3.05            238             22675           0.4             Ethylene        0.02
                                ----            -----
```

Page: 1 of: 1

LLN.T-1

Fig. 23: Acetylene reduction curve of six different Isolates (Selected for 16S rDNA analysis).



```
                                        Institute of Bioresources and Sustainable Development
                                                                       Imphal. Manipur 795 001.
                                                              Thermo GC Ceres 800 plus. S/N.998/0310

Method filename:       C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed:              05/18/2012  11:51
Sample ID:             LLNIE-1
Calculation method:    External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\LLNIE-1B (18-05-12).dat

S/N.      RT        Height    Area           Conc      Component   Conc
(#)       (min)     (uV)      (.1*uV*sec)    PPM                   nM
--------- --------- --------- -------------- --------- ----------- ---------
1         0.73      23318     959173         0.0                   0.00
2         3.23      9342      1024443        19.8      Ethylene    0.81
                    -----     -------

                                  Page: 1 of: 1
```

```
                                        Institute of Bioresources and Sustainable Development
                                                                       Imphal. Manipur 795 001.
                                                              Thermo GC Ceres 800 plus. S/N.998/0310

Method filename:       C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\ARA(20-03-12).mth
Analysed:              05/17/2012  15:46
Sample ID:             LLNB-1
Calculation method:    External STD (Area)
Chromatogram filename: C:\Program Files\Thermo\Chemito Chrom-Card\data\First Run\SURAJ\LLNB-1 (17-05-12).dat

S/N.      RT        Height    Area           Conc      Component   Conc
(#)       (min)     (uV)      (.1*uV*sec)    PPM                   nM
--------- --------- --------- -------------- --------- ----------- ---------
1         0.72      30195     1477403        0.0                   0.00
2         3.17      15463     1787887        34.6      Ethylene    1.42
                    -----     -------

                                  Page: 1 of: 1
```

LLN.IE-1 **LLN,B-1**

Fig. 24: Acetylene reduction curve of two Isolates (Selected for 16S rDNA analysis).

4.6. NifH gene amplification

All the selected twenty-six isolates from Rhizosphere and the twenty isolates obtained from Root Nodules were subjected to nifH gene amplification through polymerase chain reaction after ARA. Identification of replicon with a molecular weight of approximately 300 bp indicates the presence of nif gene in the isolates. In some isolates multiple replicons were formed which may be due to minute variations in the concentration and purity of template DNA as observed by Berg *et al.* (1994).

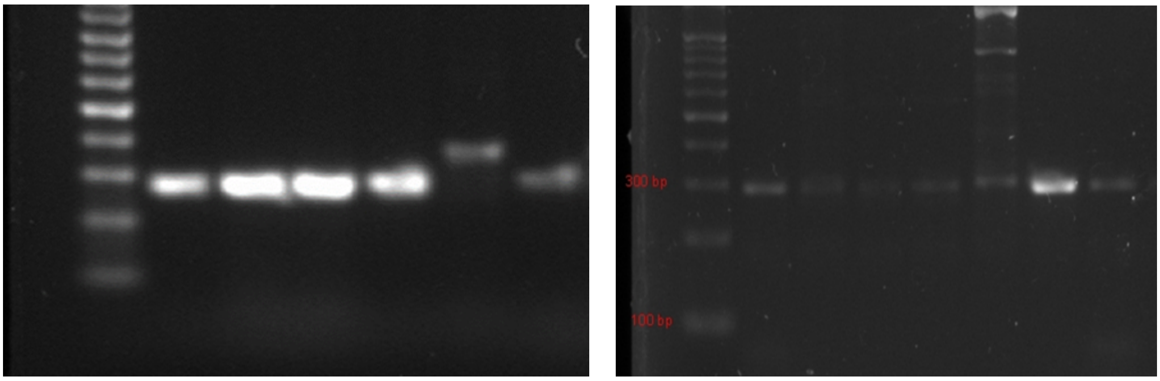


Fig.25: Gel image for nifH gene amplification.

4.7. 16S rDNA Amplification

Amplification of 16S rDNA was carried out for twelve selected isolates from rhizosphere and fourteen selected isolates from amongst the Root Nodule isolates. Selection of the isolates were done after observing and comparing both the results from ARA and NifH gene amplification. Both the ARA results and NifH amplification were taken into consideration and in few cases either of the two results was taken into consideration. Amplification of the 16S rDNA of all the selected samples through PCR gives band between 1400bp to 1600bp as shown in the gel image below (Fig.21). Amplification between 1400bp to 1600bp indicates the amplification of the targeted 16S rDNA. The PCR product was then sent for sequencing to perform further sequence analysis and phylogenetic studies.

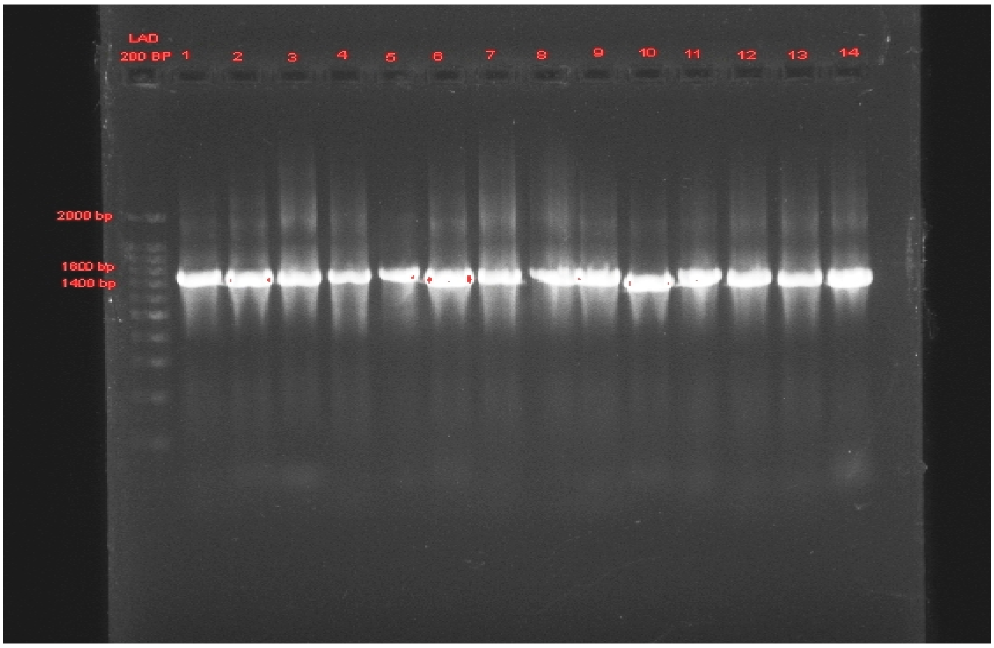


Fig. 26: Gel image for 16S rDNA amplification

4.8. Phylogenetic analysis of 16S rDNA sequences

After ARA and NifH gene amplification, the following twelve stains *viz.* SS.T-1, SS.IW-3, CPS.B-1, CPS.B-2, CPS.IW-3, CPS.T-1, CJS.IE-1, LLS.T-1, LLS.IE(B)-1, PS.IE-2, PS.IW-1 and PS.T(B)-2 were subjected to 16S rDNA phylogenetic analysis. These isolates were subjected to 16S rDNA gene sequencing in accordance with their result regarding the previous two confirmatory steps. However, some isolates are still selected for 16S rDNA gene sequencing even if the result from either of the previous test were not convincing. This is mainly due to the fact that both the ARA and NifH gene amplification cannot give perfect and accurate result everytime as many factors including culture condition and the state of the extracted DNA sometimes dictate the outcome of the test. The sequences of all the above 12 strains were deposited in GenBank under accession numbers: SS.T-1 (KM456220), SS.IW-3 (KM925076), CPS.B-1 (KM382276), CPS.B-2 (KM456219), CPS.IW-3 (KM925077), CPS.T-1 (KM925078), CJS.IE-1 (KM598638), LLS.T-1 (KM925075), LLS.IE(B)-1 (KM396262), PS.IE-2 (KM396263), PS.IW-1 (KM269071) and PS.T(B)-2 (KM598639) respectively. The bacterial isolates obtained from rhizosphere conforms to different organisms *viz. Bacillus spp.*, *Enterobacter spp.*, *Beijerinckia spp.*, *Cedecea spp.*, *Klebsiella spp.* and *Pseudomonas spp.* Details of organisms established with the isolates and their GenBank accession numbers are furnished in Table.16.

Table.16: Rhizosphere isolates with organism name and Accession number.

SL. NO.	ISOLATES	ORGANISM	ACCESSION NO.
1.	SS.T-1	Enterobacter cloacae	KM456220
2.	SS.IW-3	Cedecea davisae	KM925076
3.	CPS.B-1	Beijerinckia fluminensis	KM382276
4.	CPS.B-2	Enterobacter asburiae	KM456219
5.	CPS.IW-3	Bacillus subtilis	KM925077
6.	CPS.T-1	Enterobacter asburiae	KM925078
7.	CJS.IE-1	Cedecea davisae	KM598638
8.	LLS.T-1	Enterobacter kobei	KM925075
9.	LLS.IE(B)-1	Bacillus altitudinis	KM396262
10.	PS.IE-2	Klebsiella oxytoca	KM396263
11.	PS.IW-1	Bacillus subtilis	KM269071
12.	PS.T(B)-2	Pseudomonas cedrina	KM598639

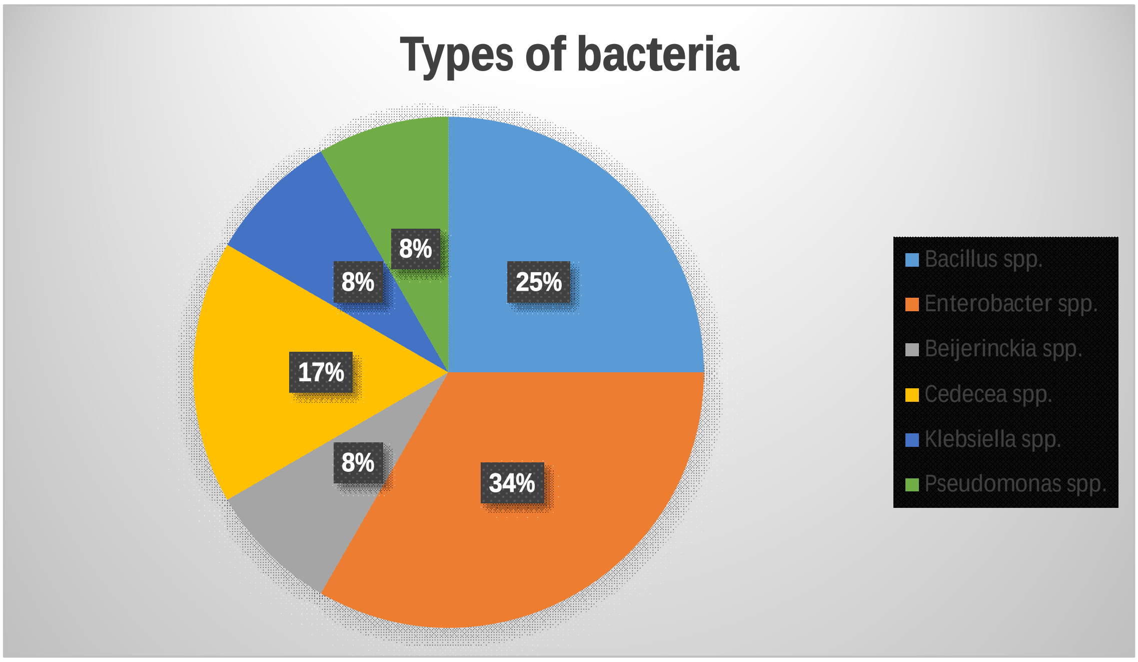


Fig.27: Pie diagram showing percentage of different species isolated from Rhizosphere.

From the total of twenty bacterial samples isolated from the root nodules of the source plants and selected for ARA and NifH gene amplification, 16S rDNA amplification and sequencing have been performed for fourteen bacterial sample in accordance with their results from ARA and NifH gene amplification. However, some isolates are still selected for 16S rDNA gene sequencing even if the result from either of the previous test were not convincing. Again this is mainly due to the same reason as mentioned before. The sequences of the said bacterial sequences deposited in GenBank along with their accession numbers are as follows: SN.T (KP331546), SN.IE-1 (KU355544), SN.B-1 (KX281718), CJN.T-1 (KP331547), CJN.B-1 (KU355542), CJN.IW-1 (KU355543), CJN.IE-2 (KX434625), CPN.B (KU935450), CPN.IW-1 (KU935451), CPN.T-1 (KU935452), CPN.T-4 (KU935453), LLN.B-1 (KU955582), LLN.T-1 (KU955583) and LLN.IE-1 (KX281719). The bacterial isolates obtained from rhizosphere conforms to different organisms *viz. Mesorhizobium spp., Pseudomonas spp., Rhizobium spp., Pantoea spp., Bacillus spp., Bradyrhizobium spp., Enterobacter spp., Stenotrophomonas spp.* and *Cedecea spp.* Details of organisms established with the isolates and their GenBank accession numbers are furnished in Table.18.

Table.17: Root nodule isolates with organism name and Accession number.

SL. NO.	ISOLATES	ORGANISM	ACCESSION NO.
1	SN.T	Mesorhizobium huakuii	KP331546
2	SN.IE-1	Pseudomonas azotoformans	KU355544
3	SN.B-1	Rhizobium huautlense	KX281718
4	CPN.B	Enterobacter hormaechei	KU935450
5	CPN.IW-1	Stenotrophomonas maltophilia	KU935451
6	CPN.T-1	Pantoea agglomerans	KU935452
7	CPN.T-4	Cedecea davisae	KU935453
8	CJN.T-1	Pantoea agglomerans	KP331547
9	CJN.B-1	Pantoea agglomerans	KU355542
10	CJN.IW-1	Bacillus subtilis	KU355543
11	CJN.IE-2	Bradyrhizobium japonicum	KX434625
12	LLN.B-1	Bacillus toyonensis	KU955582
13	LLN.T-1	Pseudomonas hibiscicola	KU955583
14	LLN.IE-1	Mesorhizobium plurifarium	KX281719

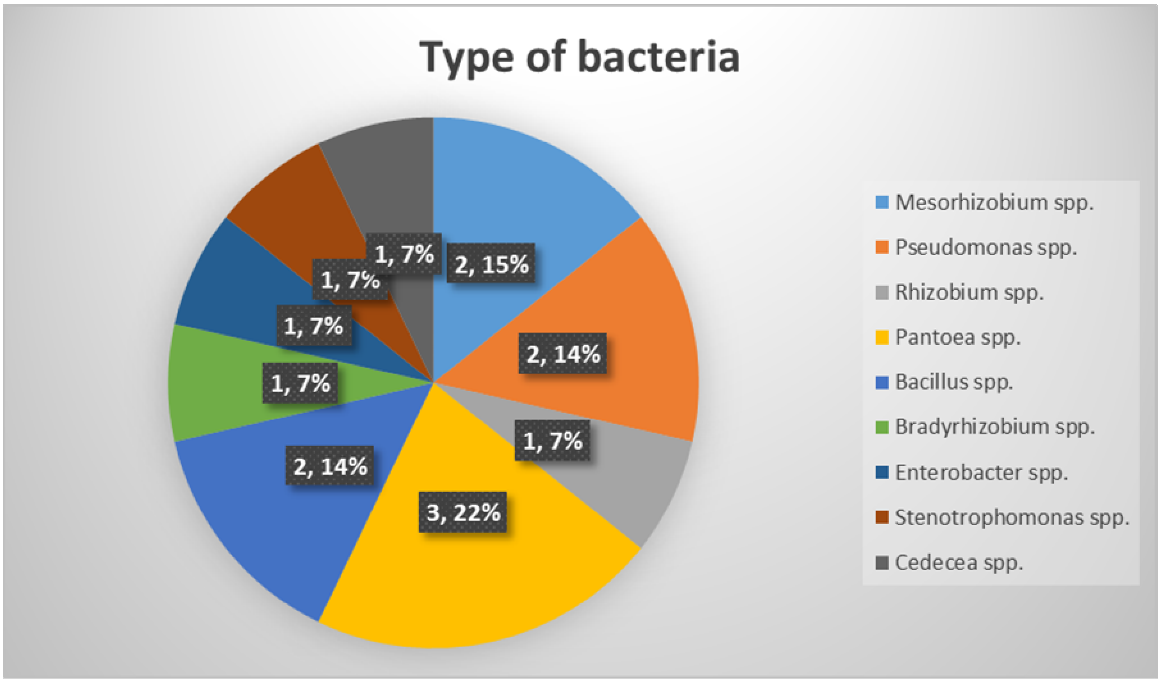


Fig.28: Pie diagram showing percentage of different species isolated from Root Nodules.

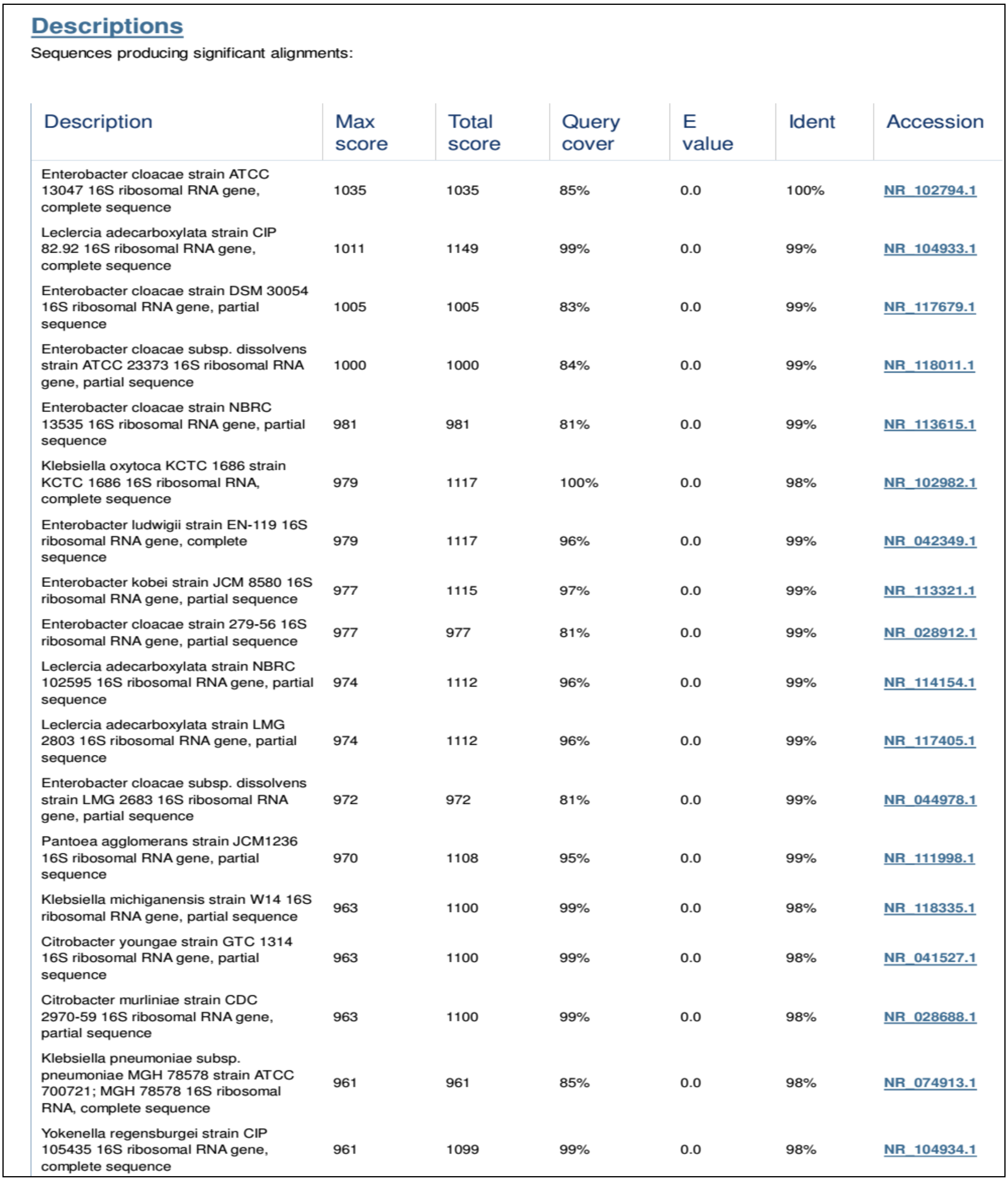
4.8.1. 16S rDNA Analysis of SS.T-1

The bacterial culture designated as SS.T-1 was established as *Enterobacter cloacae* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 654bp at GenBank NCBI through sequin submission format. KM456220 has been designated as its accsssion number.

Consensus Sequence of SS.T-1:

CGATGTCGAATTGGAAGGTTGTGCCCCTTGAGGGAGTGGCTTTCCGGAGCTAACGCGTTAA
GTCGACCGCGTGGGGAGTACGGCCGCAAGGTTAAAATTGAAGAGTTTGATCATGGCTCAGA
TTGAACGCTGGCGGCAGGCCTAACACATGCAAGTCGAACGGTAGCACAGAGAGCTTGCTCT
CGGGTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAA
CTACTGGAAACGGTAGCTAATACCGCATAATGTCGCAAGACCAAAGAGGGGGACCTTCGGG
CCTCTTGCCATCAGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTA
GGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCC
AGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCC
ATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGTGT
TGTGGTTAATAACCGCAGCAATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGC
CAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATT

Table.18: Sequences producing Significant Alignment for SS.T-1:



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Enterobacter cloacae strain ATCC 13047 16S ribosomal RNA gene, complete sequence	1035	1035	85%	0.0	100%	NR_102794.1
Leclercia adecarboxylata strain CIP 82.92 16S ribosomal RNA gene, complete sequence	1011	1149	99%	0.0	99%	NR_104933.1
Enterobacter cloacae strain DSM 30054 16S ribosomal RNA gene, partial sequence	1005	1005	83%	0.0	99%	NR_117679.1
Enterobacter cloacae subsp. dissolvens strain ATCC 23373 16S ribosomal RNA gene, partial sequence	1000	1000	84%	0.0	99%	NR_118011.1
Enterobacter cloacae strain NBRC 13535 16S ribosomal RNA gene, partial sequence	981	981	81%	0.0	99%	NR_113615.1
Klebsiella oxytoca KCTC 1686 strain KCTC 1686 16S ribosomal RNA, complete sequence	979	1117	100%	0.0	98%	NR_102982.1
Enterobacter ludwigii strain EN-119 16S ribosomal RNA gene, complete sequence	979	1117	96%	0.0	99%	NR_042349.1
Enterobacter kobei strain JCM 8580 16S ribosomal RNA gene, partial sequence	977	1115	97%	0.0	99%	NR_113321.1
Enterobacter cloacae strain 279-56 16S ribosomal RNA gene, partial sequence	977	977	81%	0.0	99%	NR_028912.1
Leclercia adecarboxylata strain NBRC 102595 16S ribosomal RNA gene, partial sequence	974	1112	96%	0.0	99%	NR_114154.1
Leclercia adecarboxylata strain LMG 2803 16S ribosomal RNA gene, partial sequence	974	1112	96%	0.0	99%	NR_117405.1
Enterobacter cloacae subsp. dissolvens strain LMG 2683 16S ribosomal RNA gene, partial sequence	972	972	81%	0.0	99%	NR_044978.1
Pantoea agglomerans strain JCM1236 16S ribosomal RNA gene, partial sequence	970	1108	95%	0.0	99%	NR_111998.1
Klebsiella michiganensis strain W14 16S ribosomal RNA gene, partial sequence	963	1100	99%	0.0	98%	NR_118335.1
Citrobacter youngae strain GTC 1314 16S ribosomal RNA gene, partial sequence	963	1100	99%	0.0	98%	NR_041527.1
Citrobacter murliniae strain CDC 2970-59 16S ribosomal RNA gene, partial sequence	963	1100	99%	0.0	98%	NR_028688.1
Klebsiella pneumoniae subsp. pneumoniae MGH 78578 strain ATCC 700721; MGH 78578 16S ribosomal RNA, complete sequence	961	961	85%	0.0	98%	NR_074913.1
Yokenella regensburgei strain CIP 105435 16S ribosomal RNA gene, complete sequence	961	1099	99%	0.0	98%	NR_104934.1

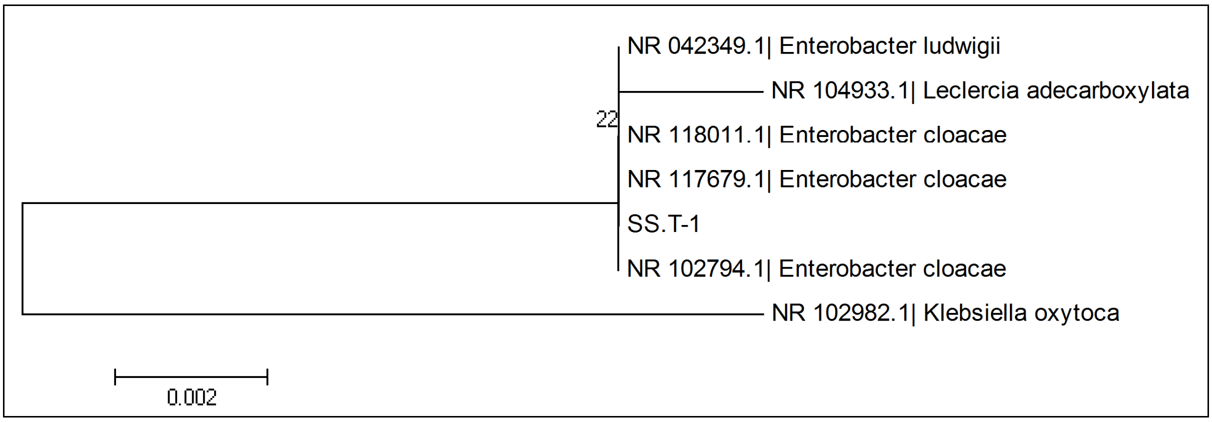


Fig.29: Evolutionary Tree for SS.T-1 with reference sequences from NCBI.

4.8.2. 16S rDNA Analysis of SS.IW-3

The bacterial culture designated as *SS.IW-3* was established as *Cedecea davisae* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 718bp at GenBank NCBI through sequin submission format. KM925076 has been designated as its accssion number.

Consensus Sequence of SS.IW-3

GAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGA
CTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGG
GGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAG
CATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTACTCTTGACATCCAGAGAACTT
TCCAGAGATGGATTGGTGCCTTCGGGAACTCTGAGACAGGTGCTGCATGGCTGTCGTCAGC
TCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCA
GCGGTTCGGCCGGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGA
CGTCAAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAA
GAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGT
CTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGA
ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAG
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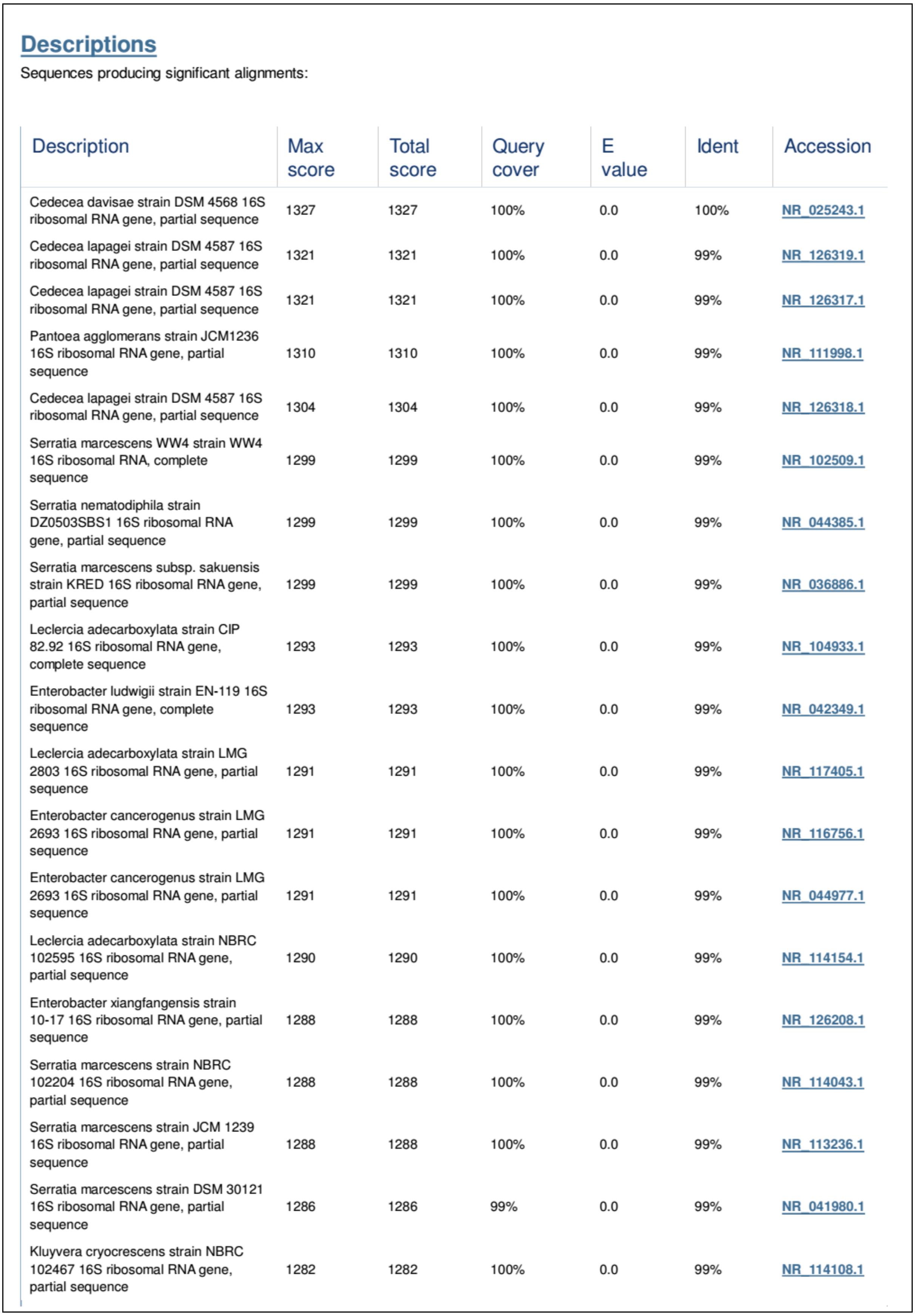
Table.19: Sequences producing Significant Alignment for SS.IW-3.



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Cedecea davisae strain DSM 4568 16S ribosomal RNA gene, partial sequence	1327	1327	100%	0.0	100%	NR_025243.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	1321	1321	100%	0.0	99%	NR_126319.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	1321	1321	100%	0.0	99%	NR_126317.1
Pantoea agglomerans strain JCM1236 16S ribosomal RNA gene, partial sequence	1310	1310	100%	0.0	99%	NR_111998.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	1304	1304	100%	0.0	99%	NR_126318.1
Serratia marcescens WW4 strain WW4 16S ribosomal RNA, complete sequence	1299	1299	100%	0.0	99%	NR_102509.1
Serratia nematodiphila strain DZ0503SBS1 16S ribosomal RNA gene, partial sequence	1299	1299	100%	0.0	99%	NR_044385.1
Serratia marcescens subsp. sakuensis strain KRED 16S ribosomal RNA gene, partial sequence	1299	1299	100%	0.0	99%	NR_036886.1
Leclercia adecarboxylata strain CIP 82.92 16S ribosomal RNA gene, complete sequence	1293	1293	100%	0.0	99%	NR_104933.1
Enterobacter ludwigii strain EN-119 16S ribosomal RNA gene, complete sequence	1293	1293	100%	0.0	99%	NR_042349.1
Leclercia adecarboxylata strain LMG 2803 16S ribosomal RNA gene, partial sequence	1291	1291	100%	0.0	99%	NR_117405.1
Enterobacter cancerogenus strain LMG 2693 16S ribosomal RNA gene, partial sequence	1291	1291	100%	0.0	99%	NR_116756.1
Enterobacter cancerogenus strain LMG 2693 16S ribosomal RNA gene, partial sequence	1291	1291	100%	0.0	99%	NR_044977.1
Leclercia adecarboxylata strain NBRC 102595 16S ribosomal RNA gene, partial sequence	1290	1290	100%	0.0	99%	NR_114154.1
Enterobacter xiangfangensis strain 10-17 16S ribosomal RNA gene, partial sequence	1288	1288	100%	0.0	99%	NR_126208.1
Serratia marcescens strain NBRC 102204 16S ribosomal RNA gene, partial sequence	1288	1288	100%	0.0	99%	NR_114043.1
Serratia marcescens strain JCM 1239 16S ribosomal RNA gene, partial sequence	1288	1288	100%	0.0	99%	NR_113236.1
Serratia marcescens strain DSM 30121 16S ribosomal RNA gene, partial sequence	1286	1286	99%	0.0	99%	NR_041980.1
Kluyvera cryocrescens strain NBRC 102467 16S ribosomal RNA gene, partial sequence	1282	1282	100%	0.0	99%	NR_114108.1

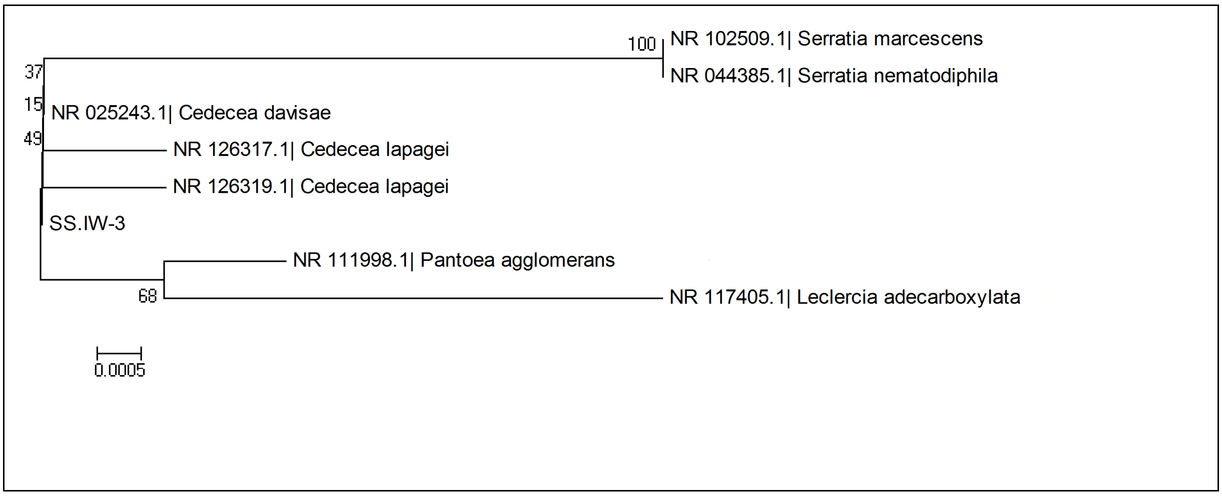


Fig.30: Phylogenetic tree of SS.IW-3 constructed by NJ method

4.8.3. 16S rDNA Analysis of CPS.B-1

The bacterial culture designated as *CPS.B-1*was established as *Beijerinckia fluminensis* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1138bp at GenBank NCBI through sequin submission format. KM382276 has been designated as its accsssion number.

Consensus Sequence of CPS.B-1

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GACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCG
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ATATTTAAGTCAGGGGTGAAATCCCAGAGCTCAACTCTGGAACTGCCTTTGATACTGGGTA
TCTTGAGTATGGAAGAGGTAAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCG
GAGGAACACCAGTGGCGAAGGGGGCTTACTGGTCCATTACTGACGCTGAGGTGCGAAAGCG
TGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGTTAGCCG
TCGGGCAGTATACTGTTCGGTGGCGCAGCTAACGCATTAAACATTCCGCCTGGGGAGTACG
GTCGCAAGATTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGT
TTAATTCGAAGCAACGCGCAGAACCTTACCAGCTCTTGACATTCGGGGTATGGGCATTGGA
GACGATGTCCTTCAGTTAGGCTGGCCCCAGAACAGGTGCTGCATGGCTGTCGTCAGCTCGT
GTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGCCCTTAGTTGCCAGCAT
TTAGTTGGGCACTCTAAGGGGACTGCCGGTGATAAGCCGAGAGGAAGGTGGGGATGACGTC
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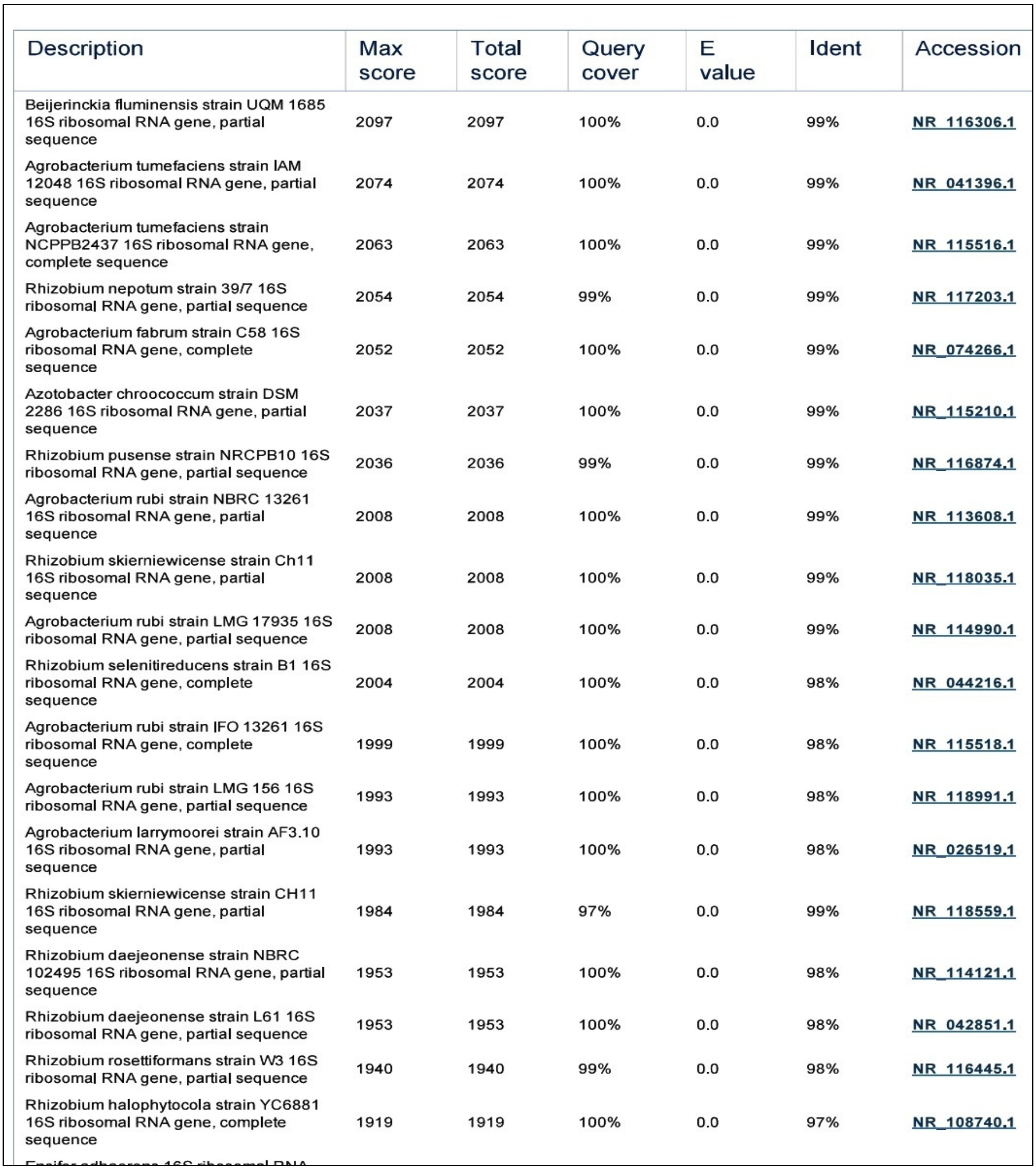
AAGTCCTCATGGCCCTTACGGGCTGGGCTACACACGTGCTACAATGGTGGTGACAGTGGGC
AGCGAGACAGCGATGTCGAGCTAATCTCCAAAAGCCATCTCAGTTCGGATTGCACTCTGCA
ACTCGAGTGCATGAAGTTGGAATCGCTAGTAATCGCAGATCAGCATGCTGCGGTGAATACG
TTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTGGTTTTACCCGAAGGTAGT
GCGCTAACCGCAAGGAGGCAGCTAACCACGGTAGGGTCAG

Table.20: Sequences producing Significant Alignment for *CPS.B-1*



Description	Max score	Total score	Query cover	E value	Ident	Accession
Beijerinckia fluminensis strain UQM 1685 16S ribosomal RNA gene, partial sequence	2097	2097	100%	0.0	99%	NR_116306.1
Agrobacterium tumefaciens strain IAM 12048 16S ribosomal RNA gene, partial sequence	2074	2074	100%	0.0	99%	NR_041396.1
Agrobacterium tumefaciens strain NCPPB2437 16S ribosomal RNA gene, complete sequence	2063	2063	100%	0.0	99%	NR_115516.1
Rhizobium nepotum strain 39/7 16S ribosomal RNA gene, partial sequence	2054	2054	99%	0.0	99%	NR_117203.1
Agrobacterium fabrum strain C58 16S ribosomal RNA gene, complete sequence	2052	2052	100%	0.0	99%	NR_074266.1
Azotobacter chroococcum strain DSM 2286 16S ribosomal RNA gene, partial sequence	2037	2037	100%	0.0	99%	NR_115210.1
Rhizobium pusense strain NRCPB10 16S ribosomal RNA gene, partial sequence	2036	2036	99%	0.0	99%	NR_116874.1
Agrobacterium rubi strain NBRC 13261 16S ribosomal RNA gene, partial sequence	2008	2008	100%	0.0	99%	NR_113608.1
Rhizobium skierniewicense strain Ch11 16S ribosomal RNA gene, partial sequence	2008	2008	100%	0.0	99%	NR_118035.1
Agrobacterium rubi strain LMG 17935 16S ribosomal RNA gene, partial sequence	2008	2008	100%	0.0	99%	NR_114990.1
Rhizobium selenitireducens strain B1 16S ribosomal RNA gene, complete sequence	2004	2004	100%	0.0	98%	NR_044216.1
Agrobacterium rubi strain IFO 13261 16S ribosomal RNA gene, complete sequence	1999	1999	100%	0.0	98%	NR_115518.1
Agrobacterium rubi strain LMG 156 16S ribosomal RNA gene, partial sequence	1993	1993	100%	0.0	98%	NR_118991.1
Agrobacterium larrymoorei strain AF3.10 16S ribosomal RNA gene, partial sequence	1993	1993	100%	0.0	98%	NR_026519.1
Rhizobium skierniewicense strain CH11 16S ribosomal RNA gene, partial sequence	1984	1984	97%	0.0	99%	NR_118559.1
Rhizobium daejeonense strain NBRC 102495 16S ribosomal RNA gene, partial sequence	1953	1953	100%	0.0	98%	NR_114121.1
Rhizobium daejeonense strain L61 16S ribosomal RNA gene, partial sequence	1953	1953	100%	0.0	98%	NR_042851.1
Rhizobium rosettiformans strain W3 16S ribosomal RNA gene, partial sequence	1940	1940	99%	0.0	98%	NR_116445.1
Rhizobium halophytocola strain YC6881 16S ribosomal RNA gene, complete sequence	1919	1919	100%	0.0	97%	NR_108740.1

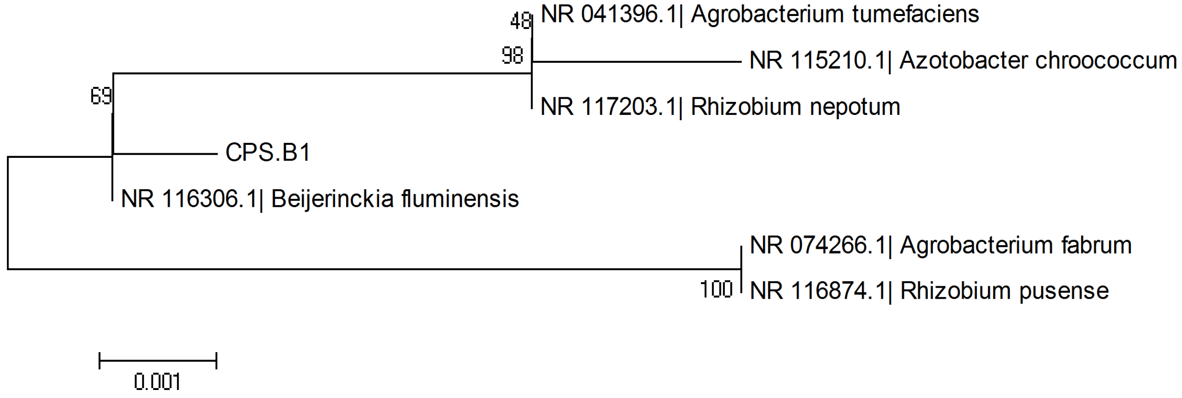


Fig.31: Phylogenetic tree of CPS.B1 constructed by NJ method

4.8.4. 16S rDNA Analysis of CPS.B-2

The bacterial culture designated as *CPS.B-2* was established as *Enterobacter asburiae* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1443bp at GenBank NCBI through sequin submission format. KM456219 has been designated as its accssion number.

Consensus Sequence of CPS.B-2

```
GGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAGCACAGGGAGCTTGCTCCTGGGTGACG
AGCGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAA
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ATCAGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGAT
CCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTA
CGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGT
GTATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCGATAAGGTTAA
TAACCTTGTCGATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCG
CGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGG
TCTGTCAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAG
GCTAGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTG
GAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCG
TGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAG
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TTTAATTCGATGCAACGCGAAGAACCTTACCTACTCTTGACATCCAGAGAACTTTCCAGAG
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GTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTCC
GGCCGGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAG
TCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGC
GACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAAC
TCGACTCCATGAAGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGAATACGTT
CCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAG
CTTAACCTTCGGGACGACCCTCCCCCACGGTGGGTTCAAT

Table.21: Sequence producing Significant Alignment for CPS.B-2.

Description	Max score	Total score	Query cover	E value	Ident	Accession
Enterobacter asburiae strain JCM6051 16S ribosomal RNA gene, partial sequence	2617	2617	98%	0.0	100%	NR_024640.1
Enterobacter cancerogenus strain LMG 2693 16S ribosomal RNA gene, partial sequence	2553	2553	98%	0.0	99%	NR_044977.1
Enterobacter asburiae LF7a strain LF7a 16S ribosomal RNA, complete sequence	2534	2534	98%	0.0	99%	NR_074722.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	2531	2531	98%	0.0	99%	NR_126319.1
Pantoea agglomerans strain JCM1236 16S ribosomal RNA gene, partial sequence	2529	2529	98%	0.0	99%	NR_111998.1
Enterobacter soli strain LF7 16S ribosomal RNA gene, partial sequence	2527	2527	98%	0.0	99%	NR_117547.1
Enterobacter aerogenes strain KCTC 2190 16S ribosomal RNA gene, complete sequence	2518	2518	98%	0.0	99%	NR_102493.1
Enterobacter aerogenes strain JCM1235 16S ribosomal RNA gene, partial sequence	2518	2518	98%	0.0	99%	NR_024643.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	2514	2514	98%	0.0	99%	NR_126317.1
Enterobacter aerogenes strain NBRC 13534 16S ribosomal RNA gene, partial sequence	2514	2514	98%	0.0	99%	NR_113614.1
Enterobacter ludwigii strain EN-119 16S ribosomal RNA gene, complete sequence	2512	2512	98%	0.0	99%	NR_042349.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	2507	2507	98%	0.0	99%	NR_126318.1
Enterobacter aerogenes strain NCTC10006 16S ribosomal RNA gene, partial sequence	2507	2507	98%	0.0	99%	NR_114737.1
Klebsiella pneumoniae strain DSM 30104 16S ribosomal RNA gene, partial sequence	2501	2501	98%	0.0	99%	NR_117683.1
Klebsiella pneumoniae subsp. rhinoscleromatis strain ATCC 13884 16S	2501	2501	97%	0.0	99%	NR_114507.1

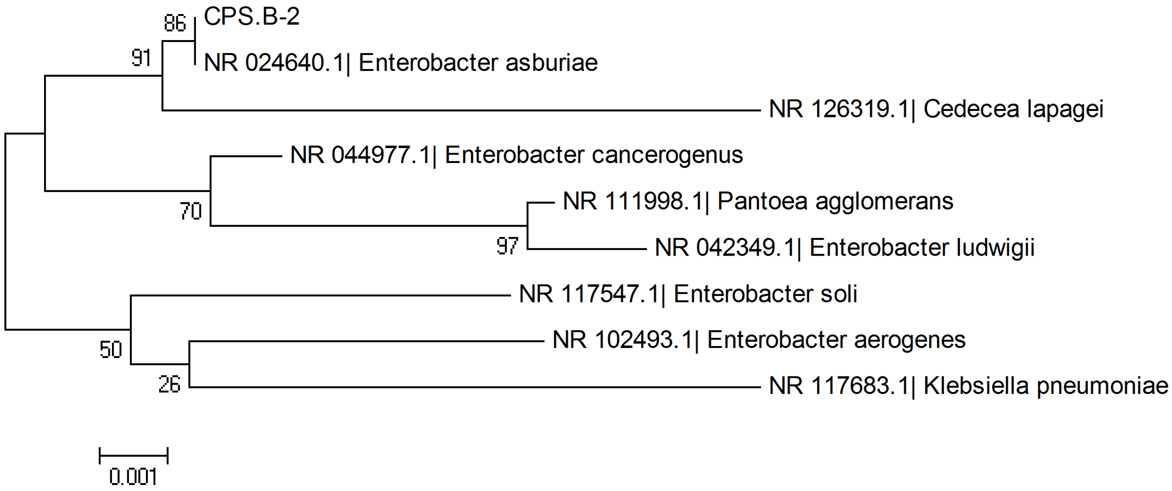

Fig.32: Phylogenetic tree of CPS.B-2 constructed by NJ method

4.8.5. 16S rDNA Analysis of CPS.T-1

The bacterial culture designated as *CPS.T-1* was established as *Enterobacter asburiae* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 519bp at GenBank NCBI through sequin submission format. KM925078 has been designated as its accsssion number.

Consensus Sequence of CPS.T-1

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CCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTACTCT
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GCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACC
CTTATCCTTTGTTGCCAGCGGTCCGGCCGGGAACTCAAAGGAGACTGCCAGTGATAAACTG
GAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCT
ACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTC
GTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTAGA
TCAGAATGCTACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGA
GTGGGTTGCAAAAGAAGTAGGTAGCTTAACC
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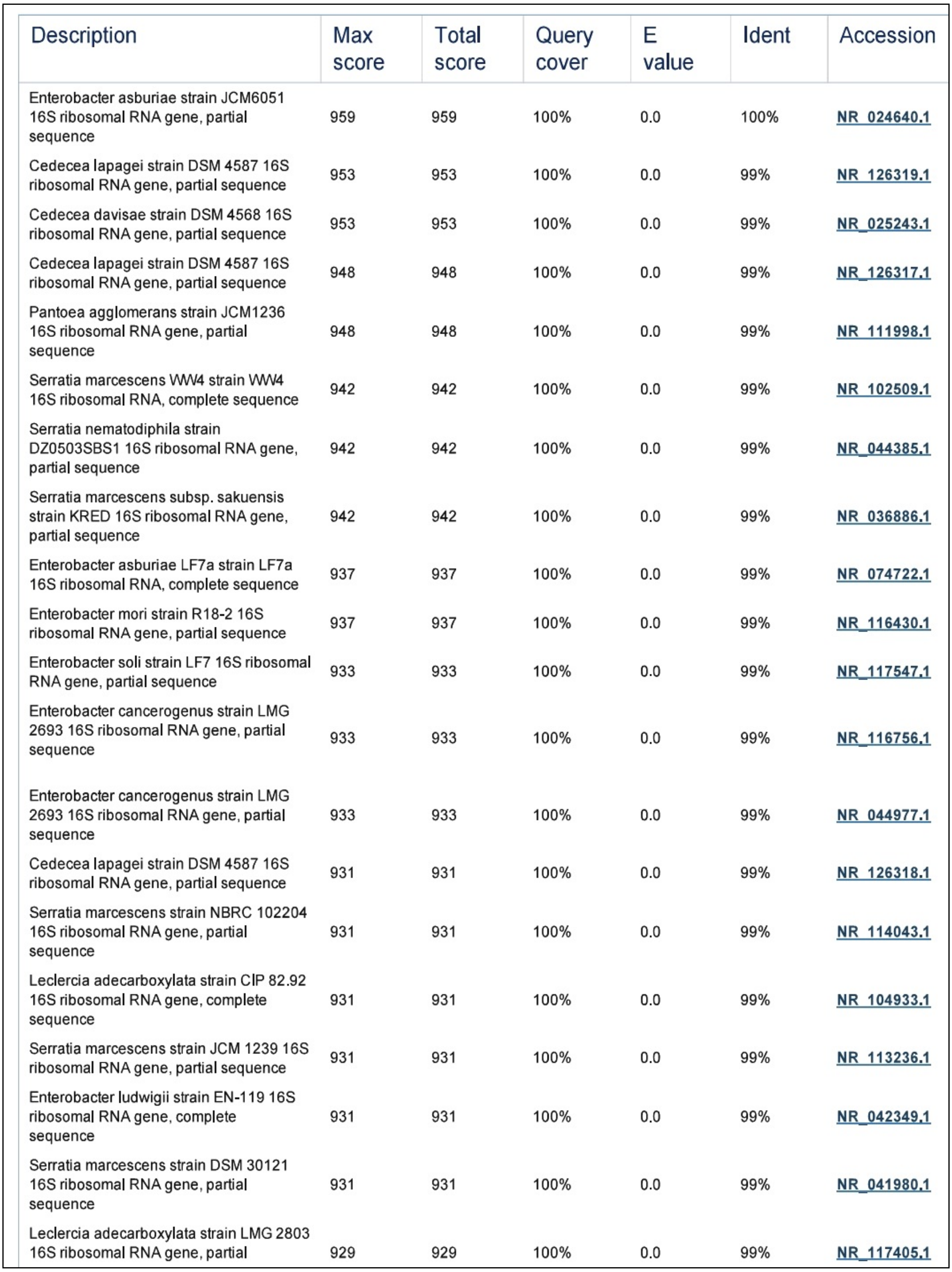
Table.22: Sequences producing Significant Alignment for CPS.T-1



Description	Max score	Total score	Query cover	E value	Ident	Accession
Enterobacter asburiae strain JCM6051 16S ribosomal RNA gene, partial sequence	959	959	100%	0.0	100%	NR_024640.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	953	953	100%	0.0	99%	NR_126319.1
Cedecea davisae strain DSM 4568 16S ribosomal RNA gene, partial sequence	953	953	100%	0.0	99%	NR_025243.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	948	948	100%	0.0	99%	NR_126317.1
Pantoea agglomerans strain JCM1236 16S ribosomal RNA gene, partial sequence	948	948	100%	0.0	99%	NR_111998.1
Serratia marcescens WW4 strain WW4 16S ribosomal RNA, complete sequence	942	942	100%	0.0	99%	NR_102509.1
Serratia nematodiphila strain DZ0503SBS1 16S ribosomal RNA gene, partial sequence	942	942	100%	0.0	99%	NR_044385.1
Serratia marcescens subsp. sakuensis strain KRED 16S ribosomal RNA gene, partial sequence	942	942	100%	0.0	99%	NR_036886.1
Enterobacter asburiae LF7a strain LF7a 16S ribosomal RNA, complete sequence	937	937	100%	0.0	99%	NR_074722.1
Enterobacter mori strain R18-2 16S ribosomal RNA gene, partial sequence	937	937	100%	0.0	99%	NR_116430.1
Enterobacter soli strain LF7 16S ribosomal RNA gene, partial sequence	933	933	100%	0.0	99%	NR_117547.1
Enterobacter cancerogenus strain LMG 2693 16S ribosomal RNA gene, partial sequence	933	933	100%	0.0	99%	NR_116756.1
Enterobacter cancerogenus strain LMG 2693 16S ribosomal RNA gene, partial sequence	933	933	100%	0.0	99%	NR_044977.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	931	931	100%	0.0	99%	NR_126318.1
Serratia marcescens strain NBRC 102204 16S ribosomal RNA gene, partial sequence	931	931	100%	0.0	99%	NR_114043.1
Leclercia adecarboxylata strain CIP 82.92 16S ribosomal RNA gene, complete sequence	931	931	100%	0.0	99%	NR_104933.1
Serratia marcescens strain JCM 1239 16S ribosomal RNA gene, partial sequence	931	931	100%	0.0	99%	NR_113236.1
Enterobacter ludwigii strain EN-119 16S ribosomal RNA gene, complete sequence	931	931	100%	0.0	99%	NR_042349.1
Serratia marcescens strain DSM 30121 16S ribosomal RNA gene, partial sequence	931	931	100%	0.0	99%	NR_041980.1
Leclercia adecarboxylata strain LMG 2803 16S ribosomal RNA gene, partial	929	929	100%	0.0	99%	NR_117405.1

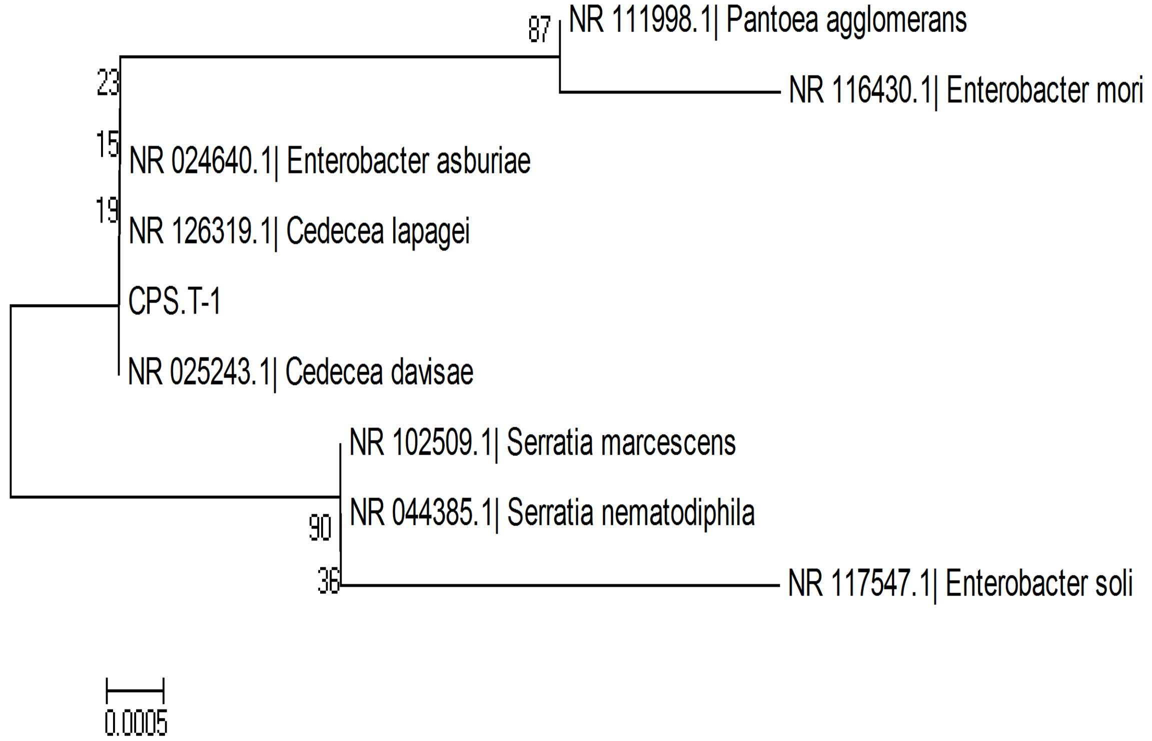


Fig.33: Phylogenetic tree of CPS.T-1 constructed by NJ method

4.8.6. 16S rDNA Analysis of CPS.1W-3

The bacterial culture designated as *CPS.1W-3* was established as *Bacillus subtilis* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1444bp at GenBank NCBI through sequin submission format. KM925077 has been designated as its accsssion number.

Consensus Sequence of CPS.1W-3

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CTTACAGATGGACCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCAACG
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TACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGC
GTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTACCGTTC
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GTGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGTCTGTAACTGACGCTGAGGAGCGAAA
GCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAA
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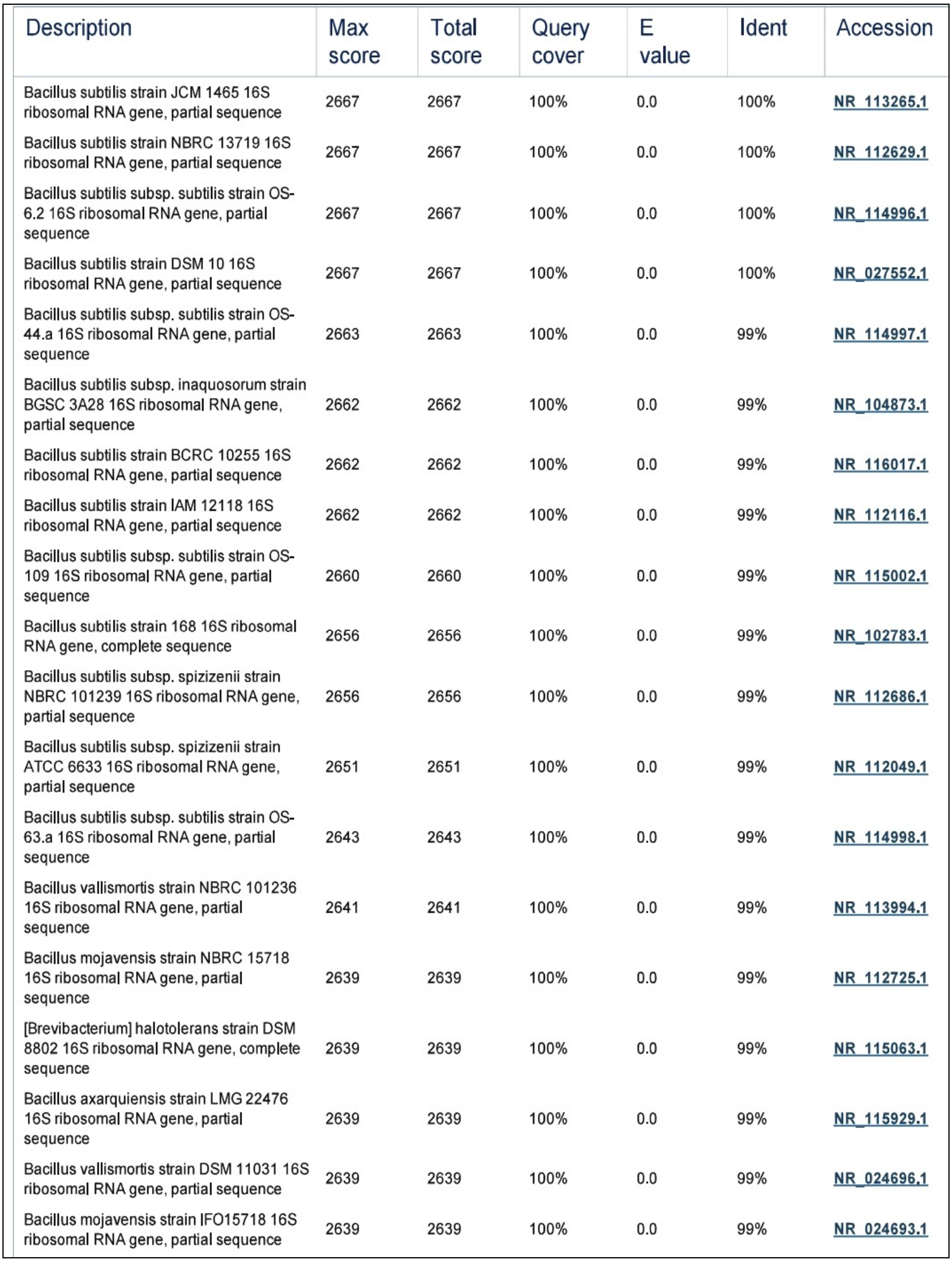
GTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCAT
GTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCTCTGACAATCCT
AGAGATAGGACGTCCCCTTCGGGGGCAGAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCG
TGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATCTTAGTTGCCAGCA
TTCAGTTGGGCACTCTAAGGTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTC
AAATCATCATGCCCCTTATGACCTGGGCTACACACGTGCTACAATGGACAGAACAAAGGGC
AGCGAAACCGCGAGGTTAAGCCAATCCCACAAATCTGTTCTCAGTTCGGATCGCAGTCTGC
AACTCGACTGCGTGAAGCTGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATAC
GTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGG
TGAGGTAACCTTTTAGGAGCCAGCCGCCGAAGGTGGGACAG

Table.23: Sequences Producing Significant Alignment for CPS.IW-3.



Description	Max score	Total score	Query cover	E value	Ident	Accession
Bacillus subtilis strain JCM 1465 16S ribosomal RNA gene, partial sequence	2667	2667	100%	0.0	100%	NR_113265.1
Bacillus subtilis strain NBRC 13719 16S ribosomal RNA gene, partial sequence	2667	2667	100%	0.0	100%	NR_112629.1
Bacillus subtilis subsp. subtilis strain OS-6.2 16S ribosomal RNA gene, partial sequence	2667	2667	100%	0.0	100%	NR_114996.1
Bacillus subtilis strain DSM 10 16S ribosomal RNA gene, partial sequence	2667	2667	100%	0.0	100%	NR_027552.1
Bacillus subtilis subsp. subtilis strain OS-44.a 16S ribosomal RNA gene, partial sequence	2663	2663	100%	0.0	99%	NR_114997.1
Bacillus subtilis subsp. inaquosorum strain BGSC 3A28 16S ribosomal RNA gene, partial sequence	2662	2662	100%	0.0	99%	NR_104873.1
Bacillus subtilis strain BCRC 10255 16S ribosomal RNA gene, partial sequence	2662	2662	100%	0.0	99%	NR_116017.1
Bacillus subtilis strain IAM 12118 16S ribosomal RNA gene, partial sequence	2662	2662	100%	0.0	99%	NR_112116.1
Bacillus subtilis subsp. subtilis strain OS-109 16S ribosomal RNA gene, partial sequence	2660	2660	100%	0.0	99%	NR_115002.1
Bacillus subtilis strain 168 16S ribosomal RNA gene, complete sequence	2656	2656	100%	0.0	99%	NR_102783.1
Bacillus subtilis subsp. spizizenii strain NBRC 101239 16S ribosomal RNA gene, partial sequence	2656	2656	100%	0.0	99%	NR_112686.1
Bacillus subtilis subsp. spizizenii strain ATCC 6633 16S ribosomal RNA gene, partial sequence	2651	2651	100%	0.0	99%	NR_112049.1
Bacillus subtilis subsp. subtilis strain OS-63.a 16S ribosomal RNA gene, partial sequence	2643	2643	100%	0.0	99%	NR_114998.1
Bacillus vallismortis strain NBRC 101236 16S ribosomal RNA gene, partial sequence	2641	2641	100%	0.0	99%	NR_113994.1
Bacillus mojavensis strain NBRC 15718 16S ribosomal RNA gene, partial sequence	2639	2639	100%	0.0	99%	NR_112725.1
[Brevibacterium] halotolerans strain DSM 8802 16S ribosomal RNA gene, complete sequence	2639	2639	100%	0.0	99%	NR_115063.1
Bacillus axarquiensis strain LMG 22476 16S ribosomal RNA gene, partial sequence	2639	2639	100%	0.0	99%	NR_115929.1
Bacillus vallismortis strain DSM 11031 16S ribosomal RNA gene, partial sequence	2639	2639	100%	0.0	99%	NR_024696.1
Bacillus mojavensis strain IFO15718 16S ribosomal RNA gene, partial sequence	2639	2639	100%	0.0	99%	NR_024693.1

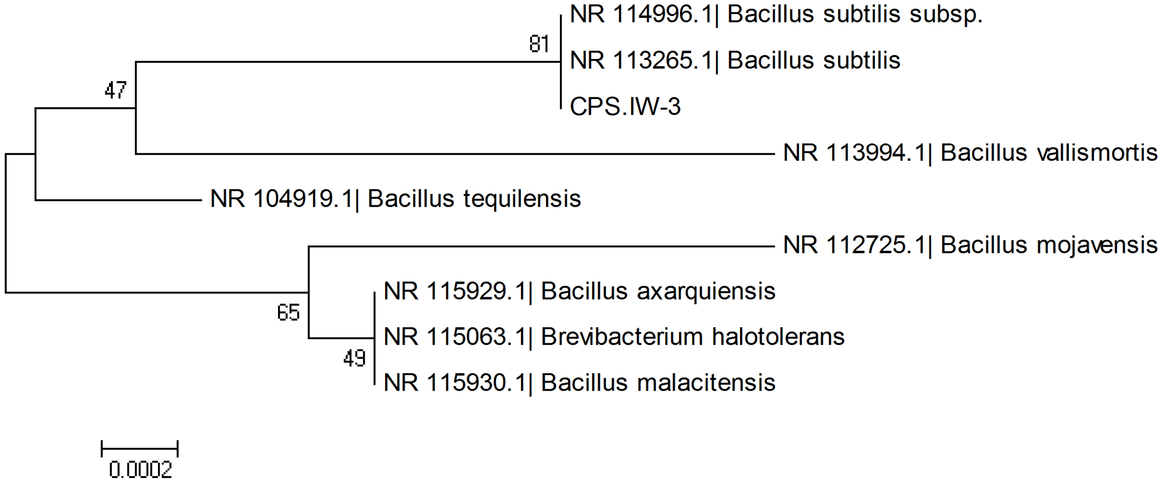


Fig.34: Phylogenetic tree of CPS.IW-3 constructed by NJ method

4.8.7. 16S rDNA Analysis of CJS.1E-1

The bacterial culture designated as *CJS.1E-1* was established as *Cedecea davisae* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 521bp at GenBank NCBI through sequin submission format. KM598638 has been designated as its accsssion number.

Consensus Sequence of CJS.1E-1

ACCTACTCTTGACATCCAGAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACT

CTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAG

TCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTTCGGCCGGGAACTCA

AAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCATG

GCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGAC

CTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCA

ACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGA

ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAA

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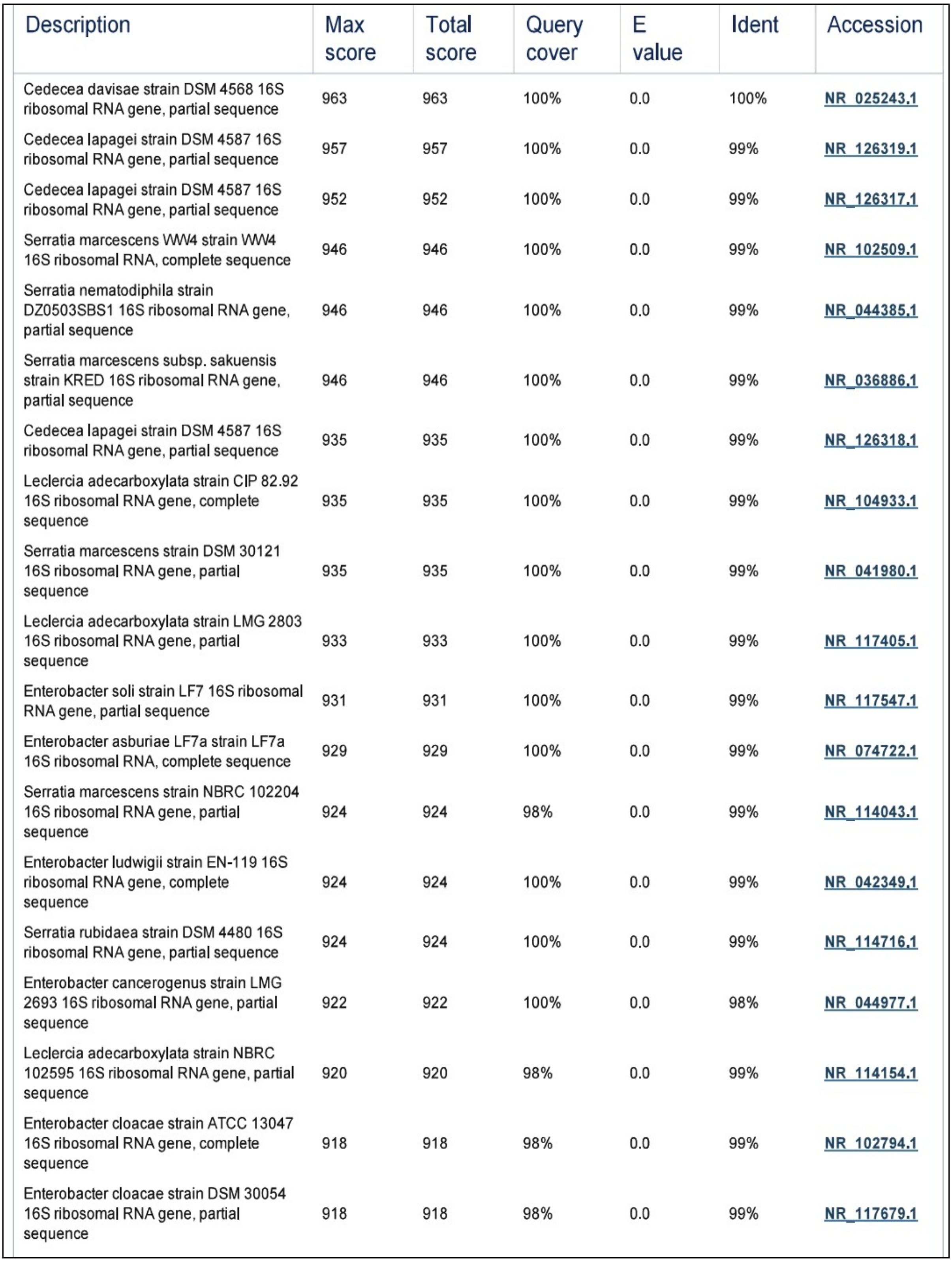
GGGTGAAGTCGTACCAA

Table.24: Sequences Producing Significant Alignment for CJS.IE-1



Description	Max score	Total score	Query cover	E value	Ident	Accession
Cedecea davisae strain DSM 4568 16S ribosomal RNA gene, partial sequence	963	963	100%	0.0	100%	NR_025243.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	957	957	100%	0.0	99%	NR_126319.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	952	952	100%	0.0	99%	NR_126317.1
Serratia marcescens WW4 strain WW4 16S ribosomal RNA, complete sequence	946	946	100%	0.0	99%	NR_102509.1
Serratia nematodiphila strain DZ0503SBS1 16S ribosomal RNA gene, partial sequence	946	946	100%	0.0	99%	NR_044385.1
Serratia marcescens subsp. sakuensis strain KRED 16S ribosomal RNA gene, partial sequence	946	946	100%	0.0	99%	NR_036886.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	935	935	100%	0.0	99%	NR_126318.1
Leclercia adecarboxylata strain CIP 82.92 16S ribosomal RNA gene, complete sequence	935	935	100%	0.0	99%	NR_104933.1
Serratia marcescens strain DSM 30121 16S ribosomal RNA gene, partial sequence	935	935	100%	0.0	99%	NR_041980.1
Leclercia adecarboxylata strain LMG 2803 16S ribosomal RNA gene, partial sequence	933	933	100%	0.0	99%	NR_117405.1
Enterobacter soli strain LF7 16S ribosomal RNA gene, partial sequence	931	931	100%	0.0	99%	NR_117547.1
Enterobacter asburiae LF7a strain LF7a 16S ribosomal RNA, complete sequence	929	929	100%	0.0	99%	NR_074722.1
Serratia marcescens strain NBRC 102204 16S ribosomal RNA gene, partial sequence	924	924	98%	0.0	99%	NR_114043.1
Enterobacter ludwigii strain EN-119 16S ribosomal RNA gene, complete sequence	924	924	100%	0.0	99%	NR_042349.1
Serratia rubidaea strain DSM 4480 16S ribosomal RNA gene, partial sequence	924	924	100%	0.0	99%	NR_114716.1
Enterobacter cancerogenus strain LMG 2693 16S ribosomal RNA gene, partial sequence	922	922	100%	0.0	98%	NR_044977.1
Leclercia adecarboxylata strain NBRC 102595 16S ribosomal RNA gene, partial sequence	920	920	98%	0.0	99%	NR_114154.1
Enterobacter cloacae strain ATCC 13047 16S ribosomal RNA gene, complete sequence	918	918	98%	0.0	99%	NR_102794.1
Enterobacter cloacae strain DSM 30054 16S ribosomal RNA gene, partial sequence	918	918	98%	0.0	99%	NR_117679.1

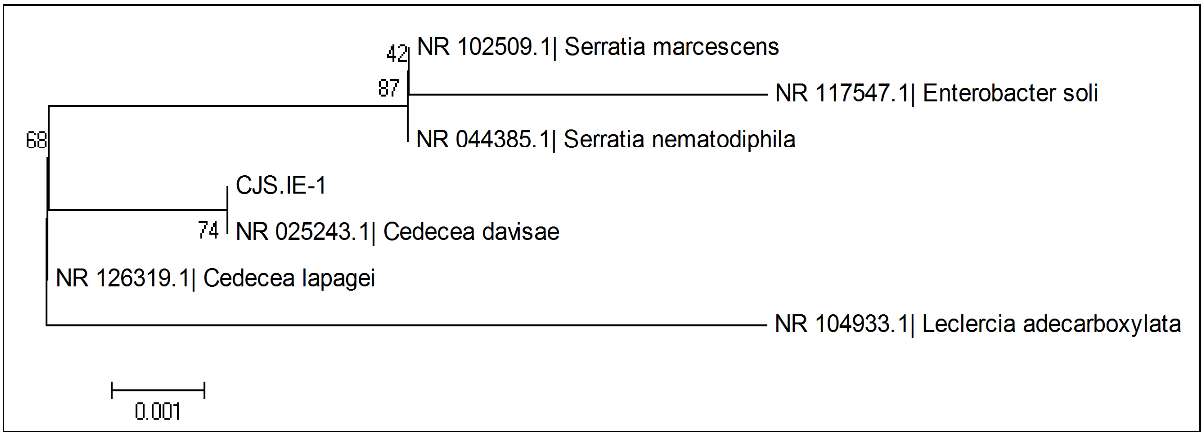


Fig.35: Phylogenetic tree of CJS.IE-1 constructed by NJ method

4.8.8. 16S rDNA Analysis of LLS.T-1

The bacterial culture designated as *LLS.T-1* was established as *Enterobacter kobei* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 837bp at GenBank NCBI through sequin submission format. KM925075 has been designated as its accssion number.

Consensus Sequence of LLS.T-1

```
GGGGTAGAATTCCCAGGTGTAGCGGTGAAAATGCGTAGAGATCTGGAGGAATACCG
GTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGTCCAGGTGCGAAAGCGTGGGGA
GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGCGG
CAGGCCTAACACATGCAAGTCGAGCGGTAGCACAGAGAGCTTGCTCTCGGGTGACG
AGCGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTAC
TGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGG
GCCTCTTGCCATCAGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCT
CACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTG
AGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG
CAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTAC
TTTCAGCGGGGAGGAAGGTGTTGTGGTTAATAACCTCAGCAATTGACGTTACCCGC
AGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAG
CGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATG
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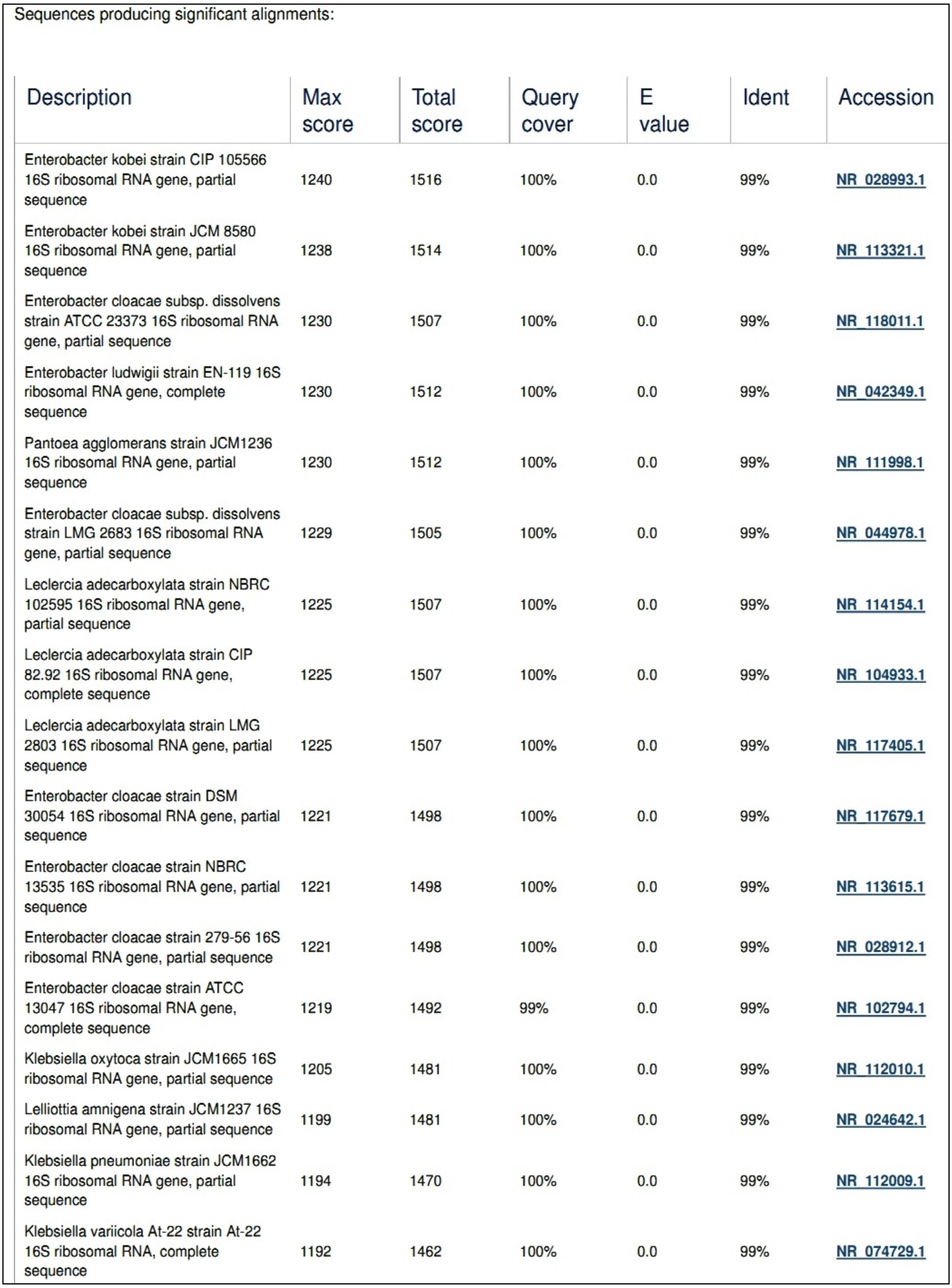
TGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAGGCTAGAGTCTT
GTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAG

Table.25: Sequences Producing Significant Alignment for LLS.T-1



Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Enterobacter kobei strain CIP 105566 16S ribosomal RNA gene, partial sequence	1240	1516	100%	0.0	99%	NR_028993.1
Enterobacter kobei strain JCM 8580 16S ribosomal RNA gene, partial sequence	1238	1514	100%	0.0	99%	NR_113321.1
Enterobacter cloacae subsp. dissolvens strain ATCC 23373 16S ribosomal RNA gene, partial sequence	1230	1507	100%	0.0	99%	NR_118011.1
Enterobacter ludwigii strain EN-119 16S ribosomal RNA gene, complete sequence	1230	1512	100%	0.0	99%	NR_042349.1
Pantoea agglomerans strain JCM1236 16S ribosomal RNA gene, partial sequence	1230	1512	100%	0.0	99%	NR_111998.1
Enterobacter cloacae subsp. dissolvens strain LMG 2683 16S ribosomal RNA gene, partial sequence	1229	1505	100%	0.0	99%	NR_044978.1
Leclercia adecarboxylata strain NBRC 102595 16S ribosomal RNA gene, partial sequence	1225	1507	100%	0.0	99%	NR_114154.1
Leclercia adecarboxylata strain CIP 82.92 16S ribosomal RNA gene, complete sequence	1225	1507	100%	0.0	99%	NR_104933.1
Leclercia adecarboxylata strain LMG 2803 16S ribosomal RNA gene, partial sequence	1225	1507	100%	0.0	99%	NR_117405.1
Enterobacter cloacae strain DSM 30054 16S ribosomal RNA gene, partial sequence	1221	1498	100%	0.0	99%	NR_117679.1
Enterobacter cloacae strain NBRC 13535 16S ribosomal RNA gene, partial sequence	1221	1498	100%	0.0	99%	NR_113615.1
Enterobacter cloacae strain 279-56 16S ribosomal RNA gene, partial sequence	1221	1498	100%	0.0	99%	NR_028912.1
Enterobacter cloacae strain ATCC 13047 16S ribosomal RNA gene, complete sequence	1219	1492	99%	0.0	99%	NR_102794.1
Klebsiella oxytoca strain JCM1665 16S ribosomal RNA gene, partial sequence	1205	1481	100%	0.0	99%	NR_112010.1
Lelliottia amnigena strain JCM1237 16S ribosomal RNA gene, partial sequence	1199	1481	100%	0.0	99%	NR_024642.1
Klebsiella pneumoniae strain JCM1662 16S ribosomal RNA gene, partial sequence	1194	1470	100%	0.0	99%	NR_112009.1
Klebsiella variicola At-22 strain At-22 16S ribosomal RNA, complete sequence	1192	1462	100%	0.0	99%	NR_074729.1

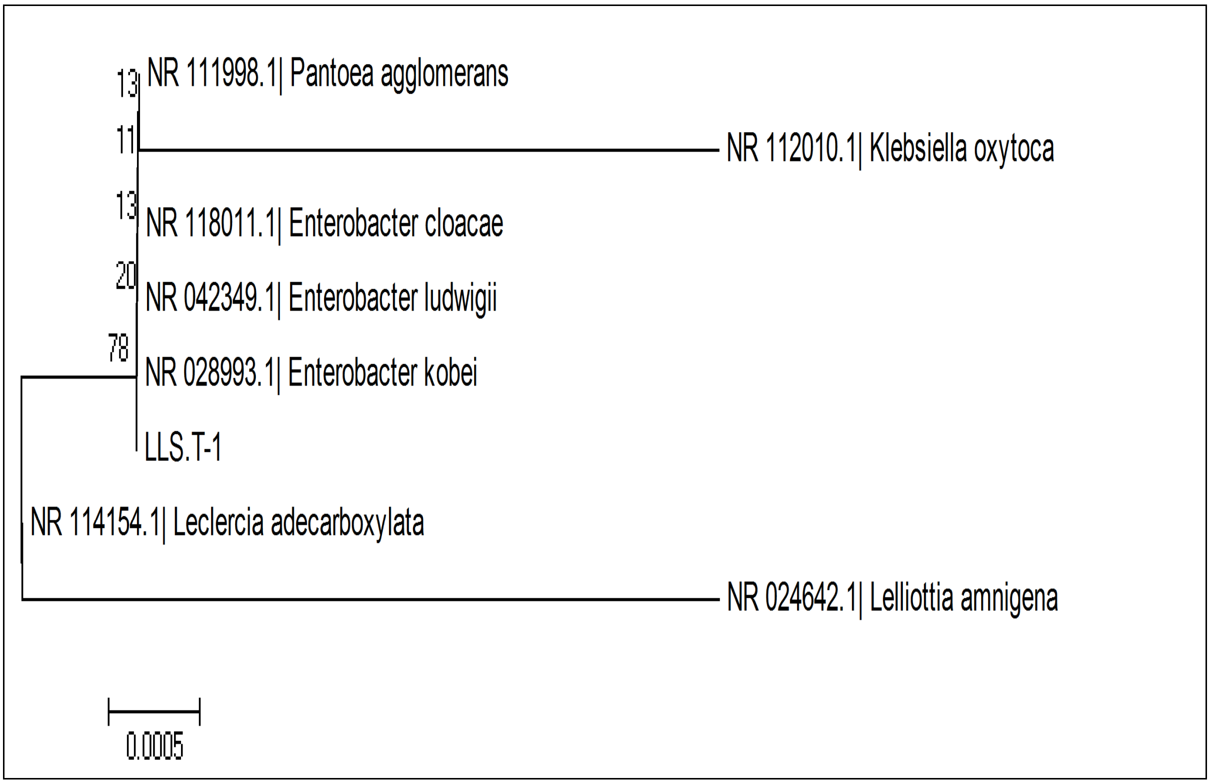


Fig.36: Phylogenetic tree of LLS.T-1 constructed by NJ method

4.8.9. 16S rDNA Analysis of LLS.1E(B)-1

The bacterial culture designated as *LLS.1E(B)-1* was established as *Bacillus altitudinis* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1440bp at GenBank NCBI through sequin submission format. KM396262 has been designated as its accsssion number.

Consensus Sequence of LLS.1E(B)-1

TCGTGCCTAATACATGCAAGTCGAGCGGACAGAAGGGAGCTTGCTCCCGGATGTTA
GCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCC
GGGAAACCGGAGCTAATACCGGATAGTTCCTTGAACCGCATGGTTCAAGGATGAAA
GACGGTTTCGGCTGTCACTTACAGATGGACCCGCGGCGCATTAGCTAGTTGGTGAG
GTAACGGCTCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACA
CTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCG
CAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATC

GTAAAGCTCTGTTGTTAGGGAAGAACAAGTGCAAGAGTAACTGCTTGCACCTTGAC
GGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTA
GGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGGGCTCGCAGGCGGTTTCTTA
AGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTGGGAAAC
TTGAGTGCAGAAGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGAT
GTGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGTCTGTAACTGACGCTGAGGAG
CGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGA
TGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCATTAAG
CACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGC
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GGTCTTGACATCCTCTGACAACCCTAGAGATAGGGCTTTCCCTTCGGGGACAGAGT
GACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCC
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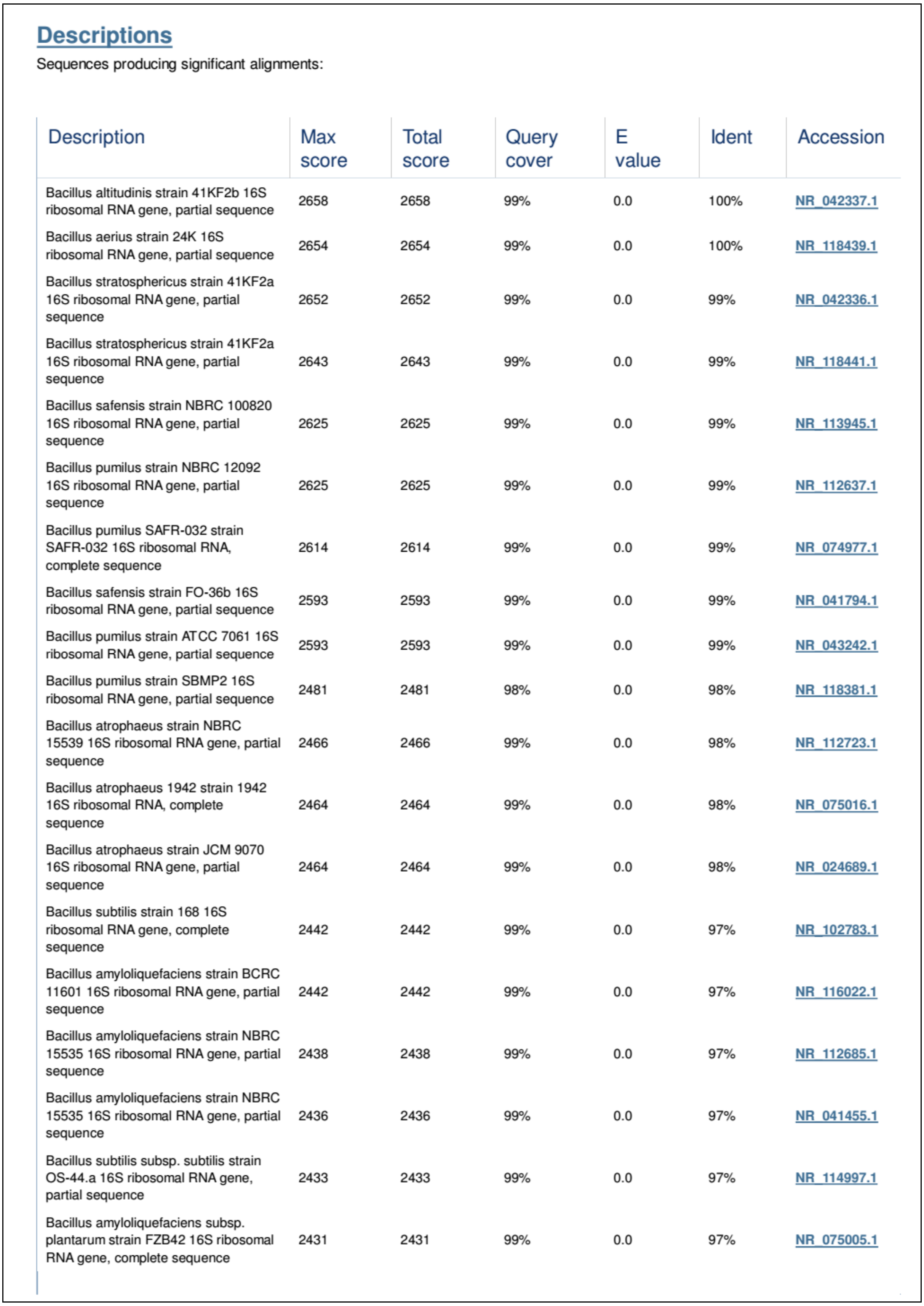
GACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCT
TATGACCTGGGCTACACACGTGCTACAATGGACAGAACAAAGGGCTGCGAGACCGC
AAGGTTTAGCCAATCCCACAAATCTGTTCTCAGTTCGGATCGCAGTCTGCAACTCG
ACTGCGTGAAGCTGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACG
TTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGCAACACCCGAAG
TCGGTGAGGTAACCTTTATGGAGCCAGCCGCCGAAGGTGG

Table. 26: Sequences Producing Significant Alignment for LLS.IE(B)-1.



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Bacillus altitudinis strain 41KF2b 16S ribosomal RNA gene, partial sequence	2658	2658	99%	0.0	100%	NR_042337.1
Bacillus aerius strain 24K 16S ribosomal RNA gene, partial sequence	2654	2654	99%	0.0	100%	NR_118439.1
Bacillus stratosphericus strain 41KF2a 16S ribosomal RNA gene, partial sequence	2652	2652	99%	0.0	99%	NR_042336.1
Bacillus stratosphericus strain 41KF2a 16S ribosomal RNA gene, partial sequence	2643	2643	99%	0.0	99%	NR_118441.1
Bacillus safensis strain NBRC 100820 16S ribosomal RNA gene, partial sequence	2625	2625	99%	0.0	99%	NR_113945.1
Bacillus pumilus strain NBRC 12092 16S ribosomal RNA gene, partial sequence	2625	2625	99%	0.0	99%	NR_112637.1
Bacillus pumilus SAFR-032 strain SAFR-032 16S ribosomal RNA, complete sequence	2614	2614	99%	0.0	99%	NR_074977.1
Bacillus safensis strain FO-36b 16S ribosomal RNA gene, partial sequence	2593	2593	99%	0.0	99%	NR_041794.1
Bacillus pumilus strain ATCC 7061 16S ribosomal RNA gene, partial sequence	2593	2593	99%	0.0	99%	NR_043242.1
Bacillus pumilus strain SBMP2 16S ribosomal RNA gene, partial sequence	2481	2481	98%	0.0	98%	NR_118381.1
Bacillus atrophaeus strain NBRC 15539 16S ribosomal RNA gene, partial sequence	2466	2466	99%	0.0	98%	NR_112723.1
Bacillus atrophaeus 1942 strain 1942 16S ribosomal RNA, complete sequence	2464	2464	99%	0.0	98%	NR_075016.1
Bacillus atrophaeus strain JCM 9070 16S ribosomal RNA gene, partial sequence	2464	2464	99%	0.0	98%	NR_024689.1
Bacillus subtilis strain 168 16S ribosomal RNA gene, complete sequence	2442	2442	99%	0.0	97%	NR_102783.1
Bacillus amyloliquefaciens strain BCRC 11601 16S ribosomal RNA gene, partial sequence	2442	2442	99%	0.0	97%	NR_116022.1
Bacillus amyloliquefaciens strain NBRC 15535 16S ribosomal RNA gene, partial sequence	2438	2438	99%	0.0	97%	NR_112685.1
Bacillus amyloliquefaciens strain NBRC 15535 16S ribosomal RNA gene, partial sequence	2436	2436	99%	0.0	97%	NR_041455.1
Bacillus subtilis subsp. subtilis strain OS-44.a 16S ribosomal RNA gene, partial sequence	2433	2433	99%	0.0	97%	NR_114997.1
Bacillus amyloliquefaciens subsp. plantarum strain FZB42 16S ribosomal RNA gene, complete sequence	2431	2431	99%	0.0	97%	NR_075005.1

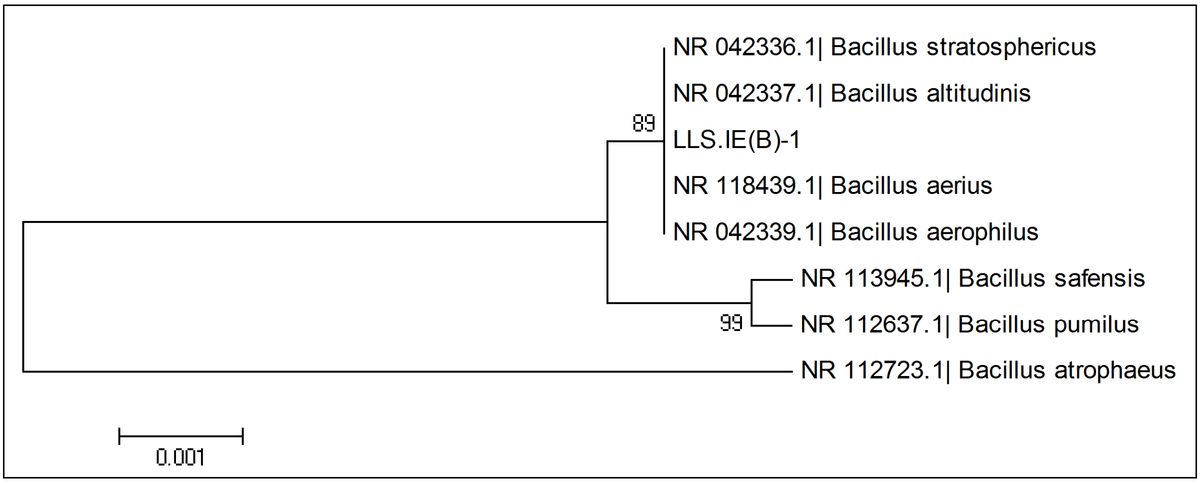


Fig.37: Phylogenetic tree of LLS.IE(B)-1 constructed by NJ method

4.8.10. 16S rDNA Analysis of PS.1E-2

The bacterial culture designated as *PS.1E-2* was established as *Klebsiella oxytoca* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1446bp at GenBank NCBI through sequin submission format. KM396263 has been designated as its accsssion number.

Consensus Sequence of PS.1E-2

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AACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGAC
CTTCGGGCCTCTTGCCATCAGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTA
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TGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGT
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AGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTG
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GAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGA
AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGT
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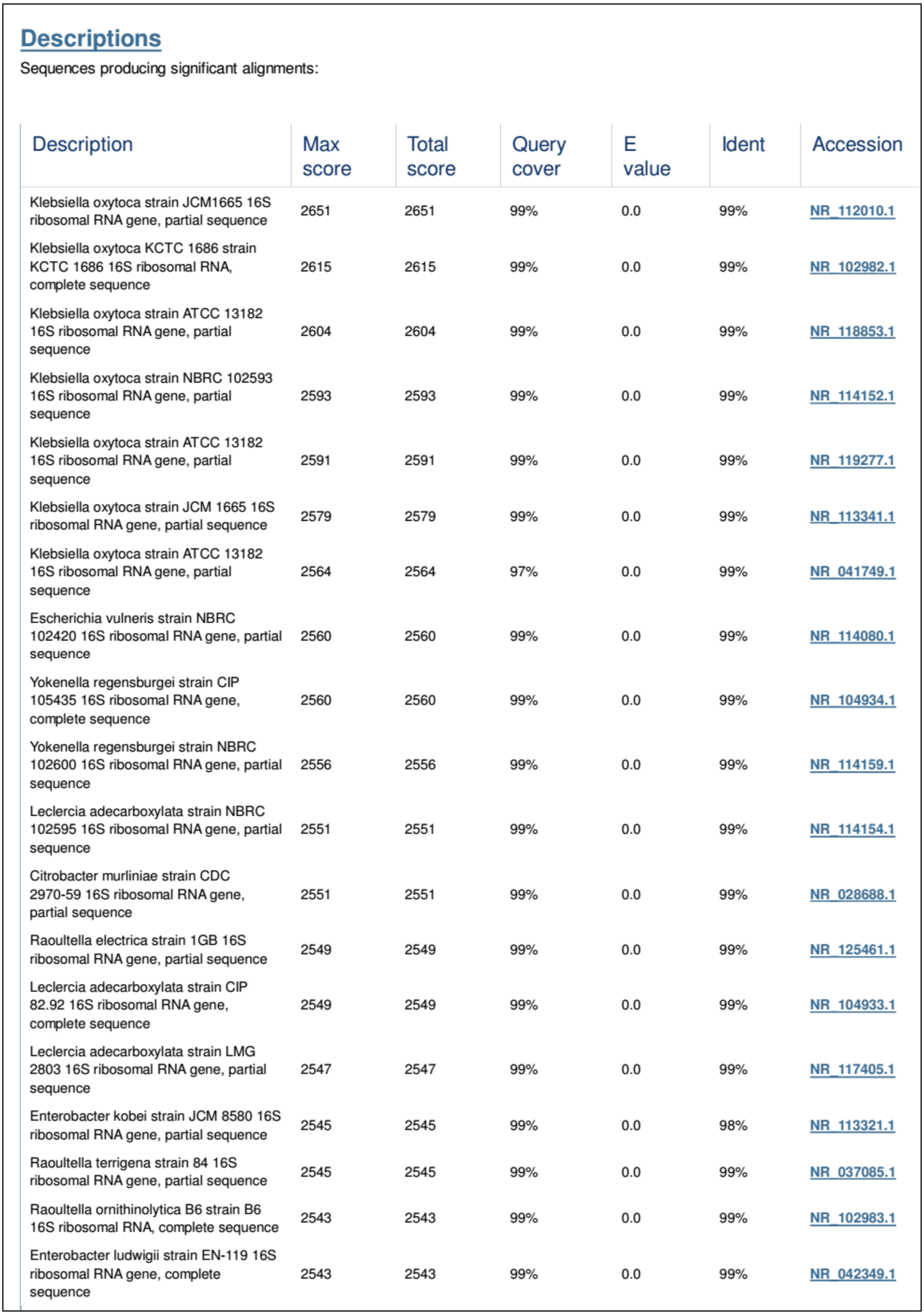
CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTACTC
TTGACATCCAGAGAACTTAGCAGAGATGCTTTGGTGCCTTCGGGAACTCTGAGACA
GGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAA
CGAGCGCAACCCTTATCCTTTGTTGCCAGCGATTCGGTCGGGAACTCAAAGGAGAC
TGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTAC
GAGTAGGGCTACACACGTGCTACAATGGCATATACAAAGAGAAGCGACCTCGCGAG
AGCAAGCGGACCTCATAAAGTATGTCGTAGTCCGGATTGGAGTCTGCAACTCGACT
CCATGAAGTCGGAATCGCTAGTAATCGTGGATCAGAATGCCACGGTGAATACGTTC
CCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAG
GTAGCTTAACCTTCGGGAGGGCGCTTACCACTTTGTGTATTTCCAG

Table.27: Sequences Producing Significant Alignment for PS.1E-2



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Klebsiella oxytoca strain JCM1665 16S ribosomal RNA gene, partial sequence	2651	2651	99%	0.0	99%	NR_112010.1
Klebsiella oxytoca KCTC 1686 strain KCTC 1686 16S ribosomal RNA, complete sequence	2615	2615	99%	0.0	99%	NR_102982.1
Klebsiella oxytoca strain ATCC 13182 16S ribosomal RNA gene, partial sequence	2604	2604	99%	0.0	99%	NR_118853.1
Klebsiella oxytoca strain NBRC 102593 16S ribosomal RNA gene, partial sequence	2593	2593	99%	0.0	99%	NR_114152.1
Klebsiella oxytoca strain ATCC 13182 16S ribosomal RNA gene, partial sequence	2591	2591	99%	0.0	99%	NR_119277.1
Klebsiella oxytoca strain JCM 1665 16S ribosomal RNA gene, partial sequence	2579	2579	99%	0.0	99%	NR_113341.1
Klebsiella oxytoca strain ATCC 13182 16S ribosomal RNA gene, partial sequence	2564	2564	97%	0.0	99%	NR_041749.1
Escherichia vulneris strain NBRC 102420 16S ribosomal RNA gene, partial sequence	2560	2560	99%	0.0	99%	NR_114080.1
Yokenella regensburgei strain CIP 105435 16S ribosomal RNA gene, complete sequence	2560	2560	99%	0.0	99%	NR_104934.1
Yokenella regensburgei strain NBRC 102600 16S ribosomal RNA gene, partial sequence	2556	2556	99%	0.0	99%	NR_114159.1
Leclercia adecarboxylata strain NBRC 102595 16S ribosomal RNA gene, partial sequence	2551	2551	99%	0.0	99%	NR_114154.1
Citrobacter murliniae strain CDC 2970-59 16S ribosomal RNA gene, partial sequence	2551	2551	99%	0.0	99%	NR_028688.1
Raoultella electrica strain 1GB 16S ribosomal RNA gene, partial sequence	2549	2549	99%	0.0	99%	NR_125461.1
Leclercia adecarboxylata strain CIP 82.92 16S ribosomal RNA gene, complete sequence	2549	2549	99%	0.0	99%	NR_104933.1
Leclercia adecarboxylata strain LMG 2803 16S ribosomal RNA gene, partial sequence	2547	2547	99%	0.0	99%	NR_117405.1
Enterobacter kobei strain JCM 8580 16S ribosomal RNA gene, partial sequence	2545	2545	99%	0.0	98%	NR_113321.1
Raoultella terrigena strain 84 16S ribosomal RNA gene, partial sequence	2545	2545	99%	0.0	99%	NR_037085.1
Raoultella ornithinolytica B6 strain B6 16S ribosomal RNA, complete sequence	2543	2543	99%	0.0	99%	NR_102983.1
Enterobacter ludwigii strain EN-119 16S ribosomal RNA gene, complete sequence	2543	2543	99%	0.0	99%	NR_042349.1

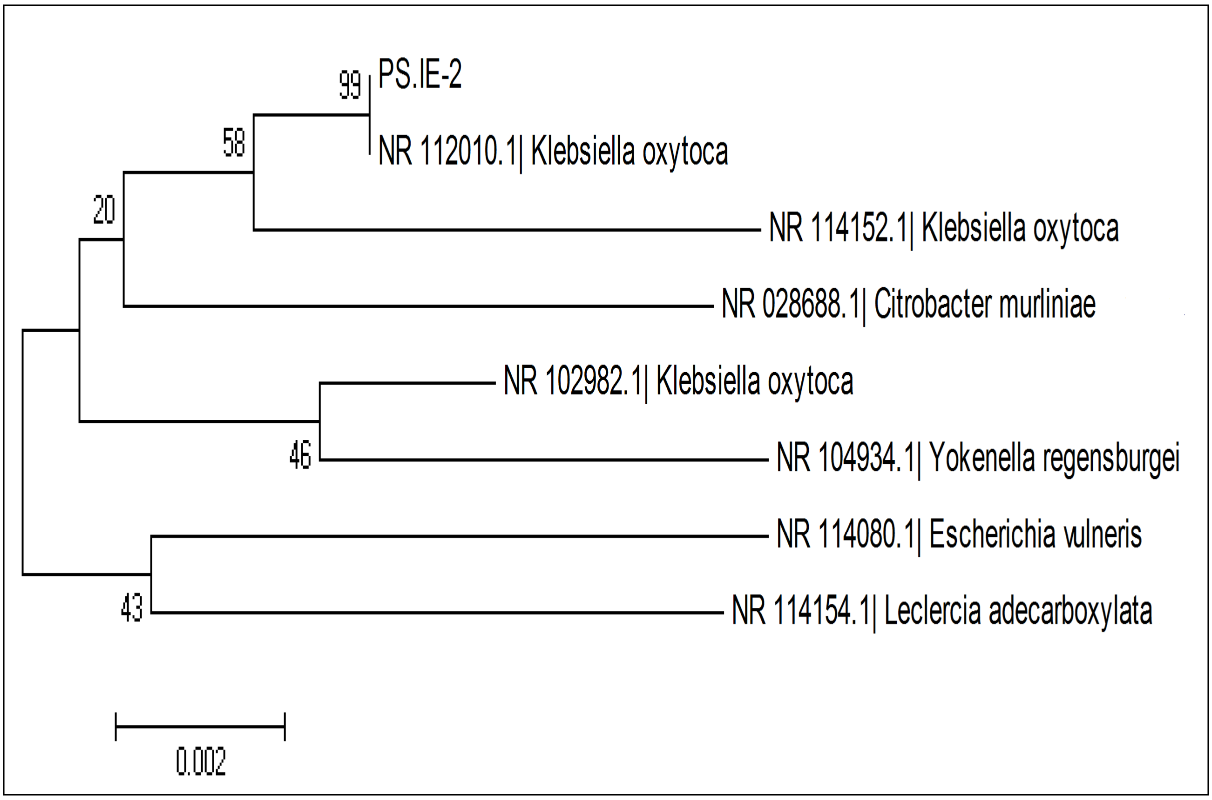


Fig.38: Phylogenetic tree of PS.IE-2 constructed by NJ method

4.8.11. 16S rDNA Analysis of PS.1W-1

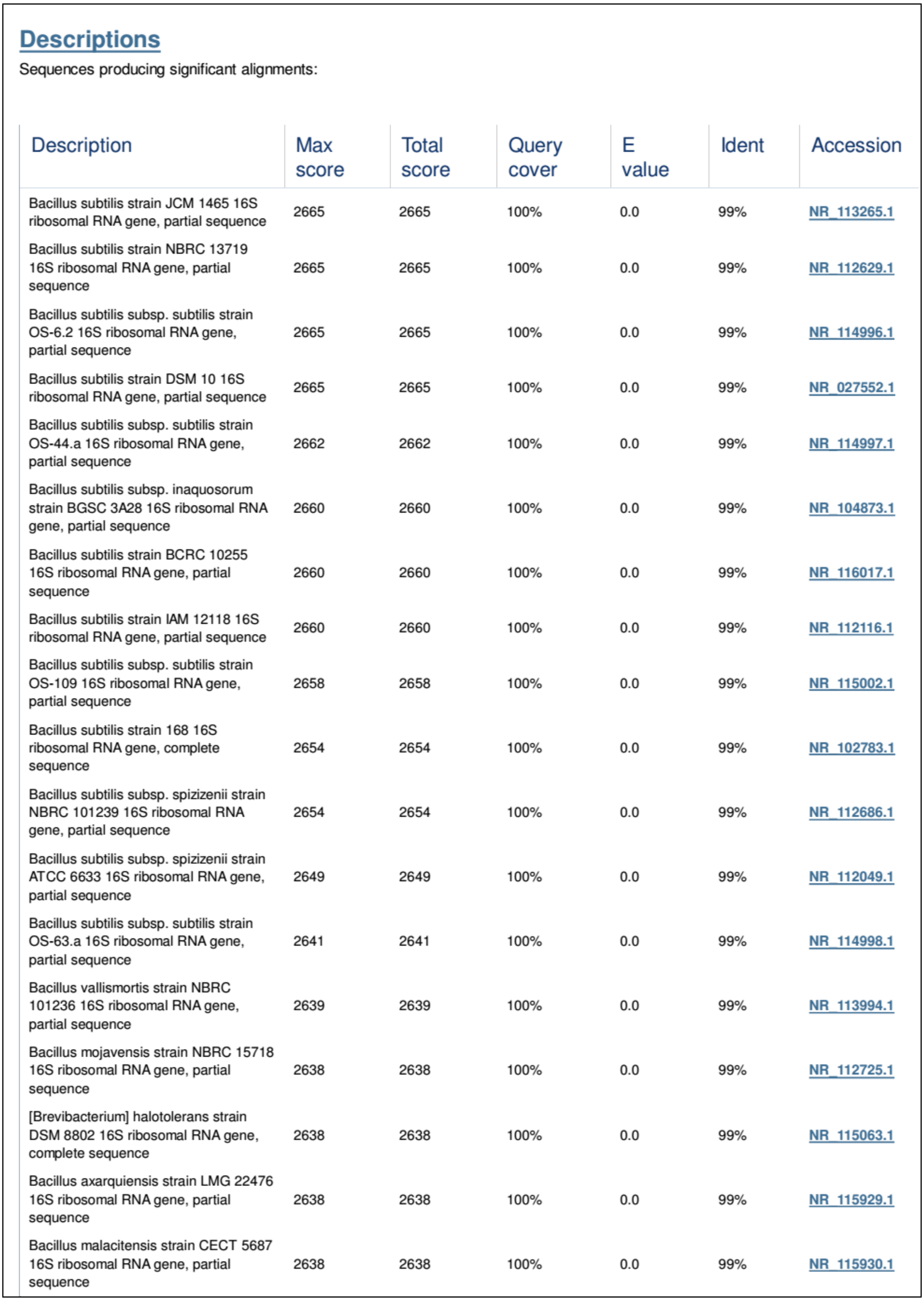
The bacterial culture designated as *PS.1W-1* was established as *Bacillus subtilis* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1449bp at GenBank NCBI through sequin submission format. KM269071 has been designated as its accsssion number.

Consensus Sequence of PS.1W-1

GGCGGCGTGTCTTATACATGCAAGTCGAGCGGACAGATGGGAGCTTGCTCCCTGAT
GTTAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGATAA
CTCCGGGAAACCGGGGCTAATACCGGATGGTTGTTTGAACCGCATGGTTCAAACAT
AAAAGGTGGCTTCGGCTACCACTTACAGATGGACCCGCGGCGCATTAGCTAGTTGG
TGAGGTAACGGCTCACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGC

CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCT
TCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCG
GATCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTACCGTTCGAATAGGGCGGTACC
TTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAAT
ACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGGGCTCGCAGGCGGTT
TCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTGG
GGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTA
GAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGTCTGTAACTGACGCTG
AGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTA
AACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCA
TTAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACG
GGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCT
TACCAGGTCTTGACATCCTCTGACAATCCTAGAGATAGGACGTCCCCTTCGGGGGC
AGAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA
GTCCCGCAACGAGCGCAACCCTTGATCTTAGTTGCCAGCATTCAGTTGGGCACTCT
AAGGTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATG
CCCCTTATGACCTGGGCTACACACGTGCTACAATGGACAGAACAAAGGGCAGCGAA
ACCGCGAGGTTAAGCCAATCCCACAAATCTGTTCTCAGTTCGGATCGCAGTCTGCA
ACTCGACTGCGTGAAGCTGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGA
ATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACC
CGAAGTCGGTGAGGTAACCTTTTAGGAGCCAGCCGCCGAAGGTGGGACA

Table.28: Sequences Producing Significant Alignment for PS.1W-1



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Bacillus subtilis strain JCM 1465 16S ribosomal RNA gene, partial sequence	2665	2665	100%	0.0	99%	NR_113265.1
Bacillus subtilis strain NBRC 13719 16S ribosomal RNA gene, partial sequence	2665	2665	100%	0.0	99%	NR_112629.1
Bacillus subtilis subsp. subtilis strain OS-6.2 16S ribosomal RNA gene, partial sequence	2665	2665	100%	0.0	99%	NR_114996.1
Bacillus subtilis strain DSM 10 16S ribosomal RNA gene, partial sequence	2665	2665	100%	0.0	99%	NR_027552.1
Bacillus subtilis subsp. subtilis strain OS-44.a 16S ribosomal RNA gene, partial sequence	2662	2662	100%	0.0	99%	NR_114997.1
Bacillus subtilis subsp. inaquosorum strain BGSC 3A28 16S ribosomal RNA gene, partial sequence	2660	2660	100%	0.0	99%	NR_104873.1
Bacillus subtilis strain BCRC 10255 16S ribosomal RNA gene, partial sequence	2660	2660	100%	0.0	99%	NR_116017.1
Bacillus subtilis strain IAM 12118 16S ribosomal RNA gene, partial sequence	2660	2660	100%	0.0	99%	NR_112116.1
Bacillus subtilis subsp. subtilis strain OS-109 16S ribosomal RNA gene, partial sequence	2658	2658	100%	0.0	99%	NR_115002.1
Bacillus subtilis strain 168 16S ribosomal RNA gene, complete sequence	2654	2654	100%	0.0	99%	NR_102783.1
Bacillus subtilis subsp. spizizenii strain NBRC 101239 16S ribosomal RNA gene, partial sequence	2654	2654	100%	0.0	99%	NR_112686.1
Bacillus subtilis subsp. spizizenii strain ATCC 6633 16S ribosomal RNA gene, partial sequence	2649	2649	100%	0.0	99%	NR_112049.1
Bacillus subtilis subsp. subtilis strain OS-63.a 16S ribosomal RNA gene, partial sequence	2641	2641	100%	0.0	99%	NR_114998.1
Bacillus vallismortis strain NBRC 101236 16S ribosomal RNA gene, partial sequence	2639	2639	100%	0.0	99%	NR_113994.1
Bacillus mojavensis strain NBRC 15718 16S ribosomal RNA gene, partial sequence	2638	2638	100%	0.0	99%	NR_112725.1
[Brevibacterium] halotolerans strain DSM 8802 16S ribosomal RNA gene, complete sequence	2638	2638	100%	0.0	99%	NR_115063.1
Bacillus axarquiensis strain LMG 22476 16S ribosomal RNA gene, partial sequence	2638	2638	100%	0.0	99%	NR_115929.1
Bacillus malacitensis strain CECT 5687 16S ribosomal RNA gene, partial sequence	2638	2638	100%	0.0	99%	NR_115930.1

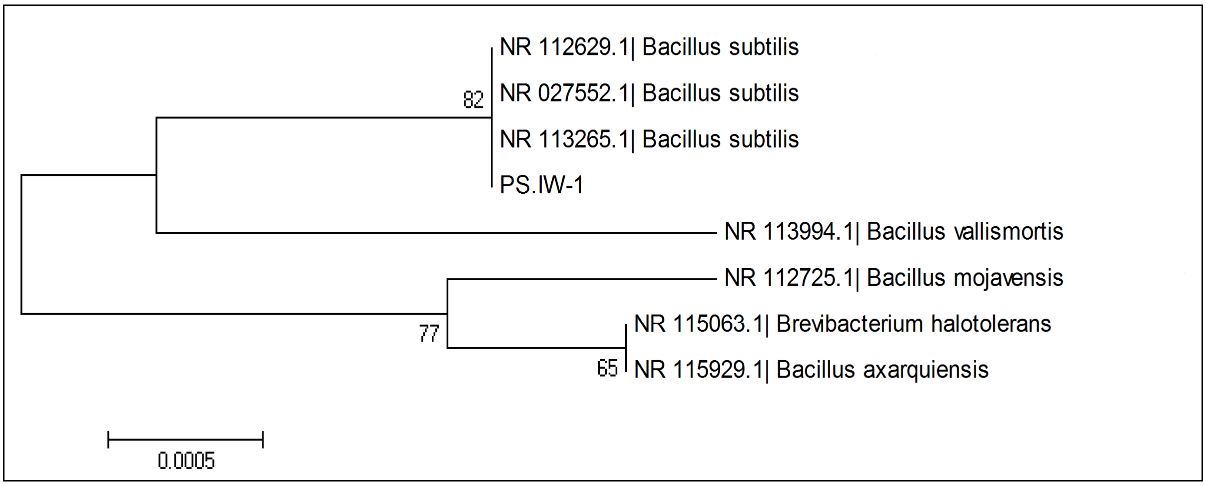


Fig.39: Phylogenetic tree of PS.IW-1 constructed by NJ method

4.8.12. 16S rDNA Analysis of PS.T(B)-2

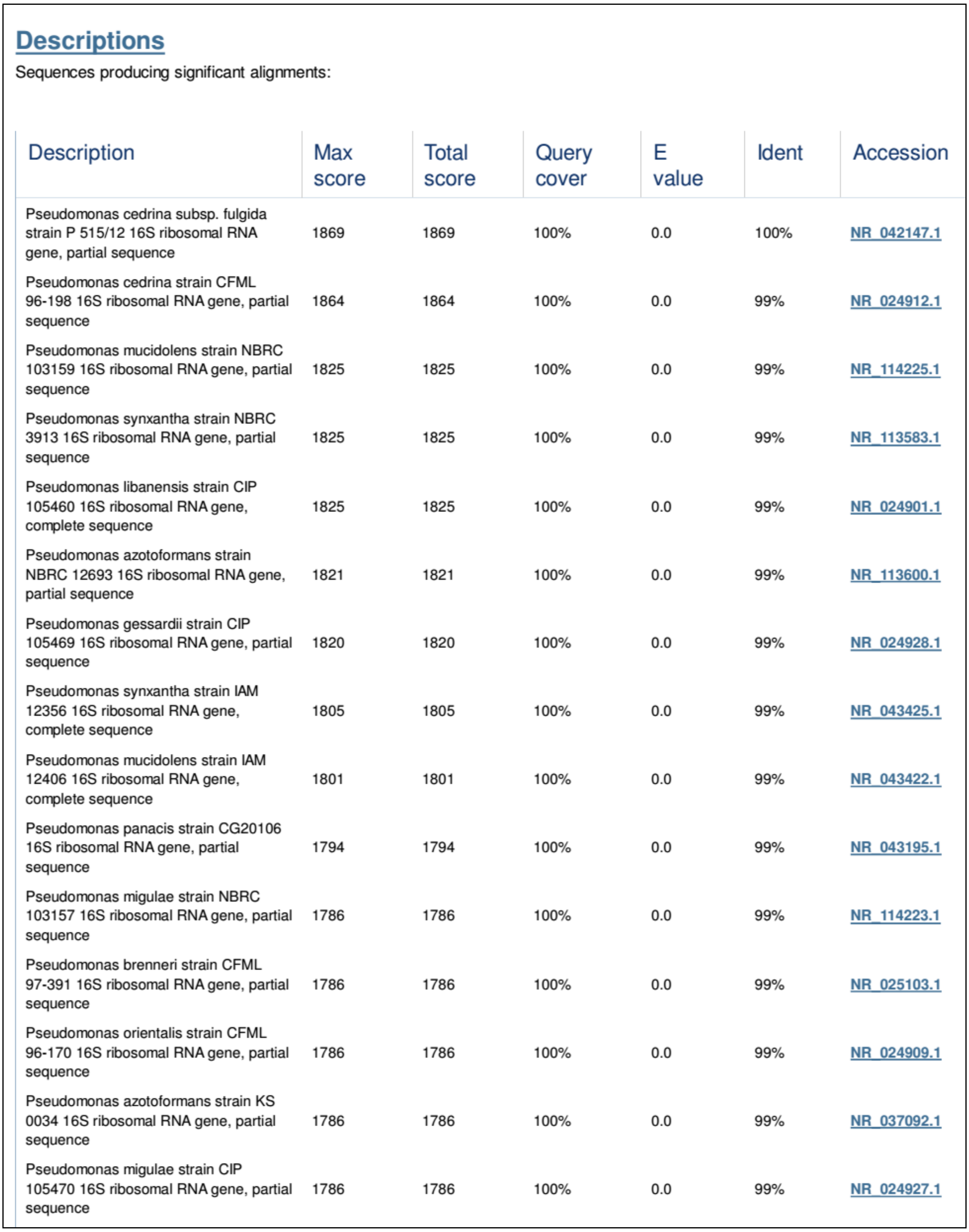
The bacterial culture designated as *PS.T(B)-2* was established as *Pseudomonas cedrina* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1012bp at GenBank NCBI through sequin submission format. KM598639 has been designated as its accssion number.

Consensus Sequence of PS.T(B)-2

GGCGGCAGGCCTAACACATGCAAGTCGAGCGGTAGAGAGAAGCTTGCTTCTCTTGAGAGCG
GCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGATAACGTTCGGAAACGG
ACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTGCGCTATCA
GATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGACGATCCGT
AACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGG
AGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGTGT
GAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGTTGTAGATTAATACT
CTGCAATTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGT
AATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTG
TTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTCAAAACTGACTGACTA
GAGTGTGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGG
AACACCAGTGGCGAAGGCGACCACCTGGACCAACACTGACACTGAGGTGCGAAAGCGTGGG
GAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCAACTAGCCGTTGG
GAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCC
GCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTA

ATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCCAATGAACTTTCCAGAGATGG ATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCA

Table.29: Sequences Producing Significant Alignment for PS.T(B)-2



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pseudomonas cedrina subsp. fulgida strain P 515/12 16S ribosomal RNA gene, partial sequence	1869	1869	100%	0.0	100%	NR_042147.1
Pseudomonas cedrina strain CFML 96-198 16S ribosomal RNA gene, partial sequence	1864	1864	100%	0.0	99%	NR_024912.1
Pseudomonas mucidolens strain NBRC 103159 16S ribosomal RNA gene, partial sequence	1825	1825	100%	0.0	99%	NR_114225.1
Pseudomonas synxantha strain NBRC 3913 16S ribosomal RNA gene, partial sequence	1825	1825	100%	0.0	99%	NR_113583.1
Pseudomonas libanensis strain CIP 105460 16S ribosomal RNA gene, complete sequence	1825	1825	100%	0.0	99%	NR_024901.1
Pseudomonas azotoformans strain NBRC 12693 16S ribosomal RNA gene, partial sequence	1821	1821	100%	0.0	99%	NR_113600.1
Pseudomonas gessardii strain CIP 105469 16S ribosomal RNA gene, partial sequence	1820	1820	100%	0.0	99%	NR_024928.1
Pseudomonas synxantha strain IAM 12356 16S ribosomal RNA gene, complete sequence	1805	1805	100%	0.0	99%	NR_043425.1
Pseudomonas mucidolens strain IAM 12406 16S ribosomal RNA gene, complete sequence	1801	1801	100%	0.0	99%	NR_043422.1
Pseudomonas panacis strain CG20106 16S ribosomal RNA gene, partial sequence	1794	1794	100%	0.0	99%	NR_043195.1
Pseudomonas migulae strain NBRC 103157 16S ribosomal RNA gene, partial sequence	1786	1786	100%	0.0	99%	NR_114223.1
Pseudomonas brenneri strain CFML 97-391 16S ribosomal RNA gene, partial sequence	1786	1786	100%	0.0	99%	NR_025103.1
Pseudomonas orientalis strain CFML 96-170 16S ribosomal RNA gene, partial sequence	1786	1786	100%	0.0	99%	NR_024909.1
Pseudomonas azotoformans strain KS 0034 16S ribosomal RNA gene, partial sequence	1786	1786	100%	0.0	99%	NR_037092.1
Pseudomonas migulae strain CIP 105470 16S ribosomal RNA gene, partial sequence	1786	1786	100%	0.0	99%	NR_024927.1

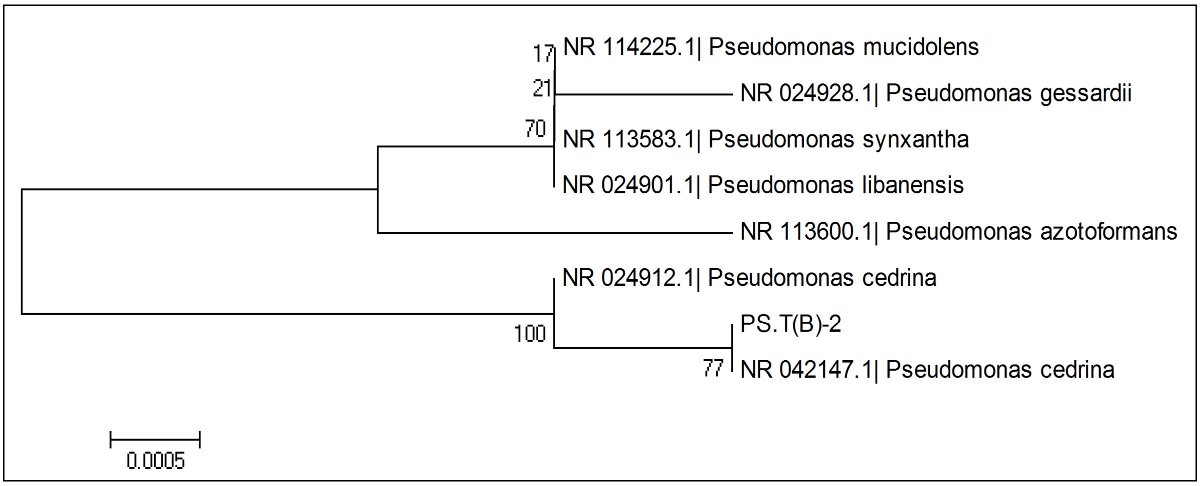


Fig.40: Phylogenetic tree of PS.T(B)-2 constructed by NJ method

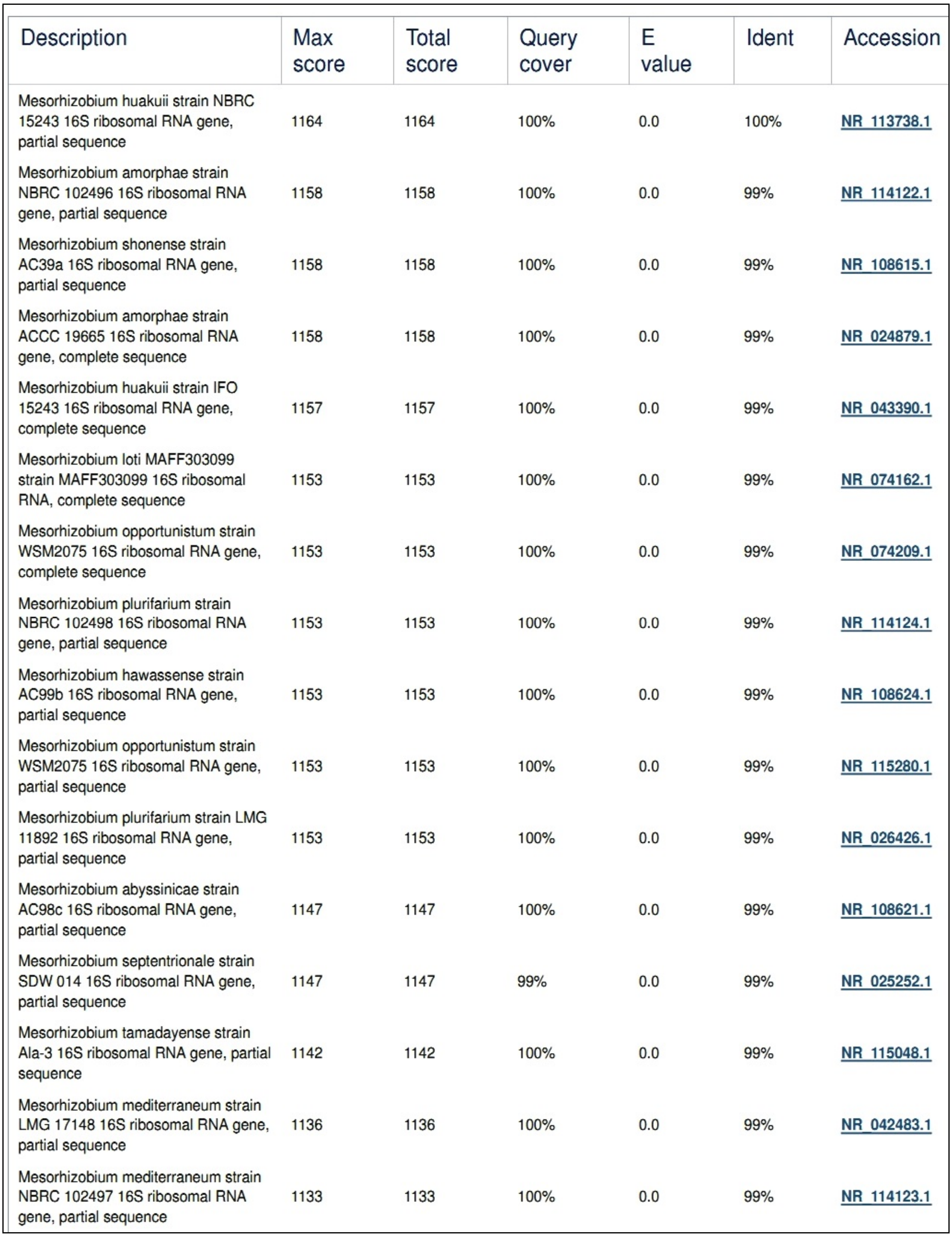
4.8.13. 16S rDNA Analysis of SN.T

The bacterial culture designated as *SN.T* was established as *Mesorhizobium huakuii* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 630bp at GenBank NCBI through sequin submission format. KP331546 has been designated as its accssion number.

Consensus Sequence of SN.T

GCGGCAGGCTTAACACATGCAAGTCGAGCGCCCCGCAAGGGGAGCGGCAGACGGGT
GAGTAACGCGTGGGAATCTACCCATCTCTACGGAACAACTCCGGGAAACTGGAGCT
AATACCGTATACGTCCTTCGGGAGAAAGATTTATCGGAGATGGATGAGCCCGCGTT
GGATTAGCTAGTTGGTGGGGTAATGGCCTACCAAGGCGACGATCCATAGCTGGTCT
GAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGC
AGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTGAG
TGATGAAGGCCCTAGGGTTGTAAAGCTCTTTCAACGGTGAAGATAATGACGGTAAC
CGTAGAAGAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGGGC
TAGCGTTGTTCGGAATTACTGGGCGTAAAGCGCACGTAGGCGGATACTTAAGTCAG
GGGTGAAATCCCGGGGCTCAACCCCGGAACTGCCTTTGATACTGGGTATCTCGAGT
CCGGAAGAGGTGAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAG
GAACACCAGTGGCG

Table.30: Sequences Producing Significant Alignment for SN.T.



Description	Max score	Total score	Query cover	E value	Ident	Accession
Mesorhizobium huakuii strain NBRC 15243 16S ribosomal RNA gene, partial sequence	1164	1164	100%	0.0	100%	NR_113738.1
Mesorhizobium amorphae strain NBRC 102496 16S ribosomal RNA gene, partial sequence	1158	1158	100%	0.0	99%	NR_114122.1
Mesorhizobium shonense strain AC39a 16S ribosomal RNA gene, partial sequence	1158	1158	100%	0.0	99%	NR_108615.1
Mesorhizobium amorphae strain ACCC 19665 16S ribosomal RNA gene, complete sequence	1158	1158	100%	0.0	99%	NR_024879.1
Mesorhizobium huakuii strain IFO 15243 16S ribosomal RNA gene, complete sequence	1157	1157	100%	0.0	99%	NR_043390.1
Mesorhizobium loti MAFF303099 strain MAFF303099 16S ribosomal RNA, complete sequence	1153	1153	100%	0.0	99%	NR_074162.1
Mesorhizobium opportunistum strain WSM2075 16S ribosomal RNA gene, complete sequence	1153	1153	100%	0.0	99%	NR_074209.1
Mesorhizobium plurifarium strain NBRC 102498 16S ribosomal RNA gene, partial sequence	1153	1153	100%	0.0	99%	NR_114124.1
Mesorhizobium hawassense strain AC99b 16S ribosomal RNA gene, partial sequence	1153	1153	100%	0.0	99%	NR_108624.1
Mesorhizobium opportunistum strain WSM2075 16S ribosomal RNA gene, partial sequence	1153	1153	100%	0.0	99%	NR_115280.1
Mesorhizobium plurifarium strain LMG 11892 16S ribosomal RNA gene, partial sequence	1153	1153	100%	0.0	99%	NR_026426.1
Mesorhizobium abyssinicae strain AC98c 16S ribosomal RNA gene, partial sequence	1147	1147	100%	0.0	99%	NR_108621.1
Mesorhizobium septentrionale strain SDW 014 16S ribosomal RNA gene, partial sequence	1147	1147	99%	0.0	99%	NR_025252.1
Mesorhizobium tamadayense strain Ala-3 16S ribosomal RNA gene, partial sequence	1142	1142	100%	0.0	99%	NR_115048.1
Mesorhizobium mediterraneum strain LMG 17148 16S ribosomal RNA gene, partial sequence	1136	1136	100%	0.0	99%	NR_042483.1
Mesorhizobium mediterraneum strain NBRC 102497 16S ribosomal RNA gene, partial sequence	1133	1133	100%	0.0	99%	NR_114123.1

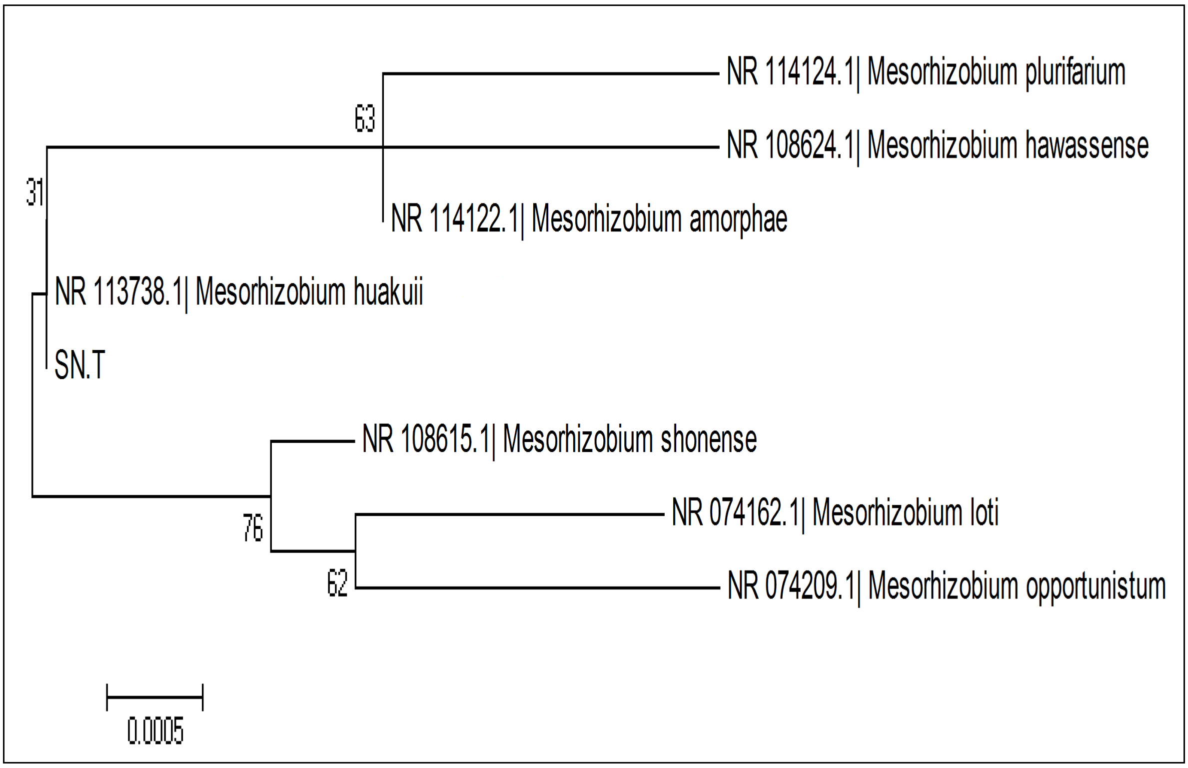


Fig. 41: Phylogenetic tree of SN.T constructed by NJ method

4.8.14 16S rDNA Analysis of SN.B-1

The bacterial culture designated as *SN.B-1* was established as *Neorhizobium huautlense* (*Rhizobium huautlense*) on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1378 bp at GenBank NCBI through Bankit submission format. KX281718 has been designated as its accsssion number.

Consensus Sequence of SN.B-1

GCGGCAGTCTTAACACATGCAAGTCGAGCGCCCCGCAAGGGGAGCGGCAGACGGGT

GAGTAACACGTGGGAATCTACCCATCCCTACGGGACAACTCCGGGAAACTGGAGCT

AATACCGGATACGCCCTTCGGGGGAAAGATTTATCGGGGATGGATGAGCCCGCGTT

GGATTAGCTAGTTGGTGAGGTAAAGGCCTACCAAGGCGACGATCCATAGCTGGTCT

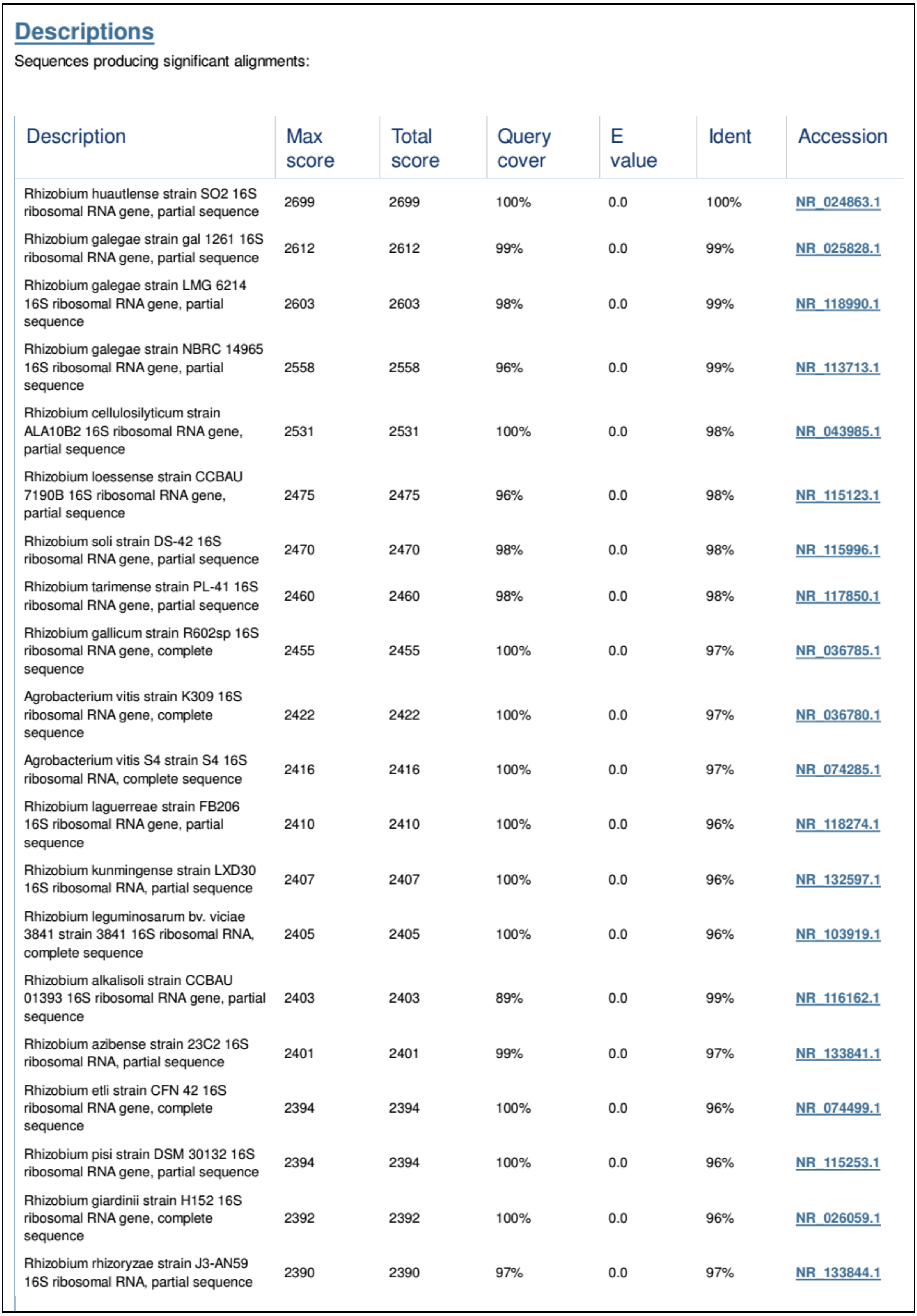
GAGAGGGTGATCAGCCACATTGGGACTGAGACACGGCCCAAACTCCTACGGGAGGC

AGCAGTGGGGAATCTTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTGAG

TGATGAAGGCCTTAGGGTTGTAAAGCTCTTTCACCGGAGAAGATAATGACGGTATC

CGGAGAAGAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTATACGAAGTGGGCT
AGCGTTGTTCGGAATTACTGGGCGTAAAGCGCACGTAGGCGGATATTTAAGTCAGG
GGTGAAATCCCAGAGCTCATCTCTGGAACTGCCTTTGATACTGGGTATCTTGAGTA
TGGAAGAGGTAAGTGGAATTGCGAGTGTAGAGGTGAAATTCGTAGATATTCGCAGG
AACACCAGTGGCGAAGGCGGCTTACTGGTCCATTACTGACGCTGAGGAGCGAAAGC
GTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATGT
TAGCCGTCGGCAAGTTTACTTGTCGGTGGCGCAGCTAACGCATTAAACATTCCGCC
TGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAG
CGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGCAGAACCTTACCAGCCCTTGAC
ATGCCCGGCCAGCCACAGAGATGTGGTGTTCCCTTCGGGGACCGGGACACAGGTGC
TGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC
GCAACCCTCGCCCTTAGTTGCCAGCATTCAGTTGGGCACTCTAAGGGGACTGCCGG
TGATAAGCCGAGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTACGGGCT
GGGCTACACACGTGCTACAATGGTGGTGACAGTGGGCAGCGAAGGAGCGATCCCGA
GCTAATCTCCAAAAGCCATCTCAGTTCGGATTGCACTCTGCAACTCGAGTGCATGA
AGTTGGAATCGCTAGTAATCGCGGATCAGCACGCCGCGGTGAATACGTTCCCGGGC
CTTGTACACACCGCCCGACACACCATGGGAGTTGGTTTTACCCGAAGGTAGTGCGC
TAACCGCAAGGAGGCAGCTAACCACGGTAGGGTC

Table.31: Sequences Producing Significant Alignment for SN.B-1.



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Rhizobium huautlense strain SO2 16S ribosomal RNA gene, partial sequence	2699	2699	100%	0.0	100%	NR_024863.1
Rhizobium galegae strain gal 1261 16S ribosomal RNA gene, partial sequence	2612	2612	99%	0.0	99%	NR_025828.1
Rhizobium galegae strain LMG 6214 16S ribosomal RNA gene, partial sequence	2603	2603	98%	0.0	99%	NR_118990.1
Rhizobium galegae strain NBRC 14965 16S ribosomal RNA gene, partial sequence	2558	2558	96%	0.0	99%	NR_113713.1
Rhizobium cellulosilyticum strain ALA10B2 16S ribosomal RNA gene, partial sequence	2531	2531	100%	0.0	98%	NR_043985.1
Rhizobium loessense strain CCBAU 7190B 16S ribosomal RNA gene, partial sequence	2475	2475	96%	0.0	98%	NR_115123.1
Rhizobium soli strain DS-42 16S ribosomal RNA gene, partial sequence	2470	2470	98%	0.0	98%	NR_115996.1
Rhizobium tarimense strain PL-41 16S ribosomal RNA gene, partial sequence	2460	2460	98%	0.0	98%	NR_117850.1
Rhizobium gallicum strain R602sp 16S ribosomal RNA gene, complete sequence	2455	2455	100%	0.0	97%	NR_036785.1
Agrobacterium vitis strain K309 16S ribosomal RNA gene, complete sequence	2422	2422	100%	0.0	97%	NR_036780.1
Agrobacterium vitis S4 strain S4 16S ribosomal RNA, complete sequence	2416	2416	100%	0.0	97%	NR_074285.1
Rhizobium laguerreae strain FB206 16S ribosomal RNA gene, partial sequence	2410	2410	100%	0.0	96%	NR_118274.1
Rhizobium kunmingense strain LXD30 16S ribosomal RNA, partial sequence	2407	2407	100%	0.0	96%	NR_132597.1
Rhizobium leguminosarum bv. viciae 3841 strain 3841 16S ribosomal RNA, complete sequence	2405	2405	100%	0.0	96%	NR_103919.1
Rhizobium alkalisoli strain CCBAU 01393 16S ribosomal RNA gene, partial sequence	2403	2403	89%	0.0	99%	NR_116162.1
Rhizobium azibense strain 23C2 16S ribosomal RNA, partial sequence	2401	2401	99%	0.0	97%	NR_133841.1
Rhizobium etli strain CFN 42 16S ribosomal RNA gene, complete sequence	2394	2394	100%	0.0	96%	NR_074499.1
Rhizobium pisi strain DSM 30132 16S ribosomal RNA gene, partial sequence	2394	2394	100%	0.0	96%	NR_115253.1
Rhizobium giardinii strain H152 16S ribosomal RNA gene, complete sequence	2392	2392	100%	0.0	96%	NR_026059.1
Rhizobium rhizoryzae strain J3-AN59 16S ribosomal RNA, partial sequence	2390	2390	97%	0.0	97%	NR_133844.1

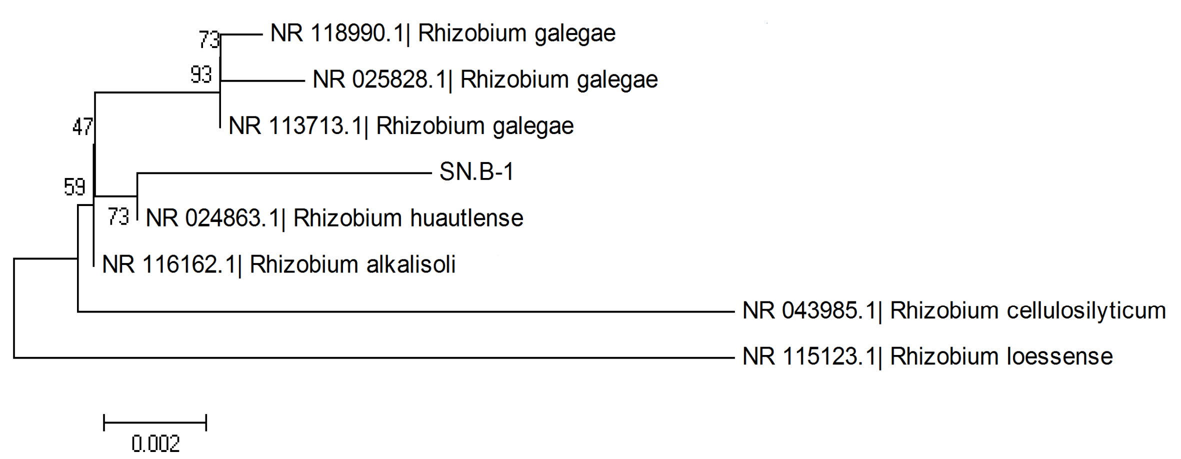


Fig.42: Phylogenetic tree of SN.B-1 constructed by NJ method

4.8.15. 16S rDNA Analysis of SN.IE-1

The bacterial culture designated as *SN.IE-1* was established as *Pseudomonas azotoformans* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 504bp at GenBank NCBI through sequin submission format. KU355544 has been designated as its accsssion number.

Consensus Sequence of SN.IE-1

AAGAACCTTACCAGGCCTTGACATCCAATGAACTTTCTAGAGATAGATTGGTGCCT
TCGGGAACATTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGT
TGGGTTAAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTAATGG
TGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCA
AGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTACAATGGTCGGTACAGA
GGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCATAAAACCGATCGTAGTCCGGATC
GCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAATCAGAAT
GTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCTCACACCATGGGAGTG
GGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT

Table.32: Sequences Producing Significant Alignment for SN.IE-1.

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pseudomonas azotoformans strain NBRC 12693 16S ribosomal RNA gene, partial sequence	584	584	80%	1e-166	92%	NR_113600.1
Pseudomonas lurida strain P 513/18 16S ribosomal RNA gene, partial sequence	584	584	80%	1e-166	92%	NR_042199.1
Pseudomonas marginalis strain ICMP 3553 16S ribosomal RNA gene, partial sequence	584	584	80%	1e-166	92%	NR_117821.1
Pseudomonas poae strain P 527/13 16S ribosomal RNA gene, partial sequence	584	584	80%	1e-166	92%	NR_028986.1
Pseudomonas simiae strain OLi 16S ribosomal RNA gene, partial sequence	584	584	80%	1e-166	92%	NR_042392.1
Pseudomonas rhodesiae strain CIP 104664 16S ribosomal RNA gene, complete sequence	584	584	80%	1e-166	92%	NR_112074.1
Pseudomonas rhodesiae strain CIP 104664 16S ribosomal RNA gene, complete sequence	584	584	80%	1e-166	92%	NR_024911.1
Pseudomonas brenneri strain CFML 97-391 16S ribosomal RNA gene, partial sequence	580	580	80%	2e-165	92%	NR_025103.1
Pseudomonas poae RE*1-1-14 strain RE*1-1-14 16S ribosomal RNA, complete sequence	579	579	80%	6e-165	92%	NR_102514.1
Pseudomonas fluorescens strain NBRC 14160 16S ribosomal RNA gene, partial sequence	579	579	80%	6e-165	92%	NR_113647.1
Pseudomonas synxantha strain NBRC 3913 16S ribosomal RNA gene, partial sequence	579	579	80%	6e-165	92%	NR_113583.1
Pseudomonas trivialis strain P 513/19 16S ribosomal RNA gene, partial sequence	579	579	80%	6e-165	92%	NR_028987.1
Pseudomonas extremaustralis strain 14-3 16S ribosomal RNA, complete sequence	579	579	80%	6e-165	92%	NR_114911.1
Pseudomonas fluorescens strain CCM 2115 16S ribosomal RNA gene, complete sequence	579	579	80%	6e-165	92%	NR_115715.1
Pseudomonas grimontii strain CFML 97-514 16S ribosomal RNA gene, partial sequence	579	579	80%	6e-165	92%	NR_025102.1
Pseudomonas antarctica strain CMS 35 16S ribosomal RNA gene, partial sequence	579	579	80%	6e-165	92%	NR_025586.1
Pseudomonas fluorescens strain ATCC 13525 16S ribosomal RNA gene, partial sequence	579	579	80%	6e-165	92%	NR_114476.1
Pseudomonas orientalis strain CFML 96-170 16S ribosomal RNA gene, partial sequence	579	579	80%	6e-165	92%	NR_024909.1

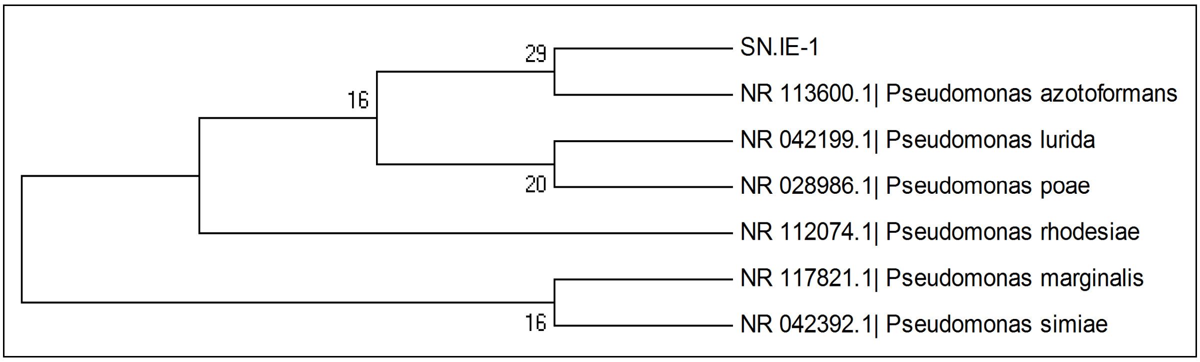


Fig.43: Phylogenetic tree of SN.IE-1 constructed by NJ method

4.8.16. 16S rDNA Analysis of CJN.T-1

The bacterial culture designated as *CJN.T-1* was established as *Pantoea agglomerans* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1214bp at GenBank NCBI through sequin submission format. KP331547 has been designated as its accssion number.

Consensus Sequence of CJN.T-1

```
ACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGA
GACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGC
AAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACT
TTCAGCGGGGAGGAAGGTGTTGTGGTTAATAACCGCAGCAATTGACGTTACCCGCA
GAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGC
GTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGT
GAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAGGCTAGAGTCTTG
TAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAAT
ACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTG
GGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTG
GAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTG
GGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCG
GTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTACTCTTGACAT
CCAGAGAACTTACCAGAGATGGTTTGGTGCCTTCGGGAACTCTGAGACAGGTGCTG
CATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGC
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AACCCTTATCCTTTGTTGCCAGCGGTCCGGCCGGGAACTCAAAGGAGACTGCCAGT
GATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGAGTAGG
GCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGAGCAAGC
GGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAA
GTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGAATACGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTT
AACCTTCGGGAGGGCGCTTACCACTTTGTGATTCATGA

Table.33: Sequences Producing Significant Alignment for CJN.T-1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pantoea agglomerans strain JCM1236 16S ribosomal RNA gene, partial sequence	2242	2242	100%	0.0	100%	NR_111998.1
Enterobacter ludwigii strain EN-119 16S ribosomal RNA gene, complete sequence	2226	2226	100%	0.0	99%	NR_042349.1
Leclercia adecarboxylata strain CIP 82.92 16S ribosomal RNA gene, complete sequence	2215	2215	100%	0.0	99%	NR_104933.1
Leclercia adecarboxylata strain NBRC 102595 16S ribosomal RNA gene, partial sequence	2211	2211	100%	0.0	99%	NR_114154.1
Leclercia adecarboxylata strain LMG 2803 16S ribosomal RNA gene, partial sequence	2207	2207	100%	0.0	99%	NR_117405.1
Enterobacter cloacae strain DSM 30054 16S ribosomal RNA gene, partial sequence	2182	2182	100%	0.0	99%	NR_117679.1
Enterobacter cloacae strain NBRC 13535 16S ribosomal RNA gene, partial sequence	2182	2182	100%	0.0	99%	NR_113615.1
Enterobacter cloacae strain 279-56 16S ribosomal RNA gene, partial sequence	2182	2182	100%	0.0	99%	NR_028912.1
Enterobacter cloacae subsp. dissolvens strain ATCC 23373 16S ribosomal RNA gene, partial sequence	2172	2172	100%	0.0	99%	NR_118011.1
Enterobacter mori strain R18-2 16S ribosomal RNA gene, partial sequence	2172	2172	99%	0.0	99%	NR_116430.1
Enterobacter cloacae subsp. dissolvens strain LMG 2683 16S ribosomal RNA gene, partial sequence	2172	2172	100%	0.0	99%	NR_044978.1
Citrobacter murliniae strain CDC 2970-59 16S ribosomal RNA gene, partial sequence	2170	2170	100%	0.0	99%	NR_028688.1
Enterobacter cloacae strain ATCC 13047 16S ribosomal RNA gene, complete sequence	2167	2167	100%	0.0	99%	NR_102794.1
Enterobacter cancerogenus strain LMG 2693 16S ribosomal RNA gene, partial sequence	2167	2167	100%	0.0	99%	NR_116756.1

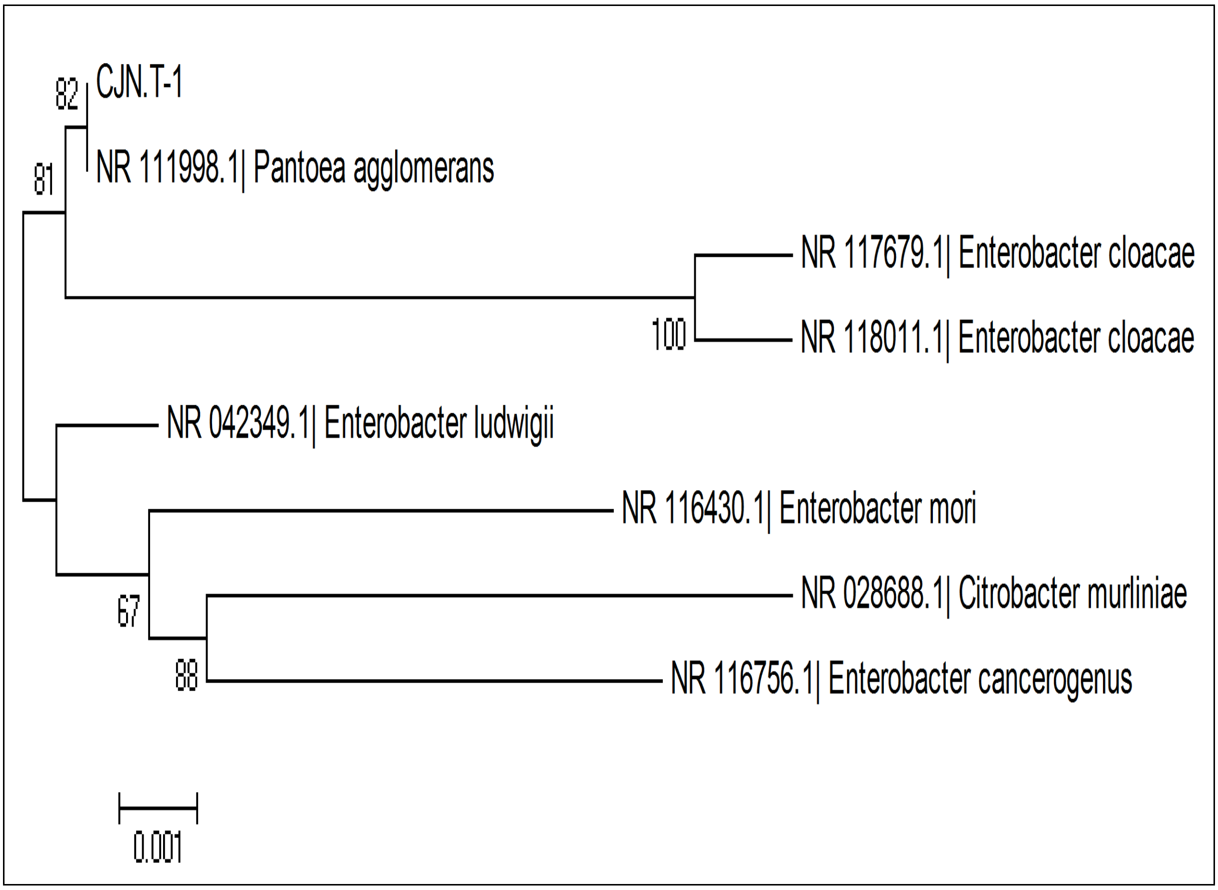

Fig.44: Phylogenetic tree of CJN.T-1 constructed by NJ method

4.8.17. 16S rDNA Analysis of CJN.B-1

The bacterial culture designated as *CJN.B-1* was established as *Pantoea agglomerans* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1445bp at GenBank NCBI through sequin submission format. KU355542 has been designated as its accession number.

Consensus Sequence of CJN.B-1

TGGGCAGCTACACATGCAGTCGAGCGGCAGCGGAAAGTAGCTTGCTACTTTGCCGG
CGAGCGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACT
ACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTC
GGGCCTCTTGCCATCAGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGG
CTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAAC
TGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATACGGCAAACGGCC

CCTTGAATGCCAGGCCCATGACAGGCGTGTAATGAATGATGCGTTCGGGGTTGTTA

AACGTACTTTCAGCGGGGGAGGGAAGGTGCTGAGGTTAATAACCTCAGCAATTGAC

GTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGA

GGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCA

AGTCGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAGGC

TAGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGAT

CTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTG

CGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGA

TGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGT

CGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCC

CGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTA

CTCTTGACATCCAGAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTCTGAG

ACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCG

CAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTTCGGCCGGGAACTCAAAGGA

GACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCT

TACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGC

GAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCG

ACTCCATGAAGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGAATACG

TTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAG

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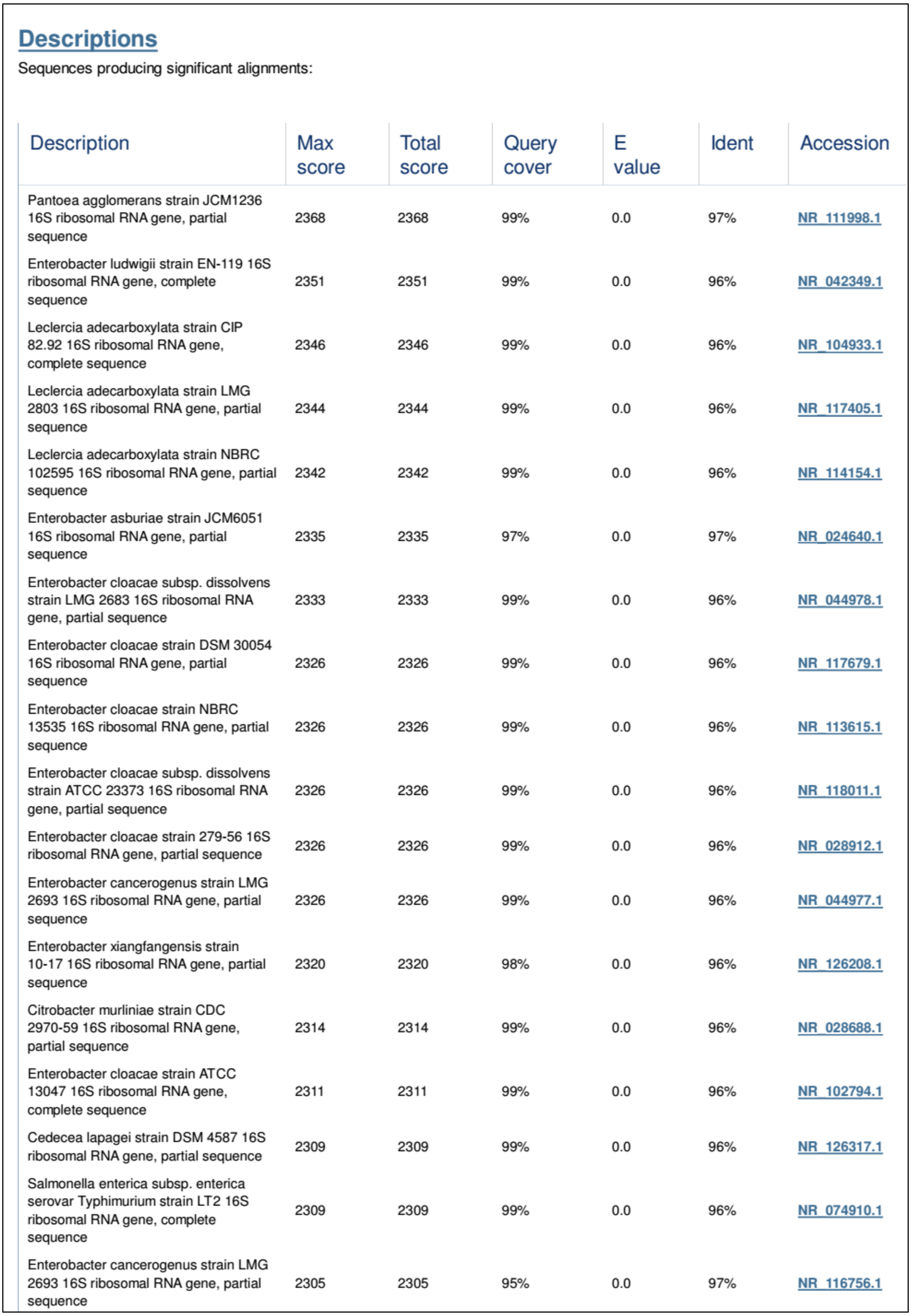
Table.34: Sequences Producing Significant Alignment for CJN.B-1



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pantoea agglomerans strain JCM1236 16S ribosomal RNA gene, partial sequence	2368	2368	99%	0.0	97%	NR_111998.1
Enterobacter ludwigii strain EN-119 16S ribosomal RNA gene, complete sequence	2351	2351	99%	0.0	96%	NR_042349.1
Leclercia adecarboxylata strain CIP 82.92 16S ribosomal RNA gene, complete sequence	2346	2346	99%	0.0	96%	NR_104933.1
Leclercia adecarboxylata strain LMG 2803 16S ribosomal RNA gene, partial sequence	2344	2344	99%	0.0	96%	NR_117405.1
Leclercia adecarboxylata strain NBRC 102595 16S ribosomal RNA gene, partial sequence	2342	2342	99%	0.0	96%	NR_114154.1
Enterobacter asburiae strain JCM6051 16S ribosomal RNA gene, partial sequence	2335	2335	97%	0.0	97%	NR_024640.1
Enterobacter cloacae subsp. dissolvens strain LMG 2683 16S ribosomal RNA gene, partial sequence	2333	2333	99%	0.0	96%	NR_044978.1
Enterobacter cloacae strain DSM 30054 16S ribosomal RNA gene, partial sequence	2326	2326	99%	0.0	96%	NR_117679.1
Enterobacter cloacae strain NBRC 13535 16S ribosomal RNA gene, partial sequence	2326	2326	99%	0.0	96%	NR_113615.1
Enterobacter cloacae subsp. dissolvens strain ATCC 23373 16S ribosomal RNA gene, partial sequence	2326	2326	99%	0.0	96%	NR_118011.1
Enterobacter cloacae strain 279-56 16S ribosomal RNA gene, partial sequence	2326	2326	99%	0.0	96%	NR_028912.1
Enterobacter cancerogenus strain LMG 2693 16S ribosomal RNA gene, partial sequence	2326	2326	99%	0.0	96%	NR_044977.1
Enterobacter xiangfangensis strain 10-17 16S ribosomal RNA gene, partial sequence	2320	2320	98%	0.0	96%	NR_126208.1
Citrobacter murliniae strain CDC 2970-59 16S ribosomal RNA gene, partial sequence	2314	2314	99%	0.0	96%	NR_028688.1
Enterobacter cloacae strain ATCC 13047 16S ribosomal RNA gene, complete sequence	2311	2311	99%	0.0	96%	NR_102794.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	2309	2309	99%	0.0	96%	NR_126317.1
Salmonella enterica subsp. enterica serovar Typhimurium strain LT2 16S ribosomal RNA gene, complete sequence	2309	2309	99%	0.0	96%	NR_074910.1
Enterobacter cancerogenus strain LMG 2693 16S ribosomal RNA gene, partial sequence	2305	2305	95%	0.0	97%	NR_116756.1

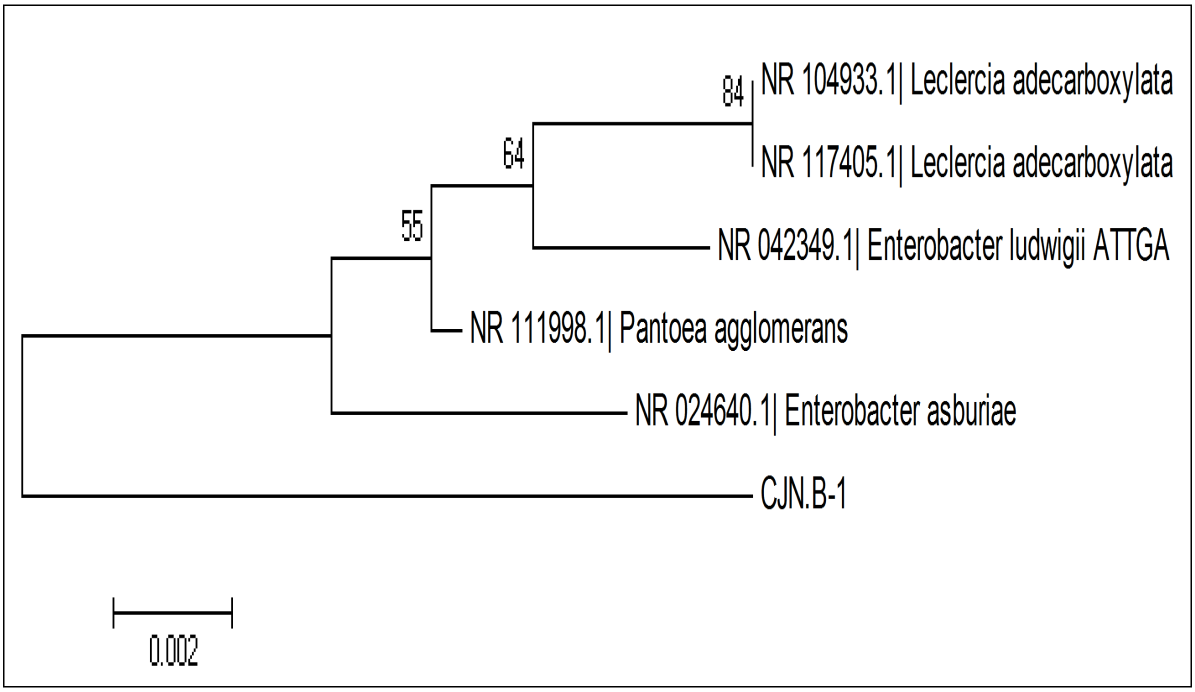


Fig.45: Phylogenetic tree of CJN.B-1 constructed by NJ method

4.8.18. 16S rDNA Analysis of CJN.IW-1

The bacterial culture designated as *CJN.IW-1* was established as *Bacillus subtilis* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1445bp at GenBank NCBI through sequin submission format. KU355543 has been designated as its accession number.

Consensus Sequence of CJN.IW-1

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TCGGGGGTCCTATCATGCAGTCGAGCGGACAGATGGGAGCTTGCTCCCTGATGTTA
GCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCC
GGGAAACCGGGGCTAATACCGGATGGTTGTTTGAACCGCATGGTTCAAACATAAAA
GGTGGCTTCGGCTACCACTTACAGATGGACCCGCGGCGCATTAGCTAGTTGGTGAG
GTAACGGCTCACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTAACCTCGGCGA
CCCTCAGTATTCTTCTGTCCCCTGATTCGCGACCGCGAGTGCAGTCTAGTATGGAC
TCTGCGAAATGTGTCGCAAGTATGATCGAAGCAATCGCCGCGTGTAGTGATGAATT
GTTCTCAGAATCGTTAAATGCTCTGATGTAGGGAAGACAAGTACCGTTCGAATAGG
GCGGTACCTTTGACGGTACCTAACAGAAAGCCACGGCTAACTACGTGCCAGCAGCG
CGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGCGTAAAGGGCTCGCAG
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GCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGCGGAGGGTCATTGGA

AACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAA

TGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGTCTGTAACTG

ACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCAC

GCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCT

AACGCATTAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAA

TTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTTGAAGCAACGCGAA

GAACCTTACCAGGTCTTGACATCCTCTGACAATCCTAGAGATAGGACGTCCCCTTC

GGGGGCAGAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTG

GGTTAAGTCCCGCAACGAGCGCAACCCTTGATCTTAGTTGCCAGCATTCAGTTGGG

CACTCTAAGGTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATC

ATCATGCCCCTTATGACCTGGGCTACACACGTGCTACAATGGACAGAACAAAGGGC

AGCGAAACCGCGAGGTTAAGCCAATCCCACAAATCTGTTCTCAGTTCGGATCGCAG

TCTGCAACTCGACTGCGTGAAGCTGGAATCGCTAGTAATCGCGGATCAGCATGCCG

CGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGT

AACACCCGAAGTCGGTGAGGTAACCTTTTAGGAGCCAGCCGCCGAAGTGGATCAG

Table.35: Sequences Producing Significant Alignment for CJN.IW-1

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Bacillus subtilis strain JCM 1465 16S ribosomal RNA gene, partial sequence	2331	2331	98%	0.0	96%	NR_113265.1
Bacillus subtilis strain NBRC 13719 16S ribosomal RNA gene, partial sequence	2331	2331	98%	0.0	96%	NR_112629.1
Bacillus subtilis subsp. subtilis strain OS-6.2 16S ribosomal RNA gene, partial sequence	2331	2331	98%	0.0	96%	NR_114996.1
Bacillus subtilis strain DSM 10 16S ribosomal RNA gene, partial sequence	2331	2331	98%	0.0	96%	NR_027552.1
Bacillus subtilis subsp. subtilis strain OS-44.a 16S ribosomal RNA gene, partial sequence	2327	2327	98%	0.0	96%	NR_114997.1
Bacillus subtilis subsp. inaquosorum strain BGSC 3A28 16S ribosomal RNA gene, partial sequence	2326	2326	98%	0.0	96%	NR_104873.1
Bacillus subtilis strain BCRC 10255 16S ribosomal RNA gene, partial sequence	2326	2326	98%	0.0	96%	NR_116017.1
Bacillus subtilis strain IAM 12118 16S ribosomal RNA gene, partial sequence	2326	2326	98%	0.0	96%	NR_112116.1
Bacillus subtilis subsp. subtilis strain OS-109 16S ribosomal RNA gene, partial sequence	2324	2324	98%	0.0	96%	NR_115002.1
Bacillus subtilis subsp. spizizenii strain ATCC 6633 16S ribosomal RNA gene, partial sequence	2322	2322	98%	0.0	96%	NR_118486.1
Bacillus tequilensis strain 10b 16S ribosomal RNA gene, partial sequence	2322	2322	98%	0.0	96%	NR_104919.1
Bacillus subtilis strain 168 16S ribosomal RNA gene, complete sequence	2320	2320	98%	0.0	96%	NR_102783.1
Bacillus subtilis subsp. spizizenii strain NBRC 101239 16S ribosomal RNA gene, partial sequence	2320	2320	98%	0.0	96%	NR_112686.1
Bacillus subtilis subsp. spizizenii strain ATCC 6633 16S ribosomal RNA gene, partial sequence	2314	2314	98%	0.0	96%	NR_112049.1
Bacillus subtilis subsp. subtilis strain OS-63.a 16S ribosomal RNA gene, partial sequence	2307	2307	98%	0.0	96%	NR_114998.1
Bacillus vallismortis strain NBRC 101236 16S ribosomal RNA gene, partial sequence	2305	2305	98%	0.0	96%	NR_113994.1
Bacillus mojavensis strain NBRC 15718 16S ribosomal RNA gene, partial sequence	2303	2303	98%	0.0	96%	NR_112725.1
[Brevibacterium] halotolerans strain DSM 8802 16S ribosomal RNA gene, complete sequence	2303	2303	98%	0.0	96%	NR_115063.1
Bacillus axarquiensis strain LMG 22476 16S ribosomal RNA gene, partial sequence	2303	2303	98%	0.0	96%	NR_115929.1

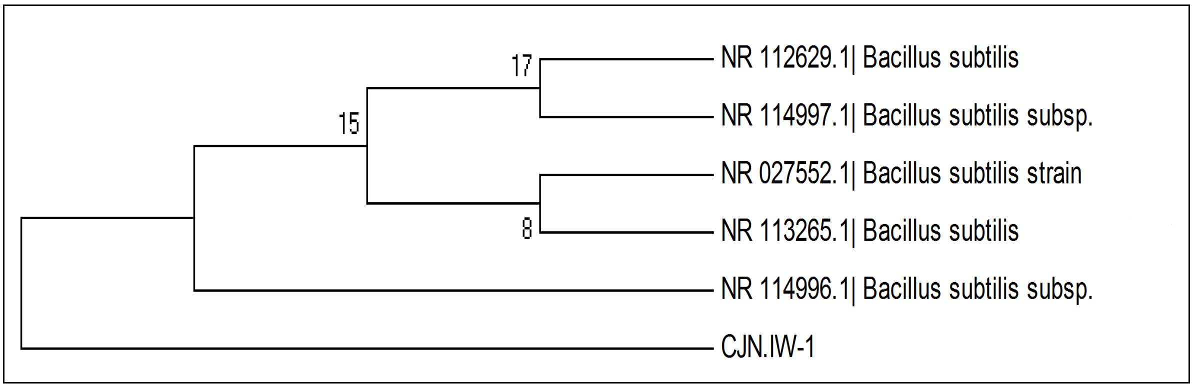

Fig.46: Phylogenetic tree of CJN.IW-1 constructed by NJ method

4.8.19. 16S rDNA Analysis of CJN.IE-2

The bacterial culture designated as *CJN.IE-2* was established as *Bradyrhizobium japonicum* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1369bp at GenBank NCBI through Bankit submission format. KX434625 has been designated as its accession number.

Consensus Sequence of CJN.IE-2

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AAATACGGTCAGCGGCAGACGGGTGAGTAACGCGTGGGCAACCTACCTTTTGGTTCGGAAC
AACACAGCGAAACTTGTGCTAATACCGCATAAGCCCTTACGGGGAAAGATTTATCGCCGAA
AGATCGGCCCGCGTCAGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGACGATCAG
TAGCTGCTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGCCCAAACTCCTACGG
GAGGCAGCAGTGGGGAATATTGGACAATGGGGGCAACCCTGAACCAGCCATGCCGCGTGAG
TGATGAAGGCCCTATGGGTTGTAAAGCTCTTTTGTGCGGGAAGATAACTCTTGACGGTACC
GCAAGAATAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGGGCTAGCG
TTGCTCGGAATCACTGGGCGTAAAGGGTGCGTAGGCGGGCCTTTAAGTCAGGGGTGAAATC
CTGGAGCTCAACTCCAGAACTGCCTTTGATACTGAGGATCTTGAGTTCGGGTGAGGTGAGT
GGAATGCGAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAGTGGCGAAGGCAG
CTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGATAC
CCTGGTAGTCCACGCCGTAAACGATGAATGCCAGCCGTTGGTGGGTTTACACAGCTAGTGG
CGCAGCTAACGCTTTAAGCATTCCACCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGG
AATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGCTTAAATTCGACGCAATCGCGCAG
AACCTTACCAGCCCTTGACATGTCCAGGACCGGTGCAGAGATCGTGACCTTCTCTTCGGAG
CCTGGAGCTCAGGTGCTGACATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGT
CCCGCAACGAGCGCAACCCCCGTCCTTAGTTGCTACCATTTAGTGGTGAGGACTCTAAGGA
GACTGCCGGTGATAAGCAGCGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTACG
GGCTGGGCTACACACGTGCTACAATGGCGGTGACAGTGGGATGCTAAGGGGCGACCCGTCG
CAAATCTCTAAAAGCCGTTCTCAGTTCGGATTGGGCTCTGCAACTCGAGCCCATGAAGTTG
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GAATCGCTAGTAATCGTGGATCAGCACGCCACGGTGAATACGTTCCCGGGCCTTGTACACA
CCGCCCGTCACACCATGGGAGTTGGTTTTACCTGAAGACTGTGCGCTAACCGCAAGGGAGC
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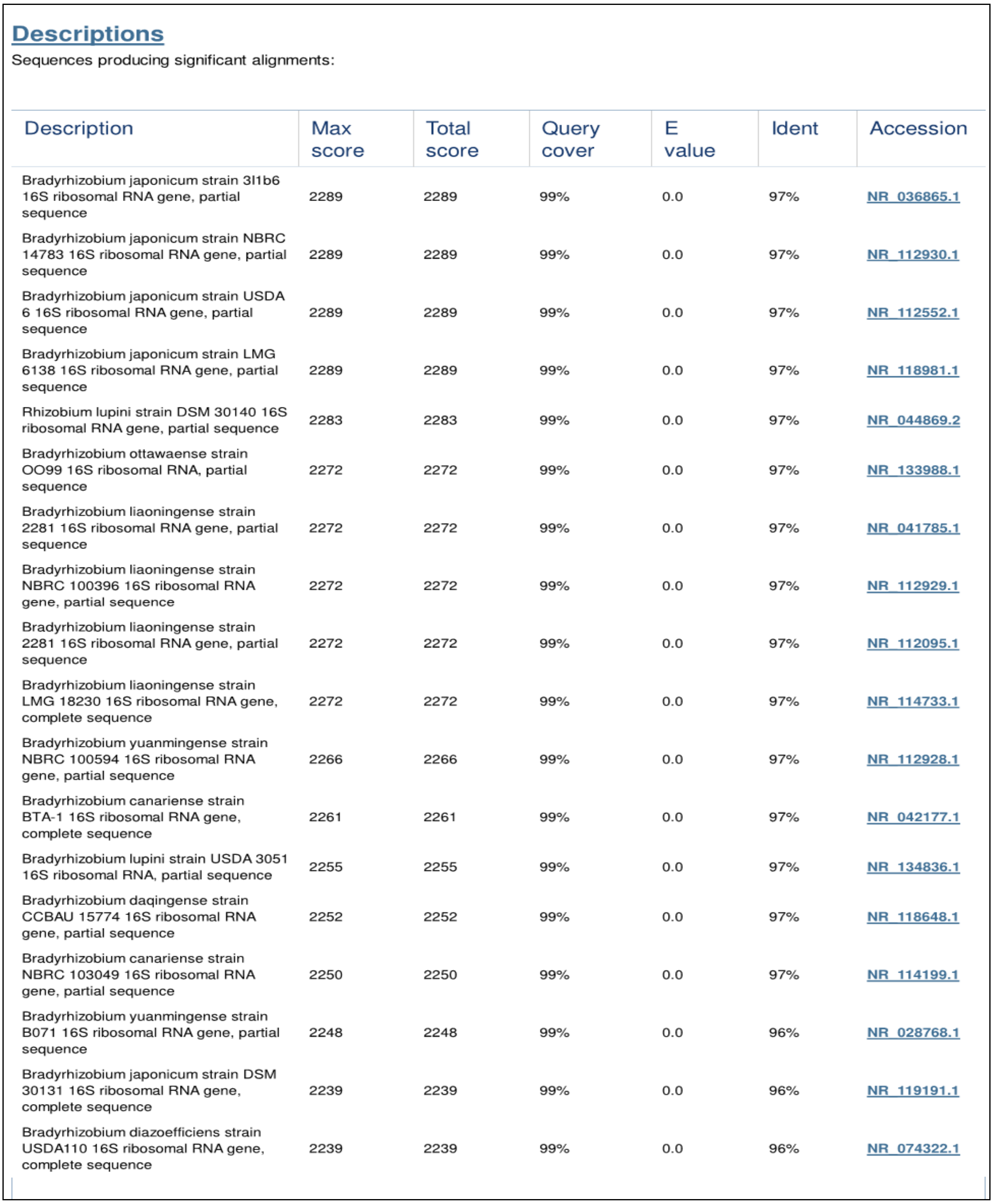
Table.36: Sequences Producing Significant Alignment for CJN.IE-2



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Bradyrhizobium japonicum strain 3I1b6 16S ribosomal RNA gene, partial sequence	2289	2289	99%	0.0	97%	NR_036865.1
Bradyrhizobium japonicum strain NBRC 14783 16S ribosomal RNA gene, partial sequence	2289	2289	99%	0.0	97%	NR_112930.1
Bradyrhizobium japonicum strain USDA 6 16S ribosomal RNA gene, partial sequence	2289	2289	99%	0.0	97%	NR_112552.1
Bradyrhizobium japonicum strain LMG 6138 16S ribosomal RNA gene, partial sequence	2289	2289	99%	0.0	97%	NR_118981.1
Rhizobium lupini strain DSM 30140 16S ribosomal RNA gene, partial sequence	2283	2283	99%	0.0	97%	NR_044869.2
Bradyrhizobium ottawaense strain OO99 16S ribosomal RNA, partial sequence	2272	2272	99%	0.0	97%	NR_133988.1
Bradyrhizobium liaoningense strain 2281 16S ribosomal RNA gene, partial sequence	2272	2272	99%	0.0	97%	NR_041785.1
Bradyrhizobium liaoningense strain NBRC 100396 16S ribosomal RNA gene, partial sequence	2272	2272	99%	0.0	97%	NR_112929.1
Bradyrhizobium liaoningense strain 2281 16S ribosomal RNA gene, partial sequence	2272	2272	99%	0.0	97%	NR_112095.1
Bradyrhizobium liaoningense strain LMG 18230 16S ribosomal RNA gene, complete sequence	2272	2272	99%	0.0	97%	NR_114733.1
Bradyrhizobium yuanmingense strain NBRC 100594 16S ribosomal RNA gene, partial sequence	2266	2266	99%	0.0	97%	NR_112928.1
Bradyrhizobium canariense strain BTA-1 16S ribosomal RNA gene, complete sequence	2261	2261	99%	0.0	97%	NR_042177.1
Bradyrhizobium lupini strain USDA 3051 16S ribosomal RNA, partial sequence	2255	2255	99%	0.0	97%	NR_134836.1
Bradyrhizobium daqingense strain CCBAU 15774 16S ribosomal RNA gene, partial sequence	2252	2252	99%	0.0	97%	NR_118648.1
Bradyrhizobium canariense strain NBRC 103049 16S ribosomal RNA gene, partial sequence	2250	2250	99%	0.0	97%	NR_114199.1
Bradyrhizobium yuanmingense strain B071 16S ribosomal RNA gene, partial sequence	2248	2248	99%	0.0	96%	NR_028768.1
Bradyrhizobium japonicum strain DSM 30131 16S ribosomal RNA gene, complete sequence	2239	2239	99%	0.0	96%	NR_119191.1
Bradyrhizobium diazoefficiens strain USDA110 16S ribosomal RNA gene, complete sequence	2239	2239	99%	0.0	96%	NR_074322.1

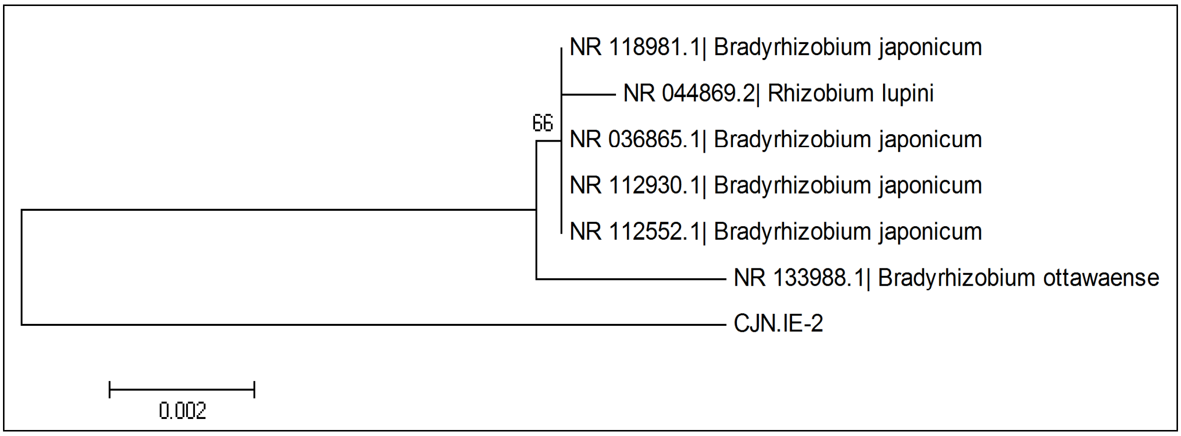


Fig.47: Phylogenetic tree of CJN.IE-2 constructed by NJ method

4.8.20. 16S rDNA Analysis of CPN.B

The bacterial culture designated as *CPN.B* was established as *Enterobacter hormaechei* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1020bp at GenBank NCBI through Bankit submission format. KU935450 has been designated as its accession number.

Consensus Sequence of CPN.B

ACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGC

ACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGT

TGTAAAGTACTTTCAGCGGGGAGGAAGGTGTTGAGGTTAATAACCTCAGCAATTGA

CGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCCAGCCGCGGTAATACG

GAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGT

CAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAG

GCTAGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAG

ATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGG

TGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAAC

GATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAA

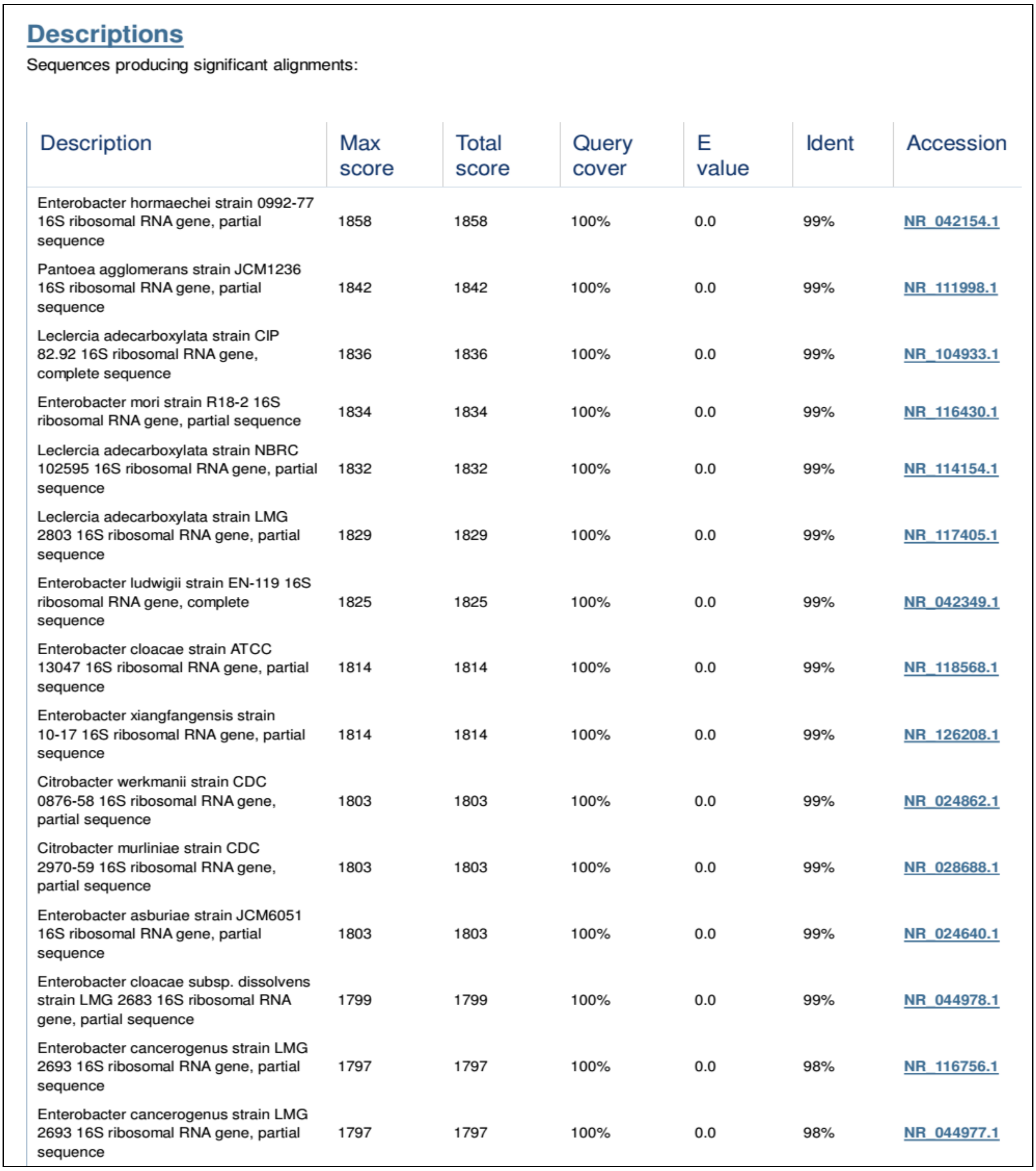
GTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGG

CCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACC

TACTCTTGACATCCAGAGAACTTACCAGAGATGGTTTGGTGCCTTCGGGAACTCTG

AGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCC
CGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTTAGGCCGGGAACTCAAAG
GAGACTGCCAGTGAATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGC
CCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCTGACC
TCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAA
CTCGACTCCATG

Table.37: Sequences Producing Significant Alignment for CPN.B



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Enterobacter hormaechei strain 0992-77 16S ribosomal RNA gene, partial sequence	1858	1858	100%	0.0	99%	NR_042154.1
Pantoea agglomerans strain JCM1236 16S ribosomal RNA gene, partial sequence	1842	1842	100%	0.0	99%	NR_111998.1
Leclercia adecarboxylata strain CIP 82.92 16S ribosomal RNA gene, complete sequence	1836	1836	100%	0.0	99%	NR_104933.1
Enterobacter mori strain R18-2 16S ribosomal RNA gene, partial sequence	1834	1834	100%	0.0	99%	NR_116430.1
Leclercia adecarboxylata strain NBRC 102595 16S ribosomal RNA gene, partial sequence	1832	1832	100%	0.0	99%	NR_114154.1
Leclercia adecarboxylata strain LMG 2803 16S ribosomal RNA gene, partial sequence	1829	1829	100%	0.0	99%	NR_117405.1
Enterobacter ludwigii strain EN-119 16S ribosomal RNA gene, complete sequence	1825	1825	100%	0.0	99%	NR_042349.1
Enterobacter cloacae strain ATCC 13047 16S ribosomal RNA gene, partial sequence	1814	1814	100%	0.0	99%	NR_118568.1
Enterobacter xiangfangensis strain 10-17 16S ribosomal RNA gene, partial sequence	1814	1814	100%	0.0	99%	NR_126208.1
Citrobacter werkmanii strain CDC 0876-58 16S ribosomal RNA gene, partial sequence	1803	1803	100%	0.0	99%	NR_024862.1
Citrobacter murliniae strain CDC 2970-59 16S ribosomal RNA gene, partial sequence	1803	1803	100%	0.0	99%	NR_028688.1
Enterobacter asburiae strain JCM6051 16S ribosomal RNA gene, partial sequence	1803	1803	100%	0.0	99%	NR_024640.1
Enterobacter cloacae subsp. dissolvens strain LMG 2683 16S ribosomal RNA gene, partial sequence	1799	1799	100%	0.0	99%	NR_044978.1
Enterobacter cancerogenus strain LMG 2693 16S ribosomal RNA gene, partial sequence	1797	1797	100%	0.0	98%	NR_116756.1
Enterobacter cancerogenus strain LMG 2693 16S ribosomal RNA gene, partial sequence	1797	1797	100%	0.0	98%	NR_044977.1

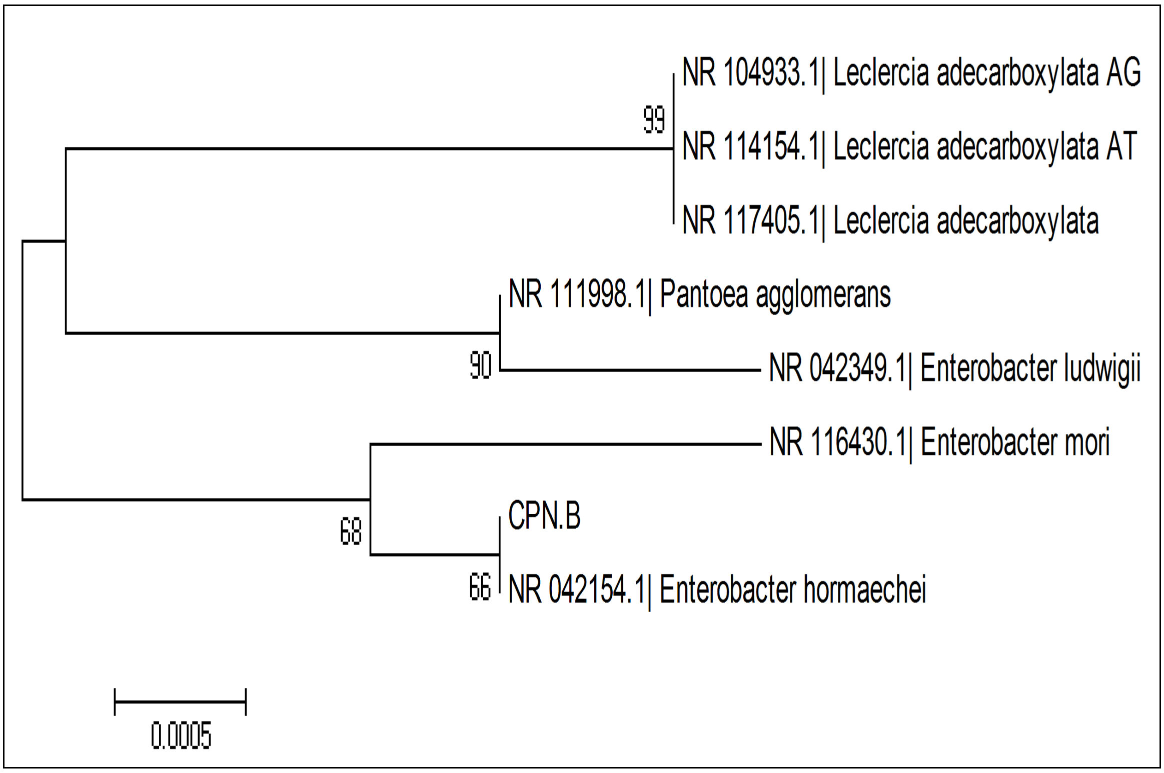


Fig.48: Phylogenetic tree of CPN.B constructed by NJ method

4.8.21. 16S rDNA Analysis of CPN.IW-1

The bacterial culture designated as *CPN.IW-1* was established as *Stenotrophomonas maltophilia* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1446bp at GenBank NCBI through Bankit submission format. KU935451 has been designated as its accession number.

Consensus Sequence of CPN.IW-1

CGGTAGGCCTAACACATGCAAGTCGAACGGCAGCACAGTAAGAGCTTGCTCTTACG
GGTGGCGAGTGGCGGACGGGTGAGGAATACATCGGAATCTACTTTTTCGTGGGGGA
TAACGTAGGGAAACTTACGCTAATACCGCATACGACCTACGGGTGAAAGCAGGGGA
TCTTCGGACCTTGCGCGATTGAATGAGCCGATGTCGGATTAGCTAGTTGGCGGGGT
AAAGGCCCACCAAGGCGACGATCCGTAGCTGGTCTGAGAGGATGATCAGCCACACT
GGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACA

ATGGGCGCAAGCCTGATCCAGCCATACCGCGTGGGTGAAGAAGGCCTTCGGGTTGT
AAAGCCCTTTTGTTGGGAAAGAAATCCAGCTGGTTAATACCCGGTTGGGATGACGG
TACCCAAAGAATAAGCACCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGG
GTGCAAGCGTTACTCGGAATTACTGGGCGTAAAGCGTGCGTAGGTGGTTGTTTAAG
TCTGTTGTGAAAGCCCTGGGCTCAACCTGGGAACTGCAGTGGAAACTGGACGACTA
GAGTGTGGTAGAGGGTAGCGGAATTCCTGGTGTAGCAGTGAAATGCGTAGAGATCA
GGAGGAACATCCATGGCGAAGGCAGCTACCTGGACCAACACTGACACTGAGGCACG
AAAGCGTGGGGAGCAAACAGGATTAGATACTCCTGGTAGTCCACGCCCTAAACGAT
GCGAACTGGATGTTGGGTGCAATTTGGCACGCAGTATCGAAGCTAACGCGTTAAGT
TCGCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCC
CGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTG
GCCTTGACATGTCGAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTCGAAC
ACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCG
CAACGAGCGCAACCCTTGTCCTTAGTTGCCAGCACGTAATGGTGGGAACTCTAAGG
AGACCGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCC
TTACGGCCAGGGCTACACACGTACTACAATGGTAGGGACAGAGGGCTGCAAGCCGG
CGACGGTAAGCCAATCCCAGAAACCCTATCTCAGTCCGGATTGGAGTCTGCAACTC
GACTCCATGAAGTCGGAATCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATA
CGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTTGTTGCACCAGA
AGCAGGTAGCTTAACCTTCGGGAGGGCGCTTGCCACGGTGTGGCCG

Table.38: Sequences Producing Significant Alignment for CPN.IW-1

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Stenotrophomonas maltophilia R551-3 strain R551-3 16S ribosomal RNA, complete sequence	492	492	19%	2e-138	96%	NR_074875.1
Stenotrophomonas maltophilia strain NBRC 14161 16S ribosomal RNA gene, partial sequence	492	492	19%	2e-138	96%	NR_113648.1
Stenotrophomonas pavanii strain LMG 25348 16S ribosomal RNA gene, partial sequence	492	492	19%	2e-138	96%	NR_118008.1
Stenotrophomonas pavanii strain ICB 89 16S ribosomal RNA gene, partial sequence	492	492	19%	2e-138	96%	NR_116793.1
Stenotrophomonas chelatiphaga strain LPM-5 16S ribosomal RNA gene, partial sequence	492	492	19%	2e-138	96%	NR_116366.1
Stenotrophomonas humi strain R-32729 16S ribosomal RNA gene, partial sequence	492	492	19%	2e-138	96%	NR_042568.1
Stenotrophomonas maltophilia strain IAM 12423 16S ribosomal RNA gene, complete sequence	492	492	19%	2e-138	96%	NR_041577.1
Stenotrophomonas maltophilia strain LMG 958 16S ribosomal RNA gene, complete sequence	492	492	19%	2e-138	96%	NR_119220.1
Pseudomonas pictorum strain LMG 981 16S ribosomal RNA gene, partial sequence	492	492	19%	2e-138	96%	NR_041957.1
Stenotrophomonas maltophilia strain ATCC 19861 16S ribosomal RNA gene, complete sequence	492	492	19%	2e-138	96%	NR_040804.1
Pseudomonas hibiscicola strain ATCC 19867 16S ribosomal RNA gene, partial sequence	492	964	55%	2e-138	96%	NR_024709.1
Pseudomonas geniculata strain ATCC 19374 16S ribosomal RNA gene, partial sequence	492	969	54%	2e-138	96%	NR_024708.1
Pseudomonas pictorum strain ATCC 23328 16S ribosomal RNA gene, complete sequence	492	492	19%	2e-138	96%	NR_112067.1
Stenotrophomonas maltophilia strain ATCC 13637 16S ribosomal RNA gene, partial sequence	492	492	19%	2e-138	96%	NR_112030.1
Stenotrophomonas terrae strain R-32768 16S ribosomal RNA gene, partial sequence	486	486	19%	1e-136	96%	NR_042569.1
Stenotrophomonas acidaminiphila strain AMX 19 16S ribosomal RNA gene, complete sequence	486	486	19%	1e-136	96%	NR_025104.1
Xanthomonas sacchari strain LMG 471 16S ribosomal RNA gene, partial sequence	481	481	19%	5e-135	96%	NR_026392.1
Stenotrophomonas daejeonensis strain MJ03 16S ribosomal RNA gene, partial	479	479	18%	2e-134	96%	NR_117259.1

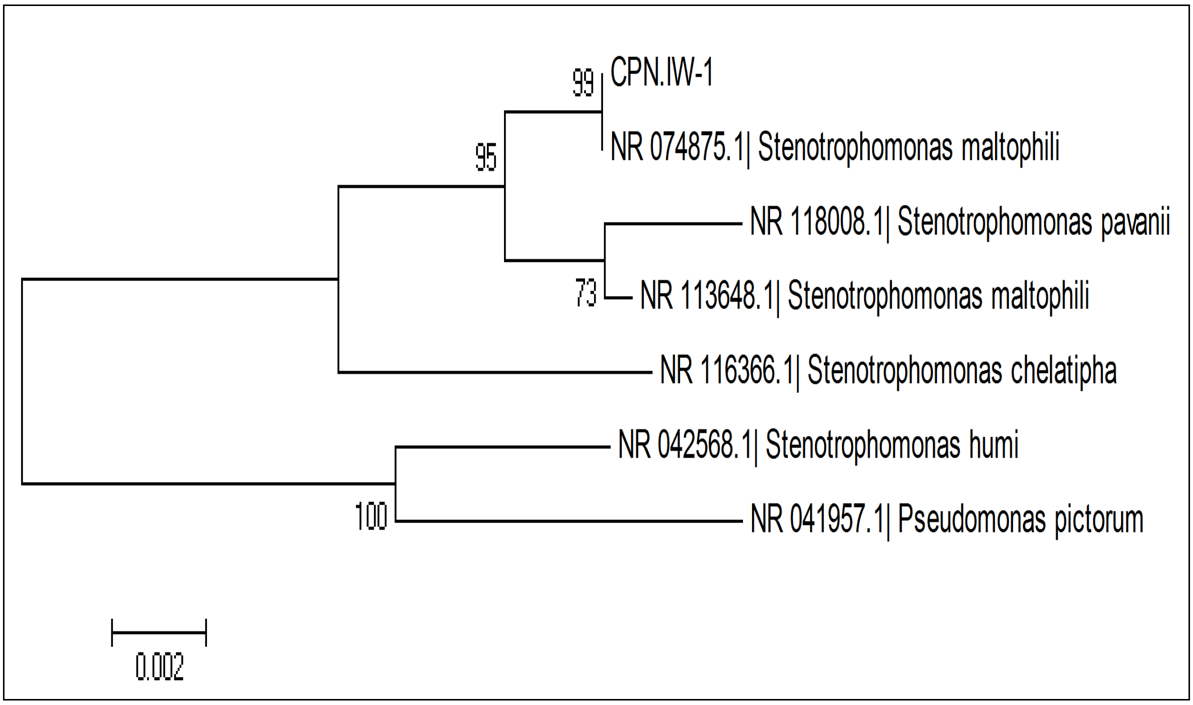


Fig.49: Phylogenetic tree of CPN.IW-1 constructed by NJ method

4.8.22. 16S rDNA Analysis of CPN.T-1

The bacterial culture designated as *CPN.T-1* was established as *Pantoea agglomerans* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1438bp at GenBank NCBI through Bankit submission format. KU935452 has been designated as its accession number.

Consensus Sequence of CPN.T-1

GGCGGCAGGCCTAACACATGCAAGTCGAACGGTAGCACAGAGAGCTTGCTCTCGGG

TGACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATA

ACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACC

TTCGGGCCTCTTGCCATCAGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAA

CGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGG

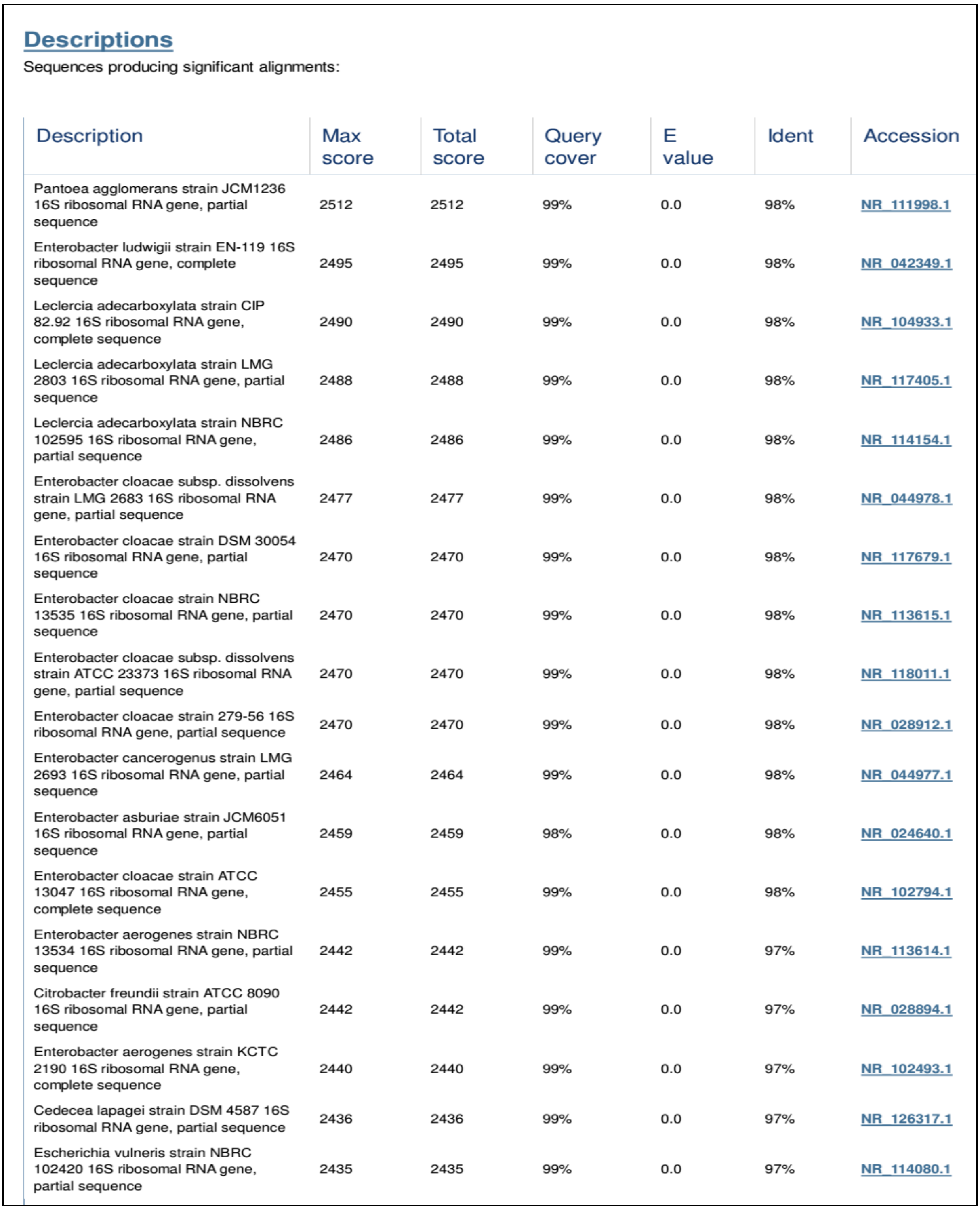
AACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAAT

GGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAA

AGTACTTTCAGCGGGGAGGAAGGTGTTGTGGTTAATAACCGCAGCAATTGACGTTA

CCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGT
GCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTC
GGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAGGCTAGA
GTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGG
AGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAA
AGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTC
GACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGAC
CGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCA
CAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTACTCT
TGACATCCAGAGAACTTACCAGAGATGGTTTGGTGCCTTCGGGAACTCTGAGACAG
GTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAAC
GAGCGCAACCCTTATCCTTTGTTGCCAGCGGTCCGGCCGGGAACTCAAAGGAGACT
GCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACG
AGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGA
GCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTC
CATGAAGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGAATACGTTCC
CGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGG
TAGCTTAACCTTCGGGAGGGCGCTTACCACTTTGTGAT

Table.39: Sequences Producing Significant Alignment for CPN.T-1



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pantoea agglomerans strain JCM1236 16S ribosomal RNA gene, partial sequence	2512	2512	99%	0.0	98%	NR_111998.1
Enterobacter ludwigii strain EN-119 16S ribosomal RNA gene, complete sequence	2495	2495	99%	0.0	98%	NR_042349.1
Leclercia adecarboxylata strain CIP 82.92 16S ribosomal RNA gene, complete sequence	2490	2490	99%	0.0	98%	NR_104933.1
Leclercia adecarboxylata strain LMG 2803 16S ribosomal RNA gene, partial sequence	2488	2488	99%	0.0	98%	NR_117405.1
Leclercia adecarboxylata strain NBRC 102595 16S ribosomal RNA gene, partial sequence	2486	2486	99%	0.0	98%	NR_114154.1
Enterobacter cloacae subsp. dissolvens strain LMG 2683 16S ribosomal RNA gene, partial sequence	2477	2477	99%	0.0	98%	NR_044978.1
Enterobacter cloacae strain DSM 30054 16S ribosomal RNA gene, partial sequence	2470	2470	99%	0.0	98%	NR_117679.1
Enterobacter cloacae strain NBRC 13535 16S ribosomal RNA gene, partial sequence	2470	2470	99%	0.0	98%	NR_113615.1
Enterobacter cloacae subsp. dissolvens strain ATCC 23373 16S ribosomal RNA gene, partial sequence	2470	2470	99%	0.0	98%	NR_118011.1
Enterobacter cloacae strain 279-56 16S ribosomal RNA gene, partial sequence	2470	2470	99%	0.0	98%	NR_028912.1
Enterobacter cancerogenus strain LMG 2693 16S ribosomal RNA gene, partial sequence	2464	2464	99%	0.0	98%	NR_044977.1
Enterobacter asburiae strain JCM6051 16S ribosomal RNA gene, partial sequence	2459	2459	98%	0.0	98%	NR_024640.1
Enterobacter cloacae strain ATCC 13047 16S ribosomal RNA gene, complete sequence	2455	2455	99%	0.0	98%	NR_102794.1
Enterobacter aerogenes strain NBRC 13534 16S ribosomal RNA gene, partial sequence	2442	2442	99%	0.0	97%	NR_113614.1
Citrobacter freundii strain ATCC 8090 16S ribosomal RNA gene, partial sequence	2442	2442	99%	0.0	97%	NR_028894.1
Enterobacter aerogenes strain KCTC 2190 16S ribosomal RNA gene, complete sequence	2440	2440	99%	0.0	97%	NR_102493.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	2436	2436	99%	0.0	97%	NR_126317.1
Escherichia vulneris strain NBRC 102420 16S ribosomal RNA gene, partial sequence	2435	2435	99%	0.0	97%	NR_114080.1

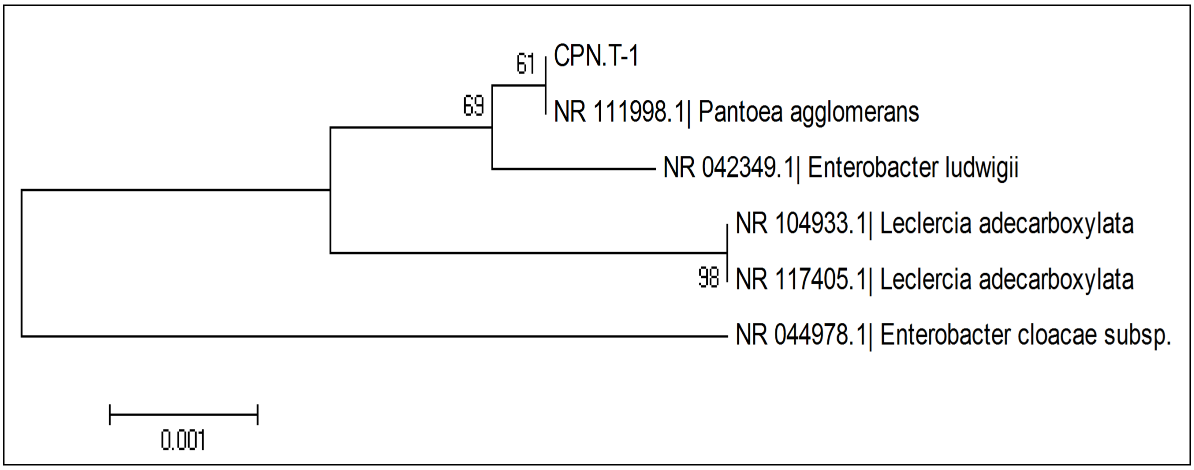


Fig.50: Phylogenetic tree of CPN.T-1 constructed by NJ method

4.8.23. 16S rDNA Analysis of CPN.T-4

The bacterial culture designated as *CPN.T-4* was established as *Cedecea davisae* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 879bp at GenBank NCBI through Bankit submission format. KU935453 has been designated as its accession number.

Consensus Sequence of CPN.T-4

TGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAAGCTTGAGTCTT

GTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAA

TACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGT

GGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTT

GGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCT

GGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGC

GGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTACTCTTGACA

TCCAGAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTCTGAGACAGGTGCT

GCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCG

CAACCCTTATCCTTTGTTGCCAGCGGTTCGGCCGGGAACTCAAAGGAGACTGCCAG

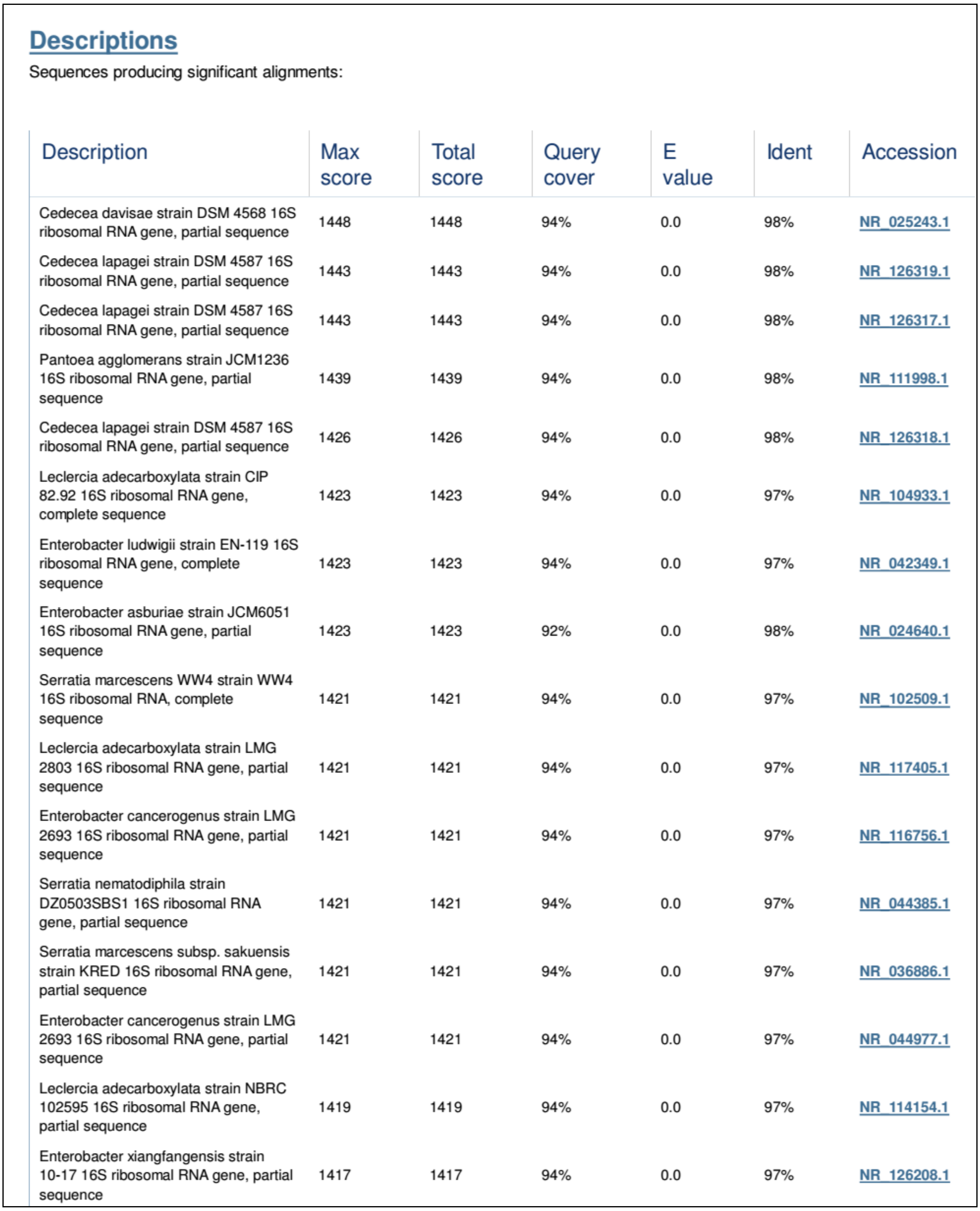
TGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGAGTAG

GGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGAGCAAG

CGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGA

AGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGAATACGTTCCCGGGC
CTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGCT
TAACCTTCGGGAGGGCGCTTACCACTTTGTGATTCATGA

Table.40: Sequences Producing Significant Alignment for CPN.T-4



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Cedecea davisae strain DSM 4568 16S ribosomal RNA gene, partial sequence	1448	1448	94%	0.0	98%	NR_025243.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	1443	1443	94%	0.0	98%	NR_126319.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	1443	1443	94%	0.0	98%	NR_126317.1
Pantoea agglomerans strain JCM1236 16S ribosomal RNA gene, partial sequence	1439	1439	94%	0.0	98%	NR_111998.1
Cedecea lapagei strain DSM 4587 16S ribosomal RNA gene, partial sequence	1426	1426	94%	0.0	98%	NR_126318.1
Leclercia adecarboxylata strain CIP 82.92 16S ribosomal RNA gene, complete sequence	1423	1423	94%	0.0	97%	NR_104933.1
Enterobacter ludwigii strain EN-119 16S ribosomal RNA gene, complete sequence	1423	1423	94%	0.0	97%	NR_042349.1
Enterobacter asburiae strain JCM6051 16S ribosomal RNA gene, partial sequence	1423	1423	92%	0.0	98%	NR_024640.1
Serratia marcescens WW4 strain WW4 16S ribosomal RNA, complete sequence	1421	1421	94%	0.0	97%	NR_102509.1
Leclercia adecarboxylata strain LMG 2803 16S ribosomal RNA gene, partial sequence	1421	1421	94%	0.0	97%	NR_117405.1
Enterobacter cancerogenus strain LMG 2693 16S ribosomal RNA gene, partial sequence	1421	1421	94%	0.0	97%	NR_116756.1
Serratia nematodiphila strain DZ0503SBS1 16S ribosomal RNA gene, partial sequence	1421	1421	94%	0.0	97%	NR_044385.1
Serratia marcescens subsp. sakuensis strain KRED 16S ribosomal RNA gene, partial sequence	1421	1421	94%	0.0	97%	NR_036886.1
Enterobacter cancerogenus strain LMG 2693 16S ribosomal RNA gene, partial sequence	1421	1421	94%	0.0	97%	NR_044977.1
Leclercia adecarboxylata strain NBRC 102595 16S ribosomal RNA gene, partial sequence	1419	1419	94%	0.0	97%	NR_114154.1
Enterobacter xiangfangensis strain 10-17 16S ribosomal RNA gene, partial sequence	1417	1417	94%	0.0	97%	NR_126208.1

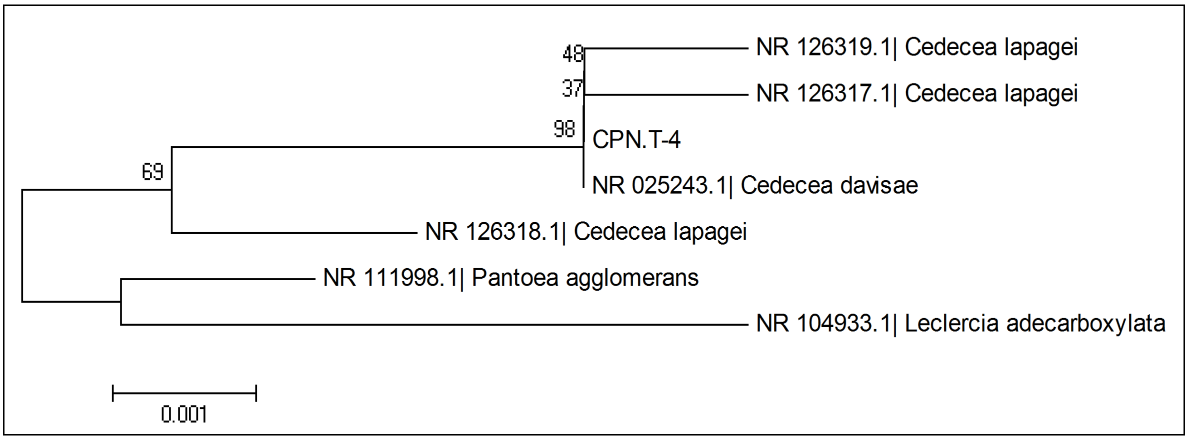


Fig.51: Phylogenetic tree of CPN.T-4 constructed by NJ method

4.8.24. 16S rDNA Analysis of LLN.B-1

The bacterial culture designated as *LLN.B-1* was established as *Bacillus toyonensis* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 898bp at GenBank NCBI through Bankit submission format. KU955582 has been designated as its accession number.

Consensus Sequence of LLN.B-1

TTGGTTTTCTTTAAGTTTGATGTCGAAGCCCCACGGCTCAACCCGTGGAGGGTCAT

TGGAAACTGGGAGACTTGAGTTCAGAAAGAGGAAAGTGAATTCCATGTGTAGCGGT

GAAATGCGTAGAGATATGGAGGAACACCAGTGGGGAAGGCGACTTTCTGGTCTGTA

ACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGT

TCACGCCGTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGA

AGTTAACGCATTAAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAA

GGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTTGAAGCAACG

CGAAGAACCTTACCAGGTCTTGACATCCTTTGACAACCCTAGAGATAGGGCTTTTC

CTTTGGGAGCAGAGTGACAGGTGGTGCATGGTTGTTGTCAGCTCGTGTCGTGAGAT

GTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATCTTAGTTGCCATCATTAAGT

TGGGCACTCTAAGGTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCA

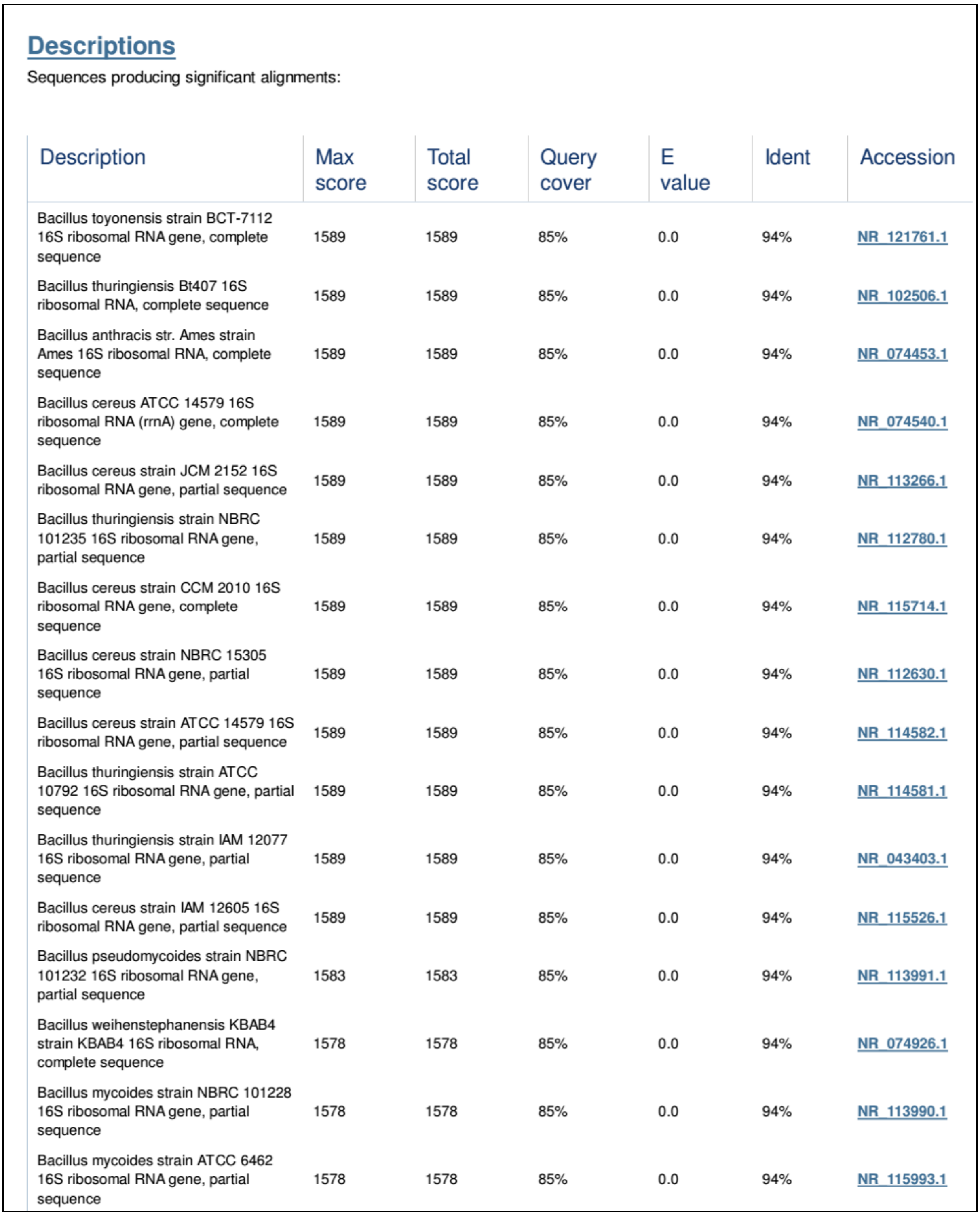
AATCATCATGCCCCTTATGACCTGGGCTACACACGTGCTACAATGGACGGTACAAA

GAGCTGCAAGACCGCGAGGTGGAGCTAATCTCATAAAACCGTTCTCAGTTCGGATT

GTAGGCTGCAACTCGCCTACATGAAGCTGGAATCGCTAGTAATCGCGGATCAGCAT

GCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGGGGTAACCTTTTGGAGCCAGCCGCCTAAGGTGGACCA

Table.41: Sequences Producing Significant Alignment for LLN.B-1



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Bacillus toyonensis strain BCT-7112 16S ribosomal RNA gene, complete sequence	1589	1589	85%	0.0	94%	NR_121761.1
Bacillus thuringiensis Bt407 16S ribosomal RNA, complete sequence	1589	1589	85%	0.0	94%	NR_102506.1
Bacillus anthracis str. Ames strain Ames 16S ribosomal RNA, complete sequence	1589	1589	85%	0.0	94%	NR_074453.1
Bacillus cereus ATCC 14579 16S ribosomal RNA (rrnA) gene, complete sequence	1589	1589	85%	0.0	94%	NR_074540.1
Bacillus cereus strain JCM 2152 16S ribosomal RNA gene, partial sequence	1589	1589	85%	0.0	94%	NR_113266.1
Bacillus thuringiensis strain NBRC 101235 16S ribosomal RNA gene, partial sequence	1589	1589	85%	0.0	94%	NR_112780.1
Bacillus cereus strain CCM 2010 16S ribosomal RNA gene, complete sequence	1589	1589	85%	0.0	94%	NR_115714.1
Bacillus cereus strain NBRC 15305 16S ribosomal RNA gene, partial sequence	1589	1589	85%	0.0	94%	NR_112630.1
Bacillus cereus strain ATCC 14579 16S ribosomal RNA gene, partial sequence	1589	1589	85%	0.0	94%	NR_114582.1
Bacillus thuringiensis strain ATCC 10792 16S ribosomal RNA gene, partial sequence	1589	1589	85%	0.0	94%	NR_114581.1
Bacillus thuringiensis strain IAM 12077 16S ribosomal RNA gene, partial sequence	1589	1589	85%	0.0	94%	NR_043403.1
Bacillus cereus strain IAM 12605 16S ribosomal RNA gene, partial sequence	1589	1589	85%	0.0	94%	NR_115526.1
Bacillus pseudomycoides strain NBRC 101232 16S ribosomal RNA gene, partial sequence	1583	1583	85%	0.0	94%	NR_113991.1
Bacillus weihenstephanensis KBAB4 strain KBAB4 16S ribosomal RNA, complete sequence	1578	1578	85%	0.0	94%	NR_074926.1
Bacillus mycoides strain NBRC 101228 16S ribosomal RNA gene, partial sequence	1578	1578	85%	0.0	94%	NR_113990.1
Bacillus mycoides strain ATCC 6462 16S ribosomal RNA gene, partial sequence	1578	1578	85%	0.0	94%	NR_115993.1

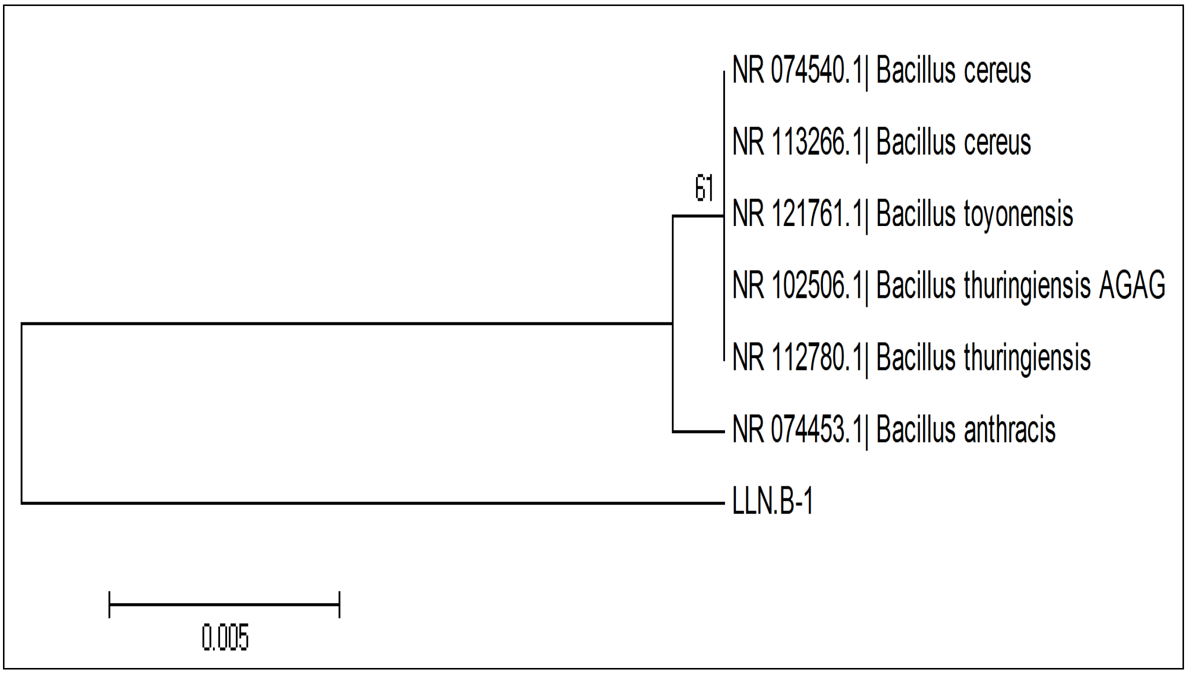


Fig.52: Phylogenetic tree of LLN.B-1 constructed by NJ method

4.8.25. 16S rDNA Analysis of LLN.T-1

The bacterial culture designated as *LLN.T-1* was established as *Pseudomonas hibiscicola* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1445bp at GenBank NCBI through Bankit submission format. KU955583 has been designated as its accession number.

Consensus Sequence of LLN.T-1

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GCGGTAGGCCTAACACATGCAAGTCGAACGGCAGCACAGGAGCTTGCTCCTTGG
GTGGCGAGTGGCGGACGGGTGAGGAATACATCGGAATCTACTTTTTCGTGGGGGAT
AACGTAGGGAAACTTACGCTAATACCGCAACTGACCTACGGGTGAAAGCAGGGGAT
CTTCGGACCTTGCGCGATTGAATGAGCCGATGTCGGATTAGCTAGTTGGCGGGGTA
AAGGCCCACCAAGGCGACGATCCGTAGCTGGTCTGAGAGGATGATCAGCCACACTG
GAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAA
TGGGCGCAAGCCTGATCCAGCCATACCGCGTGGGTGAAGAAGGCCTTCGGGTTGTA
AAGCCCTTTTGTTGGGAAAGAAATCCAGCTGGCTAATACCCGGTTGGGATGACGGT
ACCCAAAGAATAAGCACCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGG
TGCAAGCGTTACTCGGAATTACTGGGCGTAAAGCGTGCGTAGGTGGTCGTTTAAGT
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CCGTTGTGAAAGCCCTGGGCTCAACCTGGGAACTGCAGTGGATACTGGGCGACTAG

AATGTGGTAGAGGGTAGCGGAATTCCTGGTGTAGCAGTGAAATGCGTAGAGATCAG

GAGGAACATCCATGGCGAAGGCAGCTACCTGGACCAACATTGACACTGAGGCACGA

AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCCTAAACGATGC

GAACTGGATGTTGGGTGCAATTTGGCACGCAGTATCGAAGCTAACGCGTTAAGTTC

GCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCG

CACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGC

CTTGACATGTCGAGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACTCGAACAC

AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCA

ACGAGCGCAACCCTTGTCCTTAGTTGCCAGCACGTAATGGTGGGAACTCTAAGGAG

ACCGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTT

ACGGCCAGGGCTACACACGTACTACAATGGTAGGGACAGAGGGCTGCAAGCCGGCG

ACGGTAAGCCAATCCCAGAAACCCTATCTCAGTCCGGATTGGAGTCTGCAACTCGA

CTCCATGAAGTCGGAATCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACG

TTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTTGTTGCACCAGAAG

CAGGTAGCTTAACCTTCGGGAGGGCGCTTGCCACGGTGTCCCAGA

Table.42: Sequences Producing Significant Alignment for LLN.T-1

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pseudomonas hibiscicola strain ATCC 19867 16S ribosomal RNA gene, partial sequence	1978	1978	98%	0.0	92%	NR_024709.1
Stenotrophomonas maltophilia strain IAM 12423 16S ribosomal RNA gene, complete sequence	1973	1973	98%	0.0	92%	NR_041577.1
Stenotrophomonas maltophilia strain NBRC 14161 16S ribosomal RNA gene, partial sequence	1969	1969	98%	0.0	92%	NR_113648.1
Stenotrophomonas pavanii strain LMG 25348 16S ribosomal RNA gene, partial sequence	1969	1969	98%	0.0	92%	NR_118008.1
Stenotrophomonas maltophilia strain LMG 958 16S ribosomal RNA gene, complete sequence	1969	1969	98%	0.0	92%	NR_119220.1
Stenotrophomonas maltophilia strain ATCC 19861 16S ribosomal RNA gene, complete sequence	1967	1967	98%	0.0	92%	NR_040804.1
Pseudomonas geniculata strain ATCC 19374 16S ribosomal RNA gene, partial sequence	1967	1967	98%	0.0	92%	NR_024708.1
Stenotrophomonas maltophilia strain ATCC 13637 16S ribosomal RNA gene, partial sequence	1967	1967	98%	0.0	92%	NR_112030.1
Stenotrophomonas pavanii strain ICB 89 16S ribosomal RNA gene, partial sequence	1951	1951	98%	0.0	91%	NR_116793.1
Stenotrophomonas maltophilia R551-3 strain R551-3 16S ribosomal RNA, complete sequence	1947	1947	98%	0.0	91%	NR_074875.1
Stenotrophomonas chelatiphaga strain LPM-5 16S ribosomal RNA gene, partial sequence	1877	1877	98%	0.0	90%	NR_116366.1
Stenotrophomonas rhizophila strain e-p10 16S ribosomal RNA gene, complete sequence	1836	1836	98%	0.0	90%	NR_121739.1
Stenotrophomonas nitritireducens strain L2 16S ribosomal RNA gene, partial sequence	1821	1821	98%	0.0	90%	NR_025305.1
Stenotrophomonas rhizophila strain e-p10 16S ribosomal RNA gene, partial sequence	1820	1820	98%	0.0	90%	NR_028930.1
Stenotrophomonas humi strain R-32729 16S ribosomal RNA gene, partial sequence	1818	1818	98%	0.0	90%	NR_042568.1
Stenotrophomonas koreensis strain TR6-01 16S ribosomal RNA gene, partial sequence	1818	1818	98%	0.0	90%	NR_041019.1
Stenotrophomonas ginsengisoli strain NBRC 101154 16S ribosomal RNA gene, partial sequence	1814	1814	98%	0.0	90%	NR_113981.1
Xanthomonas campestris strain ATCC 33913 16S ribosomal RNA gene,	1812	1812	99%	0.0	90%	NR_074936.1

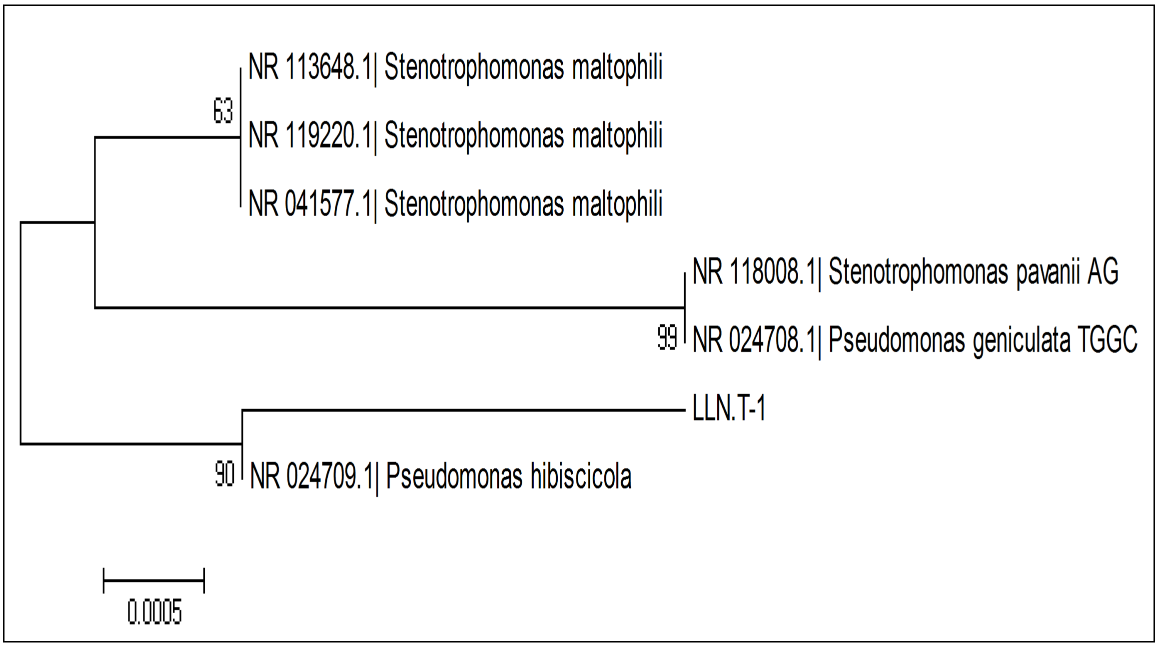


Fig.53: Phylogenetic tree of LLN.T-1 constructed by NJ method

4.8.26. 16S rDNA Analysis of LLN.IE-1

The bacterial culture designated as *LLN.IE-1* was established as *Mesorhizobium plurifarium* on the basis of nucleotide homology and phylogenetic analysis that was constructed after performing 16S rDNA sequence analysis and from BLAST (Basic Local Alignment Search Tool). The accession number of the strain has been obtained after submitting the consensus sequence of 1387bp at GenBank NCBI through Bankit submission format. KX281719 has been designated as its accession number.

Consensus Sequence of LLN.IE-1

GGCGGCAGGCTTAACACATGCAAGTCGAGCGCCCCGCAAGGGGAGCGGCAGACGGG

TGAGTAACGCGTGGGAATCTACCCATCTCTACGGAACAACTCCGGGAAACTGGAGC

TAATACCGTATACGTCCTTCGGGAGAAAGATTTATCGGAGATGGATGAGCCCGCGT

TGGATTAGCTAGTTGGTGGGGTAATGGCCTACCAAGGCGACGATCCATAGCTGGTC

TGACAGGATGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGG

CAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGG

GTGATGAAGGCCCTAGGGTTGTAAAGCTCTTTCAACGGTGAAGATAATGACGGTAA

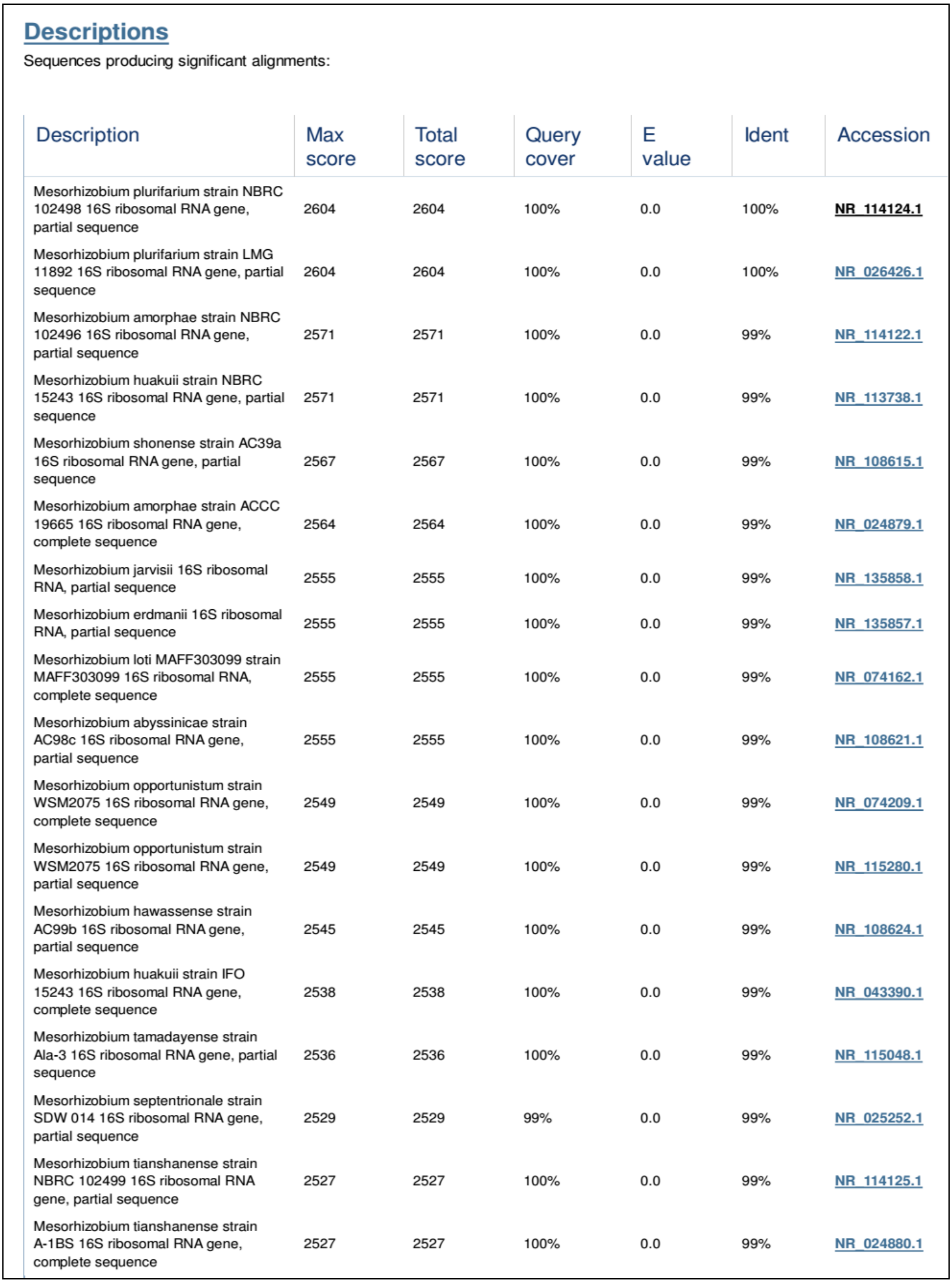
CCGTAGAAGAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGGG

CTAGCGTTGTTCGGAATTACTGGGGTTAAAGCGCACGTAGGCGGATACTTAAGTCA

GGGGTGAAATCCCGGGGCTCAACCCCGGAACTGCCTTTGATACTGGGTATCTGGAG

TCCGGAAGAGGTGAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGA
GGAACACCAGTGGCGAAGGCGGCTCACTGGTCCGGTACTGACGCTGAGGTGCGAAA
GCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGGAA
GCTAGCCGTTGGCAAGTTTACTTGTCGGTGGCGCAGCTAACGCATTAAGCTTCCCG
CCTGGGGAGTACGGTGGCAAGATTAAAACTCAAAGGAATTGACGGGGGCCCGCACA
AGCCGTGGAGCATGTGGTTTAATTCGATGCAACGCGCAGAACCTTACCTGCCCTTG
ACATCCCGGTCGCGGTTACCAGAAATGGTTTCCTTCAGTTCGGCTGGACCGGTGAC
AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCA
ACGAGCGCAACCCTCGCCCTTAGTTGCCATCATTCAGTTGGGCACTCTAAGGGGAC
TGCCGGTGATAAGCCGAGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTA
CGGGCTGGGCTACACACGTGCTACAATGGTGGTGACAGTGGGCAGCGAGACCGCGA
GGTCGAGCTAATCTCCAAAAGCCATCTCAGTTCGGATTGCACTCTGCAACTCGAGT
GCATGAAGTTGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTC
CCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTGGTTTTACCCGAAGGCG
CTGTGCTAACCGCAAGGAGGCAGGCGACCACGGTAGGGTCAGC

Table.43: Sequences Producing Significant Alignment for LLN.IE-1.



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Mesorhizobium plurifarium strain NBRC 102498 16S ribosomal RNA gene, partial sequence	2604	2604	100%	0.0	100%	NR_114124.1
Mesorhizobium plurifarium strain LMG 11892 16S ribosomal RNA gene, partial sequence	2604	2604	100%	0.0	100%	NR_026426.1
Mesorhizobium amorphae strain NBRC 102496 16S ribosomal RNA gene, partial sequence	2571	2571	100%	0.0	99%	NR_114122.1
Mesorhizobium huakuii strain NBRC 15243 16S ribosomal RNA gene, partial sequence	2571	2571	100%	0.0	99%	NR_113738.1
Mesorhizobium shonense strain AC39a 16S ribosomal RNA gene, partial sequence	2567	2567	100%	0.0	99%	NR_108615.1
Mesorhizobium amorphae strain ACCC 19665 16S ribosomal RNA gene, complete sequence	2564	2564	100%	0.0	99%	NR_024879.1
Mesorhizobium jarvisii 16S ribosomal RNA, partial sequence	2555	2555	100%	0.0	99%	NR_135858.1
Mesorhizobium erdmanii 16S ribosomal RNA, partial sequence	2555	2555	100%	0.0	99%	NR_135857.1
Mesorhizobium loti MAFF303099 strain MAFF303099 16S ribosomal RNA, complete sequence	2555	2555	100%	0.0	99%	NR_074162.1
Mesorhizobium abyssinicae strain AC98c 16S ribosomal RNA gene, partial sequence	2555	2555	100%	0.0	99%	NR_108621.1
Mesorhizobium opportunistum strain WSM2075 16S ribosomal RNA gene, complete sequence	2549	2549	100%	0.0	99%	NR_074209.1
Mesorhizobium opportunistum strain WSM2075 16S ribosomal RNA gene, partial sequence	2549	2549	100%	0.0	99%	NR_115280.1
Mesorhizobium hawassense strain AC99b 16S ribosomal RNA gene, partial sequence	2545	2545	100%	0.0	99%	NR_108624.1
Mesorhizobium huakuii strain IFO 15243 16S ribosomal RNA gene, complete sequence	2538	2538	100%	0.0	99%	NR_043390.1
Mesorhizobium tamadayense strain Ala-3 16S ribosomal RNA gene, partial sequence	2536	2536	100%	0.0	99%	NR_115048.1
Mesorhizobium septentrionale strain SDW 014 16S ribosomal RNA gene, partial sequence	2529	2529	99%	0.0	99%	NR_025252.1
Mesorhizobium tianshanense strain NBRC 102499 16S ribosomal RNA gene, partial sequence	2527	2527	100%	0.0	99%	NR_114125.1
Mesorhizobium tianshanense strain A-1BS 16S ribosomal RNA gene, complete sequence	2527	2527	100%	0.0	99%	NR_024880.1

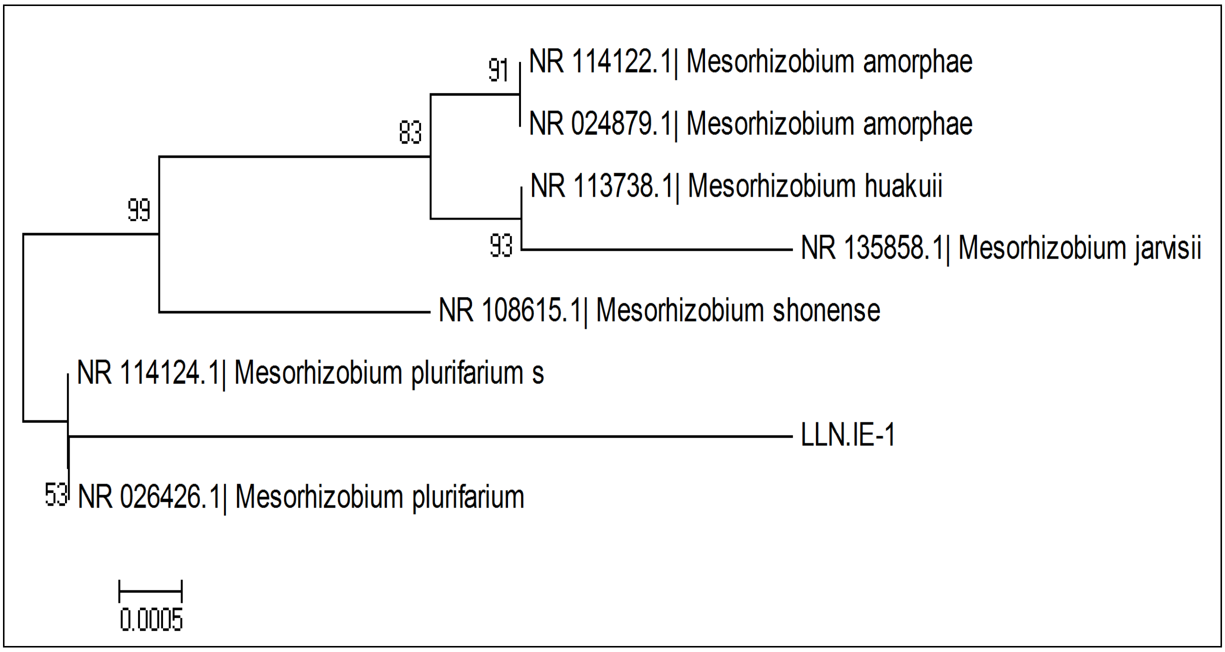


Fig.54: Phylogenetic tree of LLN.IE-1 constructed by NJ method