

1 **Title: *Rhizobium desertarenae* sp. nov., isolated from the Saline Desert Soil from the Rann**  
2 **of Kachchh, India.**

3 **Running Title:** *Rhizobium desertarenae* sp. nov.,

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16 **Keywords:** Saline Desert; Zobell marine agar; Polyphasic taxonomy; MALDI-TOF MS  
17 Biotyping

18

19 The GenBank accession numbers for the 16S rRNA gene sequences of strain ADMK78<sup>T</sup> is  
20 MK942856. The genome sequence has been deposited in GenBank under the accession number  
21 CP058350-CP058352. The type strain is available with different culture collections under the  
22 accession numbers MCC 3400<sup>T</sup>; KACC 21383<sup>T</sup>; and JCM 33657<sup>T</sup>.

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35 **Abstract:**

36 A novel bacterial strain designated ADMK78<sup>T</sup> was isolated from the saline desert soil. The cells  
37 were rod-shaped, Gram-negative, and non-motile. The strain ADMK78<sup>T</sup> grows best at 28°C and  
38 pH 7.0 and can tolerate up to 2% (w/v) NaCl. Based on 16S rRNA gene phylogeny, the strain  
39 ADMK78<sup>T</sup> belongs to the genus *Rhizobium*, with the highest similarity to *Rhizobium*  
40 *wuzhouense* W44<sup>T</sup> (98.7%) and *Rhizobium ipomoeae* shin9-1<sup>T</sup> (97.9%). Core-genes based  
41 phylogenetic analysis revealed that the strain ADMK78<sup>T</sup> forms a distinct branch in between  
42 *Rhizobium ipomoeae* shin9-1<sup>T</sup> and *Rhizobium selenitireducens* BAA-1503<sup>T</sup>. The average  
43 nucleotide identity of ADMK78<sup>T</sup> was less than 82%, to members of the family *Rhizobiaceae*.  
44 The genomic DNA G+C content of strain ADMK78<sup>T</sup> is 58.6 mol%. The major fatty acids of

45 strain ADMK78<sup>T</sup> were C<sub>18:0</sub> and C<sub>18:1 ω7c</sub>. The strain ADMK78<sup>T</sup> showed differences in  
46 physiological, phenotypic, and protein profiles estimated by MALDI-TOF MS to its closest  
47 relatives. Based on the phenotypic, chemotaxonomic properties, and phylogenetic analyses, the  
48 strain ADMK78<sup>T</sup> could be distinguished from the recognized species of the genus *Rhizobium*. It  
49 is suggested to represent a novel species of this genus, for which the name *Rhizobium*  
50 *desertarenae* sp. nov. is proposed. The type strain is ADMK78<sup>T</sup> (=MCC 3400<sup>T</sup>; KACC 21383<sup>T</sup>;  
51 JCM 33657<sup>T</sup>).

52

### 53 **Introduction:**

54 The genus *Rhizobium* is a large group of bacteria, and most species are known for their  
55 symbiotic fixation of nitrogen within the root nodules of leguminous plants. The family  
56 *Rhizobiaceae* has now been classified into 16 genera [1,2]. *Rhizobium* is one of the main genera  
57 in the family *Rhizobiaceae*, and it was first proposed in 1889 [3,4]. Presently, the genus  
58 *Rhizobium* comprises 90 recognized species (<https://lpsn.dsmz.de/genus/rhizobium>). Members of  
59 the genus *Rhizobium* are characterized as Gram-stain-negative, non-spore-forming, rod-shaped,  
60 aerobic, chemo-organotrophic, and possess C<sub>18:1</sub> and C<sub>18:1 ω7c</sub> as the predominant fatty acid and  
61 have a DNA G+C content of between 55 and 66 mol% [5,6]. Non-symbiotic and free-living  
62 members of *Rhizobium* have been found in various soils, including the rhizosphere [7,8],  
63 bioreactor [9], and beach sand [10].

### 64 **Isolation and Ecology:**

65 During the investigations on bacterial diversity of the saline desert soil collected (23.7337° N,  
66 69.8597° E) from the Rann of Kachchh, India, a bacterial strain ADMK78<sup>T</sup>, was isolated on  
67 Zobell Marine Agar. Rann of Kachchh is reputed to be the largest salt desert in the world and is a

68 transitional area between marine and terrestrial ecosystems [11]. The region experiences  
69 diagonal fluctuations of average temperatures with a high temperature of 50 °C during summers  
70 and drops below freezing during winters. Due to the hot and hypersaline environment, there is a  
71 vast possibility of identifying novel microbes with high economic and industrial potential. The  
72 newly isolated strain ADMK78<sup>T</sup> was maintained on Zobell Marine Agar at 37 °C, and preserved  
73 at -80 °C as a suspension in 20% (v/v) glycerol and by lyophilization with 20% (w/v) skimmed  
74 milk. The pure culture was processed for MALDI-TOF MS-based identification, and a  
75 comparison of the MALDI-TOF MS spectrum of ADMK78<sup>T</sup> with the Biotyper 3.0 database  
76 resulted in no reliable identification.

#### 77 **16S RNA phylogeny:**

78 High-quality genomic DNA was extracted from the strain following the JGI protocol version 3  
79 for bacterial genomic DNA isolation using CTAB [12]. The 16S rRNA gene sequence was  
80 amplified using universal primers (27f: 5'-AGAGTTTGATCCTGGCTCAG-3' and 1492r: 5'-  
81 TACGGCTACCTTGTTACGACTT-3') according to the methods described by Gulati *et al.* [13],  
82 and the amplified product was directly sequenced using the ABI PRISM Big Dye Terminator  
83 v3.1 Cycle Sequencing kit on a 3730xl Genetic Analyzer (Applied BioSystems, Thermo  
84 Scientific, USA). The similarity search for the 16S rRNA gene sequence of strain ADMK78<sup>T</sup>  
85 was performed against the type strains of prokaryotic species in the EzBioCloud's valid species  
86 database [14]. The strain ADMK78<sup>T</sup> showed the highest similarity to *Rhizobium wuzhouense*  
87 W44<sup>T</sup> (98.7%) and followed by *Rhizobium ipomoeae* shin9-1<sup>T</sup> (97.9%). The 16S rRNA gene  
88 sequence of strain ADMK78<sup>T</sup> was used as queries to closely related gene sequences using the  
89 NCBI BLASTn tool [15] and the non-redundant nucleotide database. Higher than 99% sequence  
90 similarity was recorded for two sequences. The first one was of Alpha proteobacterium

91 (EU770254.1) associated with *Microcystis aeruginosa* culture, and the second one was of  
92 *Ciceribacter* sp. strain AIY3W (MH463946.2) isolated from low salinity lakes on Tibetan  
93 Plateau. Multiple alignments of sequences of strain ADMK78<sup>T</sup> and its nearest neighbours  
94 retrieved from EzBioCloud's server and NCBI GenBank, and phylogenetic analyses were  
95 performed using MEGA software (version 7.0) [16]. Bootstrap values were determined based on  
96 1000 replications. The 16S rRNA gene sequence of *Bradyrhizobium japonicum* USDA 6<sup>T</sup> was  
97 used as an outgroup. The strain ADMK78<sup>T</sup> formed a separate branch along with the Alpha  
98 proteobacterium and *Ciceribacter* sp. AIY3W (Fig. 1). The valid species of the genus  
99 *Ciceribacter* were placed in a distinct group, which was far from the group formed by  
100 ADMK78<sup>T</sup>, Alpha proteobacterium, and *Ciceribacter* sp. AIY3W. The overall topologies were  
101 similar for the phylogenetic trees obtained with the ML, MP and NJ methods. *Rhizobium*  
102 *ipomoeae* shin9-1<sup>T</sup> appears to be the closest phylogenetic neighbour to the group formed by  
103 ADMK78<sup>T</sup>, Alpha proteobacterium, and *Ciceribacter* sp. AIY3W in all three trees constructed  
104 by different methods.

#### 105 **Genome Features:**

106 Genome sequencing was performed using a hybrid approach of two platforms, first on an  
107 Illumina MiSeq platform with 2 x 250 bp v2 chemistry, followed by sequencing with Oxford  
108 Nanopore Technology (ONT) on a minION platform. The Nanopore reads were assembled using  
109 Canu v. 2.0 [17] with default settings. The overlaps between the ends of circular contigs were  
110 identified using NUCmer v. 3.1 [18] and removed using a custom Perl script. Two rounds of  
111 polishing was performed using the paired-end Illumina reads. In each round the Illumina reads  
112 were mapped to the genome assembly using bowtie2 v. 2.3.4.1 [19] with default parameters,  
113 followed by polishing using Pilon v. 1.23 [20] with default settings. The genome sequence

114 quality of strain ADMK78<sup>T</sup> was as per the genome standards proposed by Chun et al. [21], and  
115 the detailed genome features are provided in Table 1. The genome of ADMK78<sup>T</sup> had a size of  
116 4,342,374 bp, which is smaller than the genome size of symbiotic members of *Rhizobium* and in  
117 the range of the sizes of the non-symbiotic strains of *Rhizobium* (Table 1). It consisted of a  
118 circular chromosome of 3,590,542 bp and two circular plasmids of 708,533 and 43,299 bp. The  
119 overall genome sequencing coverage for the strain ADMK78<sup>T</sup> was 147.5x, with an N50 value of  
120 3,590,542 bp. Whole-genome sequences were annotated using the RAST [22] web server  
121 (<http://rast.nmpdr.org/rast.cgi>). The genome of strain ADMK78<sup>T</sup> contains 4377 protein-coding  
122 sequences (CDS), of which 64 genes assigned to the stress response functions, like heat and cold  
123 shock, hyperosmotic stress, and protection from reactive oxygen. We could not find any  
124 nitrogen-fixation and nodulation genes in the genome of strain ADMK78<sup>T</sup>.

125 The bacterial core gene-based phylogenetic analysis was carried out using the UBCG pipeline  
126 [23] from the concatenated sequences of 92 core genes extracted by UBCG, and a maximum-  
127 likelihood phylogenetic tree was inferred using RAxML version 8.2.8 [24] with the  
128 GTRGAMMA model and 100 bootstrap replications. The Average Nucleotide Identity (ANI)  
129 was determined between strain ADMK78<sup>T</sup> and closely related strains of the *Rhizobiaceae* family  
130 using FastANI [25], and a heatmap representation of the calculated ANI values was constructed  
131 using DisplayR (<https://www.displayr.com/>). The genome-based phylogenetic analysis placed  
132 strain ADMK78<sup>T</sup> as an independent branch, with *Rhizobium ipomoeae* shin9-1<sup>T</sup> as the closest  
133 neighbour and followed by *Rhizobium rosettiformans* W3<sup>T</sup>, *Rhizobium wuzhouense* W44<sup>T</sup> and  
134 *Rhizobium glycinendophyticum* CL12<sup>T</sup> (Fig. 2). The highest ANI values of ADMK78<sup>T</sup> was for  
135 *Rhizobium rosettiformans* W3 (82%), followed by *Rhizobium wuzhouense* W44<sup>T</sup> (81.3%) and  
136 *Rhizobium ipomoeae* shin9-1<sup>T</sup> (81%) (Fig. S1; Table 1). The dDDH relatedness values of

137 ADMK78<sup>T</sup> with the reference strains were below 22% (Table 1), suggesting the strain  
138 ADMK78<sup>T</sup> is a novel species [19]. The genomic DNA G+C content of strain ADMK78<sup>T</sup> was  
139 58.6 mol%, which is well within the range (i.e., 55-66 mol %) of the genus *Rhizobium* [4].

#### 140 **Physiology and Chemotaxonomy:**

141 The type strains of *Rhizobium ipomoeae* shin9-1<sup>T</sup> and *Ciceribacter lividus* MSSRFBL1<sup>T</sup> were  
142 obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ) and the  
143 BCCM/LMG Bacteria Collection, Belgium (LMG), respectively. Both type strains were used as  
144 reference strains and evaluated together under identical experimental conditions to those for  
145 strain ADMK78<sup>T</sup>.

146 For analysis of chemotaxonomic features, the strain was grown on Zobell Marine Agar at 28 °C,  
147 and cell biomass was harvested after 24 h. Preparation and analysis of fatty acid methyl esters  
148 were performed as described by Sasser [25] using the Microbial Identification System (MIDI)  
149 and the Microbial Identification software package (Sherlock version 6.1; MIDI database,  
150 TSBA6). The primary fatty acids detected in strain ADMK78<sup>T</sup> were C<sub>18:1 ω7c</sub> and C<sub>18:0</sub> (Table  
151 S1). Small proportions of C<sub>16:0</sub>, C<sub>18:1 ω7c</sub> 11-methyl, C<sub>18:0 3OH</sub>, C<sub>20:1 ω7c</sub>, and summed feature 2 (C<sub>12:0</sub>  
152 aldehyde) were also detected for strain ADMK78<sup>T</sup>. The strain ADMK78<sup>T</sup> exhibit higher proportions  
153 of C<sub>18:0</sub>, similar to *Ciceribacter lividus* MSSRFBL1<sup>T</sup> (Table S1), which was missing in  
154 *Rhizobium wuzhouense* W44<sup>T</sup> [26] and present in relatively lower amounts in *Rhizobium*  
155 *ipomoeae* shin9-1<sup>T</sup>. A relatively higher proportion of C<sub>18:1 ω7c</sub> 11-methyl and C<sub>20:1 ω7c</sub> in the fatty  
156 acids profile of strain ADMK78<sup>T</sup>, differentiate it from the reference strains (Table S1).

157 Whole-cell proteins were extracted using ethanol/formic acid after 24 h growth on TSA, to  
158 generate the Mean Spectral Profile (MSP). The proteins ranging from 2-20 KDa were analyzed  
159 by matrix-assisted laser desorption/ionization time-of-flight mass spectrometer (MALDI-TOF

160 MS) autoflex speed (Bruker Daltonik GmbH, Germany) [27]. A total of 27 replicate spectra were  
161 used to generate a new MSP of strain [28], which was compared with MSPs of the reference  
162 strains *Rhizobium ipomoeae* shin9-1<sup>T</sup> and *Ciceribacter lividus* MSSRFBL1<sup>T</sup> generated during  
163 this study following same procedure. The mean spectra profile of strain ADMK78<sup>T</sup> has 33  
164 unique peaks in comparison to the closely related taxa out of a total of 70 peaks (Table S2),  
165 which attributed to the discrimination of ADMK78<sup>T</sup> from the closely related species.

166 Morphological, physiological, and biochemical tests for strain ADMK78<sup>T</sup> were performed on  
167 Zobell Marine Agar plates incubated under aerobic conditions. The colonies of strain  
168 ADMK78<sup>T</sup>, were circular and translucent on Zobell Marine Agar (Fig. S3). Gram-staining (K001  
169 and K004, Himedia, India) was used following the manufacturer's instructions. Hanging drop  
170 technique was used to check the motility. Scanning electron microscopy was performed to  
171 observe cell morphology as described in Rahi *et al.* [29]. These analyses revealed that strain  
172 ADMK78<sup>T</sup> is a rod-shaped bacterium with cell size ranging from 0.3-0.5×1.5-2 μm, Gram stain  
173 negative, (Fig. S2) and non-motile. Oxidase disc (DD018, Himedia, India) was used for testing  
174 oxidase activity, and catalase activity was determined by bubble formation in a 3% (v/v) H<sub>2</sub>O<sub>2</sub>  
175 solution. The strain was positive for both oxidase and catalase. Growth at different temperatures  
176 (4, 10, 15, 20, 28, 37, 45 and 55 °C), NaCl concentrations [0-2% (w/v) at 0.5% intervals] and pH  
177 values (4.0-11.0 at 1.0 pH unit intervals) was examined after incubation in Zobell Marine broth  
178 for 7 days in automated microbial growth analyzer (Bioscreen C, OY Growth Curves, Finland).  
179 The initial pH of the inoculation broth was adjusted using 1 M HCl and 1 M NaOH. The strain  
180 ADMK78<sup>T</sup> grows at 10-45 °C (optimum 28°C), pH ranging from 4-10 (optimum 7.0), and NaCl  
181 concentration tolerance up to 2%.



182 Biochemical characteristics, enzyme activities, and oxidation/or reduction of carbon sources  
183 were performed using the API 20E and API ZYM systems (07584D and 25200, bioMérieux,  
184 France) and Biolog GN III system (OmniLog, Biolog, USA) following manufacturers'  
185 instructions. The Biolog test showed that out of the substrates present in the GENIII BIOLOG  
186 microplate, ADMK78<sup>T</sup> showed activity for 71 substrates, of which a weak reaction was recorded  
187 for four substrates (Table S3). The strain ADMK78<sup>T</sup> can be distinguished from its closest  
188 phylogenetic neighbours based on features listed in Table 2.

189 The genotypic and phenotypic data generated for the strain ADMK78<sup>T</sup> revealed that the strain  
190 represents a novel species in the genus *Rhizobium*, for which the name *Rhizobium desertarenae*  
191 sp. nov. is proposed.

192 **Description of *Rhizobium desertarenae* sp. nov.**

193 *Rhizobium desertarenae* (de.sert.a.re'nae. L. neut. n. *desertum* desert; L. fem. n. *arena* sand;  
194 N.L. gen. n. *desertarenae* of desert sand).

195 Cells are Gram-negative, straight rods with round ends (0.3-0.5×1.5-2 µm), and non-motile.  
196 Colonies grown on Zobell Marine Agar are 1-3 mm in diameter, circular, raised with an entire  
197 margin, and translucent opacity. The optimal temperature for growth is 28 °C, and the optimal  
198 pH is 7.0. Growth occurs in the absence of NaCl with up to 2% tolerance in Zobell Marine broth.  
199 It is oxidase and catalase positive. The strain showed positive results in Biolog GN III analyses  
200 for utilization of D-maltose, D-trehalose, D-cellobiose, D-gentiobiose, sucrose, D-turanose, α-  
201 D-lactose, D-melibiose, β-methyl-d-glucoside, D-salicin, N-acetyl-D-glucosamine, N- acetyl-β-  
202 D-mannosamine, N-acetyl-D-galactosamine, α-D-glucose, D-mannose, D-fructose, D-galactose,  
203 D-fucose, L-fucose, L-rhamnose, inosine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol,  
204 glycerol, D-glucose-6-phosphate, D-fructose-6-phosphate, D-aspartic acid, Glycyl-L-proline,

205 glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-  
206 pyroglutamic acid, L-serine, pectin, D-galacturonic acid, D-gluconic acid, D-glucuronic acid,  
207 glucuronamide, mucic acid, D-saccharic acid, p-hydroxy-phenylacetic acid, D-lactic acid methyl  
208 ester, L-lactic acid, citric acid,  $\alpha$ -keto-glutaric acid, D,L-malic acid, bromo-succinic acid,  
209 Tween 40,  $\gamma$ -amino-butyric acid,  $\alpha$ -hydroxy-butyric acid,  $\alpha$ -hydroxy-D,L butyric acid,  $\alpha$ -keto-  
210 butyric acid, acetoacetic acid, propionic acid, acetic acid, formic acid, sodium lactate,  
211 tetrazolium violet and blue, nalidixic acid, lithium chloride (Table S3). Positive results in API  
212 ZYM strips for leucine arylamidase, trypsin, naphthol-AS-BI-phosphohydrolase,  $\alpha$ -glucosidase,  
213 N-acetyl- $\beta$ -glucosaminidase activities (Table S4). C<sub>18:0</sub> and C<sub>18:1  $\omega$ 7c</sub> are the predominant cellular  
214 fatty acids. The DNA G+C content of the type strain is 58.6 mol%.

215 The type strain ADMK78<sup>T</sup> (=MCC 3400<sup>T</sup>; KACC 21383<sup>T</sup>; JCM 33657<sup>T</sup>) was isolated from  
216 saline desert sand collected from the Kutch District of Gujarat, India. The GenBank sequence  
217 accession number of the genome sequence is CP058350- CP058352, and 16S rRNA gene  
218 sequence of strain ADMK78<sup>T</sup> is MK942856.

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226 name, species epithet and Latin etymology.

#### 227 **Conflicts of Interest:**

228 The authors declare that there are no conflicts of interest.

229 **Ethical Statement:**

230 The experiments reported in this manuscript did not involve human participants and/or animals.

231 **ABBREVIATIONS:**

232 CDS= coding sequence, CTAB= Cetyl trimethylammonium bromide; MALDI-TOF MS=  
233 Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometer; MSP= Mean  
234 Spectral Profile; UBCG= Up-to-date bacterial core genes.

235

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319 **Figure legends:**

320 **Fig. 1:** Phylogenetic tree was inferred by using the Maximum Likelihood method and Tamura-  
321 Nei model. The percentage of trees in which the associated taxa clustered together is shown next  
322 to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying  
323 Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the  
324 Tamura-Nei model, and then selecting the topology with superior log likelihood value. Empty  
325 circles indicate branches of the tree that were also recovered using the neighbour-joining method,  
326 circles with dots indicate recovery with the maximum-parsimony method, and black filled circles  
327 indicate that all three methods recovered the corresponding nodes. *Bradyrhizobium japonicum*  
328 USDA 6<sup>T</sup> (D11345) was used as an outgroup. Bar, 0.1 substitutions per nucleotide position.

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331 **Fig. 2:** Phylogenetic tree inferred by the UBCG phylogenomics pipeline using the concatenated  
332 alignment of 92 core genes, of strain ADMK78<sup>T</sup> and its closely related taxa. Percentage of  
333 bootstrap values are given at branching points. Bar, 0.05 substitution per position.

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352 **Table 1:** Standard genome features of strain ADMK78<sup>T</sup> and related type strains of the family *Rhizobiaceae*

Strain (GenBank accession numbers)	Genome size (Mbp)	Total contigs (nos.)	DNA G+C content (mol%)	N50 (kb)	Genome coverage	Genome ANI with ADMK78 <sup>T</sup> (%)	dDDH relatedness with ADMK78 <sup>T</sup> (%)	Difference in G+C content (%)
ADMK78 <sup>T</sup> (CP058350-CP058352)	4.31	03	58.6	3,590	147.5x	100.0	100	0
<i>Rhizobium wuzhouense</i> W44 (NZ_QJRY01000001)	4.93	32	61.6	493	277.4x	81.3	22.0	3.0
<i>Rhizobium rosettiformans</i> W3(NZ_STGU00000000)	4.98	86	61.7	288	200.0x	82.0	22.0	3.03
<i>Rhizobium glycinendophyticum</i> CL12(NZ_VFYP00000000)	4.84	16	61.1	2,995	206.0x	81.2	21.8	2.45
<i>Rhizobium ipomoeae</i> shin9-1 (NZ_STGV00000000)	4.39	23	60.0	535	200.0x	81.0	21.6	1.78
<i>Rhizobium selenitireducens</i> ATCC BAA-1503 (JAE00000000)	4.98	32	63.5	-	Unknown	79.9	20.7	4.88
<i>Rhizobium subbaraonis</i> JC85(NZ_OBQD00000000)	6.58	91	63.1	255	153x	78.8	20.7	4.44
<i>Ciceribacter lividus</i> DSM 25528 (NZ_QPIX00000000)	4.52	37	63.2	302	226.0x	79.2	20.2	4.58
<i>Rhizobium endolithicum</i> JC140 (NZ_CABFWF00000000)	4.18	62	62.7	206	64x	79.0	20.2	4.11
<i>Rhizobium sophoriradicis</i> CCBAU 03470(RQIH00000000)	6.67	-	61.3	-	170x	78.70	20.1	2.65
<i>Rhizobium leguminosarum</i> USDA 2370 (QBLB00000000)	7.66	108	60.8	-	50.0x	78.50	19.8	1.95

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357 **Table 2.** Differentiating characteristics of strain ADMK78<sup>T</sup> in comparison to its closest  
 358 phylogenetic neighbours.  
 359 strain 1, *Rhizobium* sp. ADMK78<sup>T</sup>; 2, *Rhizobium wuzhouense* W44<sup>T</sup>; 3, *Rhizobium ipomoeae* sp.  
 360 shin9-1<sup>T</sup>; 4, *Ciceribacter lividus* MSSRFBL1<sup>T</sup>

Characteristics	1	2*	3	4
Isolation source	Saline soil (Desert)	Roots of <i>Oryza officinalis</i>	Field	Rhizosphere soil of chickpea
Colony colour	Cream	Cream	Cream	Bluish black
pH range for growth	4.0-11(7)	5-8	7.0-9.0(7)	6.0-8.5(7)
Temperature range for growth (°C) (optimum)	10-45 (28)	15-40	10-45 (30)	10-45 (28)
NaCl range for growth (%) (optimum)	0-2.0 (1.5)	0-2.0	0-3.0 (1.5)	0.5-1.5 (1)
D-raffinose	-	+	-	+
rifamycin sv	-	-	+	+
Gelatin	-	+	-	-
L-arginine	+	-	+	+
β-galactosidase	-	+	+	-
glucosidase	-	ND	+	-
DNA G+C content (mol%)	58.6	61.6	60.0	63.2

361 \*Data from Tao Yuan et al., [27]

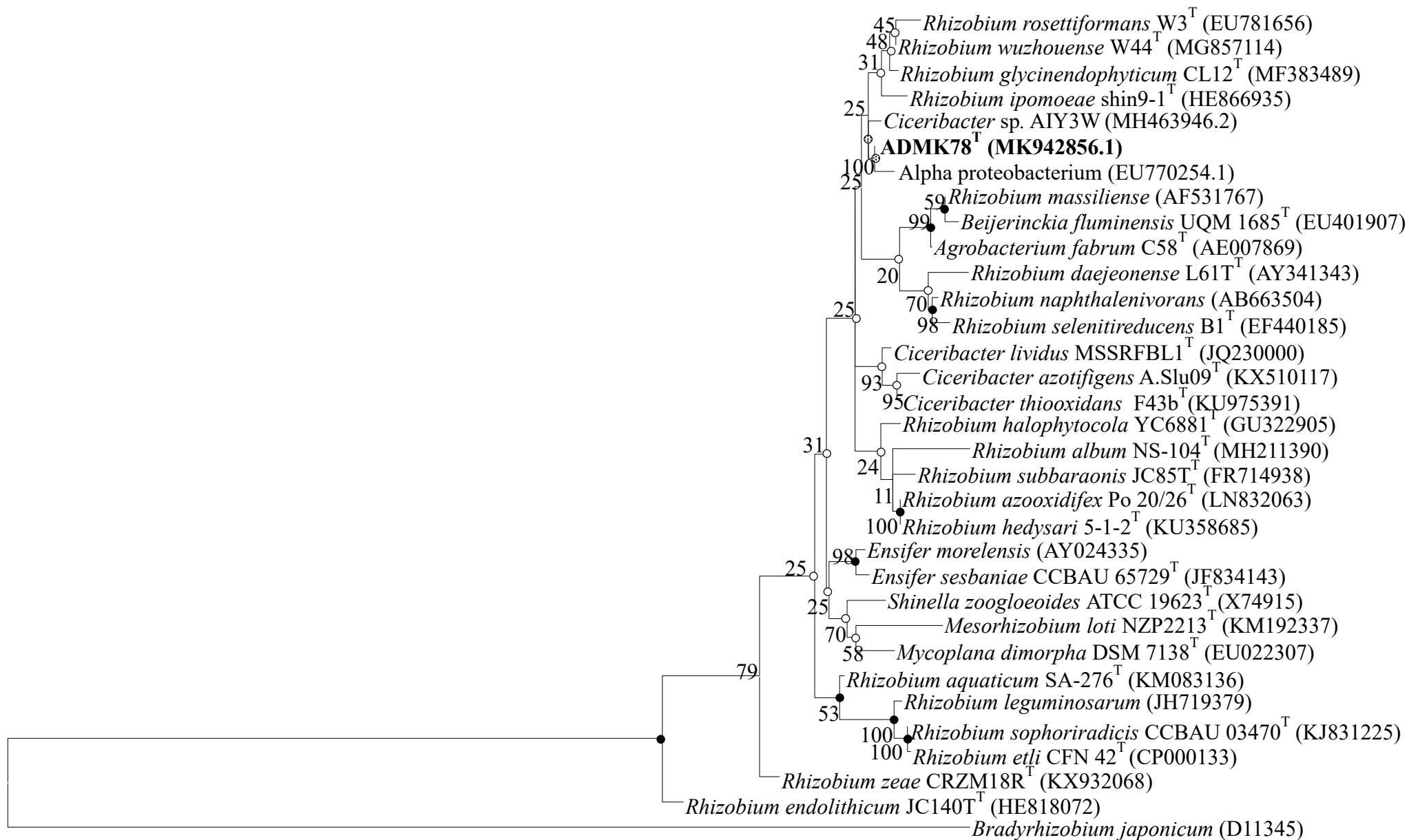
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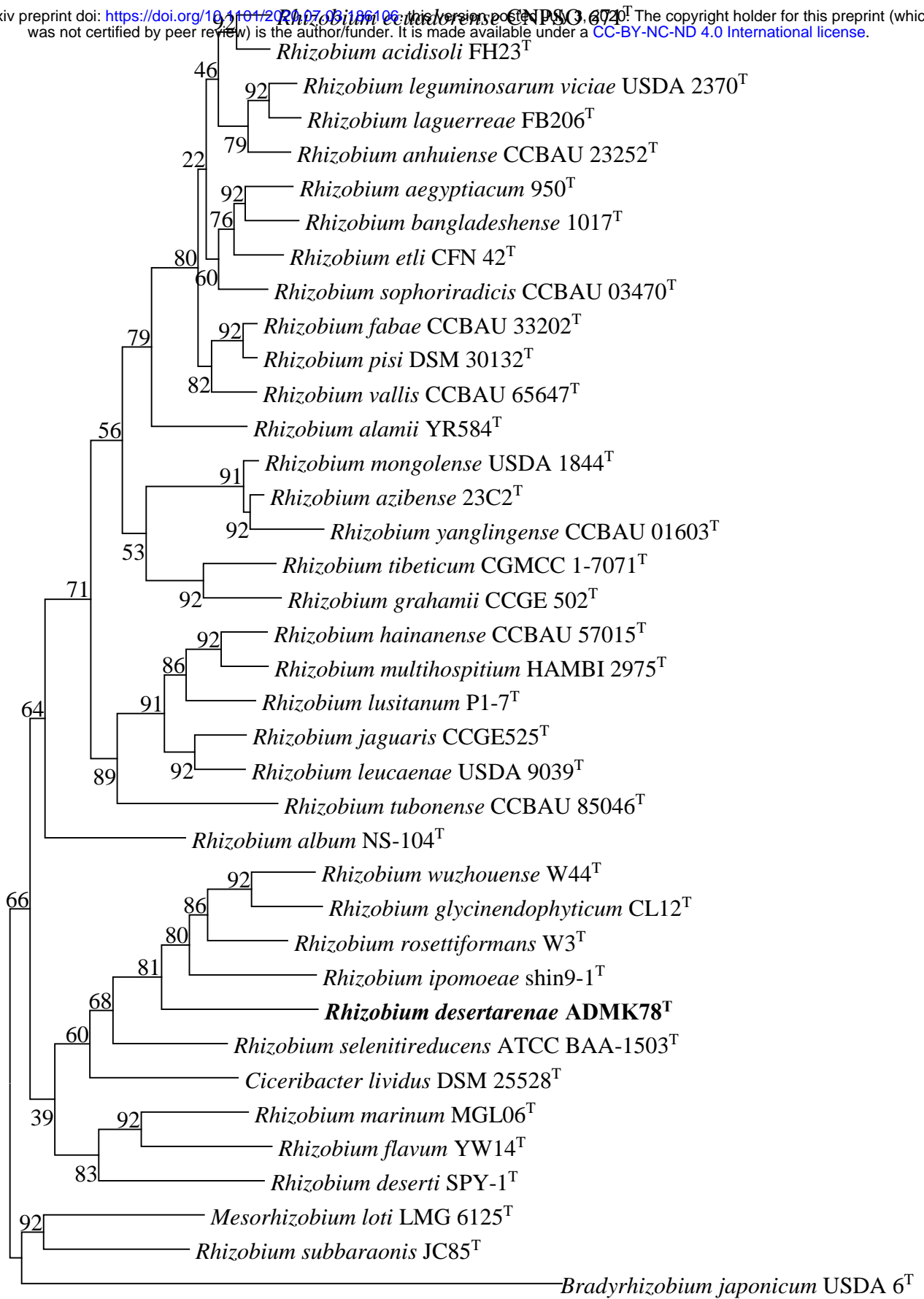
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