Table S1 The genome used in comparative genomic analysis of *A. indica Bradyrhizobium*

Aeschynomene indica *Bradyrhizobium*	Non-*Aeschynomene indica* symbiotic *Bradyrhizobium*	Non-symbiotic *Bradyrhizobium*
B. denitrificans LMG8443	*B. arachidis* LMG 26795	*B. betae* PL7HG1
B. oligotrophicum S58	*B. cytisi* CTAW11	*Bradyrhizobium* sp. AT1
Bradyrhizobium sp. DOA9	*B. daqingense* CGMCC 1.10947	*Bradyrhizobium* sp. BF49
Bradyrhizobium sp. ORS 278	*B. diazoefficiens* USDA 110	*Bradyrhizobium* sp. G22
Bradyrhizobium sp. ORS 285	*B. elkanii* USDA 76	*Bradyrhizobium* sp. LTSP849
Bradyrhizobium sp. I 82044	*B. embrapense* SEMIA 6208	*Bradyrhizobium* sp. LTSP857
Bradyrhizobium sp. I 82054	*B. guangdongense* CCBAU 51649	*Bradyrhizobium* sp. LTSP885
Bradyrhizobium sp. II 80013	*B. guangxiense* CCBAU53363	*Bradyrhizobium* sp. LTSPM299
Bradyrhizobium sp. III 80001	*B. icense* LMTR 13	*Bradyrhizobium* sp. OK095
Bradyrhizobium sp. IV 81033	*B. japonicum* USDA 6	*Bradyrhizobium* sp. S23321
Bradyrhizobium sp. V 80016	*B. jicamae* PAC68	*Bradyrhizobium* sp. URHA0002
Bradyrhizobium sp. V 80022	*B. lablabi* CCBAU 23086	*Bradyrhizobium* sp. YR681
Bradyrhizobium sp. V 80029	*B. liaoningense* CCBAU05525	
Bradyrhizobium sp. VI	*B. manausense* BR 3351	

80004

Bradyrhizobium sp. VII

81001 *B. mercantei* SEMIA 6399

Bradyrhizobium sp. VII

81035 *B. neotropicale* BR 10247

Bradyrhizobium sp. VII

82079 *B. ottawaense* OO99

Bradyrhizobium sp. VII

82084 *B. stylosanthis* BR 446

Bradyrhizobium sp. VIII

81003 *B. viridifuturi* SEMIA 690

Bradyrhizobium sp. VIII

81013 *B. yuanmingense* CCBAU 10071

Bradyrhizobium sp. VIII

83002

Bradyrhizobium sp. VIII

83012

B. denitrificans 80025

B. oligotrophicum 80005

Table S2 The gains and losses of gene families of different nodes:

Species tree node	Number of Gene Acquisition	Number of Gene Loss	Species tree node	Number of Gene Acquisition	Number of Gene Loss
B. arachidis LMG 26795^T	1325	40`	N1	1072	0
B. betae PL7HG1^T	795	131	N10	750	31
B. cytisi CTAW11^T	1577	71	N11	350	90
B. daqingense CGMCC1.10947^T	1394	59	N12	113	19
B. denitrificans 80005	232	4	N13	52	7
B. diazoefficiens USDA110^T	1561	23	N14	186	4
B. elkanii USDA76^T	1695	16	N15	104	11
B. embrapense SEMIA6208^T	1084	42	N16	1132	75
B. guangdongense CCBAU51649^T	1261	85	N17	548	27
B. guangxiense CCBAU53363^T	1351	51	N18	990	57
B. icense LMTR13^T	1064	112	N19	227	16
B. japonicum USDA6^T	853	18	N2	310	0
B. jicamae PAC68^T	778	21	N20	141	19
B. lablabi CCBAU23086^T	937	24	N21	877	11
B. liaoningense CCBAU05525^T	1210	104	N22	153	24
B. manausense BR3351^T	1317	160	N23	71	41
B. mercantei SEMIA6399^T	721	96	N24	713	13
B. neotropicale BR10247^T	1927	25	N25	188	13
B. oligotrophicum 80025	514	4	N26	785	11
B. denitrificans LMG8443^T	280	3	N27	1622	28
B. oligotrophicum S58^T	275	3	N28	300	27
B. ottawaense OO99^T	1192	47	N29	236	4
B. stylosanthis BR446^T	969	20	N3	989	0
B. viridifuturi SEMIA690^T	1084	43	N30	59	13
B. yuanmingense CCBAU10071^T	979	51	N31	219	25
Bradyrhizobium sp. AT1	669	117	N32	251	37
Bradyrhizobium sp. BF49	946	131	N33	226	16
Bradyrhizobium sp. DOA9	790	66	N34	53	2
Bradyrhizobium sp. G22	590	26	N35	436	5
Bradyrhizobium sp. I 82044	115	12	N36	386	19
Bradyrhizobium sp. I 82054	101	11	N37	563	0
Bradyrhizobium sp. Ⅱ 80013	1047	309	N38	131	57
Bradyrhizobium sp. Ⅲ 80001	667	104	N39	356	0
Bradyrhizobium sp. IV 81033	199	1	N4	257	0
Bradyrhizobium sp. LTSP849	218	6	N40	109	43
Bradyrhizobium sp. LTSP857	200	5	N41	337	19
Bradyrhizobium sp. LTSPM299	828	10	N42	34	0
Bradyrhizobium sp. LTSPM885	344	43	N43	385	3

Bradyrhizobium sp. OK095	719	33	N44	293	10
Bradyrhizobium sp. ORS 278	647	96	N45	110	86
Bradyrhizobium sp. ORS 285	580	27	N46	1197	18
Bradyrhizobium sp. S23321	734	24	N47	212	84
Bradyrhizobium sp. URHA0002	1083	140	N48	793	0
Bradyrhizobium sp. V 80016	110	1	N49	270	8
Bradyrhizobium sp. V 80022	162	2	N5	166	0
Bradyrhizobium sp. V 80029	205	0	N50	79	74
Bradyrhizobium sp. VI 80004	574	9	N51	375	22
Bradyrhizobium sp. VⅡ 81001	416	1190	N52	524	37
Bradyrhizobium sp. VⅡ 81035	548	21	N53	320	54
Bradyrhizobium sp. VⅡ 82079	174	8	N54	550	193
Bradyrhizobium sp. VⅡ 82084	247	5	N6	701	0
Bradyrhizobium sp. VⅢ 81003	626	42	N7	541	7
Bradyrhizobium sp. VⅢ 81013	194	4	N8	1162	28
Bradyrhizobium sp. VⅢ 83002	240	2	N9	137	17
Bradyrhizobium sp. VⅢ 83012	273	4			
Bradyrhizobium sp. YR681	834	31			

Table S3 Enrichment and analysis of homologous gene family difference gene KEGG in *A. indica Bradyrhizobium* and reference strain

Taxa	Same metabolic pathways	Differential metabolic pathways
Aeschynomene indica Bradyrhizobium	2-Oxocarboxylic acid metabolism，ABC transporters，Adipocytokine signaling pathway，Alanine, aspartate and glutamate metabolism，Alcoholism，Amino sugar and nucleotide sugar metabolism，Aminoacyl-tRNA biosynthesis，Aminobenzoate degradation，Amphetamine addiction，Arginine and proline metabolism，Arginine biosynthesis，Ascorbate and aldarate metabolism，Atrazine degradation，Bacterial chemotaxis，Bacterial secretion system，Base excision repair，Benzoate degradation，beta-Alanine metabolism，beta-Lactam resistance，Biofilm formation - Escherichia coli，Biofilm formation - Pseudomonas aeruginosa，Biofilm formation - Vibrio cholerae，Biosynthesis of amino acids，Biosynthesis of secondary metabolites，Biosynthesis of unsaturated fatty acids，Biotin metabolism，Butanoate metabolism，C5-Branched dibasic acid metabolism，Caprolactam degradation，Carbon fixation in photosynthetic organisms，Carbon fixation pathways in prokaryotes，Carbon metabolism，Cationic antimicrobial peptide (CAMP) resistance，Cell cycle - Caulobacter，Chemical carcinogenesis，Chloroalkane and chloroalkene degradation，Chlorocyclohexane and chlorobenzene degradation，Citrate cycle (TCA cycle)，Cocaine addiction，Cysteine and methionine metabolism，Degradation of aromatic compounds，Dioxin degradation，Dopaminergic synapse，Drug metabolism - cytochrome P450，Drug metabolism - other enzymes，Epithelial cell signaling in Helicobacter pylori infection，Ether lipid metabolism，Fat digestion and absorption，Fatty acid biosynthesis，Fatty acid degradation，Fatty acid metabolism，Ferroptosis，Flagellar assembly，Fluid shear stress and atherosclerosis，Folate biosynthesis，Fructose and mannose metabolism，GABAergic synapse，Galactose metabolism，Geraniol degradation，Glucosinolate biosynthesis，Glutamatergic synapse，Glutathione	Bacterial invasion of epithelial cells，Biosynthesis of ansamycins，Biosynthesis of enediyne antibiotics，Carotenoid biosynthesis，Cushing syndrome，Ethylbenzene degradation，NOD-like receptor signaling pathway，Other types of O-glycan biosynthesis，Photosynthesis，Plant-pathogen interaction，Polyketide sugar unit biosynthesis，Protein export，Renal cell carcinoma，Ribosome biogenesis in eukaryotes，Sphingolipid metabolism，Staphylococcus aureus infection
the reference strain of *Bradyrhizobium*		Alzheimer disease，Amoebiasis，AMPK signaling pathway，Amyotrophic lateral sclerosis (ALS)，Antifolate resistance，Apoptosis，Apoptosis - fly，Apoptosis - multiple species，Arabinogalactan biosynthesis - Mycobacterium，Biosynthesis of siderophore group nonribosomal peptides，Biosynthesis of various secondary metabolites - part 2，Caffeine metabolism，Carbohydrate digestion and absorption，Central carbon metabolism in cancer，Cholesterol metabolism，Colorectal cancer，Cyanoamino acid metabolism，D-Alanine metabolism，D-Arginine and D-ornithine metabolism，D-Glutamine and D-glutamate metabolism，DNA replication，Epstein-Barr virus infection，Fluorobenzoate degradation，FoxO signaling pathway，Furfural degradation，Glucagon signaling pathway，Hepatitis B，Hepatitis C，Herpes simplex virus 1 infection，Homologous recombination，Human cytomegalovirus infection，Human immunodeficiency virus 1 infection，Human T-cell leukemia virus 1 infection，Huntington disease，Influenza A，Kaposi sarcoma-associated herpesvirus infection，Lipoic acid metabolism，Longevity regulating pathway，MAPK signaling pathway - plant，MAPK signaling pathway - yeast，Measles，MicroRNAs in cancer，Monobactam biosynthesis，Neomycin, kanamycin and gentamicin biosynthesis，Neuroactive ligand-

	metabolism，Glycerolipid metabolism，Glycerophospholipid metabolism，Glycine, serine and threonine metabolism，Glycolysis / Gluconeogenesis，Glyoxylate and dicarboxylate metabolism，Hepatocellular carcinoma，HIF-1 signaling pathway，Histidine metabolism，Inositol phosphate metabolism，Insect hormone biosynthesis，Insulin resistance，Isoquinoline alkaloid biosynthesis，Legionellosis，Limonene and pinene degradation，Lipopolysaccharide biosynthesis，Longevity regulating pathway - multiple species，Longevity regulating pathway - worm，Lysine biosynthesis，Lysine degradation，Meiosis - yeast，Metabolic pathways，Metabolism of xenobiotics by cytochrome P450，Methane metabolism，Microbial metabolism in diverse environments，Mismatch repair，Naphthalene degradation，Necroptosis，Nicotinate and nicotinamide metabolism，Nitrogen metabolism，Nitrotoluene degradation，Non-homologous end-joining，Novobiocin biosynthesis，One carbon pool by folate，Oxidative phosphorylation，Pantothenate and CoA biosynthesis，Pathways in cancer，Pentose and glucuronate interconversions，Pentose phosphate pathway，Peptidoglycan biosynthesis，Peroxisome，Phenylalanine metabolism，Phenylalanine, tyrosine and tryptophan biosynthesis，Platinum drug resistance，Polycyclic aromatic hydrocarbon degradation，Porphyrin and chlorophyll metabolism，PPAR signaling pathway，Prodigiosin biosynthesis，Propanoate metabolism，Protein processing in endoplasmic reticulum，Purine metabolism，Pyrimidine metabolism，Pyruvate metabolism，Quorum sensing，Retinol metabolism，Riboflavin metabolism，RNA degradation，Salmonella infection，Secondary bile acid biosynthesis，Selenocompound metabolism，Serotonergic synapse，Shigellosis，Starch and sucrose metabolism，Steroid hormone biosynthesis，Streptomycin biosynthesis，Styrene degradation，Sulfur metabolism，Sulfur relay system，Synthesis and degradation of ketone bodies，	receptor interaction，N-Glycan biosynthesis，Non-alcoholic fatty liver disease (NAFLD)，Other glycan degradation，p53 signaling pathway，Pancreatic secretion，Parkinson disease，Pathogenic Escherichia coli infection，Pertussis，Phenazine biosynthesis，Phosphatidylinositol signaling system，Phosphonate and phosphinate metabolism，Primary bile acid biosynthesis，Proximal tubule bicarbonate reclamation，RNA transport，Small cell lung cancer，Steroid degradation，Thiamine metabolism，Toxoplasmosis，Ubiquinone and other terpenoid-quinone biosynthesis，Vancomycin resistance，Vibrio cholerae infection，Viral myocarditis，Vitamin B6 metabolism

	Taurine and hypotaurine metabolism，Terpenoid backbone biosynthesis，Thermogenesis，Thyroid hormone signaling pathway，Toluene degradation，Tropane, piperidine and pyridine alkaloid biosynthesis，Tryptophan metabolism，Tuberculosis，Two-component system，Tyrosine metabolism，Valine, leucine and isoleucine biosynthesis，Valine, leucine and isoleucine degradation，Xylene degradation	