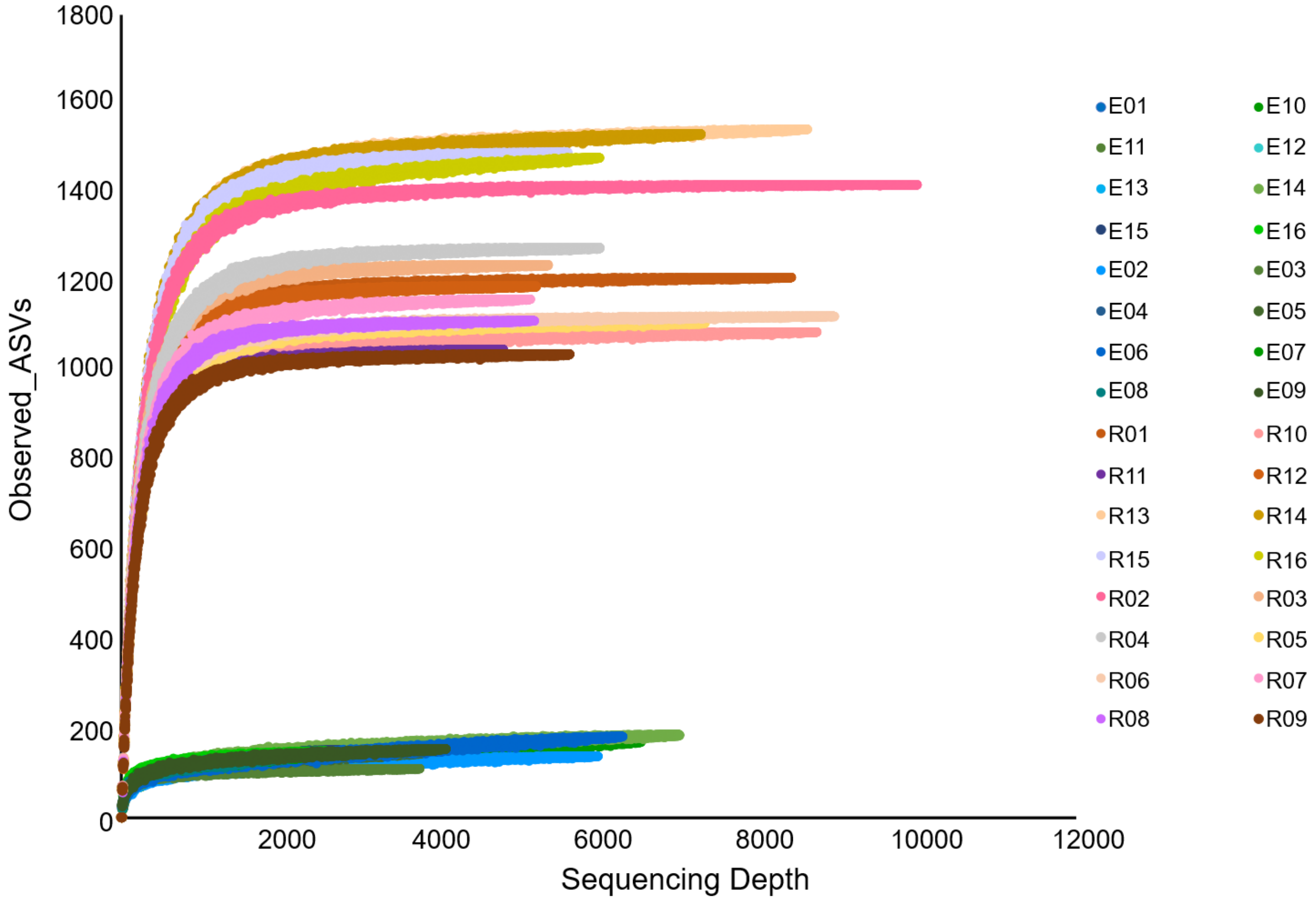

Figure S1 Rarefaction curves of 16 individual *A. sparsifolia* plants per plant compartment. Rarefaction curves were generated showing the number of amplicon sequence variant (ASVs). R01−16 represent rhizosphere samples and E01−16 represent root endosphere samples.

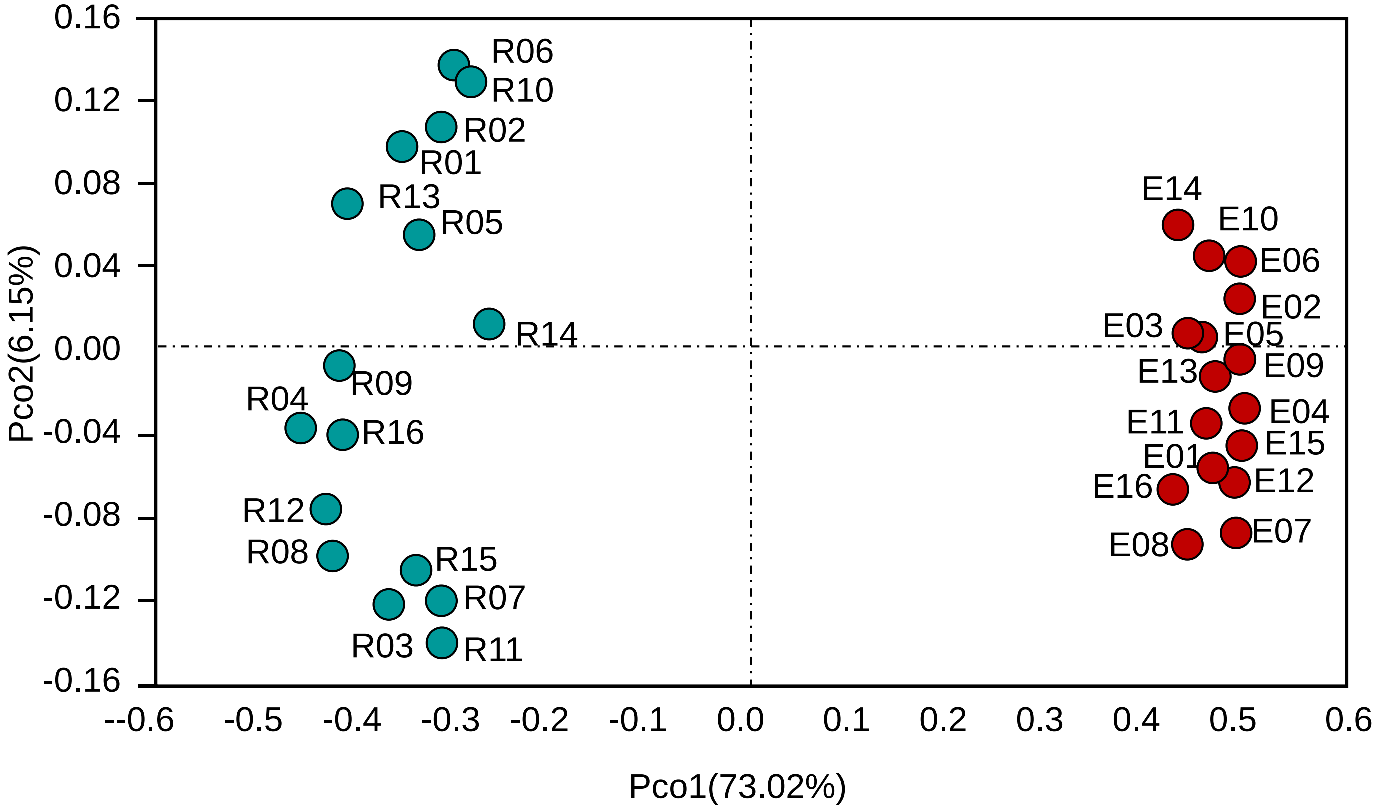

Figure S2 Similarity of the rhizosphere and endosphere samples based on ASVs composition. Principal coordinate analysis (PCoA) was performed based on Bray-Curtis method.

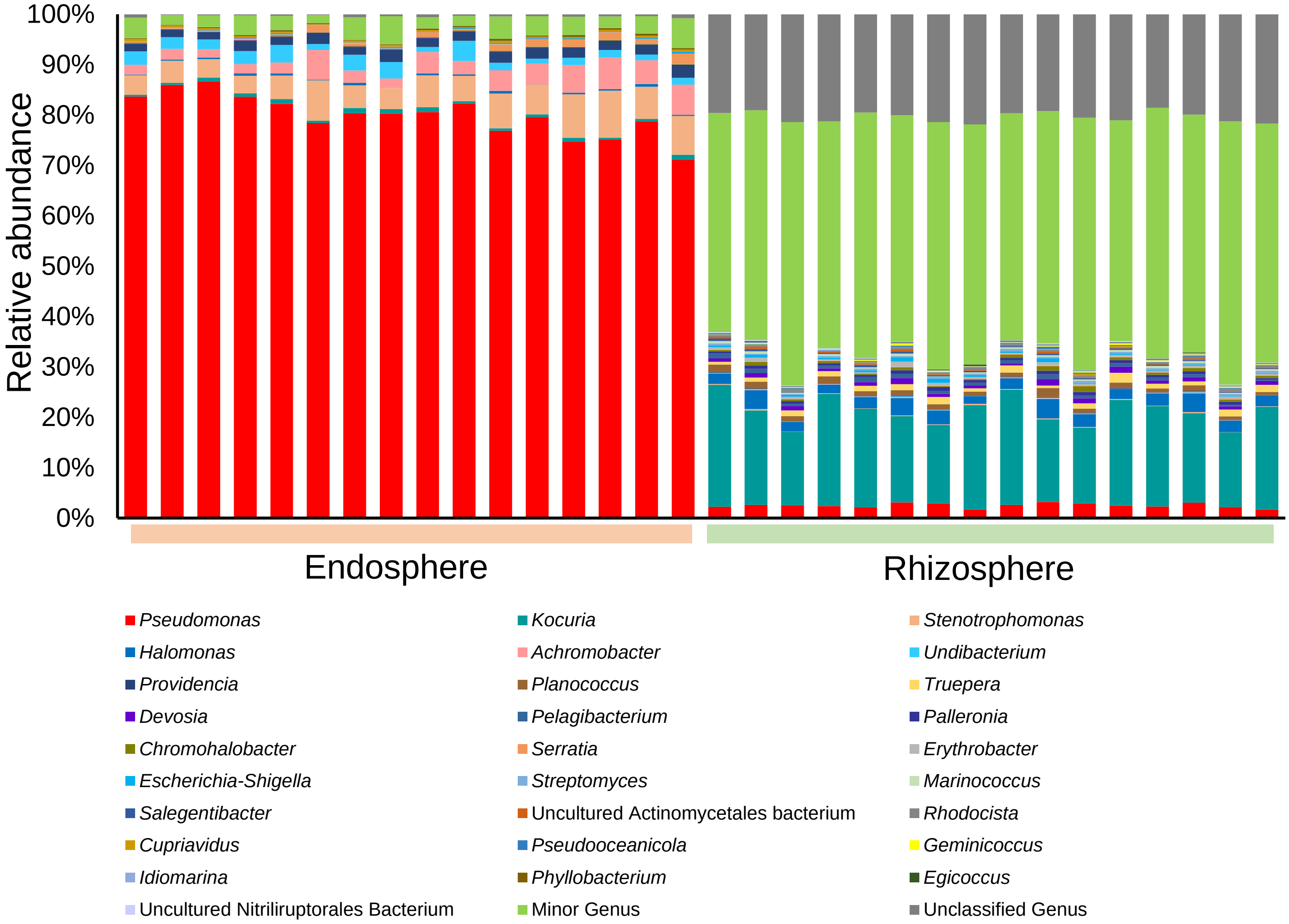

Figure S3 Comparison of the microbial community composition at the genus level between different samples. The 30 most abundant genera are listed while other genera are grouped together as "Minor genus", and their cumulative abundances are listed. Total relative abundances of the genera and differences between the rhizosphere and endosphere are listed in Table S4.

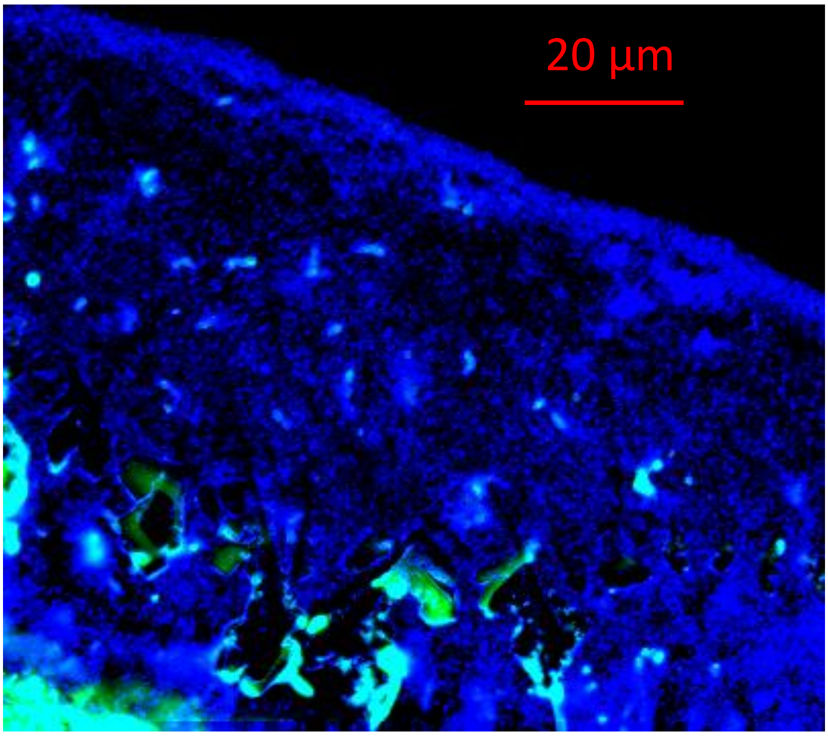

Figure S4 Confocal micrograph of the section of wheat root. Green: *Pseudomonas* sp. LTGT-11-2Z; Blue: root cells.

Table S1 Information of 16S rRNA gene amplicon sequences.

Sample	**Dataset**	**Total number of reads**	**Total number of high-quality reads**	**Percentage of high-quality reads**	**High-quality reads after assembly and removal of chloroplast and mitochondrion**
R01	LTCT-1-1	259,440	229,013	88.27%	198,262
	LTCT-1-2	259,440	229,013	88.27%	
R02	LTCT-2-1	267,571	243,452	90.99%	218,496
	LTCT-2-2	267,571	243,452	90.99%	
R03	LTCT-3-1	203,654	185,355	91.01%	167,811
	LTCT-3-2	203,654	185,355	91.01%	
R04	LTCT-4-1	244,911	227,494	92.89%	210,218
	LTCT-4-2	244,911	227,494	92.89%	
R05	LTCT-5-1	245,133	215,321	87.84%	187,872
	LTCT-5-2	245,133	215,321	87.84%	
R06	LTCT-6-1	213,070	193,275	90.71%	173,993
	LTCT-6-2	213,070	193,275	90.71%	
R07	LTCT-7-1	230,009	210,474	91.51%	191,462
	LTCT-7-2	230,009	210,474	91.51%	
R08	LTCT-8-1	195,274	180,844	92.61%	166,772
	LTCT-8-2	195,274	180,844	92.61%	
R09	LTCT-9-1	241,266	212,151	87.93%	183,611
	LTCT-9-2	241,266	212,151	87.93%	
R10	LTCT-10-1	224,643	204,821	91.18%	184,057
	LTCT-10-2	224,643	204,821	91.18%	
R11	LTCT-11-1	198,239	180,157	90.88%	162,459
	LTCT-11-2	198,239	180,157	90.88%	
R12	LTCT-12-1	228,477	212,622	93.06%	196,702
	LTCT-12-2	228,477	212,622	93.06%	

R13	LTCT-13-1	291,814	255,874	87.68%	220,248
	LTCT-13-2	291,814	255,874	87.68%	
R14	LTCT-14-1	265,672	240,461	90.51%	214,224
	LTCT-14-2	265,672	240,461	90.51%	
R15	LTCT-15-1	248,288	223,175	89.89%	200,153
	LTCT-15-2	248,288	223,175	89.89%	
R16	LTCT-16-1	227,716	210,857	92.60%	194,084
	LTCT-16-2	227,716	210,857	92.60%	
E01	LTCG-1-1	191,996	165,992	86.46%	123,848
	LTCG-1-2	191,996	165,992	86.46%	
E02	LTCG-2-1	163,832	146,658	89.52%	119,295
	LTCG-2-2	163,832	146,658	89.52%	
E03	LTCG-3-1	150,272	150,272	90.42%	113,513
	LTCG-3-2	150,272	150,272	90.42%	
E04	LTCG-4-1	170,136	155,555	91.43%	129,254
	LTCG-4-2	170,136	155,555	91.43%	
E05	LTCG-5-1	209,945	180,676	86.06%	125,833
	LTCG-5-2	209,945	180,676	86.06%	
E06	LTCG-6-1	189,371	169,340	89.42%	136,394
	LTCG-6-2	189,371	169,340	89.42%	
E07	LTCG-7-1	168,345	151,421	89.95%	125,292
	LTCG-7-2	168,345	151,421	89.95%	
E08	LTCG-8-1	149,507	137,396	91.90%	112,844
	LTCG-8-2	149,507	137,396	91.90%	
E09	LTCG-9-1	206,122	179,754	87.21%	117,370
	LTCG-9-2	206,122	179,754	87.21%	
E10	LTCG-10-1	184,289	164,671	89.35%	127,303
	LTCG-10-2	184,289	164,671	89.35%	
E11	LTCG-11-1	169,008	152,135	90.02%	125,858
	LTCG-11-2	169,008	152,135	90.02%	

E12	LTCG-12-1	173,109	158,237	91.41%	125,305
	LTCG-12-2	173,109	158,237	91.41%	
E13	LTCG-13-1	207,974	180,854	86.96%	116,804
	LTCG-13-2	207,974	180,854	86.96%	
E14	LTCG-14-1	203,749	203,749	89.39%	142,586
	LTCG-14-2	203,749	203,749	89.39%	
E15	LTCG-15-1	150,123	136,280	90.78%	115,087
	LTCG-15-2	150,123	136,280	90.78%	
E16	LTCG-16-1	159,298	145,618	91.41%	113,608
	LTCG-16-2	159,298	145,618	91.41%	

Table S2 Community richness and diversity estimates based on ASVs cluster. Values represent averages (± standard deviation) of 16 biological replicates per sample. Significant differences in the variance of root rhizosphere and endosphere were evaluated with two-tailed Student’s t-test.

Richness and diversity indices	**Rhizosphere**	**Endosphere**	***P***
Chao1	1277.440±197.639	233.244±208.502	2.05191E-16
ACE	1258.870±181.802	180.653±62.653	5.81710E-22
Observed ASVs	1219.190±165.383	130.875±11.887	4.71400E-24
Shannon_H	6.559±0.136	3.179±0.137	1.95673E-37
Simpson	0.996±0.001	0.929±0.010	1.05080E-23

Table S3 16S rRNA gene sequences assigned at the phylum level. Values represent the average relative % abundance of ASVs among the 16 *A. sparsifolia* plants and the standard deviations (SDs). Intergroup significant differences were evaluated with two-tailed Student's t-test, and the *P* values were adjusted by Benjamini-Hochberg correction.

Phyla	**Rhizosphere**		**Endosphere**		***P***
	% abundance of ASVs	**SD (%)**	**% abundance of ASVs**	**SD (%)**	
Alphaproteobacteria	16.337	1.589	1.651	0.659	1.41275E-25
Deltaproteobacteria	3.239	0.654	0.003	0.001	9.27629E-19
Gammaproteobacteria	16.107	2.000	96.390	1.214	1.51293E-43
Unclassified Proteobacteria	0.001	0.005	0.012	0.013	0.00582213
Acidobacteria	0.338	0.191	0.000	0.000	7.57978E-08
Actinobacteria	33.442	2.782	0.893	0.331	1.64342E-29
Armatimonadetes	0.012	0.024	0.016	0.042	0.743493456
Bacteroidetes	9.777	0.870	0.367	0.153	2.11343E-28
BRC1	0.149	0.115	0.000	0.000	1.36041E-05
Chlamydiae	0.043	0.063	0.000	0.000	0.010511692
Chloroflexi	1.721	0.567	0.000	0.000	4.17927E-13
Cyanobacteria	0.245	0.142	0.004	0.013	1.87796E-07
Deinococcus_Thermus	1.243	0.400	0.003	0.008	2.50466E-13
Elusimicrobia	0.003	0.013	0.000	0.000	0.325308615
Euryarchaeota	0.112	0.126	0.000	0.000	0.001236066
FBP	0.013	0.041	0.000	0.000	0.218933142
Firmicutes	9.588	1.305	0.619	0.274	1.45377E-22
Fusobacteria	0.006	0.017	0.031	0.045	0.041914524
Gemmatimonadetes	2.661	0.553	0.003	0.008	2.06821E-18
Hydrogenedentes	0.008	0.030	0.000	0.000	0.32538615
Nitrospirae	0.034	0.048	0.000	0.000	0.008453303
Patescibacteria	1.790	0.562	0.000	0.000	1.23912E-13
Planctomycetes	2.373	1.332	0.000	0.000	6.31656E-08
Tenericutes	0.001	0.002	0.000	0.000	0.325308615

Verrucomicrobia	0.624	0.471	0.000	0.000	1.00453E-05
WPS_2	0.012	0.025	0.000	0.000	0.067206089
WS2	0.013	0.053	0.000	0.000	0.325308615
Unclassified Phylum	0.110	0.142	0.008	0.012	0.007732887

Table S4 16S rRNA gene sequences assigned at the genus level. Values represent the average relative % abundance of ASVs among the 16 *A. sparsifolia* plants and the standard deviations (SDs). Intergroup significant differences were evaluated with two-tailed Student's t-test, and the *P* values were adjusted by Benjamini-Hochberg correction.

Genera	**Rhizosphere**		**Endosphere**		***P***
	% abundance of ASVs	**SD (%)**	**% abundance of ASVs**	**SD (%)**	
Pseudomonas	2.504	0.456	80.000	4.198	2.03422E-35
Kocuria	18.802	3.036	0.677	0.248	4.95807E-21
Stenotrophomonas	0.1483	0.0718	5.816	1.879	4.92752E-13
Halomonas	2.545	0.737	0.306	0.179	8.26989E-13
Achromobacter	0.087	0.048	3.589	1.687	2.93418E-09
Undibacterium	0.075	0.064	2.099	0.979	3.25616E-09
Providencia	0.087	0.041	1.912	0.358	4.76316E-19
Planococcus	1.050	0.332	0.009	0.035	2.07003E-13
Truepera	1.079	0.369	0.002	0.007	1.15611E-12
Devosia	0.812	0.253	0.050	0.049	8.41536E-13
Pelagibacterium	0.649	0.231	0.007	0.009	3.63753E-12
Palleronia	0.561	0.130	0.008	0.015	6.46803E-17
Chromohalobacter	0.507	0.256	0.085	0.050	3.76602E-07
Serratia	0.103	0.051	0.831	0.664	0.000136564
Erythrobacter	0.445	0.222	0.045	0.056	9.0754E-08
Escherichia-Shigella	0.374	0.242	0.139	0.117	0.001499749
Streptomyces	0.361	0.099	0.0017	0.004	4.84052E-15
Marinococcus	0.331	0.111	0.0019	0.008	8.53414E-13
Salegentibacter	0.285	0.107	0.0250	0.029	1.99448E-10
Uncultured Actinomycetales bacterium	0.273	0.113	0.006	0.011	1.87314E-10
Rhodocista	0.264	0.105	0.006	0.014	8.42693E-11
Cupriavidus	0.066	0.115	0.303	0.083	2.17492E-07
Pseudooceanicola	0.195	0.088	0.000	0.000	6.84696E-10

Geminicoccus	0.187	0.098	0.001	0.006	2.12858E-08
Idiomarina	0.179	0.058	0.002	0.007	5.20335E-13
Phyllobacterium	0.000	0.000	0.250	0.100	4.96669E-11
Egicoccus	0.129	0.064	0.005	0.015	1.94213E-08
Uncultured Nitriliruptorales Bacterium	0.127	0.093	0.000	0.000	5.61616E-06
Minor Genus	47.402	2.772	3.423	1.311	3.15107E-32
Unclassified Genus	20.375	1.049	0.403	0.183	1.07293E-35

Table S5 Examination of plant growth promoting (PGP) and related activities of seven endophyitc bacterial strains isolated from *A. sparsifolia* roots.

Strain name	Species name (% of similarity to strains in NCBI)	Observable PGP	Siderophore production	Exopolysaccharide production	ACC deaminase activity	Growth in 5% NaCl	Growth in 20% PEG	Growth at 42°C
LTGR-2	*Serratia marcescens* (JMPQ01000005, 99.8)	-	+	-	-	+	+	+
LTGR-2-1Z	*Stenotrophomonas maltophilia* (JALV01000036, 100)	-	+	-	-	-	+	-
LTGR-13Z	*Pseudoxanthomonas wuyuanensis* (JN247803, 100)	-	+	-	-	+	+	+
LTGR-20	*Rhizobium massiliae* (AF531767, 100)	-	-	+	-	-	-	+
LTGPAF-12F	*Pantoea dispersa* (DQ504305, 99.8)	-	-	-	-	+	+	-
LTGT-10	*Acinetobacter oleivorans* (CP002080, 100)	-	+	-	-	+	+	+
LTGT-11-2Z	*Pseudomonas* sp. (BBIS01000088, 100)	+	+	+	+	+	+	+

+, positive; -, negative.

Table S6 General information of *Pseudomonas* sp. LTGT-11-2Z isolated from the root of *A. sparsifolia.*

Strain	LTGT-11-2Z
Completeness	100%
No. of contigs	1
Genome size	6,073,276
GC content	61.88%
No. of genes	5,702
No. of proteins	5,608

Table S7 Information of selected reference strains.

Strain	Host plant	Functional role	Reference
Pseudomonas fluorescens 2P24	Wheat	Protecting plants against tomato bacterial wilt caused by *Ralstonia solanacearum* and cotton rhizoctoniosis caused by *Rhizoctonia solani*.	Ref. 1
Pseudomonas putida MTCC5279	Chickpea (Cicer arietinum L.)	Promoting growth and drought stress in chichpea.	Ref. 2
Klebsiella sp. LTGPAF-6F	Wheat	Improving growth and drought tolerance in wheat.	Ref. 3
Serratia proteamaculans 568	Poplar	Promoting root development in poplar	Ref. 4
Burkholderia phytofirmans PsJN	*Glomus vesiculiferum*-infected onion roots, Potato, tomato, grapevine, maize, barley	Promoting endophytic colonization and plant growth of potatoes, canola, maize, grapevines, herbaceous and woody species.	Ref. 5, 6
Azospirillum sp. B510	Rice (Oryza sativa cv. Nipponbare)	Promoting rice growth under both laboratory and field conditions and improving nitrogen fixation in grass.	Ref. 7
Klebsiella pneumoniae 342	Maize and wheat	Improving endophytic colonization, nitrogen fixation and plant growth in host plant.	Ref. 8
Methylobacterium populi BJ001	Poplar	Improving endophytic colonization in poplar.	Ref. 6
Pseudomonas putida W619	Poplar	Improving endophytic colonization in poplar.	Ref. 4
Enterobacter sp. 638	Poplar	Improving root development and endophytic colonization in poplar.	Ref. 9
Pseudomonas stuzeri A1501	Wheat	Improving plant growth and nitrogen fixation in host plant.	Ref. 10
Azoarcus sp. BH72	Kallar grass, rice	Improving endophytic colonization and nitrogen fixation in grass and rice.	Ref. 11
Gluconacetobacter diazotrophicus Pal5	Sugarcane, rice	Improving plant growth and nitrogen fixation in host plant.	Ref. 12

Table S8 Functions relevant for rhizosphere competence, plant colonization, plant growth promotion and stress resistance in *Pseudomonas* sp. LTGT-11-2Z and reference bacteria. Full names: *Pseudomonas* sp. LTGT-11-2Z; *Pseudomonas fluorescens* 2P24, *Pseudomonas putida* MTCC5279; *Klebsiella* sp. LTGPAF-6F; *Serratia proteamaculans* 568; *Burkholderia phytofirmans* PsJN; *Azospirillum* sp. B510; *Klebsiella pneumoniae* 342; *Methylobacterium populi* BJ001; *Pseudomonas putida* W619; *Enterobacter* sp. 638; *Pseudomonas stuzeri* A1501; *Azoarcus* sp. BH72; *Gluconacetobacter diazotrophicus* Pal5.

Functions	**LTGT-11-2Z**	**2P24**	**WTCC5279**	**LTGPAF-6F**	**568**	**PsJN**	**B510**	**342**	**BJ001**	**W619**	**638**	**A1501**	**ABH72**	**Pal5**
Motility and chemotaxis														
Type IV pili	-	+	-	+	-	+	+	+	+	+	+	-	+	+
Flagella	+	+	+	+	+	+	+	-	+	+	+	+	+	+
Chemotaxis	+	+	+	+	+	+	+	-	+	+	+	+	+	+
Methyl-accepting proteins	25	40	31	2	3	27	88	0	28	33	18	33	24	9
Che protein response regulator	7	2	3	6	10	60	71	25	73	44	26	47	51	12
Plant adhesion														
Curli fibers	1	0	0	0	1	0	0	0	2	5	5	7	0	0
Haemagglutinin protein	0	0	6	0	0	1	0	2	0	1	1	0	0	0
Agglutination protein	0	0	0	0	0	0	0	0	0	2	0	0	1	0
Plant polymer degradation														
Glycoside hydrolases (GH) total	222	247	88	104	70	41	49	68	26	26	56	29	29	35
Detoxification														
Glutathione S-transferase	10	20	9	9	11	24	11	12	16	12	9	8	10	9
Alkyl hydroperoxide reductase	1	4	4	1	0	2	1	1	0	1	1	2	1	1
Thiol peroxidase	1	1	1	1	1	1	0	1	0	1	1	1	1	0
Glutathione peroxidase	3	3	5	1	2	1	1	2	2	3	2	3	2	1
Catalase-peroxidase	1	1	1	1	1	1	0	1	0	1	1	1	1	0
SOD	2	2	2	2	2	2	2	3	2	3	3	2	2	1
Catalases	2	0	0	2	2	6	2	4	6	4	5	2	2	3
Peroxidase	3	11	13	2	2	5	2	4	1	4	4	3	4	4
SUM antioxidative enzyme	23	29	35	19	21	21	8	18	11	18	19	14	14	12
Efflux pumps	27	25	19	27	17	56	11	49	40	45	35	29	20	31

Iron uptake														
Dicitrate TonB-dependent receptor	0	0	0	1	1	1	0	0	0	1	0	0	0	0
Catecholate TonB-dependent receptor	0	0	0	1	0	1	0	1	1	1	0	1	1	2
Hydeoxymate TonB-dependent receptor	0	0	0	10	11	5	5	7	19	12	8	10	13	24
SUM Ton-dependent receptors	0	0	0	12	12	7	5	8	20	14	8	11	14	26
Siderophore biosynthesis	+	+	-	+	+	+	+	+	-	-	+	+	-	-
Compound degradation														
Alkane monooxygenase	0	8	3	0	0	1	0	0	0	0	0	0	0	0
Dioxygenases	24	0	24	12	12	15	16	9	1	11	0	8	15	0
Transporter														
ABC transporter type	34	136	122	160	130	105	51	153	63	99	145	74	51	54
ABC transporter gene	93	249	225	263	206	256	76	237	108	154	199	113	76	86
Porin	6	18	0	27	0	54	0	27	8	8	16	4	3	8
Putrescine	+	+	+	+	+	+	-	+	+	+	+	+	-	-
Spermidine/putrescine	+	+	+	+	-	+	+	+	+	+	+	+	-	-
Secretion systems														
Type I	+	-	+	-	-	-	+	+	+	+	+	+	+	+
Type II	+	-	+	+	+	+	-	-	+	+	+	+	+	-
Type III	+	+	+	-	-	+	-	-	-	-	-	-	-	-
Type IV	-	+	+	+	+	+	+	+	-	-	+	-	-	+
Type Va	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Type Vb	-	-	-	-	-	-	-	-	-	+	-	-	-	-
Type VI	+	-	+	+	+	+	+	+	-	+	-	-	+	-
Signaling														
Two component system genes	63	333	321	141	146	279	178	158	242	268	181	247	178	93
ECF sigma factor	31	17	14	17	22	40	23	19	18	619	18	28	24	18
Quorum sensing														
AI-2	-	-	-	-	-	-	-	+	-	-	+	-	-	-
DSF-system	+	-	-	+	+	-	-	-	-	-	-	-	-	-

AHL (AI-1)	+	+	+	-	-	+	+	-	+	-	-	-	-	+
LuxR (solo)	-	+	+	-	-	+	+	+	-	+	+	-	-	-
AHL degradation	-	+	-	-	-	-	+	+	-	+	-	-	-	-
Plant growth promotion and stress resistance														
Nitrogen fixation	-	-	+	+	-	-	+	+	-	-	-	+	+	+
ACC deaminase	+	-	+	-	+	+	+	-	+	+	-	+	-	-
Acetoin and 2,3-butanediol production	-	+	-	+	-	-	+	+	+	+	+	-	+	+
Spermidine/putrescine/cadaverine synthesis	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Trehalose synthesis	-	+	+	+	-	-	-	+	-	-	+	+	-	+

Table S9 Unique KEGG genes in *Pseudomonas* sp. LTGT-11-2Z in comparison with the four reference strains, including *P. putida* W619, an endophytic bacterium of poplar trees; *P. stutzeri* A1501, a rice root-associated bacterium; *P. putida* MTCC5279, a positive plant growth promoting rhizobacteria in chick pea, and the phylogenetically close strain *P. fluorescens* 2P24.

K01252	*entB*, *dhbB*, *vibB*, *mxcF*; bifunctional isochorismate lyase / aryl carrier protein [EC:3.3.2.1 6.3.2.14]
K19595	*gesA*, *mexP*; membrane fusion protein, gold/copper resistance efflux system
K00202	*fwdC*, *fmdC*; formylmethanofuran dehydrogenase subunit C [EC:1.2.7.12]
K16235	*mmuP*; S-methylmethionine transporter
K16242	*dmpN*, *poxD*, *tomA3*; phenol/toluene 2-monooxygenase (NADH) P3/A3 [EC:1.14.13.244 1.14.13.243]
K00054	*mvaA*; hydroxymethylglutaryl-CoA reductase [EC:1.1.1.88]
K00634	*ptb*; phosphate butyryltransferase [EC:2.3.1.19]
K18650	*pehX*; exo-poly-alpha-galacturonosidase [EC:3.2.1.82]
K03208	*wcaI*; colanic acid biosynthesis glycosyl transferase WcaI
K15343	*sspH1*; E3 ubiquitin-protein ligase SspH1
K07239	heavy-metal exporter, HME family
K16246	*dmpP*, *poxF*, *tomA5*; phenol/toluene 2-monooxygenase (NADH) P5/A5 [EC:1.14.13.244 1.14.13.243]
K03772	*fkpA*; FKBP-type peptidyl-prolyl cis-trans isomerase FkpA [EC:5.2.1.8]
K03148	*thiF*; sulfur carrier protein ThiS adenylyltransferase [EC:2.7.7.73]
K01739	*metB*; cystathionine gamma-synthase [EC:2.5.1.48]
K07459	*ybjD*; putative ATP-dependent endonuclease of the OLD family
K00876	*udk*; uridine kinase [EC:2.7.1.48]
K00016	*ldh*; L-lactate dehydrogenase [EC:1.1.1.27]
K19176	FAAH2; fatty acid amide hydrolase 2 [EC:3.5.1.99]
K19592	*golS*; MerR family transcriptional regulator, gold-responsive activator of gol and ges genes
K16245	*dmpO*, *poxE*, tomA4; phenol/toluene 2-monooxygenase (NADH) P4/A4 [EC:1.14.13.244 1.14.13.243]
K07316	*mod*; adenine-specific DNA-methyltransferase [EC:2.1.1.72]
K20927	*mpdB*; 2-methyl-1,2-propanediol dehydrogenase [EC:1.1.1.400]
K07494	putative transposase
K18098	*bjaR1*, *rpaR*, *rhiR*; LuxR family transcriptional regulator, quorum-sensing system regulator BjaR1
K16165	*nagK*; fumarylpyruvate hydrolase [EC:3.7.1.20]
K10947	*padR*; PadR family transcriptional regulator, regulatory protein PadR
K01474	*hyuB*; N-methylhydantoinase B [EC:3.5.2.14]
K10857	*exoX*; exodeoxyribonuclease X [EC:3.1.11.-]
K13243	*dos*; c-di-GMP-specific phosphodiesterase [EC:3.1.4.52]
K14257	*ctcP*, *cts4*, *prnC*; tetracycline 7-halogenase / FADH2 O2-dependent halogenase [EC:1.14.19.49 1.14.19.-]
K00183	prokaryotic molybdopterin-containing oxidoreductase family, molybdopterin binding subunit
K16093	*bacA*; bacitracin synthase 1
K07729	putative transcriptional regulator
K06324	*cotA*; spore coat protein A, manganese oxidase [EC:1.16.3.3]
K12452	*ascC*, *ddhC*, *rfbH*; CDP-4-dehydro-6-deoxyglucose reductase, E1 [EC:1.17.1.1]
K11909	*vasI*; type VI secretion system protein VasI

K16249	*dmpK*, *poxA*, *tomA0*; phenol/toluene 2-monooxygenase (NADH) P0/A0
K12991	*rfbG*; rhamnosyltransferase [EC:2.4.1.-]
K11894	*impI*, *vasC*; type VI secretion system protein ImpI
K04782	*pchB*; isochorismate pyruvate lyase [EC:4.2.99.21]
K18334	*fucD*; L-fuconate dehydratase [EC:4.2.1.68]
K17716	*capD*; UDP-glucose 4-epimerase [EC:5.1.3.2]
K19597	*golT*; Au^+-exporting ATPase [EC:3.6.1.-]
K16244	*dmpM*, *poxC*, *tomA2*; phenol/toluene 2-monooxygenase (NADH) P2/A2 [EC:1.14.13.244.14.13.243]
K01473	*hyuA*; N-methylhydantoinase A [EC:3.5.2.14]
K01829	protein disulfide-isomerase [EC:5.3.4.1]
K19449	*sinR*; XRE family transcriptional regulator, master regulator for biofilm formation
K19171	*dndD*; DNA sulfur modification protein DndD
K02472	*wecC*; UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase [EC:1.1.1.336]
K16701	*amsD*; amylovoran biosynthesis glycosyltransferase AmsD [EC:2.4.-.-]
K02849	*waaQ*, *rfaQ*; heptosyltransferase III [EC:2.4.-.-]
K06400	*spoIVCA*; site-specific DNA recombinase
K19594	*gesB*, *mexQ*; gold/copper resistance efflux pump
K05797	*pchF*; 4-cresol dehydrogenase (hydroxylating) flavoprotein subunit [EC:1.17.9.1]
K18983	*gci*; D-galactarolactone cycloisomerase [EC:5.5.1.27]
K19425	*epsH*; glycosyltransferase EpsH [EC:2.4.-.-]
K03718	*asnC*; Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC and gidA
K03420	*psmR*; proteasome regulatory subunit
K16243	*dmpL*, *poxB*, *tomA1*; phenol/toluene 2-monooxygenase (NADH) P1/A1 [EC:1.14.13.244 1.14.13.243]
K06996	uncharacterized protein
K03765	*cadC*; transcriptional activator of cad operon
K15521	*mshA*; D-inositol-3-phosphate glycosyltransferase [EC:2.4.1.250]

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