

**Table S1A. Geolocation of the sites sampled in the provinces of Salta and Jujuy and the host plant species at those sites.**

Sampled Site	ID <sup>a</sup>	Province	Department	GPS coordinates	Plant-host species
6	6995	Salta	Rosario de la Frontera	64° 56' 40,8'W 25° 45' 17,7'S	<i>D. paspalaceus</i>
7	7005	Jujuy	El carmen	65° 04' 50,7'W 24° 32' 15,15'S	<i>D. virgatus</i>
8	7059	Jujuy	Ledesma	64° 43' 21,8'W 23° 45' 40,1'S	<i>D. virgatus</i>

**a:** Corresponding collection number in the catalog of Dr. Pensiero, Facultad de Ciencias Agrarias, Universidad Nacional del Litoral, Argentina.

**Tabla S1B. Climatic and edaphic characteristics of the sampled sites.**

Sampled site <sup>a</sup>	Climatic data		Edaphic data						
	Annual rainfall (mm)	Mean Temperature (°C)	Soil order <sup>b</sup>	Texture	Chemical properties				
					OM <sup>c</sup> (%)	TON <sup>d</sup> (%)	AP <sup>e</sup> (ppm)	pH <sup>f</sup>	EC <sup>g</sup> (dS/m)
6	924.9	19.2	Entisols	sandy-gravelly	1.99	0.091	7	7.2	0.145
7	742.9	17.8	Molisol	Loamy-clay-loam	2.59	0.123	23	6.8	0.089
8	761.9	18.2	Molisol	Clay loam	2.11	0.100	17	6.9	0.105

**a:** Geolocation of the host plant species are detailed in Table S1.

**b:** Soil Taxonomy Classification System

**c:** MO: Organic Matter

**d:** TON: Total Organic Nitrogen

**e:** AP: Available phosphorus

**f:** pH (soil:water ratio, 1:2)

**g:** EC:Electrical conductivity.

**Table S2. Best hits resulting from the EZBiocloud searches against partial 16S rDNA sequences of isolates 6-70, 6-117, 7-81 and 8-89.**

<b>Local isolate 16S rDNA query <sup>1</sup></b>	<b>Best hit in EZBiocloud</b>	<b>Identity (%)</b>
<b>6-70 (Salta)</b>	<i>Sinorhizobium mexicanum</i> ITTG R7	99.93
	<i>Sinorhizobium chiapanecum</i> ITTG S70	99.71
<b>6-117 (Salta)</b>	<i>Sinorhizobium mexicanum</i> ITTG R7	99.61
	<i>Sinorhizobium chiapanecum</i> ITTG S70	99.37
<b>7-81 (Jujuy)</b>	<i>Sinorhizobium psoraleae</i> CCBAU 65732	100.00
<b>8-89 (Jujuy)</b>	<i>Sinorhizobium arboris</i> LMG 14919	97.64

<sup>1</sup> Query sequence for each isolate corresponding to the sequence stretch that covered the positions homologous to nucleotides 78–1,355 (1,278 bp) of the 16S rDNA in *Sinorhizobium medicae* NBRC100384<sup>T</sup> (GenBank AB681159). The parentheses indicate the province of origin for each isolate (*cf.* the information of the site sampled in Table S1).

**Table S3. MALDI-TOF typing of bacteria from root nodules of *D. virgatus* and *D. paspalaceus* which were nodulated in the field (Jujuy and Salta) or in the laboratory with soil samples.**

Isolate name	Best candidate in data base	Biotyper Score <sup>1</sup>	Group <sup>2</sup>	Identification
6-70	6-70	2.84	$\alpha$	<i>Sinorhizobium</i> spp.
6-71	6-70	1.9	$\alpha$	<i>Sinorhizobium</i> spp.
6-117	6-117	2.84	$\alpha$	<i>Sinorhizobium</i> spp.
7-73	6-117	2.01	$\alpha$	<i>Sinorhizobium</i> spp.
7-74	8-89	2.423	$\alpha$	<i>Sinorhizobium</i> spp.
7-75	7-81	2.088	$\alpha$	<i>Sinorhizobium</i> spp.
7-76	8-89	2.488	$\alpha$	<i>Sinorhizobium</i> spp.
7-77	7-81	2.138	$\alpha$	<i>Sinorhizobium</i> spp.
7-78	8-89	2.155	$\alpha$	<i>Sinorhizobium</i> spp.
7-79	8-89	2.548	$\alpha$	<i>Sinorhizobium</i> spp.
7-80	7-81	2.41	$\alpha$	<i>Sinorhizobium</i> spp.
7-81	7-81	2.84	$\alpha$	<i>Sinorhizobium</i> spp.
7-82	8-89	2.46	$\alpha$	<i>Sinorhizobium</i> spp.
8-83	7-81	2.55	$\alpha$	<i>Sinorhizobium</i> spp.
8-84	8-89	2.13	$\alpha$	<i>Sinorhizobium</i> spp.
8-85	8-89	2.10	$\alpha$	<i>Sinorhizobium</i> spp.
8-86	8-89	1.70	$\alpha$	<i>Sinorhizobium</i> spp.
8-87	8-89	2.52	$\alpha$	<i>Sinorhizobium</i> spp.
8-88	7-81	2.15	$\alpha$	<i>Sinorhizobium</i> spp.
8-89	8-89	2.85	$\alpha$	<i>Sinorhizobium</i> spp.
8-90	8-89	2.08	$\alpha$	<i>Sinorhizobium</i> spp.
8-91	8-89	2.58	$\alpha$	<i>Sinorhizobium</i> spp.
8-92	8-89	2.45	$\alpha$	<i>Sinorhizobium</i> spp.
8-93	8-89	2.58	$\alpha$	<i>Sinorhizobium</i> spp.
8-94	6-70	1.85	$\alpha$	<i>Sinorhizobium</i> spp.
8-95	8-89	2.56	$\alpha$	<i>Sinorhizobium</i> spp.
8-96	7-81	1.73	$\alpha$	<i>Sinorhizobium</i> spp.

1: Bacterial identification was performed with the MALDI Biotyper Software (Bruker) through the use of the score values proposed by the manufacturer, with a score  $\geq 2$  indicating species identification (green), a score between 1.7 and 1.9 genus identification (yellow), and a score  $< 1.7$  no identification [30, 33].

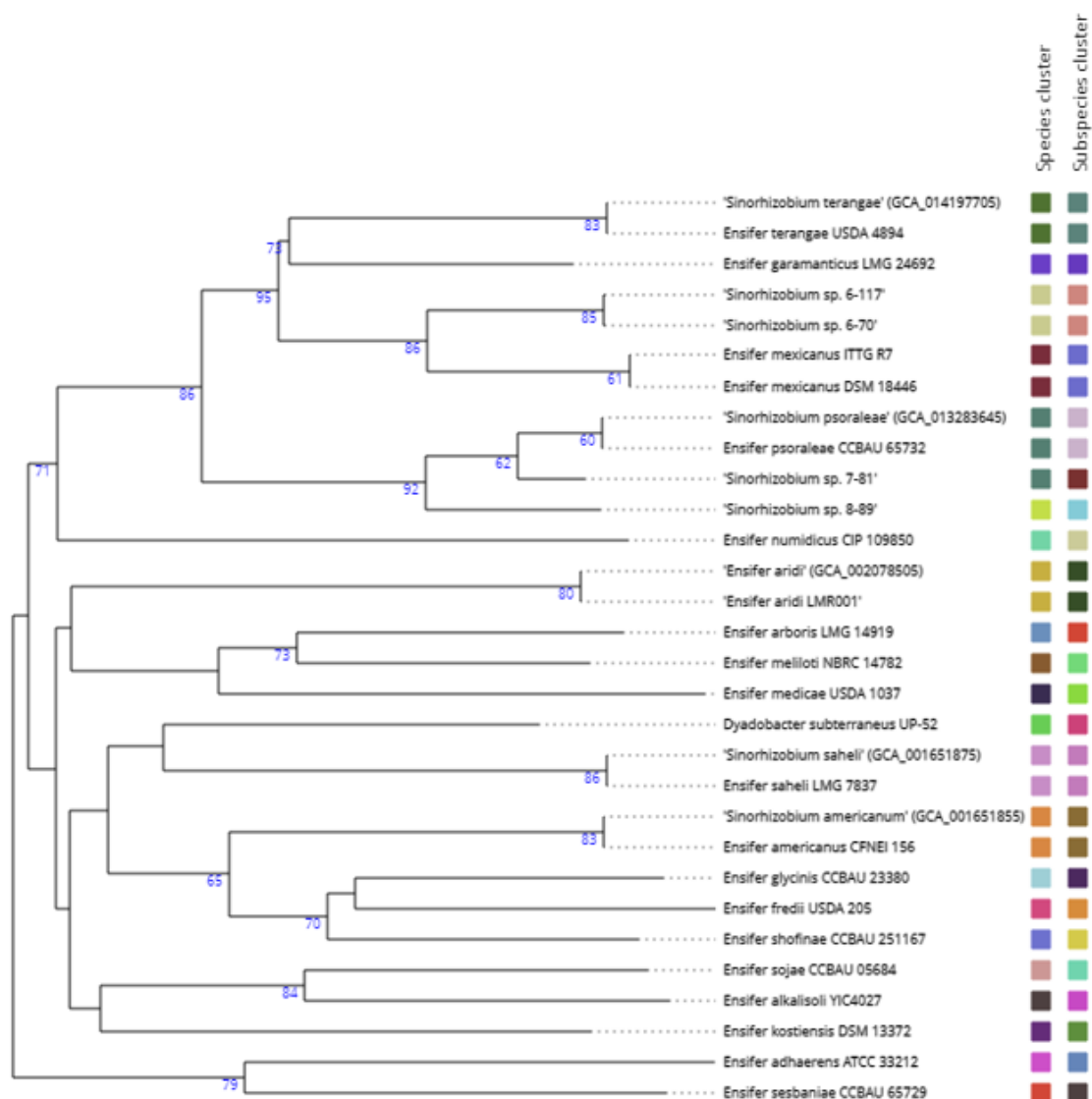
2: Cf. See manuscript text, first section in Results and Fig. 1.

**Table S4. Growth of rhizobia that nodulate *D. virgatus* and *D. paspalaceus* evaluated under different abiotic stressing conditions in agarized-YEM medium.**

Isolate	Growth at the indicated temperature (°C) <sup>1</sup>			Growth at indicated pH <sup>1,2</sup>						Growth at NaCl (%w/v) concentration <sup>1</sup>				Province
	28	35	40	4	5	6	7	8	9	0.5%	1%	2%	3%	
6-67	5	5	2	2	2	5	5	5	5	5	4	0	0	Salta
6-69	5	4	1	2	4	5	5	5	5	5	4	0	0	Salta
6-70	5	5	2	2	4	5	5	5	5	5	4	0	0	Salta
6-71	5	5	2	2	4	5	5	5	5	5	4	0	0	Salta
6-72	5	5	2	2	4	5	5	5	5	5	4	0	0	Salta
6-117	5	5	2	2	4	5	5	5	5	5	4	0	0	Salta
7-73	5	4	0	3	3	5	5	3	1	5	5	4	2	Jujuy
7-74	5	4	0	3	3	5	5	3	1	5	5	2	1	Jujuy
7-75	5	4	0	3	3	5	5	3	1	5	5	4	2	Jujuy
7-76	5	4	0	2	3	5	5	3	1	5	5	2	1	Jujuy
7-77	5	4	0	3	3	5	5	3	1	5	5	2	1	Jujuy
7-78	5	4	0	2	3	5	5	3	1	5	5	2	1	Jujuy
7-79	5	4	0	2	3	5	5	3	1	5	5	2	1	Jujuy
7-80	5	5	0	5	5	5	5	5	4	5	4	3	2	Jujuy
7-81	5	4	0	3	4	5	5	3	1	5	4	2	1	Jujuy
7-82	5	4	0	2	3	5	5	3	1	5	4	2	1	Jujuy
8-83	5	5	1	1	4	5	5	4	3	5	4	2	0	Jujuy
8-84	5	5	1	1	4	5	5	1	0	5	4	2	0	Jujuy
8-85	5	5	1	1	4	5	5	4	3	5	4	1	0	Jujuy
8-86	5	5	1	1	4	5	5	4	3	5	4	1	0	Jujuy
8-87	5	5	2	1	4	5	5	5	4	5	4	1	0	Jujuy
8-88	5	5	2	1	4	5	5	5	4	5	4	1	0	Jujuy
8-89	5	5	5	1	4	5	5	5	4	5	4	1	0	Jujuy
8-90	5	5	2	1	4	5	5	5	4	5	4	1	0	Jujuy
8-91	5	5	5	1	4	5	5	5	4	5	4	1	0	Jujuy
8-92	5	5	3	1	4	5	5	5	4	5	4	1	0	Jujuy
8-93	5	5	4	1	4	5	5	5	4	5	4	1	0	Jujuy
8-94	5	4	2	1	4	5	5	5	4	5	3	2	0	Jujuy
8-95	5	4	2	1	4	5	5	5	4	5	4	1	0	Jujuy
8-96	5	5	0	0	1	5	5	5	4	5	4	1	0	Jujuy
CB3126	5	5	4	0	4	5	5	5	4	4	2	1	0	Commercial inoculant

1: Scores from 5 to 0 indicate the ability of rhizobia to grow under the condition investigated (5 = full development in 2 days, 0 = absence of growth).

2: YEM medium at pH 4 was softer, as expected, than the medium at pH 7 but stable enough to properly streak isolates on the surface



**Figure S1. Phylogenetic tree inferred with FastME from GBDP distances calculated from genome sequences.** The tree was generated with the tools available at <https://tygs.dsmz.de/> (TSGS, Type Strain Genome Server). GBDP refers to genome Blast distances and FastME is an accurate and fast distance-based phylogeny inference program (<http://www.atgc-montpellier.fr/fastme/>). The numbers above branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications. The tree was rooted at the midpoint. Results indicate that the four sequenced isolates most likely belong to three different species: a same species for isolates 6.70 and 6-117, and two different species in case of isolates 7-81 and 7-89) (see color boxes at the first column on the right side of the tree). According to this result and to the ANIb values (Table 2), isolate 7-81 might thus belong to the *S. psoraleae* species.