

Soybean-nodulating strains with low intrinsic competitiveness for nodulation, good symbiotic performance, and stress-tolerance isolated from soybean-cropped soils in Argentina

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Supplementary Material

Including:

Table S1: Accession numbers of SNAP-isolates gene sequences used for species determination.

Figure S1: DNA sequences of *nodC* and *nifH* PCR-fragments from *Rhizobium radiobacter*.

Figure S2: Maximum likelihood cladogram for *Rhizobium radiobacter nodC* and *nifH*.

Table S1 Accession numbers of SNAP-isolates gene sequences used for species determination.

Gene	Isolate	Accession number
16S rRNA	<i>Bradyrhizobium diazoefficiens</i> NUJ/N-43	MK228877
	<i>Bradyrhizobium japonicum</i> CAS/S-02	MK228874
	<i>Bradyrhizobium japonicum</i> CAS/N-10	MK228875
	<i>Bradyrhizobium japonicum</i> CAV/S-15	MK22879
	<i>Bradyrhizobium japonicum</i> CUR/N-28	MK228876
	<i>Bradyrhizobium japonicum</i> SAA/S-48	MK228878
	<i>Bradyrhizobium elkanii</i> CAV/S-14-1	MK228883
	<i>Bradyrhizobium elkanii</i> CUR/S-25-2	MK228880
	<i>Rhizobium radiobacter</i> NUJ/N-44-1	MK228881
	<i>Rhizobium radiobacter</i> NUJ/N-44-2	MK228882
	<i>Paenibacillus glycanilyticus</i> CUR/S-25-1	MK243450
recA	<i>Bradyrhizobium diazoefficiens</i> NUJ/N-43	MK246834
	<i>Bradyrhizobium japonicum</i> CAS/S-02	MK246831
	<i>Bradyrhizobium japonicum</i> CAS/N-10	MK246832
	<i>Bradyrhizobium japonicum</i> CAV/S-15	MK246836
	<i>Bradyrhizobium japonicum</i> CUR/N-28	MK246833
	<i>Bradyrhizobium japonicum</i> SAA/S-48	MK246835
atpD	<i>Bradyrhizobium diazoefficiens</i> NUJ/N-43	MK246822
	<i>Bradyrhizobium japonicum</i> CAS/S-02	MK246819
	<i>Bradyrhizobium japonicum</i> CAS/N-10	MK246820
	<i>Bradyrhizobium japonicum</i> CAV/S-15	MK246824
	<i>Bradyrhizobium japonicum</i> CUR/N-28	MK246821
	<i>Bradyrhizobium japonicum</i> SAA/S-48	MK246823
glnII	<i>Bradyrhizobium diazoefficiens</i> NUJ/N-43	MK246828
	<i>Bradyrhizobium japonicum</i> CAS/S-02	MK246825
	<i>Bradyrhizobium japonicum</i> CAS/N-10	MK246826
	<i>Bradyrhizobium japonicum</i> CAV/S-15	MK246830
	<i>Bradyrhizobium japonicum</i> CUR/N-28	MK246827
	<i>Bradyrhizobium japonicum</i> SAA/S-48	MK246829

NUJ/N-44-1 *nodC*

CTGATGCCAAAGAACGTCGGAAAGCGCAAGGCGCAGATTGTCGCAATACGGGAATCATCGGGAGATTTGGTGCTCAA
CGTTGACTCGGACACGACCATTGCGCCGACGTAGTCACGAACTTGCCTGAAGATGTACAGTCCCGCGGTCGGCG
CGGCGATGGGTACGTTGACGGCCAGCAACCGCAGCGACACATGGCTGACGCGGTTGATCGACATGGAGTACTGGCT
CGCCTGCAACGAGGAACGAGCAGCACAGGCTCGCTTTGGAGCCGTTATGTGTTGCTGCGGCCGTGTGCCATGTACC
GGCGGTCCGCACTCCTATTGCTGCTCGATAAATACGAGACGCAACTGTTTCGAGGCAGGCCAAGCGACTTCGGGGAA
GACCGCCACCTCACAATCCTCATGCTGAATGCAGGCTTTCGAACCGAGTACGTTCCGGACGCCATCGCGGCGACGGTC
GTTCCAAACTCGATGGGGCCTATCTGCGCCAACAACCTGCGCTGGGCACGCAGCACGTTTCGCGACACATTGCTCGCG
CTCCGCTACTGCCGGCCTTGATCGCTATCTTACGCTGGACGTGATCGGACAGAATCTTGGTCCGCTGCTCCTAGCCC
TCTCGTCTGACGGGGCTAGCACAGCTCGCTCTGACGGCCACAGTGCCTTGGTCGACGATCCTGATGATTGCATCTA
TGACAATGGTCCGCTGCGGCGTGGCGGCGTTTCGAGCGCGAGAGCTGCGATTCTTGGGTTTTTCGCTGCACACCCTCC
TCAACGTCGCTCTCCTGCTCCCCCTCAAAGCATATGCGTTGTGCACGTTGAGCAATAGCGACTGGGC

NUJ/N-44-2 *nodC*

AATCGCAACGCCATCATACTGTACACGATCATTATGCGTGCGACCCGAGGTTCCGCTTATCCTGATGCCAAAGAACG
TCGAAAAGCGCAAGGCGCAATGTCGCAATACGGGAATCATCGGGAGATTTGGTGCTCAACGTTGACTCGGACACGAC
CATTGCGCCGACGTAGTCACGAACTTGCCTGAAGATGTACAGTCCCGCGGTCGGCGCGGCGATGGGTACGTTGA
CGCCAGCAACCGCAGCGACACATGGCTGACGCGGTTGATCGACATGGAGTACTGGCTCGCCTGCAACGAGGAACG
AGCAGCACAGGCTCGCTTTGGAGCCGTTATGTGTTGTGCGGCCCGTGTCCATGTACCGGCGGTCCGCACTCCTATTGC
TGCTCGATAAATACGAGACGCAACTGTTTCGAGGCAGGCCAAGCGACTTCGGGGAAGACCGCCACCTCACAATCCTCAT
GCTGAATGCAGGCTTTGAACCGAGTACGTTCCGGACGCCATCGCGGCGACGGTCGTTCCAAACTCGATGGGGCCTA
TCTGCGCCAACAACCTGCGCTGGGCACGCAGCACGTTTCGCGACACATTGCTCGCGCTCCGCTACTGCCGGCCTTGA
TCGCTATCTTACGCTGGACGTGATCGGACAGAATCTTGGTCCGCTGCTCCTAGCCCTTCGGTCTGACGGGGCTAGCA
CAGCTCGCTCTGACGGCCACAGTGCCTTGGTCGACGATCCTGATGATTGCATCTATGACAATGGTCCGCTGCGGCGTG
GCGGCGTTTTTCGAGCGCGAGAGCTGCGATTCTTGGGTTTTTCGCTGCACACCCTCCTCAACGTCGCTCTCCTGCTCCCC
TCAAAGCA

NUJ/N-44-2 *nifH*

GGCAAGTCCACCACCACCCAGAACCTCGTCTCCGCCCTGGCCGAAGCCGGTCAGAAGGTGATGATCGTCGGCTGCGA
TCCGAAGGCGGACTCCACCCGTCTGATCCTGCACGCCAAGGCCAGAACTCGATCATGGAAATGGCCGCCGAAGCCG
GCAGCGTGAAGACCTCGAGCTCGAAGACGTGCTCAAGGTCGGCTATCGCGACATCAAGTGCCTCGAGTCGGGCGG
CCCTGAGCCGGGCGTTGGCTGCGCTGGCCGCGGTGTGATCACCGGATCAACTTCTCGAAGAGGAAGGCGCCTACG
AGGAAGACCTCGACTTCGTGTTCTACGACGTAACGCGACGTGGTCTGCGGTGGCTTCGCCATGCCGATCCGCGAG
AACAAGGCGCAGGAGATCTACATCGTCTGCTCCGGCGAAATGATGGCCATGTACGCGGCCAACAACATCGCCAAGGG
CATCGTGAAGTACGCCAACTCCGGCAGCGTGCCTGTCGAGGCTGATCTGCAACAGCCGCAACACCGCCCGCGAAG
ACGAACTGATCATGGAACCTGGCCGTCAGCTGGGCACCCAGATGATCCACTTCGTGCCGCGGACAACGTCGTACAG
CGCGCCGAGATCCGCCGATGACCGTAGTCGAGTACGACCCGACGGMCAAGCGGCCGACGAGTACCGCCAGCTGGC
GAACAAGATCGTCAACAACCGCAACTTCGTGATTCCGACGCCATCACCATGGACGAACTCGAAGACAT

Fig. S1 DNA sequences of *nodC* and *nifH* PCR-fragments obtained from the *Rhizobium radiobacter* SNAP-isolates. The *nifH* fragment could not be amplified from NUJ/N-44-1. The highest identities were obtained with *R. radiobacter* (*Agrobacterium tumefaciens*) MQ-110s for both *nodC* and with *R. radiobacter* (*Agrobacterium tumefaciens*) gx-178 for *nifH*.

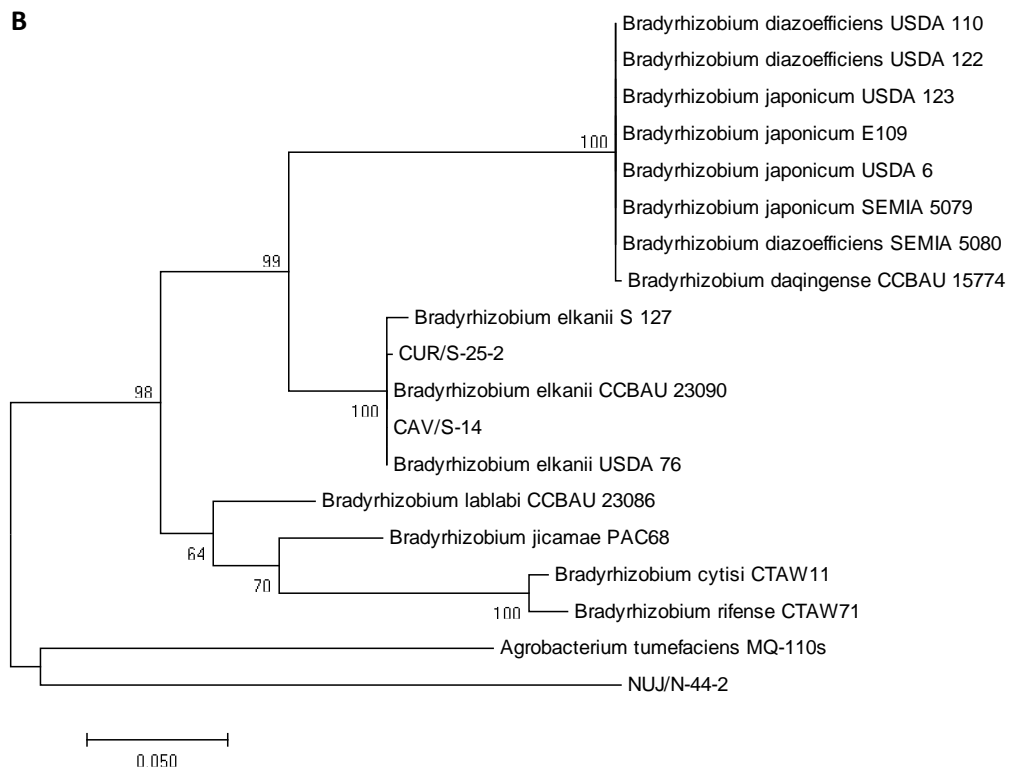
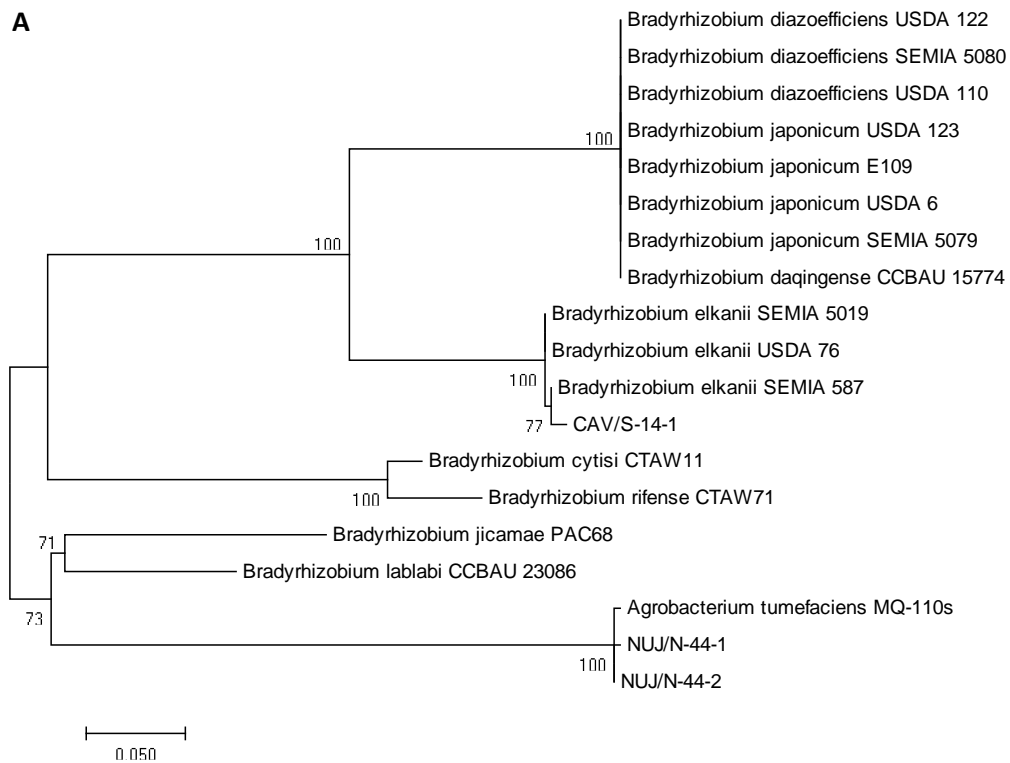


Fig. S2 Maximum likelihood cladogram for *Rhizobium radiobacter* NUJ/N-44-1 and NUJ/N-44-2 *nodC* (A) and NUJ/N-44-2 *nifH* (B). Next to the nodes the percentage of replicate trees in which the associated taxa clustered together in the bootstrap test with 1000 replicates are shown. Branch lengths in the tree are scaled in the same units as those of the evolutionary distances (scale bar) used to infer the phylogenetic tree.