



**Legend**

**Taxon Phenotypes**  
 Nitrogen fixation (atm%<sup>15</sup>N)

> 2.0	White
= 1.1 – 1.9	Light Yellow
= 0.81 – 1.0	Yellow
= 0.66 – 0.8	Orange
< 0.66	Red

\*Ineffective strains have an asterisk

**Ancestral nodes**  
 Proportional Likelihood of N-Fixation

● (Red)	> 0.950
● (Yellow)	0.900 → 0.949
● (Light Yellow)	0.600 → 0.899

(Nodes with PP>0.8 are numbered)

**S4 Figure. Bayesian cladogram inferred with the *nodZ* and *nolL* loci (SI).** The tree is rooted with homologous sequences from *Mesorhizobium loti* MAFF303099. Only nodulating isolates are included in the SI tree since the SI loci could not be amplified for the isolates that failed to form nodules. Four species-like clades are identified with the outermost curved bars. A continuous measure of nitrogen fixation is indicated on the tips of the tree, via colored rectangles (colored rectangles = significant nitrogen fixation, white rectangles = no significant nitrogen fixation). Ancestral nodes are labeled and numbered for all clades with Bayesian posterior probabilities  $\geq 0.80$ . Ancestral states for nitrogen fixation (on *A. strigosus*) are estimated for all well-supported internal nodes using maximum likelihood. Proportional likelihood of the nitrogen fixation is reported via the color of the node labels. In the parsimony analysis all 18 well-supported ancestral nodes were inferred to be nitrogen fixing. See S4 Table for full parsimony analysis, node support values, and proportional likelihood values of ancestral states of nitrogen fixation. Each of the four major clades on the symbiosis island tree exhibited evidence of incongruence with the chromosomal phylogeny, consistent with recurrent transfer of the symbiosis island among chromosomal lineages (S2,4,5 Figures). In particular, the largest clade on the symbiosis island tree (i.e., SI clade 11, pp=0.88) encompassed only *B. canariense* isolates but for three exceptions, consistent with horizontal transfer of the SI (i.e., #132, *B. spp. nov. X*; #175, *B. spp. nov. II*; #185, *B. liaoningense*). Similarly, the next largest symbiosis island clade (i.e., node 14, pp=1.00) encompassed mostly *B. spp. nov. I* and related chromosomal taxa, but for one exception consistent with horizontal transfer of the SI (i.e., #149, *B. canariense*).