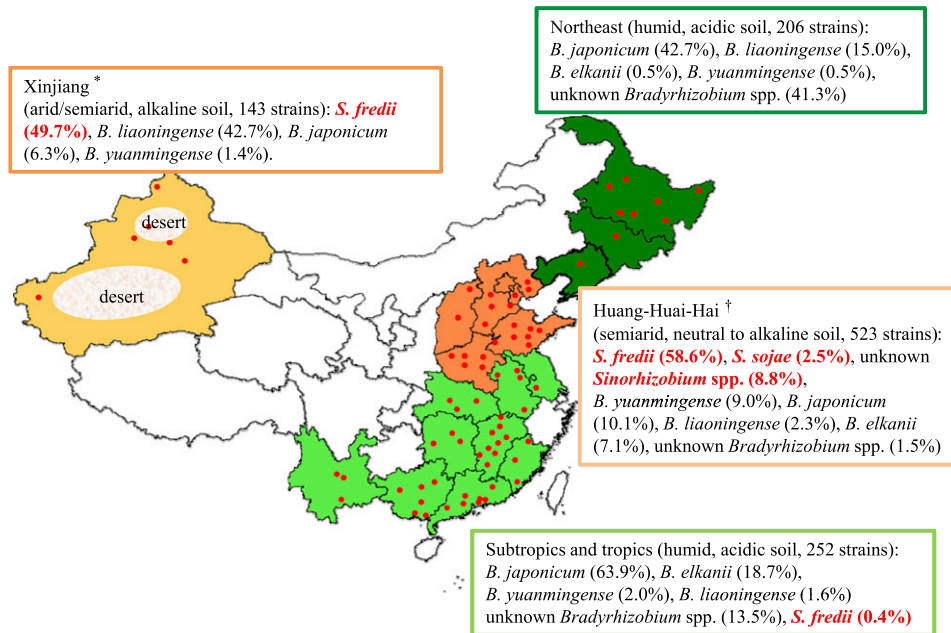


# Supporting Information

Tian et al. 10.1073/pnas.1120436109



**Fig. S1.** Genetic diversity and biogeography of rhizobia nodulating soybean. Red points indicate sampling sites. The species in red belongs to *Sinorhizobium*. Relative abundance of each species is also indicated. \*In Xinjiang (1); 98.6% of *Bradyrhizobium* strains were isolated from soybean nodules in soils with low values of electronic conductivity (EC) (77–178  $\mu\text{S}/\text{cm}$ ), and 69.4% of them were collected from a sampling site of near-neutral soil (pH 7.3; EC, 77  $\mu\text{S}/\text{cm}$ ), whereas 93.0% of *S. fredii* strains were isolated from nodules in alkaline soils (pH 7.6–8.04), and 66.2% of them were found at a site with relatively high value of soil EC (1,090  $\mu\text{S}/\text{cm}$ ). †In Huang-Huai-Hai (2, 3); *Bradyrhizobium* dominated (89.9%) soybean nodules in soils with pH 6.91–7.73, whereas *Sinorhizobium* was the major (85.5%) microsymbiont of soybean in soils with higher pH values (pH  $\geq$  7.81).

- Han LL, et al. (2009) Unique community structure and biogeography of soybean rhizobia in the saline-alkaline soils of Xinjiang, China. *Plant Soil* 324:291–305.
- Li QQ, et al. (2011) Diversity and biogeography of rhizobia isolated from root nodules of *Glycine max* grown in Hebei Province, China. *Microb Ecol* 61:917–931.
- Zhang YM, et al. (2011) Biodiversity and biogeography of rhizobia associated with soybean plants grown in the North China Plain. *Appl Environ Microbiol* 77:6331–6342.





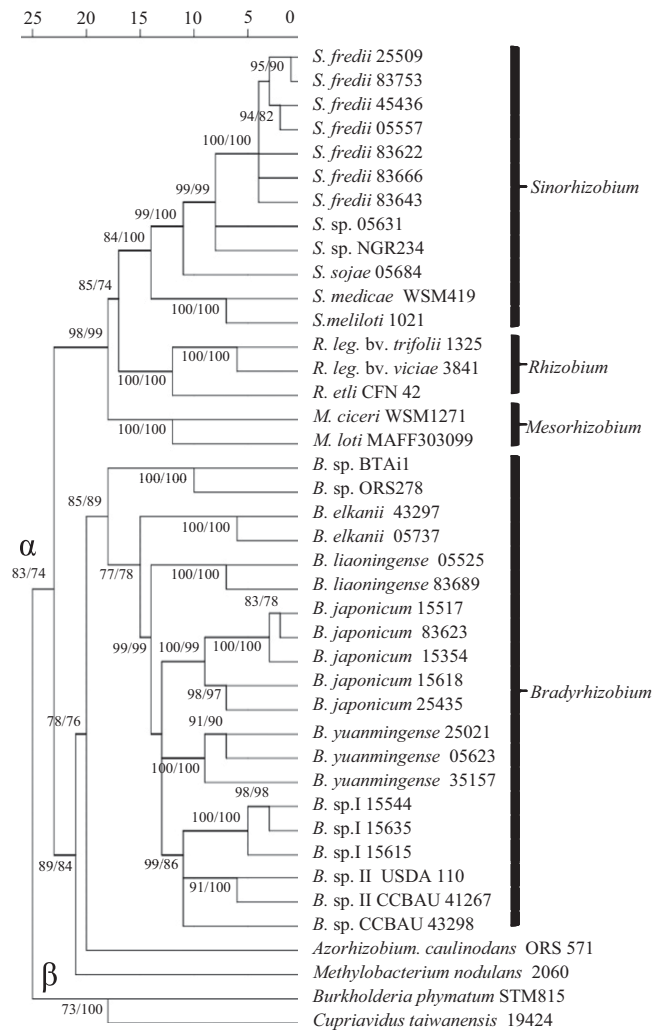
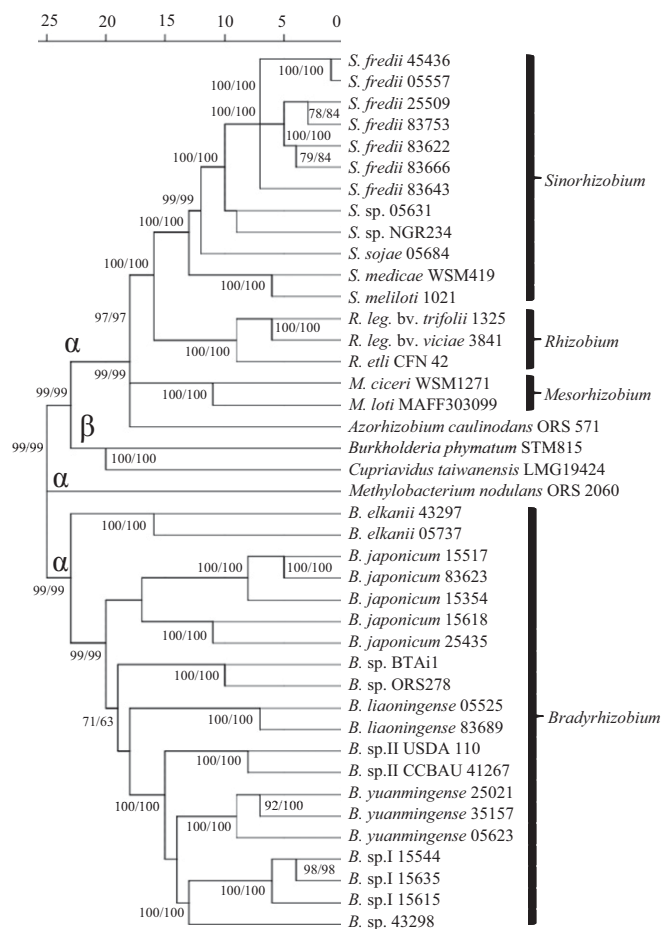


Fig. 54. Hierarchical clustering of rhizobia based on heat map of 887 functional genes. Approximately unbiased probability and bootstrap probability (au/bp) values of >70% were indicated at each node.  $\alpha$ , the branch of  $\alpha$ -proteobacteria;  $\beta$ , the branch of  $\beta$ -proteobacteria.





**Fig. S6.** Hierarchical clustering of rhizobia based on heat map 66,150 pan genes. Approximately unbiased probability and bootstrap probability (au/bp) values of >70% were indicated at each node.

## Other Supporting Information Files

- [Table S1 \(DOC\)](#)
- [Table S2 \(DOC\)](#)
- [Table S3 \(DOC\)](#)
- [Table S4 \(DOC\)](#)
- [Table S5 \(DOC\)](#)
- [Table S6 \(DOC\)](#)
- [Dataset S1 \(XLS\)](#)