

Supplementary Table S6. Information regarding the phylogenetic analyses for each *recA* dataset

	<i>Ensifer</i>	<i>Mesorhizobium</i>	<i>Paraburkholderia</i>	<i>Rhizobium</i>	<i>Bradyrhizobium</i>
Number of isolates	32	27	19	6	1
<b><i>recA</i></b>					
Initial number of taxa	160	174	213	132	272
Number of haplotypes	94	131	156	115	194
Length of alignment	525	474	549	480	492
Evolutionary model <sup>a</sup>	TrN+I+G	TrN+I+G	TIM2+I+G	HKY+I+G	TIM2+I+G

<sup>a</sup> Specifics for the evolutionary models used: TrN (Tamura and Nei, 1993); TIM2 (“transitional model”; Posada, 2008) and HKY (Hasegawa et al. 1985). For each of these models the datasets had a proportion of invariable sites (+I) and had rate variation among sites (+G).