

Table S1. Amplification primers for bacterial and chloroplast regions used in this study.

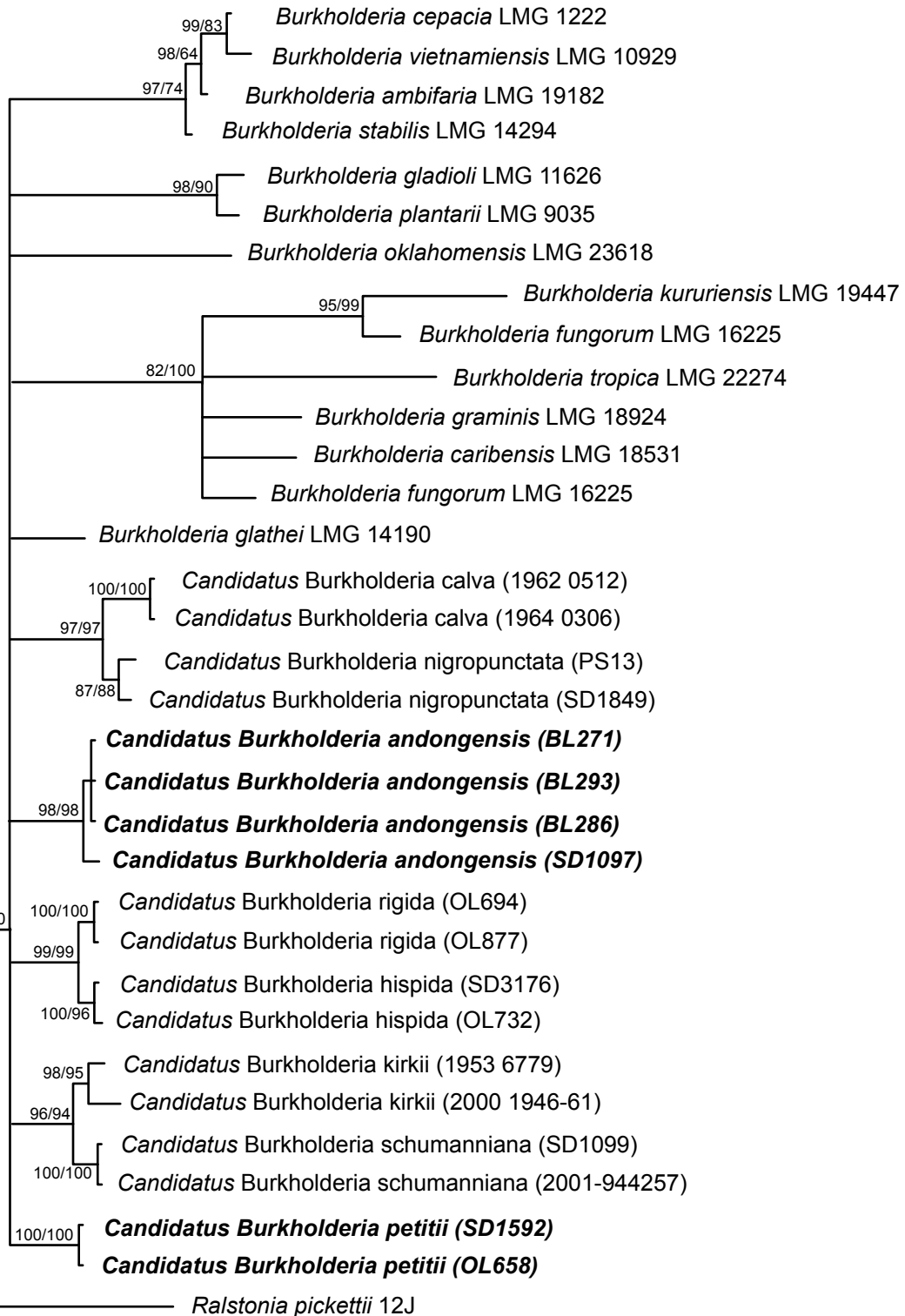
Region	Primer	Primer sequence (5'-3')	Reference
16S rDNA	16SB (forward)	AGAGTTTGATCCTGGCTCAG	Van Oevelen et al. 2001
	16SE (reverse)	AAGGAGGTGATCCAGCCGCA	
<i>recA</i>	<i>recA</i> -F (forward)	AGGACGATTCATGGAAGAWAGC	Spilker et al. 2009
	<i>recA</i> -R (reverse)	GACGCACYGAYGMRTAGAACTT	
<i>gyrB</i>	<i>gyrB</i> -F (forward)	ACCGGTCTGCAYCACCTCGT	Spilker et al. 2009
	<i>gyrB</i> -R (reverse)	YTCGTTGWARCTGTCGTTCCACTGC	
<i>rps16</i>	<i>rps16</i> -F (forward)	GTGGTAGAAAGCAACGTGCGACTT	Oxelman et al. 1997
	<i>rps16</i> -R2 (reverse)	TCGGGATCGAACATCAATTGCAAC	
<i>trnG</i>	<i>trnG</i> -1F (forward)	TAGCGGGTATAGTTTAGTGG	Tesfaye et al. 2007
	<i>trnG</i> -725R (reverse)	ATCGTTAGCTTGGAAAGGCT	
<i>trnL-trnF</i>	<i>trnL</i> -c (forward)	CGAAATCGGTAGACGCTACG	Taberlet et al. 1991
	<i>trnL</i> -f (reverse)	ATTTGAACTGGTGACACGAG	
<i>petD</i>	<i>petD</i> -1365 (forward)	TTGACYCGTTTTTATAGTTTAC	Löhne & Borsch 2004
	<i>petD</i> -738 (reverse)	AATTTAGCYCTTAATACAGG	
<i>petA-psbJ</i>	<i>petA</i> (forward)	AACARTTYGARA AGGTTCAAT T	Shaw et al. 2005
	<i>psbJ</i> (reverse)	ATAGGTACTGTARCYGGTATT	
<i>atpI-atpH</i>	<i>atpI</i> (forward)	TATTTACAAGYGGTATTCAAGCT	Shaw et al. 2005
	<i>atpH</i> (reverse)	CCAAYCCAGCAGCAATAAC	

Table S2. Characteristics of plastid datasets.

	<i>rps16</i>	<i>trnG</i>	<i>trnL-trnF</i>	<i>petD</i>	<i>petA-psbJ</i>	<i>atpI-atpH</i>
Number of taxa	9	9	9	8	9	5
Aligned characters (bp)	784	642	811	930	692	855
Length variation (minimum-maximum)	781-783	636-640	798-811	928-929	689-692	830-850
Identical sites	778	622	791	922	686	825
Variable sites	6 (0.8 %)	20 (3.1 %)	20 (2.5 %)	8 (0.7 %)	6 (0.9 %)	30 (3.5 %)
Indels	3	2	6	2	1	4

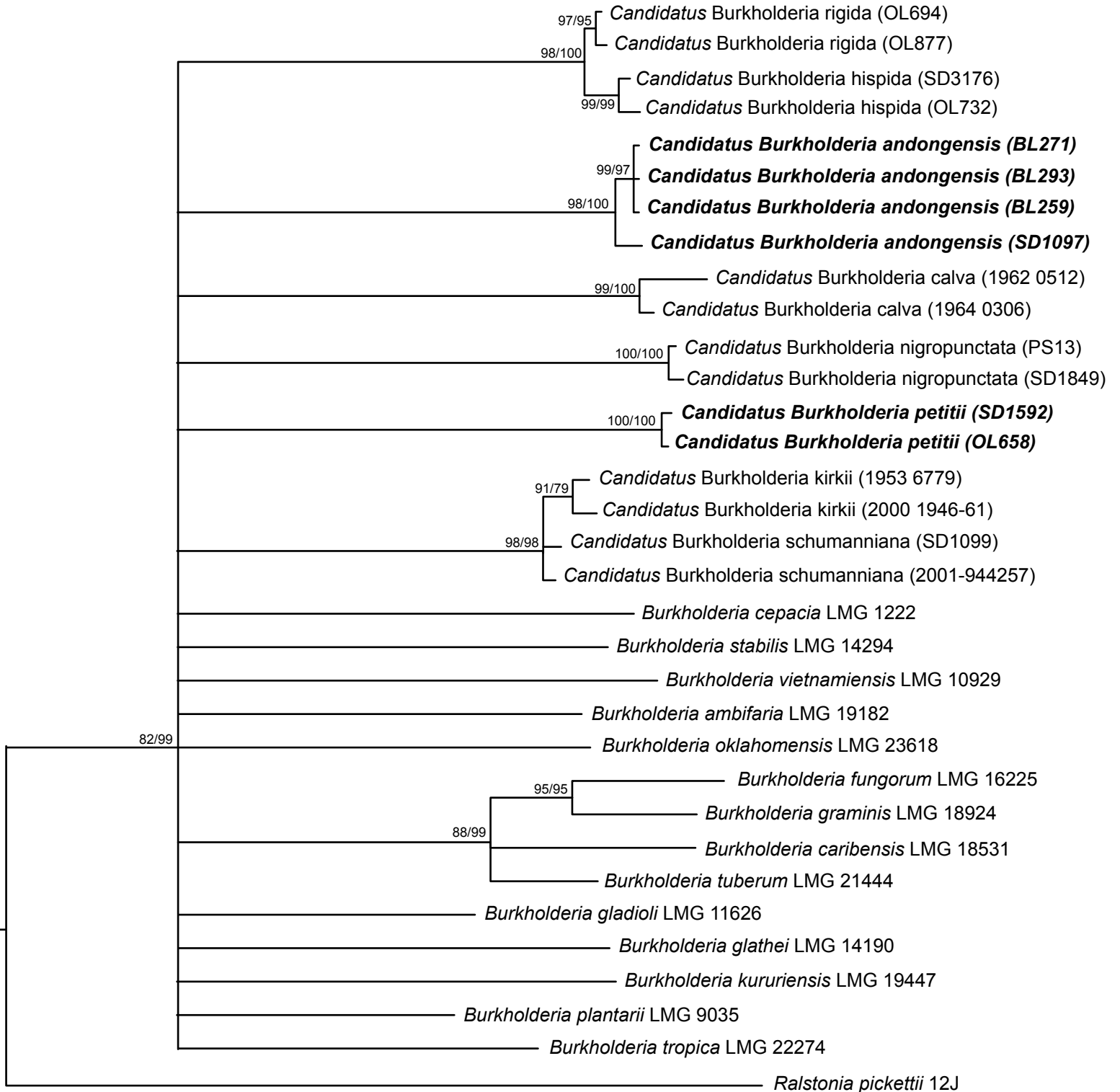
Fig. S1. Phylogenetic relationships within *Burkholderia* based on phylogenetic analysis of **(a)** 16S rDNA, **(b)** *recA* and **(c)** *gyrB* data. Support values for the Bayesian and Maximum Likelihood analysis are given at the nodes (Bayesian posterior probabilities - bootstrap values from the Maximum Likelihood analysis). Branches of leaf nodulating endosymbionts are shown in bold.

(A)



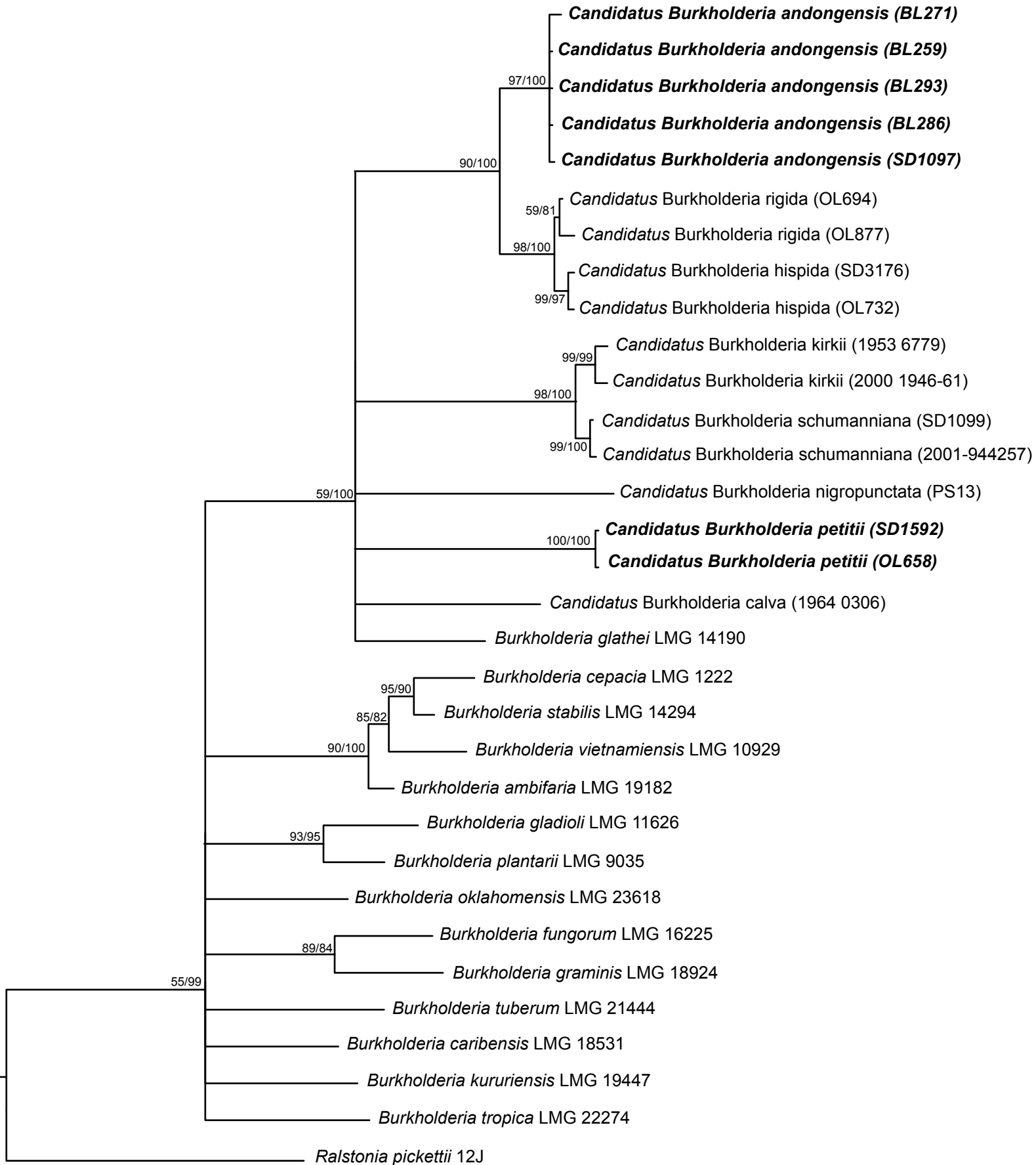
0.06 substitution/site

(B)



0.05 substitution/site

(C)



0.08 substitution/site