

Supplemental Material



Fig. S1. Map showing the sampling locations. Cattle with clinical babesiosis were sampled in the Badulla, Kilinochchi, and Jaffna districts in Sri Lanka.

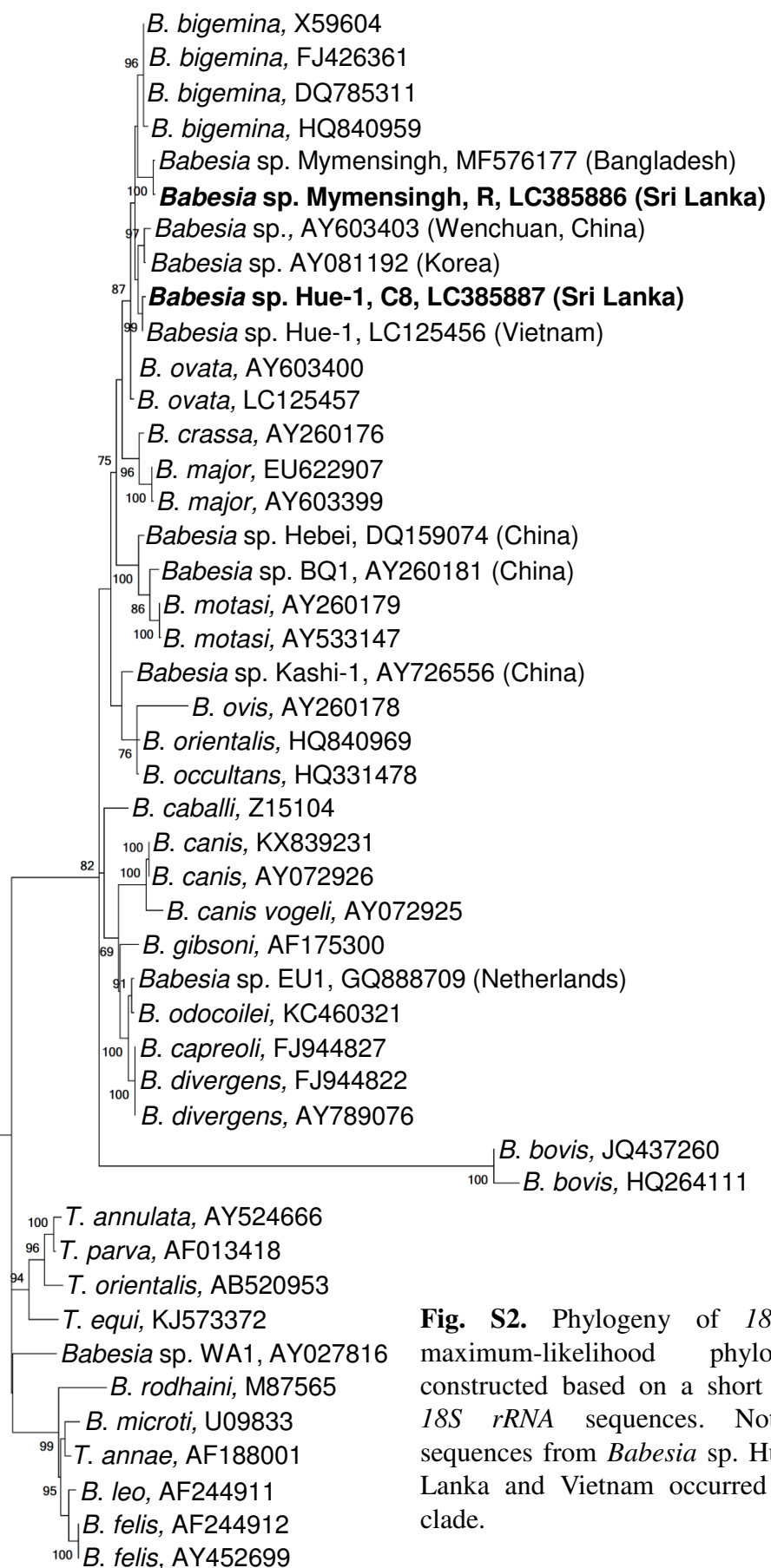


Fig. S2. Phylogeny of 18S rRNA. A maximum-likelihood phylogeny was constructed based on a short alignment of 18S rRNA sequences. Note that the sequences from *Babesia* sp. Hue-1 from Sri Lanka and Vietnam occurred in the same clade.

Table S1. Primers used in diagnostic PCR assays

Pathogen	Target gene	Primer sequence (5' - 3') ^a		Amplicon size (bp)	Reference
		Forward	Reverse		
<i>B. bovis</i>	<i>rap-1</i>	TCAACAACGTA CTCTATATGGCTACC	CTACCGACCAGAACCTTCTTCACCAT	298	(1)
<i>B. bigemina</i>	<i>ama-1</i>	TACTGTGACGAGGACGGATC	CCTCAAAAGCAGATTCGAGT	211	(2)
<i>B. ovata</i>	<i>ama-1</i>	GATACGAGGCTGTCGGTAGC	AGTATAGGTGAGCATCAGTG	504	(3)
<i>Th. annulata</i>	<i>tams-1</i>	ATGCTGCAAATGAGGAT	GGA CTGATGAGAAGACGATGAG	768	(4)
<i>Th. orientalis</i>	<i>mpsp</i>	CTTTCCTAGGATACTTCCT	ACGGCAAGTGGTGAGAACT	776	(5)
<i>Tr. theileri</i>	<i>catl</i>	CGTCTCTGGCTCCGGTCAAAC	TTAAAGCTTCCACGAGTTCTTGATGATCCAGTA	289	(6)
<i>A. marginale</i>	<i>msp5</i>	GTGTTCTGGGGTACTCCTATGTGAACAAG	AAGCATGTGACCGCTGACAACTTAAACAG	547	(7)

^a All parasite species were detected by single-step PCR, although the *B. bovis*-, *B. bigemina*-, and *A. marginale*-specific PCR assays were originally described as nested PCR assays.

Table S2. PCR detection of *Babesia*, *Theileria*, *Trypanosoma*, and *Anaplasma* species in clinical cases of bovine babesiosis in Sri Lanka

No.	Animal ID	<i>B. bovis</i>	<i>B. bigemina</i>	<i>B.ovata</i>	<i>Th. annulata</i>	<i>Th. orientalis</i>	<i>Tr.theileri</i>	<i>A. marginale</i>
1	I	+	-	-	+	-	+	-
2	L1	-	+	-	-	+	+	-
3	L2	-	+	-	-	-	+	-
4	R	-	-	-	-	+	+	-
5	S	+	+	-	-	+	+	-
6	T1	+	+	-	-	+	+	-
7	T2	+	+	-	-	-	+	-
8	V	+	+	-	-	-	+	-
9	C2	-	+	-	+	+	-	-
10	C5	+	-	-	+	+	-	-
11	C6	+	-	-	+	+	-	-
12	C7	+	+	-	-	-	-	-
13	C8	+	+	+	+	+	-	+
Total		9	9	1	5	8	8	1

PCR, polymerase chain reaction; ID, identification; +, positive; -, negative

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