

Epidemiology and Diversity of Rickettsiales Bacteria in Humans and Animals in Jiangsu and Jiangxi provinces, China

Running title: Infection of Rickettsiales bacterial in China

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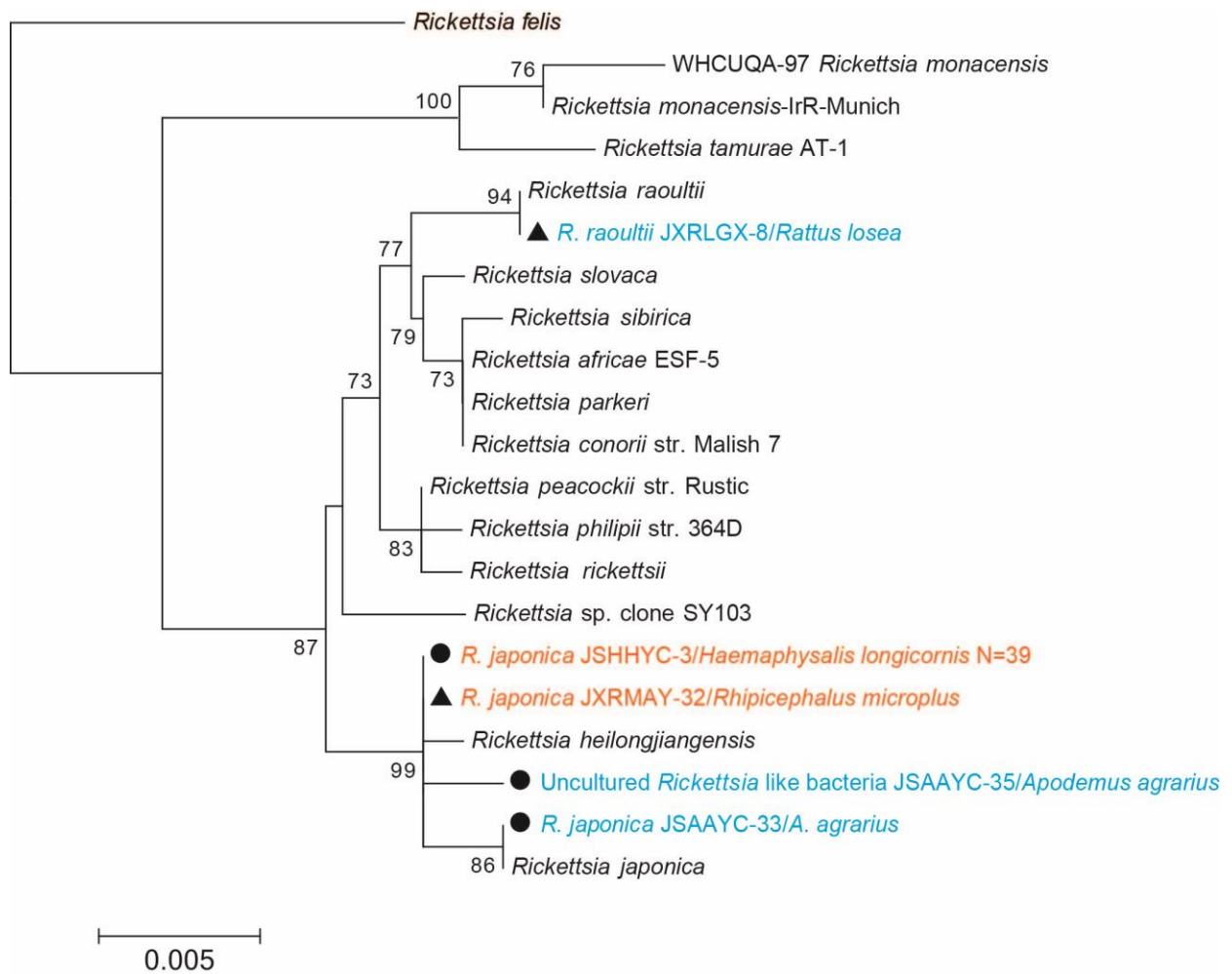
Supplementary Table S1. Bacterial sequences obtained in this study.

Strains	Genes(nt)			Bacteria ^a
	<i>rrs</i>	<i>groEL</i>	<i>TSA56</i>	
Jiangsu Province				
Human				
JSHMFN-77	1356 (99.41%) ^b	- ^c	-	<i>R. monacensis</i>
JSHFFN-74	-	-	540 (99.44%)	<i>O. tsutsugamushi</i>
<i>Apodemus agrarius</i>				
JSAAYC-40	-	-	738 (99.86%)	<i>O. tsutsugamushi</i>
JSAAYC-43	-	-	708 (99.86%)	<i>O. tsutsugamushi</i>
JSAAYC-57	-	-	882 (98.60%)	<i>O. tsutsugamushi</i>
JSAAYC-59	-	-	711 (99.86%)	<i>O. tsutsugamushi</i>
JSAAYC-61	1091 (100.0%)	-	-	<i>R. heilongjiangensis</i>
JSAAYC-87	1091 (100.0%)	-	-	<i>R. heilongjiangensis</i>
JSAAYC-19	795 (99.87%)	-	-	<i>R. japonica</i>
JSAAYC-33	790 (100.0%)	807 (100.0%)	-	<i>R. japonica</i>
JSAAYC-35	910 (99.89%)	663 (99.50%)	-	<i>R. japonica</i>
JSAAYC-39	910 (99.89%)	-	-	<i>R. japonica</i>
JSAAYC-58	910 (99.89%)	-	-	<i>R. japonica</i>
<i>Mus musculus</i>				
JSMMYC-52	910 (99.89%)	-	-	<i>R. japonica</i>
<i>Haemaphysalis longicornis</i>				
JSHHYC-3 (N=39)	1303 (100%)	702 (99.75%)	-	<i>R. japonica</i>
Jiangxi Province				
Human				
JXHFRJ-71	957 (98.75%)	-	-	<i>A. bovis</i>
<i>A. agrarius</i>				
JXAASY-38	1376 (99.78%)	-	-	<i>Ca. N. mikurensis</i>
JXAAGX-49	1316 (99.70%)	-	-	<i>A. phagocytophilum</i>
JXAASY-51	1406 (99.57%)	1248 (92.16%)	-	<i>A. phagocytophilum</i>
<i>Rattus losea</i>				
JXRLYD-97	1122 (99.73%)	-	-	<i>R. parkeri</i>
JXRLGX-8	895 (100.0%)	750 (100.0%)	-	<i>R. raoultii</i>
JXRLGX-13	1376 (100.0%)	-	-	<i>Ca. N. mikurensis</i>
JXRLGX-16	1376 (100.0%)	-	-	<i>Ca. N. mikurensis</i>
JXRLSY-59	1384 (99.93%)	-	-	<i>Ca. N. mikurensis</i>
JXRLSY-54	717 (99.72%)	1000 (94.44%)	-	<i>E. chaffeensis</i>
JXRLSY-56	717 (99.30%)	1003 (91.75%)	-	<i>E. chaffeensis</i>
JXRLGX-39	1406 (99.72%)	1248 (91.74%)	-	<i>A. phagocytophilum</i>
<i>Suncus murinus</i>				
JXSMYD-70	1376 (100.0%)	-	-	<i>Ca. N. mikurensis</i>
<i>Rhipicephalus microplus</i>				
JXRMAY-32	1337 (100.0%)	801 (99.75%)	-	<i>R. japonica</i>

^a The abbreviation is the same as used in Table3.

^b The length of sequence amplified from the samples (Nucleotide sequence identity compared to the reference sequences from GenBank).

^c “-”, not available.



Supplementary Figure S1: Phylogenetic tree based on partial *groEL* gene sequences of *Rickettsia*. The tree was mid-point rooted for clarity only. Bootstrap values (>70%) are shown for appropriate nodes. The scale bar represents number of nucleotide substitutions per site. The sequences from rodents and shrews are marked in blue, and those from ticks are marked in orange.