

Table S1. Pairwise K2P genetic distances between *Cox1* sequences involved in the analyses. The number of base substitutions per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. Analyses were conducted using the Kimura 2-parameter model. The rate variation among sites was modeled with a gamma distribution (shape parameter = 1). The analysis involved 11 nucleotide sequences. Codon positions included were 1st+2nd+3rd. All ambiguous positions were removed for each sequence pair. There were a total of 1166 positions in the final dataset. Evolutionary analyses were conducted in MEGA7.

##	Sequence accession number and mite species	1	2	3	4	5	6	7	8	9	10	11
1	OP730707 <i>N. limpopoensis</i> n. sp.		0.02	0.02	0.02	0.02	0.02	0.03	0.04	0.03	0.03	0.08
2	OP730708 <i>N. zuluensis</i> n. sp.	0.24		0.02	0.02	0.02	0.02	0.03	0.03	0.03	0.03	0.07
3	KY922365 <i>N. rostratae</i>	0.22	0.22		0.02	0.02	0.02	0.03	0.03	0.03	0.03	0.07
4	MT712729 <i>N. longissimus</i>	0.23	0.23	0.24		0.02	0.02	0.03	0.03	0.03	0.03	0.07
5	MT712731 <i>Novophytoptus</i> sp.	0.26	0.27	0.28	0.27		0.02	0.03	0.04	0.04	0.03	0.08
6	MT712730 <i>N. luzulis</i>	0.23	0.23	0.21	0.21	0.26		0.03	0.03	0.00	0.03	0.07
7	KT070240 <i>N. cf rostratae</i>	0.24	0.23	0.21	0.25	0.30	0.21		0.03	0.03	0.07	0.12
8	KT070241 <i>N. cf rostratae</i>	0.27	0.26	0.21	0.25	0.35	0.21	0.20		0.03	0.06	0.12
9	KT070242 <i>N. cf luzulis</i>	0.25	0.24	0.20	0.23	0.31	0.00	0.21	0.21		0.06	0.10
10	KY922364 <i>Oziella atherodes</i>	0.40	0.39	0.36	0.39	0.46	0.38	0.52	0.51	0.50		0.05
11	MN905325 <i>Pentasetacus araucariae</i>	0.86	0.78	0.79	0.77	0.80	0.73	0.87	0.88	0.80	0.55	