

Table S1

Estimates of evolutionary divergence of *cox1* over sequence pairs between groups. Analyses were conducted using the Tamura 3-parameter model (Tamura, 1992). Standard error estimate(s) are shown above the diagonal and were obtained by a bootstrap procedure (1000 replicates). This analysis involved 9 nucleotide sequences with *C. imicola* as outgroup. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated (complete deletion option). There were a total of 614 positions in the final dataset. Evolutionary analyses were conducted in MEGA11 (Tamura et al., 2021).

	<i>C. foxi</i> (LC704477) D.R.	<i>C. foxi</i> (LC704478) D.R.	<i>C. foxi</i> (LC704479) D.R.	<i>C. foxi</i> (LC704480) D.R.	<i>C. foxi</i> (LC704481) D.R.	<i>C. foxi</i> (LC704482) D.R.	<i>C. foxi</i> (PLECH1418-20) C.R.	<i>C. foxi</i> (PLJAY474-20) C.R.	<i>C. imicola</i> (KT307823) (outgroup)
<i>C. foxi</i> (LC704477) D.R.		0,00233	0,00000	0,00000	0,00163	0,00000	0,00166	0,00228	0,01767
<i>C. foxi</i> (LC704478) D.R.	0,00327		0,00233	0,00233	0,00284	0,00233	0,00162	0,00327	0,01787
<i>C. foxi</i> (LC704479) D.R.	0,00000	0,00327		0,00000	0,00163	0,00000	0,00166	0,00228	0,01767
<i>C. foxi</i> (LC704480) D.R.	0,00000	0,00327	0,00000		0,00163	0,00000	0,00166	0,00228	0,01767
<i>C. foxi</i> (LC704481) D.R.	0,00163	0,00491	0,00163	0,00163		0,00163	0,00231	0,00162	0,01786
<i>C. foxi</i> (LC704482) D.R.	0,00000	0,00327	0,00000	0,00000	0,00163		0,00166	0,00228	0,01767
<i>C. foxi</i> (PLECH1418-20) C.R.	0,00163	0,00163	0,00163	0,00163	0,00327	0,00163		0,00283	0,01768
<i>C. foxi</i> (PLJAY474-20) C.R.	0,00327	0,00656	0,00327	0,00327	0,00163	0,00327	0,00491		0,01802
<i>C. imicola</i> (KT307823) (outgroup)	0,17669	0,17885	0,17669	0,17669	0,17883	0,17669	0,17670	0,18096	

D.R.= Dominican Republic, R.C.= Costa Rica