

**Appendix 2.** Results for statistical tests analysing the relationship between body size and substitution rate for nonsynonymous (dN) and synonymous (dS) substitutions for the protein coding genes. The “no. of +ve signs” indicate the number of comparisons in which the bigger species had a faster rate of molecular evolution than the smaller species, out of the total “no. of pairs” for the data set. Significant results are shown with an asterisk. Bonferroni’s corrected values are indicated in parentheses. Dashes indicate that a large number of zero-length branches precluded use of the test.

Data set	Gene	No. of pairs	No. of +ve signs		Sign test <i>P</i> value		Signed rank test <i>P</i> value		Spearman’s rank		Spearman <i>P</i> value	
			dN	dS	dN	dS	dN	dS	dN	dS	dN	dS
Species-level comparisons												
Lepidoptera	COI	63	29	31	0.684	1.000	0.877	0.701	0.080	0.039	0.618	0.774
	COII	38	19	22	0.487	0.418	0.056	0.350	-0.343	-0.075	0.075	0.652
	ND5	28	11	15	0.839	0.851	0.786	0.891	-0.124	0.251	0.561	0.215
Arachnida	COI	17	3	9	0.035* (0.352)	1.000	0.083	0.554	-0.084	0.164	0.800	0.528
Cephalopoda	COI	34	19	14	0.201	0.392	0.382	0.039* (0.394)	-0.420	0.021	0.052	0.905
Gastropoda	COI	14	8	8	0.581	0.581	0.424	0.946	-0.007	-0.646	0.991	0.037* (0.370)
Platyhelminthes	COI	10	5	5	1.000	1.000	0.910	0.910	0.595	0.191	0.132	0.665
Family-level comparisons												
Hymenoptera	COI	8	5	6	0.727	0.289	0.484	0.109	-0.119	-0.024	0.793	0.977
Bivalvia	COI	10	3	3	0.344	0.344	0.557	0.106	0.317	0.115	0.410	0.759
Annelida	H3	8	6	3	0.289	0.727	0.063	0.547	-	-0.048	-	0.935