Table S2. Numbers of characters, base frequencies and maximum uncorrected pairwise distances. * *cox1* mtDNA aligned only by ClustalX..

alignment/	number of	constant	variable	parsimony	base frequencies (%)				max. uncorrec.
partition	characters	characters	uninformative	informative	A	C	G	T	pairw. dist. (%)
BlastAlign									
Total dataset	4675	2781	441	1453	27.17	21.08	24.38	27.38	15.41
18S rDNA	2186	1587	163	436	24.03	24.44	27.94	23.59	08.90
28S rDNA	1001	635	128	238	25.49	23.46	30.93	20.12	16.74
rrnl mtDNA	765	334	104	327	32.28	09.73	17.13	40.87	26.58
cox1 mtDNA*	723	225	046	452	33.25	17.86	14.51	34.39	35.00
ClustalX									
Total dataset	4330	2245	372	1713	27.12	20.99	24.37	27.53	19.07
18S rDNA	2130	1449	160	521	23.94	24.52	27.97	23.57	12.40
28S rDNA	910	396	123	391	25.33	23.57	30.97	20.13	30.47
rrnl mtDNA	567	175	43	349	32.18	09.47	17.01	41.33	32.28
cox1 mtDNA*	723	225	046	452	33.25	17.86	14.51	34.39	35.00