Table A.4. Estimates of genetic diversity for populations of the clade A (based on COI): number individuals for group (*n*), number of haplotypes (*h*), number of segregating sites (*S*), nucleotide diversity ($\pi \pm$ SD) and haplotype diversity H_d ± SD and test for demographic expansion accounted

Id	*n*	*h*	*S*	π	H_d	Tajima's D	Fu's Fs
54	4	3	10	0.0116 ± 0.0043	0.833 0.222	−0.2223	1.606
55	2	2	1	0.0022 ± 0.0011	1.000 ± 0.500	–	0.000
56	1	1	0	0	–	–	–
57	1	1	0	0	–	–	–
58	1	1	0	0	–	–	–
59	3	3	2	0.0029 ± 0.0010	1.000 ± 0.272	–	−1.216
60	1	1	0	0	–	–	–
61	10	4	15	0.0101 ± 0.0025	0.889 ± 0.075	−0.8460	0.203
62	2	2	5	0.0109 ± 0.0055	1.000 ± 0.500	–	1.609
63	2	1	0	0	–	–	–
64	1	1	0	0	–	–	–
65	1	1	0	0	–	–	–
66	1	1	0	0	–	–	–
87	4	1	0	0	–	–	–
115	5	2	3	0.0039 ± 0.0012	0.600 ± 0.175	1.5727	2.429
116	5	1	0	0	–	–	–
117	5	1	0	0	–	–	–
118	2	1	0	0	–	–	–
119	5	1	0	0	–	–	–
120	5	1	0	0	–	–	–
121	4	2	3	0.0033 ± 0.0017	0.500 ± 0.265	−0.7544	1.716
122	3	1	0	0	–	–	–
123	3	1	0	0	–	–	–
124	5	1	0	0	–	–	–
125	2	1	0	0	–	–	–
126	3	2	9	0.0116 ± 0.0030	0.833 ± 0.222	0.8602	1.606
127	6	3	23	0.0249 ± 0.0055	0.733 ± 0.155	0.8275	5.222
211	4	1	0	0	–	–	–
214	5	3	12	0.0109 ± 0.0057	0.800 ± 0.164	−0.9543	2.306
215	3	2	3	0.0044 ± 0.0021	0.667 ± 0.314	–	1.609
225	4	1	0	0	–	–	–
229	2	2	1	0.0022 ± 0.0011	1.000 ± 0.250	–	0.000
251	3	1	0	0	–	–	–
253	1	1	0	0	–	–	–
254	2	1	0	0	–	–	–
255	3	1	0	0	–	–	–
257	3	1	0	0	–	–	–
258	3	1	0	0	–	–	–
259	3	1	0	0	–	–	–
260	4	2	1	0.0011 ± 0.0006	0.500 ± 0.265	−0.6124	0.172
261	3	1	0	0	–	–	–
262	3	1	0	0	–	–	–
263	3	1	0	0	–	–	–
264	3	1	0	0	–	–	–
265	5	1	0	0	–	–	–
266	5	1	0	0	–	–	–
267	4	2	3	0.0033 ± 0.0017	0.500 ± 0.265	−0.7544	1.716
268	5	1	0	0	–	–	–
270	1	1	0	0	–	–	–

* $P<0.005$.