Table A.2. 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 $H_d \pm$ SD and test for demographic expansion accounted

Id	n	h	S	π	H_d	Tajima's D	Fu's Fs
1	3	1	0	0	–	–	–
2	4	1	0	0	–	–	–
3	3	3	2	0.0019 ± 0.0007	0.600 ± 0.215	–0.0500	– 0.427
4	7	1	0	0	–	–	–
5	5	1	0	0	–	–	–
6	1	1	–	–	–	–	–
7	2	1	0	0	–	–	–
8	2	1	0	0	–	–	–
9	2	1	0	0	–	–	–
10	2	1	0	0	–	–	–
11	2	1	0	0	–	–	–
12	2	1	0	0	–	–	–
13	4	2	1	0.0015 ± 0.0004	0.667 ± 0.204	1.6330	0.540
14	1	1	–	–	–	–	–
15	1	1	–	–	–	–	–
16	1	1	–	–	–	–	–
17	4	2	1	0.0015 ± 0.0004	0.667 ± 0.204	1.6330	0.540
18	4	2	1	0.0015 ± 0.0004	0.667 ± 0.204	1.6330	0.540
19	1	1	–	–	–	–	–
20	1	1	–	–	–	–	–
21	1	1	–	–	–	–	–
22	2	1	0	0	–	–	–
23	2	1	0	0	–	–	–
24	1	1	–	–	–	–	–
25	1	1	–	–	–	–	–
26	1	1	–	–	–	–	–
27	3	1	0	0	–	–	–
28	1	1	–	–	–	–	–
29	2	1	0	0	–	–	–
30	1	1	–	–	–	–	–
31	1	1	–	–	–	–	–
33A	1	1	–	–	–	–	–
34	2	2	1	0.0022 ± 0.0011	1.000 ± 0.500	–	0.000
36	1	1	–	–	–	–	–
37	2	1	0	0	–	–	–
38	2	1	0	0	–	–	–
40	2	2	2	0.0044 ± 0.0022	1.000 ± 0.250	–	0.693
41	1	1	–	–	–	–	–
42	1	1	–	–	–	–	–
43	1	1	–	–	–	–	–
44	2	1	0	0	–	–	–
45	2	1	0	0	–	–	–
46	2	1	0	0	–	–	–
47	2	1	0	0	–	–	–
52	1	1	–	–	–	–	–
53	1	1	–	–	–	–	–
85	1	1	–	–	–	–	–
129	3	1	0	0	–	–	–
130	3	1	0	0	–	–	–
131	4	1	0	0	–	–	–

Id	*n*	*h*	*S*	π	H_d	Tajima's D	Fu's Fs
132	2	1	0	0	–	–	–
133	4	1	0	0	–	–	–
134	2	1	0	0	–	–	–
135	3	2	6	0.0087 ± 0.0041	0.667 ± 0.314	–	2.639
136	1	1	–	–	–	–	–
137	3	3	4	0.0058 ± 0.0027	0.667 ± 0.314	–	2.022
138	4	1	0	0	–	–	–
139	4	1	0	0	–	–	–
140	4	2	1	0.0011 ± 0.0006	0.500 ± 0.265	–0.6124	0.172
141	3	2	1	0.0015 ± 0.0007	0.667 ± 0.314	–	0.201
142	5	1	0	0	–	–	–
143	3	1	0	0	–	–	–
144	5	1	0	0	–	–	–
145	6	1	0	0	–	–	–
146	1	1	–	–	–	–	–
147	4	1	0	0	–	–	–
148	1	1	–	–	–	–	–
160	2	1	0	0	–	–	–
183	2	1	0	0	–	–	–
231	2	1	0	0	–	–	–
232	1	1	–	–	–	–	–
233	1	1	–	–	–	–	–
234	3	2	1	0.0015 ± 0.0007	0.667 ± 0.314	–	0.201
299	1	1	–	–	–	–	–

* $P<0.005$.