Table S1. Information of Microsatellite primer in this study.

Primers	Sequence	Repeat Unit	Annealing Temperature (°C)
Tail A	GCCTCCCTCGCGCCA		63
DJ234	F:ATGAATTGGACAGGAAGAGA R:ATGCTATTCCACTGTGAATG	$(AG)_{16}$	55
DJ516	F:GCTGTCCACAATAGAATTACC R:CTCTGTCTTTGCTGTCCAT	$(GA)_{18}$	50
DJ276	F:CAACATGGAGACAGATAGAGT R:TTGGGCTATGCTGATAAGC	$(AG)_6… (GA)_{25}$	59
D13	F:AGTAACCAGCGGCTATGT R:GGTACTACTACTGCCTGAAA	$(AC)_{13}$	62
DJ360	F:TTGGAGACTGCTGTTACAC R:ATCCTCTCACTGCATTCATT	$(GA)_{21}$	57

Table S2. Mitochondrial molecular (D-loop & cyt b) indices.

Sequence	Population	N	S	K	Hap	Hd	π	Tajima's D	Fu's
D-loop	HM	27	30	4.145	19	0.943	0.0038	−1.78965	−2.58805
	HX	28	6	0.429	2	0.071	0.00039	−2.09646*	−3.4717**
	QY	24	16	4.547	11	0.841	0.00417	0.21814	−0.35339
	LX	29	6	1.153	3	0.532	0.00106	−0.70656	0.75111
	BL	24	19	3.924	12	0.874	0.00327	−0.08174	−0.5662
	HZ	23	15	3.565	9	0.812	0.00361	−1.1258	−1.26537
	Total	155	40	4.25002	37	0.853	0.0039	−1.25037	−2.82355*
Cyt b	HM	23	10	0.949	10	0.688	0.0009	−2.1913**	−3.2657**
	HX	28	2	0.143	3	0.14	0.00014	−1.5106	−2.35188
	QY	16	3	0.592	3	0.242	0.00053	−1.0018	−0.33572
	LX	20	0	0	1	0	0	0	0
	BL	24	7	1.15238	4	0.414	0.00104	−1.32187	−1.46387
	HZ	21	7	0.583	4	0.239	0.00053	−2.15287*	−3.45939*
	Total	132	22	0.569	18	0.306	0.00051	−2.4382**	−4.6887**

The population genetic statistics includes N: total number of individuals sampled in the population; Hap: number of haplotypes; S: number of segregating sites; K: average number of nucleotide differences; Hd: haplotype diversity; π: nucleotide diversity; Tajima'sD: Tajima's D test value; Fu's: Fu's Fs-test value.

**P < 0.02; * P < 0.05

Table S3. Distribution of haplotypes and polymorphic sites based on D-loop.

Hap	Sequence	Number	Component
Hap_1	GCATTTGGATAGGAGCACTTCCGAGAGAGAAGGCCTTCTC	2	BL :1 HZ:1
Hap_2	. . . . G . . A . . . . T . . . . T	22	BL:8 HM:5 HZ:7 QY:2
Hap_3	. . . . G . . A	15	BL: 7 HM: 1 HX:1 HZ:5 QY:1
Hap_4	. . G C . . . . G . . A A . . . . T . . T . . . . C .	1	BL:1
Hap_5	. . . . G C . . A . . . . . . T . . . . T . . . C .	3	BL:1 HZ:2
Hap_6	. . . . . . A . G C . . A G . . . . . . T . . . . C .	3	BL:3
Hap_7	. . . . . . A . G . . . A . . . . . T . . . . C .	1	BL:1
Hap_8	A . G . . . . . G . . A A . . . . . . T . . . . T C .	1	BL:1
Hap_9	. . G . . . A A G . . A A G . . . . . T . . . . C .	2	BL:1 HZ:1
Hap_10	. . . . G C . . . . T . . . . T . . . . . . T . A . . .	50	HM:5 HX:27 HZ:1 LX:9 QY:8
Hap_11	. . . . G . . A . . . . T . . . . A . . T	2	HM:1 HZ:1
Hap_12	. . . . G . . A . . . . T . . . . . G A . . . . . T	1	HM:1
Hap_13	. . . . G . . A . . . . . . T . . . . G . . . T	1	HM:1
Hap_14	. . . . . . A . G C . A A G . . . . C . T T . . . . G . . . G . . . . C .	1	HM:1
Hap_15	. . . . G . . . . . A . . . . . T . . . . T	1	HM:1
Hap_16	. . . . G . . A . . . . T . . . G . . . . T	1	HM:1
Hap_17	. . . . G . . A . . A T . . . . T C	1	HM:1
Hap_18	. . . . G . . A . G . . . . T	7	HM:1 QY:6
Hap_19	. . . . . . A G . . A . . . . T T . . . . T	1	HM:1
Hap_20	. . . . G . . A . . . . . T . . . A . . . . T	4	HM:1 HZ:1 LX:2
Hap_21	. . . . G . . A . . . T . . . . . A . . . . A . T	1	HM:1
Hap_22	. . . . G . . A . . . . . . T . . . . T . C . . .	1	HM:1
Hap_23	. T . . . . . . G . . A . . . . . . T . . . . G . . . T	1	HM:1
Hap_24	. . . . G . . A . . . . T . . . . A	1	HM:1
Hap_25	. . . . C . . . G . . A . G . . G . . T . . . . T	1	HM:1
Hap_26	. . . . G . . . . T	1	HM:1
Hap_27	. T . . . . . . G . . A . . . . . . T . . . . T	1	HM:1

Hap_28	. . . . G . . A . . . . T	2	HZ:1
			QY:1
Hap_29	. . . . . C . . G . . A . . . . T . . . . T	1	HZ:1
Hap_30	. . G . . . A A G C . A A G . . . . . . T T . G . . . . C .	1	HZ:1
Hap_31	. . . . G C . . . . T . A . . . T . . . . . . T . A . . .	18	LX:18
Hap_32	. . . . G C . . A . . . . T . . . . C .	1	QY:1
Hap_33	. . . . C . . . G . . A . G . . G . . C T . . . . T	1	QY:1
Hap_34	. . . . . . A . G . . A A G . . . . . T . . . . C .	1	QY:1
Hap_35	. . . . G . G A . . . . T . . . . T	1	QY:1
Hap_36	. . . . . . A . G . . . A G . . . . . . T T . . . . C .	1	QY:1
Hap_37	. . G . . . A . G . . A A G . . . . . . T . . . . C .	1	QY:1

Table S4. Distribution of haplotypes and polymorphic sites based on Cyt b.

Hap	Sequence	Number	Component
Hap_1	T G A T C G C A C G G G A T T A C G T A G G	110	BL :16 HM:13 HX:26 HZ:21 LX:20 QY:14
Hap_2	. . . . . . T	1	BL:1
Hap_3	. . . . T . . . . G . . C . . .	3	BL:3
Hap_4	. . . . A . G A .	3	BL:1 HZ:1 QY:1
Hap_5	. . . . . A	2	HM:1
Hap_6	. . . . G	1	HM:2
Hap_7	. . . . A	1	HM:1
Hap_8	. . . . A . C	1	HM:1
Hap_9	. . G	1	HM:1
Hap_10	. . . . T	1	HM:1
Hap_11	. . . . A	1	HM:1
Hap_12	. . . . T	1	HM:1
Hap_13	. . . . C	1	HM:1
Hap_14	A	1	HX:1
Hap_15	. . . . A	1	HX:1
Hap_16	. A	1	HZ:1
Hap_17	. . . C . . . G T	1	HZ:1
Hap_18	. . . . A . G . .	1	QY:1

Table S5. Pairwise F$_{ST}$ (lower diagonal) and P-values (upper diagonal) between populations based on 5 microsatellite loci.

	HM	HX	LX	QY	HZ	BL
HM		0.000	0.207	0.036	0.009	0.279
HX	0.072 **		0.000	0.000	0.000	0.000
LX	0.005	0.036 **		0.027	0.000	0.144
QY	0.011 *	0.039 **	0.019*		0.000	0.009
HZ	0.021*	0.058 **	0.031**	0.023 **		0.144
BL	0.004	0.048**	0.006	0.017**	0.007	

*P<0.05, ** P<0.001