

Table 1 Gene regions sequenced, number of individuals used, results revealed from the of the sequencing process and Genbank Accession numbers

Gene region	Sample number per population	Length of the seq. (bp)	Mean nucleotide composition (%)				No. of haplotypes produced from each population		No of shared haplotypes	Genbank Accession numbers
			A	C	G	T	Northern	Southern		
Mitochondrial 16S rRNA	08	550	33.27	13.09	20.36	33.27	01	01	01	KM486609
Mitochondrial 12S rRNA	08	407	35.63	14.25	18.18	31.94	01	01	01	KM486608
Mitochondrial COI	10	690	34.97	17.87	19.86	27.29	02	02	01	KM528139– KM528141
Mitochondrial Control	15	522	42.45	9.24	6.78	41.52	07	07	07	KM486612– KM486618
Nuclear 18S RNA	08	735	22.86	23.13	29.39	24.63	01	01	01	KM486610
Nuclear H3	08	376	21.01	34.04	25.53	19.41	01	01	01	KM486611