

Genetic diversity and population structure in *Bactrocera correcta* (Diptera: Tephritidae) inferred from mtDNA *cox1* and microsatellite markers

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Table S1 Characterization of 12 microsatellite markers of *B. correcta*

Locus	<i>N</i>	<i>N_E</i>	<i>I</i>	<i>H_O</i>	<i>H_E</i>	<i>F_{IS}</i>	PIC
Bcor1	15	2.8137	1.4339	0.4968	0.6450	0.1068*	0.612
Bcor2	11	3.2737	1.4151	0.5931	0.6950	0.0957*	0.646
Bcor3	20	4.0562	1.7661	0.3446	0.7540	0.5277*	0.725
Bcor4	21	4.9162	1.9526	0.5212	0.7971	0.3042*	0.772
Bcor5	13	3.5342	1.4175	0.5419	0.7175	0.1830*	0.670
Bcor6	21	4.2824	1.8330	0.5631	0.7670	0.2544*	0.741
Bcor7	8	1.3776	0.5876	0.2670	0.2743	-0.0111	0.258
Bcor8	11	2.5975	1.3240	0.5610	0.6154	-0.0133	0.569
Bcor9	15	3.4835	1.5092	0.4968	0.7134	0.2907*	0.671
Bcor10	18	3.7198	1.8088	0.5308	0.7316	0.2516*	0.713
Bcor11	13	1.6979	0.7898	0.3864	0.4113	0.0019*	0.363
Bcor12	19	3.8287	1.7901	0.3691	0.7393	0.4730*	0.715

N: number of alleles; *N_E*: mean number of effective alleles; *I*: mean Shannon's information index; *H_O*: mean observed heterozygosity; *H_E*: mean expected heterozygosity; *F_{IS}*: within population inbreeding coefficient; PIC: polymorphic information content. *: deviation from HWE at P<0.05 after Bonferroni correction

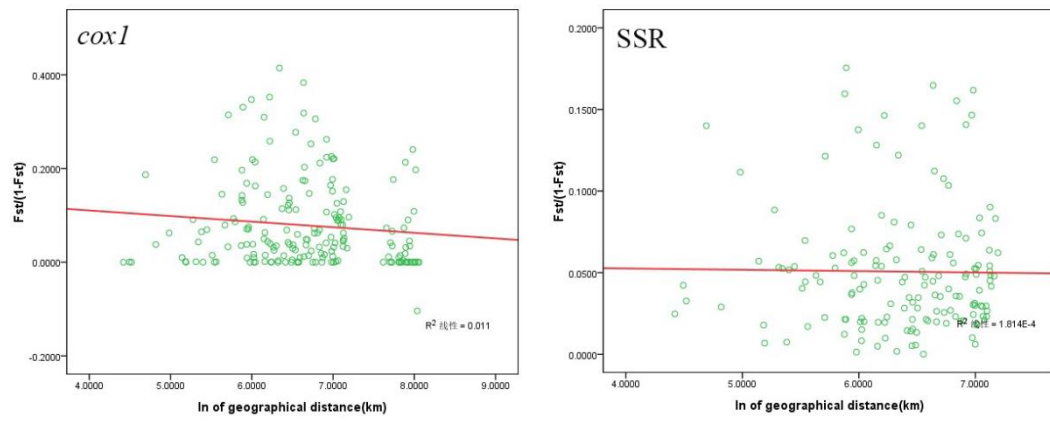


Figure S1. Mantel correlation tests of geographical and genetic distances based on two set of molecular makers of *B. correcta*

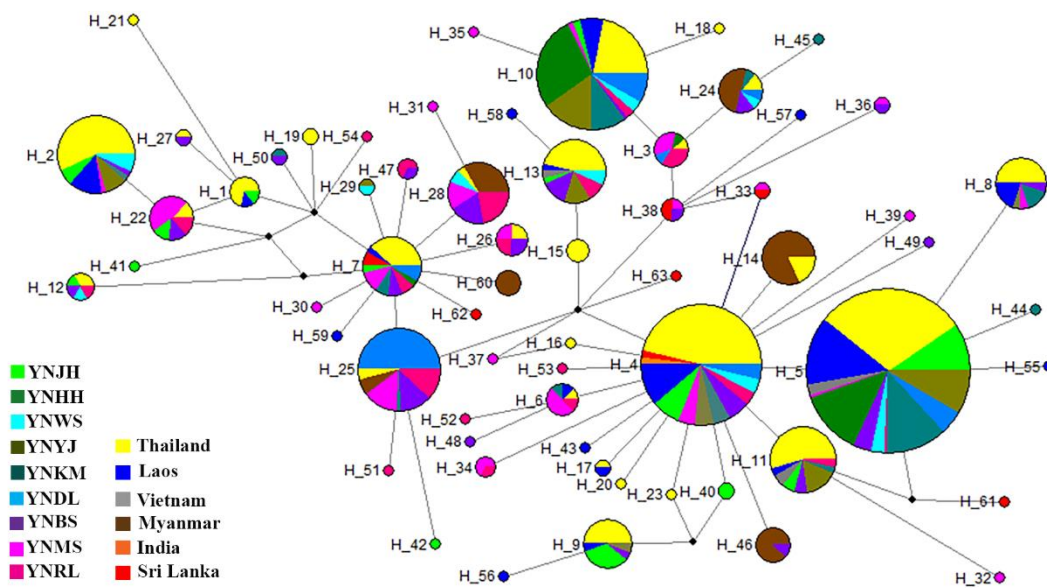


Figure S2. Median-Joining haplotype network of *B. correcta* based on mtDNA *cox1* data.

Note: Size of nodes and pie segments were proportional to haplotype frequency; small black circles represent median vectors (roughly equivalent to hypothetical unsampled haplotypes); length of the branched is proportional to number of mutational changes between haplotypes.

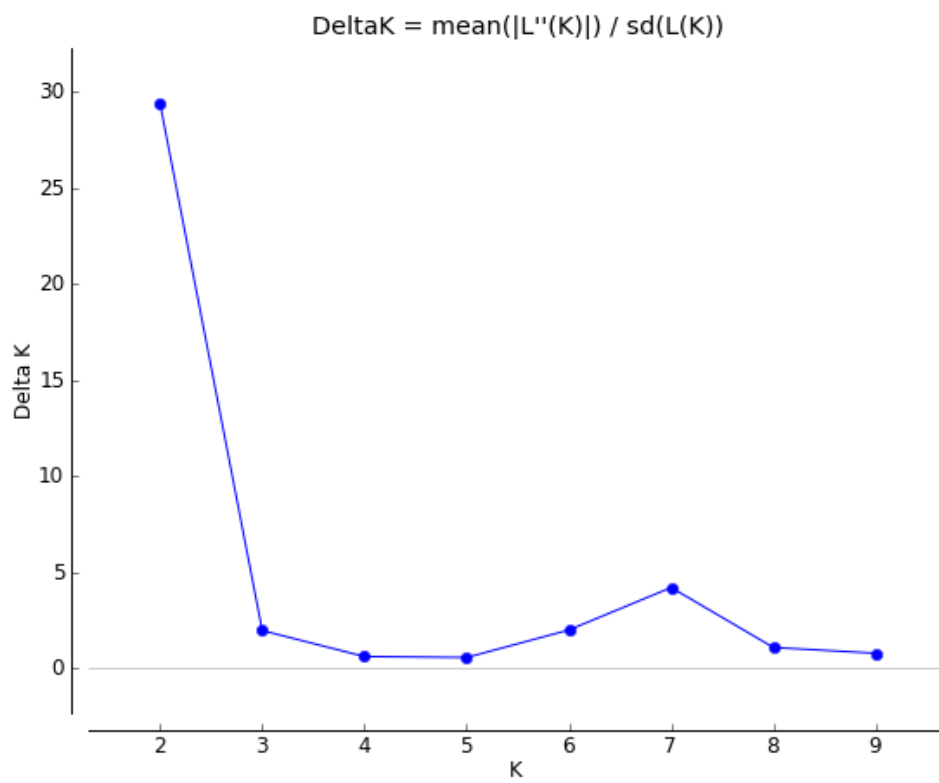


Figure S3. The graph of the best number of cluster of *B. correcta* from Structure Harvester

Table S2 SAMOVA results of *B. correcta* based on *cox1* data (K=2)

Source of Variation	d. f.	Sum of squares	Variance components	Percentage of Variation	Fixation Indices
Among groups	1	38.296	0.31330Va	12.28	$F_{SC} = 0.06143$
Among populations within groups	18	133.503	0.13743Vb	5.39	$F_{ST} = 0.17673$
Within populations	773	1623.062	2.09969Vc	82.33	$F_{CT} = 0.12284$
Total	792	1794.861	2.55042		

Table S3 AMOVA results of *B. correcta* based on *cox1* and microsatellite markers

	Source of Variation	d. f.	Sum of squares	Variance components	Percentage of Variation	Fixation Indices
cox 1	Among groups	1	38.917	0.31904Va	12.34	$F_{SC} = 0.06112^{**}$
	Among populations within groups	18	134.782	0.13853Vb	5.36	$F_{ST} = 0.17697^{**}$
	Within populations	773	1644.917	2.12796Vc	82.30	$F_{CT} = 0.12339^{**}$
	Total	792	1818.615	2.58554		
SSR	Among groups	1	68.760	0.28152 Va	7.46	$F_{IS} = 0.21817^{**}$
	Among populations within groups	16	229.773	0.11994 Vb	3.18	$F_{SC} = 0.03434^{**}$
	Among individual within populations	763	3134.964	0.73587 Vc	19.50	$F_{CT} = 0.07459^{**}$
	Within individuals	781	2059.500	2.63700 Vd	69.87	$F_{IT} = 0.30133^{**}$
	Total	1561	5492.996	3.77433		

****P<0.001**

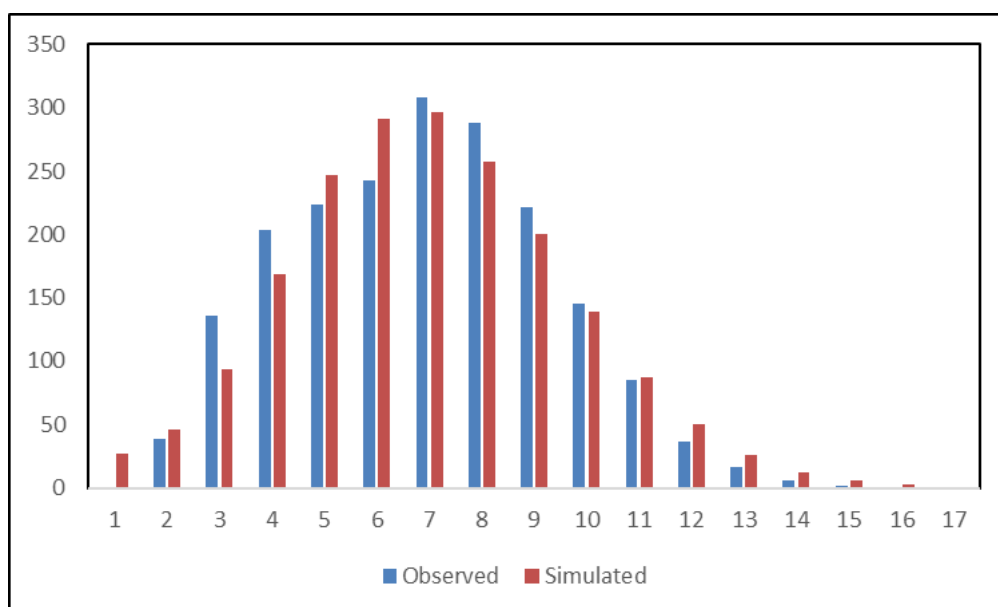


Figure S4. Mismatch distributions of the 793 *cox1* sequences of *B. correcta*