

Table S1. Primers and optimized amplification conditions for ten microsatellite loci used in *T. dimidiata*.

T_m = Annealing Temperature; Na = Number of alleles. PCR reactions were conducted in a final volume of 10 µl; using 50 ng/µl templates DNA and 2.5 U/µl of Go-Taq polymerase (Promega®). All forward primers were 5' labelled with HEX or 6-FAM dyes. Loci pairs TDMS16-TDMS22 and Tinf_ms42 -TDMS4 were amplified in a multiplex reaction.

Locus [Ref]	Primers (5'- 3')	T _m (°C)	PCR reaction Cycling conditions	Reported product (bp)	Observed product (bp)	Genbank access code	Na
TDMS1 [15]	6-FAM GGA AAT ACA GGT TTT CAC A AAT TGC ACT TTC GGA TGA	57.5	2ul of 5X buffer; 0.6ul of MgCl ₂ at 25 mM; 0.8ul of DNTp at 2.5 mM	133–221	133-194	AF487982	15
TDMS3 [15]	6-FAM GGA AAT ACA GGT TTT CAC A ACG ACC TCA ACA TCC CTT TC	57.5	0.4ul of each labeled F-primer at 20uM and 1.0ul of R-primer at 50nr/ul.	129–146	141	AF487983	1
TDMS4 [15]	6-FAM CAG TTG TTC ATC AGG AAG TGA ATC GCT CAG AAA ATA TGT TCC CAG T	55.6	95°C x 5'; [95°C x 30'' ; T _m °C x 30''; 72°C x 1'] *30; 72°C X 30'	150–186	134-180	AF487984	9
TDMS9 [15]	HEX CAT TGC AAT CGT GTC GAA AT TGC CCA AAA TTT TCG TGT CT	57.5		194–230	133-204	AF487985	19
TDMS11 [15]	HEX GGT GCA CCA TGT TTA AAG AGC GAA TGG TCT GTG AAT TG	55.6		132–230	117-249	AF487986	24
TDMS16 [15]	HEX GGT GCA CCA TGT TTA AAG TTT CAA AAG GTC CCA TTT AAC ATT	55.6		144–272	124-240	AF487987	15
TDMS19 [15]	6-FAM CTC AAG GGA TTTA TTC CCA GAA TCT CTG AGA AGC CCT ATC ACA TC	55.6		138–194	143-201	AF487988	13

TDMS22 [15]	6-FAM TAT TAT GGT TGC CGG TAT TAA GG CCA CCC AAG TTT TAC TAT CCA T	55.6		101–109	59-116	AF487989	12
Tinf_ms42 [16]	HEX GAC GCT CCA GCT ATC GAT TC GGC CAA TTG GTT TGG TAG TG	57.5	2ul of 5X buffer; 0.3ul of MgCl2 at 25 mM; 0.8ul of DNTp at 2.5 mM 1.5ul of labeled F-primer at 5uM and 2.5ul of R- primer at 50nr/ul 95°C x 5'; [95°C x 30'' ; Tm°C x 30''; 72°C x 1'] *30; 72°C X 30'	206–246	152-238	AY742683	34
Tp544 [8]	HEX TGT TAG AAT GAA TGC CAC TA GCA ATA CAA TAG AGG ACT GA	45	2ul of 5X buffer; 1.0ul of MgCl2 at 25 mM; 3.2ul of DNTp at 2.5 mM 0.4ul of labeled F-primer and R- primer at 20uM 94°C x 3'; [94°C x 30'' ; 45°C x 1'; 72°C x 30'''] *35 ; 72°C X 12'	148–172	134-240	EF672097	19

Table S2. COI Haplotype distribution of *T. dimidiata* used in this study. Map numbers and geographic origin are detailed in Table 1.

COI Haplotype code	Genbank access	Region / Map No.	Inter Andean valleys						Caribbean region				SNSM	
			1	2	3	4	5	6	7	8	9	10	11	12
Tdim_Hap1	KC489226								1					
Tdim_Hap2	KC489227								1					
Tdim_Hap3	KC489228								1					
Tdim_Hap4	KC489229								1					
Tdim_Hap5	KC489230								1					
Tdim_Hap6	KC489231								1					
Tdim_Hap7	KC489232			1										
Tdim_Hap8	KC489233			1										
Tdim_Hap9	KC489234						1							
Tdim_Hap10	KC489235						1							
Tdim_Hap11	KC489236						1							
Tdim_Hap12	KC489237						1							
Tdim_Hap13	KC489238			1										
Tdim_Hap14	KC489239						1							
Tdim_Hap15	KC489240						1							
Tdim_Hap16	KC489241						1							
Tdim_Hap17	KC489242			1	1									
Tdim_Hap18	KC489243			1										
Tdim_Hap19	KC489244			2										
Tdim_Hap20	KC489245			1	1		1							
Tdim_Hap21	KC489246			1										
Tdim_Hap22	KC489247					1								
Tdim_Hap23	KC489248					1								
Tdim_Hap24	KC489249					1								
Tdim_Hap25	KC489250									1				
Tdim_Hap26	KC489251									1				
Tdim_Hap27	KC489252									1				
Tdim_Hap28	KC489253									1				
Tdim_Hap29	KC489254											1		
Tdim_Hap30	KC489255											1		
Tdim_Hap31	KC489256									1				

Tdim_Hap32	KC489257		2	1		
Tdim_Hap33	KC489258		1			
Tdim_Hap34	KC489259		1			
Tdim_Hap35	KC489260			2		
Tdim_Hap36	KC489261		1			
Tdim_Hap37	KC489262		1		8	
Tdim_Hap40	KC489265					1
Tdim_Hap41	KC489266					3
Tdim_Hap42	KC489267					1
Tdim_Hap43	KC489268					1
Tdim_Hap44	KC489269					1
Tdim_Hap45	KC489270					1
Tdim_Hap46	KC489271					1
Tdim_Hap47	KC489272					1
Tdim_Hap48	KC489273					1
Tdim_Hap49	KC489274					1
Tdim_Hap50	KC489275	1				
Tdim_Hap51	KC489276	1				
Tdim_Hap52	KC489277	1				
Tdim_Hap53	KC489278	1				
Tdim_Hap54	KC489279	1				
Tdim_Hap55	KC489280	1				
Tdim_Hap56	KC489281				1	
Tdim_Hap57	KC489282				1	
Tdim_Hap58	KC489283				1	
Tdim_Hap59	KC489284				1	
Tdim_Hap60	KC489285				1	
Tdim_Hap61	KC489286				1	
Tdim_Hap62	KC489287				1	
Tdim_Hap63	KC489288				1	
Tdim_Hap64	KC489289				1	
Tdim_Hap65	KC489290					

Table S3. Supplementary data of observed and expected heterozygosity and *p-value* of HWE test. Bold significant unbiased HWE (Bonferroni correction 0.0071 to amplified loci K=7). Notations: Ho= observed heterozygosity; He= expected heterozygosity, NA= alleles; na= no amplified > 90% of individuals; M=monomorphic locus. *Non-estimated due to low sample size

Location ID	N	TDMS1				TDMS3				TDMS4				TDMS9				TDMS11			
		NA	Ho	He	p	NA	Ho	He	p	NA	Ho	He	p	NA	Ho	He	p	NA	Ho	He	p
1	21	3	0.368	0.373	0.027	1	M	M	M	3	0.095	0.092	1.0	na	-	-	-	9	0.429	0.563	0.006
2	19	7	0.789	0.615	0.11	1	M	M	M	4	0.105	0.359	0.001	na	-	-	-	7	0.211	0.681	<0.001
3	14	2	0.357	0.375	1.0	1	M	M	M	1	M	M	M	na	-	-	-	4	0.143	0.360	0.007
4	12	3	0.417	0.538	0.369	1	M	M	M	2	0.083	0.080	1.0	5	0.364	0.446	0.06	4	0.250	0.406	0.02
5	18	3	0.111	0.526	<0.001	1	M	M	M	4	0.056	0.252	<0.001	na	-	-	-	6	0.222	0.343	0.01
6	6*	2	-	-	-	1	M	M	M	4	-	-	-	6	-	-	-	6	-	-	-
7	10	2	0.100	0.095	1.0	1	M	M	M	2	0.300	0.455	0.48	2	0.0	0.180	0.05	3	0.500	0.585	0.32
8	25	4	0.520	0.554	0.05	1	M	M	M	4	0.400	0.562	0.02	na	-	-	-	10	0.920	0.857	0.61
9	15	2	0.467	0.420	1.0	1	M	M	M	3	0.600	0.651	0.07	1	M	M	M	5	0.800	0.780	0.45
10	18	4	0.389	0.366	0.37	1	M	M	M	6	0.611	0.698	0.29	3	0.056	0.156	0.03	8	0.778	0.850	0.03
11	12	5	0.333	0.476	0.005	1	M	M	M	3	0.250	0.434	0.08	4	0.250	0.462	0.02	3	0.333	0.601	0.07
12	19	7	0.526	0.627	0.01	1	M	M	M	4	0.474	0.528	0.61	4	0.368	0.456	0.004	7	0.579	0.698	0.06
Mean over all	189	3.7	0.379	0.427	0.449	1	-	-	-	3.3	0.301	0.428	0.361	3.6	0.340	0.408	0.029	6.0	0.500	0.622	0.207
*Continuation																					
Location ID	N	TDMS16				TDMS19				TDMS22				Tinf_42				TP544			
		NA	Ho	He	p	NA	Ho	He	p	NA	Ho	He	p	NA	Ho	He	p	NA	Ho	He	p
1	21	2	0.050	0.049	1.0	na	-	-	-	3	0.143	0.135	1.0	8	0.667	0.797	0.01	7	0.158	0.407	0.003
2	19	5	0.158	0.391	0.001	na	-	-	-	3	0.053	0.234	0.002	14	0.632	0.880	0.004	5	0.316	0.627	<0.001
3	14	2	0.071	0.069	1.0	na	-	-	-	2	0.000	0.245	0.005	9	0.643	0.849	0.009	4	0.286	0.411	0.02
4	12	1	M	M	M	na	-	-	-	1	M	M	M	8	0.583	0.819	0.03	4	0.273	0.698	<0.001
5	18	2	0.000	0.198	<0.001	na	-	-	-	2	0.000	0.105	0.03	13	0.889	0.877	0.57	na	-	-	-
6	6*	na	-	-	-	3	-	-	-	1	M	M	M	4	-	-	-	4	-	-	-
7	10	3	0.556	0.475	0.34	3	0.556	0.537	0.73	2	0.000	0.198	0.06	1	M	M	M	5	0.900	0.660	0.57
8	25	6	0.609	0.624	0.25	5	0.417	0.702	<0.001	5	0.600	0.590	0.19	7	0.600	0.611	0.29	5	0.400	0.566	0.03
9	15	na	-	-	-	5	0.400	0.609	0.03	6	0.714	0.605	0.19	6	0.467	0.613	0.03	5	0.429	0.686	0.06
10	18	6	0.556	0.667	0.15	6	0.222	0.674	<0.001	4	0.412	0.642	0.06	4	0.389	0.665	0.03	6	0.778	0.719	0.71
11	12	6	0.455	0.748	0.04	6	0.417	0.830	<0.001	3	0.250	0.538	0.01	7	0.500	0.792	0.01	6	0.364	0.711	0.04
12	19	6	0.556	0.693	0.02	7	0.333	0.718	<0.001	7	0.579	0.659	0.04	8	0.579	0.691	0.08	6	0.333	0.744	<0.001
Mean over all	189	3.9	0.334	0.435	0.350	5.0	0.359	0.623	0.283	3.3	0.275	0.395	0.159	7.4	0.601	0.750	0.108	5.2	0.430	0.619	0.273

Table S4. Microsatellite loci variability parameters among Colombian regions. N = total number of specimens analyzed. NL = number of loci successfully amplified on >90% of the individuals. Lp = number of polymorphic loci (defined as more than 2 alleles and with >0.8 frequency). AM = mean number of alleles overall loci. AR = allele richness averaged overall loci. Ho, He = Observed and Expected Heterozygosity averaged overall loci respectively. F_{IS} = Inbreeding Coefficient averaged over all loci. F_{IS} values with $p < 0.05$ are in bold. *Non-estimated due to low sample size.

Eco-geographic region	Community location ID	N	Nl	Lp	AM	AR	Ho	He	Fis
Inter Andean Valleys	1	21	8	7	5.2	4.8	0.3	0.3	0.21
	2	19	8	7	6.4	6.4	0.3	0.5	0.4
	3	14	8	6	3.4	3.4	0.2	0.3	0.41
	4	12	8	6	3.5	3.4	0.2	0.4	0.3
	5	18	7	6	5.1	1.2	0.2	0.4	0.44
Mean overall loci and all locations of Inter Andean Valleys		84	8	6.4	4.7	4.5	0.3	0.4	0.3
Caribbean Plains	6*	-	-	-	-	-	-	-	-
	7	10	10	8	2.6	1.3	0.4	0.4	0.11
	8	25	9	8	5.7	5.7	0.6	0.6	0.1
	9	15	9	7	4.1	1.9	0.5	0.5	0.12
	10	18	10	9	5.2	5.1	0.5	0.6	0.2
Mean overall loci and all locations of Caribbean Plains		74	9.4	7.8	4.3	4.8	0.5	0.5	0.2
Sierra Nevada de Santa Marta	11	19	10	9	6.2	6.1	0.5	0.6	0.33
	12	12	10	9	4.8	4.7	0.4	0.6	0.4
Mean over all loci and all locations of Sierra Nevada de Santa Marta		31	10	9	5.5	5.4	0.4	0.6	0.3
Overall all loci, locations and regions		189	9.1	7.7	4.8	4.9	0.4	0.5	0.3

Table S5. Supplementary data of population structure of *T. dimidiata* from Colombia based on Multilocus microsatellites analysis. Summarized results of hierarchical analysis of molecular variance (AMOVA) and population structure index F (Cockerham and Weir, 1986) with its respective *p-value*. Key: n.s=not significant, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

Source of variation	df	Percent of variation	F index
All populations from Colombia			
Among regions	2	22.1	Fct: 0.221***
Among all communities	11	22.5	Fst: 0.225***
Among communities within regions	9	5.8	Fsc: 0.074***
Among individuals within communities	177	19.2	Fis: 0.267***
Pairwise comparison between regions			
Inter Andean Valleys and Caribbean Plains	1	26.7	Fct: 0.267**
Among communities within regions	8	6.1	Fsc: 0.083***
Among individuals within communities	148	16.9	Fis: 0.253***
Inter Andean Valleys and SNSM	1	32.2	Fct: 0.322*
Among communities within regions	5	1.7	Fsc: 0.024***
Among individuals within communities	108	22.4	Fis: 0.338***
Caribbean Plains and SNSM	1	1.4	Fct: 0.014n.s
Among communities within regions	5	10.6	Fsc: 0.107***
Among individuals within communities	98	22.4	Fis: 0.255***