

Supplementary Material

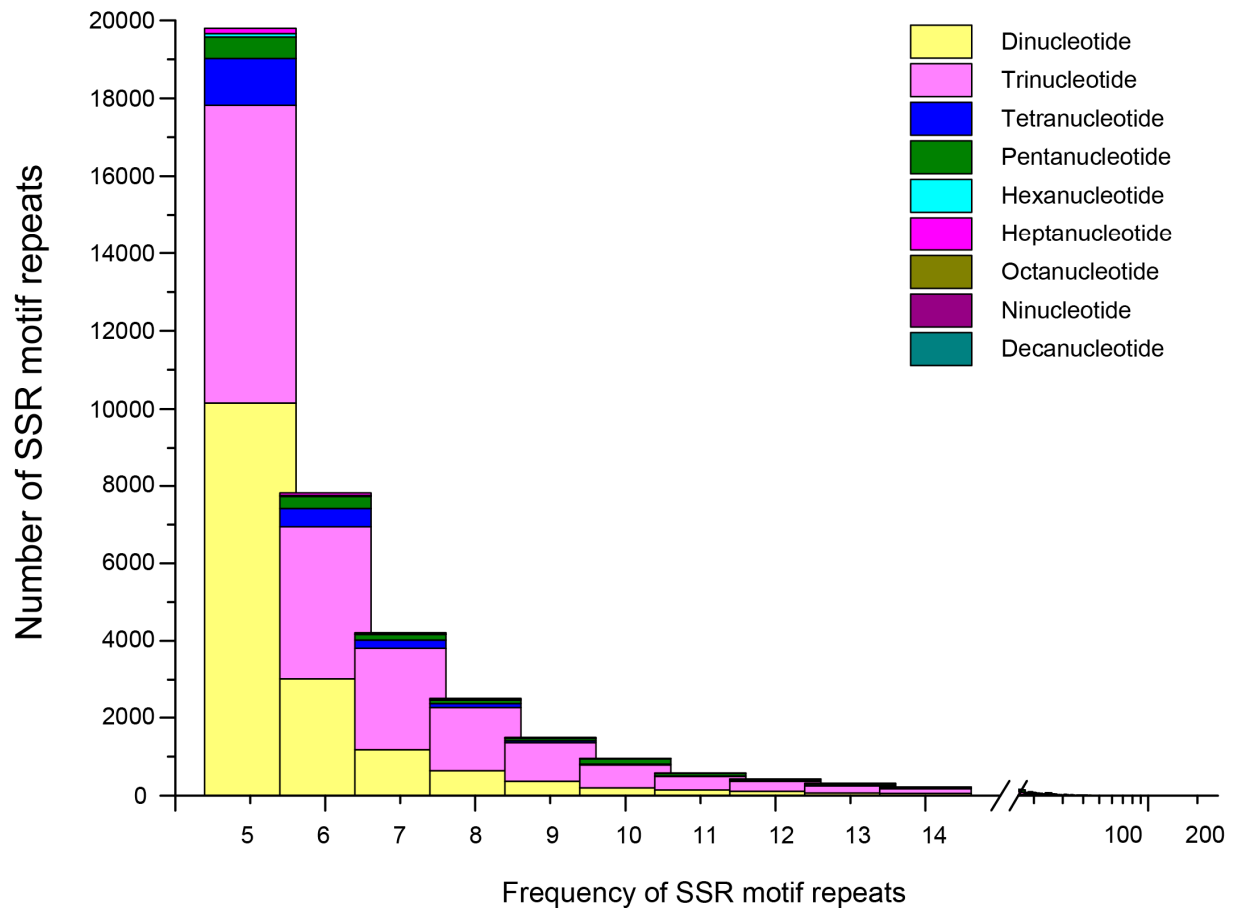


Figure S1 Distribution and frequency of SSR motif repeat numbers. The X-axis shows the frequencies of SSR types, while the Y-axis shows SSR repeat numbers.

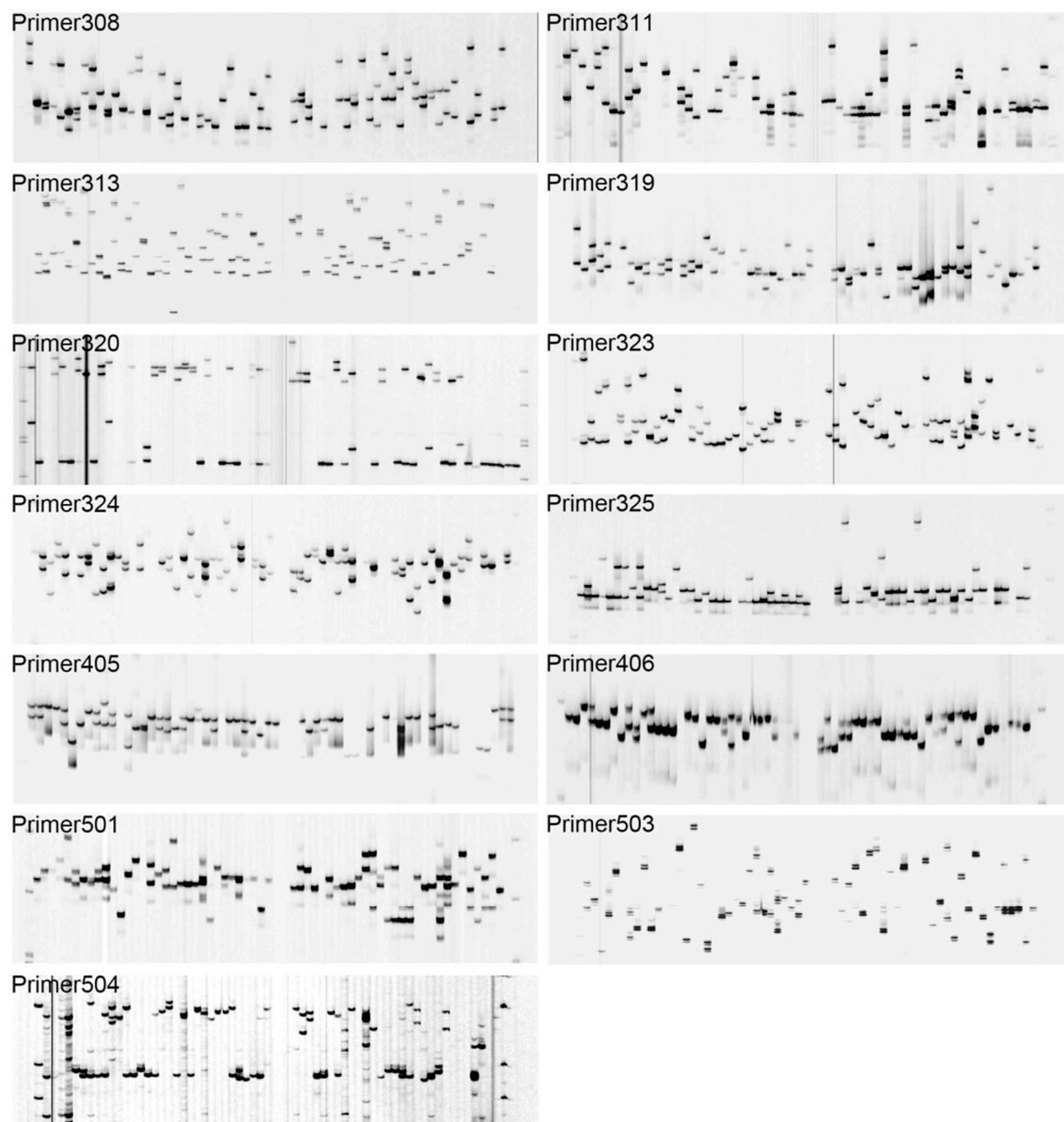


Figure S2 PCR amplification result of 13 SSR loci. 13 pairs of primers showed clear and numerous polymorphism fragments in 6.5 % polyacrylamide gel.

Table S1. SSR markers and characteristics of primers used in genetic analysis of *P. pectoralis*

No	SSR name	Chr	Start	End	Forward primer (5'-3')*	Reverse primer (5'-3')	motif	Res ult
1	SSR301	LG1 0	29525644	29524978	TCGGTGTTCAGTGT TGT	AACCAGGAGCCAAA GTGT	(gat)6	
2	SSR302	LG0 7	8220518	8221252	AAAGCAGAAGCCCTA CTAAA	AAACGGCCAATACC AGAA	(aat)6	
3	SSR303	LG0 7	12624283	12624781	CCCTTGGAAGATTTA CAC	AAGACTTGAAGAAA GCTGC	(aat)8	
4	SSR304	LG0 3	38954751	38955635	AAAAGCTGTGCCTTCT TG	TATTGCTGCTGTTTGG GT	(tta)8	
5	SSR305	LG0 2	81923098	81922806	ATACATCCATCGCAG AGG	GTGAAGCATTCCCAA CAT	(aga)9	
6	SSR306	LG0 9	13832527	13832008	GCGTGTAAGCATTGTC TC	GCCAAGAATCGGAT ACATAA	(tac)21	
7	SSR307	LG0 7	41331038	41330555	CCGCTTACCTCGCTTA TT	AAAACATTAGGCGA GGCT	(tat)9	
8	SSR308	LG0 7	39678327	39677588	CAAAGCGGAACCTCA AAC	AACCAGGTAAAGGT AGCG	(aat)8	OK
9	SSR309	LG0 6	21371206	21370365	CCGCGCCACTGCTTTA ATTT	GAGACGGTCTGTGCT CGATT	(tat)21	
10	SSR310	LG0 9	27597563	27596993	ATCGTGTTTGTGCCTTT C	GTTTTACCGCTCGTT CC	(att)13	
11	SSR311	LG0 4	30577309	30578070	GAACAAATGGTTGAA AGGAA	GCCGTTGCTATGAG AAT	(taa)12	OK
12	SSR312	LG0 3	51062472	51062109	GTGAGCGAGTCTCCA GTG	TGTATTCGGTTTGTGC TA	(taa)12	

13	SSR313	LG0 7	40348582	40349582	ACAAGGCAAACAGAG CAT	CTTCGATCATCTCCGT CA	(gaa)16	OK
14	SSR314	LG0 6	4767339	4766948	ATTACTTACTCCCGTG TAGAGT	ATGCGGCGTGAAACA ACT	(tat)11	
15	SSR315	LG0 5	47310835	47311093	AGCAATTTCTTGGTGT GGA	ACGACTGACTCGGTC TTAG	(att)16	
16	SSR316	LG0 7	30337313	30336867	TCACTTTGCTAAGCTG ATAAC	TGTGCTAATGCGGAC CTA	(aat)13	
17	SSR317	LG0 2	70162475	70162966	GGAGCAAAACTGGTT CGG	TTATTGCACGACACG GAG	(ttgaa)7	
18	SSR318	LG0 1	44698570	44697852	TGCCCATTTCTTTTGTG AATGCT	CGCGAGATGTTGAAC ATGGG	(ata)17	
19	SSR319	LG0 6	19495493	19494463	ATTTGGGTTAGTTTAG GC	CACGCAAGAAGTGG AGATA	(tat)13	OK
20	SSR320	LG0 3	48825694	48825192	TAATCCGCGACTGTTT TG	TTGACTCTACCGCAC CTC	(ata)12	OK
21	SSR321	LG0 6	40535170	40536088	TTGACTCTACCGCACC TC	TGGGCGAAAGATGG ATGT	(aac)16	
22	SSR322	LG0 1	63400534	63400170	CAAAGCTGCGTTCATA AT	TTGCCACCATCACAA TCT	(tta)14	
23	SSR323	LG0 8	19419411	19418388	AGGACAGGGCACTCA CAT	TGGACATCGCAATCA CTA	(ata)15	OK
24	SSR324	LG0 3	41425698	41426739	TATGTGCTTTGGCTTGT G	AAGTTCGGATGCTAA TGC	(tat)12	OK
25	SSR325	LG0 5	8988867	8989383	CGCTTTTtagCACCTT CA	ACATACTTCGCCCAC TCT	(aat)15	OK
26	SSR401	LG0	24945156	24944269	CTGAGAAACCAGCAT	CGAATCGCATTAAAC	(ttta)8	

		7			CCG	ACATA		
27	SSR402	LG0	21650906	21651620	TGAACCTATGACCCTT	TTCGTAATCTTTCACC	(tgtc)8	
		4			GC	GC		
28	SSR403	LG0	42181662	42181439	TGATTACTTCAATACC	TCCAGATTACATCGC	(aatc)6	
		6			CACC	ACC		
29	SSR404	LG0	40217516	40217970	CAGGGATTCTTGAGAC	GCTAACTTGACGTAA	(attg)7	
		3			ACTT	CCCTAAC		
30	SSR405	LG1	10750335	10749891	TTATTTACTGCAAACG	GCGAAAGACAGAAA	(tatt)6	OK
		0			GTGAG	GGGAC		
31	SSR406	LG0	21272843	21273264	TCTTGAATGGACGGAC	TTTCTATCCTTGAACG	(aaat)6	OK
		7			CTA	CTGT		
32	SSR501	LG0	43934651	43935197	GCGTGGGCTGAAGAG	TTGTGGAGGTGGCGA	(ttgaa)7	OK
		6			GAT	AGG		
33	SSR502	LG0	40887538	40887995	ACGCACGGGCATTGTC	AACCACCCTGGATCA	(ttgta)7	
		4			TT	CCT		
34	SSR503	LG0	7096085	7095375	TGAGCATATATCGAAC	AACAAAGGTGGTTGG	(tacaa)1	
		6			GTAA	TGA	9	OK
							(tacag)7	
35	SSR504	LG0	12384299	12383838	CTAAAAGTGCTGCTGG	TGTTTCAAATACAAT	(atatt)5(OK
		6			CG	GGTCTAA	att)7	
36	SSR505	LG0	11190281	11189675	ATTCCTCGCACCCCTG	CCAAAAGGGATGTA	(tattg)16	
		6			TA	AATGAT		
37	SSR506	LG0	29254037	29255032	CTGACTTATGGCGGCG	TGACACCCCAAAAAT	(attac)7	
		7			AA	ACTGA		
38	SSR507	LG0	28880322	28880503	AGGCGTGTTACCTTTT	GCTTCCCATGCAAAC	(taata)6	
		3			CA	CTT		
39	SSR508	LG0	11190281	11189675	ATTCCTCGCACCCCTG	TCCAAAAGGGATGTA	(tattg)16	

		6			TA	AATGA	
40	SSR509	LG0	9202972	9203267	GTCGCCTGAACAAAC	TCACATTGGCAAATG	(ataac)8
		9			ACC	ACG	
41	SSR510	LG0	29254037	29255032	GACTTATGGCGGCGA	ACATAGATCGTAACA	(attac)7
		7			ACC	AGGCG	
42	SSR511	LG0	8254712	8253654	TTCCTCAGGTAAGTCC	GCCCTATCCACCATT	(tatgg)6
		7			ACCAC	TCG	
43	SSR512	LG0	2591547	2591933	CGCAAGGGCATTACA	TCAGGCGAAAATCA	(taatt)7
		1			CGA	GAAA	
44	SSR513	LG0	19116736	19117247	GCGTCACAATCAACA	GGCTTTTACAGAATC	(tttg)7
		2			CCT	TACCG	
45	IRDye 800-labeled M13f-29 primer				CACGACGTTGTAAAA		
					CGAC		

*Each forward SSR primer has a universal M13 19 bp tail sequence added at the 5' end (5'- CAC GAC GTT GTA AAA CGA C-3')

Table S2 The body length, width, and weight of mating fireflies (25 female and 59 male).

Firefly	body lengt h (mm)	body widt h (mm)	weigh t (g)	Firefly	body lengt h (mm)	body widt h (mm)	weigh t (g)	Firefly	body length (mm)	body width (mm)	weight (g)
Female-1	21.23	7.53	0.2740	Male-4	17.10	6.33	0.0822	Male-32	15.33	6.14	0.0631
Female-2	22.11	7.26	0.3132	Male-5	15.74	5.68	0.0711	Male-33	15.26	6.40	0.0622
Female-3	27.08	8.59	0.5890	Male-6	16.68	6.45	0.0663	Male-34	16.88	6.35	0.0678
Female-4	26.49	6.95	0.3303	Male-7	16.32	6.22	0.0698	Male-35	17.27	6.56	0.0631
Female-5	29.21	8.05	0.4718	Male-8	16.41	6.70	0.0611	Male-36	15.76	5.88	0.0468
Female-6	27.76	7.64	0.3482	Male-9	16.59	6.33	0.0647	Male-37	15.67	5.95	0.0450
Female-7	23.45	6.30	0.2992	Male-1 0	16.44	6.28	0.0764	Male-38	19.23	7.17	0.0946
Female-8	21.37	7.43	0.2780	Male-1 1	16.94	6.73	0.0829	Male-39	18.67	6.58	0.0679
Female-9	21.51	7.49	0.2785	Male-1 2	16.69	6.55	0.0964	Male-40	18.86	7.35	0.0832
Female-1 0	24.03	6.70	0.2884	Male-1 3	15.10	5.74	0.0699	Male-41	17.96	7.33	0.0836
Female-1 1	22.00	7.22	0.3032	Male-1 4	16.86	6.74	0.0739	Male-42	18.38	7.37	0.0793
Female-1 2	21.44	7.46	0.2782	Male-1 5	15.34	6.41	0.0532	Male-43	17.66	6.45	0.0833
Female-1 3	22.00	7.25	0.3092	Male-1 6	15.35	5.87	0.1121	Male-44	18.70	6.70	0.0685
Female-1 4	29.10	8.22	0.4705	Male-1 7	16.88	6.82	0.1028	Male-45	17.54	6.55	0.0617
Female-1 5	22.83	6.01	0.2693	Male-1 8	15.93	6.68	0.1112	Male-46	15.05	5.70	0.0444
Female-1 6	23.03	6.11	0.2993	Male-1 9	16.69	5.89	0.1231	Male-47	15.88	6.54	0.0575
Female-1 7	24.04	6.69	0.2783	Male-2 0	17.04	6.90	0.1013	Male-48	19.39	7.21	0.0944
Female-1 8	22.00	7.03	0.2650	Male-2 1	16.81	6.31	0.0919	Male-49	19.03	7.09	0.0744
Female-1 9	26.42	7.91	0.4464	Male-2 2	17.54	7.34	0.1022	Male-50	19.49	7.86	0.0977
Female-2 0	27.00	8.03	0.4760	Male-2 3	16.77	6.87	0.0978	Male-51	19.27	7.67	0.0968

Female-2 1	21.59	6.75	0.2633	Male-2 4	15.95	6.36	0.1003	Male-52	18.66	7.18	0.0833	
Female-2 2	27.00	8.33	0.5877	Male-2 5	15.80	6.30	0.0643	Male-53	17.93	7.31	0.0841	
Female-2 3	27.03	8.51	0.5891	Male-2 6	14.32	5.70	0.0635	Male-54	16.34	6.14	0.0623	
Female-2 4	24.04	6.70	0.2777	Male-2 7	15.45	5.80	0.0667	Male-55	16.48	6.32	0.0654	
Female-2 5	22.00	7.25	0.3092	Male-2 8	15.74	5.77	0.0622	Male-56	17.89	7.17	0.0610	
Male-1	16.24	5.96	0.1524	Male-2 9	15.42	5.91	0.0656	Male-57	17.70	7.17	0.0767	
Male-2	16.38	6.26	0.1400	Male-3 0	14.68	5.79	0.0637	Male-58	15.92	6.13	0.1121	
Male-3	16.13	5.84	0.1424	Male-3 1	16.28	5.87	0.0666	Male-59	17.14	6.57	0.0690	
									Female average	24.23±	7.34±	0.36±
										2.61	0.70	0.11
									male average	16.80±	6.50±	0.08±
										1.27	0.55	0.02

Table S3 Identification and characteristics of SSR motifs in the *P. pectoralis* genome

Motif	Repeats	Length	Percentage of repeats	Max motif length	Min motif length	Average motif length
Dinucleotide	16370	209166	41.04	538	10	12.76
Trinucleotide	18725	379920	46.94	153	15	20.28
Tetranucleotide	2131	53100	5.34	312	20	24.88
Pentanucleotide	1956	109200	4.9	600	25	55.8
Hexanucleotide	228	12972	0.57	330	30	56.88
Heptanucleotide	297	14091	0.74	294	35	47.39
Octanucleotide	125	6424	0.31	144	40	51.36
Ninucleotide	51	3006	0.13	261	45	58.86
Decanucleotide	7	430	0.02	80	50	61.4
Total	39890	788309	100	600	10	40.8

Table S4 Top15 repeat of different types of SSR motif.

name	Repeats	length	Percentage of repeats
Total dinucleotide	16370	209166	100%
TA/AT	6290	80020	38.42%
TG/CA	4977	60186	30.40%
TC/GA	4215	58936	25.75%
GC/CG	888	10024	5.42%
Total trinucleotide	18725	379920	100%
ATT/AAT	15578	319896	83.19%
AGA/TCT	1183	24123	6.32%
ACT/AGT	466	9441	2.49%
ATG/CAT	433	7659	2.31%
AGG/CCT	316	6243	1.69%
AAC/GTT	301	5115	1.61%
ACG/CGT	162	2649	0.87%
ACC/GGT	126	2052	0.67%
AGC/GCT	108	1890	0.58%
CCG/CGG	52	852	0.28%
Total tetranucleotide	2131	53100	100%
TTTA/TAAA	1190	28912	55.84%

Table S5 Genetic characterization of 13 polymorphic SSR loci of 60 males.

Locus	N	Na	Ne	I	Ho	He	uHe	PIC	HWE
SSR308	60	10	8.706	2.215	0.767	0.885	0.893	0.874	ns
SSR311	60	13	10.811	2.429	0.75	0.908	0.915	0.9	ns
SSR313	60	22	13.74	2.829	0.867	0.927	0.935	0.923	ns
SSR319	60	10	8.582	2.193	0.75	0.883	0.891	0.872	ns
SSR320	60	13	10.169	2.408	0.883	0.902	0.909	0.893	ns
SSR323	60	15	11.392	2.561	0.833	0.912	0.92	0.906	ns
SSR324	60	15	10.762	2.521	0.9	0.907	0.915	0.9	ns
SSR325	60	12	3.169	1.532	0.433	0.684	0.69	0.637	***
SSR405	60	9	7.725	2.111	0.767	0.871	0.878	0.857	ns
SSR406	60	4	2.463	1.042	0.4	0.594	0.599	0.516	***
SSR501	60	9	8.295	2.156	0.733	0.879	0.887	0.867	ns
SSR503	60	34	16.552	3.169	0.483	0.94	0.947	0.937	***
SSR504	60	12	10.959	2.438	0.767	0.909	0.916	0.901	ns
Mean	60	13.692	9.487	2.277	0.718	0.862	0.869	0.845	
SE	0	2.052	1.053	0.148	0.047	0.028	0.029	0.119	

***Highly significant from HWE ($P < 0.001$).

N = Number of examined individuals

Na = No. of different alleles.

Ne = No. of effective alleles = $1/(\sum p_i^2)$.

I = Shannon's Information Index = $-1 * \sum (p_i * \ln(p_i))$.

Ho = observed heterozygosity = no. of Hets/N.

He = expected heterozygosity = $1 - \sum p_i^2$.

uHe = unbiased expected heterozygosity = $(2N/(2N - 1)) * He$.

PIC = polymorphism information content.

HWE = Hardy–Weinberg equilibrium

ns = no significance

Table S6 Summary of Chi-Square Tests for Hardy-Weinberg Equilibrium (HWE).

Locus	Degrees of freedom	Chi-square value	P-value	Significance
SSR308	45	37.176	0.79	ns
SSR311	78	85.672	0.258	ns
SSR313	231	244.279	0.262	ns
SSR319	45	45.32	0.459	ns
SSR320	78	71.676	0.68	ns
SSR323	105	126.831	0.072	ns
SSR324	105	81.5	0.957	ns
SSR325	66	231.958	0	***
SSR405	36	42.219	0.22	ns
SSR406	6	35.566	0	***
SSR501	36	44.995	0.145	ns
SSR503	561	1088.711	0	***
SSR504	66	82.82	0.079	ns

***Highly significant from Hardy–Weinberg equilibrium ($P < 0.001$)

Ns=no significance

	progeny number allocation			percentage		
Replicates	P1	P2	P3	P1	P2	P3
F1×M2-1	36	15	—	0.7059	0.2941	—
F1×M2-2	20	33	—	0.3774	0.6226	—
F1×M2-3	68	8	—	0.8947	0.1053	—
F1×M2-4	10	40	—	0.2000	0.8000	—
F1×M2-5	2	99	—	0.0198	0.9802	—
F1×M2-6	50	38	—	0.5682	0.4318	—
F1×M2-7	83	48	—	0.6336	0.3664	—
F1×M2-8	55	10	—	0.8462	0.1538	—
F1×M2-9	70	9	—	0.8861	0.1139	—
F1×M2-10	69	6	—	0.9200	0.0800	—
F1×M2-11	21	46	—	0.3134	0.6866	—
F1×M2-12	4	78	—	0.0488	0.9512	—
F1×M2-13	77	23	—	0.7700	0.2300	—
F1×M2-14	9	129	—	0.0652	0.9348	—
F1×M2-15	43	48	—	0.4725	0.5275	—
F1×M2-16	88	11	—	0.8889	0.1111	—
F1×M3-1	19	27	41	0.2184	0.3103	0.4713
F1×M3-2	6	6	81	0.0645	0.0645	0.8710
F1×M3-3	18	0	63	0.2222	0.0000	0.7778
F1×M3-4	0	39	39	0.0000	0.5000	0.5000
F1×M3-5	37	7	14	0.6379	0.1207	0.2414
F1×M3-6	7	5	55	0.1045	0.0746	0.8209
F1×M3-7	4	25	53	0.0488	0.3049	0.6463
F1×M3-8	1	55	5	0.0164	0.9016	0.0820
F1×M3-9	0	0	49	0.0000	0.0000	1.0000
Descriptive Statistics of F1×M2						
	N	Mean	SD	SEM		
F1×M2-P1	16	0.53816	0.32971	0.08243		
F1×M2-P2	16	0.46184	0.32971	0.08243		
Difference		0.07633				
t-Test Statistics of F1×M2						
	t Statistic	DF	Prob> t			
Equal Variance Assumed	0.65478	30	0.5176			
Equal Variance NOT Assumed	0.65478	30	0.5176			
Descriptive Statistics of F1×M3						

	Sample Size	Mean	Standard Deviation	SE of Mean
F1×M3-P1	9	0.14586	0.20319	0.06773
F1×M3-P2	9	0.25297	0.29593	0.09864
F1×M3-P3	9	0.60118	0.30403	0.10134

One Way ANOVA of F1×M3

	DF	Sum Squares	of Mean Square	F Value	Prob> F
Model	2	1.02012	0.51006	6.91458	0.00425
Error	24	1.77038	0.07377		
Total	26	2.7905			

Means Comparisons by Fisher Test of F1×M3

	MeanDiff	SEM	t Value	Prob	Alpha	Sig
F1×M3-P2 F1×M3-P1	0.10711	0.12803	0.83658	0.41108	0.05	0
F1×M3-P3 F1×M3-P1	0.45532	0.12803	3.55628	0.0016	0.05	1
F1×M3-P3 F1×M3-P2	0.34821	0.12803	2.7197	0.01195	0.05	1