10.1071/BT10291_AC

Australian Journal of Botany, 2011, 59(4), 351–362

Accessory Publication

Locus level genetic diversity

*TABLE 4. Characteristics and population genetic values for each of six nucleic loci used in this study, obtained from 334 individuals from 27 populations: locus name, repeat type and frequency, forward (*F*) (not including the M13 addition) and reverse (*R*) primer sequences, (T_a) annealing temperature, allelic size range, (*N*) number of individuals amplified from total 334, (N_A) total number of alleles, (H_O) observed heterozygosity, (H_E) expected heterozygosity and GenBank Accession number.*

Locus	*Repeat*		**Primer sequences (5'-3')*	T_a (°C)	*Allele size range (bp)*	*N*	N_A	H_O	H_E	*GenBank Acc. no.*
PeA16BGT	$(CT)_{11}$	F	GCTAAACCTTACCCATCAAT	61	405-481	328	22	0.435	0.383	FJ935795
		R	TATGTGGCAAACTCACTCTGT							
PeB31BGT	$(CT)_9$	F	GGCATTGGCTCAACAGA	61	209-235	305	9	0.161	0.280	FJ935797
		R	TCGTGGAGAGGTACTTCATT							
PeC19BGT	$(AG)_{21}$	F	GAGACCAGACAAAGATGAAGA	61	195-247	316	21	0.555	0.618	FJ935799
		R	GAGTAAGAGCAAGACACCAAA							
PeD9BGT	$(CT)_4CC(CT)_{10}$	F	GTGCTTGTAAATGAGAGAGAG	61	363-379	332	9	0.214	0.462	FJ935801
		R	GGGCGAGGAGAGAATC							
PeD13BGT	$(AT)_7$ $(CT)_7$ $(GT)_{10}$	F	CTACCCGAACATTGCTCTA	61	329-371	314	9	0.238	0.388	FJ935802
		R	CTCCCATCGTTTCCAATT							
PeD14BGT	$(GT)_{24}$	F	GAATGGATGGGTAATGGC	61	275-327	324	20	0.775	0.681	FJ935803
		R	GGAACATAACTTGAATGCTTT							

TABLE 5. Locus level genetic diversity for the 15 populations sampled for genetic diversity (refer to Table 1 for population name and location), including genetic diversity per locus and population, number of alleles, allelic richness based on minimum sample size of seven individuals, F_{is} *per locus and population (including significance), and* P*-values for* F_{is} *within samples. (NA) indicates monomorphism. (-) indicates missing data (*P<0.05, ** P<0.01, *** P<0.001)*

POP	*1*	*2*	*3*	*4*	*5*	*9*	*10*	*15*	*16*	*17*	*18*	*19*	*22*	*23*	*27*
Gene diversity per locus and pop															
A16	0.29	0.632	0.332	0.396	0.295	0.765	0.336	0.633	0.49	0.321	0.411	0.307	0.689	0.317	0
B31	0.251	0.445	0.541	0.74	0.688	0.641	0	0.163	0.154	0.396	0.433	0.585	0.189	0.195	0.262
C19	0.749	0.873	0.908	0.859	0.729	0.881	0.888	0.595	0.519	0.659	0.71	0.732	0.655	0.718	0.817
D9	0.704	0.706	0.325	0.674	0.719	0	0.756	0.689	0.76	0.462	0.641	0.69	0.5	0.493	-
D13	0.47	0.337	0.471	0.484	0.392	0	0.724	0.75	0.574	0.72	0.661	0.435	0.622	0.546	-
D14	0.765	0.814	0.67	0.659	0.728	0.853	0.66	0.818	0.753	0.783	0.788	0.807	0.833	0.596	0.5
no. of alleles sampled :															
A16	5	5	5	5	3	5	4	5	4	3	8	6	6	5	1
B31	4	4	3	5	6	4	1	3	2	2	4	4	2	3	2
C19	9	10	12	14	9	9	8	5	4	5	7	7	4	7	4
D9	6	5	3	3	4	1	4	5	5	5	4	5	3	5	-
D13	3	2	2	2	2	1	4	4	4	6	5	5	4	4	-
D14	9	9	7	5	8	6	7	8	6	8	9	8	7	4	2
mean	6	5.8	5.3	5.7	5.3	4.3	4.7	5	4.2	4.8	6.2	5.8	4.3	4.7	2.3
Allelic Richness per locus and population															
based on min. sample size of:			7 diploid individuals.												
A16	2.655	3.669	3.104	2.843	2.262	4.418	3.152	4.127	3.323	2.451	3.811	3.189	5.225	3.02	1
B31	2.466	3.166	2.5	4.287	4.578	3.752	1	2.167	1.797	1.997	2.819	3.33	1.921	2.167	1.989
C19	5.267	7.321	8.202	7.261	5.694	7.194	6.513	4.237	3.076	4.018	4.676	5.282	4	5.118	4
D9	4.208	4.201	2.32	2.993	3.859	1	3.933	4.004	4.334	3.582	3.197	3.856	2.918	3.402	-
D13	2.231	1.98	1.999	1.999	1.993	1	3.93	3.934	3.334	4.82	3.386	3.341	3.621	3.084	-
D14	5.528	5.986	4.32	3.876	4.985	5.77	5.176	6.384	4.999	6.05	5.638	6.014	6.224	3.087	2
mean	3.73	4.39	3.74	3.88	3.9	3.86	3.95	4.14	3.48	3.82	3.92	4.17	3.98	3.31	2.25
Fis per locus/pop															
A16	-0.113	0.367	-0.11	0.001	0.516	0.02	0.189	0.21	-0.255	0.556	0.012	-0.085	0.129	-0.104	NA
B31	0.54	0.207	0.208	0.827	0.612	0.64	NA	-0.023	1	0.458	0.711	0.525	-0.059	1	-0.091
C19	0.126	0.045	0.014	0.054	0.4	-0.047	0.48	0.159	0.111	0.675	0.295	0.598	0.127	0.443	0.184
D9	0.51	0.606	0.838	0.381	0.431	NA	0.593	0.637	-0.013	0.333	0.648	0.728	0.6	0.696	-
D13	0.929	1	1	0.957	0.884	NA	0.363	0.111	0.464	0.405	0.101	0.744	0.839	0.359	-
D14	0.053	0.079	0.057	-0.012	-0.186	-0.083	0.301	-0.019	-0.328	-0.004	-0.07	-0.101	-0.2	0.245	0.143
All	0.32***	0.313***	0.268***	0.359***	0.39***	0.1	0.416***	0.2**	0.03	0.373***	0.261***	0.411***	0.234**	0.407***	0.125
sig	0.0006	0.0006	0.0006	0.0006	0.0006	0.1144	0.0006	0.0039	0.3933	0.0006	0.0006	0.0006	0.0056	0.0006	0.3044
P-value for Fis within samples.				based on :	1800 randomisations.			Indicative adjusted nominal level (5%) for one table is :					0.00056		
Proportion of randomisations that gave a LARGER Fis than the observed:															
A16	1	0.0183	1	0.5833	0.0344	0.5661	0.2839	0.1939	1	0.0294	0.5711	1	0.3294	1	NA
B31	0.0039	0.1772	0.3	0.0006	0.0006	0.0022	NA	1	0.0433	0.1394	0.0006	0.0022	1	0.0011	1
C19	0.1589	0.4228	0.5344	0.2133	0.0017	0.825	0.0006	0.2722	0.4339	0.0011	0.0044	0.0006	0.4411	0.0006	0.32
D9	0.0006	0.0006	0.0006	0.0006	0.0022	NA	0.0011	0.0022	0.6428	0.1	0.0006	0.0006	0.03	0.0006	-
D13	0.0006	0.0006	0.0006	0.0006	0.0006	NA	0.0356	0.3628	0.03	0.0094	0.2483	0.0006	0.0006	0.0356	-
D14	0.3572	0.2961	0.4389	0.6039	0.9722	0.8778	0.0472	0.7156	1	0.6494	0.8556	0.9061	1	0.1156	0.6794
All	0.0006	0.0006	0.0006	0.0006	0.0006	0.1144	0.0006	0.0039	0.3933	0.0006	0.0006	0.0006	0.0056	0.0006	0.3044

Bottleneck results

TABLE 6. Summary table of Sign Test BOTTLENECK results for the 15 populations, sampled for genetic diversity. Assuming all loci fit a Stepwise Mutation Model (S.M.M) expected for microsatellite markers in mutation-drift equilibrium., including population name, number of loci with heterozygosity deficiency in each population, number loci with heterozygosity excess in each population, (P) BOTTLENECK probability, and F_{is} *per population (including significance) (*P<0.05, ** P<0.01, *** P<0.001)*

	POPULATION (N=15)	**No. of loci with heterozygosity deficiency**	**No. of loci with heterozygosity excess**	***P***	F_{is}
1	Target Beach, Jervis Bay, NSW	6	0	0.005**	0.32***
2	Fox Ground Rd, Kiama, NSW	4	2	0.220	0.313***
3	Porrots Brush, Jamberoo, NSW	3	3	0.453	0.268***
4	Bass Point, Shellharbour, NSW	3	3	0.524	0.359***
5	Mungo Brush, Tea Gardens, NSW	4	2	0.203	0.39***
9	Bundagen, Raleigh, NSW	1	3	0.461	0.1
10	Victoria Park, Alstonville, NSW	2	3	0.670	0.416***
15	Mt Glorious, Maiala N.P., QLD	5	1	0.046*	0.2**
16	Neurum Creek, Mt Delaney, QLD	5	1	0.047*	0.03
17	Buderim Forest Park, Nambour, QLD	5	1	0.048*	0.373***
18	Burumba, Wrattens N.P., QLD	6	0	0.005**	0.261***
19	Wrattens Camp, Wrattens N.P., QLD	6	0	0.005**	0.411***
22	Bulburin S.F., Bundaberg, QLD	4	2	0.190	0.234**
23	Eurimbula N.P., Seventeen Seventy, QLD	6	0	0.004**	0.407***
27	Bakers Blue, Mt Molloy, QLD	1	2	0.580	0.125
	TOTAL MEAN	4.1	1.5	0.23	0.308

TABLE 7. Likely dispersers of P. elatus seed.

Superb Fruit-Dove (*Ptilinopus superbus*)
Rose-crowned Fruit-Dove (*Ptilinopus regina*)
Wompoo Fruit-Dove (*Ptilinopus magnificus*)
Topknot Pigeon (*Lopholaimus antarcticus*)
Grey-headed Flying Fox (*Pteropus poliocephalus*)
Little Red Flying Fox (*Pteropus scapulatus)*
Black Flying Fox (*Pteropus alecto*)