Levels of genetic differentiation and gene flow between four populations of the Scaly-naped Pigeon, *Patagioenas squamosa*: implications for conservation

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Supplementary Materials

Table S1: Summary of sampling scheme for each island.

Islands	Sampling type	Biological samples	Year of sampling	N
Puerto-Rico	Trapping	Blood	2009-2010	9
	Trapping	Feather	2009-2010	32
Guadeloupe	From hunters	Toe	2010	36
Martinique	From hunters	Liver	2009	11
	Trapping	Feather	2011	3
	From hunters	Feather	2011	8
	From hunters	Toe	2012	9
Barbados	Trapping	Blood	2010	49
			TOTAL	**157**

Table S2: Estimate of null allele frequency using EM algorithm (Dempster et al. 1977) per population and microsatellite loci.

Microsatellite Loci	Estimate of null allele frequency/Populations			
	Puerto-Rico	Guadeloupe	Martinique	Barbados
PsA130	0.0515	0.000	0.00054	0.000
PsC11	0.00318	0.0401	0.0371	0.000
PsC101	0.000	0.00031	0.000	0.0377
PsC120	0.120	0.112	0.0322	0.0207
PsC128	0.000	0.000	0.000	0.0519
PsD2	0.0227	0.0319	0.0510	0.000
PsD5	0.000	0.0187	0.109	0.000

Table S3: Estimates of Fst using or not ENA correction for each locus and statistical results for a Paired Wilcoxon rank-test.

Microsatellite Loci	Using ENA correction	Not using ENA correction
PsA130	0.00331	0.00331
PsC11	0.0398	0.0399
PsC101	0.0424	0.0403
PsC120	0.0251	0.0224
PsC128	0.0843	0.0775
PsD2	0.0309	0.0318
PsD5	0.0208	0.0230
Average	0.0352	0.0340
All loci	0.0374	0.0362

Paired Wilcoxon rank-test: V =17 ; P = 0.688

Table S4: Basic summary statistics of genetic variation within different islands based on the seven microsatellite loci. Average number of nucleotides per microsatellite loci (N_a), Allelic Richness (R_a), observed and expected heterozygosity (H_o and H_e, respectively), P-value from Hardy-Weinberg exact test (P_{HWE}) and the inbreeding coefficient (Fis). Significant values considering BY's correction (αBY = 0.0204) are in bold (NS = not significant; * = P < 0.0193; ** = P < 0.00396; *** = P < 0.000386)

	Microsatellite loci						
Populations	PsA130	PsC11	PsC101	PsC120	PsC128	PsD2	PsD5
All (n = 128)							
N_a	6	14	10	8	12	15	8
R_a	5.865	13.806	9.999	7.879	11.850	15	7.999
H_o	0.626	0.785	0.789	0.444	0.828	0.839	0.804
H_E	0.579	0.823	0.848	0.581	0.833	0.921	0.836
P_{HWE}	0.067	0.005*	0.011*	0.003*	0.076	0.025	0.236
F_{is}	-0.083	0.047	0.070	0.236	0.006	0.089	0.038
PR (n = 32)							
N_a	3	8	9	4	11	12	7
R_a	2.894	8.000	8.178	3.992	10.067	10.779	6.671
H_o	0.571	0.786	0.857	0.478	0.955	0.864	0.850
H_E	0.539	0.815	0.848	0.656	0.886	0.902	0.836
P_{HWE}	0.027	0.352	0.228	0.028	0.581	0.598	0.152
F_{is}	-0.062	0.037	-0.011	0.275	-0.080	0.043	-0.017
GUA (n = 36)							
N_a	5	11	7	4	10	13	8
R_a	4.250	9.243	6.468	3.883	8.665	12.00	7.007
H_o	0.742	0.828	0.800	0.333	0.968	0.850	0.788
H_E	0.636	0.887	0.821	0.481	0.870	0.924	0.817
P_{HWE}	0.092	0.060	0.503	0.035	0.387	0.238	0.709
F_{is}	-0.170	0.069	0.026	0.312	-0.115	0.082	0.036
MAR (n = 28)							
N_a	4	10	9	6	8	11	8
R_a	3.733	8.934	8.611	5.336	7.643	11.00	7.929
H_o	0.500	0.783	0.938	0.409	0.941	0.786	0.667
H_E	0.544	0.855	0.853	0.493	0.859	0.918	0.862
P_{HWE}	1.000	0.391	0.736	0.176	0.611	0.414	0.187
F_{is}	0.084	0.081	-0.103	0.173	-0.099	0.149	0.233
BAR (n = 32)							
N_a	5	7	7	6	9	10	6
R_a	3.901	5.939	6.238	4.988	6.826	9.028	5.864
H_o	0.621	0.741	0.643	0.556	0.517	0.839	0.862
H_E	0.564	0.647	0.781	0.641	0.561	0.872	0.800
P_{HWE}	0.688	0.548	0.007*	0.443	0.255	0.351	0.912
F_{is}	-0.102	-0.148	0.179	0.135	0.079	0.038	-0.079