

Erratum to: Pronounced genetic structure and low genetic diversity in European red-billed chough (*Pyrrhocorax pyrrhocorax*) populations

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In the original publication, Tables 3 and 6 were published with incorrect estimates of population heterozygosities. All other diversity statistics were correct as originally presented. Updated versions of Tables 3 and 6 with corrected heterozygosity estimates confirmed using Arlequin 3.5 (Excoffier and Lischer 2010) as in Dávila et al. (2014) are provided in this erratum. Discrepancies were minor for populations on the British Isles. The correct estimates for

Spain are slightly larger than those reported for La Palma by Dávila et al. (2014), but this does not necessarily affect their interpretation that choughs on La Palma may have originated from multiple migration events. The original conclusion that chough populations on the British Isles have low genetic diversity compared to continental European populations remains and is now, in fact, strengthened.

The online version of the original article can be found under doi:[10.1007/s10592-012-0366-6](https://doi.org/10.1007/s10592-012-0366-6).

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Table 3 Genetic diversity statistics (means \pm 1 SD) derived from 16 microsatellite loci across 348 red-billed choughs from 11 populations

Population	<i>n</i>	Missing data (%)	<i>n_a</i>	<i>a_r</i>	<i>n_e</i>	<i>n_p</i>	<i>H_O</i>	<i>H_E</i>	<i>F_{IS}</i>
Colonsay	40	4.85 \pm 9.01	2.88 \pm 1.15	1.95 \pm 0.58	1.60 \pm 0.52	1	0.28 \pm 0.19	0.32 \pm 0.20	0.131*
Islay	77	6.51 \pm 10.63	3.13 \pm 1.31	1.97 \pm 0.67	1.62 \pm 0.62	2	0.31 \pm 0.22	0.31 \pm 0.22	0.024
Isle of Man	41	5.95 \pm 10.85	3.13 \pm 1.50	1.98 \pm 0.67	1.63 \pm 0.55	4	0.32 \pm 0.22	0.32 \pm 0.22	0.019
Ireland	26	6.31 \pm 10.30	3.63 \pm 1.50	2.53 \pm 0.89	2.16 \pm 0.95	1	0.41 \pm 0.21	0.46 \pm 0.22	0.130*
North Wales	73	7.18 \pm 12.48	3.38 \pm 1.54	2.46 \pm 0.79	2.29 \pm 0.83	1	0.50 \pm 0.26	0.49 \pm 0.24	-0.009
South Wales	11	6.55 \pm 6.27	2.69 \pm 1.01	2.34 \pm 0.70	2.03 \pm 0.63	0	0.51 \pm 0.27	0.45 \pm 0.21	-0.078
Cornwall	9	19.78 \pm 25.04	2.25 \pm 0.77	2.05 \pm 0.62	1.75 \pm 0.55	0	0.41 \pm 0.26	0.37 \pm 0.21	-0.031
Brittany	18	3.67 \pm 4.67	2.81 \pm 1.17	2.23 \pm 0.70	1.96 \pm 0.74	1	0.45 \pm 0.25	0.42 \pm 0.22	-0.040
French Alps	14	13.07 \pm 18.43	4.88 \pm 1.67	3.55 \pm 0.86	3.33 \pm 1.30	5	0.58 \pm 0.16	0.66 \pm 0.12	0.167**
Spain	17	4.35 \pm 10.22	6.38 \pm 2.55	4.11 \pm 1.17	4.51 \pm 1.92	28	0.77 \pm 0.18	0.73 \pm 0.15	-0.038
Paradise Park	22	3.86 \pm 8.77	2.81 \pm 1.05	2.38 \pm 0.67	2.15 \pm 0.61	0	0.53 \pm 0.23	0.48 \pm 0.20	-0.063
Total	348	6.57 \pm 11.58	—	—	—	—	—	—	—

Population size (*n*) is given alongside the average percentage of missing genotype data, number of alleles (*n_a*), allelic richness (*a_r*), effective number of alleles (*n_e*), number of private alleles (*n_p*), observed heterozygosity (*H_O*), expected heterozygosity (*H_E*) and Wright's *F_{IS}* with significance indicated at the 5 % level (*) and strict Bonferroni-corrected level ($\alpha = 0.00028^{**}$)

Table 6 Characterisation of 16 microsatellite loci for red-billed chough

Locus name	Repeat unit	<i>T_a</i>	<i>n_a</i>	Allele range	<i>H_O</i>	<i>H_E</i>	<i>p_{HWE}</i>	Null-allele frequency
Ppy-001	TACA	60 \rightarrow 50	4	151–179	0.42 \pm 0.21	0.41 \pm 0.19	0.148	-0.04 \pm 0.13
Ppy-002	ATCT	60 \rightarrow 50	4	151–179	0.39 \pm 0.19	0.39 \pm 0.20	0.993	-0.05 \pm 0.12
Ppy-003	AGAT	60 \rightarrow 50	11	292–344	0.55 \pm 0.24	0.55 \pm 0.15	<0.001	0.01 \pm 0.11
Ppy-004	AGAT	60 \rightarrow 50	7	173–239	0.45 \pm 0.22	0.45 \pm 0.19	0.183	-0.04 \pm 0.13
Ppy-005	TATC	60 \rightarrow 50	7	226–250	0.36 \pm 0.27	0.36 \pm 0.26	0.028	-0.02 \pm 0.14
Ppy-006	CATC	60 \rightarrow 50	8	139–175	0.13 \pm 0.30	0.12 \pm 0.28	0.729	0.00 \pm 0.05
Ppy-007	GATA	55 \rightarrow 45	9	161–193	0.58 \pm 0.16	0.60 \pm 0.15	0.425	0.00 \pm 0.08
Ppy-008	GATA	60 \rightarrow 50	9	221–265	0.57 \pm 0.14	0.60 \pm 0.16	0.018	-0.02 \pm 0.17
Ppy-009	AAGT	60 \rightarrow 50	6	222–242	0.56 \pm 0.25	0.51 \pm 0.19	0.420	-0.06 \pm 0.11
Ppy-010	CA	60 \rightarrow 50	14	108–146	0.50 \pm 0.26	0.43 \pm 0.23	0.187	-0.11 \pm 0.17
Ppy-011	TAGA	60 \rightarrow 50	10	163–191	0.68 \pm 0.16	0.63 \pm 0.14	0.190	-0.08 \pm 0.13
Ppy-012	TAGA	60 \rightarrow 50	13	210–266	0.47 \pm 0.23	0.51 \pm 0.15	<0.001	0.00 \pm 0.23
Ppy-013	GATA	60 \rightarrow 50	10	197–221	0.64 \pm 0.12	0.65 \pm 0.08	0.493	0.01 \pm 0.07
Ppy-014 ^a	GATG	60 \rightarrow 50	5	239–275	0.39 \pm 0.11	0.40 \pm 0.10	0.615	0.02 \pm 0.08
Ppy-015 ^a	TATG	60 \rightarrow 50	3	152–158	0.13 \pm 0.26	0.11 \pm 0.19	0.120	-0.04 \pm 0.15
Ppy-016	GGAT	60 \rightarrow 50	13	200–244	0.53 \pm 0.23	0.56 \pm 0.22	0.022	0.02 \pm 0.07

Statistics (\pm 1 SD) were calculated from 348 individuals in 11 populations

The microsatellite repeat unit is given alongside TouchDown annealing temperature gradient (*T_a*), number of alleles (*n_a*), allele range (*bp*), observed (*H_O*) and expected (*H_E*) heterozygosity, the probability of Hardy–Weinberg equilibrium (*p_{HWE}*) and null allele frequency (van Oosterhout et al. 2004). See Wenzel et al. (2011) for full characterisation

^a Locus also isolated by Jaari et al. (2008)

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