

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

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ABSTRACT

The red-billed chough (*Pyrrhocorax pyrrhocorax*) is of conservation concern in the British Isles and continental Europe, with historically declining populations and a highly fragmented distribution. We quantified the distribution of genetic variation within and among European populations to identify isolated populations that may need to be managed as demographically independent units, and assess whether individual populations are denuded of genetic diversity and so may show reduced viability.

We genotyped 326 choughs from ten wild populations and 22 from one captive population at 16 nuclear microsatellite loci, and sequenced 34 individuals across three mitochondrial regions to quantify genetic structure, diversity and phylogeography.

Microsatellite diversity was low (often <4 alleles per locus), but pairwise population differentiation was high (often $D_{est} > 0.1$), with a signature of isolation-by-distance. Bayesian-inferred a posteriori genetic clusters coincided with a priori populations, supporting strong genetic structure. Microsatellites also allowed us to identify the probable origin of the captive choughs and one recently founded wild population. Mitochondrial DNA sequence diversity was low ($\pi = 0.00103$). Phylogeographic structure was consequently poorly resolved, but indicated that sampled continental-European populations are ancestral to British Isles populations, which comprised a single clade.

Our data suggest that British Isles chough populations are relatively isolated with infrequent gene flow and relatively genetically depauperate, potentially requiring genetic management. These findings should be integrated into conservation management policy to ensure long-term viability of chough populations.