Journal of Avian Biology

JAV-02633
Rodríguez, A., Rodríguez, B., Montelongo, T., Garcia-Porta, J., Pipa, T., Carty, M., Danielsen, J., Nunes, J., Silva, C., Geraldes, P., Medina, F. M. and Illera, J. C. 2020. Cryptic differentiation in the Manx Shearwater hinders the identification of a new endemic subspecies. – J. Avian Biol. 2020: e02633

Supplementary material

Supporting material

Figure S1 Underwing

Figure S1. The axillary underwing pattern variation of Manx Shearwater *Puffinus puffinus* and codes used in this study: 1) birds showing a clean white underwing, 2) birds showing a dark spot in the articulation, 3) birds with a dark spot and a diagonal axillary bar, and 4) birds with a dark spot in the articulation, a diagonal axillary bar and a conspicuous dark flank bar.

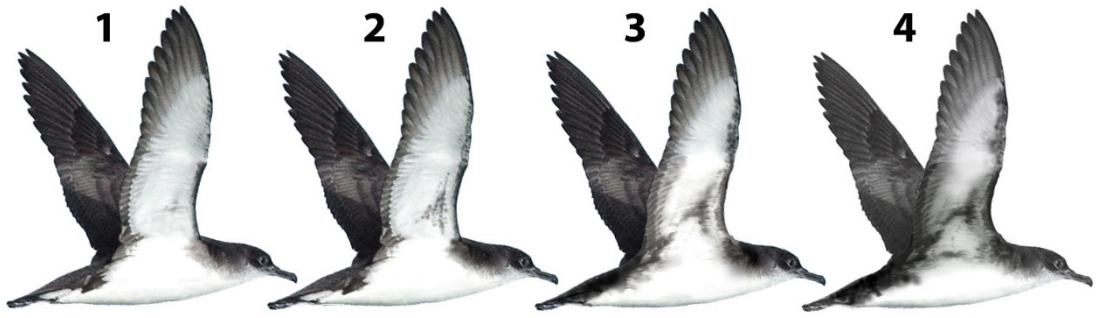

Figure S2 Sonograms

Figure S2. Examples of sonograms of male Manx shearwater *Puffinus puffinus*. Upper recorded on Tenerife, Canary Islands (February 2020), and lower recorded on St. Kilda, Scotland (Robb et al. 2008).

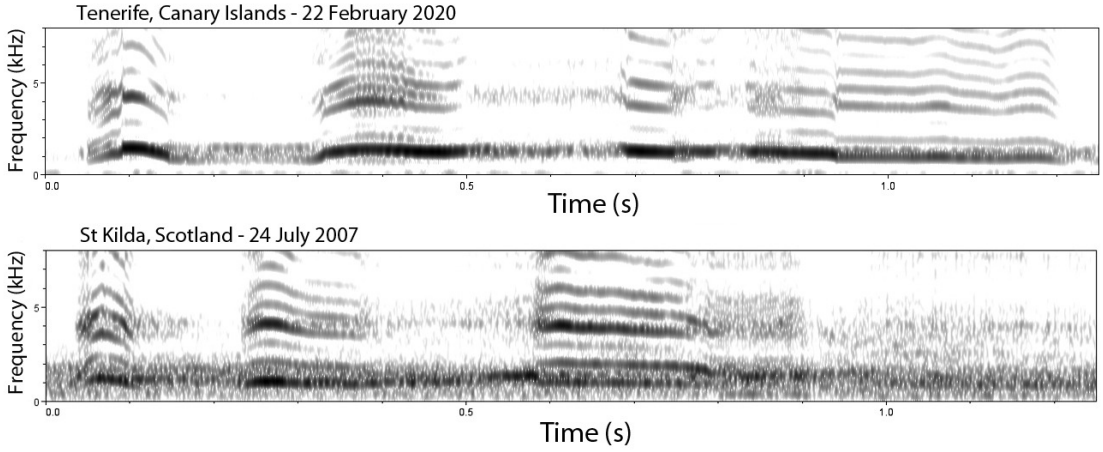

Figure S3 Wing length Zonfrillo

Figure S3. Mean wing lengths compiled by Zonfrillo (2001) from six breeding colonies across a latitudinal gradient of 34 degrees. Dots and whiskers indicate mean wing and standard deviation. Numbers indicate sample size. Different letters indicate statistical significant differences among groups according to post-hoc Tukey tests (see main text).

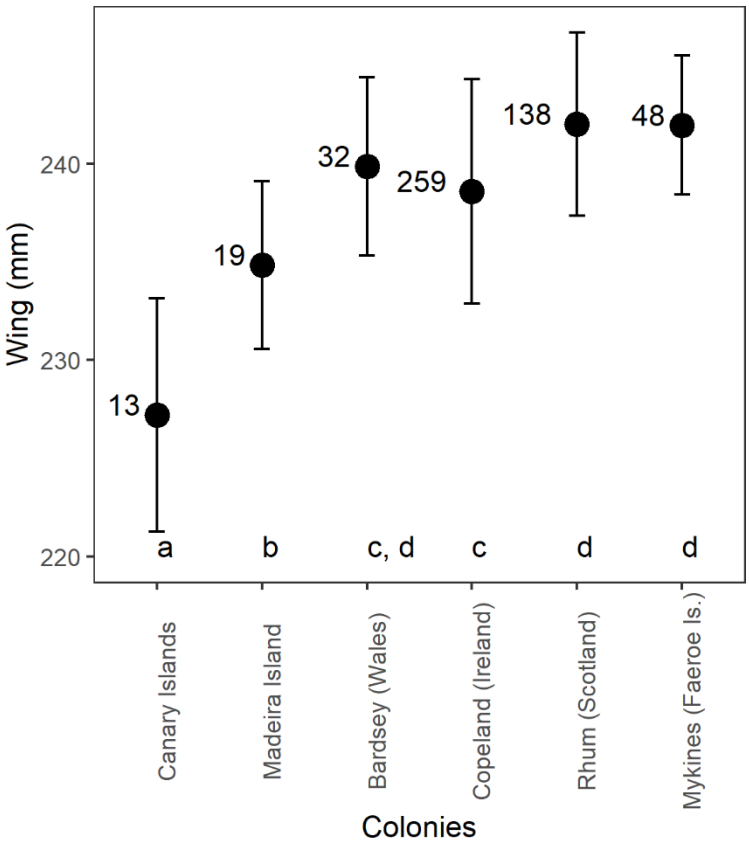

Figure S4 Skeletal traits

Figure S4. Distribution of skeletal traits of northern European individuals (black circles) hosted at the collections of the Natural History Museum, Tring (UK), and the types (red circles) hosted at the collection of the Doñana Biological Station, EBD-CSIC, Seville (Spain). Abbreviations of the skeletal traits used by McMinn et al. 1991 are showed in brackets.

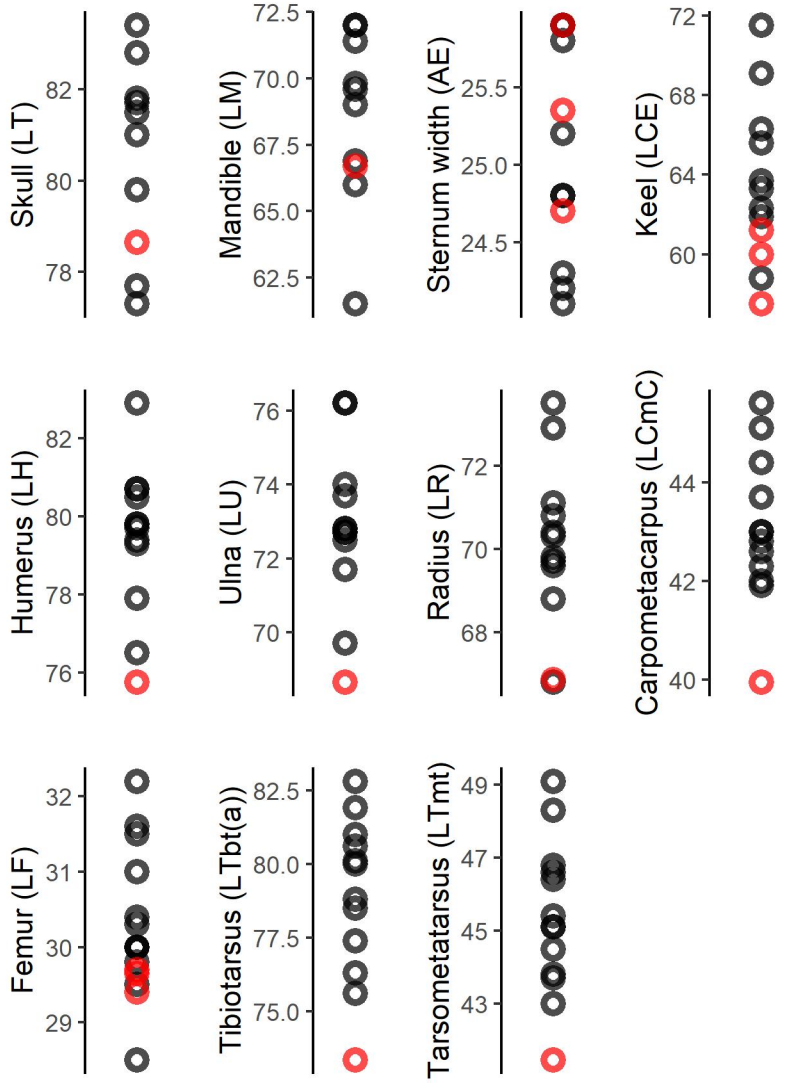

Figure S5 Network

Figure S5. Parsimony network of the Manx shearwaters *Puffinus puffinus*, based on a 319 bp fragment of the control region mitochondrial gene, obtained with the programme TCS (v.1.21). Open small circles depict one-step mutation edge. The size of haplotypes (circles) represents its abundance, that is, the number of individuals sharing such haplotype.

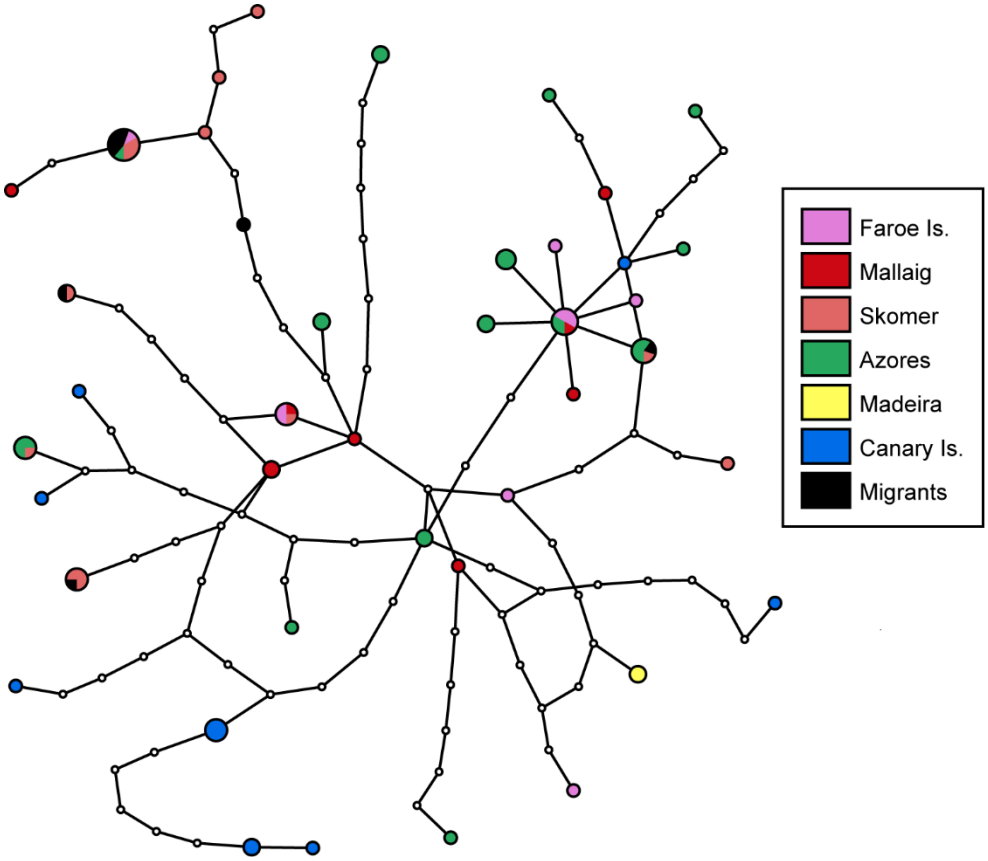

Figure S6 Summary (Bayesian) tree

Figure S6. Summary tree including *Puffinus puffinus* sequences obtained in the present study and all *Puffinus* spp. sequences available in GenBank (Dataset2; see details in Methods). Black dots indicate posterior probabilities ≥ 0.95.

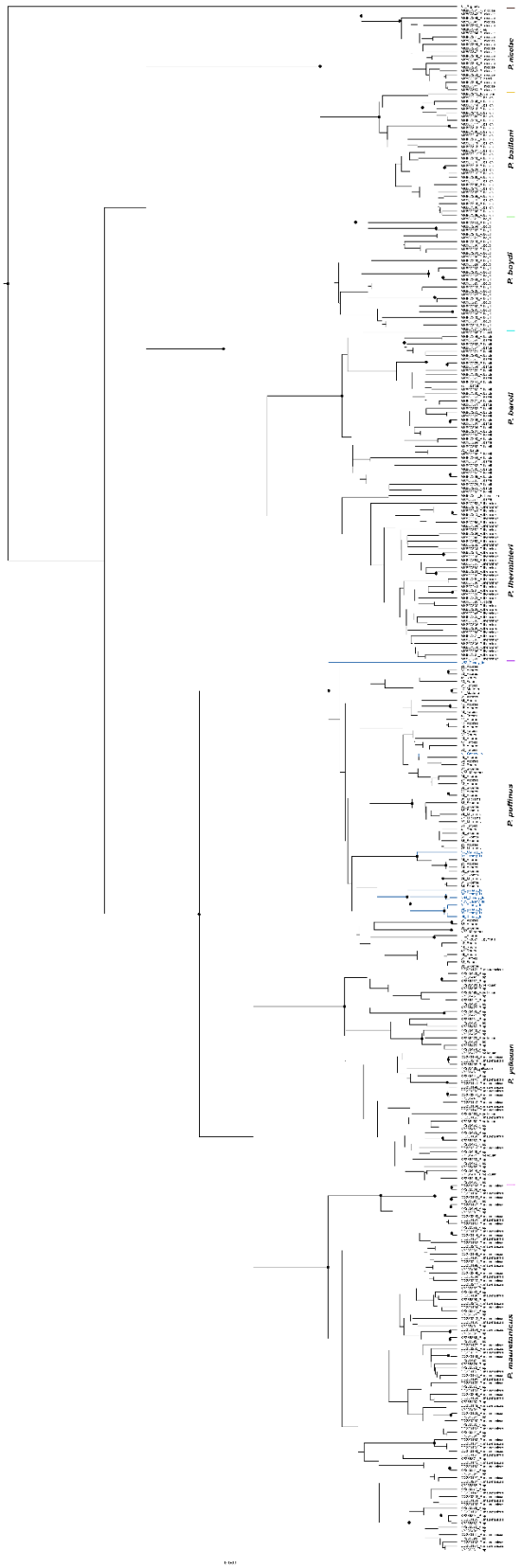

Figure S7 Ring Map1

Figure S7. Inter-colony movements of Manx shearwater *Puffinus puffinus*. Birds were ringed as nestlings, and recovered as breeders (Status code = N) or in a colony (not necessarily breeding, Status code = K). Arrows indicate the direction of movement. Only inter-colony movements larger than 100 Km are shown. Ringing data comes from EURING Data Bank.

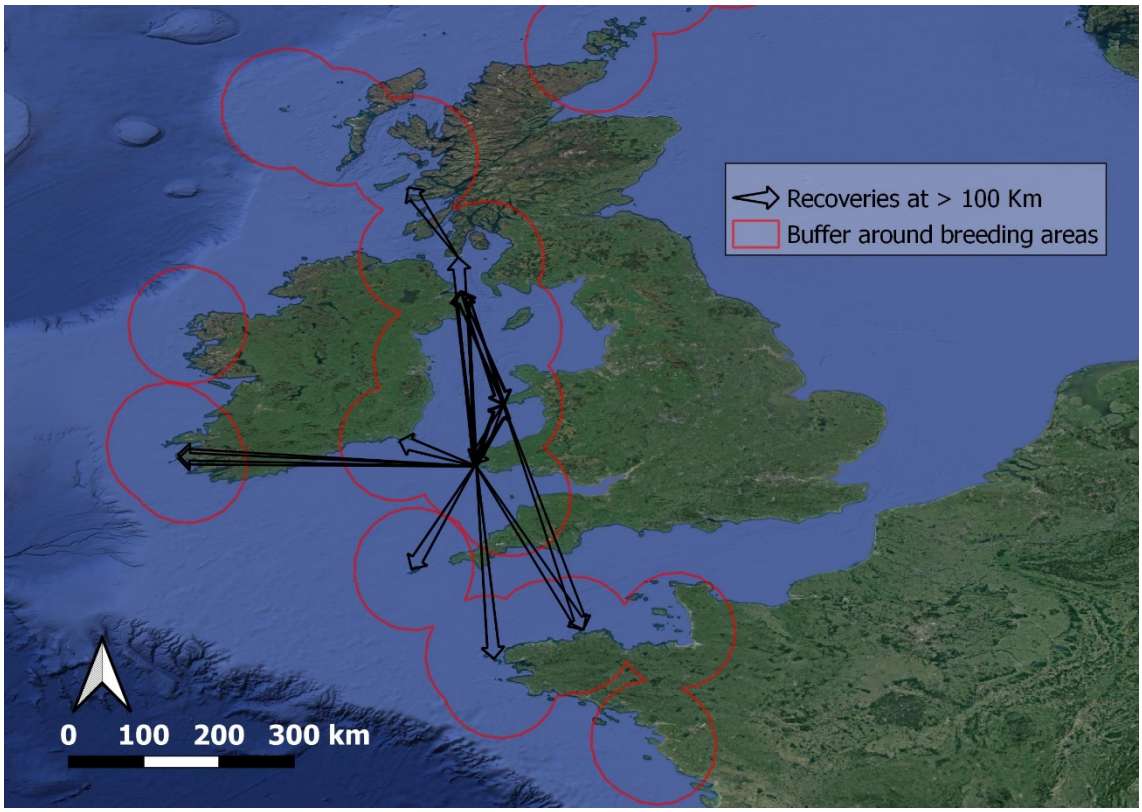

Figure S8 Ring Map2

Figure S8. Long-distance movements from European breeding areas to peripheral breeding areas (Azores, Maderia, Canary Islands, and East coast of North America) recorded in the Manx shearwater *Puffinus puffinus*. The Manx shearwater nestlings were ringed at their natal colonies in Iceland, Faroe Islands, and United Kingdom, and recovered at any circumstances. Ringing data comes from EURING Data Bank.

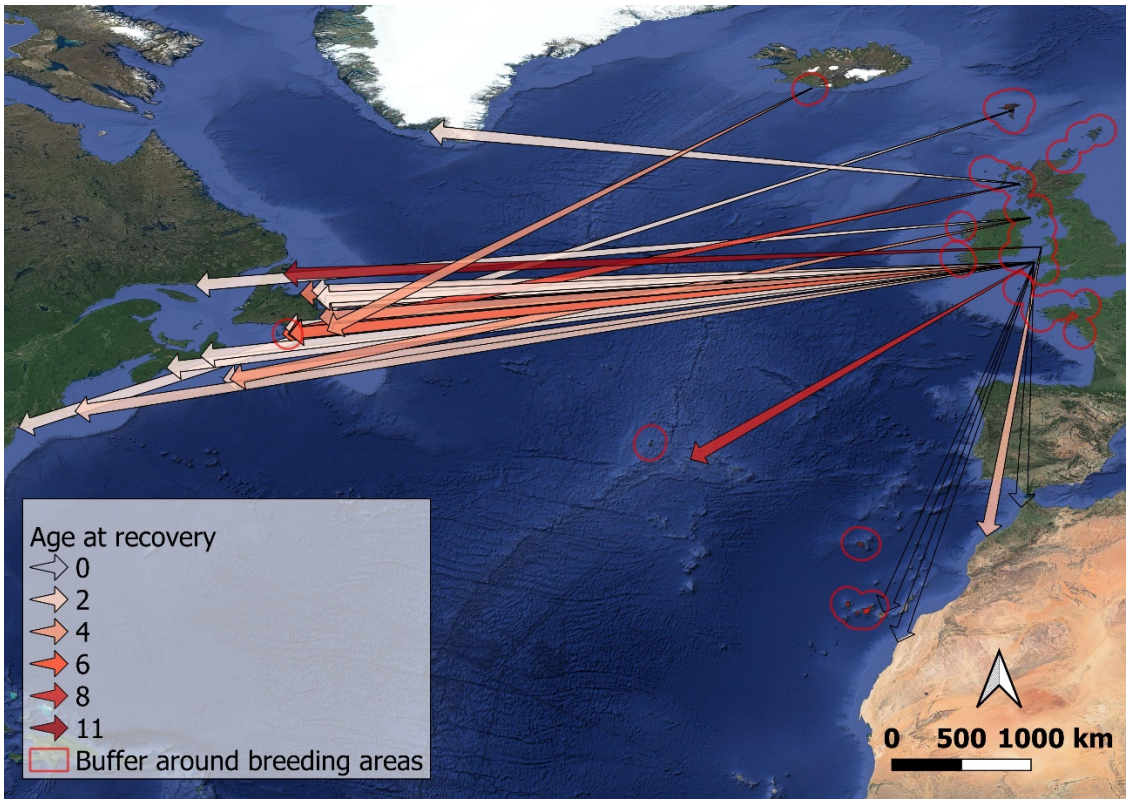

Figure S9 Photographs

Figure S9. Photographs of Manx shearwaters *Puffinus puffinus* showing differences in colouration. A bird photographed around Scilly, United Kingdom, on 7 August 2014 (a; Photo courtesy of Zac Hinchcliffe). Three birds photographed on the North shore of Tenerife, Canary Islands, on 18 June 2017 (b, c, and d; Photos courtesy of Beneharo Rodríguez).

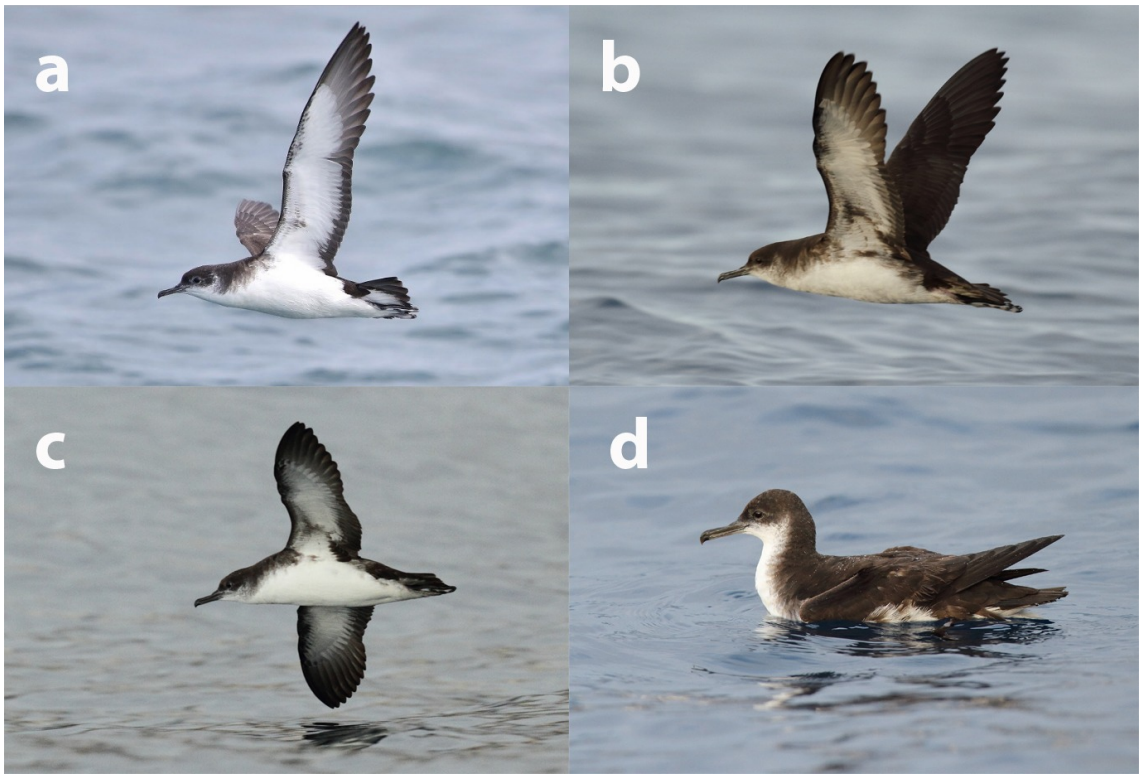

Table S1

Table S1. Factor loadings of the principal components and importance of the components of the principal components analysis (PCA) on the eight biometric variables measured in three breeding populations (Mallaig, Azores and the Canary Islands).

	PC1	PC2	PC3
Variables			
Weight	0.32	-0.44	0.13
Wing	0.29	0.01	0.64
Tarsus	0.29	0.25	0.57
Skull	0.28	0.41	-0.04
Culmen	0.33	0.49	-0.27
Bill length at nostril	0.43	0.24	-0.32
Bill depth at nostril	0.42	-0.35	-0.09
Bill depth	0.43	-0.39	-0.27
Importance of components			
Standard deviation	1.65	1.24	1.07
Proportion of Variance	0.34	0.19	0.14
Cumulative Proportion	0.34	0.53	0.67

Table S2

Table S2. Factor loadings of the principal components and importance of the components of the principal components analysis (PCA) on the seven acoustic variables measured in the northern populations (including Iceland, Ireland and United Kingdom) and in the Canary Islands population.

	PC1	PC2	PC3
Variables			
Fundamental frequency	0.00	-0.57	0.00
Mean frequency	0.46	-0.31	-0.01
Peak frequency change	-0.14	0.00	-0.74
Harmonicity	-0.19	-0.50	-0.01
Wiener entropy	-0.55	0.05	0.05
Frequency bandwidth	0.54	0.04	-0.07
Amplitude	-0.18	-0.32	0.54
Vibrato amplitude	0.20	0.35	0.40
Vibrato asymmetry	-0.25	0.32	0.05
Importance of components			
Standard deviation	1.78	1.66	1.12
Proportion of Variance	0.35	0.31	0.14
Cumulative Proportion	0.35	0.66	0.79

Table S3

Table S3. Genetic diversity estimates from the mitochondrial control region gene for the *Puffinus puffinus* complex group using the DnaSP programme (v 5.10.01). N: Sample size. Hap: Number of haplotypes. HD: Haplotype diversity and standard deviation (SD). ND: Nucleotide diversity and standard deviation. θ: Theta (2Neμ) per site from number of variable sites and standard deviation (SD). Ambiguity nucleotide codes with two or three variants per position were substituted for a general (n) ambiguity code.

			Control Region (CR)					
Populations	N	Hap	HD	SD	ND	SD	θ	SD
Total	80	33	0.943	0.014	0.01907	0.00096	0.00249	0.00738
Canary Islands	12	8	0.894	0.078	0.02605	0.00371	0.02716	0.01148
Madeira	2	1	0.000	0.000	0.00000	0.00000	0.00000	0.00000
Azores	25	13	0.933	0.028	0.01878	0.00230	0.02555	0.00925
Skomer	14	10	0.934	0.051	0.02233	0.00201	0.02189	0.00913
Mallaig (Rum)	9	7	0.944	0.070	0.01464	0.00303	0.01518	0.00736
Faroes	10	7	0.911	0.077	0.01644	0.00343	0.01908	0.00876
Migrants	8	5	0.786	0.151	0.02118	0.00531	0.02190	0.01048

Supplementary Data

Dataset. Excel file containing the raw data supporting the findings of this study. The file has six spreadsheets with the data on phenology, morphometrics, skeletons, colouration, acoustics and genetics.