Forensic Science International: Genetics 3 (2009) e63–e69

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Announcement of population data

Genetic data from 28 STR loci for forensic individual identification and parentage analyses in 6 bird of prey species

Nick Dawnay [a,*], Rob Ogden [b], Jon H. Wetton [c], Roger S. Thorpe [a], Ross McEwing [b]

[a] School of Biological Sciences, Bangor University, Deiniol Road, Bangor LL57 2UW, United Kingdom
[b] Wildlife DNA Services, Tepnel RPS, Appleton Place, Livingston EH54 7EZ, United Kingdom
[c] The Forensic Science Service, 2960 Trident Court, Solihull Parkway, Birmingham Business Park, Solihull B37 7YN, United Kingdom

ARTICLE INFO

Article history:
Received 28 April 2008
Received in revised form 6 June 2008
Accepted 1 July 2008

Keywords:
Wildlife forensics
Population genetics
Bird of prey
Validation
STR

ABSTRACT

Twenty-eight STR loci were screened in wild populations of six bird of prey species providing allele frequencies and population genetic parameters necessary for the application of STRs in wildlife forensic genetic casework. Individual STR loci were validated according to forensic recommendations in specimens of golden eagle (*Aquila chrysaetos*), goshawk (*Accipiter gentilis*), merlin (*Falco columbarius*), peregrine falcon (*Falco peregrinus*), gyr falcon (*Falco rusticolus*) and saker falcon (*Falco cherrug*). Deviations from Hardy–Weinberg expectations and linkage disequilibrium between locus pairs were examined. The average probability of identity (PI_{ave}) and power of exclusion (PE) suggest the profiling systems of golden eagle, goshawk, merlin and peregrine falcons are capable of providing robust and highly discriminatory forensic evidence for legal proceedings. Due to low sample numbers the allele frequency data for gyr and saker falcons is not currently capable of providing an effective probability of identity. Further work should focus on increasing the size of these data sets.

1. Populations

Fig. 1 shows United Kingdom (UK) subpopulations of (A) golden eagle $n = 178$, (B) goshawk $n = 99$, (C) merlin $n = 190$ and (D) peregrine $n = 45$. Swedish gyr falcon $n = 18$ and Asian saker $n = 14$ data was also collected.

2. Extraction

DNA was extracted from blood, tissue, buccal swab or feather following standard QIAGEN DNeasy tissue kit protocols and was quantified against a known standard using the fluorescent dye PicoGreen (Molecular Probes, Inc.), and Galaxy Fluostar apparatus (BMG Labtechnologies Ltd.).

3. PCR

PCR reaction conditions and thermocycling parameters are available online (http://www.tracenetwork.org).

4. Genotyping

Genotypes for golden eagle were resolved on an Applied Biosystems, Inc. 3730xl. All remaining species were genotyped on a Beckman Coulter CEQ8000 platform. Details from previously isolated STR loci [1–5] used in the population screen are provided in supplemental data Table 1.

5. Quality control

Laboratory accredited to ISO 9001. All loci were validated according to SWGDAM guidelines prior to population screen.

6. Analyses of data

MSA [6], GENEPOP [7], API-CALC [8], and GENALEX [9] programs.

7. Results

See Tables 1–6.

* Corresponding author. Tel.: +44 1506 424290; fax: +44 1506 424280.
E-mail address: nick.dawnay@yahoo.com (N. Dawnay).

1872-4973/$ – see front matter © 2008 Elsevier Ireland Ltd. All rights reserved.
doi:10.1016/j.fsigen.2008.07.001

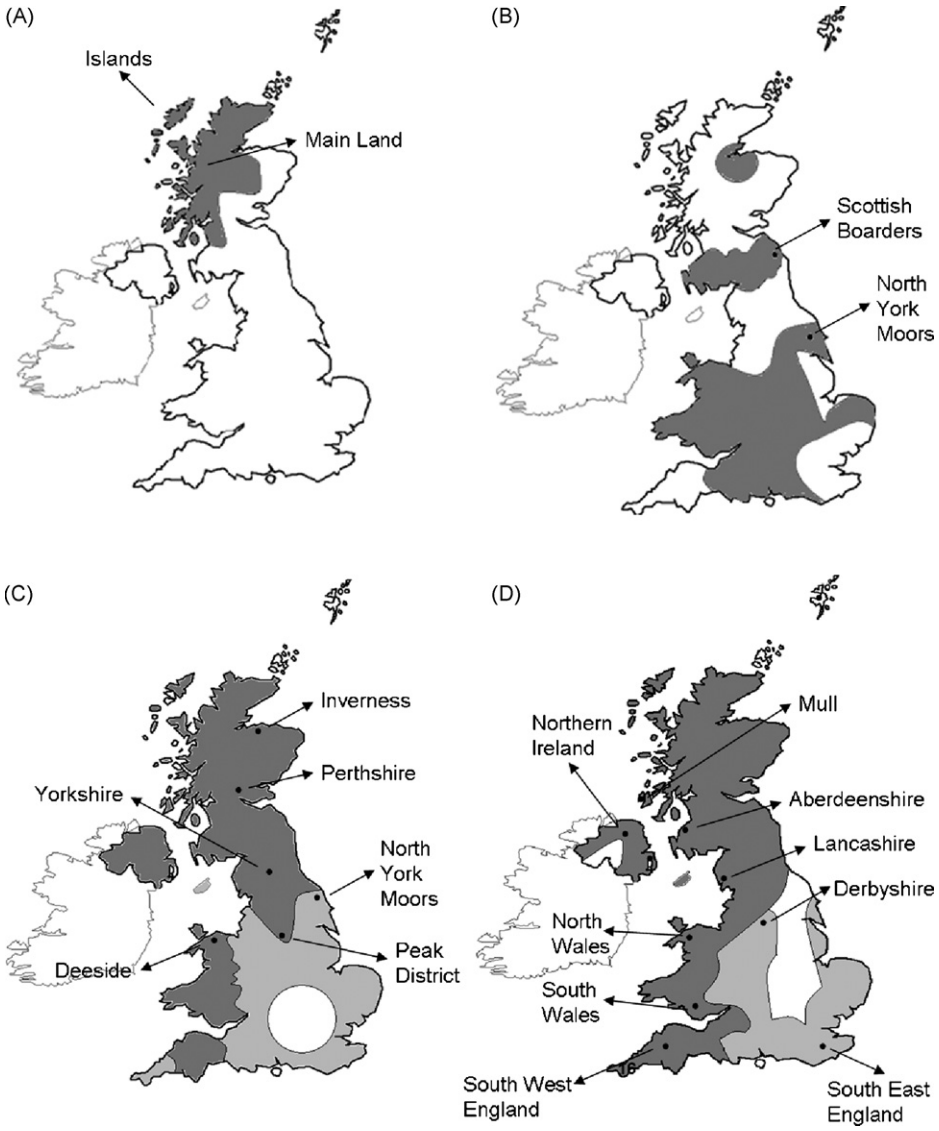

Fig. 1. Species distribution data from United Kingdom populations of A = golden eagle, B = goshawk, C = merlin and D = peregrine falcon showing sample site locations. Merlin and peregrine have both a full year resident distribution range (dark grey) and an extended winter distribution range (light grey). Un-shaded areas contain no populations. Distribution data modified from Royal Society for the Protection of Birds data available at http://www.rspb.org.uk/wildlife/birdguide.

8. Access to the data

Available on request: nick.dawnay@yahoo.com.

9. Other remarks

The legitimate trade in captive bred birds of prey is well established both in the UK and internationally. However, illegal trade in wild caught individuals particularly through attempts to legitimize wild birds into the legal captive bred market by false claims of captive breeding [10,11] threatens the conservation of protected species with 39 reported incidents of this nature in the UK in 2006 [12]. An additional threat is persecution in the form of poisoning, shooting and egg collecting [12]. The data provided in this study can be used in forensic genetic casework investigating false parentage claims or to establish a link between trace evidence and crime scene through the generation of a forensic match probability.

Validation experiments were performed on each locus following recent forensic recommendations in animal identity testing [13,14]. All loci displayed Mendelian inheritance, and gave consistent genotypes in five independent PCR amplifications. Full validation results are available (http://www.tracenetwork.org).

In golden eagle, goshawk and merlin populations sample numbers were sufficient to allow for genetic analyses of separate geographical populations (Fig. 1A–C). Tests for deviations from HWE in individual populations showed significant heterozygote deficiency after Bonferroni correction at three loci in golden eagle (Aa02, Aa26 and Aa39), one locus in goshawk (Age4) and one locus in merlin (μFpe2-Mer). However, loci did not display the same pattern in all tested populations. In peregrine, gyr and saker population sample numbers were insufficient to allow for separate population analyses and therefore global allele frequencies were used. Tests for deviations from HWE showed significant heterozygote deficiency at one locus in gyr (NVH fp54). Independence of loci was tested by performing linkage disequilibrium analyses between locus pairs in each population. After Bonferroni correction, significant linkage between loci was observed in 1 of 56 (1.8%) locus pair combinations in golden eagle, 1 of 56 (1.8%) combinations in goshawk and 5 of 206 (2.49%) combinations in merlin.