Citation for published version:

Digital Object Identifier (DOI):
10.1016/j.fsigen.2011.04.015

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Peer reviewed version

Published In:
Forensic Science International: Genetics

General rights
Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy
The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.
Forensic Population Genetics—Short Communication

Genetic data from 15 STR loci for forensic individual identification and parentage analyses in UK domestic dogs (*Canis lupus familiaris*)

Rob Ogden a,b,*, Richard J. Mellanby c, Dylan Clements c, Adam G. Gow c, Roger Powell d, Ross McEwing a,b

1. Populations

United Kingdom (UK) dogs obtained from domestic dog collections held in Edinburgh (Scotland) and Cambridge (England). Samples included dogs from 12 major contributing breeds\(^1\) (\(n = 301\)), 22 minor breeds\(^2\) (\(n = 47\)) and 27 mixed breed individuals.

2. Extraction

DNA was extracted from whole frozen blood samples following standard QIAGEN DNeasy blood and tissue kit protocols.

3. PCR amplification

Amplification of eighteen STR loci and one sex determination zinc-finger protein-linked locus was performed using the Finnyzymes Canine 2.1 STR Multiplex Reagent Kit.

4. Electrophoresis and genotyping

Genotypes were resolved under capillary electrophoresis on an Applied Biosystems, Inc 3730xl and subsequently analysed using proprietary GeneMapper v4.0 software. A standard system of allele nomenclature for these canine STRs has previously been developed [3] and was followed in this study.

5. Analysis of data

GenePOP [4], POWER-STAT [5], and GENALEX [6] programs were used to calculate population genetic parameters and estimate discrimination power (Table 1).

6. Results

The mean allele frequencies per locus across breeds are shown in Table 1, together with locus specific Hardy–Weinburg test results, probabilities of discrimination and probabilities of exclusion.
<table>
<thead>
<tr>
<th>Allele</th>
<th>FH2001</th>
<th>FH2004</th>
<th>FH2010</th>
<th>FH2054</th>
<th>FH2088</th>
<th>FH2107</th>
<th>FH2309</th>
<th>FH2328</th>
<th>FH377</th>
<th>PEZ02</th>
<th>PEZ05</th>
<th>PEZ16</th>
<th>PEZ17</th>
<th>PEZ21</th>
<th>VWF.X</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.804</td>
<td>0.586</td>
<td>0.356</td>
<td>0.617</td>
<td>0.499</td>
<td>0.517</td>
<td>0.534</td>
<td>0.543</td>
<td>0.552</td>
<td>0.561</td>
<td>0.562</td>
<td>0.563</td>
<td>0.564</td>
<td>0.565</td>
<td>0.566</td>
</tr>
<tr>
<td>2</td>
<td>0.677</td>
<td>0.601</td>
<td>0.471</td>
<td>0.693</td>
<td>0.604</td>
<td>0.744</td>
<td>0.680</td>
<td>0.662</td>
<td>0.659</td>
<td>0.623</td>
<td>0.421</td>
<td>0.617</td>
<td>0.620</td>
<td>0.499</td>
<td>0.538</td>
</tr>
<tr>
<td>3</td>
<td>0.662</td>
<td>0.586</td>
<td>0.488</td>
<td>0.723</td>
<td>0.603</td>
<td>0.778</td>
<td>0.708</td>
<td>0.702</td>
<td>0.693</td>
<td>0.609</td>
<td>0.510</td>
<td>0.647</td>
<td>0.595</td>
<td>0.523</td>
<td>0.542</td>
</tr>
<tr>
<td>4</td>
<td>0.804</td>
<td>0.281</td>
<td>0.906</td>
<td>0.119</td>
<td>0.412</td>
<td>0.548</td>
<td>0.527</td>
<td>0.717</td>
<td>0.022</td>
<td>0.356</td>
<td>0.006</td>
<td>0.001</td>
<td>0.987</td>
<td>0.481</td>
<td>0.084</td>
</tr>
</tbody>
</table>

Table 1
Allele frequencies for 15 loci in the Finnzymes Canine 2.1 STR panel genotyped across 375 individuals and 34 breeds of UK dog.
Table 1 (Continued)

| Allele | FH2001 | FH2004 | FH2010 | FH2054 | FH2088 | FH2107 | FH2309 | FH2328 | FH3337 | PEZ02 | PEZ05 | PEZ16 | PEZ17 | PEZ21 | VWF.X |
|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| PD     | 0.904  | 0.926  | 0.815  | 0.936  | 0.891  | 0.957  | 0.970  | 0.957  | 0.957  | 0.917  | 0.835  | 0.941  | 0.902  | 0.821  | 0.819  |
| PE     | 0.320  | 0.276  | 0.164  | 0.402  | 0.239  | 0.483  | 0.380  | 0.368  | 0.405  | 0.308  | 0.160  | 0.322  | 0.333  | 0.196  | 0.201  |

Obs. H and Exp. H are observed and expected heterozygosities averaged across breed, P-value = Hardy–Weinberg equilibrium exact test, PD = power of discrimination, PE = power of exclusion.

7. Other remarks

Canine DNA is being increasingly used as evidence in a wide range of crimes. Domestic dogs may be involved as the perpetrator or victim of crime, or as a contributor to trace DNA evidence that may link suspects, evidence items and crime scenes [7]. Within the UK, canine DNA profiling has been successfully used to investigate crimes including murder, dog-fighting and animal abuse for over five years. However until now, the application of profile matching has been limited by the lack of available population data for UK dogs, necessitating the use of a US database with highly conservative match probability statistics to estimate the probability of a random DNA profile match. The data provided in this study can be used to calculate more accurate estimates of forensic genetic parameters associated with canine DNA profiling in the UK.

The Finnzymes Canine 2.1 STR Multiplex Reagent Kit includes eighteen STR markers and a sex determinant zinc-finger protein-linked locus. Tests for deviation from Hardy–Weinberg equilibrium (HWE) showed highly significant (P < 0.001) differences between observed and expected genotype frequencies at one locus (FH2017) across multiple breeds, suggesting the presence of null alleles. This locus was therefore excluded from subsequent analysis. Significant deviations at loci PEZ05 and PEZ16 (Table 1) were driven by results within single breeds (Staffordshire Bull Terriers and Yorkshire Terriers respectively) and are not considered to be problematic. Loci FH2361 and FH3313 were excluded due to the presence of microvariants that complicated allele calling. The future development of an allelic ladder should resolve this issue.

The relative genetic distances among breeds were examined by calculating pairwise FST values among all breeds. All pairwise comparisons among true breeds showed significant FST values (FST > 0, P = 0.01) confirming the expected reduction in gene flow among breeds due to separation of breeding lines. The mean FST estimate across all breeds was 0.186, which is the value used to represent theta in the match probability equation [8]. As previously discussed by Dawnay et al. [9], there is currently no consensus about how best to account for individual inbreeding within breeds, f, commonly estimated as FIS. Inbreeding within UK breeds is high [10] and will bias match probability estimates in favour of the prosecution. Existing published methods to mitigate this [11] are not always applicable [9]. The only current alternative is to use sibling match probabilities; the PIobs estimate for this current study is 2.49 × 10⁻⁷.

8. Quality control

All data were generated in a GLP certified laboratory operating in compliance with ISO17025 testing standards. ISFG recommendations on the analysis of the DNA polymorphisms [12] and non-human DNA [13] were followed throughout. This publication follows ISFG guidelines for the publication of population genetic data [14].

Acknowledgements

This work was funded by Petsavers and a Genesis-Faraday SPARK award to RO, RM, DC and RMcE. The authors thank Sree Kanthaswamy (UC Davis) and Mikko Koskinen (Finzymes) for advice during the preparation of this manuscript.

References