

# Conservation Genetics of British Traditional Chicken Breeds

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The Rare Breeds Survival Trust collaborated with The Roslin Institute to bring about the first investigation into the genetic diversity of British traditional chicken breeds. The results of the study were recently published in the journal *Animal Genetics*<sup>1</sup>. Samantha Wilkinson and colleagues discuss the findings of this study and the implications for conservation of traditional chicken breeds in Britain.

Britain has one of the largest numbers of different chicken breeds. A vast array of diverse morphological characteristics can be witnessed at any poultry show. Organisations like RBST, breed societies and individual breeders have put immense time and effort into safeguarding rare and traditional breeds. With such investments it is important that the genetic aspects of these breeds are taken into consideration. Breeds, in particular the rare ones, can suffer from loss of genetic diversity due to small population

sizes. An up-to-date genetic characterisation of breeds can not only give a picture of the current genetic states of breeds, but also inform management initiatives to preserve genetic diversity.

## Analysis

A panel of DNA markers was used to characterise the genetic diversity of 24 British traditional chicken breeds listed in Table 1. The breeds are a highly diverse set, ranging from old indigenous breeds to imported breeds that are well established in Britain to

breeds developed from crossing. The genetic markers were used to estimate (i) the levels of genetic diversity within each breed, (ii) the levels of genetic divergence and relationships amongst the breeds, and (iii) the nature of the genetic structure within breeds.

## Genetic diversity within the breeds

The levels of genetic diversity estimated for each breed are presented in Table 1. Two measures of genetic diversity within breeds are displayed. The first diversity estimate is the number of alleles<sup>2</sup> found in each breed and the second is the heterozygosity<sup>3</sup> found within each breed, with higher numbers indicating higher levels of genetic diversity. As can be seen, based on the number of alleles, the highest levels of genetic diversity were found in Maran and the lowest in Spanish. Based on heterozygosity, the highest levels of genetic diversity were found in Araucana and the lowest again in Spanish. To determine if the levels of genetic diversity found in the British traditional chicken breeds are reasonable we can look at other European chicken breeds to compare and contrast the estimates of genetic diversity. By comparison to other studies we found that the levels of genetic diversity in the British traditional chicken breeds are similar to those found in European chicken breeds (using similar panels of genetic markers). We can conclude that, encouragingly, for most breeds the levels of genetic diversity within breeds are high.

The one exception is the Spanish breed where, in comparison to the other

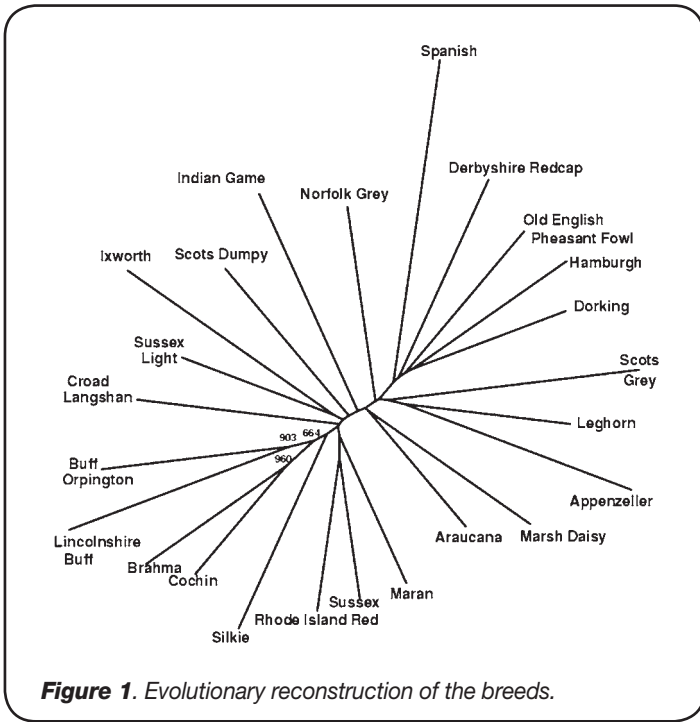
British breeds, there is very limited genetic diversity in this breed. The Spanish is a well-established breed in Britain and it has a uniquely distinctive morphological feature: a white face. In addition, it has a very small population size. The low genetic diversity in this breed could be due to limited introduction of other breed genetic material in order to maintain this physically distinctive characteristic and genetic processes enhanced by the small population size could have decreased the genetic diversity in this breed over the years.

## Genetic divergence and relationships amongst the breeds

The levels of genetic divergence of breeds were estimated and are presented as an evolutionary tree in Figure 1. The length of a branch of a breed is a visual representation of the genetic distance of a breed to all the other breeds, with a longer branch indicating higher genetic differentiation. As can be seen, most breeds have very long branches indicating high levels of genetic divergence of the breeds. This indicates that the chicken breeds are genetically distinct populations and there has been limited contemporary gene flow between breeds, probably to maintain the morphological distinctiveness of the breeds. The most genetically distinctive breeds were also amongst the most morphologically distinctive. For example, Indian Game (short legs, squat and wide), Silkie (degenerate feathers, dark skin) and Spanish (white face) possess traits not found in other breeds in

Breed	Breed origin	Status <sup>1</sup>	Number of alleles	Heterozygosity
1 Appenzeller	Switzerland, imported in 1970s	Endangered	94	0.43
2 Araucana	Chile, imported in 1930s		129	0.62
3 Brahma	China, imported (via USA) in 1800s	At Risk	124	0.53
4 Buff Orpington	Britain, developed from breed crosses in 1800s	At Risk	118	0.55
5 Cochon	China, imported in 1800s	At Risk	124	0.56
6 Croad Langshan	China, imported in late 1800s		107	0.49
7 Derbyshire Redcap	Old indigenous		94	0.42
8 Dorking	Old indigenous		107	0.47
9 Hamburg	Old indigenous		98	0.42
10 Indian Game	Britain, developed from breed crosses in 1800s	Endangered	100	0.49
11 Ixworth	Britain, developed from breed crosses in 1930s	Critical	90	0.43
12 Leghorn (coloured)	Italy, imported (via USA) in 1800s		119	0.54
13 Lincolnshire Buff	Britain, developed from breed crosses in 1980s	Critical	105	0.48
14 Maran	France, imported in early 1900s		132	0.58
15 Marsh Daisy	Britain, developed from breed crosses in 1900s	Endangered	96	0.49
16 Norfolk Grey	Britain, developed from breed crosses in 1930s	Critical	89	0.50
17 Old English Pheasant Fowl	Old indigenous	Endangered	105	0.48
18 Rhode Island Red	USA, imported in 1900s		121	0.57
19 Scots Dumpy	Old indigenous		126	0.51
20 Scots Grey	Old indigenous	At Risk	95	0.40
21 Silkie	Asia, imported in 1600s		115	0.56
22 Spanish	Mediterranean, imported in 1700s	Critical	60	0.20
23 Light Sussex	Britain, developed from breed crosses in 1800s		121	0.54
24 Sussex	Britain, developed from breed crosses in 1800s		117	0.57

**Table 1.** Summary details of 24 chicken breeds. 1 Population size status measured by the number of breeding females as follows: Critical = 100, Endangered = 200, Vulnerable = 300, At Risk = 500 (DEFRA 2010) (The adopted quantification was previously used by RBST to categorise breed status.)



**Figure 1.** Evolutionary reconstruction of the breeds.

this study. Furthermore, the most genetically distinctive breeds also tended to have low population sizes (e.g. Appenzeller, Indian Game, Ixworth, Lincolshire Buff, Scots Grey and Spanish).

The genetic distances between breeds can be used to estimate the genetic relationships between breeds which in turn tell us about the history of breeds. By reconstructing an evolutionary tree using the genetic distances between breeds, a number of genetic relationships between breeds are observed (Figure 1). Although the British chicken breeds were highly differentiated, genetic similarities between certain breeds were observed. The evolutionary tree shows that there are two principal genetic groups.

The first group consists of the Derbyshire Redcap, Dorking, Hamburg, Old English Pheasant Fowl and Spanish. Excluding the Spanish, these are old indigenous breeds of the British Isles, are closely related and may have contributed to the breed improvement of each other (Hams 2004). The second group consists of the Buffs (Buff Orpington and Lincolshire Buff), Asian (Cochin, Brahma and Croad Langshan), Sussex, Ixworth, Maran and Rhode Island Red breeds. It has been suggested that Asian breeds may have been used to improve the Sussex breed (Vorwalkd Dohner 2001). The

Asian breeds also influenced the development of Buff Orpington and Lincolshire Buff (Hams 2004). In turn, the Light Sussex contributed to the development of the white-feathered Ixworth (Roberts 1994). Cross-breeding of the Light Sussex and Rhode Island Red in the 1940s became the basis of commercial poultry enterprises in Britain (Hams 2004) and could have had an effect on non-commercial stocks of these breeds. Before the importation of Maran to Britain the breed was improved using, amongst other breeds, Croad Langshan stock.

It was not possible to resolve the genetic relationships amongst the remaining breeds (Appenzeller, Araucana, Indian Game, Leghorn, Marsh Daisy, Norfolk Grey, Silkie, Scots Dumpy and Scots Grey). The predominantly long branches indicate that these breeds are genetically distinct and share little recent genetic relatedness.

### The nature of genetic structure within breeds

A clustering analysis of individuals was performed to determine if individuals can be assigned to their pre-defined breed origin based on their genetic composition. The rationale behind this analysis is that if individuals are more genetically similar they will cluster together and as breeds (or populations) should not

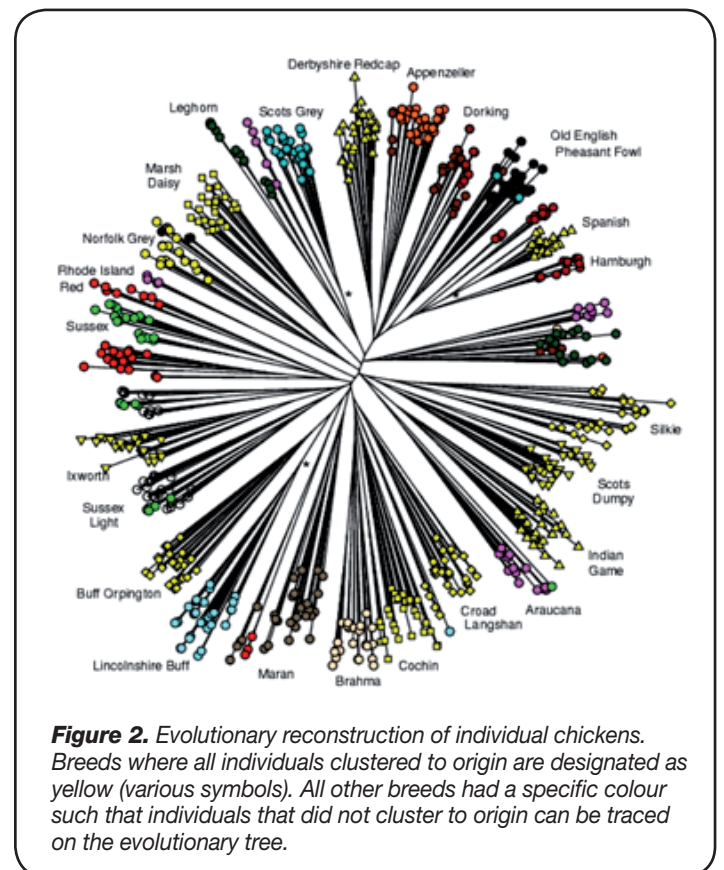
interbreed, individuals within breeds will be more genetically similar to one another than to individuals from another breed. These results are presented as an evolutionary tree shown in Figure 2. As can be seen, eleven chicken breeds formed single distinct genetic units where all individuals clustered to breed origin: Buff Orpington, Cochin, Croad Langshan, Derbyshire Redcap, Indian Game, Ixworth, Marsh Daisy, Norfolk Grey, Scots Dumpy, Silkie and Spanish (all designated as yellow in various shapes). Five other breeds formed single distinct genetic units, with the exception of a couple of individuals: Appenzeller (1 individual clustered with a mixed clade), Brahma (1 clustered with mixed clade), Lincolshire Buff (1 clustered with Croad Langshan), Old English Pheasant Fowl (2 clustered with Norfolk Grey) and Scots Grey (2 clustered with Old English Pheasant Fowl). (These mis-assignments could be the result of mis-labelling during the data collection process.)

However, the remaining breeds did not form single distinct genetic units and instead were genetically split with 4 groups each detected in Dorking and Light Sussex, 3 groups

each detected in Araucana, Hamburg, Rhode Island Red and Sussex and 2 groups each detected in Leghorn and Maran. It became apparent that the patterns of genetic subdivision within the Leghorn and Sussex breeds were associated with morphological type. However, genetic subdivision could not be explained by morphological type in the Araucana, Dorking, Hamburg, Maran, Rhode Island Red and Light Sussex. Instead, the observed genetic partitions in these breeds reflected suppliers, whereby all individuals from a particular flock were genetically separated from the rest of the same breed. This pattern of genetic substructure within breeds suggest that certain management practices (e.g. restricted gene flow between farmers through geographical isolation or line breeding) have produced subtle genetic differences amongst flocks within these breeds.

### Implications of genetics for breed conservation

The application of population genetics to breed conservation essentially encompasses two different components: within-breed genetic diversity (measured by average number



**Figure 2.** Evolutionary reconstruction of individual chickens. Breeds where all individuals clustered to origin are designated as yellow (various symbols). All other breeds had a specific colour such that individuals that did not cluster to origin can be traced on the evolutionary tree.

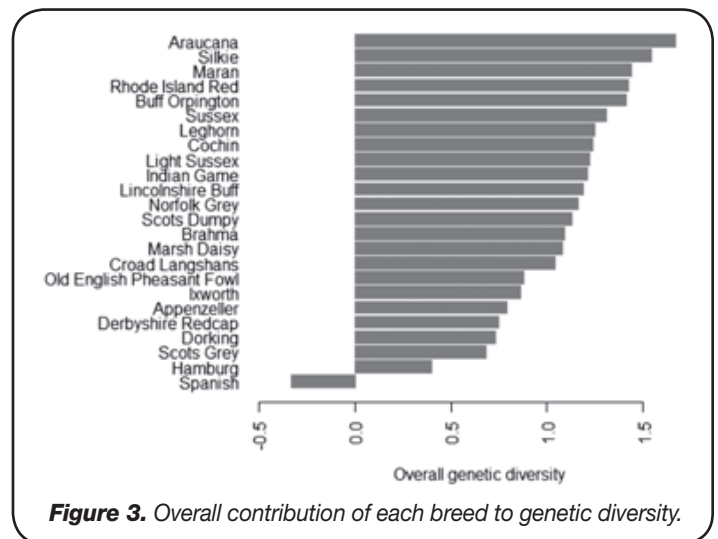
of alleles or heterozygosity) and between-breed genetic diversity (genetic distance). These two components were combined to provide an overall measure of genetic diversity of a breed which is presented in Figure 3. This can be used to identify genetically robust breeds and those of potential concern (i.e. genetically vulnerable).

Although the Spanish is genetically distinct, it also possesses very low genetic variation (Table 1) and was the lowest contributor to overall genetic diversity (Figure 3). Conversely, the highest contributors to overall diversity were breeds with high levels of genetic diversity such as Araucana, Buff Orpington, Maran, Rhode Island Red and Sussex. Two breeds, Buff Orpington and Silkie, were not only genetically distinct, but also possessed high levels of genetic diversity, and should be considered as genetically robust. The reverse perspective can be adopted to identify genetically vulnerable breeds (i.e. those

that possess both low genetic diversity and uniqueness). Three breeds satisfied these criteria: Dorking, Hamburg and Old English Pheasant Fowl and this was confirmed by the low contribution of these breeds to overall genetic diversity. The genetic results highlight that the future viability of these breeds is of potential concern.

### Conclusion

In conclusion, British chicken breeds have a high level of genetic diversity. However, genetic substructure within breeds was observed indicating limited exchanging of genetic material between breeders. If certain flocks are to be treated as isolated genetic islands the breed as a whole could lose genetic diversity, consequently care has to be taken in the management of these breeds. In addition, certain breeds had low levels of both genetic diversity and uniqueness. Consideration is required for the conservation and preservation of these potentially vulnerable breeds.



**Figure 3.** Overall contribution of each breed to genetic diversity.

### Footnotes

<sup>1</sup> S. Wilkinson, P. Wiener, D.

Teverson, C.S. Haley and P. M.

Hocking (2012) Characterisation of the genetic diversity, structure and admixture of British chicken breeds. *Animal Genetics* (in press). doi: 10.1111/j.1365-2052.2011.02296.x.

<sup>2</sup> An allele is a copy of a gene that is inherited from one parent and may be the same or different from the allele that is inherited from the other

parent. A gene may have more than two alleles.

<sup>3</sup> Heterozygosity is a measure of the proportion of genes that are represented by different alleles. In this study heterozygosity is an average statistic based on 30 genes.

### References

A list of references is available from RBST.



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