# Geographical isolation of native sheep breeds in the UK—Evidence of endemism as a risk factor to genetic resources

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## ARTICLE INFO

## ABSTRACT

This study addresses the potential risk to the genetic resources of UK sheep breeds from endemism. Twelve native breeds are analysed that exist in significant numbers and continue to be commercially farmed livestock. The breeds were selected to represent regions of the British Isles: North of England hill breeds (Herdwick, Rough Fell, Lonk, Dalesbred), South of England breeds (Southdown, Romney, Devon Closewool, Exmoor Horn), Scottish breed (South Country Cheviot) and Welsh/Welsh border breeds (Welsh Hill Speckled Face, South Wales Mountain (Nelson), Clun Forest).

For each breed, numerical data were collected in collaboration with breed society members and analysed in terms of population size and structure together with the extent of their geographical range. The number of flocks per breed proved to be highly variable, questioning the assumption that has been made that the number of breeding units can be disregarded in the calculations of endangerment. The data also indicated that an average flock size for a breed cannot be estimated to gain an insight of the population structure, since this parameter was found to vary considerably within and between breeds. The endemism was best illustrated in the breed maps which clearly highlighted the degree to which each breed was associated with a distinct geographical area. From the maps, ten of the twelve breeds analysed were concentrated, but the flocks of two breeds were visually more dispersed. In numerical terms, the ten breeds were found to have up to 95% of their breed numbers concentrated within a radius of 65 km from the mean centre of each breed.

The study provides a valuable foundation for future research into genetic diversity within and between the sheep breeds analysed, a baseline of information to enable population trends to be examined and a robust evidence-base for policy decisions on Farm Animal Genetic Resources (FAnGR).

## 1. Introduction

It is well recognised that effective management of farm animal genetic diversity is important for sustainable economic development and food security across the world. This biodiversity is increasingly at risk from a number of threats including animal disease, the consequences of climate change and government policy and programmes (Canali, 2006). Also, the rapid spread of intensive livestock production, often using only a narrow range of breeds, has led to a significant decline in traditional production systems and the associated use of regional breeds. These regional breeds are usually highly adapted to their environments and are often farmed in low input extensive agricultural systems.

The 2007 FAO report, State of The World's Animal Genetic Resources for Food and Agriculture, highlighted that 20% of the world's livestock breeds could be classified as at-risk.

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Significantly, the European and Caucasus regions, with specialised livestock industries, were found to have the highest number of at-risk breeds in absolute terms. The report emphasised that there was an urgent need for improved surveying and reporting of breed population size and structure, given that one of the prerequisites for sustainable management of farm animal genetic resources (FAnGR) was an improved awareness of breed distribution (FAO, 2007).

An essential aspect of breed distribution is the extent to which a breed is concentrated in a geographical area. The potential risk to genetic resources arising from geographical concentration has been recognised for many years, but data have not been available to determine the extent of the risk, particularly when the native breeds exist in significant numbers and contribute to the livestock industry.

An insight into this potential impact of geographical concentration was gained in the UK during the Foot and Mouth Disease epidemic of 2001. Greater than 44% of the farms whose animals were slaughtered were located in the Cumbrian region of the North–West of England (FMD, 2001 Inquiry Report, 2002). As a consequence, the two local sheep breeds, the Herdwick and Rough Fell, both commercially farmed by their regional communities suffered disproportionate losses (Bowles et al., 2003). The catastrophe led to renewed awareness in the UK that geographical concentration alone could represent a considerable risk to FAnGR (Defra, 2006).

However, conservation programmes to mitigate this risk require a robust evidence-base for prioritisation of breeds to inform policy and future strategy (Simon, 1999). Considerable information has been collected on native breeds that are numerically scarce and represent the rare breeds protected by national and international NGOs such as RBST and RBI (Rare Breeds Survival Trust, 2002). In contrast, little attention had focussed on those native breeds existing in significant numbers until the FMD epidemic highlighted the risk of geographical concentration.

Regional sheep breeds have evolved in and become adapted to their environments, often thriving under extreme and stressful conditions. These breeds may therefore have unique characteristics providing a valuable resource of genetic variation. This variation is essential both to develop sustainable animal production systems and to mitigate against unpredictable future events. Regional sheep breeds are also fundamental to the social and economic structure of rural communities in their locality, and local knowledge of livestock is recognised to be an essential contributor to both economic and environmental sustainability (Tempelman and Cardellino, 2007). Of the 85 sheep breeds recognized in the UK, 59 breeds are considered native. Many of these native breeds have proved very successful in the stratified sheep industry of the UK and have become widely distributed. However there are other breeds which are thought to be localised in distinct regions although the extent of their geographical concentration is unknown.

This study explores the distribution and flock size of twelve commercially farmed, regional native sheep breeds to determine their degree of concentration and provide a factual evidence-base for conservation priorities. Significantly, the data demonstrate substantial geographical isolation of some breeds and provide a new framework for policy development to protect farm animal genetic resources.

## 2. Methodology and materials

### 2.1. Data gathering

Twelve native sheep breeds were selected to represent regions of the British Isles: North of England hill breeds (Herdwick, Rough Fell, Lonk, Dalesbred); South of England breeds (Southdown, Romney, Devon Closewool, Exmoor Horn); Scottish breed (South Country Cheviot) and Welsh/Welsh border breeds (Welsh Hill Speckled Face, South Wales Mountain (Nelson), Clun Forest). In this study the South Wales Mountain Sheep (Nelson) will be referred to as South Wales Mountain. Data gathering was achieved through a close collaboration with the respective breed societies. First, the secretaries of each society were contacted personally to request that they approach their registered membership to ask them to take part in a sheep census. This was followed by a letter outlining the proposal, further communications with each secretary and a visit to each to discuss the progress of the survey.

A questionnaire for data gathering was produced, together with an explanation of the purpose of the survey. The content of the questionnaire was reviewed by Trustees of the Sheep Trust (UK National Charity No. 1094514; www.thesheeptrust. org), a sample of farmers and by the Survey Control Liaison Unit at Defra prior to UK Ministerial approval and distribution. The questionnaire was sent out during 2007 and is provided as supplementary material. The breed societies in the study provided lists of their membership and questionnaires were sent out to all 1254 members of the twelve breed societies: in total, 929 replies were received. Thus, the average return rate from the questionnaires was 74% (ranging from 62% to 89% as detailed in Supplementary material, Table S-1). From the questionnaire, it was found that some individuals from each breed society remained members whilst no longer keeping sheep, and there were some multiple returns from members sharing a single flock. Our census identified 853 flocks and these form the basis of the data described in the results.

Whilst the return rate to the questionnaires was exceptionally high, it was nevertheless important to devise a method to determine the potential impact of "non-responders" on the geographical analyses of breed distribution. The method used was suggested by Professor John Woolliams [personal communication]. The Defra 2007/08 Annual Inventory of Sheep and Goats for Great Britain provided data on total numbers of sheep/goats at a holding number. From those data, together with Defra-held information on holdings recording sheep movements in the preceding 12 months—those holdings responding positively to earlier surveys, or those having had a flock mark registered in the preceding 12 months—it became possible to gain an insight into how many of the non-responders to the questionnaire were likely to continue to keep sheep. This assessment was made internally by Defra to preserve data confidentiality. In most cases, the addresses to which the questionnaires were sent provided sufficient information to be able to geo-reference those non-responders keeping sheep, and thereby provide a

basis to determine the impact of their locations on centres of the breeds calculated from the questionnaire returns. These data were gathered for the non-responding members of three breed societies, those of the Rough Fell, Southdown and South Wales Mountain. Return rates from the membership of the first two societies were the lowest at 66% and 62% respectively; for the South Wales Mountain breed, the response rate was high (83%) but actual numbers of sheep in the questionnaire were significantly lower than those estimated by the breed society (although it should be noted that this breed society keeps no written records).

### 2.2. Data analysis

The data from each of the returned questionnaires were transferred into an Access database showing the grid reference number for the agricultural holding, flock size, flock composition and number of purebred sheep divided into further categories (females used for breeding purebred replacements, females under 1 year, total number of females, number of rams, total number of purebred sheep, numbers of females and rams of other breeds by breeds, grand total of all sheep on the holding). The grid reference for the flock was determined either from the County Parish Holding Number (CPH), postcode or description of the location of the flock provided by each of the breeders.

Following assessment of the databases, as described in the Results section, the grid reference number together with the total number of sheep per flock for each breed was used to display geographical distribution using ESRI ArcGIS (version 9.2) mapping software and Microsoft Access. Where grid references had not been supplied or were obviously incorrect (as shown by the point references on the maps generated) these were inferred using the location attached to the unique holding identifier (the CPH number) or the postal address of the respondent. In a small number of cases (11 flocks/429 sheep) it was not possible to infer a geo-reference, for example, flocks in France or Northern Ireland, and the data relating to these were not used (Supplementary material, Table S-3).

For each flock of every breed studied, a map reference consisting of an "easting" ($x$ axis) and "northing" ($y$ axis) was identified. These data, together with the individual flock sizes, were then used in the following equation to calculate the weighted mean centre of population for each breed. The equations were applied to every flock of every breed, where

$f$ = number of sheep per flock, and the weighted mean centres (wc) were calculated from the $x$ and $y$ axes as defined below.

$$\bar{x}_{wc} = \frac{\sum f_i x_i}{\sum f_i} \qquad \bar{y}_{wc} = \frac{\sum f_i y_i}{\sum f_i}$$

wc      Weighted centre of population
$f$       Flock size (total number of sheep per flock)

Once these were determined, it was possible to go on and calculate the Euclidean distance (as the crow flies) of each flock in a breed from the weighted mean centre of that breed. Thus, moving out from the centre, the cumulative total number of sheep could be calculated to determine the percentage of the breed at any point in a radius from the weighted centre. This provided the evidence for the degree of geographical concentration for each individual breed. For three breeds, the process was repeated for non-responders to the questionnaire, in order to determine any significant shift on the mean centre that had been calculated for the breed from the questionnaire returns (Supplementary material, Table S-2).

### 3. Results

The results of the survey have been compiled into a number of Tables and the data analysed.

### 3.1. Number of purebred sheep by breed

The numerical data collected through interactions with registered members of the breed societies represent the first factual census of sheep numbers for these commercially farmed regional breeds. Typically the percentage of questionnaires completed by breed society members was high, with those from eleven of twelve breeds replying with a 66% or greater reply rate (Supplementary material, Table S-1). The questionnaire returns provided a wide range of information, including those data given in Table M-1 which describe the number of flocks per breed, the total number of purebred sheep in those flocks, together with additional data on female sheep and rams. Ewes used for breeding purebred replacements are given as

**Table M-1**
Number of purebred sheep by breed

| Breed | Number of flocks in the census | Total purebred sheep | Total female sheep | Total rams | Ewes used for breeding purebred replace-ments | Ewe lambs <1 yr old | Breed society estimate of sheep numbers |
|---|---|---|---|---|---|---|---|
| South Country Cheviot | 69 | 79,902 | 77,344 | 2558 | 53,286 | 17,004 | 80,000 |
| Clun Forest | 40 | 3353 | 3191 | 162 | 1958 | 843 | 4500 |
| Dalesbred | 74 | 21,219 | 20,875 | 344 | 9630 | 5147 | 20,000 |
| Devon Closewool | 33 | 4252 | 4159 | 93 | 2147 | 878 | 5000 |
| Exmoor Horn | 87 | 16,645 | 16,322 | 323 | 7905 | 3629 | 12,539 |
| Herdwick | 113 | 49,408 | 48,102 | 1306 | 31,137 | 12,020 | 50,000 |
| Lonk | 32 | 15,925 | 15,551 | 374 | 9985 | 4031 | 12,000 |
| Romney | 29 | 25,643 | 25,083 | 560 | 12,152 | 6595 | 7500 |
| Rough Fell | 121 | 27,876 | 27,352 | 524 | 15,862 | 7253 | 17,000 |
| Southdown | 186 | 6711 | 5867 | 844 | 3507 | 1570 | 4000 |
| South Wales Mountain | 32 | 26,226 | 25,566 | 660 | 15,880 | 11,491 | 55,000 |
| Welsh Hill Speckled Face | 37 | 19,678 | 19,299 | 379 | 9312 | 3955 | 10,000 |

a separate entry, since for some breeds, particularly hill breeds such as Dalesbred, Rough Fell and Welsh Hill Speckled Face, females are also used for breeding crossbred lambs in the stratified sheep industry of the UK. Females used in crossbreeding nevertheless represent a genetic resource for the breed.

For some breeds, the data collected from the individual breeders contrast with the numbers of sheep estimated by the
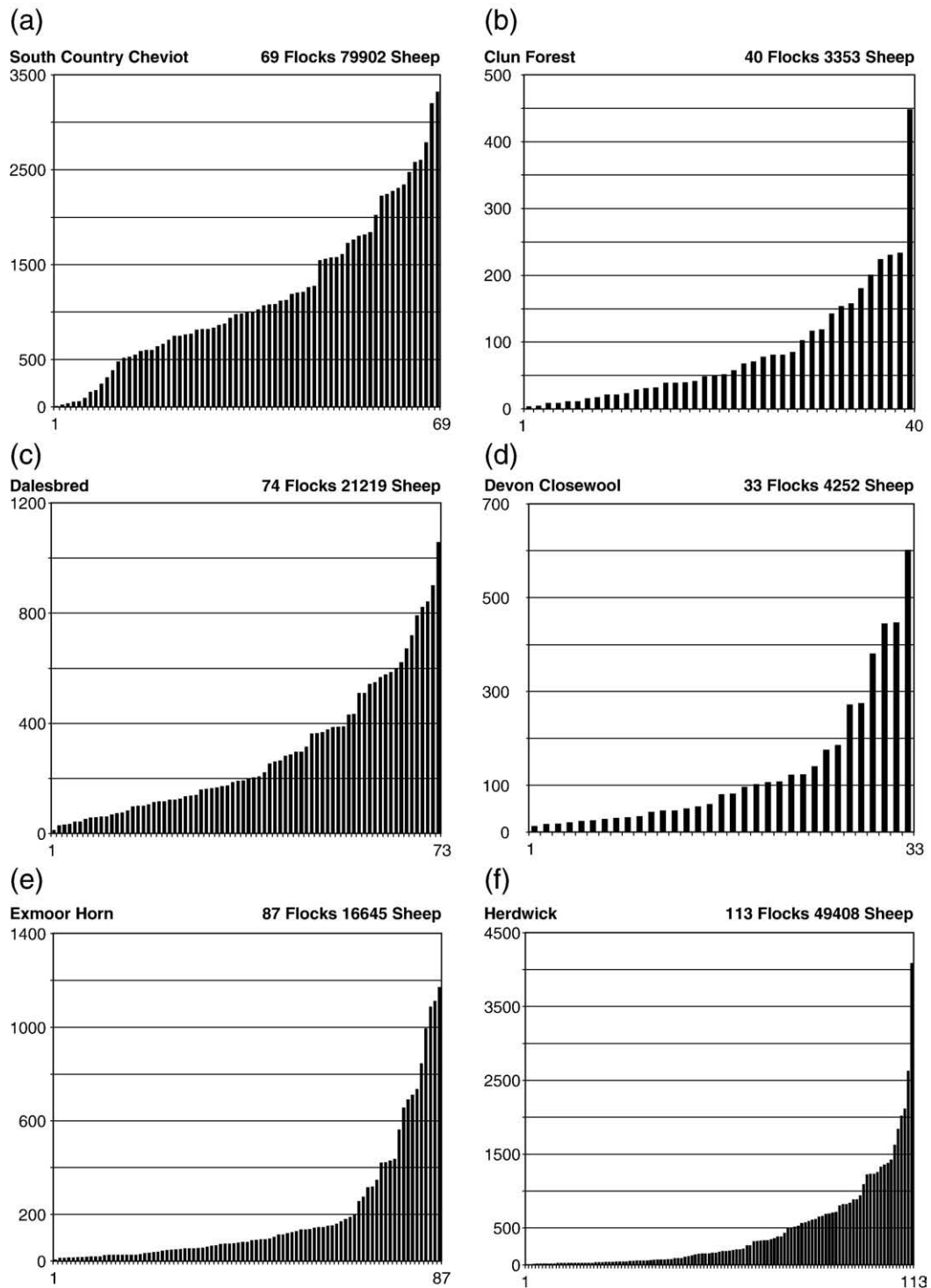


**Fig. 1.** (a) to (l) illustrates the distribution of flock sizes within twelve sheep breeds. For each breed, the number of sheep per individual flock is provided as a histogram. The x-axis provides the numbers of sheep and the y-axis provides the numbers of flocks. Note, numbers on both axes vary for each breed, reflecting the range of flocks and the numbers per flock.
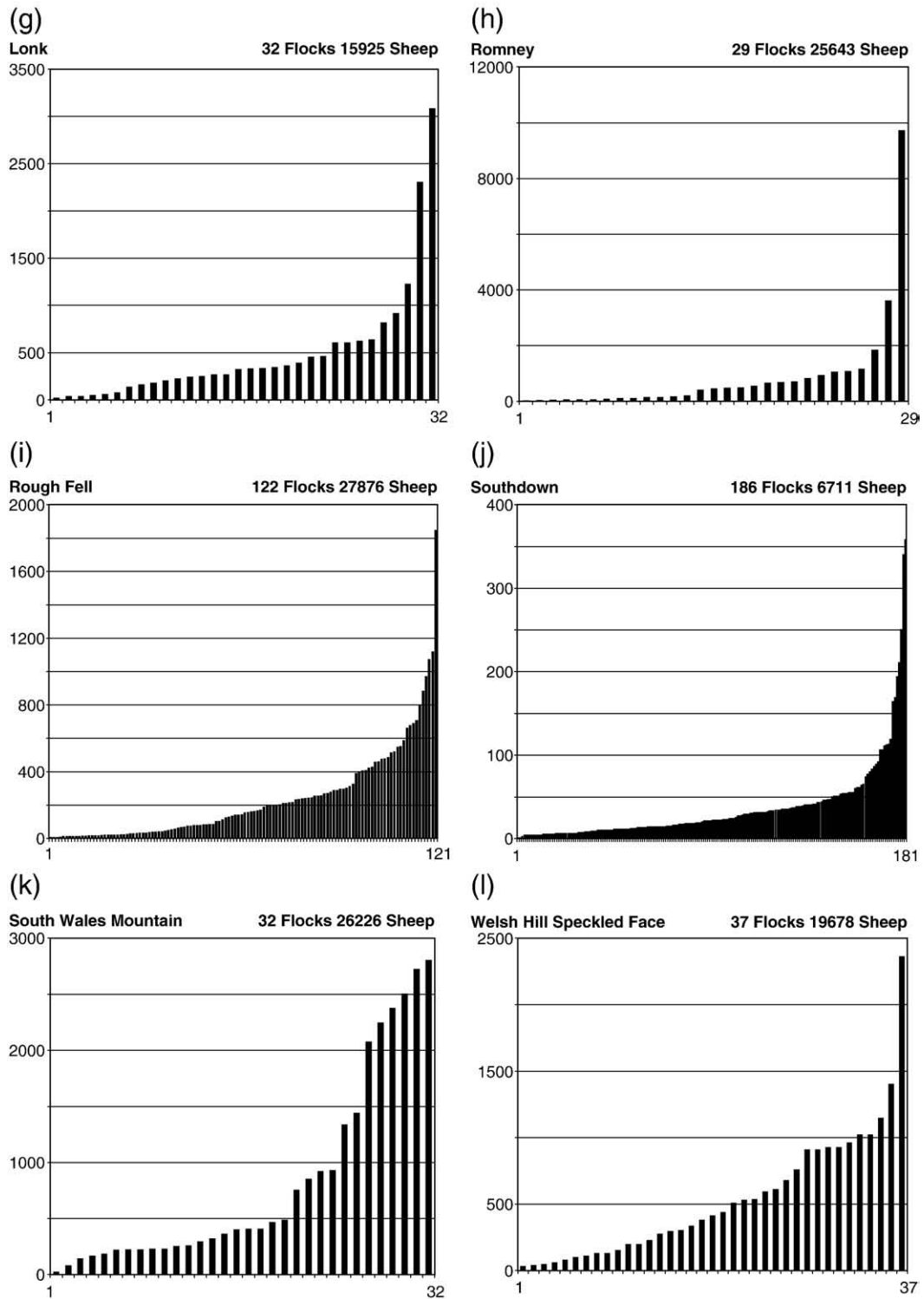
Fig. 1 (*continued*).

breed societies (Table M-1). However, the collaboration with the individual breed societies and their members revealed that each society has different processes for record-keeping and many do not update records on a regular basis. Some do not keep any written records and rely on individual breeders to maintain and pass on knowledge. Registration is typically not used to prove provenance of an animal and many breed societies do not register their females, again relying on the

breeders' experience and their awareness of accepted breed standards to define purebred animals.

These facts revealed by the collaborative nature of this study emphasise the importance of data collection from individual breeders to gain a factual census of breed numbers, an approach which underpins this study. Also, given the lack of standardisation across breed societies, the total number of purebred sheep, gathered through knowledge of the individual breeder of those sheep, is considered to be the only numerical value that can be compared across the twelve breeds. This is used in the analyses described in the following Results sections.
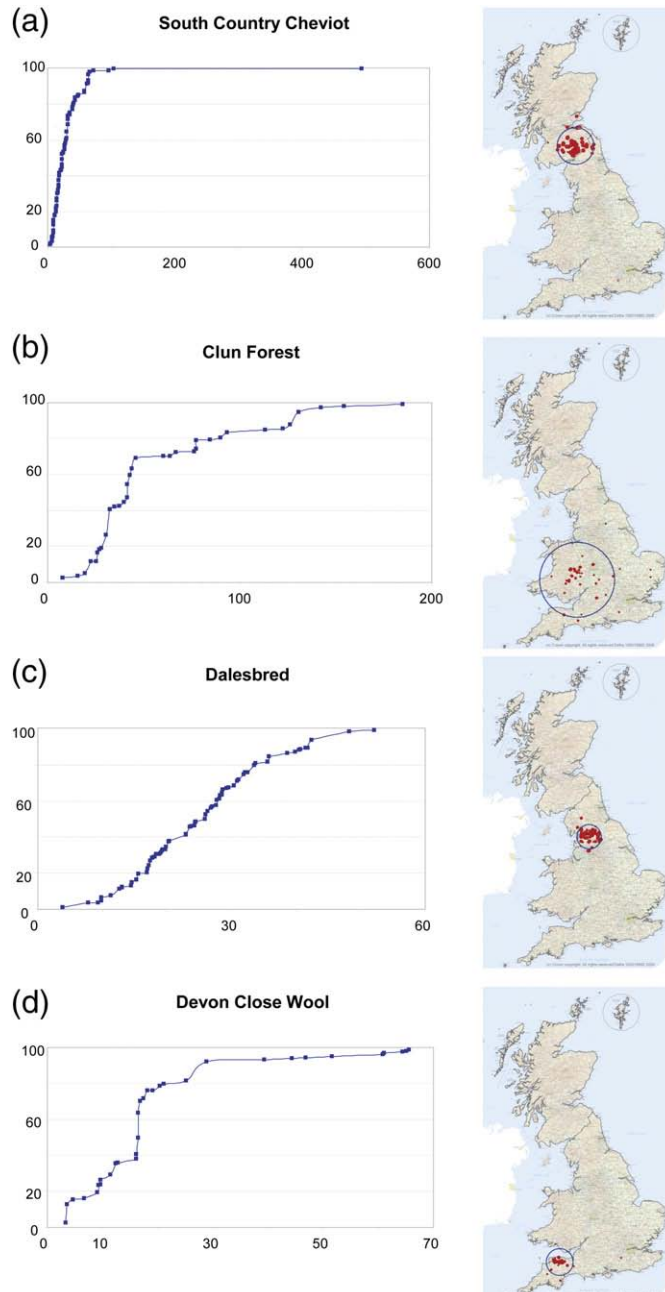


Fig. 2. (a) to (l) illustrates the geographical distribution of twelve sheep breeds. Data for each breed are given as a line drawing, in which the x-axis is cumulative percentage of purebred animals, and the y-axis is distance from the mean centre of that breed in km. The dots correspond to individual flocks. Note: distances on the y-axis vary for each breed, reflecting also the different overall distribution of the breeds. A map of Great Britain is also shown, depicting the geographical distribution of flocks of each breed as at 2007. The size-bands of the flocks range in increasing red dots from: (1) less than 50; (2) 50–99; (3) 100–499; (4) 500–999; and (5) more than 999 sheep. The area in which up to 95% of the sheep of each breed is located is highlighted by a blue circle.
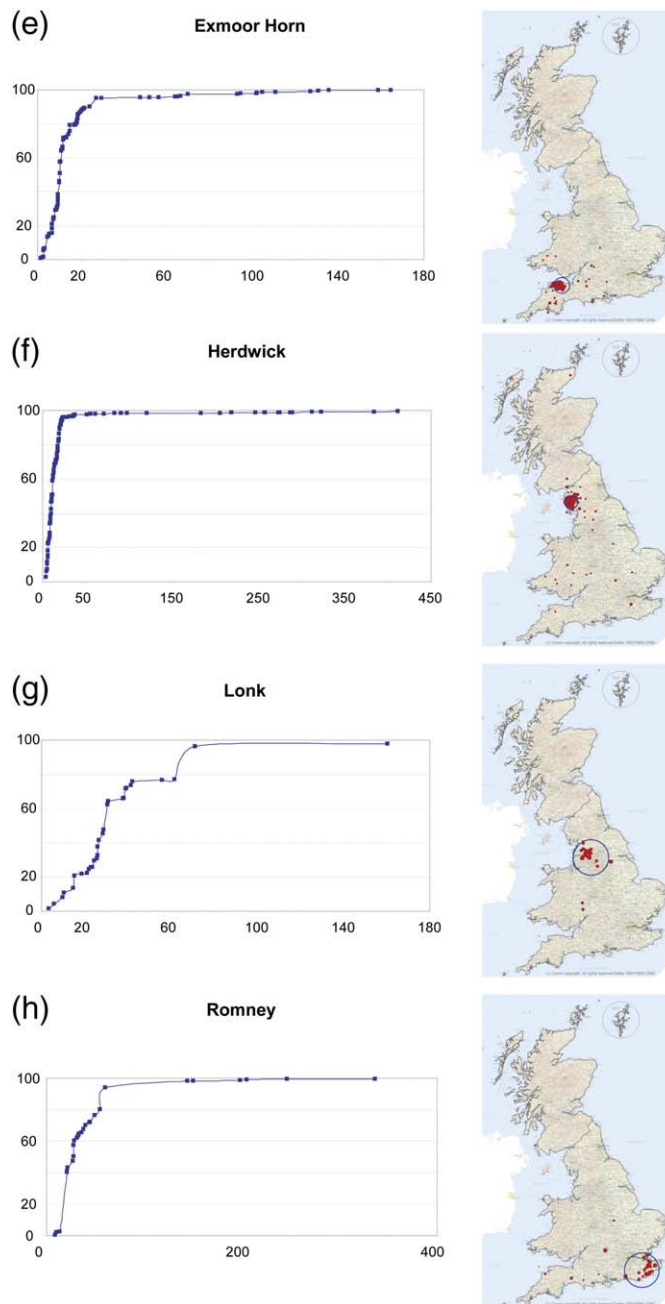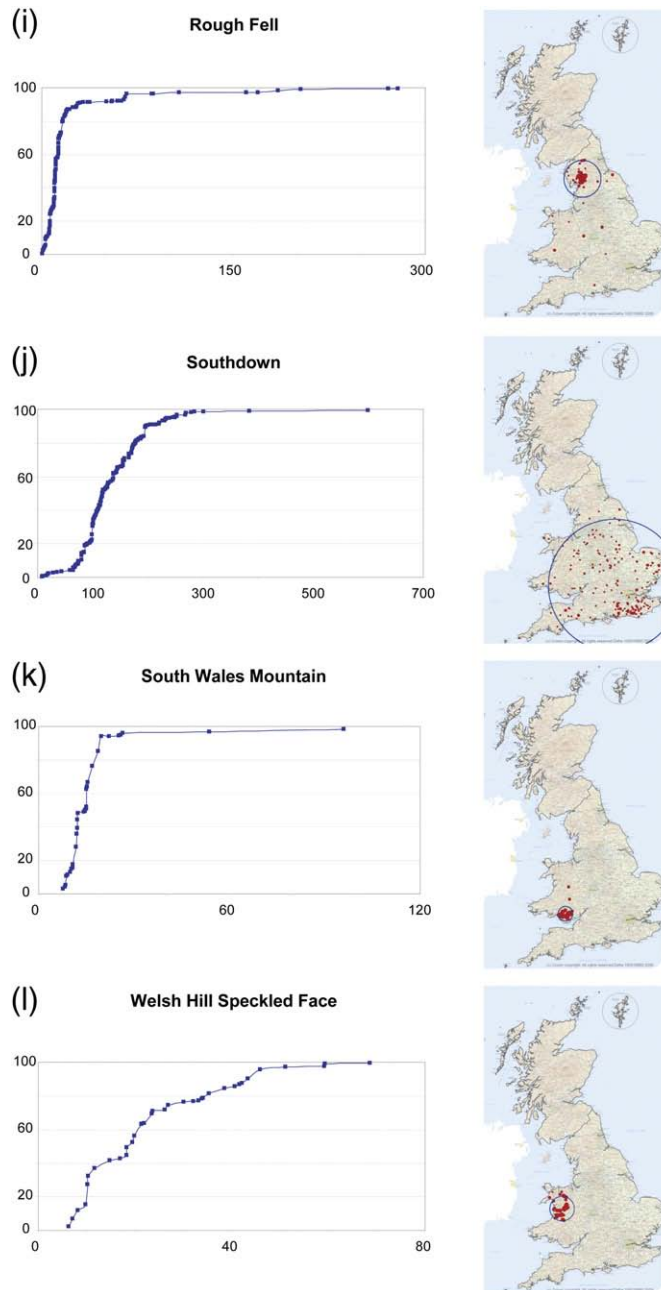
**Fig. 2** (*continued*).

### 3.2. Distribution of flock sizes across breeds

Data from the questionnaire provided information on the size of individual flocks within each of the regional, native sheep breeds. Numerical values are given in Supplementary material, Table S-4 and these are illustrated as Fig. 1a–l. For each breed, the number of sheep per individual flock is provided. Through showing individual flock sizes it is possible to assess rapidly the number of flocks per size range and how these differ for each breed. Note that the vertical axis is different for each breed, due to the very different flock sizes between breeds. The data demonstrate that for some breeds there are large numbers of small flocks and for other breeds a relatively small number of flocks containing large numbers of purebred sheep. For example the Southdown has 150 flocks with less than 50 sheep per flock. In contrast, the South Country Cheviot has 57 flocks with >500 sheep per flock.

These data clearly indicate that it is not possible to gain an insight into the average flock size from the total number of sheep and indeed any estimates could be highly misleading. Equally, sampling only a small number of flocks per breed is inappropriate.

**Fig. 2** (*continued*).

### 3.3. Geographical distribution of flocks and breed concentration

The major interest of this study was to determine the extent of regional concentration of each of the breeds. The data described above in Sections 1 and 2, together with the grid references for each flock provided in the questionnaires, enable the geographical distribution of flocks within each breed to be determined. Statistical methods were developed to demonstrate the extent of concentration of flocks and sheep numbers and plotted using GIS computer technology. The very low number of flocks based in Northern Ireland and mainland Europe, or those for which a grid reference for the flock could not be established (as detailed in Supplementary material, Table S-3), were not included in the analyses of geographical distribution.

The distance data are provided in numerical form (Supplementary material, Table S-5) and are illustrated as Fig. 2a–l. The numerical data provide numbers of purebred sheep per individual flock, the distance of each flock from the mean centre of the breed and a cumulative total presented both as population and percentage. To illustrate these data, Fig. 2a–l provide line diagrams showing the cumulative percentage of purebred animals at distances from the mean centre of each breed, together with the flock distribution

shown on a map of the UK. On each map, the area highlighted contains up to 95% of the sheep numbers of the breed. (Individual maps of each breed are provided in Supplementary material, Fig. 1, to provide greater detail of flock sizes and geographical distribution than is possible in the text.)

These data and their analysis enable the development of a definition for endangerment arising from endemism. First, the data for each individual breed will be briefly summarised and second, general trends from the data will be described.

### 3.3.1. Breed data

*3.3.1.1. South Country Cheviot (Fig. 2a).* The South Country Cheviot originated in the Cheviot Hills of the Scottish Borders and the map indicates that the breed remains highly concentrated in this region with up to 95% of sheep numbers (74,597) located within a 64 km radius of the breed's mean centre in Southern Scotland.

*3.3.1.2. Clun Forest (Fig. 2b).* The Clun Forest breed originated from a now extinct native breed, known as the Long Mynd, from a high grassland area of that name on the Shropshire/Powys border. Whilst the numbers of Clun Forest sheep are the lowest of the breeds analysed in this study and they continue to be located across the Welsh/English border, their distribution is broad with 95% of breed numbers (3007) located within a 131 km radius of the breed's mean centre.

*3.3.1.3. Dalesbred (Fig. 2c).* The Dalesbred is a black and white-faced horned hill breed which was originally developed in the North–West region of the Yorkshire Dales. Up to 95% of breed numbers (19,737) remain concentrated within a radius of 42 km of the breed's mean centre with a distribution clustered on the Pennine Hills in Lancashire and Yorkshire.

*3.3.1.4. Devon Closewool (Fig. 2d).* The Devon Closewool is a hardy, polled, white-faced breed. From the map it can be seen that the breed's distribution is concentrated on the upland heaths of the South–West of England. Up to 95% of breed numbers (4021) are located within a radius of 47 km of the breed's mean centre in North Devon.

*3.3.1.5. Exmoor Horn (Fig. 2e).* The Exmoor Horn is recorded as an ancient native sheep breed found in upland areas of the South–West of England, particularly Exmoor and Dartmoor. The map indicates that the breed has remained concentrated in this region with 95% of breed numbers (15,825) located within a radius of 27 km of the breed's mean centre.

*3.3.1.6. Herdwick (Fig. 2f).* The name Herdwick (herdvyck, meaning "sheep pasture") is recorded in documents dating back to the 12th century. The origin of the breed is unknown, but the most common theory is that the ancestors of Herdwick sheep were introduced by early Norse settlers. The map indicates that the breed is highly concentrated in the Lake District in North–West England with up to 95% of breed numbers (46,884) tightly clustered within 23 km of the breed's mean centre.

*3.3.1.7. Lonk (Fig. 2g).* The Lonk is a large horned black and white-faced breed developed in the hills of North–West Yorkshire and Lancashire. Given that three Lonk flocks, comprising 23% of the total breed numbers, are geographically distant from the breed's mean centre, the radius containing up to 95% of numbers (12,275) is relatively large at 62 km.

*3.3.1.8. Romney (Fig. 2h).* The Romney sheep breed was established in the Middle Ages as a lowland breed, taking its name from the low-lying Romney Marsh area of Kent. The Romney flocks remain concentrated in the South–East of England with up to 95% of breed numbers (24,208) located within a radius of 60 km of the breed's mean centre.

*3.3.1.9. Rough Fell (Fig. 2i).* The Rough Fell is a horned black and white-faced hill sheep which developed in the hills between the Lake District and North–West Yorkshire. As shown on the map, the breed continues to be located in the same region, spanning two National Parks, with up to 95% of numbers (26,370) within a 65 km radius of the breed's mean centre. The response rate to the questionnaire was low at 66%. However, as shown in Supplementary materials, Table S-2, the potential impact of non-responders is unlikely to affect the conclusions drawn.

*3.3.1.10. Southdown (Fig. 2j).* The Southdown is one of the oldest Down breeds of the UK. The breed society had the largest number of members (322) of any of the breed societies analysed. The map shows that the breed population is highly dispersed and this is confirmed numerically with up to 95% of breed numbers (6262) distributed across a radius of 234 km from the breed's mean centre. As shown in Supplementary materials, Table S-2, this conclusion is unlikely to be affected by the impact of non-responders to the questionnaire.

*3.3.1.11. South Wales Mountain (Fig. 2k).* As shown on the map, the South Wales Mountain breed is clustered in the hill areas of South Wales, with up to 95% of numbers (24,883) located within a radius of 26 km of the breed's mean centre. Whilst there was a high response rate to the questionnaire (83%) sheep numbers returned in the questionnaire were half of those estimated by the breed society. However, the society has no written records. Analysis of the non-responder list, (Supplementary materials, Table S-2), confirmed the likely robustness of the conclusions drawn on geographical concentration.

*3.3.1.12. Welsh Hill Speckled Face (Fig. 2l).* The Welsh Hill Speckled Face breed originated in the hills of central Wales and the map confirms the breed remains concentrated in this region with up to 95% of breed numbers (17,841) located within a radius of 43 km of the breed's mean centre.

### 3.3.2. General trends

The data described above clearly demonstrate that there is statistically significant geographical isolation. For ten of the twelve breeds analysed, up to 95% of each breed's numbers lie within a radial distance of less than 65 km from the mean centre of the breed. It is noteworthy that six of the breeds have up to 95% of their numbers within a radius less than

50 km and three of those eight breeds, the Exmoor Horn, Herdwick and the South Wales Mountain breeds have up to 95% of their numbers concentrated within a radius of less than 30 km.

Of the two breeds with a more dispersed population, up to 95% of the Clun Forest are distributed within 131 km from the breed's mean centre and for the Southdown breed, up to 95% of numbers are even more dispersed, greater than 230 km from their mean centres. These results suggest that the genetic resources of native sheep breeds with significant numbers and commercially farmed within the livestock industry can nevertheless be at threat, through clear evidence of geographical concentration.

Whilst the response rate to the questionnaire was high overall, it was important to determine whether data that could have been provided by those breeders who did not respond to the questionnaire would have led to different conclusions for the geographical distributions of the breed populations. Three breeds were chosen for further investigation into this possibility. When the impact on a breed's mean centre of these additional holdings was analysed, very little impact on the geographical locations of the centres was observed (Supplementary material, Table S-2). Essentially, the breed society members who did not respond to the questionnaire were typically located in the same geographical regions as those who did respond. This confirmed that the conclusions drawn from the questionnaire data were likely to be robust.

## 4. Discussion

Native breeds of farm animals represent an important resource, from the perspective of their genetics and their contributions to environmental and economic sustainability (Ruane, 2000). Risks facing these resources have been recognised in the 2007 FAO report, State of The World's Animal Genetic Resources for Food and Agriculture. In particular, native livestock breeds play a central role in low input extensive farming systems and in supporting rural communities both in the developed and developing nations of the world (Drucker et al., 2001). Sheep breeds, through their adaptation to local environments, are especially relevant in this respect.

Within the UK, native sheep breeds comprise a significant component of farm animal genetic resources (FAnGR) with 59 breeds recognised as originating in the British Isles (DEFRA, 2002). The risk status of breeds can be assessed in a number of ways, from overall population size and trends through to many other factors, including the number of flocks within a breed, their geographical concentration that in turn influences exposure to threats such as disease epidemics, and a variety of sociological factors, for example, the ageing populations of farmers.

Endangerment arising from numerical scarcity is a well recognised risk (Gandini et al., 2004). The EU in 2004 (Commission Regulation (EC) No. 817/2004) set out a risk status threshold for sheep of 10,000 breeding females in the context of providing incentive payments for farmers to maintain threatened breeds. Lower thresholds have been defined by the NGOs Rare Breeds International and the UK Rare Breeds Survival Trust for conservation purposes (Alder-son, 2003). These NGO definitions have also influenced policy in the UK to implement EU Directive (2003/85/EC) to protect FAnGR in the face of disease outbreaks through the formation of the Breeds at Risk Register.

Geographical isolation is often highlighted in discussions of endangerment and prioritisation of breeds for conservation but there has been no published data to inform decision-making. The concept was raised by the RBST in 1975 and most recently in their 2008 membership magazine, "The Ark".

The particular problems facing regional sheep breeds were made apparent by the UK FMD epidemic of 2001. Losses to commercially farmed breeds, such as the Herdwick and Rough Fell breeds, led to the definition of a new category of FAnGR, the Heritage Sheep Breed. Three parameters are used to define the category: proposed geographical concentration; adaptation to their local environment; and genetic distinctiveness. The European Regional Focal Point (ERFP) of FAnGR recognised the possibility that Heritage Sheep breeds may exist throughout Europe and a scoping study led to the recommendation that 154 breeds should be further considered in 14 member states (Jones and Bowles, 2006).

Of crucial significance for the development of conservation policy, is the definition of geographical isolation and the risk status threshold for endangerment through endemism. This study addresses these issues for sheep breeds that are not typically considered to be endangered, given they exist in significant numbers and contribute to the livestock industry. Unlike other livestock species, particularly cattle and horses, factual information on commercially farmed sheep breed numbers in the UK is limited. No single national database records sheep numbers and information gathering by breed societies is not standardised. A number of fundamental factors have been revealed by this study that must be taken into account in determining conservation priorities of sheep FAnGR.

### 4.1. Breed population size and structure

The population figures used in this study arose from questionnaires sent out by the authors to all members of the sheep breed societies. This was made possible by the close collaboration with breed societies and their secretaries, without whom this study would not have been possible. Return rates were high at an average of 74% giving confidence to the census. The data received contained extensive detailed information including numbers of purebred breeding females, female lambs and rams. For the analyses of breed population size and structure, total purebred animal numbers have been used to enable comparison across breeds. Many of the breed societies of the breeds studied kept no written records of breed numbers, populations or structure. Registered female numbers have been highlighted as the indicator to calculate degree of endangerment (Alderson, 2003). However, out of the twelve breeds analysed in this study, only seven societies registered females and of these, two societies registered only a proportion of females. Significantly, requirements for registration of either male or female animals were not standardised across breeds. Registration has been used to establish provenance of an animal and plays an important role in the activities of NGOs specialising in rare breeds, for which societies typically use standardised

procedures. However, this study questions the general validity of using registered female numbers for endangerment analyses. Indeed the results strongly suggest that new processes are urgently required for standardisation within and between breed societies, particularly those of the native breeds that have significant numbers and continue to be commercially farmed. This is necessary both to inform government policy on FAnGR and monitor population trends of the breeds to underpin the design of management strategies.

The study showed that the number of flocks per breed was highly variable. For example, from the returns to the questionnaire, some 26,000 South Wales Mountain sheep are managed in only 32 flocks; in contrast 6711 Southdown sheep are managed in 187 flocks. These findings fundamentally question the assumption previously made that the number of breeding units can be disregarded in the calculations of endangerment (FAO, 2007). The number of animals alone does not provide sufficient information for understanding the within-breed genetic diversity. The data also indicate that it is not possible to estimate an average flock size for a breed to gain an insight of the population structure. For example, the 187 Southdown flocks comprise only 13 flocks with >100 sheep and more than 150 flocks with less than 50 animals. The distribution of the Romney breed numbers shows that one flock contained almost half of the total breed numbers. This type of information is highly relevant in determining thresholds for endangerment of a breed.

Importantly, the data gathered on population size and structure on each of the breeds, provide an invaluable foundation for further studies including genotypic and phenotypic characterisation within and between breeds. Also, a baseline of information has been established enabling future comparisons to be made and population trends to be identified in the breeds analysed. This baseline can be readily built on in successive years and provides the enabling context for a wide range of future studies.

*4.2. Geographical distribution*

The information requested from individual breeders included data on the geographical location of their holdings. This allowed grid references to be identified for each of the flocks, which in turn enabled the distribution to be determined. Significantly both flock size and distribution were therefore available providing the information for a thorough statistical analysis and use of GIS to demonstrate flock location and degree of isolation. Statistical methods were developed to achieve these analyses, which have been presented as a cumulative percentage of population within a given radius of the mean centre of holdings and a map locating the population within the context of the UK. Thus, for each breed the analysis has involved two dimensions, the size of the population of each breed in terms of individual flocks, and the extent—narrow/wide—of their geographical range.

The data provide new robust information of geographical isolation of sheep breeds. This establishes a proof of endemism within native sheep breeds of the UK and indicates that endangerment through geographical distribution is a very real risk. The endemism is best illustrated in the breed maps which clearly highlight the degree to which each breed

is associated with a distinct geographical area. From the maps, ten of the twelve breeds analysed were concentrated but the flocks of two breeds were visually more dispersed. In numerical terms, the ten breeds were found to have up to 95% of their breed numbers concentrated within a radius of 65 km from the mean centre of each breed. The two breeds that appeared visually dispersed had up to 95% of their numbers located between 131 and 234 km.

As discussed earlier, the impact of isolation on risk status has already been illustrated in the UK by the 2001 FMD epidemic. It had been reported by breed societies that disproportionate losses were suffered by breeds farmed in a geographical region worst affected by the epidemic. This study demonstrates the degree of geographical isolation of these breeds, in particular the fact that up to 95% of their numbers are concentrated in narrow radii from the respective mean centres of each breed. This distance is 23 km for Herdwicks, 64 km for Rough Fell and 64 km for the South Country Cheviot. In numerical terms, these percentages translate into, for the Herdwick, 72 flocks (46,884 sheep) from a total of 113 flocks (49,408 sheep), for the Rough Fell 110 flocks (26,370 sheep) from a total of 121 (27,839 sheep) and for the South Country Cheviot 62 flocks (74,597 sheep) from a total of 69 (79,902). The numbers are given to highlight that these Heritage Sheep breeds are commercially farmed livestock existing in large numbers, yet must be considered to have a high risk status through their geographical isolation.

The endangerment of native sheep breeds within the UK and throughout Europe continues, with the emerging epidemic of the exotic disease caused by Blue Tongue virus (BTV). On completion of data-gathering for this study in 2007, and at an early stage of the BTV outbreak in the UK, five of the twelve breeds analysed fell within the English BTV protection zone, and within Wales, one breed (South Wales Mountain) fell within the Welsh protection zone. The emergence of BTV across European countries is a well recognised threat. However, the severity of endangerment of the geographically isolated sheep breeds continues to be largely overlooked, with attention focussing principally on the numerically scarce breeds. For example, whilst the UK has established the Breeds at Risk Register, specifically to address protection of FAnGR during disease outbreaks, only those breeds categorised as numerically rare by NGOs are included. The results presented in this study require an urgent reassessment of other native sheep breeds for inclusion on the UK Register. Also, for other countries in which BTV is circulating, and indeed other emerging diseases, it will be important to consider those sheep breeds at risk through their geographical isolation as well as through their numerical rarity.

The analyses revealed that the endemism of two of the breeds studied must remain questionable based on the data collected. Thus, the Clun Forest and Southdown were distributed relatively widely in a geographical context. For the Clun Forest, up to 95% of their numbers are found within a radius of 131 km from the respective mean centre of the breed, and for the Southdown, within a radius of 234 km. In numerical terms, for up to 95% this translates, for the Clun Forest, into 32 flocks (3007 sheep) from a total of 36 flocks (3171 sheep), and for the Southdown 167 flocks (6262 sheep) from a total of 181 (6600 sheep). It is of interest that the total number of these two breeds is relatively low. Until recently

the Southdown was categorised as a rare breed and often these are kept in small flocks by enthusiasts.

In order to design effective management strategies to prioritise and conserve breeds at risk the "value" of the breed needs to be assessed. Genetic distinctiveness is recognised to be an important component of value, since it provides evidence at the molecular level for diversity of the genetic resource (Bruford, 2004; Lawson Handley et al., 2007). There are now extensive molecular tools to characterise genotypic and phenotypic diversity, but to gain maximum value from these molecular analyses it is necessary to place the data within the context of the population size and structure. The information provided in this study on breed numbers and geographical distribution of the flocks enables a more rigorous approach for selection of the animals and populations to be characterised. In turn, the evidence-base for policy decisions on protection of livestock and conservation will be more robust.

This study and the collaboration with breed societies have demonstrated that it is possible to gain factual information on sheep breeds and their numbers from interacting directly with individual breeders registered with those societies. These numerical data can replace earlier estimated numbers and offer a useful dataset to inform management and conservation of FAnGR. The study suggests that it will be essential to establish new standardised methodology across all native breeds, both in the UK and elsewhere, to ensure valid comparisons can be made and policy-making is based on accurate information, both of numbers and of geographical distributions.

## 5. Conclusion

Information is provided on population size and structure of twelve native sheep breeds that are commercially farmed in the UK. The information is placed within a geographical context and demonstrates that the genetic resources of sheep breeds existing in significant numbers can nevertheless be endangered through their geographical concentration. Ten of the breeds were defined as geographically isolated, with up to 95% of their numbers clustered within a 65 km radius of the breeds' mean centre. This endemism presents a major risk, particularly from the threat of disease outbreaks. The study provides a new informational framework for sheep breeds and the data necessary to support the design of new policies and effective management strategies to protect and conserve their genetic resources.

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## Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.livsci.2008.11.026.

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