

Development of co-ordinated in situ and ex situ UK Farm Animal Genetic Resources conservation strategy and implementation guidance

Breeding Plans for Farm Animal Genetic Resources

Review of Conservation Strategies

Best Practice Guidance

Glossary

Technical Appendices

Stephen J.G. Hall MA PhD

Livestock Diversity Ltd.

www.livestockdiversity.com

Mention of an organization, system or procedure in this report does not imply a recommendation, endorsement, comparison, evaluation or criticism of any kind unless explicitly stated. Neither is it implied that any organization that is not mentioned is irrelevant to the topic under discussion.

Examples unless otherwise stated are illustrative only.

Executive Summary

The need for the project arises from the UK Government's international commitments to the conservation and sustainable utilization of its farm animal genetic resources (FAnGR). This report complements the other elements of the project, which have focused on background policy and specific issues of animal identification and traceability. Its aims are

- To review current activities in UK FAnGR breeding and conservation;
- To generate a best practice document for stakeholders and policy makers.

Breeding plans

"The selective breeding of livestock in order to meet commercial requirements"

1. Breeding plans operate within political, economic and scientific-technical contexts and these are reviewed;
2. UK livestock are in the private sector and while decisions are made by individual breeders, who also own the information necessary to assess the genetic consequences, but the UK Government is responsible internationally for the effects of these decisions on FAnGR;
3. Breeding plans that fail to take account of genetic conservation can lead to genetic improvement in the traits under selection being accompanied by the avoidable loss of genetic variation in other traits which may be of value either now or in the future, as has been observed in the breeding of commercial dairy cattle;
4. A practical investigation of native mainstream and at-risk breeds, using new data and methods, has shown how breeding plans and conservation strategies coexist;
5. Methodologies developed for the planning and monitoring of breeding plans can readily be adapted to perform the same functions in conservation strategies.

Conservation strategies

"The planned mating of livestock in order to retain breed genetic variation"

1. The contexts of FAnGR conservation, and the relevant stakeholders, are reviewed, with the role of breed societies being considered in detail;
2. Conservation strategies must take account of the desire of many owners of at-risk breeds to develop their breeds along commercial lines;
3. New research is reported showing that while genetic variation is, in general, being conserved, there are important areas where particular attention is needed;
4. Ex situ conservation (principally, the storage of frozen semen) is reviewed and found to compare favourably with what is practised elsewhere in Europe, except in the case of poultry;
5. Emergent issues are highlighted, notably the conservation of traditional segments within commercial breeds and of poultry in general;
6. New research is reported on the monitoring of genetic variation by means of demographic variables, for breeds where computational approaches cannot be applied.

Best practice guidance

Best Practice Guidance is presented and the principles explained. The Guidance, which is for breeders, breed societies and the UK Government, is also available as a separate document.

Table of Contents

1	General Introduction.....	6
2	Breeding Plans for Farm Animal Genetic Resources.....	7
2.1	The background to breeding plans.....	7
2.1.1	Economic context.....	7
2.1.2	Scientific and technical context	8
2.1.2.1	Molecular biosciences.....	8
2.1.2.2	Conservation biology	9
2.1.2.3	Veterinary science.....	10
2.1.3	Legal context	10
2.1.4	Social contexts	11
2.1.5	Institutional organization and stakeholder bodies	11
2.1.5.1	Breed societies	11
2.1.5.2	Umbrella organizations.....	12
2.1.5.3	Breeding companies.....	12
2.1.5.4	Industry platforms.....	12
2.1.5.5	Scientific research and knowledge transfer.....	13
2.1.5.6	Governmental bodies and levy boards	13
2.1.6	Institutional interactions.....	14
2.2	Practical breeding.....	16
2.2.1	Interface with conservation strategies	16
2.2.2	Principles applying to all species.....	16
2.2.3	Breeding structures and global needs	17
2.2.4	Crossbreeding	17
2.3	Survey of breeding plans in practice	19
2.3.1	Breed reviews.....	19
2.3.1.1	Cattle.....	20
2.3.1.2	Sheep.....	27
2.3.1.3	Goats	33
2.3.1.4	Pigs	34
2.3.1.5	Equines.....	36
2.3.1.6	Poultry.....	37
2.4	Breeding plans: summary of findings	38

3	Review of Conservation Strategies	40
3.1	The context of conservation strategies	40
3.1.1	Policy context	41
3.1.2	Regulatory context	41
3.1.3	Overseas and international organizations	42
3.1.4	Institutional context	42
3.1.4.1	Departmental Expert Committee on Farm Animal Genetic Resources	43
3.1.4.2	Umbrella organizations	43
3.1.4.3	Breed societies	44
3.1.4.4	Registration and publication of registers	45
3.2	National outcomes of UK FAnGR conservation	47
3.2.1	Maintenance of population numbers	47
3.2.2	Conservation of within-breed variation	47
3.2.3	The role of ex situ conservation	50
3.3	Conservation practice at breed level	52
3.3.1	Demographic management	52
3.3.1.1	Geographical factors	52
3.3.1.2	Traditional populations and introgression	53
3.3.2	Genetic management – general issues	54
3.3.2.1	Biodiversity indicators in relation to FAnGR	54
3.3.3	Breed-level conservation outcomes	55
3.3.3.1	Mammalian livestock	56
3.3.3.2	Poultry	60
3.3.3.3	Feral animals	63
3.3.4	An overall strategy	64
3.4	Conservation strategies: summary of findings	67
4	Best practice guidance	69
4.1	The background to recommendations	69
4.2	Specific recommendations	69
	Guidance for breeders	69
	Guidance for breed societies	69
	Guidance for the UK Government, Devolved Administrations and public bodies	70
5	Glossary	73
6	Acknowledgements	78
7	Technical Appendices	78
7.1.1	Technical Appendix 1: Population data of dairy cattle	79
7.1.2	Technical Appendix 2: Population data of non-dairy cattle	79

7.1.3	Technical Appendix 3: Population data of sheep.....	82
7.1.4	Technical Appendix 4: Population data of goats.....	84
7.1.5	Technical Appendix 5: Population data of pigs.....	85
7.1.6	Technical Appendix 6: Population data of equines.....	87
7.1.7	Technical appendix 7: Research projects relevant to FAnGR, supported under EC programmes.....	88
7.1.8	Technical appendix 8: Breed societies.....	89
7.1.9	Technical Appendix 9: Overall status of breeds listed by RBST.....	90
7.1.10	Technical Appendix 10: Ex situ breed conservation – principles and practice.....	96
7.1.11	Technical Appendix 11: Daughter breed societies.....	107
7.1.12	Technical Appendix 12: Traditional breed (Lincoln Red).....	108
7.1.13	Technical Appendix 13: Effective population sizes.....	111
7.1.14	Technical Appendix 14: Poultry.....	113
8	References.....	118

1 General Introduction

Sustainable use of farm animal genetic resources (FAnGR) requires the conservation of the breeds themselves, and of the genetic variation within them. The UK continues to be successful in the former, but success in the latter is less clear. No breeds have been lost since 1970 and many breeds which at that time were only still in existence because of the dedication of small numbers of owners have now reached numbers where they can be considered for practical purposes secure. This has been achieved by promotion of numerical growth and spread of ownership of the breeds, with the breed societies and the Rare Breeds Survival Trust having been key in the process.

However, new issues have been emerging which mean that conservation of FAnGR has become in many ways more complex. These have related to mainstream breeds rather than to those which were, certainly during the first half of the 20th century, relatively rare. A focus of this report is the pair of questions; whether the UK government can claim that breeding plans and conservation strategies as they operate in the UK actually meet these obligations, and if they do not, what can be done to rectify the situation.

Some of these mainstream breeds are themselves very local in distribution (many of them are associated strongly with a particular county) or have segments within the breed of particular conservation significance. Today a county-wide distribution does not guarantee the survival of a breed under a disease control regime which countenances the stamping out of “dangerous contacts”; due to modern patterns of livestock movement, such contacts may be geographically far more widespread than in the past.

To illustrate with specific examples: in the 1970s, interest focused on such breeds as White Park cattle; Portland sheep; Tamworth pigs; which had been rare for several decades. Now, the breeds causing most concern include, for example, the segment of the Aberdeen Angus breed that has not been influenced by introduction of genes (introgression) from overseas populations of the breed; the traditional form of Large White pig; and the Herdwick sheep which while relatively numerous is largely confined to the Lake District. But it would be wrong to be complacent about the breeds that were originally of conservation concern. In spite of stronger numbers and a heightened public profile, many are still geographically limited in their distribution (for example Gloucester cattle) or could be threatened by structural changes in their respective industries (pigs).

There is also the issue of commercial breeds losing their (usually highly specialized) roles, and declining in numbers. How this situation is managed depends on the breed society. Members may be very reluctant to be seen as “keeping a rare breed”, but they may find that the publicity which may arise from a sudden fall in numbers has attracted new people to the breed. As one might expect, this kind of situation is not well documented.

Conservation of FAnGR is probably more thoroughly enfolded into national life in the UK than anywhere else and there is probably going to be less of a “top-down” approach to its organization than in countries where the relevant institutions are non-existent, or less mature. Best practice guidance, to be acceptable, is going to have to show a keen awareness of customary practice.

This project records, analyses and evaluates the effectiveness of current programmes relating to the conservation and sustainable use of FAnGR in the UK. The information which breed societies currently place in the public domain is reviewed in terms of its suitability for monitoring national FAnGR. Drawing on new methodologies that may facilitate both the management and monitoring of FAnGR, the project offers guidance for breeders and their breed societies, and for policy makers and advisers.

2 Breeding Plans for Farm Animal Genetic Resources

2.1 The background to breeding plans

Anyone who chooses mates for his or her livestock, with a view to selecting breeding animals from among their progeny, is operating a breeding programme. Livestock breeding programmes seek to optimize the genotypes of animals in order to meet market requirements in the broadest sense, including for example traditional quality criteria such as style and aspects of conformation in the horse.

Even after millennia of husbandry, individual animals and breeds retain large amounts of genetic variation and this is continually being added to by mutation. Many traits, of which prime examples are presence or absence of horns in cattle and sheep, and coat colour generally, are determined by very small numbers of genes and these tend to have become fixed or predominant in many breeds, where they may be diagnostic of breed distinctiveness.

However very many, probably most, performance traits are controlled by large numbers of genes (they are “polygenic”) and their interactions, and animals favoured for breeding are, in principle, those whose genetically determined performance is most superior to the breed average – the net result being increases in the incidences of specific performance-related genes. Performance traits can be broadly classified as either “production” traits (such as growth rate, milk yield, carcass conformation) or as “fitness” traits (such as disease resistance or tolerance, longevity, ease of giving birth). The former tend to be easier to measure, but both sets of traits are heritable to some degree.

The four main factors affecting the annual rate of genetic improvement in polygenic traits are, to what extent the trait is genetically determined, the accuracy with which superior animals are identified, the selection intensity that is achieved, and the generation interval. The higher the values of the first three factors, and the lower the generation interval, the higher the annual rate of improvement (Simm 1998).

Programmes of genetic improvement within breeds are also partnered by mating systems whereby different breeds are mated in the process of crossbreeding. This process represents the sustainable utilization of genetic diversity, provided purebred populations are maintained to supply parents.

A key feature of breeding programmes in the UK is that they are all in the private sector, though much of the underpinning science has been conducted with public sector support.

2.1.1 Economic context

The development of a liberalized and globalized market economy has set the scene for the development of production-dominated livestock husbandry and underlies the radical and continuing changes in the genetic composition of many UK livestock breeds, particularly in dairy cattle, pigs and poultry. Some livestock sectors in the UK, such as hill sheep, previously received substantial headage-based support payments and this may well have obscured market signals (Bishop and Woolliams 2004). These signals are likely to become clearer as this kind of support is reduced, and as a result of the general privatization of breeding programmes.

With heightened awareness of sustainability issues as they relate to the food chain and to rural development (for example the Green Food Project¹) together with government commitments to mitigating global climate change, new and complex market signals and policy drivers are to be expected. Those particularly relevant to livestock will relate to ecosystem services, multifunctional landscapes, and carbon footprint. The degree to which breeding is sustainable in the genetic sense

¹ <http://www.defra.gov.uk/publications/files/pb13794-greenfoodproject-report.pdf>

must also be considered, and because the UK Government is a party to the Convention on Biodiversity (CBD) and subsequent agreements, this may well be seen as a governmental commitment.

Response to market signals and international commitments will be facilitated if breeds are adequately characterized; this will give farmers the information they need to optimize their system. Some breeds are very well characterized; for example Australian dairy farmers have access² to detailed breed-specific guidance on management of their cattle. In the UK characterization is particularly needed in native breeds at risk³, but it is also deficient in the mainstream breeds where more needs to be known about traits that are relevant to post-productivist agriculture, adaptation to climate change, and mitigation of the climate warming potential of livestock farming. In the case of commercial, but minor, breeds such as Guernsey dairy cattle, characterization of the commodities they produce is particularly important (Bichard 2002).

2.1.2 Scientific and technical context

A convenient summary of the underpinning science as presented to policy makers is provided by Parliamentary Office of Science and Technology (2011).

Many studies have shown that research on the science underlying animal breeding is fully justified in terms of the public good (Moran et al. 2007; Walters 2012) and it is also acquiring a new client group – policy makers concerned with sustainability (SAC Commercial Ltd. 2010). A shift in publicly funded research has become evident, towards “a search for new step change and/or disruptive technologies” (Amer et al. 2011).

2.1.2.1 Molecular biosciences

Breeding programmes were founded on the mature discipline of quantitative genetics (Simm 1998). The estimated breeding value (EBV) system is widely applied, whereby standardized measurements on animals are collated and processed by off-farm organizations which may indeed be located in a different continent. Performance data are merged with pedigree databases, which are usually the same as those which breed societies operate in their registration procedures, with the management and statistical calculation carried out by organizations such as Signet Breeding Services which is part of the Agriculture and Horticulture Development Board (see below). These practices are being revolutionized by the application of genomics and other so-called “omics” approaches, which are now routine in pigs and poultry (Neeteson-van Nieuwenhoven et al. 2013) and are of growing significance in cattle (Berry et al. 2013). Genomic information is used to identify animals with genes of particular commercial interest⁴ and indeed can be applied to any recorded traits or combination of traits (Eggen 2012); performance-recorded animals are typed for thousands of single-nucleotide polymorphisms (SNP) markers, and elite offspring can be reliably identified on the basis of their possession of specific alleles, altogether a much cheaper procedure than conventional breeding and performance testing (Schaeffer 2006). Recently, assays have been developed in Ireland which enable a cattle breeder to classify animals for commercial traits and recessive defects and to verify parentage in a single process which at the same time yields information of value for research and development (Berry et al. 2013). An important aspect of this particular programme is that no claim is made to the intellectual property resulting from the application of the assay.

The further contributions that fundamental biology can potentially make to livestock breeding are illustrated by the outcomes of the EU-funded SABRE project (“cutting edge genomics for sustainable

² <http://www.coolcows.com.au/tools/cost-benefit-calculator.htm>

³ Ark Spring 2012, p.31; the Ark is the journal of the Rare Breeds Survival Trust

⁴ <http://www.igenity.com/beef/whatsnew/whatsnew.aspx>; Ark Autumn 2011 p.19, as applied to Gloucester cattle, one of the UK's rarest breeds

animal breeding” – April 2006 to 2011) which involved 36 partners including several companies, and nearly 200 scientists in 14 countries⁵.

2.1.2.2 Conservation biology

Unfortunately for FAnGR, this shift away from practical breeding has also disfavoured such activities as research on the application of conservation biology to livestock biodiversity. There is much to be done. Agriculture must be reconciled with habitat protection and the conservation of wild flora and fauna. Balmford et al. (2012) summarize the “land sharing” versus “land sparing” debate – the former strategy is to integrate conservation and food production, making farmland as congenial to wild species as possible, while the latter involves increasing yields on farmland and sparing as much unmodified habitat as possible for conservation. However, this subject area is under-researched. Tellingly, Balmford et al. (2012) comment how a literature search about chickens “revealed more papers about prairie chickens (*Tympanuchus* spp.) than about the consequences for wild nature of producing tens of billions of domestic birds each year”.

FAnGR would seem to be an ideal subject area for conservation biologists, partly because of the opportunities for interdisciplinary research. Human geography (for example Gibbs et al. 2009) and ecological modelling (Hattam 2006) have been applied to the study of livestock breeding, while a systems approach is essential for understanding a possible role of genotype in mitigating the contribution of dairy cattle to greenhouse gas (GHG) emissions (O'Brien et al. 2010; Thornton 2010; Zehetmeier et al. 2012). The links between economics and livestock breeding research are strong; for very many years, economic assessment and prediction has been enfolded into animal breeding science (Simm 1998, Amer et al. 2007).

Less comfortable is the place of animal breeding science in relation to conservation of faunal and plant biodiversity. Livestock breeds are a component of global biodiversity but their place in the mainstream of species and habitat conservation is not clearly established. In fairness, two key publications arising from the 1992 Rio Convention included quite detailed accounts of global livestock biodiversity (Groombridge 1992; Heywood and Watson 1995). In some practical respects they are indeed in the mainstream; the use of traditional breeds for habitat management is well established (Small 2010), and the HR2 option of the Higher Level Stewardship programme explicitly links support for native breeds at risk to faunal and plant biodiversity outcomes (Small and Hosking 2010).

However, an interest in establishing a scientific basis to these linkages is not evident. For example, a 14-paper special profile in *Journal of Applied Ecology* in 2011 on “The future of agri-environment schemes” (Whittingham 2011) made no reference to FAnGR as components of biodiversity. Neither did FAnGR feature in publications from the recently concluded Research Councils’ Rural Economy and Land Use programme⁶ but they are mentioned at several points in the Upland Policy Review published by Defra in March 2011⁷. There are very many opportunities for scientific advance in these areas. Traditional and local breeds are strongly associated with extensive grazing systems and as such might be highly relevant to the provision of ecosystem services such as carbon sequestration in grasslands (Jones and Donnelly 2004).

As explained above, genomic tools are having great impact in commercial breeding plans. Studies of this kind can also elucidate breed history (Gautier et al. 2010) and thus contribute to appreciation of the cultural significance of FAnGR.

⁵ <http://www.sabre-eu.eu>

⁶ <http://www.relu.ac.uk>

⁷ Available at <http://www.defra.gov.uk>

2.1.2.3 *Veterinary science*

There are many valuable studies of implications of breeding programmes upon animal welfare and of the general ethical issues in livestock breeding⁸. Implications of animal health policy and practice for breeds at risk are considered in the Conservation Strategies section of this report.

Resistance to epidemic diseases like foot and mouth disease (FMD) and avian influenza is not amenable to selection because of the difficulty of identifying animals that have the desirable phenotype (due to containment regulations) and selecting animals for enhanced resistance would probably conflict with current “stamping-out” control approaches. Genetic approaches are much more appropriate for endemic diseases but must be coordinated with other strategies (emphasized by Bishop et al. 2010). Heritabilities of disease resistance or tolerance are generally rather low and an effective conventional breeding programme requires there to have been thorough monitoring of livestock for many years. It must be noted that resistance, however, is not the same as tolerance (resistance implies that the host reduces the pathogen burden, while tolerance involves counteracting the damage: Guy et al. 2012) and this has important implications for how candidate superior animals are identified. There is also the risk that what is being selected for is ability to pass a diagnostic test rather than disease resistance itself (Amos et al. 2013).

Breeding for disease resistance might be by within-breed selection in which case effects on breed genetic diversity, of intense selection against a disease-related genotype, must be considered, particularly in numerically weak breeds, for example Townsend et al. (2005). Introgression of a resistance gene is a possible approach. Epidemiological consequences of introducing a “resistance allele” into a pig population have been considered by MacKenzie and Bishop (2001); it is not necessary for all animals on a farm to be resistant to the disease for the farm to be free of epidemics.

2.1.3 **Legal context**

Breeding programmes have sometimes been organized in response to legal requirements. Concerns that bovine spongiform encephalopathy (BSE) might have entered the sheep population, and be indistinguishable from the long-established sheep disease of scrapie, gave rise to EU Commission Decision 2003/100/EC. This required member states to implement breeding programmes against susceptibility to transmissible spongiform encephalopathies (TSEs) in sheep. The UK government had already launched the National Scrapie Plan⁹ in July 2001 which aimed to reduce the frequency of the allele most associated with susceptibility, known as *VRQ*, and increase that of the one conferring least risk, *ARR*. The strategy was to genotype individual rams and a cryobank was established for sperm from rams, nominated by breed societies, of susceptible genotypes that would be culled.

The UK Climate Change Act 2008 requires a reduction, by 2020, in agriculture’s GHGs of 11% from 1990 levels. Looking further ahead it currently sets a target overall reduction of 80% in GHGs by 2050 across the UK economy. A growing area of livestock research relates to whether livestock breeding can mitigate climate change (Wall et al. 2010) or help agriculture to adapt to it (Gauly et al. 2012). Several reports and online systems have been produced in relation to this aspect of livestock production efficiency, with a focus (thus far) on management rather than breeding¹⁰. Defra has

⁸ examples of important recent contributions (March 2011 and November 2012) are accessible at <http://www.lowinputbreeds.org/> and <http://www.defra.gov.uk/fawc/> respectively

⁹ <http://archive.defra.gov.uk/foodfarm/farmanimal/diseases/atoz/bse/othertses/scrapie/nsp.htm> partnered by the Northern Ireland Scrapie Plan, <http://www.dardni.gov.uk/index/animal-health/animal-diseases/bse/scrapie-introduction/northern-ireland-scrapie-plan.htm>

¹⁰ . Examples include <http://www.eblex.org.uk/news/carbon-calculator.aspx> and the National Trust’s May 2012 report on grass-fed beef in relation to carbon footprint

already funded research on the implications for breeding programmes of this change in the policy environment (Projects AC0204 and IF0182¹¹).

2.1.4 Social contexts

Links from animal breeding sectors through to the wider public have sometimes been problematic. Public concern is often expressed over genetic changes to farm animals: when they affect welfare of the animals; when they are thought to have effects on human health; and when they are seen to be “unnatural”. The positive contribution of livestock breeding to food security is less frequently mentioned (Neeteson-van Nieuwenhoven et al. 2013). The sociocultural aspect of livestock breeding has been studied in the Netherlands and Norway (Boogard et al. 2011).

Considering the immediate social environment of livestock husbandry, Gibbs et al. (2009) contended that in the cases of beef cattle and sheep, the use of new IT-based and genomic techniques is not so much leading to corporate dominance, as has been the case in pigs, poultry and dairy, but to a more complex set of relationships between breeders, the supply chain, breed societies and consumers. The international dimension to beef cattle and sheep breeding is not characterized by dominance by multinationals; it takes the form of purchase of semen and embryos. The relationship between the breeder and the company is that of customer and supplier, rather than an incipient corporatization. Quoting Gibbs et al. (2009), we can anticipate “a nuanced co-production of political and economic structure amongst the players, shaping and reacting to the development of particular tests, databases and other technologies and techniques”.

2.1.5 Institutional organization and stakeholder bodies

Throughout livestock breeding, the defence of intellectual property rights is evident. Famously, in the 18th century the pioneer Robert Bakewell kept his livestock breeding methods secret. Under the CBD countries have rights to benefits arising from the use of their FAnGR. Breed societies own the data relating to pedigrees. The subject is reviewed with an emphasis on animal patenting by Rothschild and Newman (2002); some areas are heavily protected by patents while others are not (Richard 2002). At the same time, there are very considerable advantages to free information exchange, for example in the international evaluation of bulls. Many national and international cooperative bodies are concerned directly with livestock breeding in addition to numerous regional and national land-based and agricultural organizations.

2.1.5.1 Breed societies

Breed societies exist to advance the shared interests of their members and to maintain the status of their breeds, usually through operating breed registers. Some are very long established and many of them have charitable status. While some have professional staff many others do not. Under the EC Zootechnical Regulations¹², recognized breed societies have certain entitlements as well as obligations towards counterpart organizations overseas. Some operate commercial arms while some handle procedures such as registrations, performance and type recording, on behalf of other cattle societies (for example HUK - Holstein UK - the breed society for Holsteins and Friesians¹³). Breed societies are discussed further in the Conservation Strategies section of this report.

To comply with the EC's Zootechnical Regulations, breed societies must have certain procedures in place. Modes of registration pose particular difficulties especially for livestock where females are not

<http://www.animalwelfareapproved.org/wp-content/uploads/2012/05/067b-Whats-your-beef-full-report.pdf>.

¹¹ available at <http://randd.defra.gov.uk/>

¹² <http://www.defra.gov.uk>

¹³ (<http://ukcows.com/holsteinuk/publicweb/Services/SrvMain.aspx?page=KeyFacts&cmh=166>)

registered individually, such as in many sheep breeds. Their constitutions usually oblige them to maintain the traditional form of the breed, and usually this does not preclude them from keeping the pedigree register open to animals from overseas populations of the same breed, or from other breeds. While this gives a welcome flexibility to breeding plans, it can raise issues of genetic conservation. Finally, several new requirements are being placed on the breed society – UK Government relationship notably relating to the protection of key flocks and herds from culling during disease outbreaks.

2.1.5.2 Umbrella organizations

Organizations such as the Rare Breeds Survival Trust, British Pig Association, British Goat Society, Poultry Club of Great Britain and Rare Poultry Society function to a certain extent as breed societies in that they are involved in registration of certain breeds, but they have a much wider remit. They are considered as the context requires in the Conservation Strategies report. They parallel the organizations which are concerned with industry matters generally, such as the National Pig Association, the National Sheep Association, the National Beef Association and their Scottish, Welsh and Northern Irish counterparts. In 1974, a Combined Flock Book was established by Countrywide Livestock Ltd. for nine sheep breeds for which no such pedigree register existed. This operation continues, under the aegis of the RBST with some breeds having been added to the coverage and some removed as their own flock books have become established.

2.1.5.3 Breeding companies

Globally, breeding programmes are a major activity with substantial investment in research. In 2006 global R&D spending was \$295 million, or about 7.3% of animal genetic material (germplasm) sales (Fuglie et al. 2011). In 2006, companies based in the USA and Canada (though not necessarily in north American ownership) had about 40% of the global market for animal genetic material (germplasm) and accounted for 50% of global R&D spending. European countries, primarily Germany and the Netherlands, accounted for most of the remaining R&D and had about 57% of the world market. Worldwide cattle research is about 4.6% of sales; for pigs and chicken the figures are 7.4% and 8.1% respectively. These differences reflect economic decisions about market trends, and the relative cost/benefit ratios of investment in the respective species. For present purposes, the relevant aspect of animal breeding research is that relating to retention of genetic variation under selection regimes.

2.1.5.4 Industry platforms

FABRE TP¹⁴, the Sustainable Farm Animal Breeding and Reproduction Platform, was set up by industry and then adopted by the EC, and has contributed to formulation of the EC's biotechnology research agenda. It is now coordinated by the European Forum of Farm Animal Breeders¹⁵. For the present discussion, a particularly relevant activity of the latter has been the formulation of a 'Code of Good Practice for Farm Animal Breeding and Reproduction Organisations' which includes the following:

Breeding programmes are designed to make optimal use of existing genetic variation between and within populations. Therefore, Breeding Organisations attempt to maintain genetic diversity in their breeding populations, and to monitor and control the rate of inbreeding. Moreover, Breeding Organisations will contribute semen and/or embryos to (national) gene banks for relevant breeds/lines to ensure conservation of biodiversity.

¹⁴ <http://www.fabretp.info/>

¹⁵ <http://www.effab.org>

Bilateral arrangements are also common. At least 25 UK sheep and 9 beef cattle breed societies cooperate in their registration administration. They also cooperate with Signet and the EGENES division of SRUC in the BASCO system (Coffey et al. 2007), which has received public funding¹⁶ in order “to bring about technological development and web based interfaces for the collection and dissemination of pedigree and performance data to the industry and wider public”. Nine more beef cattle breeds operate through the ABRI/Breedplan system¹⁷.

2.1.5.5 Scientific research and knowledge transfer

The scientific community communicates through learned societies and by informal contact and has been strongly represented on the Defra Farm Animal Genetic Resources committee and its predecessors¹⁸ (Hall 2009; Roper 2004). The Biosciences KTN (Knowledge Transfer Network)¹⁹, based at the Roslin Institute and formerly known as Genesis Faraday, helps its members to seek public funding for R&D work. It managed the SABRE project mentioned above, and has Priority Areas in Innovation in Animal and Plant Production and Performance, and Sustainable Food Supply and Security.

2.1.5.6 Governmental bodies and levy boards

Defra and the Devolved Administrations converse through the FAnGR committee, and at the European level through the European Regional Focal Point (ERFP), whose activities are summarized in the Conservation Strategies section.

The Levy Boards are directly concerned with supporting genetic improvement of livestock. These organizations use levy payments to fund applied research and to promote their respective industries. DairyCo is a component of the Agriculture and Horticulture Development Board (AHDB), a non-departmental public body which liaises closely with Defra. It has a remit for the milk sector in England, Scotland and Wales. Northern Ireland’s red meat sector is covered by the Livestock and Meat Commission²⁰ and the dairy sector by the Northern Ireland Agricultural Research and Development Council²¹. For England, the meat livestock boards are EBLEX and BPEX (beef/sheep, pigs respectively)²². The Scottish and Welsh equivalents are Quality Meat Scotland²³ and Hybu Cig Cymru (HCC) – Meat Promotion Wales²⁴ - respectively. These boards have the capacity to support breed improvement²⁵ while the Horserace Betting Levy Board makes grants to breed societies “to improve and maintain the quality of pure-breeding among Britain's native breeds of horse and pony”. Eligible breeds are those on the Watchlist of the RBST; the total to be paid out in 2013 will be £100,000²⁶.

¹⁶ see for example <http://www.texel.co.uk/basco/index.php>

¹⁷ Agricultural Business Research Institute (University of New England, Armidale NSW, Australia: <http://www.abri.une.edu.au>)

¹⁸ <http://www.defra.gov.uk/fangr>

¹⁹ <https://connect.innovateuk.org/web/biosciencesktn>

²⁰ <http://www.lmcni.com/>

²¹ <http://www.agrisearch.org>

²² <http://www.eblex.org.uk/>, <http://www.bpex.org.uk/>

²³ <http://www.qmscotland.co.uk>

²⁴ <http://hccmpw.org.uk/>

²⁵ for example http://hccmpw.org.uk/publications/breed_improvement/

²⁶ <http://www.hblb.org.uk/document.php?id=110>

2.1.6 Institutional interactions

Today, many institutions are involved with the conservation and sustainable development of FAnGR. This is in sharp contrast to the situation in the 1980s and earlier. Interactions among these institutions are compared between these two periods in **Chart 1** and **Chart 2**. Emphasis is on direct concern with FAnGR; the linkages are indicative only. One prominent constituency, the agricultural societies (which would probably replicate many of the linkages) has been excluded for clarity and so too have many research funding bodies.

The natures of the linkages are left undefined, though they mainly involve formal or informal information transfer or some kind of legislative or contractual process. The aim is to emphasize the complexity that has developed.

Much of the current elaborate structure has developed since about 1989 and the situation up till then reflected how agriculture was structured in ways which reflected the 1947 Agriculture Act and the 1973 accession of the UK to the European Union and adoption of the Common Agricultural Policy. Their interactions are compared in the organization chart, with an emphasis on direct concern with FAnGR. One prominent constituency, the agricultural societies, would probably replicate all these linkages and has been excluded for clarity.

1989 was, according to Marren (2006), perhaps “the moment that politicians started taking green issues seriously”. Set-aside was introduced, the MacSharry reforms of 1992 which established environmental protection as a goal of the Common Agricultural Policy were on the horizon; the precursor of Countryside Stewardship was established. Membership of the Royal Society for the Protection of Birds and the National Trust reached half a million and 2 million respectively. Preparations were under way for the Rio Convention, to be held in 1992, that gave rise to the Convention on Biodiversity, and the Food and Agricultural Organization of the United Nations (FAO) and the European Association for Animal Production (EAAP) were developing accessible global databases on FAnGR. While there were discordances between farming and conservation, it was still possible for 1989 to be the Year of British Food and Farming in which RBST played a prominent part. This was a confident assertion of the place of agriculture in national life and heritage and a celebration of 150 years of the Royal Agricultural Society of England, and of 100 years of the Ministry of Agriculture Fisheries and Food (MAFF).

MAFF began holding informal meetings of “interested parties” concerned with FAnGR in 1995 (Hall 2009), this led to a Consultative Committee set up to prepare the 2002 UK submission to FAO’s report on the State of the World’s Animal Genetic Resources and ultimately to the Farm Animal Genetic Resources Expert Committee as it exists today.

In retrospect it seems very fortunate that MAFF’s mechanism was initiated at this time because the institutional structures relating to FAnGR were about to become much more complex. The Milk Marketing Board was privatized in 1994, the Agricultural Development and Advisory Service in 1994, devolution took place in 1997, MAFF was replaced by Defra in 2002 and the Rural Development Policies of the European Union were initiated in 2005.

Chart 1: Institutions involved with FAnGR in the 1980s

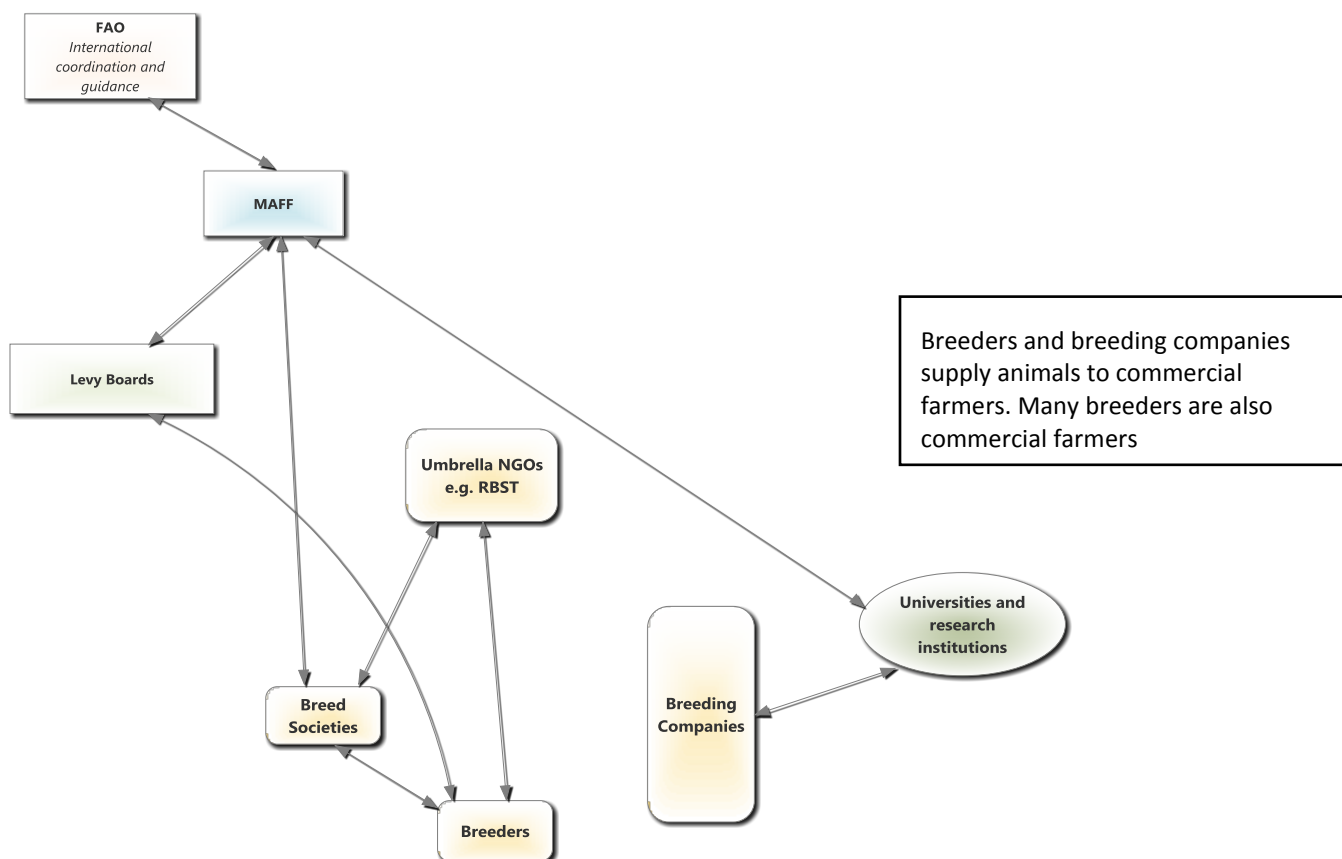
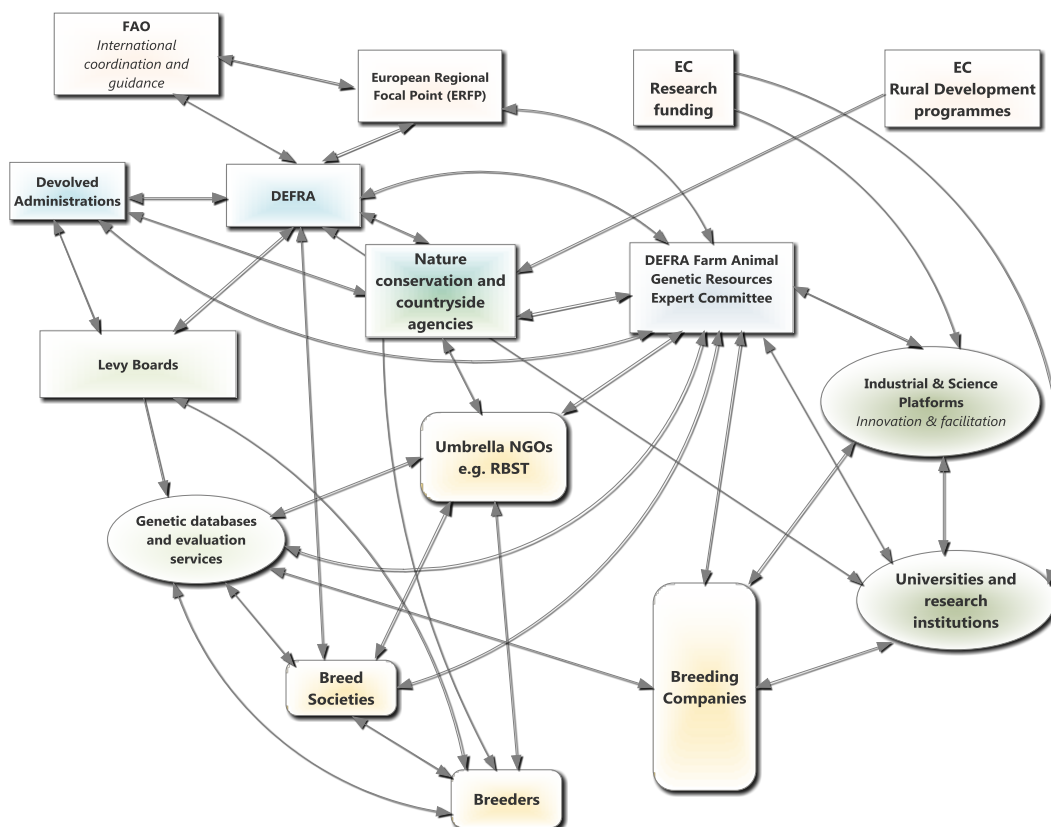


Chart 2: Institutions involved with FAnGR in 2013



2.2 Practical breeding

2.2.1 Interface with conservation strategies

Breeding plans are the procedures whereby genetic variation is exploited for commercial benefit. Conservation strategies aim at maintaining genetic variation, and making it available in a sustainable manner, for breeding plans now or in the future.

Ideally, breeding plans would embody conservation strategies and indeed this is technically feasible. Modern breeding plans identify genetically superior animals by reference to the performance of their relatives, and predict the phenotypic outcomes of particular matings; schemes which can achieve this are sophisticated enough for the effects on breed genetic diversity to be deduced using optimum contribution methods (Woolliams 2007). It is emphasized that this means that genetic improvement of a breed, targeting particular performance-related genes, can proceed without excessive loss of variation in other genes. This requires computation, EVA software being one relevant package²⁷. This identifies the best animals to breed from in terms both of predicted performance of offspring and of limiting increment of coancestry in the population.

In many breeds an important aspect of breeding plans is the management and elimination of genetic defects and general advice is available on how to achieve this²⁸. Again, this has implications for conservation strategies because heavy use of specific elite sires many of which are heterozygous for such recessives (vanRaden et al. 2011) can cause defects to become very widespread in breeds.

The reciprocal obligations of breeding plans to have an element of conservation, and of conservation strategies to have some reference to utilization, appear implicit in international commitments to biodiversity conservation. The UK government has undertaken to conserve genetic resources and it also subscribes to principles of access and benefit sharing. However, the organizations which are actually in a position to discharge these obligations are private companies, individual farmers, breed societies and NGOs. All these parties operate in accordance with their own interests and in response to market signals.

2.2.2 Principles applying to all species

Any closed population will accumulate inbreeding, and in commercial livestock it is possible to maximize the rate of genetic gain for a given rate of increase of inbreeding in properly planned breeding programmes (Villanueva et al. 2004) with research work funded by industry itself and by levy bodies (for example; Avendaño et al. 2003; Kuehn et al. 2008). Several years ago the US genetic evaluation system was already generating the expected inbreeding coefficients for future progenies of bulls, calculated from the mean relationship of a bull with a random sample of cows born during the previous three years (van Raden and Smith 1999) – by which time, unfortunately, national herds were already highly inbred. Today, dairy farmers have direct access to advice on avoiding inbreeding in their own herds (for example GMS and Herdmate Plus²⁹). One obvious strategy, to use bulls that are only distantly related to the cow population, appears suitable, but runs the risk of such bulls being used to excess.

Issues in designing relevant information technology systems are discussed by Kinghorn et al. (2002). There are essentially three classes of software architecture: central analysis using a bureau service; distributed stand-alone executable software; and internet deployment with central processing. However the problem the authors mentioned a decade ago still applies – “most existing software to

²⁷ <http://eva.agrsci.dk/index.html>

²⁸ http://www.signetfbc.co.uk/documents/content/sheepbreeder/ridgene_manual_digital.pdf

²⁹ available from <http://www.cogentuk> and <http://www.genusbreeding.co.uk> respectively

help implement genetic improvement programmes is not suitable for use by breeders who do not have access to personnel trained in quantitative genetics”.

2.2.3 Breeding structures and global needs

Animal breeding used to show a clear pyramidal structure in which elite breeders exchanged animals among themselves, practised selection and sold animals to “multipliers” who produced breeding stock for sale to commercial farmers for the production of animals and commodities for the market (Simm 1998). A problem with this structure was that pathways of information transfer from the commercial sector back to the elite were not clear. Now, with modern performance recording and information technology, information on animal performance does flow back to the elite, most notably in dairy cattle.

In dairy cattle, pigs and poultry, the elite breeders are now multinational companies and with the vertical integration of these industries and modern reproductive technology the multiplier sector has been supplanted (Laughlin 2007). However the traditional pyramid is still to be seen in beef cattle and sheep but modern IT systems make information about the genetic merit of candidate animals available to breeders – previously they had to rely on visual assessment or identification of superior animals in pedigrees.

In many of the rarest breeds and in equines breeding decisions may be better described as “mate selection”, for example when an animal is chosen because of its ancestry or because it is known to lack some harmful gene.

Breeding structures emerged in response to commercial imperatives. Whether they can accommodate the new demands being made on livestock breeding by broader global concerns is yet to be seen. There is a definite need for global approach to breeding for genetic sustainability (Ducrocq 2010). This is acquiring added urgency because it is necessary to anticipate the genetic changes needed to mitigate the effects of global climate change on dairy production (Gauly et al. 2012), and also because society demands that the livestock industries must reduce their own contribution to anthropogenic climate change. Whether this reorientation can be left to market forces operating in an environment of private-sector breeding companies remains to be seen. In the case of dairy cattle, international cooperative breeding programmes can be successful, as evidenced by the Red Scandinavian breeds (Hansen 2006).

2.2.4 Crossbreeding

Crossbreeding is the quickest way of utilizing FAnGR sustainably but at the same time, if unregulated, it is the major threat to its conservation.

There are essentially four degrees of crossbreeding:

1. Stabilized crossbreeding systems

Here, breeds are maintained as separate entities and are crossed to yield progeny which combine the merits of the parent breeds and can also exhibit heterosis (hybrid vigour). For example, “maternal breeds” (for example, hardy hill ewes) can be crossed with rams of prolific breeds (“crossing sire breeds”) to produce fertile crossbreds. Males are sold for meat but females, which are usually sold to lowland farms, are then mated with rams of meat breeds (“terminal sire breeds”) to produce lambs for slaughter. This is the crossbreeding system traditional to UK sheep farming (Pollott and Stone 2003). It can be very relevant to the survival of many breeds at risk because owners have the option of withholding temporarily a proportion of females from pedigree breeding and mating with males of commercial breeds. Hall (1989a) suggested this might apply to 42-44% of litters from UK pig breeds of conservation concern; a preliminary study (Hall and Henderson 2000) showed how marketable lambs could be produced by the use of commercial rams on ewes of the Cotswold and primitive breeds.

2. Introgression

It may be desired to bring characteristics from one breed into another without changing the latter too radically. For example, by the 1970s British beef breeds were being outcompeted by larger-bodied, faster-growing Continental breeds. Bulls of Continental breeds or from overseas populations of British origin which had already undergone selection towards the desired type were mated with British herds, the crossbred progeny being then mated (backcrossed) with purebred British animals, successive backcrosses meaning the proportion of Continental genes was progressively reduced. A prime consideration was not to lose breed identity and local adaptations, and breed societies documented the process so that in several breeds the percentage of the genotype attributable to the importation can be read from pedigree certificates and herd books. In dairy cattle, the British Friesian replaced the Shorthorn in the early 20th century by processes of introgression and has in its turn been almost completely transformed by introgression by the Holstein.

3. Composite breeds

This is introgression followed by selection for some desirable phenotype without regard to conforming to original breed type. An example is the development of Luing cattle from crosses between Highland and Beef Shorthorn followed by selection for a combination of performance characteristics coupled with genetically determined lack of horns. In pigs and poultry, production of composite breeds coexists with the maintenance of stabilized crossbreeding systems in highly complex breeding programmes which capitalize on the hybrid vigour (heterosis) which is often an outcome of matings between distinct genotypes. Developments in the design of crossbreeding programmes in the USA (Green 2009) led to the emergence of so-called composite breeds; while company lines of pigs and poultry are probably all, effectively, composite breeds. Pig breeding company websites give general indications of which breeds have contributed to their breeding programmes. For example, the Meidam and Volante dam line pigs marketed by ACMC have affinities with the Chinese Meishan and Large White respectively, while JSR's Genepacker 90 is related to the Large White and Landrace³⁰. Stabiliser cattle are a new composite beef breed³¹ based on a blend of Aberdeen Angus and continental breeds. Composite breeds in general are reviewed by Rasali et al. (2006) and Boon (2006). There is growing interest in crossbreeding in dairy cattle (Bluhm 2009) but whether this will lead to the emergence of new composite breeds remains to be seen.

4. Breed replacement

This is introgression followed by selection for the phenotype of the breed which is being introduced. Crossbreds are backcrossed to the introduced breed. Also known as upgrading, this is the process whereby the traditional dairy breeds of the UK have been largely replaced by the Holstein-Friesian.

Commercial advantages of stabilized crossbreeding systems are so great that it is only in two sectors that it is not dominant in the UK - dairy cattle and hill sheep. Here, a degree of introgression has been acceptable, sufficient to enhance production attributes but limited in order not to lose key attributes of these animals, high milk yield and fitness traits respectively. The situation is quite different in meat animals where an individual slaughter animal is likely to be, genetically, a mixture of at least three different breeds (see for example Todd et al. 2011). The dominance of stabilized crossbreeding systems is one explanation why in the UK there is such variation in the numerical sizes of commercial breeds; those with a specialized function within a crossbreeding system may exist in only small numbers but have a very great genetic influence.

³⁰ <http://www.acmc.co.uk> and <http://www.jsrgenetics> respectively

³¹ <http://www.bigbeef.co.uk>

The relevance of crossbreeding to conservation of FAnGR is that in the interests of short-term economic advantage, breeds can easily be lost through their being subsumed into composite breeds, or by being upgraded. Many specialized breeds that have been important in stabilized crossbreeding systems, such as Wensleydale and Teeswater sheep (the sires of the Masham crossbred), have had to find new uses as the systems have changed. Though keystones in their respective systems, such breeds are never very numerous as their end product is not a bulk commodity, but young breeding rams. Other breeds have been heavily introgressed so, for example, non-introgressed (“Traditional”) Aberdeen Angus cattle are now very rare. However, FAnGR may well possess specific attributes which could be introgressed into mainstream breeds, such as maternal traits, hardiness, and aspects of meat and milk quality. Better characterization of these will enable opportunities for their utilization in crossbreeding systems to be identified.

2.3 Survey of breeding plans in practice

Breeding plans operate within several contexts, as explained above, so they could be surveyed or audited at several different levels. The most obvious would be evaluation of increased profitability of the farming enterprise, but the focus in this section of the report is on sustainability in the sense of conservation and sustainable utilization of genetic resources. Appropriate metrics have been those relating to registered breeding stocks, so the investigation has been based on analysing flock-, herd- and stud books. In most cases the numbers of breeding animals presented in this report are of those which were parents of registered offspring. As such, these are fractions (Hall 2011) of the actual census population sizes.

The data presented here are partnered by extensive further analysis relevant to conservation strategies (such as effective population sizes, coefficients of inbreeding, and various demographic statistics). They are presented and discussed in the Conservation Strategies section.

Discussion of several of the most numerous and commercially significant breeds has had to be restricted to aspects relating to presence within them of animals that are of particular conservation significance because they represent “traditional” or “original” genotypes.

Confidentiality and operational issues, relating to the basis on which breeders have supplied information to breed societies, have dictated exclusion of some breeds. Implications of the resulting lack of information are discussed as they arise. Some breeds only record or publish limited data – for example, several sheep breed societies do not register ewes.

The confidentiality that surrounds commercial pig and poultry breeding has greatly restricted the scope of analysis in these sectors. The very individual natures of breeding in equine and rare poultry FAnGR, and the enfolding of breeding plans within conservation operations, have led these species to be considered more fully in the Conservation Strategies section.

For some breeds, data are available on participation in organized breeding plans. These range from extensive characterization of individuals for EBVs through the operation of sire reference schemes (where selected males sire offspring in a number of different breeding units, thus helping their genetic merit to be determined), to the simple existence of recording programmes. Schemes of these kinds probably exist in most breeds and those considered here cannot be seen as forming a complete list.

2.3.1 Breed reviews

Data were obtained from published herd- flock- and stud books, or, thanks to the kind cooperation of breed societies, direct from their databases. In many cases, particularly among the crossing and terminal sire sheep breeds, overall numbers are profoundly influenced by changes in agricultural function and the details of these changes are beyond the scope of this report. Breeds have been chosen on the basis of availability of data and the degree to which they illustrate general principles or the degree of diversity in how these principles apply.

2.3.1.1 Cattle

Population data on cattle are in Technical Appendices 1 and 2. Here, key features are emphasized. These data are the result of new research and will be analysed in detail for further publication.

Breeds evidently vary considerably in aspects of their demographic structure, which is influenced by their agricultural function and which may change from year to year. As a first step, plotting the sex ratio of parents against that of offspring separates the breeds out in ways which reflect their function (**Figure 1**).

A high ratio of dams to sires and of female calves to male calves indicates there is a tendency to use élite bulls, and to focus on cows rather than bulls as the more significant sex. This is very clear for the Guernsey, and for the segment of the Dairy Shorthorn which has received introgression from other breeds (suffixed “Grading” here). While the British Friesian³² shows a strong tendency towards the use of élite bulls, emphasis on female calves is not as strong as might be expected. If bull calves are indeed being registered in quite high proportions this could reflect a growing commercial interest in this genotype for the currently Holstein-dominated dairy industry. In some breeds, young bulls are sold in relatively high numbers for crossing programmes, explaining the location in **Figure 1** of the Herefords, Beef Shorthorn, Aberdeen Angus and Whitebred Shorthorn.

Breeds with a low dam/sire ratio include the rarer ones, which also tend to have low F calves / M calves ratios. The locations of the other breeds on the diagram probably represent individual circumstances – these are discussed below, so far as the data and space permit.

Dairy cattle

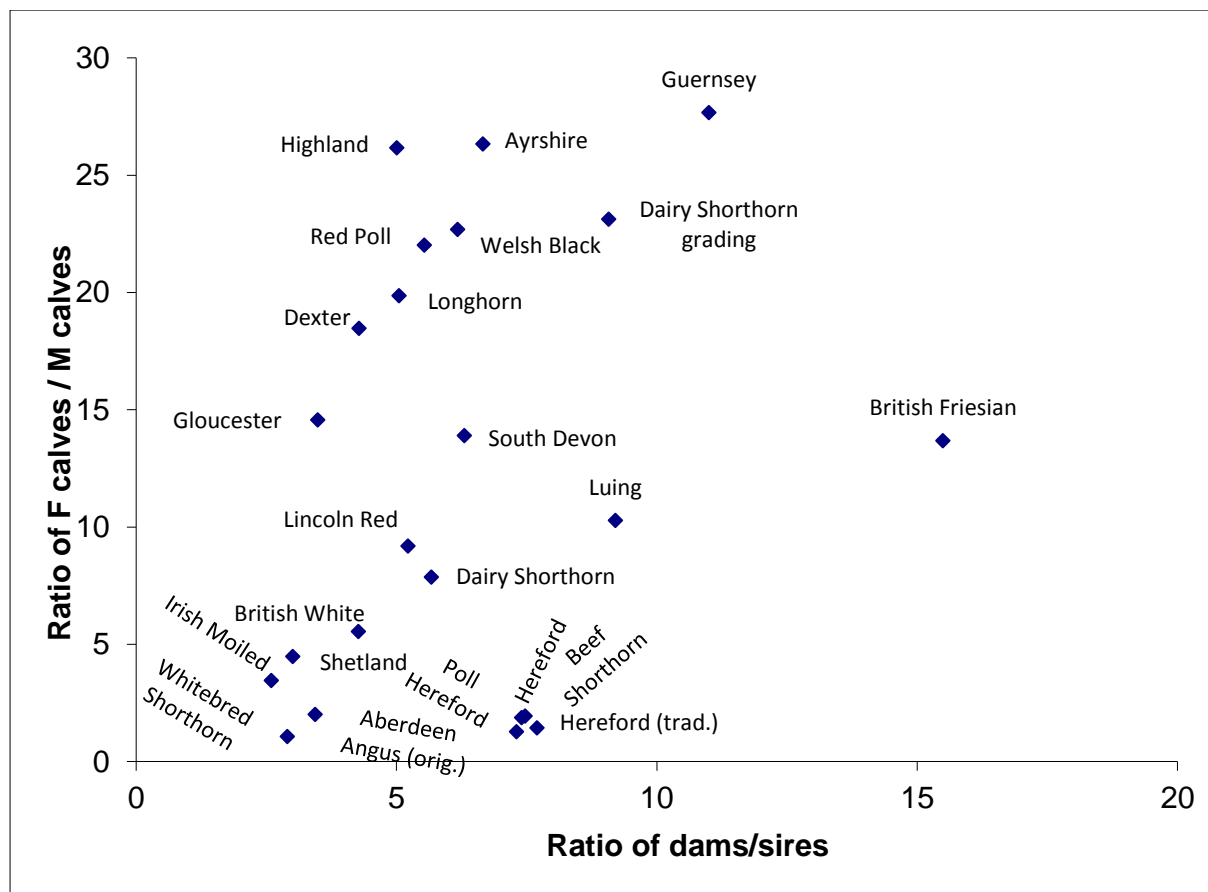
Amer et al. (2011) calculated that since 1980, genetic improvement in the UK dairy industry has been worth between £2.2 and £2.4 billion and concluded that without genetic improvement dairying would not be economically viable in the UK. Much of this benefit has been due to the availability of imported semen, principally of the North American Holstein, which has led to a dramatic increase in average milk yields over what was possible with the traditional British Friesian dairy cow. By 1993, Holstein genes contributed 64% of the genotype of the pedigree Holstein Friesian in the UK (Hill et al. 1995).

Increase in milk yield has, however, been accompanied by a drop in fertility (Royal et al. 2000). Fertility seems to be more affected than milk yield by inbreeding and in the 1990s, the contracting genetic base of UK dairy cattle was making inbreeding inevitable. In 1992, the 50 most popular Holstein Friesian sires in the UK accounted for 38% of all females registered (M. Coffey, cited by Hill et al. 1995).

Observations of the phenotypic effects of inbreeding and loss of genetic variation in dairy cattle genetic changes are plentiful (Fikse and Philipsson 2007; Hansen 2006). Inbreeding in dairy cattle is due to the use of reproductive technologies, notably artificial insemination and multiple ovulation and embryo transfer; to selection focussing on only a few traits; and also to the use of estimated breeding values in mating decisions, which tends to lead to related animals being mated (Kearney et al. 2004). Estimates of inbreeding for UK dairy cattle are not routinely published. However, in recent years and presumably reflecting a re-orientation towards traits other than milk yield, UK-bred bulls (which presumably carry a sizeable proportion of British Friesian genes) have become more economically competitive in the UK market (Amer et al. 2011).

Figure 1: Separation of cattle breeds by parental and offspring ratios.

³² Only cattle described as “British Friesian” in the herd book are considered here



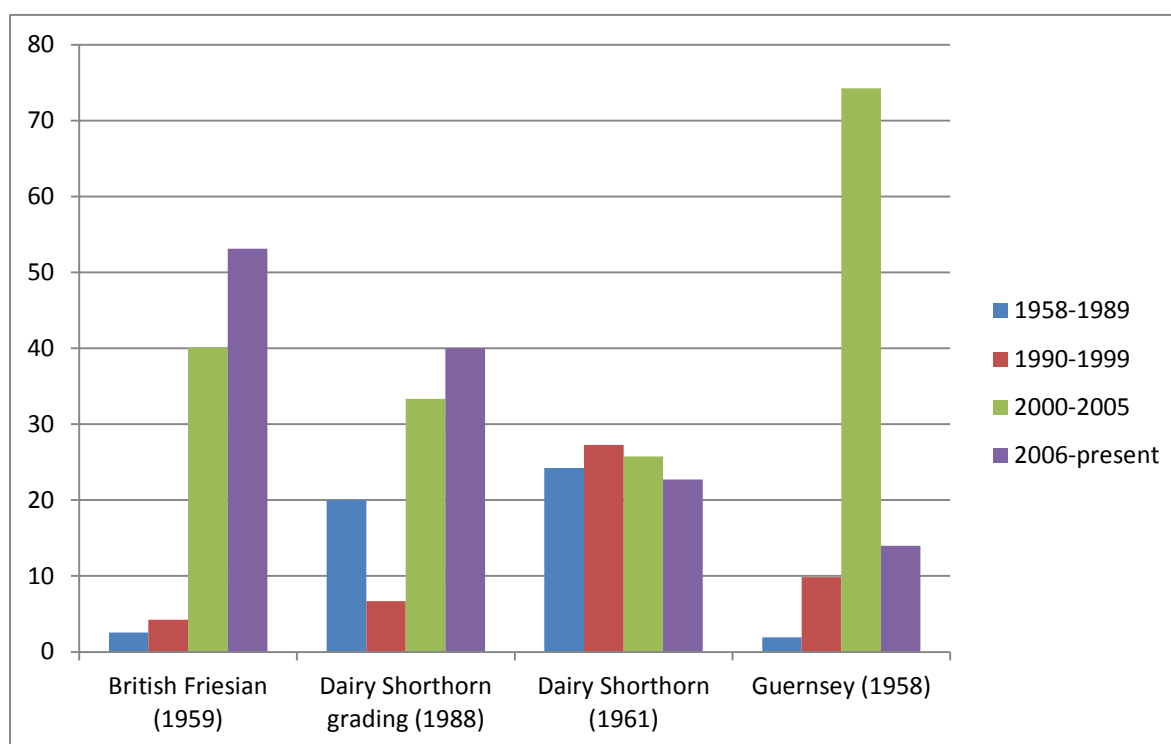
Notes:

- The three segments of the Hereford breed (Poll, Traditional, and the horned, “non-traditional” type designated here, simply, as Hereford) are distinguished
- Of the Aberdeen Angus, only the “original” type (Hart 1999a) is considered here

Population data for dairy cattle are in Technical Appendix 1. Full comparisons will be presented elsewhere; one revealing comparison is of the ages of the sires used (in practical terms “age of sire” really means “age of semen” and can be up to 50 or 60 years for semen from cryobanks).

In production terms, use of older bulls is the conservative policy as the information on performance of their daughters is more reliable; use of younger bulls implies a willingness to contribute to the accumulation of this information. Also, use of older bulls might signify a desire to revert to genotypes from a period when breeding goals were different.

Ages of dairy sires are compared in **Figure 2**, the year of birth of the oldest sire being in brackets.

Figure 2: Frequency distributions of ages of sires for each dairy cattle breed.**Notes:**

- Data relate to calves born during the years tabulated in Technical Appendix 1.
- Each column signifies the percentage of calves sired by bulls born within each period.
- Date in brackets is date of birth of oldest sire

Holstein/Friesian

In 2011/12, 207,979 females and 4,019 males were registered³³, a F/M ratio of 61.7. This very high F/M ratio is consistent with heavy use of semen from internationally proven élite bulls.

The traditional British Friesian represents an important genetic resource (Mead 2012) identifiable in the breed database by the breed code 20 which signifies the ancestry is at least 87.5% British Friesian; of these, in the calendar years 2011 and 2012 there were born 2,352 female and 236 male calves (F/M ratio of 9.9).

Red and white Holsteins can be distinguished in the register. In 2010 2651 red and white animals were registered with Holstein UK, in 906 herds of which 28 registered 10 or more (three registered over 30; Anon 2011).

Crossbred dairy cattle will probably become more prominent in the UK; advantages are evident, under some conditions, of sacrificing some of the milk yield of the pure Holstein for increased longevity and other fitness traits (Bluhm 2009). The January 2013 semen catalogue from Genus Breeding supports this prediction. Breed distribution of the 198 dairy bulls on offer is as follows: Friesian 13; Holstein 120; Red & White Holstein 13; Ayrshire 2; Jersey 17; Dairy Shorthorn 2; Guernsey 4; Brown Swiss 5; Montbeliarde 8; Viking Red 14. The Viking Red is a red and white dairy animal of Scandinavian origin. It appears that the company has received market signals from farmers, that they wish to diversify their dairy herds.

³³ <http://www.ukcows.com>, Annual Report 2012

Guernsey

This specialized dairy breed shows a high F/M registration ratio and, consistent with this, a high ratio of dams to sires. Further examination of the parentages of registered calves reflects the Guernsey's status as a global breed (Luff 2010) with considerable use being made of sires of overseas origin (**Table 1**). Thus, for example, for only 14.3% of male and 25.4% of female Guernsey calves were both parents of UK origin.

Table 1: Parentages (sire and dam) of Guernsey calves born 2008-2012.

Parentage:	Of male calves		Of female calves	
	n	%	n	%
Guernsey x Guernsey	18	14.3	855	25.4
N American Guernsey x Guernsey	30	23.8	1213	36.0
N American Guernsey x Island Guernsey	8	6.3	164	4.9
N American Guernsey x N American Guernsey	70	55.6	1135	33.7
	126	100	3367	100

Guernsey (Island)

Mr. W. Luff and Dr. Janet Roden³⁴ have kindly provided the following information on Island-bred Guernsey cattle. Purebred Guernsey semen has been imported since 1975 from the UK, USA and Canada; cattle of over 65% Island genotype still exist in significant numbers, but in only a small proportion of the Island herds. Inbreeding, which had fallen after these importations has been increasing since the mid 1990s at the rate of about 1% per generation, which is similar to the rate of increase in the USA and Canada and rather higher than in South Africa (Melka et al. 2012). Of calves born in 2011, 48% had an inbreeding coefficient lower than 3.125%, and only 12% of calves had one higher than 6.25%. The average inbreeding coefficient of registered calves born in the island in 2011 was 4.2% compared with 7.3% in the US population.

Jersey

The cattle population on the island of Jersey, though isolated (by some definitions) from all other cattle since 1789, proved in a microsatellite study to retain much genetic variation (Chikhi et al. 2004) but was not considered large enough, with about 3,000 cows, to maintain genetic progress (Hambrook 2008). In 2008 it was agreed that importation of semen should be permitted (Anon 2010) and by December 2009, 7,800 units from at least 55 bulls had been imported, 50% of the units from seven bulls. Effects on registrations are summarized in **Table 2**.

Table 2: Comparison of basic registration data of Jersey Island cattle before and after importation of semen was permitted.

year	Bulls siring progeny	Male calves registered	Female calves registered	Number of bulls siring 50% of progeny	% of females sired by 5 most popular bulls
2003-2008 average	119	36	884	16	26.0
2009	143	33	965	21	22.0

In 2009, 39% of calves were sired by means of imported semen, 61% by local bulls.

³⁴ Personal communications, April 2013

The breed society is mindful of the need to maintain the distinctive identity of cattle of pure Island lineage and these are distinguished in the herd book.

Ayrshire

Table 3 shows that bulls from overseas Ayrshire populations and of non-Ayrshire breeds, are siring a high proportion of the calves registered, particularly of males.

Table 3: Parentages of sires of male and of female Ayrshire calves, 2010-2012 registrations.

	Male calves	%	Female calves	%
Ayrshire	122	57.3	3759	69.4
Holstein	14	6.6	569	10.5
Overseas Ayrshire	75	35.2	851	15.7
Red Hybrid (<50% Ayrshire)	2	0.9	172	3.2
Others	0	0	63	1.2
Total	213	100		100

Dairy Shorthorn

311 sires listed are listed, 118 are stated as “100% Shorthorn”. For 130 (42%) of the 311 sires, information on EBVs is available, and these sires tend to be older (9.15 cf. 5.72 years for other sires) and in the 2008 calf crop, on average they sired twice as many calves. Together with the Northern Dairy Shorthorn³⁵, it is registered by the Shorthorn Society. The Dairy Shorthorn has received introgression from other dairy breeds (Bowman and Hocking 1974) and the pedigree registration system documents this, with non-introgressed animals being identifiable³⁶.

Non-dairy cattle

Population data for non-dairy cattle are in Technical Appendix 2. Comparison of age of sire (**Figure 3**), as described for dairy cattle above, is particularly revealing because of the larger number of breeds. The Beef Shorthorn and Welsh Black stand out by virtue of their use of the youngest bulls, while all the others are broadly similar. The Original Aberdeen Angus and Traditional Hereford³⁷ are not distinct, implying that breeders who are conserving the original segments of the breed are not dependent on very old frozen semen to do so.

Genetic improvement in UK beef cattle has proceeded by within-breed selection, usually in conjunction with controlled introgression from overseas breeds which may or may not be historically linked, or from overseas populations of the same breed which for historic reasons are mostly in the USA or Commonwealth countries.

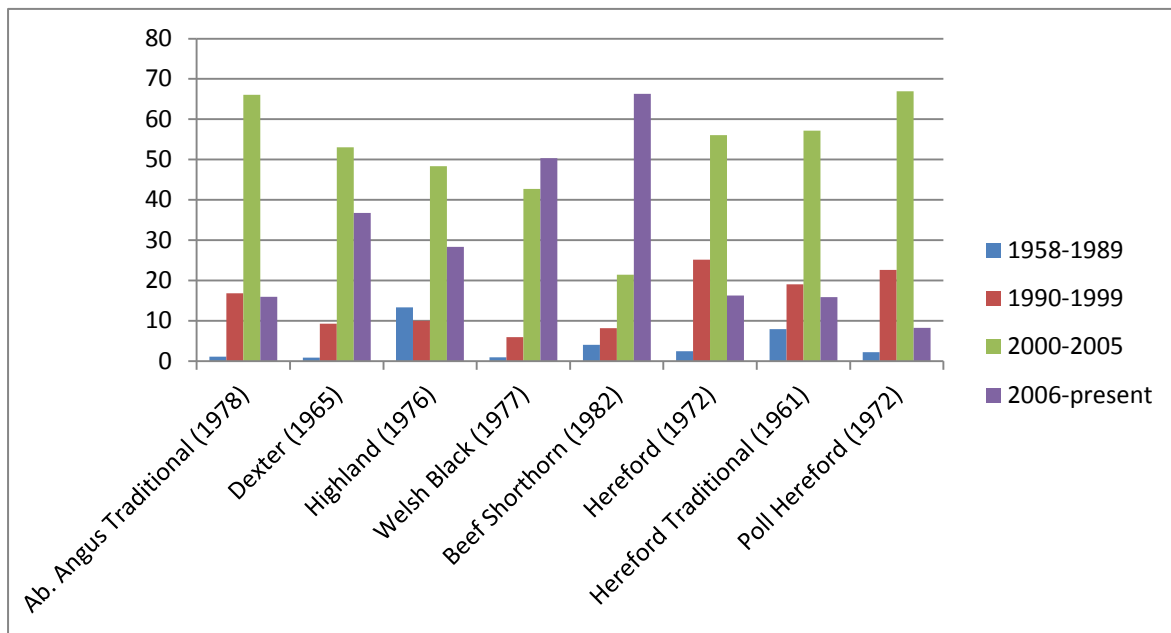
In commercial beef cattle, there is a rise in composite breeds and indeed the traditional UK lowland beef breeds are all now to some extent composites with continental breeds or USA or Commonwealth counterparts, though traditional segments are identifiable in several.

³⁵ Ark Summer 2010 p.15; Summer 2011 p.28

³⁶ Ark Summer 2012 p.18

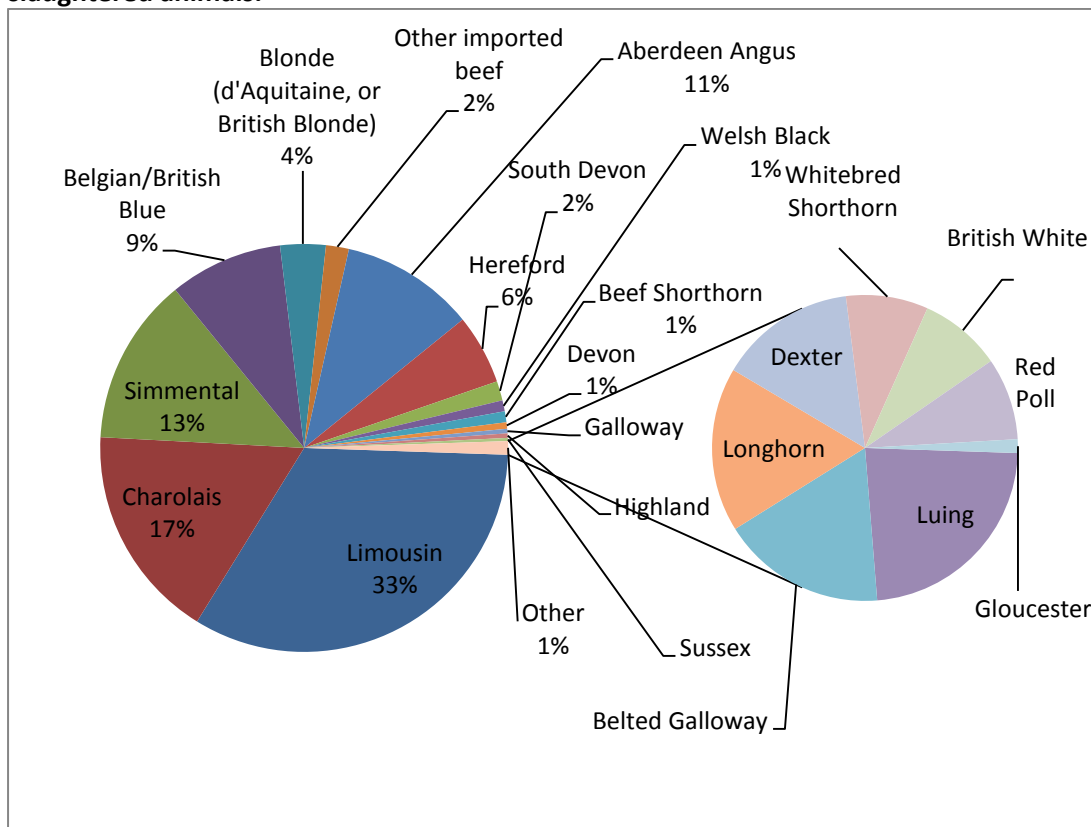
³⁷ Traditional Hereford Breeders' Club: <http://www.traditionalherefords.org>

Figure 3: Frequency distributions of ages of sires for non-dairy cattle breeds (see Fig. 2)



The dominance of the continental breeds in UK beef supply is very clear. Todd et al. (2011) found that breed genetic contributions were, from “imported beef breeds” 50%, from “native beef breeds” 14% and from “dairy breeds”, 36%. The percentage breakdown of the first two sets of contributions is illustrated in **Figure 4** (from unpublished data kindly supplied by Dr. Darren Todd). For clarity the values of the smallest contributions have not been distinguished.

Figure 4: Breed composition of the UK beef supply 2008, in terms of proportions of genes of slaughtered animals.



Against this background of the British native breeds supplying only a very small proportion of the total market, it is noteworthy that of the 142 beef herds participating in Signet recording schemes, 63 are of UK breeds (**Table 4**: February 2013 data kindly supplied by Mr. Sam Boon). Why some breeds are strongly represented in these schemes has not been formally reviewed.

Table 4: Number of herds of beef breeds in Signet recording, February 2013 (whole UK).

UK native breeds		Other breeds	
Sussex	45	British Blonde	7
Red Poll	7	Salers	4
Lincoln Red	6	Stabiliser	66
Highland	5		

Western and northern breeds

Breeds in this group are very diverse in function and in population status.

Chillingham

Although there is circumstantial evidence that selection was practised in the 19th century (a substantial proportion of bulls were castrated: Hall and Hall 1988), and the herd was reduced by about 50% around 1918, selective breeding has been avoided since then. For the present discussion the most interesting feature of the breed is its continued viability in spite of the genetic uniformity attributable to bottlenecks in its history (Ballingall et al. 2012; Hudson et al. 2012; Visscher et al. 2001), though this is probably not of relevance to the design of conservation strategies for FAnGR generally.

Dexter

Here, the low ratio of dams to sires and the low variance of female calves sired per bull may imply small herd size and/or a preference for natural service over artificial insemination (AI). The important distinction of a “traditional” non-introgressed type within the Dexter breed³⁸ was explored using molecular genetics by Bray et al. (2009).

Welsh Black

Demographic statistics for this breed are similar to those of beef breeds of similar numerical status. EBV bulls, which are on average 2.7 years older than others, have almost completely replaced non-EBV bulls as sires of registered males; non-EBV bulls have consistently been siring fewer female calves than have EBV bulls.

Highland

This breed, like the Dexter, has a low ratio of dams to sires. There is evidence of directional breeding - 39 of the bulls cited as sires in the 2008 herd book have EBVs and these sired on average 0.21 male and 5.92 female calves each, compared with 0.18 and 4.72 respectively for non EBV bulls.

Short-horned cattle

The Shorthorn has been an immensely influential breed not just in the UK. The histories of the Whitebred Shorthorn, Lincoln Red and Blue Albion trace back to the Shorthorn, but these are not

³⁸ Ark Spring 2003, p.7 The Ark is the journal of the Rare Breeds Survival Trust

parts of the Shorthorn breed as it is constituted today. The Beef Shorthorn has its own breed society and registration system.

Beef Shorthorn

This breed has a very high incidence of registration of male calves. Like the Hereford it is important as a crossing sire and there is evidence of the emergence of élite bulls.

Lincoln Red

This breed does not differ markedly from other beef breeds except in a remarkably low variance of age of sires of bulls. It is however of especial value for the current discussion because its registration data are particularly tractable and this has enabled introgression, in the last 60 years, from other beef breeds to be analysed.

The Lincoln Red was developed in eastern England from the Shorthorn, the breed society of the former being established in 1895 with an annual herd book being published subsequently. Links between the two breeds persisted such that some Lincoln Reds of dairy type were acceptable for entry into Coates Herd Book (the UK herd book for Shorthorns) and these were distinguished in the Lincoln Red herd book. From 1957 cattle of accepted Lincoln Red type derived from Aberdeen Angus (both black animals, and their red derivatives) and polled American Shorthorn cattle were used to introduce polling to the breed and from the early 1970s other beef breeds principally the Limousin were used in a breed development programme (BDP) to develop traits related to beef production. The regulations for these programmes are given in relevant volumes of the herd book.

Lincoln Red cattle tracing back to the introgressions are identifiable in the herd book by prefixes to their registration numbers. Animals without such a prefix are therefore to be seen as original (pre-polling) Lincoln Red cattle. The last such registrations were made in 1977 (male) and in 1980 (female). Animals lacking any of the prefixes that denote affinity to the BDP or subsequent introgressions are now known as Traditional Lincoln Reds and are recognized as a genetic resource of conservation significance.

English lowland cattle

The Hereford, like the Beef Shorthorn, has a clear function as a crossing sire and this is borne out by the large numbers of male registrations. Most of these bulls, as in the Beef Shorthorn, will be used in crossbreeding rather than in pedigree breeding.

The South Devon and Red Poll are very different in function from all three Hereford types, the former two being maternal breeds with rather low rates of registration of male calves. Indeed, the Red Poll Cattle Society has recently adopted a strategy that includes developing the milking attributes of the breed³⁹. This is one of the very few genetically hornless breeds of cattle with a dairy reputation⁴⁰.

2.3.1.2 Sheep

Population data for sheep are in Technical Appendix 3.

Breeding plans in UK sheep are most clearly understood with reference to the function of each breed in the crossbreeding systems that are the foundations of the sector.

³⁹ <http://www.redpoll.org/strategydoc.shtml>

⁴⁰ Though not identified as a prime welfare concern (<http://www.fawc.org.uk/pdf/dcwelfar-091022.pdf>) in some dairy systems the polled condition is highly desirable; this is a selling point for Norwegian Red cattle (<http://www.genoglobal.no>)

In sheep the traditional stratified crossbreeding system “survives and continues to evolve” (Pollott and Stone 2003) though in Scotland at least it is probable that a growing proportion of hill ewes are being mated with terminal sires (Rodriguez-Ledesma et al. 2011). The diversity within British hill sheep has become better appreciated (Jones and Bowles 2006).

The UK sheep industry showed rapid change from 1996 to 2003 mainly due to structural developments and some breeds changed spectacularly in recorded numbers (Table 6 of Pollott and Stone 2003). The percent genetic contribution of the different breed types to lamb carcass meat were as follows: hill 27%, crossing sire 15% terminal sire 47%, self-contained 12%. The dominant terminal sire breeds used in 2003 were Texel (100,350 rams) and Suffolk (93,900 rams) being mated to respectively 3.6 and 3.4 million ewes. While there is clear merit in genetic improvement to hill breeds the most cost effective route is to develop the terminal sires because a small number of individuals have a big impact on the final marketed product and this is illustrated by the initial concentration of the Scottish Sheep Strategy⁴¹ on promoting the use of terminal sires of high EBV.

Participation in Signet recording schemes is one indicator of a commitment to breed development, and in the context of this section of the report it is noteworthy how this is shown by the Shropshire and Southdown, native breeds which are not numerous (February 2013 data kindly provided by Mr. Sam Boon). Commercial breeds of foreign origin are tabulated for comparison (**Table 5**). Perhaps also indicative of an interest, among the keepers of the less numerically strong breeds, in computational approaches to selection for production characteristics, is the presence among the list of breeds represented in the BASCO system of the Leicester Longwool⁴², Border Leicester, Shropshire, Southdown and Wiltshire Horn. Data from these schemes can be used in research. For example Conington et al. (2013) used data from 70 Scottish Blackface flocks, over the period 1976-2011 to derive general principles for improving lamb survival.

Table 5: Numbers of flocks in Signet schemes (mean flock size in brackets).

Maternal breeds		Terminal sire breeds	
South Country Cheviot	1	Beltex	17(32)
North Country Cheviot (Hill)	1(106)	Berrichon du Cher	2
N.C. Cheviot (Park)	5(69)	Bleu du Maine	4
N.C. Cheviot (unspecified)	15	Blue Texel	4
Welsh Mountain	9(187)	Charmoise Hill	1
Beulah	5(120)	Charollais	68(71)
Easycare	7	Hampshire Down	62(25)
Romney Marsh	4	Ile de France	2
Scottish Blackface	19(145)	Rouge de l'Ouest	1
S. Wales Mountain	2	Meatlinc	7(168)
Hardy Speckle	1	Texel	215(51)
Wiltshire Horn	11(39)	Suffolk	74(55)
Crossing sire breeds		Shropshire	22(36)
Bluefaced Leicester	34(37)	Southdown	16(44)
Border Leicester	2		

⁴¹ <http://www.scottishsheepstrategy.org.uk>

⁴² Ark Summer 2006, p.21

Pollott and Stone (2003) also mention the willingness of sheep farmers to try “new” breeds – one such is the Easycare mentioned above.

The early years of this century saw an unanticipated development in the operation of breeding programmes in sheep. Imposed on the established routines of breeding for better performance (and in the case of breeds at risk, of breeding for genetic conservation), were requirements to select against genes apparently predisposing sheep to scrapie. This has had several lessons for the development and operation of conservation strategies. So too, but less directly, did the foot and mouth disease outbreak of 2001 which brought into focus the importance of demographic and geographic factors in planning conservation strategies (Bowles et al. 2004; Carson et al. 2009).

Some of the interactions between strong selection against scrapie-susceptible genotypes and other genetic processes have been studied. Earlier concerns that the *ARR/ARR* genotype was associated with poorer performance have been addressed (Moore et al. 2009), though relationships with atypical scrapie⁴³ and other health traits require further study (Sweeney and Hanrahan 2008). Effects on population genetic processes were not explicitly studied in the UK though special procedural measures were instituted for rare breeds (Townsend 2003a) and a modelling study was performed by Man et al. (2007). An extensive cryobank was established⁴⁴ which ultimately comprised 540,000 straws of semen from 75 breeds. Studies elsewhere highlighted the risks of this selection (Palhière et al. 2008; Windig et al. 2007)

The French equivalent to the UK scrapie plans was launched in October 2001. Backed up by a cryobank, the plan concentrated on strong selection within nucleus flocks with a view to their providing resistant rams to flocks lower down the pyramid (Palhière et al. 2008). Effects on genetic variability elsewhere in the genome were studied using pedigrees and neutral microsatellite markers, in four breeds representing a range of management systems. Neutral markers near the PrP locus were affected, but not those further away. Neither pedigree nor molecular data showed strong bottleneck effects attributable to the scrapie plan, but in the two breeds in which concurrent selection for production traits was strongest there was evidence of reduced genetic variability.

The Dutch scrapie-eradication programme started in 2002 and involved only *ARR/ARR* rams being allowed to breed. Special provisions were made for rare breeds with few *ARR/ARR* rams which were allowed to use rams of less resistant genotypes provided they set up special breeding programmes for both scrapie eradication and restriction of inbreeding. Using population data from the rare Mergellander sheep, Windig et al. (2007) showed that the use of *ARR* homozygotes and heterozygotes was consistent with restriction of inbreeding, if optimum contribution methodology were used. However it is not reported whether any breeders actually took advantage of this concession, the evidence was that breeders used the relatively scarce *ARR* rams that were available.

A complete tabulation of basic population data for all native sheep breeds is given in the UK Country Report⁴⁵. Those considered in the present report are (a) breeds at risk for which population data are obtainable; (b) breeds for which formal breeding plans are known to exist; (c) certain breeds not at risk for which a more detailed demographic analysis can help to elucidate general principles.

Outline registration data only are given here. The full dataset has been used to develop procedures for use in assessment of conservation status and the formulation of strategies and this work is described in the Conservation Strategies section of the report.

⁴³ <http://www.defra.gov.uk/ahvla-en/disease-control/notifiable/scrapie/>

⁴⁴ Ark Spring 2009, p.7

⁴⁵ <https://www.gov.uk/government/publications/uk-country-report-on-farm-animal-genetic-resources-2012>

Maternal breeds

These breeds of sheep tend to be fairly, or very, numerous and are also noted for their local adaptations (Carson et al. 2009; Jones and Bowles 2006). Genetic improvement is less of a concern here than, probably, in any other sector of commercial FAnGR, yet economic benefits can be derived through selective breeding (Simm 1998).

The Devolved Administrations are prominent in this activity⁴⁶. In addition to those in **Table 5**, breeding programmes are also in operation in Wales for the Llandoverly Whiteface (recording scheme since 2002); Tregaron (sire reference group since 2001) and the Brecknock Hill Cheviot (recording programme in operation). The last named breed is in a marketing partnership with Marks & Spencer⁴⁷. For the Beulah and Hardy Speckle, there have been HCC sire reference groups since 1979 and 1999 respectively, and for the South Wales Mountain a sire reference group is also active. For Welsh Mountain there are local group breeding schemes, including the CAMDA scheme started in 1976. In Scotland, maternal breeds were the subject of the Highlands and Island Sheep Strategy (HISS), which was set up in 1998 by the Blackface Sheep Breeders Association, the North Country Cheviot Sheep Society, the Meat and Livestock Commission, and Highlands and Islands Enterprise. This was part funded by SERAD and the European Commission⁴⁸. Later, Lleyn and Shetland sheep were included. The successor to HISS has been the Scottish Sheep Strategy of Quality Meat Scotland⁴⁹. It is available to all sheep producers and breeds in the country and will encompass more sheep breeding technologies than previously.

North Country Cheviot

This breed is of particular interest for analysis of breeding plans because of the tractable nature of its registration data and because within it two sectors exist – the Park and the Hill flocks. These are found in, respectively, comparatively benign and comparatively harsh environments. Within the former, breeding plans might be expected to focus more on market factors while in the latter, emphasis might be expected on traits relating to survival. Park flocks number 179 with a total of 11957 ewes (mean flock size 67 ewes). Hill flocks number 172 with 59528 ewes (mean 346 ewes).

The two sectors differ in overall structure, in participation in breeding programmes, and in the usage of rams for which performance EBVs are available (**Table 6**).

Table 6: Comparison of management practices in North Country Cheviot (Park and Hill) flocks.

(a) Participation in breeding programmes

Scottish Sheep Strategy	Park: 6 flocks Hill: 8 flocks
Welsh Sheep Strategy	Park: 3 flocks
Performance recorded	Park: 11 flocks Hill: 4 flocks

(b) Median number of ewes put to each ram ($p < 0.001$, Mann-Whitney test)

Park flocks	20.0
Hill flocks	39.2

⁴⁶ Details of the Welsh programmes are given in http://hccmpw.org.uk/publications/breed_improvement/sheep_breed_groups_factsheets

⁴⁷

<http://producerexchange.marksandspencer.com/sites/default/files/fields/file/Brecknock%20Hill%20Cheviot%20Group%20case%20study.pdf>

⁴⁸ <http://www.scottish-blackface.co.uk/blackface-sheep-information.cfm?InfoID=4>

⁴⁹ <http://www.scottishsheepstrategy.org.uk>

Table 6: continued

(c) Source of rams

	Park	Hill
n homebred rams (%)	57 (12.6%)	397 (33%)
n flocks using homebred rams (%)	36 (20%)	57 (33%)
n flocks using rams with published EBVs (%)	32 (18%)	6 (3%)

(d) Comparison, between Park and Hill flocks, of sources of rams

	Park flocks	Hill flocks
n rams used that were bred in "EBV flocks"	264 (59.5% of all rams)	88 (11.6% of all rams)
n ewes to which these rams were put	6820 (60.5% of all ewes)	3737 (9.9% of all ewes)

The influence of flocks which have bred EBV-rated rams may also make itself evident through provision of rams which do not themselves have EBV values, but which presumably have some degree of superiority by virtue of a genealogical relationship.

Scottish Blackface

The Lewis strain of Scottish Blackface, documented by Munro (1962) seems no longer to be distinguished, although the (conserved) Boreray is presumably related to this strain. Jones and Bowles (2006) draw attention to the differences between the Newton Stewart or Galloway type, and the Perth, Lanark and Northumberland types. Crossing the Scottish Blackface with the Swaledale (and other breeds) has been shown experimentally by Annett et al. (2011) to be advantageous⁵⁰ and, learning from history, there is probably a case for keeping the progress of introgression and of crossing among Blackface strains, under review. As with all breeds where individual females are not registered, demographic information is very incomplete and flock-by-flock surveys are the only reliable source of information.

Other hill breeds

Of 317 Dalesbred rams registered in the 2009-2010 flock book, 38 (11.9%) were homebred, i.e. the progeny of a homebred sire and/or a homebred ewe. For the Herdwick in the 2012 flock book, 66 of the 309 ram lambs registered (21.4%) for whom flock of sire was given, were from homebred rams. Of 57 flocks where the deduction was possible, only 4 registered only ram lambs sired by homebred rams, 40 registered only ram lambs by bought-in rams and the other 13 registered ram lambs some of which were by homebred and others by bought-in sires. For the South Country Cheviot, of 94 rams recorded in the 2010 flock book as having been used, 35 (37.2%) were homebred. These differences in the use of homebred rams are clearly expressions of breeding policy. Conceivably the use of home-bred rams implies a desire to maintain or enhance local adaptation of a hefted flock.

Crossing sire breeds

These breeds, pivotal in the stratified breeding system, are showing rapid changes in numbers. The Teeswater and Wensleydale, historically famous as the sires of the Masham crossbred, have found new roles as purebreds while the Border Leicester has contracted in numbers, being added to the RBST Watchlist in February 2013⁵¹.

⁵⁰ see also <http://www.afbini.gov.uk/sheepbooklet.pdf>

⁵¹ <https://www.rbst.org.uk/rbst-announces-watchlist-2013>

In spite of the importance of these breeds, population studies are effectively non-existent (but see Young and Purser 1962).

The Border Leicester and Bluefaced Leicester have had sire reference groups in Wales since 1990⁵².

Terminal sire breeds

Many of these breeds are descended from the Southdown which itself has an interesting recent history illustrating many of the general features of breeding plans.

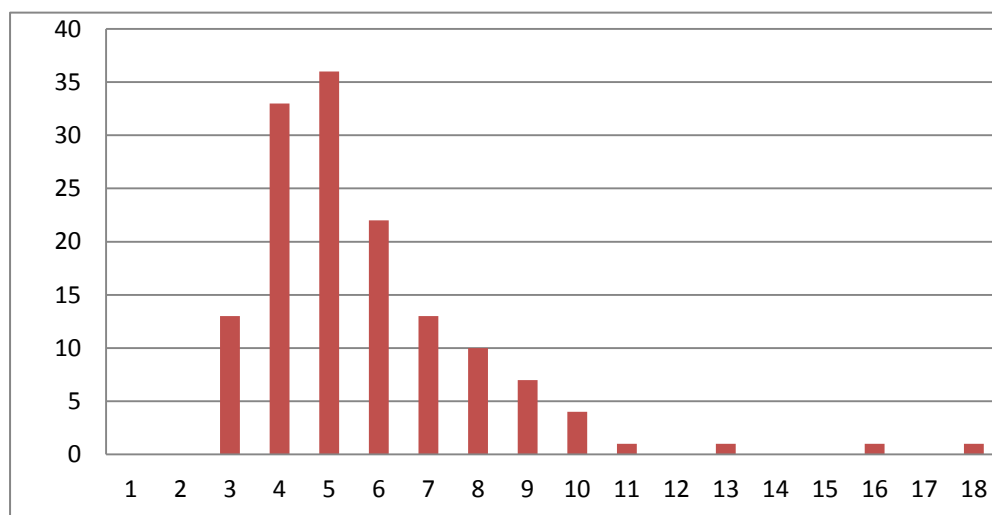
Southdown

This breed provides one of the few examples of the pedigree consequences of introgression. Pedigree analysis showed (Hall 1989b) how introgression of New Zealand and French Southdowns took place. In the late 1960s the breed was in decline (5475 ewes in 1957, 1202 in 1985) and in order to modernize the growth rate and conformation 10 rams were imported between 1966 and 1980, and there have been subsequent importations that have not been analysed formally. Many pedigree offspring were sired by these 10 rams – 392 males and 374 females. Only 42 of these sons were put to ewes in pedigree breeding, but they were intensely used, siring 468 males and 553 females. As a result, the New Zealand influence spread very rapidly through the breed. A sample of 68 rams, namely those that sired ram lambs in the 1985/86 flock book, was analysed; of these, 53 had some French or New Zealand ancestry.

Hampshire Down

In 2011, 142 ram lambs by 100 sires were registered. All sires were in the BASCO/Egenes system so a very high usage of EBV rams was likely. The oldest sire used was born in 1994 implying use of frozen semen in this breed. The ways ram lambs were distributed among sires of different ages is illustrated in **Figure 5**.

Figure 5: Hampshire Down sheep, 2011 registrations. Numbers of ram lambs born to sires of different ages (years). Median age of sire 3 years



Self-contained breeds

This group includes several of the rare and formerly rare breeds some of which have acquired distinct roles in the rural economy. The breeds at risk are considered in more detail in the Conservation Strategies section of the report.

⁵² http://hccmpw.org.uk/publications/breed_improvement/sheep_breed_groups_factsheets

Poll Dorset and Dorset Horn

Of 405 ram lambs registered in the 2012 Flock Book, 30 were classed as Dorset Horn and the rest as Poll Dorset. Of the 405 lambs, only 76 were sired by rams from flocks which had had no animals represented in the BASCO/Egenes database. It appears therefore that 81% of ram lambs are bred in flocks which take part in EBV-based improvement schemes.

2.3.1.3 Goats

Population data for goats are in Technical Appendix 4.

In 2005 the UK population of farmed goats was estimated at 88,000-93,000 (Anon 2005). Pedigree breeding is overseen by the British Goat Society⁵³ with nine Sections (registers) in its herd book. Three of these registers are closed, meaning that upgrading is not permitted (**Table 7**). The Bagot goat has its own breed society and registry, after many years in the RBST Combined Flock Book system.

The English goat is being bred as a utility goat and does not have a formal register. The only feral population to be recognized as a breed is the Cheviot goat. Paradoxically, and because of the absence of grading programmes, it is the Toggenburg and Saanen rather than their British eponyms that are of conservation significance in the UK (along with the Golden Guernsey and Bagot).

Goat dairying

Goat dairying in the UK satisfies about 35% of the market and is practised on a fully commercial scale by perhaps 45 herds, averaging 900 head (Anon 2008).

While the herd books of the British Goat Society devote considerable space to accounts of championship milk yields, this does not approach the scale of dairy goat recording in France where every year about 40 young bucks per breed enter progeny testing and, in 1996, 60,000 goats were artificially inseminated and 290,000 were officially milk recorded (Leboeuf et al. 1998). Genetic studies have recently been initiated in the UK (Mucha et al. 2013).

Table 7: Breeds overseen by the British Goat Society.

Register	Upgrading?	Outline history
Anglo-Nubian	yes	Originated from crosses of English goats with dairy goats from Middle, Near and Far East, first named in 1893
British	yes	Registered, eligible for upgrading
British Alpine	yes	Developed in UK, varied origin
British Guernsey	yes	Breed being formed by crossing Golden Guernsey bucks on females of other breeds
British Saanen	yes	Developed in UK with Saanen influence
British Toggenburg	yes	Breed being formed by crossing Toggenburg bucks on females of other breeds
Golden Guernsey	no	First imported to UK from Guernsey in 1965
Saanen	no	Imported from Netherlands in 1922, subsequent importations 1965, 1993, 1997/98
Toggenburg	no	First in UK in 1882, subsequent importations 1922, 1965, 1993

⁵³ <http://www.allgoats.com>

Fibre production

The diversity of natural fibres was celebrated under the leadership of FAO in 2009 which was the International Year of Natural Fibres⁵⁴. Cashmere is the valuable fibre undercoat found to varying degrees on all goats except for Angora, whose product is mohair (Angora wool comes from the Angora rabbit not from the Angora goat). These fibres differ in such aspects as softness, ability to take up dyes, and insulation properties. Fibre diameters are, cashmere: < 19 microns; mohair: 25-38 microns; angora wool 14-16 microns. In the 1980s particularly, large numbers of feral goats (which still retained the cashmere character lost from the dairy breeds) were taken from the wild mainly in southwest Scotland to build up cashmere herds. The genetic basis was extensively characterized (Bishop and Russel 1994). About 50 producers operate in the UK with 2,500 goats in total (Anon 2005); Angora herds bring the total number of fibre goats up to 10,000 (Little 2010). The British Angora Goat Society operates a sire reference scheme (Anon 2005).

Meat production

Goats are raised specifically for meat in a variety of extensive or indoor systems. These are usually Boer or Boer cross and in 2009, 9,547 went through UK abattoirs (Little 2010). The Boer goat is from South Africa and the first of several importations to the UK was in 1987. The British Boer Goat Society⁵⁵ published its 22nd herd book in 2011, with more than 200 herd prefixes being registered.

2.3.1.4 Pigs

Population data for pigs are in Technical Appendix 5.

Pig production systems are very diverse in Europe, with 84 effectively distinct systems being identified in 23 countries (Bonneau et al. 2011). This diversity can be explained in terms of the relative emphasis placed on defining features of pig industries. In the UK, systems emphasizing welfare, eating quality and organic husbandry are prevalent; those emphasizing environmental compatibility, regional associations and product quality, less so.

In pigs, highly competitive hybrid lines are supplanting the British Landrace and Large White, while specialist markets in the once rare, now minority, breeds, have developed. Illustrating how breeding plans and conservation strategies can interact, Gourdine et al. (2012) simulated scenarios of breeding in a “small local” pig breed (35 herds each of 24 sows) using optimum contribution selection methodology whereby a substantial genetic response could be expected with an acceptable level of inbreeding.

The UK pig population is now (March 2013) lower than at any time since easily accessible records began in 2000⁵⁶. Whether there will be differences between the minority and rare breeds and the major commercial genotypes in their responses to this, remains to be seen. Certainly there have been very great numerical changes in the breeds which only a few years ago were indisputably in the mainstream – the pedigree Large White and British Landrace (**Figures 6 and 7**).

The UK pig industry needs to be aware of societally important aspects such as meat quality and safety, welfare and health of animals, and the environmental impact of husbandry. Most animal traits relevant to these seem to be heritable and although they may not all have a monetary value they can be included in a selection index and assigned breeding-goal weights (Kanis et al. 2005).

⁵⁴ <http://www.naturalfibres2009.org>

⁵⁵ <http://www.britishboergoatsociety.co.uk>

⁵⁶ <http://www.npa-uk.org.uk/Pages/LionsDen.html>

Figure 6: Large White pedigree pigs (registered with BPA). Changes in numbers of registrations, sires and dams

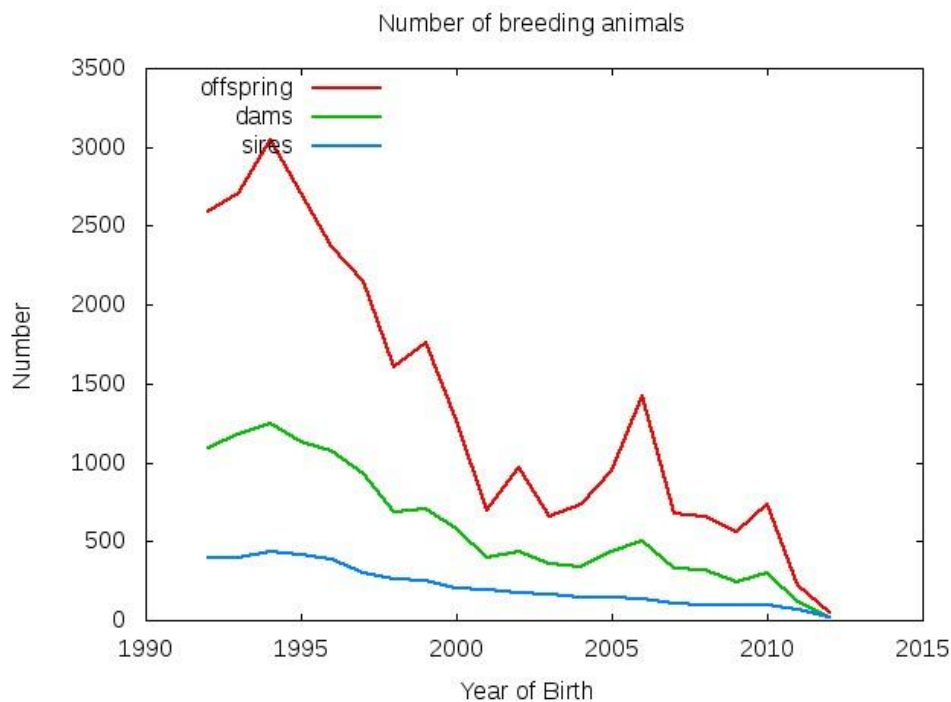
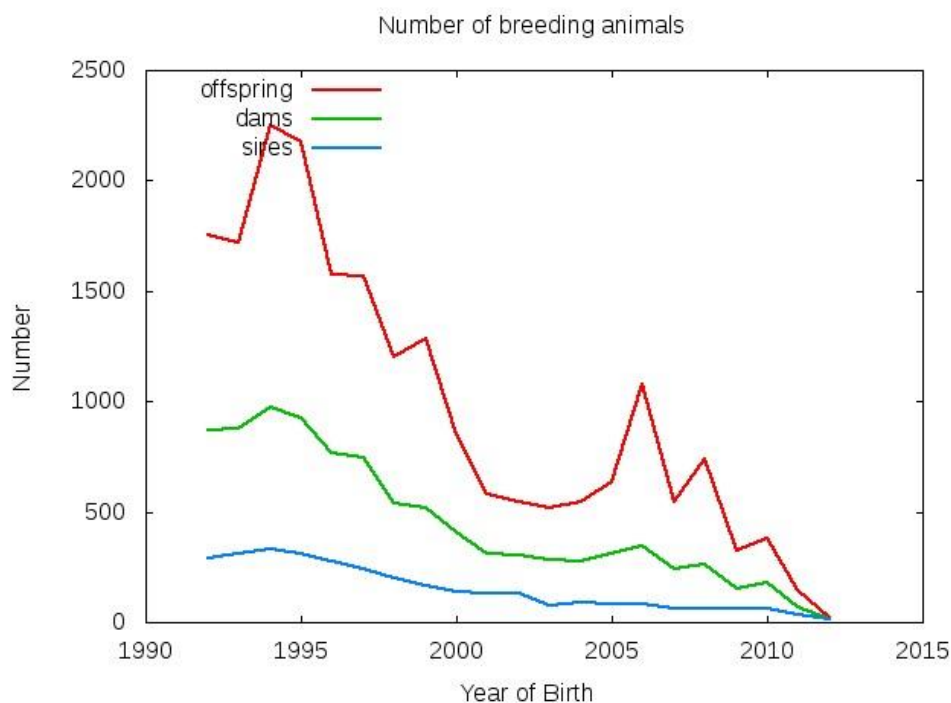


Figure 7: British Landrace pedigree pigs (registered with BPA). Changes in numbers of registrations, sires and dams



Discussion of breeding plans in pigs is hampered by the secrecy imposed by breeding companies. In the last 20 years there have been quite extensive changes in the population structures of the native pig breeds at risk. For some breeds there are new markets for speciality pigmeat products, while for others notably the Large White, British Landrace and Welsh, long-established markets for commercial breeding pigs have been lost to hybrid strains, the Large White being added to the RBST

Watchlist in February 2012⁵⁷. Some comparisons are possible between 2010 and 1979-85 using the data of Hall (1989a) and Walters (2012) on three breeds (**Table 8**). Here, generation interval is the mean number of years between birth of the parent and birth of the offspring.

Table 8: Population data for three native pig breeds: changes over 25 years.

	Berkshire		Large Black		Middle White	
	1979-85	2010	1979-85	2010	1979-85	2010
Number of herds registering	19.7 (mean)	234	17.1 (mean)	163	13.4 (mean)	133
Sows/herd	1.97	3.40	2.63	2.87	2.0	3.86
Boars/herd	0.99	0.93	1.38	0.78	1.23	0.90
Total boars	19.6	101	23.6	57	16.6	52
Total sows	38.9	795	45.1	467	27.0	513
Generation interval (boars)	1.73	3.76	1.96	2.91	1.75	3.03
Generation interval (sows)	2.13	3.56	2.76	3.16	2.16	3.40

The figures for 1979-85 are not dissimilar for those in a Spanish conservation herd of Guadyerbas pigs which during the period 1945-1998 averaged 13.6 male and 42.0 female parents, with a generation interval of 2.45 years (Toro et al. 2000). Over the whole period inbreeding was calculated as accumulating at 1.21% per year.

Today, most herds are small but in each breed there is a small number of large herds. In 2010, numbers of herds with 20 or more sows were as follows: Berkshire 2, Large Black 1, Middle White 3, Welsh 9. Numbers of herds with 5 or fewer sows were: Berkshire 195, Large Black 140, Middle White 114, Welsh 85.

Breed comparisons

British Saddleback

This breed was the result of the amalgamation in 1967 of the Essex Saddleback and the Wessex Saddleback, two breeds with widely separated distributions though no reported contemporary evidence of genetic affinity. At least 20 generations of pig breeding have passed since then. Wilkinson (2011) showed by pedigree analysis that the Essex and Wessex types are not now separable within the breed, but analysis of microsatellite DNA distinguishes a genotypic cluster of animals whose ancestry traces back to the Rainbarrow herd. These are significantly more inbred than the others. Implications for conservation are discussed in the Conservation Strategies section of the report. In relation to breeding plans, this study confirms earlier findings (Hall 1989a) that traditional pig breeds differ in the degree of genetic isolation among breeds, and provides a caution against presuming that breeding plans are uniform within this group of livestock.

2.3.1.5 Equines

Population data for equines are in Technical Appendix 6.

A comparative study does not appear to have been made of breeding plans in those breeds of horses that qualify as UK native breeds at risk. As a species the horse is of low fertility (Bruck et al. 1993) and a study of two contrasting breeds of Finnish horses concluded that breeding for fertility was “not the primary improvement option” (Sairanen et al. 2009). Dell (2010) suggested that when the

⁵⁷ <https://www.rbst.org.uk/rbst-announces-watchlist-2013>

Cleveland Bay became established in 1884 high levels of inbreeding and genetic bottlenecks were already compromising the viability of the breed. In contrast, Calder (1927) suggested that in the Clydesdale early inbreeding was avoided because of the presence of harmful recessives; later, in the 1920s, many foals were inbred to a small number of elite stallions. However, in at least some horse breeds, some traits still possess considerable genetic variation and it is predicted by Gómez et al. (2012) that Spanish heavy horse breeds could respond to selection for conformation traits, and this was shown by Druml et al. (2008) for the Austrian Noriker breed. In the UK, there will probably be selection for excellence in traits that will win prizes at such events as the annual Spring Shire Horse Show, which typically attracts at least 200 entries. In at least some breeds, aspects of gait (and presumably, therefore, of “showiness”) are heritable (Cothran et al. 1987).

A clear-cut and simple breeding plan is that applied to Fell Ponies, in order to deal with foal immunodeficiency syndrome (Fox-Clipsham 2009; Fox-Clipsham et al. 2011). The counselling on offer is to avoid carrier-carrier matings. The breed is too rare for carriers to be excluded from breeding altogether.

2.3.1.6 Poultry

Breeding plans operated by companies are commercially confidential. There have been some publicly funded breeding programmes relating to poultry, for example the application of genetic modification to produce chickens that cannot disseminate avian influenza (Lyll et al. 2011). The focus of this research on inhibiting transmission is an illustration of the principle (Bishop et al. 2010) that different approaches are needed for endemic diseases, such as salmonella, and for epidemic diseases. However, these are not strictly relevant to genetic conservation.

Breeding plans operated by individual poultry keepers have a very strong conservation element and are considered in the Conservation Strategies section of the report

With poultry it is particularly important to have a global overview of breed diversity because of the globalization of breeding activities. Muir et al. (2008) identified a serious lack of rare alleles in commercial birds and emphasized the potential importance of “non-commercial and ancestral populations”. In a simulation approach they used SNPs to create a “hypothetical ancestral population” and calculated that present-day commercial broilers had lost 60-70% of the alleles present in that population. However, inbreeding has not been an issue and is manageable, populations continuing to respond to selection. A major cause of allele loss was the use of only a limited number of breeds when the commercial lines were originally formed, though as Neeteson-van Nieuwenhoven et al. (2013) point out, most of the loss would have been when the breeds were formed and in subsequent inbreeding.

Muir et al. (2008) also found that the proportion of the genome under selection is very small and that mutations would be expected to replenish QTLs. The value of currently non-commercial stocks is conceivably in providing alleles of large effect conferring resistance to new and emerging diseases (Cheng 2010). Another valuable genetic resource could be control lines such as those that Aviagen has retained for 3 current broiler crosses (Laughlin 2007; this company now has more than 30 lines whose purpose is conservation of genetic variation, according to Neeteson-van Nieuwenhoven et al. 2013).

There are fundamental difficulties with the use of a “backyard breed” as a source of genetic variation for commercial production and these are considered in the Conservation Strategies section. From the viewpoint of breeding companies many problems can be avoided by the use of techniques such as the commercial sibling trial (Neeteson-van Nieuwenhoven et al. 2013). Here, the nucleus population is maintained in biosecure conditions while siblings are kept in non-secure commercial husbandry. Data from the latter are used to guide the selection of the nucleus population.

2.4 Breeding plans: summary of findings

- Breeding plans are the systems whereby genetic improvement is achieved in livestock. The principal tools are the establishment of a genetic basis, the recording of performance of individuals and their family relationships, and the selective mating of individuals to produce animals of optimized genotype.
- Breeding plans are long term but the contexts within which they operate may vary from region to region and change from year to year. Breeding plans are heavily influenced by the economic context and are now having to take account of the social and political environments. Productivity has always been an important objective, to which welfare and health have been added in recent years, and now ecosystem service and environmental footprint issues are becoming of interest.
- For livestock systems to be able to adapt rapidly, access to a wide range of breeds is essential.
- Breeding plans are partnered by mating systems whereby different breeds are mated in the process of crossbreeding.
- Livestock in the UK is in the private sector and for the most part is highly fragmented, so breeding decisions are taken by owners and managers, and there is a mature system of stakeholder bodies, industry platforms and support networks funded by levy and the taxpayer.
- There is increasing awareness of genetic issues and better information and tools all of which facilitate genetic management and, in principle, monitoring. However, commercial confidentiality constrains the extent to which genetic status and trends can be assessed, especially pigs and poultry
- The basic population data for specific livestock breeds presented in this report provide previously unavailable benchmarks for practical use, which are elaborated and discussed further in the Conservation Strategies section of the report.
- Breeding plans and conservation strategies are not separable. Each automatically includes elements of the other. This is particularly evident in cattle, where in several breeds, directional selection for commercial attributes coexists with the maintenance of traditional strains.
- In sheep, breeding activities aimed at improving performance are widespread, though most intense in a small number of breeds that perform particular key functions within the system and where improvement is most immediately cost-effective. Selection for local adaptation is evident in several hill breeds.
- In goats, crossbreeding is particularly significant because of the benefits to milk production, though breeds specialized for fibre and meat are important.
- With pigs, the breeding plans operated by companies are commercially confidential though inferences can be drawn about breeding plans in the non-corporate minority and native breeds sectors. Currently the sector is under intense economic pressure.
- Breeding plans as they operate in equines and in non-corporate poultry are almost entirely of conservation orientation and are considered in the Conservation Strategies section of the report.
- Crossbreeding, if properly managed, enables FAnGR to be utilized sustainably, in the case of the rarer breeds principally through the use of commercial sires for production of marketable crossbred young stock. This can be a useful adjunct to the development of niche markets for the purebred progeny.
- There is a fundamental tension between a) desire of breeders for introgression to maintain or improve breed quality and b) the need to conserve original stocks. A range of responses to such

situations is found in practice. Transparent and consistent pedigree registration protocols are a necessity for sustainability.

- Exploitation of within-breed genetic variation runs the risk of accidental loss of genes which do not happen to feature in the selection process; such genes may be of potential value. The use of EBVs has become much more widespread and although this facilitates the use of genetic resources, it could also lead to inbreeding through excessive use of animals of high genetic merit.
- Poorly planned breeding programmes can also lead to avoidable and unnecessary increases in inbreeding, and reduced overall effectiveness of the programme. The science underpinning the management of these risks is well established and the software for managing genetic improvement can itself be used to limit the accumulation of inbreeding. However these programmes are not generally accessible by non-specialists.
- Ideally, monitoring of the effects of breeding programmes on genetic conservation of FAnGR would be done by interrogating a centralized database, but until such a database can be achieved a practicable approach is by drawing inferences from data in published flock- herd- or stud books. Such data can yield estimates of several parameters which are key to genetic conservation, namely: numbers of sires, generation length (both to be maximized in the interests of conservation), and measures of the variabilities in numbers of breeding offspring produced by parents (to be minimized). These all influence the rate of increase of inbreeding and contribute to the determination of effective population size, though methods are yet to be refined.
- This study has assembled new data on demographic parameters; their value and practical application for monitoring are described in the Conservation Strategies and Best Practice Guidance sections.

3 Review of Conservation Strategies

3.1 The context of conservation strategies

FAnGR pose special problems for their conservation. The UK has international commitments to conserving its FAnGR, and under the terms of the CBD, of making them available and deriving benefits from them. There is a real and urgent interest in the formulation and supervision of conservation strategies even though the FAnGR themselves are in private, or corporate, ownership, and their governance reposes in autonomous breed societies. The UK Government is, effectively, answerable to the global community for the conservation of UK FAnGR, and much of the direction of livestock policy is within the purview of the devolved administrations.

Not only does the UK Government hold this responsibility, the nature of the responsibility is not of its own making in that the fundamental strategy was settled at least two decades prior to the CBD. Conservation of biodiversity can be *in situ* (where life forms are maintained in their respective habitats) or *ex situ* (maintenance in managed conditions such as zoos, botanical gardens or, as germplasm, in frozen storage). In the UK, *in situ* conservation is the favoured overall strategy with *ex situ* conservation being seen as a supplement, not an alternative; this was effectively a strategic decision taken by the private sector pioneers of UK FAnGR conservation. Elsewhere in the world, or perhaps in the specific case of livestock being kept as research or development populations (Woolliams 2004; Silversides et al. 2012) this balance between *in situ* and *ex situ* conservation is a strategic decision to be taken in the light of local circumstances.

The primacy of *in situ* conservation in the UK context means that demographically viable populations of living animals must be maintained, often in commercially unfavourable circumstances. In terms of conservation biology theory and practice, FAnGR conservation has to take account of both the “declining population paradigm” (where the challenge is to manage and reverse population decline and where practice is abundant and theory sparse) and the “small population paradigm” (relating to effects of numerical smallness on viability, where practice is scarce and theory abundant). This duality (Caughley 1994) is reflected very clearly in UK FAnGR conservation. Here, maintenance of population sizes is predominantly a practical activity that owes more to policy than to theory, and there are practical issues of breed conservation where theory can be effectively applied.

Genetics is the theoretical underpinning for the management of FAnGR, but this knowledge has not been easy to apply. Data on individual animals, whether relating to numbers and locations of animals (essential for demographic management) or their pedigrees (essential for genetic management) are, like the animals themselves, in private ownership, and often either unobtainable or intractable. In the absence of adequate knowledge, detailed strategy cannot be formulated and the most practicable general approach is the provision of an enabling environment with monitoring of outcomes and the generation of information that can be used for auditing and dissemination of best practice. The importance, Europe-wide, of FAnGR support being flexible and adaptable to local situations was shown by Gandini et al. (2010).

A number of instruments are available to encourage breeders and their societies to operate in ways which enable the UK Government to discharge its international responsibilities. Rural development support is one such instrument, though its mode of operation differs among the countries of the UK. Another is European zootechnical legislation, whereby official recognition of a breed society may depend on its modes of operation meeting approval. This legislation is expected to be “recast” during 2013⁵⁸. A review of how FAnGR conservation operates in the UK, and how this can be improved, is therefore timely as it may be able to contribute to this recasting process.

⁵⁸ <https://www.gov.uk/government/publications/uk-country-report-on-farm-animal-genetic-resources-2012> page 52

In the UK the appropriate strategic framework, building on the activities that are already established, is a National Action Plan (Roper 2004). UK Government actions in the realm of FAnGR conservation are all consistent with the overarching strategy being more accurately described as a policy; of providing an enabling environment in which private FAnGR conservation initiatives can flourish and the UK Government be helped to show how it is discharging its international obligations for biodiversity. On that basis, this section of the report considers how such an environment can be maintained and how the outcomes can be monitored.

3.1.1 Policy context

Under the Common Agricultural Policy (CAP), Pillar I of CAP effectively, though indirectly, provides a support system for breeding plans by virtue of its promotion of agricultural production, while Pillar II can be seen as supporting conservation strategies, because it now has a degree of functionality in relation to enacting the EU Biodiversity Strategy.

Action 10 of the EU Biodiversity Strategy to 2020, which aims to “Conserve Europe’s agricultural genetic diversity” is as follows: “The Commission and Member States will encourage the uptake of agri-environmental measures to support genetic diversity in agriculture and explore the scope for developing a strategy for the conservation of genetic diversity”. Action 20 aims to “Regulate access to genetic resources and the fair and equitable sharing of benefits arising from their use”.

In principle, the CAP with its facility for modulation should enable conservation of flora and fauna, and of agricultural genetic resources, to proceed in parallel. England has supported Native Breeds under the Higher Level Stewardship scheme (Natural England, 2008) which has explicit linkages between environmental and FAnGR conservation support. The Scottish, Welsh and Northern Irish devolved administrations have counterpart schemes which also have linkages to environmental conservation⁵⁹ though these do not support the range of breeds eligible in England. Elsewhere in the EU, support for native breeds is independent of participation in environmental conservation (Small and Hosking 2010). In the UK, this has disqualified non-grazing livestock (i.e. pigs and poultry) from support under agri-environment schemes. Indeed, a “potentially unclear demarcation between this [870/2004] Community Programme and the Rural Development policy” was highlighted in the June 2012 independent report on the Programme⁶⁰.

The effectiveness of European agri-environment schemes might be debated (Whittingham 2011). Unfortunately data are lacking on how many animals of which breeds are supported under the UK schemes but in England alone there are over 1100 agri-environment agreements in operation where native breeds at risk are being supported.

EU policy has been to support research into aspects of FAnGR conservation. Relevant projects, past and present, are listed in Technical Appendix 7. Outputs of particular relevance to this report are cited individually in the text.

3.1.2 Regulatory context

Under the Zootechnical Standards (England) Regulations 2012⁶¹, recognized breed societies are expected to be able to prove they have the capacity to perform, among other functions, the following⁶²:

⁵⁹ summary and comparison: <http://www.assemblywales.org/11-012.pdf>

⁶⁰ http://www.rfp-europe.org/fileadmin/SITE_ERFP/EU/870_evaluation_01062012.pdf

⁶¹ <http://www.legislation.gov.uk/uksi/2012/2665/made>

⁶² <http://www.defra.gov.uk/fangr/files/ZootechRegsGuidanceNov.pdf>

to possess “a sufficiently large herd to carry out a breed improvement programme, or ... to preserve the breed where this is considered necessary”;

to be able to “make use of the livestock performance data necessary for carrying out their breed improvement or preservation programme”;

to “have a set of rules covering the definition of its breeding objectives” (Defra guidance is that selection can be “to preserve the breed and to maintain certain characteristics of the breed”).

The Regulations as they currently exist are not hostile to breed conservation, but the apparent requirement for both males and females to be registered makes their application to many UK breeds, particularly hill sheep, problematic.

3.1.3 Overseas and international organizations

The international policy background and context of UK FAnGR activities has been reviewed (Small 2013). The European Regional Focal Point (ERFP)⁶³ merits further consideration because it is a major forum for policy makers.

Setting the context of the ERFP, Martyniuk (2004) describes the history of breed conservation from a pan-European perspective. The first activities were at national level with several government initiatives and, in the UK, the formal establishment of the RBST in 1973. In 1979 the Nordic countries began to organize and coordinate regional activities and the next year, following recommendations from FAO, the EAAP established a working group to carry out breed surveys which led to the European Animal Genetic Data Bank.

In 1993 FAO’s Global Strategy for Management of Farm Animal Genetic Resources invited countries to establish National Focal Points and to nominate National Coordinators. Most countries have followed FAO guidelines to establish advisory committees for FAnGR. Since 1995 a network of National Coordinators has operated, as a clearing house for information and experience.

Since 1998 this informal regional co-ordination has been elaborated into a European Regional Focal Point, funded by government donations. The ERFP has promoted regional activities including the EC-funded project EFABIS⁶⁴ which has helped to develop national databases and to facilitate information transfer. Through a Working Group and Task Force system ERFP has produced reports on issues such as the status of AnGR within national agri-environment measures, access and benefit sharing, risk status and indicators. Its priority activities can be briefly summarized as follows:

- Characterization and inventory, and monitoring of trends and associated risks,
- Sustainable use and development,
- Conservation,
- Policies, institutions and capacity building.

3.1.4 Institutional context

The policy and institutional frameworks encompassing FAnGR within the UK have been reviewed (Small 2013). The ERFP network provides the means for comparisons with the frameworks that apply in other countries and Small and Hosking (2010) summarize the different ways in which Rural Development Programme funding has been secured for FAnGR conservation.

Within Europe the institutional framework for FAnGR shows considerable differences between countries and even within countries, as would be expected when regions have a degree of autonomy in relation to rural policy. Thus for example in Italy of the twenty regions, only six mention FAnGR in

⁶³ <http://www.rfp-europe.org>

⁶⁴ Technical Appendix 7; also <http://efabis.tzv.fal.de/>

their Rural Development Plans. Examples from overseas can provide valuable insights into how FAnGR conservation might be put into effect, and these are discussed at relevant points in this section of the report, but in many cases the institutional environments are so different from what applies in the UK that the comparisons are rather limited in their applicability. For example in Spain, from 1995 an extensive five-year programme operated in Spain, with funding from the European Agricultural Guidance and Guarantee Fund (total: equivalent to £10.3 million) to support the conservation of 55 breeds; approximately £37,000 per year per breed (Vega et al. 1997). In Ireland, the Kerry Cattle premium scheme is of interest for many reasons, including the costings data that are available. There has been government support for the Kerry cattle in one form or another since at least 1888, and the scheme that operates currently provides for a premium of €66.18 (£57) per eligible calf. The enabling EC Regulation is No 1535/2007 on the application of Articles 87 and 88 of the Treaty to *de minimis* aid in the sector of agricultural production⁶⁵. “*De minimis* aid” can be awarded without reference to the European Commission as the aid is considered too small significantly to affect trade or competition in the common market. With 443 calves having been registered in 2009⁶⁶ a total equivalent to about £25,000 might have been paid out. In France livestock breed conservation programmes are well documented in the academic and professional literature – much better than in the UK – and are a fairly frequent topic for doctoral dissertations (for example Fouvez 2008; Lauvie 2007). Considering French FAnGR generally, breed conservation programmes are very diverse in how they are managed (Danchin-Burge et al. 2010) and in how conservation interacts with commercialization (Lauvie 2007; Lauvie et al. 2011), and there is very considerable professional input from state organizations. Facilitating review of the success of conservation activities, France has a national sheep database that operates in the context of official performance recording enabling pedigrees of rare breeds as well as commercial breeds to be traced back at least to 1970 (Palhière et al. 2008).

3.1.4.1 Departmental Expert Committee on Farm Animal Genetic Resources

Defra and its predecessor MAFF held “meetings of interested parties” starting in 1995 (Hall 2009) and modest research funding was made available at an early stage (see for example Mercer et al. 1997). In December 2001 a Consultative Committee was set up to prepare the UK submission to FAO’s “State of the World’s Animal Genetic Resources” (Roper 2004). This led to a Defra National Steering Committee to prepare an Action Plan for Farm Animal Genetic Resources which was published in November 2006 and the Government including the Devolved Administrations accepted all 38 of its Recommended Actions. The first of these was the establishment of the National Standing Committee on Farm Animal Genetic Resources, which held its first meeting in March 2008. In April 2011, following the Government’s review of “arms length bodies” the Committee was reclassified as a Departmental Expert Committee. Its activities are reported on a dedicated website⁶⁷. Here can be found the Native Breeds at Risk (NBAR) list which is a key policy instrument in the support of UK FAnGR.

3.1.4.2 Umbrella organizations

The Rare Breeds Survival Trust (RBST) is probably the best known, though very important functions are also performed by, among others, the British Pig Association, British Goat Society, Sheep Trust, Rare Poultry Society, Poultry Club of Great Britain, Goose Club, and British Waterfowl Association. In addition there are the industry organizations mentioned in the Breeding Plans section.

⁶⁵ (Official Journal No. L337 of 21 December 2007, page 35)
<http://www.agriculture.gov.ie/farmingsectors/animalbreeding/cattle/>

⁶⁶ <http://www.kerrycattle.ie/news.asp>

⁶⁷ <http://www.defra.gov.uk/fangr/>

Historical accounts of the foundation of the RBST are available (Alderson and Porter 1994; Zuckerman 1994). A series of interviews with a selection of experts in 2007 concluded (Kubbinga et al. 2007) that the foundation of this pioneering non-governmental organization (NGO) was one of the three milestones in the history of farm animal genetic resource management (the others were an FAO conference and the Rio Convention). The journal of RBST, the Ark, published monthly from May 1974 to March 1996 and quarterly thereafter, is an important literature source, though with its primary function as a lively magazine for the membership it is neither peer-reviewed nor comprehensively indexed. The position of the RBST in the rural and conservation contexts and in relation to other institutions has attracted academic attention (Evans and Yarwood 2000), partly because rural human geography is an important subdiscipline but also because as a pioneering, relatively small, highly specialized, internationally known institution the RBST is of considerable interest in its own right. It has co-funded a number of scientific studies including those reported by Wilkinson (2011) and Bray (2009).

3.1.4.3 Breed societies

The fundamental role of breed societies in farm animal genetic resources is evidenced by the final two words of the current definition⁶⁸ of a livestock breed “... in the UK context ... an interbreeding population of husbanded or formerly husbanded domesticated animals of consistent genotype and phenotype with a recognized history and administrative framework”.

Through operating pedigree registers, and through breed promotion, breed societies are fundamental to maintaining breed diversity and, thereby, the proportion of genetic variation that resides in between-breed variation. Because many have charitable status there is a form of state support through the tax system but most costs are borne by society members. If breed societies did not exist, between-breed variation would be eroded so the operating costs of the societies can be seen as the costs of maintaining this variation, which would otherwise fall on the state.

Total annual value of breed society support for the NBAR cattle, sheep and equines (25, 46, 16 breeds respectively) is estimated (Technical Appendix 8) as £3.7 million.

The diversity of breed society modes of operation is well shown by the range of registration fees they charge and the ways the registers are formatted. These differences are highly relevant to the present discussion because registration fees offer a mechanism for incentives (as suggested by Hasler et al. 2011), and the format of the registers gives an indication of what kind of information the breed societies generate for the public domain.

Many very important initiatives often come from individual society members. Examples of leadership shown in the conservation of traditional or original segments of commercial cattle include Lincoln Red (Stennett 1999), Aberdeen Angus and Hereford (Hart 1999a,b) and British Friesian (Mead 2012), and Dairy Shorthorn⁶⁹.

To comply with the EC's Zootechnical Regulations, breed societies must have certain procedures in place. Modes of registration pose particular difficulties especially for livestock where females are not registered individually, such as hill sheep. Their constitutions usually oblige them to maintain the traditional form of the breed and this is often problematic when the pedigree register is open to animals from overseas populations of the same breed, or from other breeds. While some have professional staff others do not, and providing the information that UK Government needs for its monitoring function can be burdensome. Finally, several new expectations are being placed on the breed society – UK Government relationship notably relating to the protection of key flocks and herds from culling during disease outbreaks.

⁶⁸ <http://www.defra.gov.uk/fangr/2011/03/17/national-inventory/>

⁶⁹ Ark Winter 2012, p.14

3.1.4.4 Registration and publication of registers

Registration fees vary considerably among breeds, but are usually higher for males than for females, and are not trivial. Examples are in **Table 9** (in most cases the fee will be increased for late registration). All values are £. In several cattle and horse breeds, a DNA test is required. In some horse breeds, a passport and DNA test are included in the fee.

Registers include statements as to the parentages of animals. These can be validated by DNA-based tests. Recent technical developments (see for example Kijas et al. 2012; Berry et al. 2013) have dramatically reduced costs. Quoting Dr. James Kijas⁷⁰: “The current SNP based parentage test is available to Australian sheep producers at [£12] per animal. This covers the cost of the blood card, SNP genotyping and provision of a parentage result. The SNP test is composed of 192 SNP selected for analysis of parentage (high minor allele frequency across breeds and genomic spacing). It will also be useful for genetic diversity and the assessment of relatedness between animals, however this application wasn’t considered during assay design”.

Table 9: Examples of current or recent registration fees.

		Male	Female
		£	£
Cattle	Shetland	7.50	7.50
	Beef Shorthorn	25	25
	Welsh Black	30	12
	Aberdeen Angus	50	50
	Longhorn	100	16.50
Sheep	North Country Cheviot	2	n/a
	RBST Combined Flock Book	9.70-21.45	1.50-10.70
	Shropshire	15	5
	Dorset (Poll & Horn)	20	2
Horse	Dales Pony	25	25
	Clydesdale	107	105
Goat		20	8
Pig	(+ £3 / litter)	6.50	6.50

Herd books - cattle

Cattle herd books vary considerably in style and content and for many the published volume is backed up by databases accessible through breed society websites. Most, probably all cattle breed societies register females as well as males and some register steers (castrated males). Some publish herd returns (the numbers of animals of each sex/age class in the herd).

For the purposes of the present discussion, a major feature of herd books is that most have multiple registers enabling the progress of upgrading or introgression to be followed (Lincoln Red example discussed earlier). Some breed societies denote animals whose genotype is, to a very small proportion, derived from other breeds through introgression, as “pure”. Given that the computerized databases are usually truncated, it is often not possible to identify “traditional” or “original” (i.e. non-introgressed) segments within a breed except by tracking pedigrees through herd book volumes. Some breeds publish the percentage of genotype ascribable to the pure ancestral breed, but in some cases a visual check of the pedigrees indicates that these percentages cannot have been deduced arithmetically.

⁷⁰ Personal communication, 11 March 2013

Herd books - pigs

Pig herd books are digitized and of uniform format greatly facilitating analysis (see examples earlier in this section of the report).

Flock books

The first flock book for sheep was published in 1882, for the Shropshire, and since then the diversity of sheep breeds has been partnered by a diversity of registration systems. Typically flock books might include address lists of breeders, breed information (such as show results and sale prices), flock returns (numbers of ewes and rams kept or “put to the ram” by each breeder, and register information, usually with some parentage information and sometimes with dates of birth and indications of whether the animal registered was of a single or multiple birth. Flock books are probably without exception annual or biennial and usually include errata and late registrations, carried over from previous years. For several breeds there is password access for society members to an online database.

Full registration of males and females is associated with the rarer breeds and with crossing and terminal sire breeds. Hill breeds typically register males only. For all breeds in **Table 10**, it is discernible whether sires are homebred or bought-in. The relevance of phone or email information is that is of obvious value in emergencies, particularly in relation to geographically localized breeds. Postcodes enable geographical location to be established unequivocally and are given, along with addresses, in all these examples, though the Hebridean flock book for one does not give addresses or postcodes.

Table 10: The range of detail published in a selection of sheep flock books.

Breed and year	Sexes registered	Flock return	For rapid contact	In BASCO / Egenes	Other features
Dorset Down 2012	M & F	yes	Phone, email	no	Separate section for sheep of New Zealand breeding
Shropshire 2012	M & F	yes	Phone, email	Yes	
Hebridean 2012	M & F	no		no	Summary statistics (sons/daughter registered per ram)
RBST Combined Flock Book 2007	M & F	yes		no	Periodic detailed flock survey results
Poll Dorset & Dorset Horn 2012	M, but F reg. not published	yes	Phone, email	yes	Health scheme and <i>PrP</i> genotype information
North Country Cheviot 2012	M	yes	Phone, email	yes	Health scheme information
Dalesbred 2010	M, dam's sire noted	no	Phone	no	<i>PrP</i> genotype information
South Country Cheviot 2010	M	no	Phone	no	<i>PrP</i> genotype information
Devon Closewool 2009	M	yes	Phone	no	
Herdwick 2012	M	no		no	

Stud books

Equine registers also vary considerably in style and content and can be very difficult to analyse mainly because dates of birth often do not correspond with the volume in which animals are registered.

3.2 National outcomes of UK FAnGR conservation

The UK Country Report 2012⁷¹ summarizes the overall state of national FAnGR, primarily in terms of numbers of animals, and notes progress since the last Country Report was published in 2002.

It has often been repeated that none of the UK's breeds have gone extinct since the Lincolnshire Curly Coat pig in the early 1970s. A useful summary of the situation is the RBST's Watchlist which tabulates breeds according to their degree of endangerment, which is measured against a set of criteria not limited to numerical status but including demographic, genetic and geographic considerations.

A historical overview of the RBST Watchlist is in Technical Appendix 9. Most of the breeds that have been on this list since its inception in 1977 have improved in status. Additions to the Watchlist are generally either "original" or "traditional" (non-introgressed) segments of native British breeds, or of breeds previously considered ineligible which have succeeded in demonstrating a continuity of existence or other aspect of compliance with the Watchlist criteria. Formerly numerous, commercial breeds have on occasion declined in numbers to such an extent that they have fallen within the numerical criteria for inclusion.

3.2.1 Maintenance of population numbers

For 32 breeds using Grassroots systems⁷², changes in registrations over the period 2007-2011 are summarized as follows. Considering just numbers of dams whose offspring were registered, 11 have shown a decline over the period. However considering each species as a whole, the 8 breeds of cattle showed on average an annual increase of 3.9% in numbers of dams, the 13 breeds of sheep an average of 4.1%, the 5 breeds of goat, 5.6%, but the 6 breeds of equine an average annual decrease of 5.7% (full data not presented here).

The greatest annual rates of increase in this parameter for each species were, for cattle, 10.7% (Luining), for equines 2.6% (Clydesdale), for goats 22.3% (British Guernsey), and for sheep, 16.0% (Boreray). These rates are indicative of the rates of growth of registered breeds under conservation (or, in the case of the Luining, being commercially developed but with an eye to restriction of inbreeding) as practised in private sector systems such as those operating in the UK.

The British Cattle Movement Service can provide data which can be used to infer overall processes of change in numbers⁷³, it must be appreciated that the data relate to commercial animals including crossbreeds. Comparisons are made between 2006 and 2012⁷⁴, in **Table 11**.

3.2.2 Conservation of within-breed variation

In 2002 the Conference of the Parties to the CBD made a commitment to reduce the rate of global biodiversity loss; this resolve was subsequently echoed and strengthened by the EU. Biodiversity indicators were accepted as a necessary instrument for monitoring this process. In 2007 the Interlaken Declaration on Animal Genetic Resources affirmed the relevance of the CBD commitment to activities in FAnGR conservation, and this led Villanueva et al. (2010) to develop an indicator of the within-breed genetic diversity in UK sheep and cattle, for inclusion in the UK suite of biodiversity indicators overseen by the Joint Nature Conservation Committee⁷⁵. The general finding was that

⁷¹ <https://www.gov.uk/government/publications/uk-country-report-on-farm-animal-genetic-resources-2012>

⁷² <http://www.grassroots.co.uk/>

⁷³ <https://www.gov.uk/government/publications/the-cattle-book-2008>

⁷⁴ Data kindly made available by Mr. Tim Brigstocke

⁷⁵ <http://jncc.defra.gov.uk/page-4240>

from 2001 to 2007 “The mean effective population size for breeds most at risk of loss of genetic diversity has risen by 4.5 individuals for sheep breeds (12 per cent) and by 8.3 individuals for cattle (32 per cent). This increase for sheep breeds is not statistically significant due to variability in the data, and the measure is therefore assessed as showing little or no overall change”.

Table 11: Changes from June 2006 to June 2012 in UK populations of selected cattle genotypes.

Reported number on:	1 June 2006	1 June 2012	Average annual % change
Dairy cattle			
Holstein/Friesian	3083000	2928000	-0.86
Jersey	85184	116486	5.22
Ayrshire	62767	66336	0.92
Guernsey	17696	12620	-5.63
Dairy Shorthorn	9738	17132	9.42
Beef cattle (selection)			
Limousin & crosses	1959670	1615521	-3.22
Charolais & crosses	897943	635080	-5.77
Some native breeds & their crosses			
Aberdeen Angus & crosses	647979	733923	2.08
Hereford & crosses	362438	311863	-2.50
South Devon & crosses	91525	96200	0.83
Welsh Black & crosses	59787	54752	-1.47
Galloway & crosses	38733	43486	1.93
Highland & crosses	38047	39323	0.55
Devon & crosses	36592	47189	4.24
Beef Shorthorn & crosses	24176	47466	11.24
Dexter & crosses	22772	31699	5.51
Longhorn & crosses	15117	21562	5.92

Effective population size is explained below but it is critically important to appreciate that it is a genetic measure, it is not (as is sometimes thought) the number of breeding animals. As will be explained, if its value is calculated as below 50 for a particular breed, then there should be conservation concern.

In the published paper (Villanueva et al. 2010), breed names were anonymized but breed societies have kindly given permission for inclusion in this report of the calculated values for N_e in 2001 and 2007 (Table 12).

It is imperative to appreciate that this study was intended to compare the situation in 2007 with that in 2001. Values are unlikely to have changed greatly since then, except that for most breeds with N_e below 50 in 2007 the evidence from the present study is that this value has increased.

Table 12. Comparisons of effective population sizes of cattle and sheep breeds, 2001 and 2007. Compiled from Villanueva et al. (2010), with breed society permissions.

Cattle	2001	2007	Sheep	2001	2007	Sheep	2001	2007
Ayrshire	119	94	Black Welsh Mtn.	312	135	Oxford Down	112	83
British White	34	36	Border Leicester	-	100	Portland	96	96
Chillingham	10	10	Boreray	14	25	Ryeland	86	93
Dairy Shorthorn	290	500	Cambridge	91	44	Soay	36	30
Devon	nd	90	Castlemilk Moorit	48	61	Suffolk	500	420
Guernsey	145	105	Clun Forest	172	156	Swaledale	500	420
Guernsey (Island)	197	173	Cotswold	79	61	Teeswater	179	-
Highland	110	118	Devon Closewool	172	152	Wensleydale	500	238
Jersey	195	268	Dorset Down	250	227	Whitefaced Woodland	63	98
Jersey (Island)	127	500	Hampshire Down	122	86			
Lincoln Red	107	82	Hebridean	426	443			
Lincoln Red (orig.)	16	24	Herdwick	500	500			
Longhorn	73	82	Kerry Hill	312	500			
Luing	78	112	Leicester Longwool	35	47			
Red Poll	42	65	Lincoln Longwool	56	122			
South Devon	71	97	Manx Loaghtan	29	38			
Sussex	179	294	Norfolk Horn	500	90			
Welsh Black	500	500	North Ronaldsay	204	124			
Whitebred Shorthorn	113	97						

Indicator sets that assess livestock biodiversity in more contextual ways (with reference to the production environment) have been proposed (Martyniuk et al. 2010) but not yet evaluated or applied in the UK.

This study has also enabled an assessment of degree of conservation of within-breed genetic variation since the 2002 Country Report⁷⁶, though as it is on the basis of comparison of mean inbreeding coefficients of offspring it does not have the predictive capacity of an analysis of breed coancestry. However, the general picture is encouraging (**Figures 8 – 11**; breeds anonymized) with most breeds showing a decline in the inbreeding of current crops of calves, lambs or kids, the means

⁷⁶ <https://www.gov.uk/government/publications/uk-country-report-on-farm-animal-genetic-resources-2002>

being mostly below 0.10 in 2011, signifying overall, successful avoidance of inbreeding of these cohorts, bearing in mind that for most of these breeds the inbreeding has accumulated over many generations.

Figure 8: Changes in mean offspring inbreeding coefficients of 8 cattle breeds.

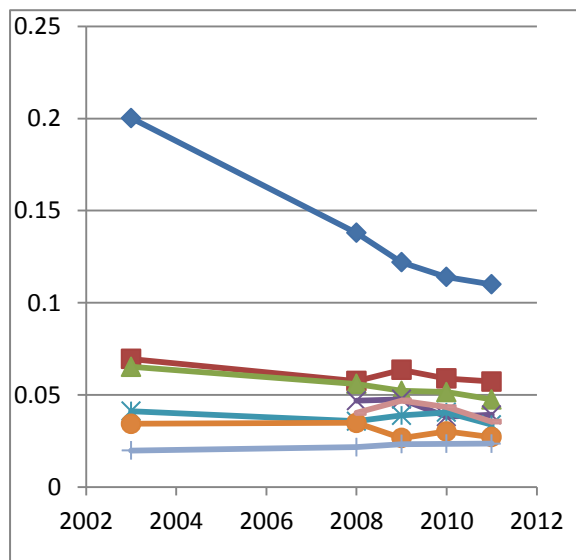


Figure 9: Changes in mean offspring inbreeding coefficients of 13 sheep breeds.

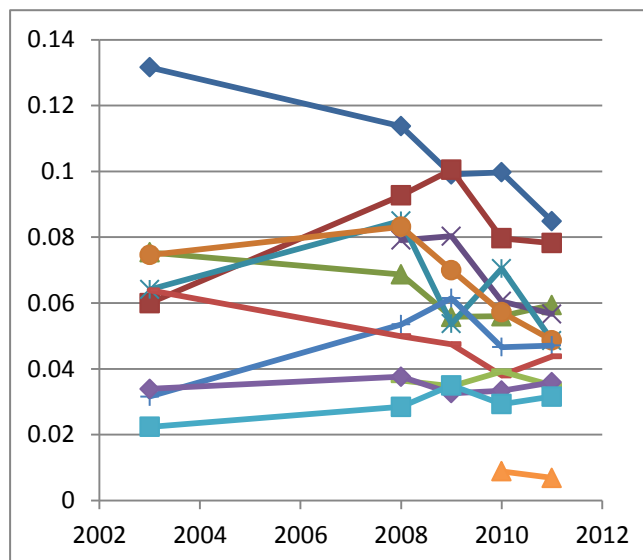


Figure 10: Changes in mean offspring inbreeding coefficients of 5 goat breeds.

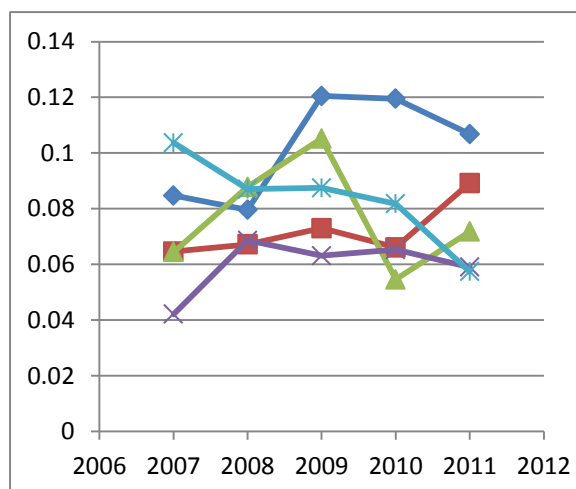
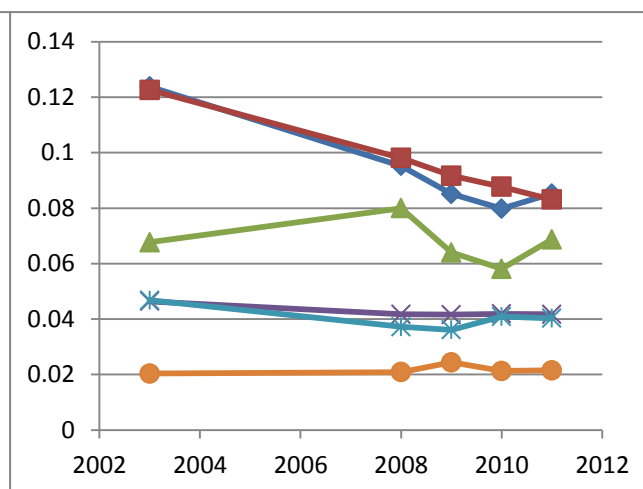


Figure 11: Changes in mean offspring inbreeding coefficients of 6 equine breeds.



3.2.3 The role of ex situ conservation

Ex situ conservation involves the collection and storage of reproductive cells and embryos, with a view to their utilization for the following purposes:

- To recover a lost breed;
- To address new breeding goals within an existing breed;
- To support breeding schemes in small populations, principally in order to minimize inbreeding;
- For research in conservation genetics and genomics.

Scientific advance in reproductive technologies has come about primarily because of their very substantial economic benefits.

The most mature technologies relate to collection, processing, freezing, storage and utilization of semen. These processes are essentially routine in cattle, sheep, goat, horse, pig and poultry. A fundamental disadvantage is that if a breed is to be recovered from extinction by the use of stored semen, without females of that breed being available it is impossible to recreate the extinct breed completely as genes from whatever breed has been fertilized by the stored semen will persist in the progeny and their descendants.

Embryo collection and transfer are routine in cattle, sheep and goat but are either very difficult or still at the R&D stage in horse and pig, and simply not possible in birds.

A rapidly-developing set of technologies is that relating to cloning. Here, an oocyte from which the nucleus (and, therefore, most of the genetic material) has been removed can, in effect, “host” a nucleus from a non-reproductive cell (such as skin) and this laboratory construct (the result of somatic cell nuclear transfer, or SCNT) can then be transferred to a surrogate mother and develop into a viable animal.

Difficulties of scientific and ethical natures persist with the SCNT process and it is on the presumption that these can be overcome that conservation of somatic cells has been proposed as a low-cost ex situ option. Cells (collected, for example, by ear punch) can be stored and, in principle, used to produce clones of long-dead animals.

None of these technologies is free from constraints. Some, though perhaps incapable of resolution directly, can be sidestepped. In all cases, the requirement that animals must be in demonstrable good health before collection of cells or embryos might make emergency collection impossible. Cloning is expensive and contentious.

The available technologies for the respective species are reviewed by Mara et al. (2013), their practical applications being considered in more detail in Technical Appendix 10 and summarized as follows:

Cattle

Semen and embryos: no serious issues, commercially viable.

Sheep and goats

Semen: no serious issues for collection and freezing, apart from issues of training rams and of coping with their reproductive seasonality. Practical issues of successful artificial insemination are evident. Salvage of sperm post-slaughter thoroughly practicable.

Embryos: commercially viable.

Horse

Semen: fundamental issue of individual stallions differing markedly in post-thawing viability of sperm. Issues of basic species biology make artificial insemination very expensive.

Embryos: very difficult.

Pigs

Semen: no serious issues though individual boars can differ markedly in post-thawing viability of sperm.

Embryos: at R&D stage.

Poultry

Semen: some laboratories have particular expertise, for example in the Netherlands (Woelders et al. 2012).

Embryos: not viable but cryopreservation of isolated embryonic cells is possible.

3.3 Conservation practice at breed level

Breed conservation involves demographics and genetics. Demographic management involves maintaining adequate numbers of breeding females while genetic management is concerned with maintaining within-breed genetic variation. Conservation of between-breed genetic variation depends on the former; of that within-breed, on the latter.

3.3.1 Demographic management

Breeds often have fairly complex demographic substructures, whose effects on genetic diversity can be quantified. Usually some elite flocks and herds supply high proportions of the breeding males used (the “breeding pyramid: Simm 1998, Pollott and Stone 2003). Pedigree (or molecular) studies can be used to partition the amount of inbreeding that an animal has acquired, between that due to its relationships within a subgroup, and that due to its subgroup’s relationships with the rest of the breed; this process generates so-called F statistics (Frankham 2002) and when they are statistically significant, substructuring is indicated. Changes over time in these statistics can often be linked to demographic events. Examples include Dexter cattle (Bray et al. 2009) and British Saddleback pigs (Wilkinson 2011); both these studies used molecular data. F statistics derived from pedigree data were first described by Wright (1977) for pre-1920 Shorthorn cattle but most recent examples are from non-UK breeds (for example Cervantes et al. 2008; Dunner et al. 1998; Gutiérrez et al. 2005).

Substructuring may be formally recognized, as when a herd book includes subregisters. Breeders may also classify animals according to their matrilineal or patrilineal descent and this may be verbalized in terms of “bloodlines” or similar. For example, the Aberdeen Angus herd book lists 82 “cow families”. Lineages are particularly evident in equines, the best known being the Lipizzan horse (Kavar et al. 1999) where the matrilineal descent is evident in the pedigrees and reflected in mitochondrial DNA variation. In pigs, conservation of bloodlines is widely supported (the BPA coordinates an annual survey of rare pig bloodlines, reported in the RBST’s “Ark” journal every spring). Bloodlines are often used to guide choice of mates, shown by animals with the same bloodline name tending to be more closely related than those whose bloodline names differ (Hall 1989a). Bloodlines can be shown to be genetically distinct in terms of microsatellites (in the British Saddleback pig: Wilkinson 2011) though in this case, for several acknowledged bloodlines, genetic distinctiveness has not been supported. In rare sheep, particular blood group alleles have been shown to be associated with specific foundation flocks (Clarke et al. 1989).

In principle, demographic monitoring should be relatively straightforward. An essential part of the monitoring operation is census activities, and numerical strength of a breed is a criterion for conservation status and for eligibility for support⁷⁷. While some breed societies publish information on individual herd or flock sizes many do not and, often, a survey of breeders is the only way to establish the numerical strength of a breed (but approximate methods do exist: e.g. Hall 2011).

3.3.1.1 Geographical factors

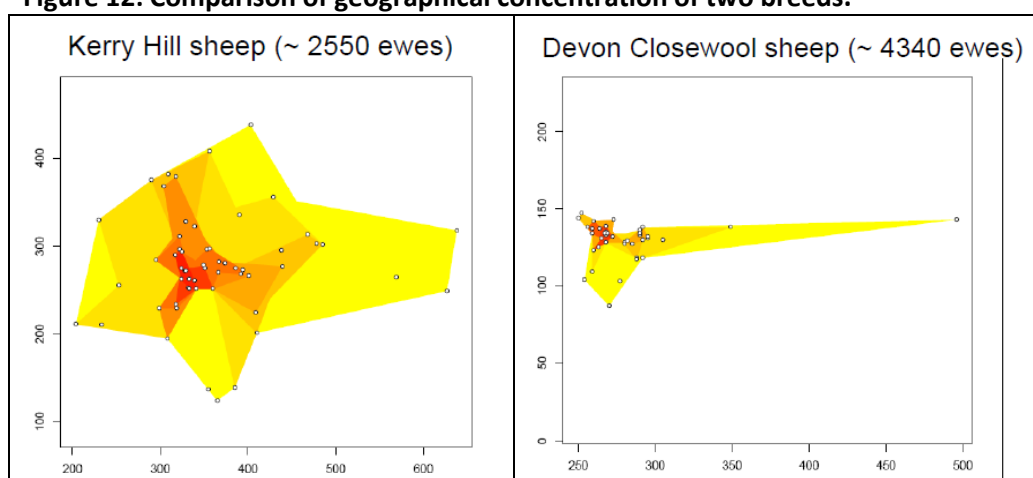
Immediate and visible threats to breed conservation are much more likely to be demographic in nature than genetic, and they can be very rapid in onset, particularly under a veterinary regime dependent on stamping out foot-and-mouth and other such diseases by slaughter. This became evident during the FMD outbreak in 2001 when areas were depopulated of livestock, with substantial effects both on rare breeds (Townsend et al. 2002) and on numerically strong yet geographically localized breeds (Carson et al. 2009). According to Wright et al. (2002), prior to 2001 ... “South Country Cheviot [ewes] ... [numbered] approximately 65,000 ... Up to 17 April 2001 ... some 16,000 ewes had been slaughtered.” Of the breeders selling rams at the autumn 2000 ram sale at Lockerbie, 25% subsequently had their flocks destroyed.

⁷⁷ <http://www.defra.gov.uk/fangr/2012/05/03/inventory-lette/>

Research is urgently needed on the geography of breed distribution, to extend the work of Carson et al. (2009). A criterion taking the form of “a breed with “x%” of its total population within “y km” of a geographical location defined on the basis of “z”, appears necessary but this has not been studied scientifically. This is urgent, because in the event of an emergency such a definition could be subject to legal challenge. **Figure 12** illustrates some of the problems. These are the results of applying a home-range (radiotracking) program to map references of locations of sheep flocks and to the number of ewes in each flock. The diagrams give the relative geographical locations of the different flocks, each marked by a symbol. The darkest shading is the polygon which, proceeding out from the centre of gravity of distribution of ewes and including the flocks which mark its boundary, includes 50% of the ewes in the breed. Successive shadings account for 60, 70, 80, 90, 100%; clearly breeds are not distributed in an even, concentric manner.

As local adaptation is considered a major merit of such breeds (Jones and Bowles 2006) the priority should probably go to large flocks or herds located towards the centre of gravity of the distribution.

Figure 12: Comparison of geographical concentration of two breeds.



Note:

- From 1994 data (S.J.G. Hall, unpublished).
- The centroids are in the Welsh Marches (Kerry Hill) and near Barnstaple (Devon Closewool); each division on the axes is 100 km. The furthest east flock of the latter was near Godalming, Surrey.

3.3.1.2 Traditional populations and introgression

There is probably no breed society which has as its aim the maintenance of the breed in an unchanged state. A rapid route to genetic improvement is the use of animals from other populations, but at the same time, breeders wish to retain many of the traditional characteristics of their breed. Introducing genes from overseas populations of the same breed is an attractive option, and because British breeds have been adopted worldwide suitable animals can be sought in “daughter” breed societies abroad (see Technical Appendix 11). A general review on this subject does not exist, but in view of the operation of the Zootechnical Regulations it might be presumed that the barriers to importation from such daughter breed societies would be relatively low.

Breed societies usually have mechanisms for enfolded such animals into the breed. It is often possible to admit animals from breeds with no shared history, and registration of their descendants usually involves progression through grading registers (a process governed by the Zootechnical Regulations). Very many, perhaps most commercial livestock breeds have received introgression from other breeds or from animals registered with daughter breed societies elsewhere. An account of how the process operated in the Lincoln Red is given in Technical Appendix 12. In some breeds the use of imports has been pervasive, and purebred descendants of the “Traditional” or pre-

importation breeds have in some breeds (notably Aberdeen Angus, Hereford, Ayrshire and Dairy Shorthorn) been identified and marked out for particular attention by conservationists.

Management of introgression has been on a breed-by-breed basis and a general review has not been made. There are accounts of specific breeds and these can give useful insights into how breed societies operate (French example: Lauvie et al. 2008). As these studies can be laborious when based on pedigree analysis this could be a situation where molecular methods will be especially valuable. Programs such as STRUCTURE⁷⁸ can be very effective at apportioning the genotypes of animals among different ancestral populations (for example, Bray et al. 2009; Wilkinson 2011). New molecular work on Lincoln Red cattle has confirmed the pedigree evidence that the Traditional Lincoln Red is in fact free of introgression from continental beef breeds (Bray TC, Hall SJG, Bruford MW, unpublished).

3.3.2 Genetic management – general issues

Breeds, by definition, tend to be maintained as closed populations and within them, breeders will tend to select particular individuals for breeding because of their heritable merits and by doing so will change the genetic composition of the population – this is artificial selection. Also, and this is inevitable in a closed population, animals will tend to be related to their mates, and inbreeding is the result. Some animals may possess particular rare genes and for one reason or another fail to leave descendants so these genes are lost from the population, while elite animals which are particularly favoured for breeding may disseminate genes through the breed which were not explicitly selected for – these are processes of genetic drift.

Conservation strategies and breeding programmes have the same scientific underpinning and it is now appreciated that they complement each other rather than being adversarial. But very many conservation strategies are essentially monitoring operations whereby the breed-level outcomes of decisions made by individual breeders are kept under review. Material for these reviews is most easily obtained from herd-, flock- or stud-books, which are published by breed societies as a record of births of registered (pedigree) stock and are in the public domain. Deaths of registered animals and births of non-registered or crossbred progeny are not usually recorded, and for many breeds (particularly in the UK of hill sheep) only males are registered.

Genetic conservation is a matter of sustaining current diversity (Woolliams 2007; Woolliams and Toro 2007), and the primary strategy for achieving it is the long term management of the process of accumulation of inbreeding. This mechanism operates by advising on individual matings. There are a few published examples, none of them from the UK, of rare breeds that are managed by total control of matings (Toro et al. 2000). The vast majority of UK breeds exist as independently managed herds or flocks, and individual breeders operate in a diversity of ways – they may apply formally designed mating plans or simply follow general principles of breeding management.

3.3.2.1 Biodiversity indicators in relation to FAnGR

Genetic diversity of FAnGR resides within breeds and between breeds, and the status of this diversity and the prospects for its conservation depend on geographic and demographic factors. A discussion has been opened on how an indicator might be developed for FAnGR (Martyniuk et al. 2010) but further work is needed. Villanueva et al. (2010) have developed and tested a genetic indicator based on effective population size, N_e . They conceded that assembling the data required is difficult under current conditions but argue that rather than compromise on quality and reliability by operating an indicator that uses more freely available data, effort should focus on developing a national database that can provide the data as and when required. Whether breed societies are able, or willing, to provide such data is clearly a relevant consideration.

⁷⁸ <http://pritch.bsd.uchicago.edu/software.html>

An overview of genetic conservation in a particular breed can be provided by the calculation of key population parameters. The key one is the rate of increase of average inbreeding ΔF . This is conveniently expressed in terms of effective population size N_e . In a single statistic, N_e gives a measure of the effects of management practice or breeding policy on the genetic composition of a breed. Indeed, there are rather few published reports of the effective population size of the rarer breeds (Toro et al. 2011) and they are of much potential value. If values for N_e that have all been obtained by the same method and with the same assumptions are compared among breeds, breeds could be identified which are unusual in some respect and which may deserve further investigation. Practical experience has shown that in livestock N_e should have a value of at least 50. If N_e is too small, the resilience to environmental challenges conferred by the presence of genetic variation is likely to be compromised. Unfortunately effective population size is a technical term that can be very hard to grasp and it is often used inconsistently.

N_e is only correctly defined in terms of the rate of increase of inbreeding, but certain equations have been developed which enable it to be predicted from demographic data. The accuracy of these predictions has not been formally reviewed, but demographic predictions of N_e could be very attractive for the monitoring process because they can be obtained from public domain data, i.e. herd books and their equivalents. This has several advantages – principally, that access may not be possible to the digitized databases necessary for mass calculations of inbreeding, and also that with the herd book process being so deeply embedded in pedigree livestock breeding, concepts derived directly from herd books are relatively easily understood. Further research is clearly needed and the use of demographic equations to estimate N_e in this report must be seen in this light.

The respective equations for N_e are explained in Technical Appendix 13. Briefly, the simplest-looking equation, that of Wright (eqn. 3), estimates N_e in terms of the numbers of sires and dams. The more complex, that of Hill (eqn. 4) is more realistic because it takes into account certain demographic variables; it accounts for N_e tending to be increased by numbers of sires, numbers of dams and generation interval; while N_e will tend to be decreased if these variables are reduced or if sires and dams vary considerably in the numbers of breeding offspring they leave.

3.3.3 Breed-level conservation outcomes

A theme of this project has been to see whether the currently existing frameworks for FAnGR conservation are in fact achieving outcomes that are as good as those that are theoretically possible. Ideally fully digitized pedigree databases would be available and their analysis would reveal the extent to which inbreeding is accumulating. A complete picture would require breed-specific investigations of demographic issues and other issues such as introgression and the retention of traditional segments within breeds.

Databases of this kind might become available, but until then, approximate methods must be used with appropriate caveats, and this section describes the results of investigations primarily based on public domain data obtained by the analysis of published herd- flock- and stud books.

“They order, said I, this matter better in France”⁷⁹. What can be done with a fully digitized database is well illustrated by publications of the Institut de l’Elevage, France; see for example a report⁸⁰ in which the genetic variability of 19 cattle breeds is documented and reviewed.

⁷⁹ Laurence Sterne, *A Sentimental Journey*, 1768

⁸⁰ <http://idele.fr/recherche/publication/idelesolr/recommends/estimation-de-la-variabilite-genetique-de-19-races-bovines-a-partir-de-leurs-genealogies.html> (0009 72 125 of September 2009)

3.3.3.1 Mammalian livestock

Cattle

Full data are in Technical Appendices 1 and 2. The N_e figures calculated by the equations of Wright (Frankham 2002, p. 241) and Hill (1979) are compared in **Table 13**.

As indicated in Technical Appendix 13 Wright's equation is based simply on numbers of parents. Hill's equation usually yields a different value, because it takes account of how parents differ in number of offspring and of how increasing generation length slows inbreeding.

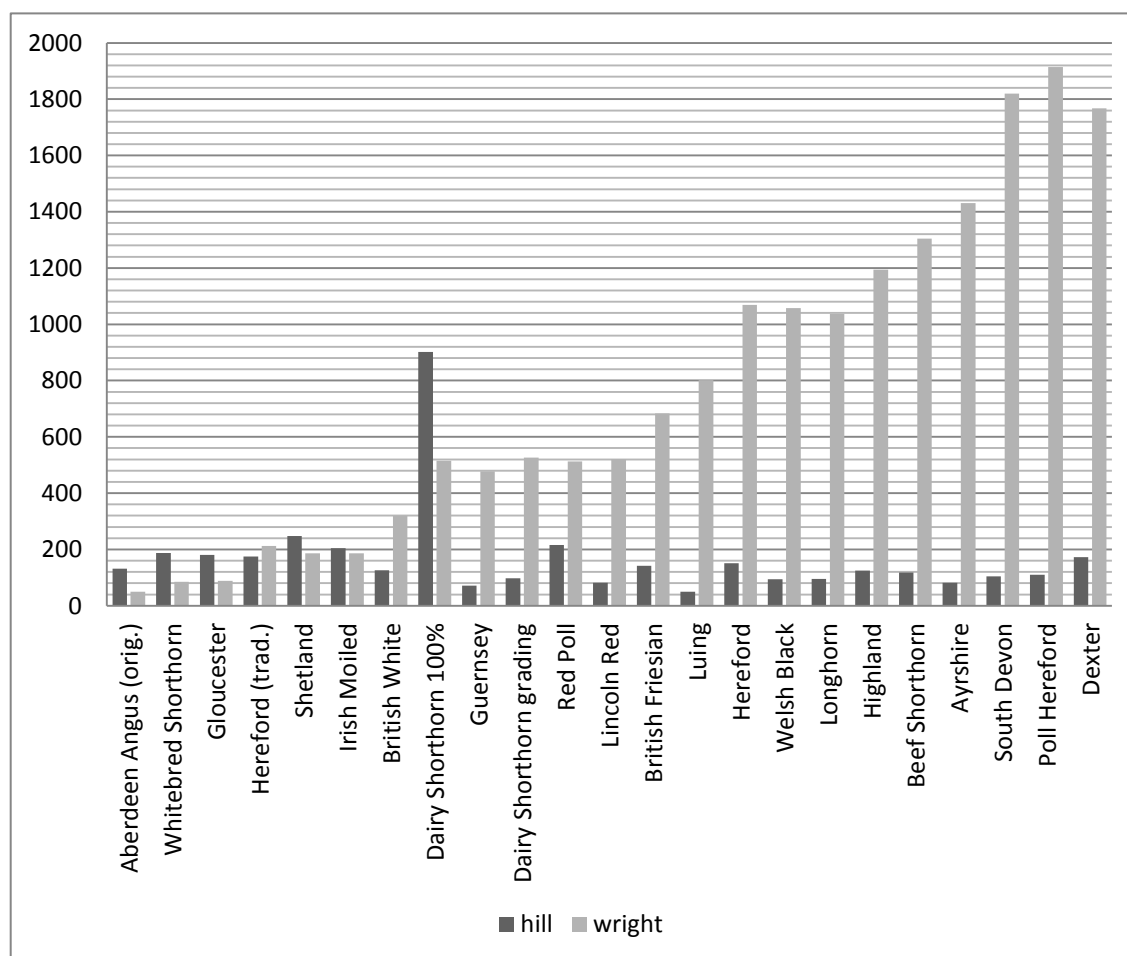
Table 13: Effective population sizes of cattle breeds, by the methods of Wright and of Hill.

	Sires	Dams	Generation interval	N_e (Hill)	N_e (Wright)	N_e (Wright) / N_e (Hill)
Aberdeen Angus (orig.)	16	57	5.5	131	50	0.4
Ayrshire	405	3053	6	82	1430	17.5
Beef Shorthorn	370	2740	5	118	1304	11.0
British Friesian	182	2820	10	141	684	4.8
British White	100	398	5	126	320	2.5
Dairy Shorthorn grading	146	1325	6.7	97	526	5.4
Dairy Shorthorn	136	2405	10	902	515	0.6
Dexter	545	2335	6.5	173	1767	10.2
Gloucester	32	70	5.4	180	88	0.5
Guernsey	136	971	5.6	71	477	6.7
Hereford	302	2326	5.3	151	1069	7.1
Hereford (trad.)	60	456	8.7	175	212	1.2
Highland	358	1793	6	125	1194	9.6
Irish Moiled	66	157	5.3	205	186	0.9
Lincoln Red	155	810	5	82	520	6.4
Longhorn	309	1613	5.6	96	1037	10.8
Luing	224	1893	4.9	50	801	16.2
Poll Hereford	544	3974	4.1	110	1914	17.4
Red Poll	151	850	9.4	216	513	2.4
Shetland	63	180	6	248	187	0.8
South Devon	527	3322	6	104	1819	17.5
Welsh Black	302	2131	6.2	94	1058	11.3
Whitebred Shorthorn	28	90	5.7	188	85	0.5

"Wright N_e " is expected to be larger than "Hill N_e " and should it actually be the same or smaller – as is the case for several breeds in **Table 13** - perhaps here variances in offspring number are very small and/or generation interval particularly long. In **Figure 13**, the comparison is set in the context of the number of sires active in the breed (a similar pattern is seen if number of dams is used instead) and it is striking that that the rarest breeds – to the left – show the greatest similarity of "Hill N_e " and "Wright N_e ". It seems unlikely that matings in these breeds have been planned with an explicit aim

of minimizing variance in offspring number and/or maximizing generation length, but that seems to have been the net effect, a relatively high N_e being obtained as a result.

Figure 13. Comparison of effective population sizes deduced by Hill's equation with those from Wright's equation.



The position of Dairy Shorthorn on the diagram shows that a breed with a particularly high mean generation interval can have exceptionally high N_e . With over 50% of the sires in Dairy Shorthorn being older than 13 years (**Figures 2 and 3**; clearly, insemination has been with frozen sperm) this segment within the breed appears to have a tendency towards a conservative breeding policy either preferring well-characterized older bulls or those of a more traditional type. An obvious risk of using frozen semen is that it will have been derived from popular sires which may well already feature in the pedigrees of the animals inseminated, thus increasing inbreeding. The high proportion of young sires in the Guernsey is in contrast; this is in accordance with policy for that breed which favours the evaluation of young bulls (Luff 2010; Luff and Bichard 2002). High use of young sires is also the case in the British Friesian.

In relation to the more numerous breeds with rather low effective population sizes, such as the Guernsey and the Luving, it should be noted that if N_e is very large this can indicate that selection is unlikely to be strong enough to be able to achieve breeding goals, so a breed with N_e of 50 may be one where fairly intensive selection is being applied but at the same time inbreeding is being avoided. In commercial dairy cattle a minimum N_e of 40 is required for maximizing net genetic response for total economic merit and theory indicates that there is a range of values from 30 to 250 within which a balance can be achieved between decreases in fitness due to inbreeding and increases in fitness due to natural selection (references in Avendaño et al. 2003).

Sheep

Data presented here are supplemented in Technical Appendix 3. These data clearly require further analysis because certain aspects of the calculation of variance of family size for females have not yet been elucidated. Why the calculated values for N_e (Hill) in some cases exceed the numbers of breeding animals obviously needs to be explained. The general uniformity of the results in **Table 14** suggests that none of these breeds is under particular demographic challenge. Mean generation times are probably long compared to commercial breeds where 2 years would be more normal. Ways in which the Portland, Manx Loaghtan, Hebridean and Southdown breeds are structured demographically will be compared with findings from the 1980s (Hall 1986, 1989b).

Demographic management in sheep must take account of artificial insemination (and, thereby, the extension of generation times by use of frozen sperm) being, technically, not straightforward.

Table 14: Effective population sizes for sheep, 2011, by the methods of Wright and of Hill.

	Sires	Dams	Generation interval	N_e (Hill)	N_e (Wright)	Wright / Hill
Boreray	31	110	3.6	381	97	0.3
North Ronaldsay	46	151	4.0	249	131	0.5
Leicester Longwool	42	204	3.9	220	136	0.6
Whitefaced Woodland	43	216	2.9	392	143	0.4
Castlemilk Moorit	61	219	3.3	654	191	0.3
Lincoln Longwool	72	279	3.2	913	229	0.3
Manx Loaghtan	85	337	3.4	766	272	0.4
Portland	99	373	3.7	1143	313	0.3
Norfolk Horn	96	390	3.5	978	308	0.3
Oxford Down	105	410	3.6	1165	334	0.3
Soay	160	539	3.6	1464	494	0.3
Southdown	291	1541	3.6	3063	979	0.3
Wiltshire Horn	324	2448	2.0	919	1145	1.2

Goats

Data presented here are supplemented in Technical Appendix 4. The situation is similar to what is observed in sheep (**Table 15**), the estimates of N_e (Hill) in some cases considerably greater than the census population.

Table 15: As for Table 14, but for goats.

	Sires	Dams	Gen. interval	N_e (Hill)	N_e (Wright)	Wright / Hill
Toggenburg	17	28	3.3	229	42	0.2
British Guernsey	14	36	2.2	71	40	0.6
Saanen	19	42	2.7	106	52	0.5
British Alpine	37	75	3.1	405	99	0.2
British Toggenburg	69	154	3.1	556	191	0.3
British Saanen	60	157	2.3	300	174	0.6
Golden Guernsey	76	177	3.2	779	213	0.3
Anglo Nubian	88	222	2.7	545	252	0.5

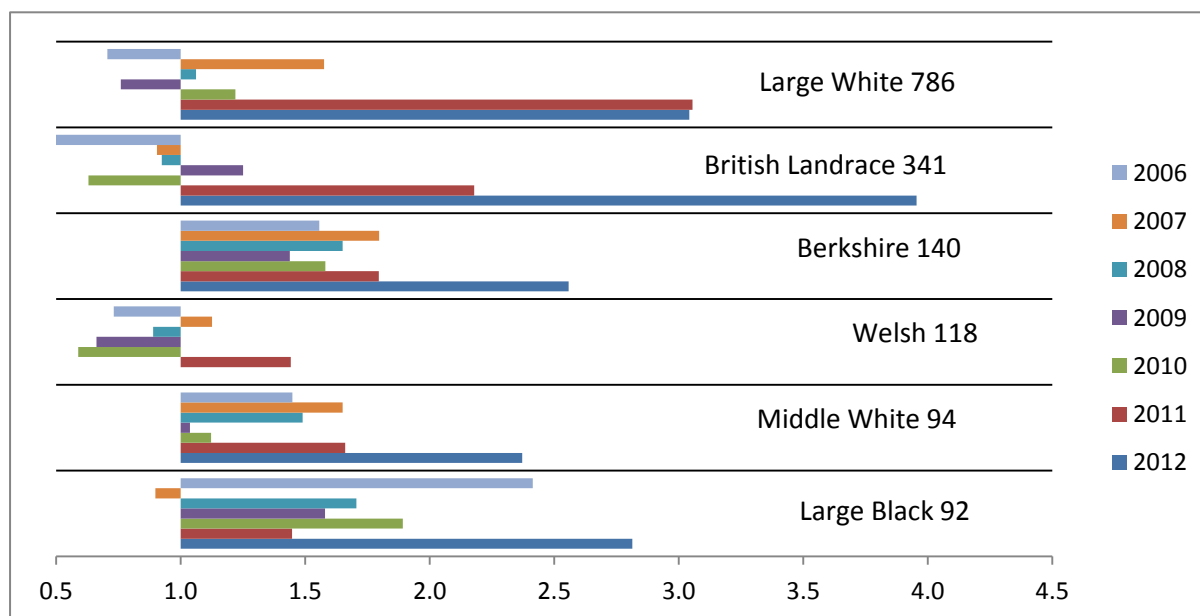
Pigs

Data presented here are supplemented in Technical Appendix 5. Also see **Table 8** above.

Half a century ago, N_e values were around 83 for 17 breeds (McPhee 1965). More recently N_e values for commercial herd book populations have generally been found to be above 50 (77 to 113 for 5 American breeds, calculated from pedigrees; 61 and 91 for two Finnish breeds, calculated from linkage disequilibrium of SNPs: (Welsh et al. 2010; Uimari and Tapio 2011, respectively). For Piétrain pigs in Bavaria, N_e was around 160 depending on method of calculation (Habier et al. 2009). This breed is administered by different, autonomous breed associations across Germany and N_e calculated at national level depends on which method is used, while four regional breeds of more conservation concern have N_e between 23.1 and 48.4 (Tholen et al. 2010). For the conserved Guadyerbas pigs mentioned above, N_e averaged 13.8 (Toro et al. 2000).

The calculated values of N_e (Hill) and N_e (Wright) are compared in **Figure 14**, by plotting the value of N_e (Hill) / N_e (Wright) for each breed each year. The breeds which have been considered as rare (Berkshire, Middle White and Large Black; Hall 1989a) are the ones which have consistently shown high values for this ratio. This could, as in cattle, indicate a general policy of breeding with conservation in mind in these breeds. In contrast, the Large White, British Landrace and Welsh (all considered historically as mainstream breeds) have frequently shown a lower value for N_e (Hill).

Figure 14. Comparison of effective population sizes calculated by two methods. Symbols to the right of the value of 1.0 represent N_e (Hill) being larger than N_e (Wright)



Note:

- Breeds are in descending order of number of dams in 2006, which are given next to the breed names

Equines

Data presented here are supplemented in Technical Appendix 6.

In two breeds, it is striking how the N_e values calculated using Hill's equation are considerably higher than those from the Wright equation. In Spanish heavy horses (four breeds, between 595 and 6307 animals) "Wright N_e " was between 5.8 and 14.9 times the "Hill N_e " value (Gómez et al. 2012).

Detailed study of the Cleveland Bay by Dell (2010) yielded values of "Wright N_e " of 145, and N_e calculated from increase in inbreeding of 85 (52 sires, 120 dams active during period 2005-2007).

Table 16: As for Table 14, but for equines. Breeds anonymized.

	Sires	Dams	Generation interval	N_e (Hill)	N_e (Wright)	Wright / Hill
-	<50	<50	8.5	112	48	0.4
-	<50	100-150	9.8	153	122	0.8
-	50-100	150-200			180	
-	50-100	150-200	10.2	171	177	1.0
-	50-100	200-300	11.9	100	244	2.4
-	100-150	300-500	10.8	161	387	2.4
-	100-150	500-1000	11.1		500	

Notes:

- N_e (Hill) cannot yet be realistically calculated for two breeds because there are anomalies in the demographic data for these breeds.

3.3.3.2 Poultry

In the absence of pedigree data most of our knowledge of genetic conservation of poultry in the UK is dependent on periodic surveys. The numerical status of UK non-corporate poultry has been reviewed (Defra 2010). That rare poultry breeds are indeed repositories of variation – at least of microsatellites and SNPs - has been shown on the global level by Hillel et al (2003) and at the UK level by Wilkinson et al. (2012) who also reported that British poultry breeds are more inbred than continental European breeds suggesting a greater degree of substructuring within breeds.

In the light of the difficulties of cryoconservation in poultry (Technical Appendix 10) it seems clear that systematic conservation in the form of *in vivo* stocks is the preferable option.

Poultry pose special issues, as without pedigree registration systems and with a multiplicity of (often very small) breed societies monitoring is very difficult (Defra 2010). There are some examples of formal institution-based genetic conservation programmes (Spain: Campo et al. 2000) but no equivalents in the UK. Even so, within - and between – breed diversity is still very evident (Technical Appendix 14).

The way in which UK non-corporate poultry breeds are structured, with private ownership, information networks that are at best informal, an almost complete lack of objective information on every aspect of the subject apart from molecular genetics, poses problems of auditing and it may be worth developing completely novel ways of monitoring this resource. The genetic data published by Wilkinson et al. (2012) suggest that breeding practices do not differ among breeds. A study of Internet traffic suggests (Technical Appendix 14) that overall, breeds that have more breeders also tend to have more traffic, but that when number of Google hits is corrected for number of members, the breeds overseen by the Rare Poultry Society have more Google hits per breeder. Breeds where the number of Google hits per breeder is particularly out of step are the Cochin and Andalusian, and the Welbar, Rhodebar and Campine; these might be breeds where interest in the breed, and by inference numbers of flocks, are greater than the numbers of known breeders would imply.

In this institutional environment breed societies have particularly important roles. The Animal Health and Veterinary Laboratories Agency⁸¹ advises that in a biosecurity emergency context being able to verify that a particular flock is of conservation significance, through breed society affiliation, would be very important.

Regarding inventories, experimental lines have been catalogued (references in Tixier-Boichard et al. 2009). A number of formal conservation programmes for poultry operate overseas. These are not

⁸¹ Ark Winter 2013, p.20; advice is posted at <http://www.defra.gov.uk/fangr>

numerous, and the reports tend to be case studies, though the report by Spalona et al. (2007) is of particular value in that it compares activities in five countries – Denmark, Hungary, Italy, Poland and Slovakia – and effective population sizes and inbreeding rates are estimated.

In Belgium, 40 breeds and several hundred varieties are not conserved under formal conservation programmes, though a 2005 survey was supported by the Ministry of the Walloon region which inventoried 1,140 flocks of which 97% were privately conserved⁸². but there has been quite extensive characterization work especially of eggs, and the use of local stocks for niche production has been promoted (Moula 2012).

In Denmark poultry conservation was, according to Spalona et al. (2007), entirely by private breeders. The focus of interest is the Danish Landrace fowl, but there seems to be little or no institutional interest in this long-established breed (recorded in 1879).

From 1998, a network of farms has operated in Finland for *in situ* conservation of the Finnish landrace chicken, overseen by MTT Agrifood Research Finland (the relevant state organization). There are about 80 farms, which are categorized as chick producers or chicken keepers (numbering 48 and 299 respectively) and the programme is more a network of keepers than a formal conservation programme⁸³. There are 10-12 varieties within the breed and altogether there were about 5000 chickens in 2012, four times the number in 1998.

In France, breed is frequently stipulated in the product description lodged as part of the Appellation d'Origine Contrôlée system (Institut National de l'Origine et de la Qualité⁸⁴), a well-known example is the Bresse chicken, with its characteristic blue legs (Verrier et al. 2005). Genotypes associated with schemes of this kind have been characterized in considerable detail (for example Baéza et al. 2009). Generally, the conservation and development of local and the more ornamental breeds has been by amateur breeders whose interests are looked after by the Fédération Française des Volailles (FFV).

Conservation in Germany of the Vorwerkhühn chicken is described by Weigend et al. (2009). This has research institute collaboration and is partnered by the development, in collaboration with Lohmann, of a line based on hybridizing with a commercial stock. Unusually for poultry and waterfowl, the Diepholzer Gans goose of Lower Saxony has a long-established flock book, and numbered 153 male and 382 females in 2005⁸⁵.

In Hungary, poultry conservation has been of private-sector interest at least since the 1950s with a national programme being started in the 1970s. This is supported through an agri-environment programme (Spalona et al. 2007).

In Italy, many universities are involved in conservation of avian genetic resources and public funds have been allocated to these activities for many years (Spalona et al. 2007) with a "huge activity of hobbyists in cooperation with research institutes". Now, support is also received through Rural Development Plans which operate on a regional basis. The Veneto region (in the north east) has supported conservation of local poultry (6 breeds of chicken, 2 duck, 1 turkey, 1 guinea fowl) since 2000. According to De Marchi et al. (2005) the project involves 4 widely dispersed organic farms and a total of 25 lines are managed following a defined plan with between 6 and 36 males and 5 and 49

⁸²

http://www.cabi.org/animalscience/Uploads/File/AnimalScience/additionalFiles/WPSA2_files/Lariviere.pdf

⁸³ <http://www.nordgen.org/index.php/en/content/view/full/1869>; Prof. Asko Mäki-Tanila, personal communication 11 April 2013

⁸⁴ <http://www.inao.gouv.fr>

⁸⁵ <http://naturlandhof-buening.de>

females in each (median composition chicken 28M, 44F, duck 25M, 39F, turkey 16M, 34F, guinea fowl 26M, 36F). Males are rotated as part of a breeding plan, and heterozygosity monitored by molecular methods.

In Latvia, the Vishtines goose is of particular significance and there are two conservation flocks of 150 birds, with a further 3000-5000 in private ownership (Juodka et al. 2012). All birds were taken to Russia during the Soviet era and the current population is descended from 100 eggs that were repatriated in 1994.

In the Netherlands, ex situ conservation of poultry is partnered by a programme of research and development. The Dutch cryobank is reviewed in Technical Appendix 10.

In Norway, the Jær hen is managed primarily as a conservation flock by the Norwegian Poultry Association. Numbers are given as 44 males and 273 females (no date)⁸⁶, all apparently descended from a single pair.

There has been national support for poultry conservation in Poland since 1972 (Spalona et al. 2007). Wężyk (2009) reviewed the conservation programme operated under the National Poultry Board, for six chicken varieties, 14 goose and six duck. A flock book system is implied. A problem has been the relatively high costs of maintenance of the ducks, which are not actually native breeds. There has been extensive characterization including fitness traits. With reference to the Greenleg Partridge chicken this account can be extended with an article from the Globaldiv newsletter⁸⁷: the population consists of 2 separate flocks of about 60 M and 700 F each. In one flock the birds are mated in groups of 1 M and 12-20 F. Matings of birds with 1 common grandparent are avoided. In the other there is rotational mating, the flock is in 4 groups and males from each group are mated to females in the next. Utility traits are recorded (survivability, growth rate, egg production & quality) but are not used in formulating breeding goals. Support for this breed has also been provided locally under a Biodiversity Conservation Programme (Spalona et al. 2007).

Conservation of local breeds, at least some of which are the outcomes of crossing with imports such as New Hampshire, Rhode Island Red and White Sussex, has been supported by research institutes in Slovakia since the 1970s (Spalona et al. 2007).

In Spain a programme conserving 13 varieties of poultry was started in 1975 (Campo et al. 2000) and continues⁸⁸. The annual cost is 54,500 euros (£47,000) (J.L. Campo pers. comm., INIA Madrid, February 2013). Characterization has taken place; populations are kept partly as pedigreed populations and partly random bred with inbreeding calculated by Wright's formula. Since 1998 the breeding scheme of Wang (1997) has been used. N_e values have been calculated as between 72 and 256.

In Switzerland, there are three native breeds (Poule Suisse (Schweizerhühn), Appenzelloise huppée (Appenzeller Spitzhaubenhühn) and Appenzelloise barbu (Appenzeller Barthühn). and maintenance of a flock book is managed by Förderverein Schweizer Kleinterrassen⁸⁹ with funding from the Federal Office for Agriculture, Switzerland and the NGO ProSpecieRara⁹⁰.

⁸⁶ <http://www.nordgen.org/husdyrdb/visrase.php?id=80&langid=1>

⁸⁷ issue 9, June 2009, http://www.globaldiv.eu/NL/GlobalDiv_Newsletter%20no%209.pdf by A. Witkowski and colleagues from universities of Lublin and Bydgoszcz

⁸⁸

http://wwwsp.inia.es/Publicaciones/PublicacionesInstitucionales/Documents/Memoria_INIA_2011.pdf

⁸⁹ <http://www.schweizer-kleinterrassen.ch>

⁹⁰ http://www.prospecierara.ch/de/projekte/erhaltungsprojekt_huehner

The Poltava Clay chicken of Ukraine is the subject of institute-based conservation activities which date back to 1948 when steps were taken to develop native chicken populations as an alternative to the poultry production system that was then dominant in collectivized Soviet Union agriculture (Moiseyeva et al. 2007).

Poultry breeding companies acknowledge that retention of genetic variation is vital for the future of their industry (Neeteson-van Nieuwenhoven et al. 2013) but there are serious obstacles to the use of “backyard breeds” as a source of this variation. At least in the last 10-15 years there have been no reported cases of this having been done⁹¹. There are genetic and practical obstacles. Along with the desired alleles such introgression would bring portions of the genome which would depress many aspects of the performance of the recipient stock. Compliance with biosecurity requirements could be difficult and there would be a substantial R&D requirement.

The process would in any case be time consuming. From pedigree to broiler production takes around 5 years, this can be doubled if the new variety is not developed from existing lines (Laughlin 2007). In principle introgression could be accelerated using molecular markers but there are no known instances of this having been achieved, at least for disease resistance traits (Cheng 2010). Transgenic processes might be practicable though the technology in poultry has lagged behind that in mammals (Nishijima and Iijima 2013).

In contrast, there are several examples, particularly from continental Europe, where local breeds have formed the basis of niche poultry production. Should it be decided to support poultry conservation more actively in the UK, this should be partnered by breed characterization and market analysis.

3.3.3.3 Feral animals

Feral animals have no special status in the EU. The Switzerland/Germany based NGO SAVE has been collating information and experiences and has identified 65 breeds and populations in Europe⁹².

Feral animals are those that live in a self-sustained population after a history of domestication and husbandry (Clutton-Brock 1999). The degree of human involvement in these populations varies. There is no management nor welfare culling for Soay and Boreray sheep on the St. Kilda archipelago nor for many, perhaps most feral goats. Chillingham cattle receive hay in winter and euthanasia on ground of individual welfare is practised. Cheviot goats are occasionally gathered. Other feral goats might be subject to shooting for trophies or because of a perceived nuisance, and for some populations immunocontraception (Kirkpatrick et al. 2011) has been under discussion (R.W. Small, pers. comm.).

There are many populations described as semi-feral and typically these are individually identifiable, there is some control of breeding or of overall numbers and they often have links with pedigreed populations of the same breed. Examples include Manx Loaghtan sheep on the Calf of Man⁹³ and Cheviot goats in a number of locations⁹⁴ also at least three populations of ponies including Welsh Mountain semi-feral (Winton et al. 2013)⁹⁵, Exmoor⁹⁶ and New Forest⁹⁷.

⁹¹ Dr. Santiago Avendaño, personal communication, 9 April 2013

⁹² http://www.save-foundation.net/docu/reports/SAVE_activity_2012.pdf

⁹³ <http://www.manxloaghtansheep.org>

⁹⁴ <http://www.lyntongoats.org.uk/relocation.php>

⁹⁵ <http://www.eryri-npa.gov.uk/park-authority/newsroom/press-releases-2007/safeguarding-the-future-of-the-carneddau-ponies>; <http://www.bbc.co.uk/news/uk-22204077>

⁹⁶ <http://www.moorlandmousietrust.org.uk>

⁹⁷ <http://www.newforestpony.com/newforest.php>

There are also instances of animals from feral populations being taken back into husbandry; this is the origin of the registered mainland populations of Soay and Boreray sheep (Jewell 1980), and of herds of Cheviot goats now established away from their historic range (Gough 2012).

The number of feral goats in the UK is between 5,000 and 10,000 in 40 – 50 locations (Smith 2005). Feral livestock represent an area of FAnGR where the policy environment is poorly defined and SAVE's evidence shows this is the case across the EU. Possible conflicts exist between animal health and welfare laws and international commitments to conservation, because rigorous enforcement of the former could threaten the continued existence of these populations, and if they are of conservation significance international commitments could be breached. These conflicts have seldom, if ever, been put to legal test. It might be anticipated that in such a (hypothetical) test, demonstration of the conservation importance of the population would carry some weight.

The Defra FAnGR committee has contributed to the development of policy by adopting criteria for inclusion of feral FAnGR in the UK National Breed Inventory which would tend to discourage the establishment of any more feral populations in the UK, by requiring a candidate breed, in addition to satisfying the criteria for inclusion in the Inventory, to demonstrate that "more than 90% of the population have been born to feral parents, over two generations"⁹⁸.

Now that fine detail genotyping using SNPs is practicable (Winton et al. 2013) a criterion relating to demonstration of genetic distinctiveness has not yet been added but may need to be considered.

Elsewhere in Europe, some feral or extensively managed breeds that live in herds with more than one active sire have parentages assigned to them on the basis of microsatellite typing (Bomcke and Gengler 2009; Fina et al. 2008).

3.3.4 An overall strategy

A general framework for a breed conservation scheme is given in **Figure 15** (after FAO 1998). This design is applicable across the world and can be fine-tuned for UK conditions.

The overarching conservation strategy needs to promote the maintenance of genetic diversity, which is measured in two ways; (1) the continued existence of breeds and (2) the maintenance of the genetic diversity within them. The breeds and the data relating to them are in private ownership while the international responsibility for them resides with the UK Government.

The strategy has to be able to encompass mainstream, numerically strong breeds such as cattle as well as poorly documented and rare breeds, notably many poultry.

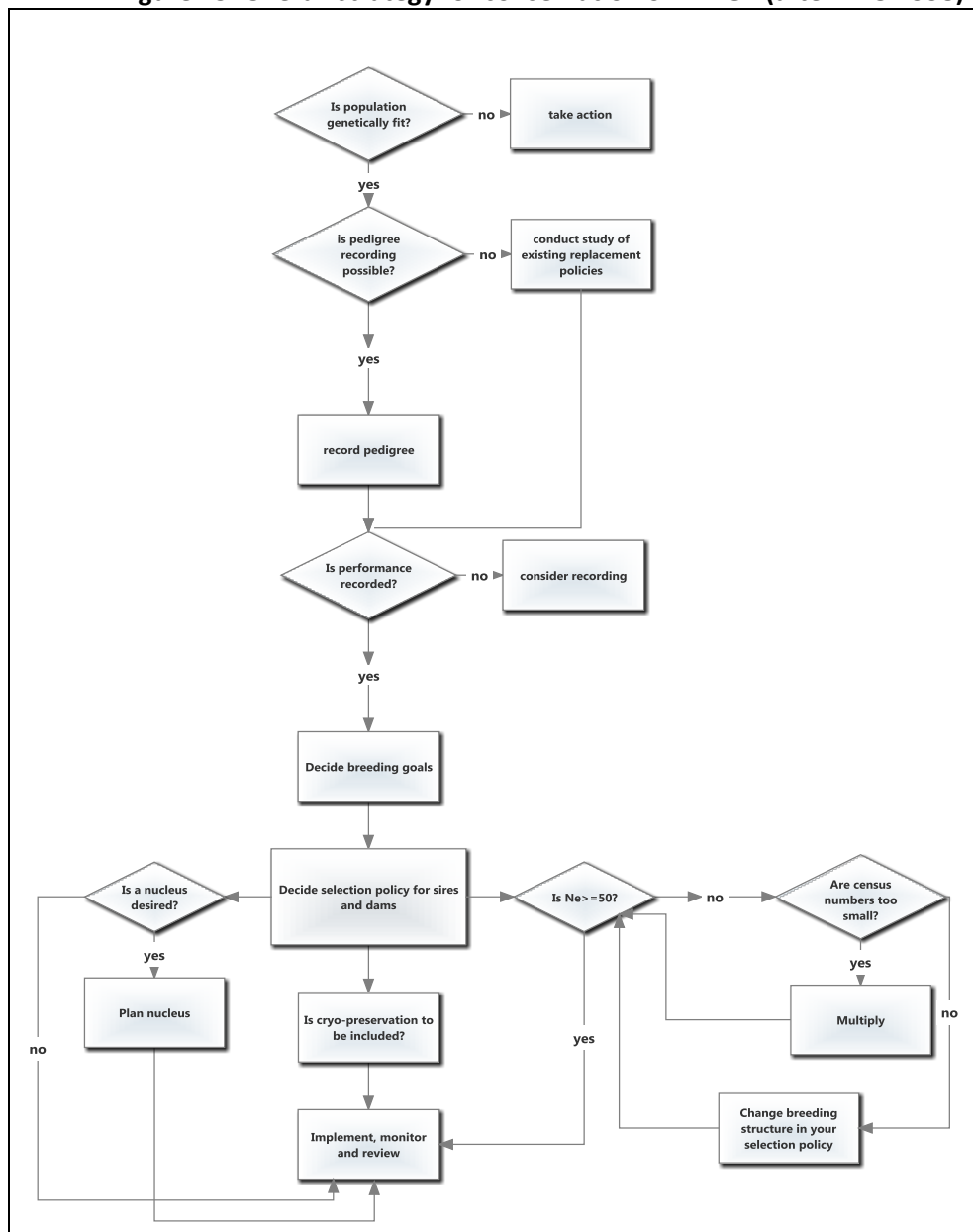
The general principles of conservation strategies based on live animal populations have been succinctly stated by Simm (1998, p.103):

- (i) start with as variable a population as possible;
- (ii) start with as large a population as possible;
- (iii) turn over generations as slowly as possible;
- (iv) use enough parents (especially males) to keep inbreeding at acceptable levels;
- (v) minimize the variation in family sizes to reduce inbreeding; and
- (vi) subdivide the breeding population to reduce inbreeding and genetic drift.

That N_e should be at least 50, in commercial breeds as well as in breeds where genetic conservation is the priority, is a firmly embedded and enduring rule of thumb (Kristensen and Sørensen 2005). In the guidelines from FAO (1998), how N_e was to be audited at breed level was not examined.

⁹⁸ <http://www.defra.gov.uk/fangr/files/BreedSocietyInventoryLetter.pdf>

Figure 15: Overall strategy for conservation of FAnGR (after FAO 1998).



Recently, genetic contribution and optimization approaches; Woolliams 2007; Fernández et al. 2011) have been applied to the theory of breed genetic management, sometimes with reference to specific breeds (Engelsma et al. 2011; Fabuel et al. 2004; Mucha and Windig 2009; Windig et al. 2007). Application to the process of choosing animals for representation in genebanks seems relatively straightforward but there do not seem to be any indications in the formal literature of these new methodologies being put into practice in the ongoing management of breeds. In principle, modifications to the software already widely used for the utilization of EBV data, would be able to perform relevant analysis (Woolliams 2007).

The theory of N_e has led, by admittedly complicated processes, to some simple rules about genetic management and a convenient table has been produced by Woolliams (2007, p.163), redrawn as **Table 17** which gives the minimum number of sires needed so that a population of particular demographic properties will have N_e of at least 50. The heavily outlined box represents the breeding system probably most likely in practice namely mass selection, where individuals are selected for breeding purely on the basis of their own merits for some sufficiently heritable character. Thus for example when females produce 4 breeding offspring in a lifetime and typically one male serves 5 or

more females, the breed would require 21 males and at least (21 x 5) females to achieve N_e of 50 or more. Wright's equation would yield N_e of 70 for that population and the difference is because the calculations that led to **Table 17** have taken account of the selection system (Woolliams 2007).

So far as number of breeding offspring produced during a female's lifetime is concerned, the ideal is for a female to be replaced in the breed by a single daughter and if she produces more, then more males will be needed otherwise overall inbreeding will increase. The chart presented as **Table 18**, which is reproduced from FAO (1998), is in fact an earlier version of **Table 17** and probably less applicable because the values for a given number of sires and dams are calculated on the basis of sires and dams per generation.

Species obviously differ in generation interval and litter size, but because the tables relate to numbers of animals retained for breeding rather than to total production, the differences between species do not have a very great effect on the calculations.

Table 17: Numbers of sires to be used to achieve N_e of at least 50, under different demographic conditions and selection regimes.

Ratio of F to M	Under mass selection						Random selection	Within-family selection
	Mean number of breeding offspring anticipated during lifetime of a female							
	4	8	12	16	20	36		
5 or more	21	23	25	27	28	30	15	10
4-5	21	25	27	28	29	32	16	11
3-4	23	26	28	30	31	35	17	11
2-3	25	29	32	34	36	40	19	11
1-2	31	38	43	46	48	55	25	13

Within-family selection is the process when a breed is divided into lineages and in selection all families are represented, the best individuals from each being used for breeding. The net effect is that a sire is replaced by one of his sons and a dam by one of her daughters, certain principles of inbreeding avoidance being observed. This can greatly reduce the number of sires needed to restrict increase in inbreeding.

Table 18: Numbers of sires and dams needed per generation to achieve N_e of at least 50.

Random selection		Mass selection		Within-family selection	
Sires	Dams	Sires	Dams	Sires	Dams
25	25	35	35	13	13
20	34	30	45	12	14
16	56	25	65	10	50
14	116	20	300	9	1000
Smaller numbers of sires: not possible					

With tables like this, breeders have the basic information needed to run a selection programme which still conserves genetic variation.

Formal breeding schemes can be organized and have attracted particular attention in France but these require strong central control; they might be appropriate for breeds with perhaps no more than five flocks or herds (Danchin-Burge et al. 2010). In the UK context the scientifically robust scheme that would be most straightforward to operate would be the minimization of average coancestry (MAC; Caballero and Toro 2000). Though intuitively attractive, programmes based on maximum avoidance of inbreeding and on equalizing founder contributions are not supported by

theory. Caballero and Toro (2000) point out that though MAI will reduce or delay inbreeding in the generations immediately following establishment of such a programme, as the programme proceeds and the variance of family size declines, the degree of genetic drift will increase. Equalizing founder contributions would minimize the variance of contributions from founders, but not those contributions from individuals of the generations intervening between the founders and their present-day descendants, so a population might show a good balance of contributions from the original founders but animals from intermediate generations may be over- or under-represented.

Guidance for organizations proposing to operate MAC programmes requires specialist input and would be expensive, particularly as follow-up analysis and auditing is needed. First steps would be:

- (i) to select as mates animals whose kinships with themselves and the rest of the breed do not greatly exceed the average mean kinship, and
- (ii) to pair mates with similar levels of mean kinship (Ballou and Lacy 1995).

What appears to be the only documented example of such a programme in the UK, the Cleveland Bay programme⁹⁹, is detailed by Dell (2010). While a range of software is available¹⁰⁰ specialist advice and input is necessary. A system widely used in the UK is Geneped, an add-on to the Breed Society Record package operated by Grassroots Systems Ltd. Geneped was developed in collaboration with RBST (Townsend 2003b) and has been used to compute inbreeding coefficients and to trace founder representation in many breeds, though accessible reports are rare¹⁰¹ (other examples: Roberts 2008; Walters 2012; Wilkinson 2012). The RBST analyses Geneped outputs on behalf of breed societies, because specialist input is needed for interpretation. Recently founder representation has been emphasized less and the advice is being oriented more towards kinship analysis¹⁰².

3.4 Conservation strategies: summary of findings

- While the UK Government is internationally accountable for the success of the UK's efforts at conservation of FAnGR, whether or not this achieved depends on the private sector.
- Individual breeders operate within a framework of breed societies with important input from umbrella organizations. The activities of these bodies are funded by breeders, breed societies and certain charitable organizations and the annual value of this contribution to conservation of the genetic resource represented by native breeds is estimated at £3.7 million.
- Even though in many cases numbers are rather small, breeders of commercial native breeds are often involved in systematic genetic improvement. In some cases, improvement has involved introgression. This process needs to be monitored and managed and in several cases the acknowledgement of a segment of the breed as being "traditional", "original" or "native" has been beneficial. Generally, effective population sizes seem large enough for most breeds to be able to accommodate directed selection activities provided inbreeding is limited.
- A key measure of success in conserving FAnGR is maintenance of effective population size at 50 at the least. As part of the JNCC Biodiversity Indicators study, an audit of effectiveness of conservation as it operates in cattle and sheep was carried out in 2007 (published 2008) with reassuring results, namely that effective population sizes in sheep and cattle had, overall, either

⁹⁹ Ark Winter 2008, p.6

¹⁰⁰ http://www.save-foundation.net/docu/en/Pedigree_Analysis_Software.pdf

¹⁰¹ <http://www.hebrideansheep.org.uk/Downloads/Blackboard/2010%2003%20Blackboard.pdf>;
<http://www.castlemilkmooritsociety.co.uk/Pages/TheBreedingProgramme.aspx>;
<http://www.allgoats.org.uk/Downloads/BGS%20Grassroots.pdf>

¹⁰² Ark Autumn 2012, p.24

increased or remained the same. However, further work is needed on indicators of livestock biodiversity.

- The present study, which is extended to pigs, goats, equines and poultry suggests that effective population sizes continue to be healthy. However, there are important emerging issues, including the management of traditional sectors within commercial breeds; the ways in which breeds that were once commercially significant can decline very rapidly in numbers when the commercial environment changes; and the degree of variation in the demographic structures of breeds.
- The UK's record in establishing and maintaining gene banks for mammalian livestock compares favourably with those of other countries.
- The UK compares very unfavourably with many European countries in institutional support of poultry conservation.
- Genetic variation resides in the variation among animals within a breed, but also in the differences between breeds. Thus, an enabling environment is needed both for the maintenance of the breed as an entity, and for the conservation of the genetic variation therein.
- At the same time, breeders and breed societies need guidance regarding the conservation of genetic variation within breeds. This is influenced by demographic variables and highlights the importance of maximizing some variables (notably generation length and the numbers of sires) while minimizing others (notably the variability in numbers of offspring that subsequently breed, produced by parents), and avoiding excessive use of particular sires.
- The existing legal and regulatory framework is broadly conducive to FAnGR conservation, and private sector objectives and practice are generally in line with conservation needs. Best practice advice is however needed to address some existing and emerging issues, and to highlight opportunities to strengthen the reconciliation of conservation and commercial objectives.
- In particular, there are opportunities to improve utilization of public domain information in the form of herd- flock- or stud book data, both to manage and audit the maintenance of a satisfactory effective population size. There is also a need and opportunity to:
 - improve the scope, quality and availability of some of the information collected and monitored (for example breed characterization);
 - make full use of a range of modern analytical tools; and
 - strengthen organization and representation of breeders in some sub-sectors, notably poultry.

4 Best practice guidance

4.1 The background to recommendations

Conservation of FAnGR depends on breeds continuing to exist as distinct entities, each adequately widespread and in sufficient abundance to minimize the risk of extinction through collapse in numbers.

The genetic variation within breeds that are numerically small (and this includes that within “traditional” segments of mainstream breeds) can be conserved if proper breeding plans are being followed.

Breeds are owned by private individuals. If these individuals are not members of a breed society, their animals cannot be considered as part of the breed. The role of the breed society is therefore central.

How breed societies ensure that proper breeding plans are in effect will vary across societies. In some a general policy may be achievable, but for most the practicable approach will be a periodic review to ensure that the totality of breeding plans practised by individuals is leading to a satisfactory outcome, which would to a major extent be indicated by increase of inbreeding being kept sufficiently low in the breed as a whole.

Key findings of the present study, that underpin the recommendations offered here, are reported in Sections 3.4 and 4.3 of this document.

This guidance is also available as a separate document.

4.2 Specific recommendations

Guidance for breeders

1. Guidance on the practical husbandry, welfare and management of breeding animals is readily available from college courses, networks and societies, veterinary surgeons, published books and periodicals;
2. All breeders should join their breed society. If one already exists, do not form a new one, even if you believe your animals are a distinct type within a currently accepted breed. If in doubt, consult the Rare Breeds Survival Trust, Rare Poultry Society or other umbrella organizations;
3. If intending to practise selection, consider joining a centralized scheme;
4. If breeding mainly for conservation, consider lengthening generation intervals or using a wider spread of males;
5. If keeping poultry, note the recent guidance from the Animal Health and Veterinary Laboratories Agency on the advantages of documented membership of a breed society and of unique individual identification of your birds¹⁰³.

Guidance for breed societies

- (i) In the case of breeds at particular risk, the priority should be on building up numbers and minimizing overall risk. Once progress has been made in this direction, breeding schemes that manage effective population size should be implemented;

¹⁰³ This is to be published on the Defra FAnGR website.

- (ii) Particularly in the case of numerically strong breeds, traditional or original lines within the breed should be inventoried and electronic databases reviewed to ensure pedigrees are accurately documented;
- (iii) For breeds where there has been upgrading or breed development by introgression, there should be a clear designation to be applied to animals that have no ancestry from outside the UK population. This must be established rigorously, if necessary by tracing animals back beyond electronic records and into hard copy volumes;
- (iv) For pedigreed breeds, if one is not already in existence, establish a breed conservation committee which will, every year, report on retention of genetic variation within the registered portion of the breed. Recommended mode of operation of the committee is presented below;
- (v) For non- or partially-pedigreed sheep breeds, breed societies should consider comparing their flock books with those of other breeds and finding ways of making them as informative as possible; specifically
 - a) Flock returns should be included in as much detail as possible;
 - b) Rams should be identifiable as home-bred or bought-in;
 - c) Periodic surveys of breed numerical status should be made and trends identified;
- (vi) Poultry breed societies should consider options for pedigree recording and operation of breeder and animal databases; these must be electronic.

Guidance for the UK Government, Devolved Administrations and public bodies

1. Improve the current enabling environment for breed societies and breeders;
 2. Implement urgently research on identifying significant flocks/herds, in all breeds but with special emphasis on those which are geographically localized;
 3. Arrange with other government agencies and bodies that such flocks/herds receive special protection when needed, for example from culling during disease outbreaks;
 4. Review all proposed regulatory requirements which may be particularly financially burdensome on keepers of breeds of conservation significance;
 5. Monitor effective population sizes of breeds;
 6. Implement urgently research and development relating to the conservation of poultry breeds;
 7. Achieve a cost-effective national database of electronic breed registration and census data including development of software for monitoring and periodic review and for facilitating routine activities of breed societies.
-

Recommended mode of operation for a breed conservation committee

First steps

Encourage all breeders to adopt an overall breeding policy and to see it as a group activity.

Arrange for the exchange of information so there can be breed-wide networks for exchanging parent stock. Remember that many breeders will not be confident internet users.

Avoid having overly exclusive rules for registration of animals.

If there are genetic faults in the breed, deal with them openly¹⁰⁴.

If there are problems, find out how these have been dealt with in other breeds, and seek advice.

The key- have as many active sires as practicable, all siring much the same number of young.

This is how you can calculate a minimum number of sires for your breed.

If this calculation is not possible, then a rule of thumb is to have at least 25 sires active in each generation, each siring similar numbers of offspring. This is broadly true for all species.

1. How many dams are there on average for each sire? This will probably be 5 or more for cattle, 5 for sheep and goats, 3 for horses and poultry, 2 for pigs. There is no need to try and change this.
2. Deduce how many breeding offspring (sexes combined) the average female produces during her lifetime. For all species, this will probably be between 4 and 12.
3. Are there at least the following numbers of males siring registered stock in the current year:
 - a. For a lifetime production of 4, 21 bulls, rams or bucks; 24 stallions or male birds; 25 boars
 - b. For a lifetime production of 12, 25 bulls, rams or bucks; 28 stallions or male birds; 43 boars
4. If your breed uses EBVs, specialist advice is needed to confirm the above numbers.
5. Discuss with your database manager ways of keeping the mating structure of your breed, and its consequences for increase of inbreeding, under review.

The target is to have at least the number of sires given in (3) above for your species.

¹⁰⁴ http://www.signetfbc.co.uk/documents/content/sheepbreeder/ridgene_manual_digital.pdf

Possible ways of achieving this number of sires – also, ask your membership for ideas

1. Possible incentives to breeders might include:
 - a. With advice from your database manager, provide a list of recommended sires
 - b. Make available stored semen; have a rationing/archiving scheme so stocks never become exhausted; encourage purchasers of semen to contribute to restocking
2. Manipulate registration fees perhaps as follows:
 - a. Free registration for first son/daughter registered from a given sire that year
 - b. Increased registration fee for subsequent progeny, maybe on a sliding scale
 - c. Funds raised from (b) could be used to subsidize (a) or for some other conservation purpose for example collection of semen or funding periodic external review of breed conservation activities

And here are some things your committee should do every year or every two years:

1. Calculate effective population size by whatever method your database manager can offer (preferably by at least 2 methods). Ensure exactly the same methods are used each year and that the calculations are documented. Compare with previous years, add new methods should they become available
If you are unable to do this, then report the number of sires that have been in use, which should be at least 25. If you can also illustrate that numbers of offspring per sire are getting more even, so much the better – this is easy to do with spreadsheets
2. Review whether there are specific sires that are being heavily used
3. If not operating a semen bank, consider doing so
4. If your breed uses computerized evaluation including the recording of performance data for pedigreed animals, ask your service provider whether optimum contribution methodology can be applied and consider how to implement it

5 Glossary

Note: the meaning of many terms is specific to their use within FAnGR conservation

Allele: each alternative form that a gene can take.

Area based: of support or subsidy regimes: payment on the basis of the land area under a particular system, rather than on the number of animals kept. See Headage based.

Backcross: see Upgrading.

Biodiversity: biological diversity, here, encompassing the variety of breeds and the genetic variation within them.

Biodiversity indicator: measure of diversity of some biological system whether at regional, ecosystem, habitat, population or individual level. Indicators need to summarize often complex data in a standardized way and provide a clear message for decision-makers and the public.

Biotechnology: physical manipulation of the genome for industrial or agricultural purposes.

Bloodline: see Lineage.

Bottleneck: a temporary restriction of population size. As a result, the post-bottleneck population can be genetically different from the pre-bottleneck population, through chance.

Bought-in: converse of homebred.

Breed: a livestock breed, in the UK context, is an interbreeding population of husbanded or formerly husbanded domesticated animals of consistent genotype and phenotype with a recognised history and administrative framework.

Breed code: prefix or suffix to an animal's serial number indicating the breed or type to which it belongs. For this report, most relevant in dairy cattle where many breeds allow introgression; can be a useful shorthand in summarizing pedigrees. Breed codes are operated by other organizations including the British Pig Association and the British Cattle Movement Service.

Breed society: duly constituted administrative framework in which a breed operates; typically responsible for registration of animals, maintenance of breed standards, breed promotion, and regulation of development of the breed.

Breed standard: the accepted description of a breed, as adopted and maintained by a breed society.

Breeding programme: organized programme aimed at heritable improvement in some aspect of livestock phenotype. When properly organized, improvement can be achieved in several aspects and inbreeding and loss of genetic variation minimized.

Breeding value: see Estimated breeding value.

BSE: bovine spongiform encephalopathy ("mad cow disease")

Chromosome: the physical entity within a cell upon which genes are located. Replicate themselves during the processes of cell division.

Cloning: production of genetically identical individuals usually by embryo splitting.

Coancestry: Relationship between two animals expressed as the inbreeding coefficient of their hypothetical offspring. Also known as kinship.

Coefficient of inbreeding: measure of how inbred an animal is. Range is 0 to 1, often expressed as a percentage. Formally, the proportion of the genotype at which both of the two alleles trace back to the same ancestor.

Cohort: group of animals born or hatched at approximately the same time period or season (period defined in terms of the individual species).

Commercial: (of a breed) see Mainstream.

Composite breed: see Hybrid.

Conformation: body proportions of an animal.

Continental breed: usually refers to terminal sire cattle and sheep breeds originating from continental Europe.

Covariance: statistical measure of the degree to which two values vary together.

Crossbreeding: mating of animals of two different breeds to give a crossbred, which may have its own name (e.g. Scotch Halfbred which is the progeny of a Border Leicester ram and a Cheviot ewe) or be denoted in terms of the parental breed, the sire being given first (e.g. Hereford x Friesian).

- Crossbreeding is relatively unusual between two crossbreds in practical husbandry though it features strongly in the development and production of commercial/corporate pigs and poultry.
- Crossing sire breed: a breed selected for prolificacy, mated with animals where prolificacy has not been particularly favoured. The crossbred progeny usually combine the merits of both parents and often show heterosis.
- Cryobank: see Germplasm.
- Dam line: see Maternal breed.
- Demographic: relating to age and sex structure and to (age-specific) birth and death rates of a breed, and how the breed is organized into breeding groups.
- DNA test: used in many cattle and horse breeds to authenticate declared parentage.
- Domesticated: having undergone an evolutionary process involving biological and cultural change leading to animals being enfolded into human society with a view to economic profit or other benefit.
- EBV: see Estimated breeding value.
- Ecosystem services: functions of general community benefit ascribable to a particular farming or land management operation, not appearing on a balance sheet or profit and loss account but quantifiable in cash terms. Examples include water quality and carbon sequestration.
- Effective population size: When calculated for a breed, the size of a theoretical population of idealized individuals that would exhibit the same rate of increase of inbreeding as that shown by the breed in question. Not the number of breeding animals.
- Endemic: (adjective) found in only one region; native to a region.
- Epidemic: (adjective or noun) infectious disease prevalent within a population.
- Estimated breeding value: the degree to which an animal is genetically superior to the breed average. Can be calculated from the performance of its relatives.
- Ex situ conservation: (commonly italicized) conservation of a breed away from its normal environment, principally as frozen germplasm or somatic cells. Strictly speaking would include farm park populations but seldom if ever used in that sense.
- Feral: living in a self-sustained population after a history of domestication and husbandry, without direct control of mating.
- Fitness traits: traits relating to survival, such as maternal behaviour, longevity, ease of giving birth. See Production traits.
- Flock book: periodically published (printed or electronic) list of animals registered by a breed society in a defined period. Term applies to sheep and poultry.
- Flock prefix: the prefix to an animal's registered name, agreed with the breed society, that indicates the flock in which the animal is born (also defines Herd prefix)
- Foundation flock/herd: flock/herd which was in the first volume of a flock/herd book.
- Gene: the physical entity carrying genetic information. A piece of DNA occupying a particular locus on a chromosome.
- Gene flow: transfer of breeding stock or germplasm from one breeder to another.
- Genebank: see Germplasm
- GENEPED: widely used proprietary software operated by Grassroots Ltd. for characterizing inbreeding coefficients and other population genetic parameters.
- Generation interval: time elapsed between birth of a parent and birth of its offspring, averaged across all offspring. Not the same as age of parent at birth of first offspring.
- Genetic drift: changes in genetic composition of a population due to random effects, most probable in small populations.
- Genetic marker: see molecular marker.
- Genetic modification: see Transgenic.
- Genetic: relating to inherited variation.
- Genome: term overlaps with genotype, but "genome" tends to be used when the breed or species as a whole is being considered, genotype tends to relate to individuals, breeds or groups within breeds.

Genomic selection: selection that uses SNPs to characterize segments of the chromosome; the contribution of each segment to fitness or production is deduced facilitating the calculation of breeding values of individuals.

Genomics: study of the processes linking the physical structure of genes to interactions among those genes and to the determination of the phenotype. Heavily dependent on computation of very large datasets.

Genotype: the genetic endowment of an animal; the inherited component of its phenotype. Sometimes used in the sense of a group of animals of similar genotype, that are rather distinct from others within a breed.

Germplasm: reproductive cells or embryos, typically stored in a genebank in liquid nitrogen at minus 196degC.

Grading: (adjective, applied to animal) animal which is in an upgrading programme.

Grading-up: see Upgrading

Headage based: of support or subsidy regimes: payment on a per head basis. See Area based.

Herd book: as for Flock book, but applies to pigs, cattle and goats.

Herd prefix: see Flock prefix.

Heritability: proportion (range 0 – 1; often expressed as percentage) of the variation of a quantitative trait that is determined by the genotype. A character with high heritability is one that is likely to respond to selection.

Heterosis: Hybrid vigour. Extent to which the performance of a crossbred is greater than the average performance of its parents. Attributable to outbreeding, as a result of which an individual is likely to receive different alleles from its parents; should one of these alleles be relatively impaired in function, the other is likely to compensate. The converse of inbreeding depression.

Heterozygote: (adjective – heterozygous; state – heterozygosity) an individual with a different allele at a given locus on the members of a chromosome pair.

Homebred: (adjective) an animal that is retained in the flock or herd in which it was born.

Homozygote: (adjective – homozygous; state – homozygosity) an individual with the same allele at a given locus on both members of a chromosome pair.

Husbandry: maintenance of livestock or tamed non-domesticated animals under conditions of shelter from environmental conditions, and control of breeding, with a view to economic profit.

Hybrid: In zoological terms means the progeny of two different species. In livestock, an animal derived from a crossbreeding programme where the relative proportions of the genotype ascribable to the breeds from which it originated are maintained at stable levels through planned mating. Tends to be applied to commercial pig and poultry breeds. For cattle and sheep, the term “composite breed” is more commonly used.

Hybrid vigour: see Heterosis.

Immunocontraception: process whereby a female is rendered immune to her own ova or embryos or to sperm.

In situ conservation: (commonly italicized) conservation of a breed as live animals within a farming system.

Inbreeding: the mating of individuals whose parents have common ancestors, e.g. brother and sister, or cousin matings, or indeed any mating where there is one or more individual featuring on both the maternal and paternal sides of the animal's ancestry.

Inbreeding depression: Extent to which the performance of a crossbred is inferior to the average performance of its parents. Attributable to inbreeding, as a result of which an individual is likely to receive the same alleles from both parents. The converse of heterosis.

Indicator: see Biodiversity indicator.

Interbreeding: mating animals that are all in the same population, with each other.

Introgression: introduction of genetic material from another breed.

Kinship: see Coancestry

Lineage: line of descent. Also termed bloodline or matriline/patriline. A common human example of a patriline is a surname.

Locus: location on a chromosome of a gene.

Mainstream: breeds which make a sizeable contribution to agricultural output. They may be numerically strong, or may, because of their position in crossbreeding systems, make a key contribution while being numerically quite small.

Maternal breed: a breed selected for such attributes as twinning rate, mothering qualities. Same as dam line.

Matriline: see Lineage.

Maximum avoidance of inbreeding: mating plan based on minimizing the inbreeding of offspring. Not now considered sufficient for maintenance of genetic diversity in the medium or long term.

Microsatellite: class of loci distributed throughout the genome with highly variable alleles comprising apparently non-functional DNA. Extensively used as molecular markers and to measure genetic relationships among breeds and the general level of genetic variation within breeds.

Mitochondrial DNA: DNA carried by organelles within the cells involved in energy production; it enables matriline to be identified because it is not transmitted by sperm during fertilization, only by eggs, and remains relatively stable because there is no recombination. Has mainly been found useful for tracing relationships among breeds which have been developing separately for hundreds of generations.

Molecular characterization: measuring within-breed genetic variation primarily by the use of molecular markers and SNPs.

Molecular marker: microsatellite locus or other genetic system which is relatively easy to characterize and which is closely linked on the chromosome to some functional locus or loci of importance in determining phenotype but which may be difficult to characterize. Animals with a particular marker allele may also possess advantageous alleles at the functional loci. Used in marker-assisted selection, which exploits linkages between a marker and the trait of interest.

Multifunctional landscapes: farmed landscapes usually of scenic quality or performing ecosystem services which provide public benefit in more ways than just agricultural output.

Mutation: a sudden genetic change, i.e. parents lack that particular form of the allele but it appears in one or more offspring.

Native: see Native breed; also see Traditional

Native breed: breed complying with Defra criteria conferring conservation status befitting a UK farm animal genetic resource.

Omics: molecular genetic approaches that focus on a specific aspect of the phenotype, for example metabolomics (relating to metabolic processes) or proteomics (relating to the totality of proteins in the body).

Oocyte: female reproductive cell prior to release from the ovary.

Optimum contributions: computational methodology applicable to managing or documenting inbreeding in populations under selection.

Original: see Traditional.

Passport: document allocated to an equine for purposes of identification and tracking.

Pedigree: (noun or adjective) ancestry of an animal; statement of the individual animals from which it is descended. May or may not signify purebred.

Percentage of genotype: see Upgrading.

Performance recording: documentation of animal data such as weight gain, milk yield, fertility etc. Can be used in breeding plans and in some breeds can be necessary for an animal to be acceptable for registration.

Phenotype: the observable characteristics of an individual.

Polled: (adjective) genetically without horns, as opposed to dehorned. Genetically dominant to horned.

Polygenic: (adjective) a character that is determined by the genes at more than one locus.

Population: genetic term meaning the unit within which genetic change takes place. Can be a breed, or a flock or herd, or an entire species, depending on the context.

Post-productivist agriculture: farming where production of bulk commodities is of secondary importance.

Primitive breed: general term often used for the small-bodied sheep breeds of northern short-tailed type.

Production traits: traits relevant to milk yield, carcase conformation, meat quality and other attributes of marketable product. See Fitness traits.

Progeny testing: estimating the breeding value of an animal by performance recording its offspring.

Prolific: (adjective) producing, rearing and weaning large numbers of young.

Purebred: Strictly, an animal of pure descent from the breed whose name it carries. Breed societies can, under the EU Zootechnical Regulations, grant purebred status to animals which include a proportion of ancestry from some other breed

Quantitative genetics: study of the inheritance of quantitative variation, for example body size or behaviour, which depend on large numbers of genes each of relatively small effect.

Quantitative trait locus: a locus whose genes have a relatively large effect on a quantitative trait.

:

Registration: process operated by breed societies whereby an animal conforming to regulations is entered in a register, which is published as a herd-, flock- or stud book. The animal is allocated a serial number and a pedigree certificate may be issued. There are often sub-registers for animals which only comply with some of the regulations, for example those which are in upgrading programmes, and registration numbers may carry prefixes or suffixes which identify such animals.

Reproductive technology: science-based interventions manipulating aspects of reproductive biology, such as artificial insemination, embryo transfer, transgenics and cloning.

Scrapie: the sheep equivalent of BSE, though apparently without the serious consequences for humans.

Selection intensity: a measure of how superior animals selected for breeding are to the rest of the population. Related to the proportion of animals selected for breeding.

Single-nucleotide polymorphism: genetic variation in the fundamental element of the genetic code, the actual base sequence of DNA. "SNP chips" are a rapidly developing technology enabling the alleles an animal possesses at very large numbers of loci to be established and this can enable the animal to be characterized for production and other traits. In a related approach SNPs can be used to define regions of the genome with particular phenotypic effects.

SNP: see Single-nucleotide polymorphism.

Stud book: as for Flock book, but applies to equines.

Substructuring: consequences of patterns of gene flow within a population. Measurable from inbreeding coefficients (by " F_{IS} statistics").

Sustainable: in genetic conservation terms, not involving the excessive and over-rapid loss of genetic variation, whether neutral or functional.

Terminal sire breed: a breed selected for rapid and high-quality meat production. When mated with a crossbred or some other breed, fast-growing, marketable progeny result.

Traditional: sector within a breed which has received no introgression. The time period over which this has been the case has not been defined and "traditional" status is assigned on a case by case basis. Depending on the breed, the term used might be "original" or (confusingly) "native".

Transgenic: (adjective) resulting from genetic modification procedures whereby one or more genes or chromosomal fragments from another life form are incorporated into the heritable genome.

Upgrading: process whereby introgression of breed A into breed B is managed. If the daughters of a mating of a male of breed A with a breed B female are themselves mated (backcrossed) with a breed A male, and this process is continued, a herd originally of breed B will in successive generations consist of animals of average percentage genotype (1) 50:50 A:B, (2) 75:25 A:B, (3) 87.5:12.5 A:B, (4) 93.75:6.25 A:B.

Variance: statistical measure of the degree to which a value is variable.

Welfare: (of an animal) Its state as regards coping with the environment.

Within-breed genetic variation: a key target for conservation. Measured by the numbers of different alleles present at given loci and the extent to which loci are heterozygous.

6 Acknowledgements

Without the generous and helpful support provided by a large number of individuals and organizations this project would not have been possible. They are not, however, responsible for the analyses conducted and the conclusions drawn which are due to the author alone.

In Defra, valuable and sympathetic support has been provided throughout the duration of the project by Bill Lyons.

The Steering Committee (Professor Asko Mäki-Tanila, Dr. Claire Barber, Collette Connor, Rob Havard, Julian Hosking, Louisa Bagshaw, Professor Charlotte Maltin, Roy McLachlan and Bryn Jones) have provided helpful guidance throughout.

Libby Henson of Grassroots Systems Ltd. provided indispensable help with obtaining the use of data from breed societies, and Margaret Hargreaves extracted relevant statistics with patience, insight and thoroughness.

Marcus Bates of British Pig Association kindly arranged for the provision of relevant data.

Rachel Farrow patiently and impeccably transcribed herd book and flock book information, Mme Virginia Kouyoumdjian kindly helped with information from France.

Many breed society secretaries and other office holders generously gave permission to use statistics derived from their data and in several cases provided data directly for analysis.

Professional colleagues provided unpublished materials, advice and other indispensable help. Particular acknowledgement is made to Dr. Santiago Avendaño, Dr. Maurice Bichard, Sam Boon, Mr. Tim Brigstocke, Dr. José Luis Campo, Mrs. Amanda Carson MRCVS, Dr. Coralie Danchin-Burge, Dr. Andy Dell, Mr. Bill Luff, Mr. Stuart Mullan MRCVS, Dr. Janet Roden, Dr. Darren Todd and Professor John Woolliams.

7 Technical Appendices

Demographic and genetic information were obtained either via Grassroots Systems Ltd., or from published flock books and herd books. The kind cooperation of breed societies is gratefully acknowledged; any interpretation placed on the data is solely due to the author.

7.1.1 Technical Appendix 1: Population data of dairy cattle

Basic population data of dairy cattle

Breed	year	Total sires	M calf regs	F calf regs	Ratio F/M calves	Ratio dams/sires	Total dams	Mean sons/sire	Variance sons/sire	Mean dau. / sire	Variance dau. / sire	covariance
Ayrshire	2011	405	123	2930	23.8	7.5	3053	0.31	1.18	7.23	138.3	4.645
Dairy Shorthorn grading	2008	146	51	1179	23.1	9.1	1325	0.30	0.71	6.97	82.26	1.769
Dairy Shorthorn	2008	136	87	684	7.9	5.7	2405	0.64	2.08	5.02	69.12	2.371
Guernsey	2011	99	28	943	33.7	9.8	971	0.29	0.41	9.56	163.3	3.477
British Friesian	2011-2012	182	236	2352	9.96	15.0	2820	0.81	3.52	10.31	313.2	21.450

7.1.2 Technical Appendix 2: Population data of non-dairy cattle

Basic registration data for western and northern cattle breeds

Breed	year	Total sires	M calf regs	F calf regs	Ratio F/M calves	Ratio dams/sires	Total dams	Mean sons/sire	Variance sons/sire	Mean dau. / sire	Variance dau. / sire	covariance
Aberdeen Angus (orig.)	2011	16	20	37	1.9	3.6	57	1.19	2.30	2.38	8.25	1.592
Dexter	2008	545	120	2215	18.5	4.3	2335	0.22	0.32	4.06	13.71	1.728
Highland	2009	358	53	1708	32.2	4.9	1793	0.18	0.43	4.82	19.32	0.423
Irish Moiled	2011	68	33	136	4.1	2.4	157	0.50	0.75	2.06	4.19	0.631
Luig	2011	227	168	1795	10.7	8.5	1894	0.75	3.72	8.01	31.94	1.344
Shetland	2011	63	33	147	4.5	2.9	180	0.52	0.74	2.33	4.68	0.449
Welsh Black	2010	345	90	2041	22.7	6.2	2131	0.26	0.54	5.92	24.48	1.121

Basic registration data for beef breeds of historical short-horned type

Breed	year	Total sires	M calf regs	F calf regs	Ratio F/M calves	Ratio dams/sires	Total dams	Mean sons/sire	Variance sons/sire	Mean daughters / sire	Variance daughters / sire	covariance
Beef Shorthorn	2008	370	956	1784	1.9	7.4	2740	2.58	12.86	4.82	25.53	9.947
Lincoln Red	2011	155	74	771	10.4	5.2	810	0.4	1.04	4.97	18.80	0.961
Lincoln Red (orig.)	2008	33	9	171	19.0	5.5	180	0.27	0.33	5.18	20.15	-0.199
Whitebred Shorthorn	2011	28	48	49	1.0	3.2	90	1.71	4.80	1.75	3.60	1.852

Basic registration data for English lowland cattle

Breed	year	Total sires	M calf regs	F calf regs	Ratio F/M calves	Ratio dams/sires	Total dams	Mean sons / sire	Variance sons / sire	Mean dau. / sire	Variance dau. / sire	covariance
British White	2011	100	70	343	4.9	4.0	398	0.70	1.34	3.43	6.89	0.292
Gloucester	2011	32	8	66	8.3	2.2	70	0.25	0.26	2.07	4.83	-0.484
Hereford	2011	302	957	1369	1.4	7.7	2326	3.18	12.65	4.53	17.82	9.767
Hereford (trad.)	2011	60	155	301	1.9	7.6	456	2.58	18.756	5.02	26.22	13.346
Longhorn	2009	309	72	1606	22.3	5.4	1613	0.23	0.38	5.20	23.41	0.204
Poll Hereford	2011	544	1747	2227	1.3	7.3	3974	3.20	14.45	4.12	18.20	9.644
Red Poll	2011	159	46	901	19.6	5.63	868	0.305	0.052	5.967	35.15	-0.210
South Devon	2011	527	223	3099	13.9	6.3	3322	0.423	1.408	5.880	20.714	0.794

7.1.3 Technical Appendix 3: Population data of sheep

Basic data for maternal breeds

Breed	year	Total sires	Total dams	M lamb regs	F lamb regs	Ratio F/M lambs	Ratio dams / sires	Mean sons / sire	Variance sons / sire	Mean dau. / sire	Variance dau. / sire	covariance
Dalesbred	2010	169		488	1554	3.18		2.89	6.37	9.19		
N.C. Cheviot (Park)	2011	451	11957				26.5					
N.C. Cheviot (Hill)	2011	1203	59528				49.5					
S. C. Cheviot	2010	94		159								
W.F. Woodland	2011	43	216	25	245	9.8	5.0	0.58	0.73	5.70	46.31	-0.582
Wiltshire Horn	2011	324	2448	391	2851	7.3	7.6	1.44	5.34	10.48	86.59	4.752

Basic flock data for self-contained breeds

Breed	year	Total sires	Total dams	M lamb regs	F lamb regs	Ratio F/M lambs	Ratio dams/sires	Mean sons / sire	Variance sons / sire	Mean dau. / sire	Variance dau. / sire	covariance
Boreray	2011	31	110	23	102	4.4	3.5	0.74	25.9	3.29	10.88	0.177
C'milk Moorit	2011	61	219	50	250	5.0	3.6	0.93	1.47	4.63	12.50	-0.7827
Devon Closewool	2009	85	3279									
Dorset Horn	2011	95	1698	30			17.9					
Leicester L'wool	2011	42	204	42	235	5.6	4.9	1.02	1.60	5.73	151.4	2.282
Lincoln L'wool	2011	72	279	36	299	8.3	3.9	0.50	0.59	4.15	13.03	-0.401
Manx Loaghtan	2011	85	337	65	356	5.5	4.0	0.82	1.28	4.51	20.79	1.039
Norfolk Horn	2011	96	390	65	434	6.7	4.1	0.69	1.15	4.62	15.84	1.031
N. Ronaldsay	2011	46	151	43	146	3.4	3.3	1.02	4.91	3.48	18.70	2.720
Poll Dorset	2011	676	16898	375			25.0					
Portland	2011	99	373	45	361	8.0	3.8	0.45	0.68	3.65	21.66	0.152
Soay	2011	160	539	141	543	3.9	3.4	0.90	1.63	3.48	14.40	0.647
Hebridean	2011	217	1586				7.31	1.69 in 2012	1.46 in 2012	7.51 in 2012	61.70 in 2012	0.476 in 2012

Mean progeny per male and generation intervals for sheep (mean 2008-2011; age x y: mean age of m or f parent at birth of m or f offspring, in years)

	m per sire	f per sire	age s m	age s f	age d m	age d f
Boreray	0.7	3.3	3.17	3.64	4.80	4.18
Castlemilk Moorit	0.8	4.1	2.80	2.78	3.82	4.06
Leicester Longwool	1.0	5.6	3.76	10.93	3.98	4.21
Lincoln Longwool	0.5	4.2	2.90	2.94	3.44	3.55
Manx Loaghtan	0.8	4.2	2.40	2.70	4.37	4.19
Norfolk Horn	0.7	4.5	3.07	3.13	3.49	3.53
North Ronaldsay	0.9	3.2	3.23	3.57	4.14	4.06
Oxford Down	0.5	3.9	3.07	2.92	4.00	4.16
Portland	0.5	3.6	3.91	3.30	4.10	4.06
Soay	0.9	3.4	3.06	3.38	3.81	3.71
Southdown	1.2	5.3	3.29	3.20	3.66	3.59
Whitefaced Woodland	0.6	5.7	3.53	3.17	3.44	3.67
Wiltshire Horn	1.2	8.8	1.84	1.98	1.50	1.56
mean of means	0.8	4.6	3.08	3.67	3.73	3.73
median of means	0.8	4.2	3.07	3.17	3.82	4.06

Basic data for terminal sire breeds

Breed	year	Total sires	Total dams	M lamb regs	F lamb regs	Ratio F/M lambs	Ratio dams / sires	Mean sons / sire	Variance sons / sire	Mean dau. / sire	Variance dau. / sire	covariance
Dorset Down	2011	56		63	402	6.4		1.125	4.257	7.179	75.895	3.432
Oxford Down	2011	105	410	49	414	8.4	3.9	0.49	0.71	4.14	20.66	0.102
Shropshire	2011	169		126	1194	9.5		1.85	1.38	7.51	51.35	1.815
Southdown	2011	291	1541	358	1545	4.3	5.3	1.27	3.97	10.48	86.59	3.137
Hampshire Down	2011	142		142				1.42	0.81			

7.1.4 Technical Appendix 4: Population data of goats

Basic registration data for British Goat Society breeds

Breed	year	Total sires	Total dams	M kid regs	F kid regs	Ratio F/M kids	Ratio dams/sires	Mean sons / sire	Variance sons / sire	Mean daughters / sire	Variance daughters / sire	covariance
Anglo-Nubian	2011	95	222	98	271	2.8	2.3	1.11	2.11	3.08	5.66	0.945
British Alpine	2011	40	75	24	81	3.4	1.9	0.65	0.77	2.19	2.78	-0.182
British Guernsey	2011	19	39	17	42	2.5	1.9	1.21	3.67	3	3.62	-0.769
British Toggenburg	2011	72	154	51	190	3.7	2.1	0.74	1.04	2.75	10.02	0.067
Golden Guernsey	2011	84	180	62	209	3.4	2.1	0.82	0.94	2.75	6.58	-0.233

Mean progeny per male and generation intervals for goats (mean 2007-2011; age x y: mean age of m or f parent at birth of m or f offspring, in years)

	m per sire	f per sire	age s m	age s f	age d m	age d f
British Guernsey	0.9	2.2	2.64	2.47	2.28	2.47
British Alpine	0.6	2.0	2.76	2.84	3.81	3.31
British Toggenburg	0.7	2.6	2.41	2.32	3.72	3.41
Golden Guernsey	0.7	2.5	2.17	2.26	3.26	3.06
Anglo Nubian	1.0	2.9	2.17	2.26	3.26	3.06
mean of means	0.8	2.5	2.43	2.43	3.26	3.06
median of means	0.8	2.4	2.41	2.32	3.26	3.06

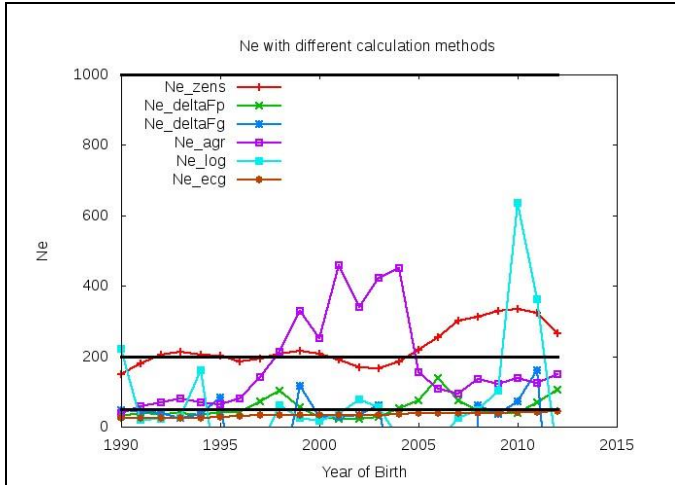
7.1.5 Technical Appendix 5: Population data of pigs

Basic registration data for pig breeds with generation intervals (age x y: mean age of m or f parent at birth of m or f offspring, in years)

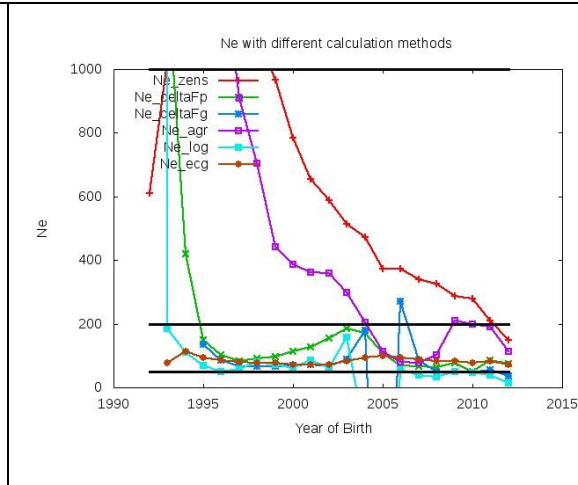
Breed	year	Total sires	Total dams	Total registrations	age s m	age s f	age d m	age d f
Berkshire	2011	75	122	279	3.1	2.3	3.8	3.3
-	2012	36	48	106				
British Landrace	2011	37	71	146	1.5	2.0	2.8	2.1
-	2012	12	13	20				
Large Black	2011	58	84	256	3.6	2.3	3.2	2.8
-	2012	36	51	118				
Large White	2011	69	119	218	2.4	2.2	4.5	3.7
-	2012	17	24	49				
Middle White	2011	47	75	182	2.9	3.6	3.0	2.4
-	2012	32	47	102				
Welsh	2011	75	157	316	1.6	2.3	2.6	2.6
-	2012	29	51	104				

Effective population sizes of six UK pig breeds, calculated by the six different methods offered by POPREP (Groeneveld et al. 2009). *Ne_zens* is by Wright's formula (Technical Appendix 13), the others are based on rate of increase of inbreeding.

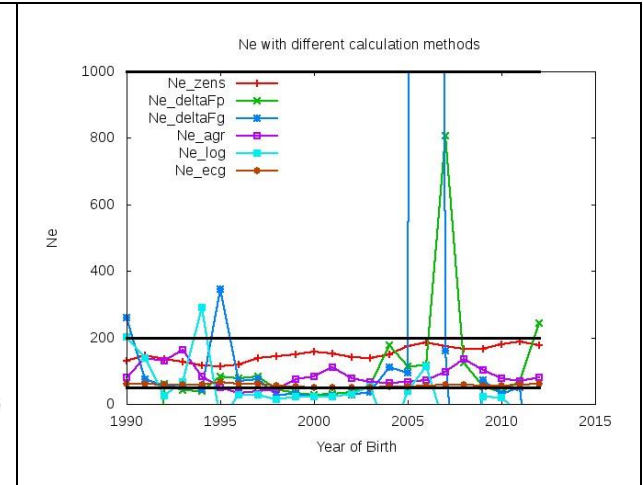
Berkshire



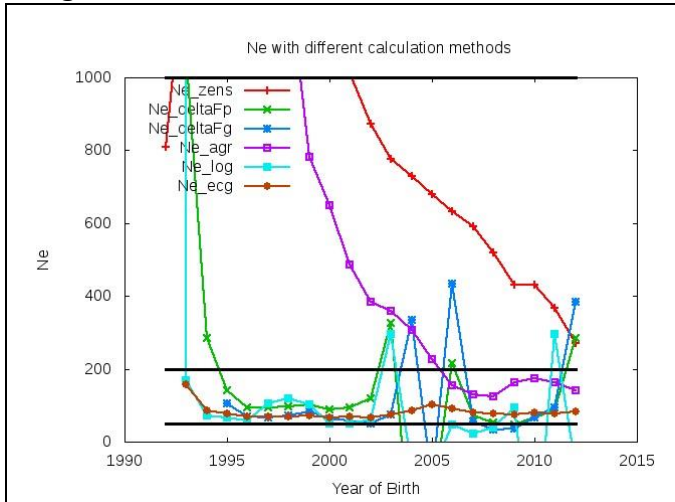
British Landrace



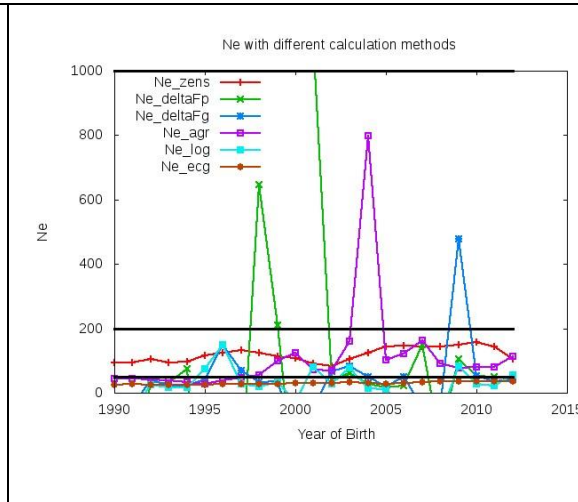
Large Black



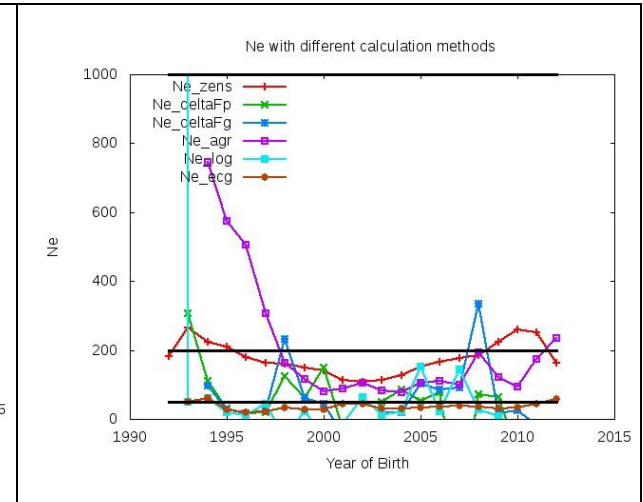
Large White



Middle White



Welsh



7.1.6 Technical Appendix 6: Population data of equines

Basic registration data for equine breeds

Breed	year	Total sires	Total dams	M foal regs	F foal regs	Ratio F/M foals	Ratio dams / sires	Mean sons / sire	Variance sons / sire	Mean dau. / sire	Variance dau. / sire	covariance
Cleveland Bay	2011	22	38	19	19	1.00	1.73	0.864	0.504	0.864	0.409	0.485
Clydesdale Horse	2011	60	182	122	140	1.15	3.03	2.033	3.539	2.333	5.189	0.209
Dales Pony	2011	43	104	41	63	1.54	2.42	0.954	0.928	1.465	1.551	-0.002
Dartmoor Pony	2011	62	155	86	71	0.83	2.50	1.387	2.653	1.145	1.252	0.205
Highland Pony	2011	134	349	182	176	0.97	2.60	1.358	1.767	1.313	1.678	0.263
New Forest Pony	2011	145	911	566	428	0.76	6.28	3.903	22.179	2.952	24.809	19.391

Generation intervals for equines

	year	m per sire	f per sire	age s m	age s f	age d m	age d f
Cleveland Bay	2005-2008			13.55	12.87	11.17	9.24
Clydesdale	mean 08-11	2.3	2.7	2.84	3.17	3.64	4.13
Dales Pony	mean 08-11	0.9	1.5	10.81	9.90	10.27	10.63
Dartmoor Pony	mean 08-11	1.4	1.5	10.09	9.42	10.32	10.04
Highland Pony	mean 08-11	1.4	1.4	11.37	11.24	10.33	10.47
New Forest Pony	mean 08-11	3.9	3.6	10.63	10.61	11.40	11.52

7.1.7 Technical appendix 7: Research projects relevant to FAnGR, supported under EC programmes

A summary of EC projects relating to FAnGR is as follows (revised from Ajmone-Marsan 2012 and Ligda and Zjalic 2011). Many of these had, or have, UK participants:

	Title	Examples of outputs
Concerted Action BIO4-CT96-0197 (1996)	Genebanks and the conservation of farm animal genetic resources	Oldenbroek (1999)
BIOTECH2-BIO4-96-1189 (funded 1996)	Development, optimisation and validation of molecular techniques for the measurement of genetic diversity in domestic ungulates	Dataset from this project is not readily available (but see Handley et al. 2007)

The first EU Community programme (RESGEN) funded four programmes (http://ec.europa.eu/agriculture/publi/genres/prog94_99_en.pdf) as named below, plus one on rabbits

Concerted Action CT96-83 (1997)	Farm animals: a permanent inventory of European farm animal genetic resources and of activities on characterisation, conservation and utilisation of those resources	http://www.eaap.org/content/RESGEN.htm
PL98-118	Towards a strategy for the conservation of the genetic diversity of European cattle	Wiener et al. (2004)
CT95-12	European gene banking project for pig genetic resources	Ollivier et al. (2001)

Programmes funded under Framework Programmes are as follows:

PIGBIODIV: characterization of genetic variation in the European pig to facilitate the maintenance and exploitation of biodiversity	Wilkinson et al. (2011); reviewed along with 2 other EU-funded pig projects by Ollivier (2009) http://bioinformatics.roslin.ac.uk/diversity/
AVIANDIV: development of strategy and application of molecular tools to assess biodiversity in chicken genetic resources	http://aviandiv.tzv.fal.de/ Wilkinson et al. (2011)
ECONOGENE: combines molecular analysis of biodiversity, socio-economics and geostatistics to address the conservation of sheep and goat genetic resources and rural development in marginal agrosystems in Europe	Canali and Econogene Consortium (2006); Bertaglia et al. (2007) http://www.econogene.eu/
NEXTGEN Next generation methods to preserve farm animal biodiversity by optimizing present and future breeding options	http://nextgen.epfl.ch/ Formally commenced in April 2011. Linked to European Science Foundation research networking programme "Genomic Resources" http://www.esf.org/index.php?id=7009

The following five projects were funded within the EU Community programme in the frame of the Biodiversity Action Plan for Agriculture (Council Regulation 870/2004). An independent review was published in June 2012 (http://www.rfp-europe.org/fileadmin/SITE_ERFP/EU/870_evaluation_01062012.pdf)

AGRI GEN RES 040	Heritage Sheep – aimed at establishing European programme for conservation of local breeds	http://www.heritagesheep.eu
012 AGRI GEN RES 870/2004	EURECA Towards self-sustainable European regional cattle breeds	http://www.regionalcattlebreeds.eu Hiemstra et al. (2010) Maki-Tanila and Hiemstra (2010)
AGRI GEN RES 066	ELBARN European livestock breeds ark and rescue net	http://www.elbarn.net/ Network of conservation units http://www.elbarn.net/Elbarn/Portals/0/Basics-ELBARN/Elbarn_Book.pdf
QLRT-2001-00026	EFABIS European Farm Animal Biodiversity Information System	http://efabis.net/ Integrated breeds database
AGRI GEN RES 067	GLOBALDIV A global view of livestock biodiversity and conservation	http://www.globaldiv.eu/ Ajmone-Marsan and GLOBALDIV (2010); Boettcher et al. (2010); Groeneveld et al. (2010)

7.1.8 Technical appendix 8: Breed societies

The stated aims of most breed societies are to protect, and in almost all cases develop, their breeds, while maintaining breed standards. These activities cost money and represent a contribution from the livestock constituency towards the cost of conservation. This is the first study on an overall cash value for this activity, not including in-kind voluntary contributions. Summary accounts, which are publicly available for those breed societies with have charitable status, have been used.

Umbrella organizations

	2011 income £'000		2011 income £'000
RBST	710	British Goat Society	62
BPA	298	British Waterfowl Association	21
Poultry Club of GB	86	Sheep Trust	0.1 (53 in 2010)

Breed societies

Breeds on the NBAR list are for the most part overseen by individual breed societies, though pigs, some of the rarest sheep, most goats and many poultry are overseen by umbrella organizations. Many breed societies have charitable status and summaries of their accounts are public.

The aim of this analysis is to estimate the cost of breed society activities for the NBAR breeds. Numbers of breeding females are tabulated and annual breed society costs per breeding female can be estimated by division. This ratio can then be multiplied by the total number of breeding females of all NBAR breeds to give an overall estimate.

Income in 2011 was considered. Only certain breeds are suitable for this derivation. Cattle breeds excluded were Chillingham (because the cattle are managed as part of an estate), and the "traditional" or "original" subsets of commercial breeds because the proportion of breed society they are assigned could not be determined; this also applied to the Dorset Horn sheep, as an affiliate of the Poll Dorset. Results are in the Table:

	N societies	Total 2011 income (max-min) (£'000)	mean	median	Total breeding females	Annual society cost per female £
cattle	12	966 (163-11)	81	81	40165	24.1
sheep	14	209 (414-3)	15	11	25609	8.2
equine	10	898 (311-6)	90	73	5568	161.3

For cattle and sheep, but not for equines, correlation between breeding females and income was highly significant, as would be expected given the importance of registration income to societies ($r=0.07$, $p<0.01$; $r=0.84$, $p<0.001$; $r=0.12$ respectively).

Application of these ratios to the totality of NBAR breeds gave the following estimates of total costs:

	Total breeding females all NBAR	Cost £million
cattle	61893	1.488
sheep	117371	0.957
equines	7822	1.261

This total of £3.7 million can be compared with the income in 2011 of some of the breed societies of major commercial breeds: Holstein/Friesian £8.06 million, British Limousin £1.01 million, Aberdeen Angus £0.74 million.

7.1.9 Technical Appendix 9: Overall status of breeds listed by RBST

Changes in the RBST watchlist are summarized in the following pages. Criteria for classification changed on a number of occasions and new categories were added. Terminology changed, but the symbols used here are standardized to those applying in 2013, as follows:

XXXX	Critical (most threatened)
xxx	Endangered
xx	Vulnerable
x	At risk
5	Minority
6	Other native breeds
99	Not classified

Changes in 2013 to sheep breeds were as follows:

Border Leicester added as “Minority” (5 in chart)

Leicester Longwool and North Ronaldsay (underlined in chart) uprated to “Endangered” (xxx in chart)

Changes to other species are as indicated on the charts

There were no changes between 1977 and 1979.

	Ab. Ang (trad.)	B Sh'hn	Belted G'way	BrWh	Ch' ham	D. Sh'hn (orig)	Dexter (orig)	Dexter	Gloucs	Ir-Moil	Kerry	Ln Red (trad.)	Long- horn	N. Dy Sh'hn	Red Poll	Shetld	H'Ford (trad.)	Vaymol	White Park	Whbrd Sh'hn	
1977-79			xx	XXXX				xxx	XXXX	XXXX	XXXX		xxx	XXXX		XXXX				XXXX	
1980			xx	XXXX				xxx	XXXX	XXXX	XXXX		xxx	XXXX		XXXX				XXXX	
1981			xx	XXXX				xxx	XXXX	XXXX	XXXX		xxx	XXXX		XXXX				XXXX	
1984			xx	xxx	6			xx	XXXX	XXXX	XXXX		xx		x	XXXX				XXXX	
1985				xx	6			x	XXXX	XXXX	XXXX		xx		x	XXXX				XXXX	
1986				xx	6			x	XXXX	XXXX	XXXX		xx		x	XXXX				XXXX	
1988		xx		xx	6			x	XXXX	XXXX	XXXX		xx		x	XXXX				XXXX	
1989		xx		xx	6			x	XXXX	XXXX	XXXX		xx		xx	XXXX		XXXX		XXXX	
1990		xx		xx	6			x	XXXX	XXXX	XXXX		xx		xx	XXXX		XXXX		XXXX	
1991		xx		xx	6			x	XXXX	XXXX	XXXX		x		xx	XXXX		XXXX		XXXX	
1992		xx		xx	6			x	XXXX	XXXX	XXXX		x		xx	XXXX		XXXX		XXXX	
1993		xx		x	6				xx	XXXX	xxx				xx	XXXX		XXXX		xxx	
1994		xx		x	6				xx	XXXX	xxx				xx	XXXX		XXXX		XXXX	
1995		xx		x	6				xxx	XXXX	xxx					XXXX				XXXX	
1996		xx			6				xxx	XXXX	xx				xx	XXXX		XXXX		XXXX	
1997		xx			6				xxx	XXXX	xx				xx	XXXX	7	XXXX		XXXX	
1998		xx			6				xxx	XXXX	xx	7			xx	XXXX	7	XXXX		xxx	
1999		xx			6				xxx	XXXX	xx	7			xx	XXXX	7	XXXX		xxx	
2000		xx			6				xxx	XXXX	xx	7			xx	XXXX	7	XXXX		xxx	
2001		xx			6				xxx	XXXX	xx	7			xx	XXXX	7	XXXX		xxx	
2002		xx	7	7	6				xxx	XXXX	6	XXXX	7		xx	XXXX	xx	XXXX		xxx	
2003	XXXX	xx	7	7	5		XXXX		xxx	XXXX	6	XXXX	7		xx	XXXX	xx	XXXX		xxx	
2004	XXXX	xx	7	7	5		6		xxx	xxx	6	XXXX	7		xx	XXXX	xx	XXXX		xxx	
2005	XXXX	xx	7	7	5		6		xxx	xxx	6	XXXX	7	XXXX	xx	XXXX	xx	XXXX		xxx	XXXX
2006	XXXX	x	5	5	XXXX				xx	xxx		xxx		XXXX	x	xxx	x	XXXX		xx	XXXX
2007	XXXX	6		5	XXXX				x	xxx		xxx		XXXX	6	xx	x	XXXX		x	XXXX
2008	XXXX	6	6	5	XXXX				x	xx		xx	6	XXXX	6	x	x	XXXX		x	xxx
2009	XXXX	6	6	5	XXXX				x	xx		xxx	6	XXXX	6	x	5	XXXX		5	xxx
2010	XXXX	6	6	6	XXXX				x	xx		xx	6	XXXX	6	x	5	XXXX		5	xxx
2011	XXXX	6	6	6	XXXX				x	x		xx	6	XXXX	6	x	5	XXXX		5	XXXX
2012	XXXX	6	6	6	XXXX	99			x	x		xx	6	XXXX	6	x	5	XXXX		5	XXXX
2013	xxx	6	6	6	XXXX	XXXX			x	x		xx	6	XXXX	6	x	5	XXXX		5	XXXX

	B'wen	Black Welsh Mtn	B'eray	C'milk M'it	Cots	D & Cll L'wool	Dor. Down	Dor. Horn	G'way	G'face Dart	Heb	Hill Rad	Jacob	Kerry Hill	Leics L'wool	Linc L'wool	Llan'rog	Lleyn
1977-80					xxx						xx				XXXX	xxx		x
1980		x			xxx						xx				XXXX	xxx		x
1981					xxx						xx				XXXX	xxx		x
1984			6	XXXX	xxx						5				XXXX	xxx		
1985			6	XXXX	xxx						5				XXXX	xxx		
1986			6	XXXX	xxx					xx	5				XXXX	xx		
1988			6	XXXX	xxx					xx	5				XXXX	xx		
1989			6	XXXX	xxx					xx	5				XXXX	xx		
1990			6	XXXX	xxx					xx	5				XXXX	xx		
1991			6	XXXX	xx					x	xx				xxx	x		
1992			6	XXXX	xx					x	xx				xxx	x		
1993			6	XXXX	xx					x	xx	xx			xxx	x		
1994	xx		6	XXXX	xx		x			x	xx	xxx			xx	x	xx	
1995	xx		6	XXXX	xx		x			x	x	xxx	x		xx	x	xx	
1996	xx		6	XXXX	xx		x		xxx	x	x	xx	x		xx	x	xx	
1997	xx		6	XXXX	xx		x		xxx	x	x	xx	x		xx	x	xx	
1998	xx		6	XXXX	xx		x		xxx	x		xx			xxx	x	x	
1999	xx		XXXX	XXXX	xx		x		xxx	x		x			xxx	x	x	
2000	xx		XXXX	XXXX	xx		x		xxx	x		x			xxx	x	x	
2001	xx		XXXX	XXXX	xx		x		xxx	x		x			xxx	x	x	
2002	xx		XXXX	XXXX	xx		x		6	x	7	x		7	xxx	x	x	
2003	xx		XXXX	XXXX	xx		x		6	x	7	x		7	xxx	x	x	
2004	xx		XXXX	xxx	xx		x		6	x	7	x		7	xxx	xx	x	
2005	xx		XXXX	xxx	xx	7	x		6	x	7	x		7	xxx	xx	x	
2006	x		XXXX	xxx	xx	x	xx	x		5		xx			xxx	xx	5	
2007	x		XXXX	xxx	x	x	x	5		5		xx			xxx	x	5	
2008	x	6	XXXX	xx	x	xx	5	5		5	6	xx		6	xxx	x	6	
2009	x		XXXX	xx	5	xx	5	5		5	6	xx		6	xxx	x	6	
2010	x	6	XXXX	xx	5	xx	5	5		5	6	xx		6	xxx	x	6	
2011	x	6	XXXX	xx	x	xx	5	5		5	6	xx	6	6	xxx	x	6	6
2012	x	6	XXXX	xx	x	xx	5	5		5	6	xx	6	6	xxx	x	6	6

	Manx Loghtan	Norfolk Horn	North Ronaldsay	Oxford Down	Portland	Ryeland	Shetland	Shropshire	Soay	Soay island	South Wales Mountain	Southdown	Teeswater	Wensleydal e	Whiteface Dartmoor	Whitefaced Woodland	Wiltshire Horn
1977--79	XXXX		xx	xxx	XXXX	xxx	xx	xxx	xx			xx	xxx	XXXX		xxx	xx
1980	XXXX		xx	xxx	XXXX	xxx	xx	xxx	xx			xx	xxx	XXXX		xxx	xx
1981	XXXX		xx	xxx	XXXX	xxx	xx	xxx	xx			xx	xxx	XXXX		xxx	xx
1984	xxx		xxx	xx	XXXX	x	5	xx	5			xx	xxx	xxx		xx	x
1985	xxx		xxx	x	XXXX	x	5	xx	5					xxx		xx	x
1986	xxx	XXXX	xxx	x	XXXX		5	xx	5					xxx		xx	x
1988	xxx	XXXX	xxx	x	XXXX		5	x	5			x		xxx		xx	x
1989	xxx	XXXX	xxx		XXXX		5	x	5			x		xxx		xx	x
1990	xxx	XXXX	xxx		xxx		5	x	5			x		xxx		xx	x
1991	xxx	XXXX	xxx		xxx			x	xx			x		xx		xx	x
1992	xx	XXXX	xxx		xxx			x	xx			x		xx		xx	x
1993	xx	XXXX	xxx		xxx			x	xx			x		xx		xxx	x
1994	xx	XXXX	xx		xx			x	xx		xx	x		xx	xx	XXXX	x
1995	xx	XXXX	xx		xx			x	xx		x	x		xx	xx	XXXX	x
1996	xx	XXXX	xx		xx			x	xx			x		x		xxx	x
1997	xx	xxx	xx		xx			x	xx			x		x		xxx	x
1998	x	xxx	xx		xx			x	xx			x	xx	x		xxx	
1999	x	xxx	xx		xx			x	xx			x	xxx	x		xxx	
2000	x	xxx	xx		xx			x	xx			x	xxx	x		xxx	
2001	x	xxx	xx		xx			x	xx			x	xxx	x		xxx	
2002	x	xxx	xx	7	xx	7		x	xx	5		x	xxx	x	7	xxx	7
2003	x	xxx	xx	7	xx	7		x	xx	5		x	xxx	x	7	xxx	7
2004	x	xx	xx	7	x	7		x	x	5		x	xxx	x	7	xx	7
2005	x	xx	xx	7	x	7		7	x	5		x	xxx	x	7	xx	7
2006	x	xx	XXXX	x	x	5		x	xx			5	xxx	x	x	xx	
2007	x	x	xxx	5	x			5	xx				xxx	x	x	xx	
2008	x	x	xxx	5	x	6	6	5	x			6	xxx	x	x	xx	
2009	x	x	xxx	x	x	6	6	5	x		6	6	xx	x	x	x	6
2010	x	x	xxx	x	x	6	6	5	x		6	6	xx	x	x	x	6
2011	x	x	xxx	x	x	6	6	5	x		6	6	xx	x	x	xx	6
2012	x	x	xxx	x	x	6	6	5	x		6	6	xx	x	x	xx	6

	Bagot	Golden Guernsey	Berks	Bri Lop	British S'back	Glos. Old Spot	Lg. Black	Lg. White	Mid. W	Oxford S.& Black	T'worth	Welsh
1977-79	XXXX	xxx	XXXX	XXXX	x	XXXX	xxx		XXXX		XXXX	
1980	XXXX	xxx	XXXX	XXXX	xx	XXXX	xxx		XXXX		XXXX	
1981	XXXX	xxx	XXXX	XXXX	x	XXXX	xxx		XXXX		XXXX	
1984	XXXX	xxx	XXXX	XXXX	xx	xxx	XXXX		XXXX		XXXX	
1985	XXXX	xxx	XXXX	XXXX	xxx	xxx	XXXX		XXXX		XXXX	
1986	XXXX	xxx	XXXX	XXXX	XXXX	xxx	XXXX		XXXX		XXXX	
1988	XXXX	xxx	XXXX	XXXX	XXXX	xxx	XXXX		XXXX		XXXX	
1989	XXXX	xxx	XXXX	XXXX	XXXX	xxx	XXXX		XXXX		XXXX	
1990	XXXX	xxx	XXXX	XXXX	XXXX	xxx	XXXX		XXXX		XXXX	
1991	XXXX	x	XXXX	XXXX	XXXX	xxx	XXXX		XXXX		XXXX	
1992	XXXX	x	XXXX	XXXX	XXXX	xxx	XXXX		XXXX		XXXX	
1993	XXXX	x	xxx	XXXX	xxx	xxx	XXXX		XXXX		XXXX	
1994	XXXX	xx	xxx	XXXX	xxx	xxx	XXXX		XXXX		XXXX	
1995	XXXX	xx	xxx	XXXX	xxx	xxx	XXXX		XXXX		XXXX	
1996	XXXX	xx	xxx	XXXX	xxx	xxx	XXXX		XXXX		XXXX	
1997	XXXX	xx	xxx	XXXX	xxx	xxx	XXXX		XXXX		XXXX	
1998	XXXX	xx	xxx	XXXX	xxx	xxx	XXXX		XXXX		XXXX	
1999	XXXX	xx	xxx	XXXX	xxx	xxx	XXXX		XXXX		XXXX	
2000	XXXX	xx	xxx	XXXX	xxx	xxx	XXXX		XXXX		XXXX	
2001	XXXX	xx	xxx	XXXX	xxx	xxx	XXXX		XXXX		XXXX	
2002	XXXX	xxx	xx	xxx	x	x	xx		xx		xxx	
2003	XXXX	xxx	xx	xxx	x	x	xx		xx		xxx	
2004	XXXX	xxx	xx	xxx	x	x	xx		xx		xxx	
2005	XXXX	xx	xx	xxx	x	7	xx		xx		xxx	x
2006	XXXX	x	xx	xxx	x	5	xx		xx		xxx	xx
2007	XXXX	5	xx	xxx	x	5	xx		xxx		xx	xx
2008	XXXX	5	xx	xxx	x	5	xx	6	xxx		xx	xx
2009	xxx	5	xx	xxx	x	5	xx		xxx		xx	xx
2010	xxx	5	x	xxx	5	5	xx	6	xx		x	x
2011	xx	5	x	xx	5	5	xx	6	xx		x	x
2012	xx	5	x	xx	5	5	xx	6	xx	5	x	x
2013	xx	5	x	xx	5	5	xx	5	xx	5	x	x

	Cleveland Bay	Clydesdale	Dales Pony	Dartmoor Pony	Feriskay Pony	Exmoor Pony	Fell Pony	Feral Welsh Mountain (section A)	Hackney Horse & Pony	Highland Pony	Irish Draught	New Forest Pony	Shetland Pony	Shire	Suffolk	Welsh Pony & Cob
1977-79		xx	xx			XXXX	xx							xx	xxx	
1980		xx	xx			XXXX	xx							xx	xxx	
1981		xx	xx			XXXX	xx							xx	xxx	
1984	x	xx	xxx			XXXX	xx								xxx	
1985	x	xx	xxx			XXXX									xxx	
1986	x	x	xx			xxx									xxx	
1988	x	x	xx		7	xxx									xxx	
1989	x	x	xx		7	xxx									xxx	
1990	x	x	xx		7	xxx									xxx	
1991	xx	x	xx		7	XXXX									XXXX	
1992	xxx	x	xx		7	XXXX					x				XXXX	
1993	XXXX	x	xx			XXXX					x				XXXX	
1994	XXXX	x	xx			xxx					xx				XXXX	
1995	XXXX	x	xx			xxx					xx				XXXX	
1996	XXXX	x	xx			xxx					xx				XXXX	
1997	XXXX	x	xx		XXXX	xxx					xx				XXXX	
1998	XXXX	x	xx	xx	XXXX	xxx	xx				xx				XXXX	
1999	XXXX	x	xx	xx	XXXX	xxx	xx				xx				XXXX	
2000	XXXX	x	xx	xx	XXXX	xxx	xx				xx				XXXX	
2001	XXXX	x	xx	xx	XXXX	xxx	xx				xx				XXXX	
2002	XXXX	x	xx	xx	XXXX	xxx	xxx			xx	6			7	XXXX	
2003	XXXX	x	xx	xx	XXXX	xxx	xxx	xx		xx	6			7	XXXX	
2004	XXXX	x	xx	xx	XXXX	xxx	xxx	xx		xx	6			7	XXXX	
2005	XXXX	x	xx	xx	XXXX	xxx	xxx	xx	xxx	xx	6			7	XXXX	
2006	XXXX	x	XXXX	xx	XXXX	xxx	xx	xx	xxx	xx				5	XXXX	
2007	XXXX	xx	XXXX	xx	XXXX	xxx	x	xx	xxx	x				x	XXXX	
2008	XXXX	xx	xxx	xx	XXXX	xxx	x	xx	xxx	x	6	6		x	XXXX	6
2009	XXXX	xx	xx	xx	XXXX	xxx	x	xx	xxx	x			6	x	XXXX	
2010	XXXX	xx	xxx	xx	XXXX	xxx	x	xx	xxx	x	6	6		x	XXXX	6
2011	XXXX	xx	xxx	xx	XXXX	xxx	x	xx	xxx	x	6	6		x	XXXX	6
2012	XXXX	xx	xxx	xx	XXXX	xxx	x	xx	XXXX	x	6			x	XXXX	6
2013	XXXX	xx	xxx	xx	XXXX	xxx	x		XXXX	x				x	XXXX	

7.1.10 Technical Appendix 10: Ex situ breed conservation – principles and practice

Ex situ breed conservation is also known as gene banking. While other meanings of the term might be encountered in relation to wild animals, in the context of FAnGR it has customarily meant, the collection, processing, storage at very low temperature, recovery and utilization of gametes (reproductive cells) and embryos. Now, the term also applies to somatic (non-reproductive) cells intended for use in cloning. For reasons of space, the veterinary health implications of these techniques have to be omitted (but see Wrathall and Simmons 2004). The policy background including the enabling EU legislation is covered by Small (2013).

The ex situ collections within the UK have been assembled as a result of targeted initiatives by RBST, BPA and the Sheep Trust, by breed society initiatives, and by RBST taking over collections that had been assembled by other organizations, including one substantial collection held in partnership with the NSA. As a result, all UK FAnGR are represented, with the exception of poultry, though the small numbers of individual animals represented and the paucity of stored embryos mean that these collections would, in almost all cases, be insufficient to restore breeds to 100% original genotype after extinction.

Ex situ collections are acknowledged as “backup insurance” by FAO¹⁰⁵ but there seems to be no guidance as to the proportion of FAnGR spending that should be allocated to gene banks. In any insurance decision an accurate assessment of risk is needed (risk is the probability of an event occurring, multiplied by a measure of its severity).

Scientific principles

The scientific principles are explained in the formal literature (recent reviews: Woelders et al. 2012; Men et al. 2012; also see Woelders and Hiemstra 2012). Certainly in emerging technologies the laboratory procedures involved are highly innovative and as a result expertise in some aspects of the subject may be confined to centres of excellence. This means that most state-of-the-art reproductive technologies are not generally available, but in rare cases, innovative scientific research may be conducted using breeds at risk whose conservation status is improved as a result. The Enderby Island cattle of New Zealand are a prime example; this vanishingly rare breed was rescued through a very early application of cloning (Wells et al. 1998). In the UK fundamental research on immunology and mitochondrial genetics, using the Chillingham cattle (Ballingall et al. 2012; Hudson et al. 2012), has led to the cryopreservation of cell cultures of possible use in cloning.

Scientific research is, of course, also driven by market requirements so some technologies have advanced further than others. Thus for example embryo technologies are highly developed in cattle, where they can compensate for the cow's low reproductive rate and are relatively straightforward in practical terms because embryo transfer is non-surgical, and there are several examples of embryo transfer in rare breeds¹⁰⁶. In pigs the high reproductive rate and necessity of surgery for embryo transfer (Hazeleger and Kemp 1999) mean the incentive for technical development has been less evident, though transfer of unfrozen embryos has been used to increase numbers of Mangalitsa pigs in Hungary (Rátky et al. 2001).

In all farm animal species, cryopreservation of semen is commercially available and reliable. Fundamental biological problems persist in some species (Holt and Watson 2004). For example, individual stallions can differ markedly in how their semen survives the freezing-thawing process (Katila 2001); the same is probably also true of boars and cocks (Boe-Hansen et al. 2005; Blesbois et al. 2008; Siudzińska and Łukaszewicz 2008). In the case of sheep, reproductive seasonality and anatomy can make semen collection and artificial insemination difficult (Barber 2010; Woelders et al. 2012), and there are probably breed differences in this species as well (Fair et al. 2005).

Transfer of cryopreserved embryos is not routinely available for pigs, biologically impossible for birds, and effectively impracticable for horses (where embryos for transfer are kept at +5 degC: Squires et al. 1999). It is commercially viable for cattle, sheep and goats; females are induced to produce multiple ova, insemination proceeds naturally or artificially, embryos are collected and transferred either immediately or after frozen storage to surrogate mothers where gestation proceeds.

¹⁰⁵ Interlaken Declaration Strategic Priority 9, page 23, <http://www.fao.org/docrep/010/a1404e/a1404e00.htm> (2007). Also see Small (2013).

¹⁰⁶ Ark Summer 2010 p.28; Summer 2011 p.15; Winter 2012 p.19

In cattle, taking into account the success rates to be expected at each stage of the process, the general estimate for cost of embryo transfer per live calf born is £300-350¹⁰⁷.

In all livestock species, cryopreservation of semen does not conserve the entire genome but this problem might be sidestepped in that cryopreserved ovaries can, after thawing and transplantation, be functional in recipient animals. This is briefly considered with reference to poultry by Silversides et al. (2012). However, this is not yet a mature technology. Oocytes (the cells which, as ova, are fertilized by sperm) can be cryopreserved but this is not favoured for farm animal gene banks (Gandini and Oldenbroek 2007). Work in Canadian poultry on cryopreservation of embryonic cells for possible reconstitution as germline chimaeras is summarized by Silversides et al. (2007).

Gene banking could in principle be based on cloning technology, somatic cells being collected and stored in anticipation of future developments making the production of cloned animals a realistic conservation option. However the use of somatic cell nuclear transfer in livestock, particularly those entering the food chain, may continue to be contentious (Lassen et al. 2006). In horses the process is relatively straightforward, unfrozen, cloned embryos derived from high-value individuals being traded internationally (Asseged et al. 2012).

Data management and international inventories

Guiding principles for establishment, maintenance and use of ex situ collections are given by FAO (1998) as updated by Woolliams (2004).

Several studies have been conducted on how animals should be chosen for inclusion in a gene bank, for example Gandini and Oldenbroek (2007). The numbers of doses of semen stored has to relate to the objectives to be met after withdrawal from the bank (Woolliams et al. 2008). Groeneveld et al. (2008) have proposed a structure for a project database. How conservation of live animals can be made more effective by the planned use of stored semen has been considered by Meuwissen (2007).

A centralized list of European gene banks is available¹⁰⁸, reviewed by Ligda and Zjalic (2011). This list enables countries to see how they compare in terms of meeting international obligations to conduct ex situ conservation, and it can help with studies on whether genetic resources of global breeds are being adequately conserved (for example Danchin-Burge et al. 2011).

Costs of techniques

The different cryopreservation approaches differ in “biological effectiveness” (Gandini and Oldenbroek 2007) as well as in cost. In many, perhaps most circumstances the most cost-effective approach will involve a combination of approaches and technologies.

With chickens, keeping live populations is the most cost-effective approach up to a period of three years, and for any chicken population that will not be used within five years replacement of the live population by a gene bank is the most cost-effective option (Silversides et al. 2012).

For mammalian livestock Gandini et al. (2007) simulated the reconstruction of a population of 25 males and 25 females, enough semen and/or embryos being collected and stored to furnish duplicate gene banks, it being assumed that current problems with embryo technologies can be overcome. Collection strategies considered were as follows.

- 1) Embryos only: sufficient embryos are collected to be 90% certain of reconstructing the 25M/25F population;
- 2) Embryos and semen: to take account of embryos being more expensive to collect and store than semen, various combinations were defined ranging from 90% of the number in (1) above with sufficient semen doses for subsequent insemination, down to 10% of that number, with a correspondingly increased number of semen doses;
- 3) Semen only, for a backcrossing programme over 5 generations (the semen used to inseminate females of some other breed, the female progeny being inseminated with the semen, this process repeated

¹⁰⁷ Personal communication, Mr. Stuart Mullan MRCVS, 10 January 2013

¹⁰⁸ http://www.rfp-europe.org/fileadmin/SITE_ERFP/WG_ex_situ/ERFP_Genebanks.pdf

and leading to the reconstituted population whose genotype approaches 100%, asymptotically, to that of the extinct breed).

Predicted costs (£, 2007 prices) of creating a gene bank for a single breed are in **Table EX1**. Here, YKF means “years-keeping-females”, which is a measure of the costs of the reconstitution process (the cumulated number of years of herd life for females raised during the reconstruction process). For cattle, this value is much reduced when embryo transfer is used in reconstitution. The cheapest option for each species is in **bold** while the most rapidly completed (minimum YKF) is underlined. Costs of maintenance of the stores were not included in this study.

Table EX1: Predicted costs of establishment of gene banks (after Gandini et al. 2007)

	Horse	Cattle	Pig	Cattle (ET)	Sheep
Embryo 90% + semen	£200,000	£35,000	<u>£28,000</u>	<u>£35,000</u>	<u>£24,000</u>
YKF	49	40	<u>5</u>	<u>11</u>	<u>18</u>
Embryo 50% + semen	£130,000	£29,000	£24,000	£29,000	£17,000
YKF	201	166	16	38	52
Semen only	£390,000	£26,000	£18,000	£20,000	£17,000
YKF	15,581	12,878	84	341	1,776
Embryos only	<u>£230,000</u>	<u>£38,000</u>	£29,000	£38,000	£26,000
YKF	<u>42</u>	<u>35</u>	19	35	21

Semen collection and the artificial insemination process in general are least straightforward in horses, partly explaining the high costs and long duration of the reconstitution process in this species. These calculations emphasize the value of a dual approach, with both embryos and semen being stored; not just because this means the full matrilineal genome is conserved, but also because restoration of a viable live population is accelerated.

Table EX2 reproduces the possible storage inventories proposed by Gandini and Oldenbroek (2007) for a goat breed, taking into account survival rates and other relevant variables, the aim being reconstruction of a population of 25 males and 25 females.

Table EX2: Storage inventory options for a hypothetical gene bank for a goat breed (after Gandini and Oldenbroek 2007)

	Number stored	Reconstruction period
Storage of embryos only	174 embryos	2 years
Storage of semen doses only	270 doses	9.4 years, reconstruction not 100%
Embryos and semen	43 embryos 65 doses	5.4 years
	108 embryos 45 doses	3.2 years

For some very rare breeds it may be difficult to commit enough females to an embryo recovery programme, remembering that yields of embryos per females can be very low (for example Schmutz et al. 2001) and might be reduced further by inbreeding (Alvarez et al. 2005; van Eldik et al. 2006).

The potential appeal of somatic cell nuclear transfer was demonstrated by Groeneveld et al. (2008) who conducted a pilot experiment in Vietnam and established a gene bank of somatic cells representing 300 individuals of 6 breeds, with full documentation, for the equivalent of £3,600. The cost of producing clones from these cells and completing the reconstruction of the six breeds was not estimated.

Costings for large scale poultry conservation programmes are scarce. Piseni et al. (1999) made a detailed proposal for conserving north American poultry stocks totalling 361 genotypes of five species and including commercial and

research populations, by a combination of in situ and ex situ methods. Estimated costs at 2012 sterling prices were £14.8 million for establishment, and £630,000 for annual running costs.

Practical outcomes

Reconstruction of breeds from gene banks is clearly very likely to be expensive and whether it succeeds is likely to vary from case to case. For example, the Enderby Island cattle¹⁰⁹ are all descended from clones derived from a single cow (approximately 13 years old) removed from the eponymous New Zealand island in 1993 (Wells et al. 1998) after extermination of a feral herd in the interests of habitat conservation. Previously, sperm had been obtained post mortem from the herd, but this cow was the sole representative of the female genome; she was cloned because she was subfertile. By March 2013, the breed numbered 4 mature bulls, 4 young males, 16 cows and 8 young females¹¹⁰. It has taken 20 years for the population to build up to this number. At a rough estimate with several assumptions this could correspond to 160 “years keeping females”, four times that predicted from the simulated embryo/semen option of Gandini et al. (2007) described above. The projections in that study are probably “best case scenarios”.

A commitment to ex situ conservation is embodied in international undertakings relating to FAnGR (Small 2013). If the chosen gene banking approach can also be used to reduce the risks of extinction then there are several reasons to favour it, even though, should extinction happen, it may not be the biologically ideal strategy for full recovery of the breed. A semen cryopreservation scheme combining a utilization function with that of an archive, would seem the most appropriate. This could help the breed to address new breeding goals and support breeding schemes aimed at minimizing inbreeding, both necessary if it is to continue in existence.

Ex situ conservation of FAnGR in the UK

There are limited stocks of semen relevant to UK native breeds in gene banks within the EU or elsewhere.

Cattle: breeders of British Friesians have been using frozen semen from Dutch bulls¹¹¹. Outside Europe, Jersey Island semen is conserved under the US National Animal Germplasm Program with 400 bulls (total 2,473 straws) represented¹¹².

Sheep: breeds with daughter breed societies elsewhere in Europe are listed in Technical Appendix 11. None appear to have semen stores, except for the Cheviot in Norway¹¹³, counterpart of the South Country Cheviot.

Horses: For the British Percheron, frozen semen is available in France from the counterpart Percheron breed society¹¹⁴ but there is not a breed society gene bank as such. Semen from three Percheron and three New Forest stallions is also kept by the French national stud¹¹⁵.

The early history of the RBST's gene banking activities is summarized by Alderson and Porter (1994). The processes have not been fully documented, but RBST has acquired semen that was collected for commercial purposes from many mainstream native breeds, with an emphasis on bulls which had not been introgressed. Semen is available for current use¹¹⁶.

¹⁰⁹ <http://www.rarebreeds.co.nz/enderby.html>

¹¹⁰ Personal communication, Dr. Dave Matheson, 22 March 2013

¹¹¹ Personal communication Mary Mead, 5 April 2013

¹¹² <http://www.ars-grin.gov:8080/j2ee/nagppub/jsp/nagp/drilldown2.jsp>

¹¹³ <http://www.nordgen.org/husdyrdb/visrase.php?id=57&langid=1>

¹¹⁴ Personal communication Virginia Kouyoumdjian, 8 April 2013

¹¹⁵ http://www.france-haras.fr/etalons/recherche-avancee/?no_cache=1

¹¹⁶ <https://www.rbst.org.uk/semen-for-sale>

Table EX3: Combined list of UK cattle semen resources

RBST genebank	bulls	doses	Mean doses/bull	Documented breed society gene banking activity
Aberdeen Angus (Original)	28	3150	113	None advertised on website
Ayrshire	4	218	55	None advertised on website
Beef Shorthorn	9	2285	254	None advertised on website
Belted Galloway	2	1337	669	None advertised on website
Belted Welsh	1	341	341	None advertised on website
Blue Albion	5	1582	316	None advertised on website
British Friesian (original)	170	16149	95	None advertised on website
British White	8	786	98	21 bulls advertised on website, including one born in 1978 and another in 1982
Chillingham				Cell cultures stored for research. Small amounts of semen are in store.
Dairy Shorthorn	8	1004	126	No Society semen or embryos. RBST bank includes semen from 3 Original bulls ¹¹⁷
Devon	13	1622	125	None advertised on website
Dexter	26	500	19	Society semen classified: 1. For general use (3 bulls); 2. For specialist breeding projects (12 bulls); 3. Retained by Society for "research and heritage" (18 bulls). Society semen includes 9 Original bulls ¹¹⁸
Galloway	4	711	178	None advertised on website
Gloucester	28	5900	211	None advertised on website
Guernsey	5	316	63	Currently advertised: 12 proven and young sires, all with North American Guernsey influence, mean percentage of genotype attributable to UK or Island 19% (range 0-37.5). No embryos.
Guernsey (Island)				Society has mean of 112 straws from 92 Island bulls in "Museum stock". 16 UK and 18 North American bulls (mean 13 straws) also represented.
Hereford	14	485	35	23 bulls advertised of which 6 horned and 17 polled
Highland	6	477	80	5 bulls advertised
Irish Moiled	12	5012	418	Semen from 10 bulls stored at 2 centres, for sale to breeders
Jersey (Island)				Semen from 400 bulls in USDA repository, duplicated in Island
Kerry	15	3276	218	None advertised on website
Lincoln Red	19	2241	118	No embryos. Society sells semen from 4 Original bulls (website)
Longhorn	27	2538	94	Society has 20 bulls in AI catalogue, median year of birth 1988, oldest 1975, youngest 2004. Graded fees relate to conservation significance of bull
Luing				Society has no stock, private breeders have semen and embryos
Northern Dairy Shorthorn	9	3185	354	None advertised on website

¹¹⁷ Ark Winter 2012, p.14¹¹⁸ Ark Spring 2003, p.7

Table EX3: Continued

	bulls	doses	Mean doses/bull	Breed society activity
Red Dane	7	7770	1110	No breed society
Red Poll	12	2398	200	Society semen: 31 bulls of which 18 have dairy records. Semen of 12 bulls is rationed
Shetland	16	3555	222	None advertised on website
South Devon	26	3813	147	28 bulls in semen catalogue, rationed when depleted
Sussex	30	10079	336	14 bulls in semen catalogue
Traditional Hereford	77	8002	104	Also 64 bulls, total 27063 straws with Traditional Hereford Breeders' Club ¹¹⁹
Vaynol	11	2413	219	Ark Autumn 2005 p.24
Welsh Black	17	1525	90	Private and company semen sales notified on website
White Park	11	4428	403	None advertised on website
Whitebred Shorthorn	6	3913	652	Website advertises RBST semen

Pigs

The British Pig Association¹²⁰ and the RBST¹²¹ have both assembled pig semen banks and have operated schemes whereby boars are kept at stud for natural mating¹²².

Table EX4: Combined list of UK pig semen resources

Breed	RBST			BPA			
	Total boars	Total doses	Mean doses / boar	Total boars	No. of lines sampled / total lines available	Total doses	Mean doses / boar (range)
Berkshire	6	300	50	7	6/7	161	24 (10-42)
British Lop	2	100	50				
British Saddleback	4	200	50	9	6/14	199	22 (17-40)
Gloucestershire Old Spots	7	350	50	7	4/4	172	25 (13-55)
Large Black	4	200	50	5	5/6	89	18 (9-20)
Middle White	5	250	50	5	4/5	114	19 (15-20)
Oxford Sandy & Black	Semen announced as available for use ¹²³						
Tamworth	5	250	50	6	6/8	131	21 (17-34)
Welsh	4	200	50	4	4/11	80	20 (20-20)
Oxford Sandy & Black				2	2/4	50	25 (20-30)

¹¹⁹ <http://www.thcbc.co.uk/Albulls.htm>

¹²⁰ <http://www.britishtpigs.org.uk/aisemen.htm>

¹²¹ <https://www.rbst.org.uk/semen-for-sale>

¹²² For example, Ark Winter 2012 p.32

¹²³ Ark Winter 2013, p.40

Equines

In addition to the RBST gene bank there are many private holdings of equine semen.

Table EX5: Combined list of UK equine semen resources

RBST	Total stallions	Total doses	Mean doses/stallion	Breed society activity
British Percheron				Semen stored from 6 stallions ¹²⁴ .
Cleveland Bay	11	525	48	
Clydesdale	3	288	96	
Dales	2	198	99	Limited stocks from one stallion ¹²⁵
Dartmoor	5	316	63	
Eriskay	4	246	62	
Exmoor	2	123	62	
Fell	5	254	51	
Hackney	2	247	124	
Highland	3	221	74	
Irish Draught	2	66	33	
New Forest				Some semen stored ¹²⁶
Shire	3	271	90	
Suffolk	2	216	48	

Goats**Table EX6: Combined list of UK goat semen resources**

Breed	Total bucks	Total doses	Mean doses / buck
Bagot	13	888	68
Golden Guernsey	10	902	90

¹²⁴ Conservation gene bank started in 2000 (3 of the stallions are now deceased). Release of semen restricted. Personal communication, Muriel Bond, 2 April 2013

¹²⁵ Personal communication Jo Ashby 8 April 2013

¹²⁶ Personal communication Jane Murray, 5 April 2013

Sheep

In the UK there have been 3 coordinated gene banking initiatives for sheep, all started in response to emergencies, organized by 3 different agencies.

During the foot-and-mouth disease outbreak of 2001 the RBST commenced emergency collection of sheep semen¹²⁷ from its highest priority sheep breeds and this was extended into a multi-species programme with a fundraising target of £2.5 million (Mansbridge 2004). Establishment and operation of the RBST sheep semen bank were reviewed by Barber (2010); funding of £425,000 over eight years from the Tubney Trust led to 38,000 semen straws being obtained from 350 collections from sheep and goats of the highest conservation priorities. The strategy has been to partition the semen from each animal as follows: 55% for permanent storage, 30% for use in conservation breeding programmes, 15% stored free of charge for the owner of the animal at the time of collection.

Also in 2001 the same time the Heritage GeneBank project was launched, inspired by the threat to Herdwick sheep (Bowles et al. 2004); this project was extended into embryo cryopreservation for the Herdwick (178 embryos, from 6 donor farms) and Rough Fell (71 embryos, 2 donor farms; Jones and Bowles 2006).

Thirdly, concern that BSE could become established in UK sheep where it might be masked by the well-established ovine encephalopathies, classical and atypical scrapie, led in 2003 to the National Scrapie Plan and Northern Ireland Scrapie Plan Sheep Semen Archive being launched with EC funding¹²⁸ to the extent of £1.44 million. The stated aim was "... to create an archive from which viable populations of sheep could be produced and re-admitted to the national flock if it was found that genotypes removed from the national sheep flock were needed in a future animal disease situation ...". Restoration from extinction was not an aim. In 2006 it was concluded¹²⁹ that the threat of ovine BSE was too low to justify public funding for the Archive, and in 2008 responsibility for it was shouldered by a joint venture of RBST and the National Sheep Association¹³⁰. For the Archive, collection costs were estimated at £300 per ram (Woelders and Kaal 2008) and annual costs of maintenance of the complete archive were anticipated in 2008 to be £20-25,000 though after some "de-accessioning" these were reduced to approximately £12,000 in 2011 (personal communication Frances Radcliffe). Reports on how sheep gene banks have been established in other countries are given by Woelders and Kaal (2008).

¹²⁷ Ark, Autumn 2001, p.105

¹²⁸ Aid scheme N659/2002: http://ec.europa.eu/eu_law/state_aids/agriculture-2002/n659-02.pdf

¹²⁹ <http://archive.defra.gov.uk/foodfarm/farmanimal/diseases/atoz/bse/othertses/scrapie/>

¹³⁰ <https://www.rbst.org.uk/rbst-take-action-serve-native-sheep-genetics>

Table EX7: Combined list of UK sheep semen resources

National Scrapie Plan Semen Archive			RBST Sheep Semen Bank			Sheep Trust Heritage Gene Bank			
	Total rams	Total doses	Mean doses / ram	Total rams	Total doses	Mean doses / ram	Total rams	Total doses	Mean doses / ram
BADGERFACE WELSH MOUNTAIN	24	3286	137						
BALWEN	9	1787	199	9	984	109			
BELTEX	26	3019	116						
BEULAH SPECKLED FACE	26	3525	136						
BLACK FRIESLAND	3	212	71						
BLACK WELSH MOUNTAIN	17	2550	150						
BLEU DE MAINE	8	1111	139						
BLUEFACED LEICESTER	44	5712	130						
BORDER LEICESTER	13	1730	133						
BORERAY	3	412	137	11	1166	106			
BRECKNOCK HILL CHEVIOT	19	1767	93						
BRITISH MILKSHEEP	9	1795	199						
CAMBRIDGE	16	2630	164						
CASTLEMILK MOORIT	11	1215	110	19	2047	108			
CHAROLLAIS	23	3225	140						
CLUN FOREST	7	1562	223						
COTSWOLD	14	1757	126	10	958	96			
DALESBRED	6	1128	188				4	58	15
DERBYSHIRE GRITSTONE	2	308	154						
DEVON & CORNWALL LONGWOOL	3	623	208	7	782	112			
DEVON CLOSEWOOL	9	1891	210						
DORSET DOWN	5	957	191	6	622	104			
DORSET HORN	15	2422	161	7	770	110			
EASYCARE	12	1439	120						
EXMOOR HORN	11	1452	132						
FRIESLAND	17	2768	163						
GALWAY	1	150	150	1	42	42			
GREYFACE DARTMOOR	20	2528	126	20	1857	93			
HAMPSHIRE DOWN	11	1457	132						

Table EX7: continued

	National Scrapie Plan Semen Archive			RBST Sheep Semen Bank			Sheep Trust Heritage Gene Bank		
	Total rams	Total doses	Mean doses / ram	Total rams	Total doses	Mean doses / ram	Total rams	Total doses	Mean doses / ram
HEBRIDEAN	15	2704	180	18	1543	86			
HERDWICK	0	0	0				85	1118	13
HILL RADNOR	19	2566	135	6	681	114			
JACOB	14	2067	148						
KERRY HILL	10	1991	199	2	308	154			
LEICESTER LONGWOOL	2	486	243	21	2121	101			
LINCOLN LONGWOOL	4	987	247	14	2214	158	6	245	41
LLANDOVERY WHITEFACE	5	750	150						
LLANWENOG	20	2969	148	17	1728	102			
LLEYN	64	10226	160						
LONK	1	200	200				6	100	17
MANX LOGHTAN	18	2610	145	19	1931	102			
NORFOLK HORN	2	320	160	31	2912	94			
NORTH COUNTRY CHEVIOT	42	6000	143						
NORTH RONALDSAY	9	1100	122	21	2339	111			
OXFORD DOWN	10	1176	118	11	1204	109			
POLL DORSET	43	4818	112						
PORTLAND	7	1279	183	12	1352	113	5	62	12
ROMNEY MARSH	17	3526	207	17	3526	207			
ROUGH FELL	16	2048	128	9	175	35	9	175	35
RYELAND	8	1414	177	6	644	107			
SCOTTISH BLACKFACE (LANARK)	41	5364	131						
SC BLACKFACE (N ENGLAND)	16	2297	144						
SCOTTISH BLACKFACE (PERTH)	11	1357	123						
SHETLAND (ISLAND)	31	4215	136						
SHETLAND (MAINLAND)	33	3948	120						
SHROPSHIRE	26	3812	147	10	1238	124			
SOAY	16	2168	136	1	1987	105			

Table EX7: continued

National Scrapie Plan Semen Archive			RBST Sheep Semen Bank			Sheep Trust Heritage Gene Bank			
	Total rams	Total doses	Mean doses / ram	Total rams	Total doses	Mean doses / ram	Total rams	Total doses	Mean doses / ram
SOUTH COUNTRY CHEVIOT	42	5077	121						
SOUTH WALES MOUNTAIN	20	2767	138						
SOUTHDOWN	6	747	125	11	1164	106			
SUFFOLK	54	7121	132						
SWALEDALE	43	9261	215						
TALYBONT WELSH MOUNTAIN	8	1077	135						
TEESWATER	3	656	219	14	1701	122			
TEXEL	35	4361	125						
TREGARON WELSH MOUNTAIN	23	3106	135						
WELSH HILL SPECKLED FACE	20	2708	135						
WELSH MOUNTAIN - PEDIGREE	8	1022	128						
WENSLEYDALE	4	854	214	16	1784	112			
WHITE FACED WOODLAND	12	1678	140	19	2045	108			
WHITEFACE DARTMOOR	7	1274	182	3	300	100			
WILTSHIRE HORN	19	2588	136	1	92	92			
ZWARTBLES	20	2693	135						

7.1.11 Technical Appendix 11: Daughter breed societies

Numbers of countries with daughter breed societies for UK breeds (derived from Porter 2002). European countries with societies are indicated.

Cattle				Sheep				Horse			Pig	
Aberdeen Angus IE,EL,DK FI,NO,SE	18	Lincoln Red	4	Bluefaced Leicester	1	Oxford Down CZ,CH	3	Cleveland Bay	1	Berkshire	2	
Ayrshire CZ	11	Luing	4	Border Leicester	3	Romney CZ,PL	5	Clydesdale	5	British Saddleback	1	
Belted Galloway DE	4	Red Poll	8	Clun Forest FR	3	Ryeland	2	Dartmoor NL,FR,DE	5	Large Black	3	
British White	2	Shorthorn (incl. Beef)	9	Cotswold	2	Scottish Blackface	2	Exmoor	1	Large White	Many FI,IE IT	
Devon	5	South Devon IE	6	Dorset Down FR	2	Shetland	1	Hackney horse NL	6	Middle White	2	
Dexter	4	Sussex	4	Dorset Horn	5	Shropshire	4	Hackney pony NL	2	Tamworth	1	
Galloway DE,FR,CZ IS	10	Welsh Black	3	Hampshire Down FR	7	South Country Cheviot NO	5	Highland Pony FR	2			
Guernsey IE	8	White Park	1	Jacob	2	South-down	4	Shetland BE,DK,FR DE,SE,NL	7	Goat		
Hereford DK,FR,PT ES,SE,CZ EE,NO,DE HU,NL	26			Leicester Longwool	2	Suffolk IE,FR,DE NL,CZ	10	Shire	1	Anglo Nubian	3	
Highland SE,DE,FR	5			Lincoln Longwool	4	Wensleydale	1	Suffolk	1	Br. Alpine	3	
Jersey FR,SE,DE NL,BE,IE NO	22			North Country Cheviot	2	Wiltshire Horn	1	Welsh BE,DK,NL FR,SE	10			

Country codes: see

http://epp.eurostat.ec.europa.eu/statistics_explained/index.php/Glossary:Country_codes

7.1.12 Technical Appendix 12: Traditional breed (Lincoln Red)

The Lincoln Red was developed in eastern England from the Shorthorn, the breed society of the former being established in 1895 with an annual herd book being published subsequently. Links between the two breeds persisted such that some Lincoln Reds of dairy type were acceptable for entry into Coates Herd Book (the UK herd book for Shorthorns) and these were distinguished in the Lincoln Red herd book. From 1957 cattle of accepted Lincoln Red type derived from Aberdeen Angus (both black animals, and their red derivatives) and polled American Shorthorn cattle were used to introduce polling to the breed and from the early 1970s other beef breeds principally the Limousin were used in a breed development programme (BDP) to develop traits related to beef production. The regulations for these programmes are given in relevant volumes of the herd book.

Lincoln Red cattle tracing back to the introgressions are identifiable in the herd book by prefixes to their registration numbers. Animals without such a prefix are therefore to be seen as original (pre-polling) Lincoln Red cattle. The last such registrations were made in 1977 (male) and in 1980 (female). Animals lacking any of the prefixes that denote affinity to the BDP or subsequent introgressions are now known as Traditional Lincoln Reds and, following an initiative by members of the Lincoln Red Cattle Society, are recognized as a genetic resource of conservation significance (Stennett 1999).

Numbers of Lincoln Red males registered in each year, distinguished according to prefix, are illustrated in **Figure LR**. The primary trend is of a decline in numbers from 1955 to 1995, interrupted from 1971 to 1975 by a partial recovery accompanying the registration of animals derived from the polled introgression, which began in 1957. Decline after 1975 led to a low point in 1999 and a recovery thereafter, with early 21st century registrations being predominantly of animals tracing back to the BDP of the 1970s. A wide range of breeds (**Table LR**) was used in the BDP, beginning in 1975 with the entry in the herd book of one male sired by a Maine-Anjou and one male and one female sired by a Chianina. Also, the original polled introgression was supplemented from 1959 to 1961 by registration of 18 males and 25 females sired by American Polled Shorthorns.

Figure LR: Lincoln Red sires: numbers registered in each volume of the herd book. Herd book volume number + 1900 = calendar year.

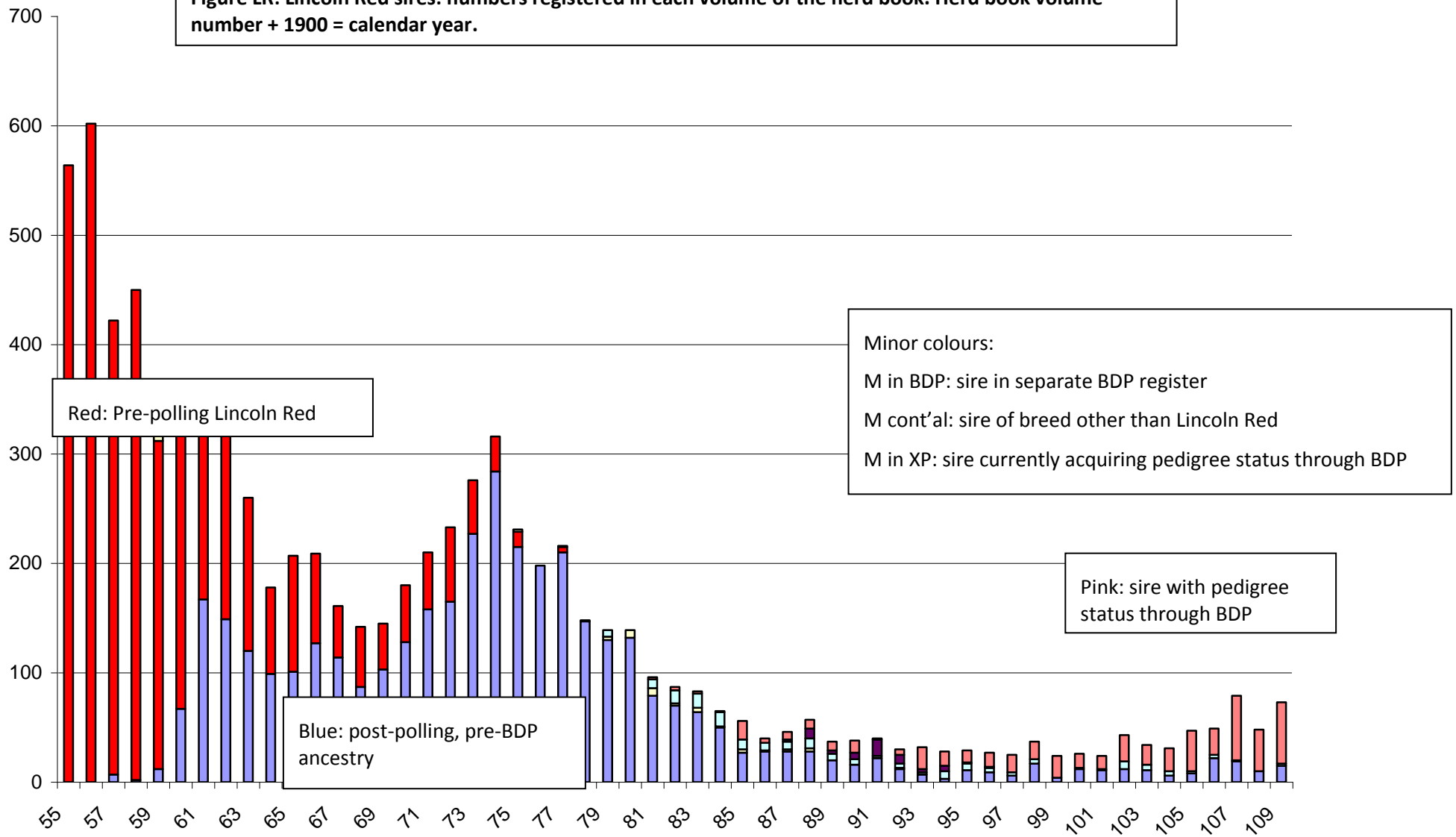


Table LR: Lincoln Red: Numbers of registered progeny in each volume of the herd book for which bulls of each breed were sires. MA: Maine-Anjou; L: Limousin; Ch: Chianina; C: Charolais; Sx: Sussex; Si: Simmental; Sa: Salers; Bl: Blonde d'Aquitaine; BB: Belgian Blue; Br: Brahman; AA: Aberdeen Angus; SD: South Devon; R: Romagnola

	MA		L		Ch		C	Sx		Si	Sa		Bl	BB	Br	AA	SD	R
	M	F	M	F	M	F	F	M	F	F	M	F	F	F	F	F	F	F
1975	1				1	1												
1977						2	21											
1978	1	5																
1979	2	1	1	3														
1980	1	7	6	16					3									
1981		6	6	14				1	15									
1982	1	18	1	18					14									
1983		4	4	6														
1984	1	7								3								
1985			3	2						1								
1986		7	1	12														
1987		5	2	15						1		6						
1988				8		2				1	3		4					
1989		10		18		3												
1990										1				6				
1991				3									1	1				
1992										4	1	1						
1993				5						2								
1994				2											1			
1995										2								
1996													2	1				
1997														4				
1998				1									3	2				
1999										2								
2000													1					
2002				4														
2003				1														
2006				2														
2007				13														
2008				1												1		
2009				5												4	1	3
total	7	70	24	149	1	8	21	1	32	17	4	7	11	14	1	5	1	3

7.1.13 Technical Appendix 13: Effective population sizes

“Effective population size” can be a confusing term because for many people it might imply numbers of breeding animals. “Equivalent population size” might have been a better choice. The concept provides the framework that connects the rate of inbreeding in a population to the size of that population.

In an idealized population that conforms to certain assumptions – notably that there is no migration nor change in population number, mating is at random among all individuals including self fertilization, there is no mutation or selection and generations do not overlap – the increase of mean inbreeding per generation ΔF was shown theoretically by the American geneticist Sewall Wright to be related to the number of individuals in the population thus:

$$\Delta F = \frac{1}{2N_e}$$

(eqn. 1)

Thus the 1% increase per generation in inbreeding mentioned above is associated with a population of 50 of these idealized individuals. However, for the theory to be applicable to livestock it has to be expressed in terms of sires and dams and the key finding from genetic theory is that, for M sires and F dams:

$$\Delta F = \frac{1}{8M} + \frac{1}{8F}$$

(eqn. 2)

Putting the two equations together yields the expression:

$$N_e = 4 \frac{MF}{(M + F)}$$

(eqn. 3). Here, this is referred to as “Wright’s equation”.

A ΔF of 1% (or 0.01), which corresponds to an N_e of 50, can be obtained in many different ways, for example:

M	F	N_e	ΔF
25	25	50	0.01
14	116	50	0.01
13	450	50	0.01

And, for a breed (like many modern dairy cattle) where there may be 2 million cows inseminated by 50 bulls:

M	F	N_e	ΔF
50	2,000,000	200	0.0025

The disproportionate importance of the number of males (the rarer sex) in determining rate of loss of genetic variation through inbreeding is very clear.

In practice, because the assumptions of idealized population are unrealistic, N_e as calculated is an overestimate and the actual ΔF is usually higher than the calculation implies.

Modifications to eqn. 3 can be made to account for real populations behaving quite differently from the idealized. These which yield values for N_e that for a given population are closer to those obtained from eqn. 1 and these are of value in permitting ΔF to be calculated or predicted for

populations whose inbreeding is unknown. They also enable the effects of population management on ΔF to be assessed.

Eqn. 3 uses the most simple form of demographic data – the number of parents of both sexes – and an obvious refinement is to take account of the fact that some parents leave far more offspring which subsequently breed, than do other parents. This is expressed by the formula of Hill (1979):

$$\frac{1}{N_e} = \frac{1}{16ML} \left[2 + \text{var}_{mm} + 2 \left(\frac{M}{F} \right) \text{cov}(mm, mf) + \left(\frac{M}{F} \right)^2 \text{var}_{mf} \right] + \frac{1}{16FL} \left[2 + \text{var}_{ff} + 2 \left(\frac{F}{M} \right) \text{cov}(fm, ff) + \left(\frac{F}{M} \right)^2 \text{var}_{fm} \right]$$

(eqn. 4)

In this report, this is referred to as “Hill’s equation”.

M is the number of sires and F the number of dams. L is the generation length. var_{mm} and var_{mf} are the variances of number of breeding sons and daughters per sire, and var_{ff} and var_{fm} those for dams. The cov terms are the corresponding covariances.

With livestock breeds, equations 2-4 tend to give higher values for N_e than equation 1 (example: Figure 2 of Toro et al. (2011)). Comparisons of N_e between studies that have used different methods may not be valid, but comparisons within studies, where the assumptions used in the equations have not changed, may be valuable.

The general form of Equations 3 and 4 has implications for practical conservation planning, which can be illustrated by using imaginary data to change the values of the terms in the equation. Any increase in the numerators of the terms will tend to diminish the estimated N_e while any increase in the denominators will tend to augment it. Reports on how these equations compare in practical situations are not yet available.

However, Eqns. 4 and 5 have still not taken selection into account; some lineages may be especially favoured by breeders (Santiago and Caballero 1995). Two principal methods for increasing N_e are, increasing mean generation interval, and managing family size. The former is the measure of how long it takes to replenish a set of parents and is the average age of parents at the birth of their replacements. By family size is meant the numbers of breeding sons and daughters produced by each sire and each dam. A dramatic effect on N_e is seen when there is pure within-family selection, a sire being replaced by one of his sons and a dam replaced by one of her daughters; here, eqn. 3 is replaced by:

$$N_e = \frac{16MF}{3F + M}$$

(eqn. 6)

N_e can be increased even more if certain further constraints are added to the mating scheme (Wang 1997).

Finally, founder genome equivalents, genetic contributions, effective numbers of founders and management of coancestry (Caballero and Toro 2000) are additional important genetic management approaches that can be applied if a full digitized dataset is available. These and other statistics can also be obtained from molecular data (Toro et al. 2011) which is very useful in populations without pedigrees. The scientifically ideal approach is known as optimal contribution selection but there are few examples of this approach having been used in a conservation population (Hasler et al. 2011; Olsen et al. 2012).

7.1.14 Technical Appendix 14: Poultry

The definitive review of the conservation status of UK poultry breeds is the 2010 Defra report¹³¹. The RBST list of breeds “at risk” was published in the Winter 2012 “Ark”, page 18. Values of the F_{is} statistic, a measure of within-population structuring and thus indicative of inbreeding, can be obtained from Wilkinson et al. (2012) and these are clearly important to conservation planning.

These F_{is} statistics are reproduced in **Table P1**. There was no correlation between F_{is} and number of breeders (members), nor did mean F_{is} for breeds with their own breed society (0.209) differ from that for breeds overseen by RPS (0.198). This implies that breeding practices do not differ among the breeds.

Familiar problems with assessment of conservation status of poultry are the lack of formal registration of birds, coupled with the likelihood that many flocks are kept by people who are not members of poultry breed societies. It is particularly important to identify breeds where the latter applies. Breeds supported by a strong breed society are almost certainly safer from extinction.

Given that much information about livestock breeds is posted on the Internet, it might be hypothesized that Internet traffic about breeds would be proportional to numbers of keepers of the respective breeds. A corollary would be that breeds where Internet traffic (assessed by numbers of Google hits) is greater than would be expected from known number of breeders, might be those with a larger proportion of flocks kept by non-members of breed societies. It would also be predicted that Google hits per breeder would be greater in breeds overseen by the Rare Poultry Society as an umbrella organization, than in breeds with their own society.

A broadly similar study of Internet traffic as related to public awareness of the conservation status of wild animal species was reported by Zmihorski et al. (2013).

The search expression “[breed name] chicken” was entered into Google, UK webpages only were stipulated. All searches were conducted at the same desktop computer session between 2000 and 2200 on Friday 27 January 2013 (to reduce the risk of Google search parameters being changed between sessions). Breeds chosen were those studied by Wilkinson et al. (2012) and those on the RBST list.

In some cases this search expression yielded clearly irrelevant information, for example “Malay chicken” and “Spanish chicken” yielded large numbers of cooking recipes. In others, for example “Old English Pheasant Fowl chicken” yielded far fewer hits than an expression consisting of just the first four words. In these situations (signalled in **Table P1**), a revised search expression was used (full details available from author).

Numbers of Google hits were divided by numbers of breeders, and mean hits per breeder compared between breeds overseen by the Rare Poultry Society (which operates a registrar system for several of the rarest breeds) and breeds with their own society.

Overall, the correlation between number of Google hits and number of members (breeders) was significant ($r = 0.36$, $df = 30$, $p < 0.05$). Mean numbers of Google hits per breeder were 1235.9 and 694.6 for breed society and RPS breeds respectively, a highly significant difference ($t = 0.379$, $p = 0.001$).

The study of Internet traffic suggests that overall, breeds that have more breeders also tend to have more traffic, but that when number of Google hits is corrected for number of members, the breeds overseen by RPS have more Google hits per breeder. Breeds where the number of Google hits per breeder is particularly out of step are the Cochin and Andalusian, and the Welbar, Rhodebar and

¹³¹ <http://www.defra.gov.uk/publications/2011/04/08/pb13451-poultry-in-the-uk/>

Campine; these might be breeds where interest in the breed, and by inference numbers of flocks, are greater than the numbers of known breeders would imply.

Table P1: F_{is} statistics and Google hits, with breed data, for poultry breeds. Underlined breeds are on the RBST Watchlist. Breeds are also distinguished according to whether or not they have their own breed society.

	F_{is}	males	females	breeders	Google hits:		notes
					total	per breeder	
With own breed society							
Ancona		20	55	72	2070	28.8	
Araucana	0.242	100	450	200	805	4.0	
<u>Australorp</u>		20	40	6			
Brahma	0.189	100	200	20			1
<u>British Faverolle</u>		80	160	40	3	0.1	2,3
Buff Orpington	0.073	110	350	119	912	7.7	
<u>Cochin</u>	0.125	125	500	50	4000	80.0	
<u>Croad Langshan</u>	0.143	90	760	120	2810	23.4	3
<u>Derbyshire Redcap</u>	0.167	144	493	53	205	3.9	
<u>Dorking</u>	0.234	292	680	111	2400	21.6	
<u>Hamburgh</u>	0.476	40	100	104	30	0.3	
<u>Indian Game</u>	0.102	39	94	58	40	0.7	
<u>Leghorn</u>	0.315	150	750	160	7490	46.8	
Light Sussex	0.111				12		4
Lincolnshire Buff	0.146	30	60	10			1
<u>Malay</u>		75	75	15	129	8.6	3
Maran	0.190	800	2000	280			
<u>Minorca</u>		160	400	80	569	7.1	
<u>Modern Game</u>		50	180		251		
<u>Old English Game</u>		100	1000		311		1
<u>Orpington (non-buff)</u>		200	500	108	6	0.1	3
Rhode Island Red	0.281	55	150	130			
<u>Rosecomb</u>		60	96	47	227	4.8	3,5
<u>Scots Dumpy</u>	0.137	200	400	125	27	0.2	
<u>Scots Grey</u>	0.200	50	200	36	440	12.2	
<u>Sebright</u>		400	1000	120	1160	9.7	5
Silkie	0.196	50	280	158			
Sussex	0.333	100	300	150	2068	13.8	2,6

Table continued					Google hits:		
	F_{is}	males	females	breeders	total	per breeder	F_{is}
Rare Poultry Society							
<u>Andalusian</u>		16	58	9	1410	156.7	
Appenzeller	0.279	30	105	8			7
<u>Brussbar</u>		5	7	1	127	127.0	
<u>Campine</u>		20	47	6	1700	283.3	
<u>Ixworth</u>	0.047	27	70	10	241	24.1	1
<u>Legbar</u>					399		
<u>Marsh Daisy</u>	0.245	52	150	19	230	12.1	
Modern Langshan		7	15	1	120	120.0	3
<u>Nankin</u>					301		
<u>Norfolk Grey</u>	0.200	14	37	9	201	22.3	
<u>North Holland Blue</u>		9	21	3	407	135.7	3
<u>Old English Pheasant Fowl</u>	0.167	27	103	11	6	0.5	3
<u>Rhodebar</u>		8	16	5	2180	436.0	3
<u>Spanish</u>	0.250	10	29	3	507	169.0	3
<u>Sultan</u>		18	42	9	1120	124.4	
<u>Welbar</u>		3	24	2	1540	770.0	3
<u>Cream Legbar</u>					231		

Notes:

- 1 lower estimate
- 2 Faverolle in Defra report
- 3 modified Google expression
- 4 included in Sussex
- 5 bantam
- 6 exclude "light sussex" hits
- 7 Appenzeller breeds combined for this analysis

Effective population sizes calculated by the Wright formula are given in **Table P2**. Retention of genetic variation within the rarest breeds will depend on whether a breeding programme can be operated, aimed at building up N_e .

The relatively high numbers of males reflect the mating systems of poultry and waterfowl. In commercial meat chickens, 8 or 9 males per 100 females is a recommendation (Hazary et al. 2001). For ducks, the ratio is one male to 4-8 females (Kasai et al. 2000). Goose breeds vary, some preferring pair bonding, the lowest male:female ratio being 1 to 4-5 females with the low body-weight breeds (Soames 1980).

Table P2: Effective population sizes of rare UK poultry breeds. All are on the RBST Watchlist.

Breed of chicken	males	females	Fis	N_e with random mating	Breeders
Brussbar	5	7		12	1
Rhodebar	8	16		21	5
Welbar	3	24		11	2
North Holland Blue	9	21		25	3
Spanish	10	29	0.250	30	3
Norfolk Grey	14	37	0.200	41	9
Australorp	20	40		53	6
Sultan	18	42		50	9
Campine	20	47		56	6
Andalusian	16	58		50	9
Ixworth	27	70	0.047	78	10
Old English Pheasant Fowl	27	103	0.167	86	11
Indian Game	39	94	0.102	110	58
Hamburgh	40	100	0.476	114	104
Malay	75	75		150	15
Rosecomb	60	96		148	47
Marsh Daisy	52	150	0.245	154	19
Modern Game	50	180		157	
British Faverolle	80	160		213	40
Scots Grey	50	200	0.200	160	36
Minorca	160	400		457	80
Scots Dumpy	200	400	0.137	533	125
Cochin	125	500	0.125	400	50
Derbyshire Redcap	144	493	0.167	446	53
Orpington (non-buff)	200	500		571	108
Croad Langshan	90	760	0.143	322	120
Leghorn	150	750	0.315	500	160
Dorking	292	680	0.234	817	111
Old English Game	100	1000		364	
Sebright	400	1000		1143	120
Cream Legbar	No data				
Legbar	No data				
Nankin	No data				

Breed of duck		males	females	Ne random	members
Abacot Ranger		7	25	22	3
Appleyard Silver		7	25	22	3
Stanbridge White		10	30	30	3
Aylesbury		12	30	34	5
Cayuga		15	35	42	7
Rouen (Exhibition)		12	40	37	5
Orpington		8	50	28	4
Magpie		12	50	39	5
Welsh Harlequin		10	55	34	6
Crested		25	60	71	8
Black East Indian		35	80	97	9
Campbell		20	400	76	8
Shetland		No data			
Silver Bantam		No data			
Breed of goose		males	females	Ne random	members
Shetland		5	5	10	2
Greyback		10	10	20	5
West of England		30	35	65	16
Pilgrim		30	40	69	14
Brecon Buff		40	45	85	32
Sebastopol		50	60	109	18
Toulouse (Exhibition)		No data			
Breed of turkey		males	females	Ne random	members
Narragansett		10	15	24	
Nebraskan		10	20	27	
Buff		10	30	30	
British White		10	35	31	
Bourbon Red		30	100	92	
Pied/Cröllwitzer		50	130	144	
Bronze		120	350	357	
Norfolk Black		180	300	450	
Blue		No data			
Slate		No data			

8 References

- Ajmone-Marsan P, GLOBALDIV. 2010. A global view of livestock biodiversity and conservation - GLOBALDIV. *Animal Genetics* 41(suppl.):1-5.
- Ajmone-Marsan P. 2012. Use of molecular information for the characterization and conservation of farm animal genetic resources: results of large scale international projects and perspectives offered by new technologies. In http://rbiglobalconf2011.nku.edu.tr/rbi/Conference_proceedings.pdf
- Alderson L, Porter V. 1994. *Saving the breeds. A history of the Rare Breeds Survival Trust*. Robertsbridge, East Sussex: Pica Press/Helm Information.
- Alvarez RH, da Silva MVGB, Pereira de Carvalho JB, Binelli M. 2005. Effects of inbreeding on ovarian responses and embryo production from superovulated Mantiqueira breed cows. *Theriogenology* 64:1669-1676.
- Amer PR, Nieuwhof GJ, Pollott GE, Roughsedge T, Conington J, Simm G. 2007. Industry benefits from recent genetic progress in sheep and beef populations. *Animal* 1:1414-1426.
- Amer PR, Wall E, Nuhs J, Winters M, Coffey MP. 2011. Sources of benefits from genetic improvement in the UK dairy industry and their impacts on producers and consumers <http://www-interbull.slu.se/ojs/index.php/ib/article/view/1227/1338>. *Interbull Bulletin Stavanger, Norway*, August 26-29, 2011[no. 44]:244-248.
- Amos W, Brooks-Pollock E, Blackwell R, Driscoll E, Nelson-Flower M. 2013. Genetic predisposition to pass the standard SICCT test for bovine tuberculosis in British cattle. *PloS One* 8:e58245.
- Annett RW, Carson AF, Dawson LER, Irwin D, Kilpatrick DJ. 2011. Effects of breed and age on the performance of crossbred hill ewes sourced from Scottish Blackface dams. *Animal* 5:356-366.
- Anon. 2005. Fibre from goats - an introduction. CALU technical notes ref. 0401003 <http://www.calu.bangor.ac.uk/technical%20leaflets/040103FibrefromgoatsintroRev2.pdf>.
- Anon. 2008. Commercial dairy goat farming: a high risk opportunity? <http://www.allgoats.com/downloads/rabdfperspective.pdf>
- Anon. 2010. The dawn of a new era in cattle breeding. *Royal Jersey Agricultural & Horticultural Society Journal*:3-8.
- Anon. 2011. UK red and white Holstein registrations in 2010. *Holstein Journal* (June 2011):15.
- Asseged BD, Habtemariam T, Tameru B, Nganwa D. 2012. The risk of introduction of equine infectious anemia virus into USA via cloned horse embryos imported from Canada. *Theriogenology* 77:445-58.
- Avendaño S, Villanueva B, Woolliams JA. 2003. Expected increases in genetic merit from using optimized contributions in two livestock populations of beef cattle and sheep. *Journal of Animal Science* 81:2964-2975.
- Baéza E, Chartrin P et al. 2009. Does the chicken genotype 'Géline de Touraine' have specific carcass and meat characteristics? *Animal* 3:764-771.
- Ballingall KT, Steele P, Hall SJG. 2012. A complete lack of functional MHC diversity within an apparently healthy population of large mammals. *Immunology* 137(Suppl. 1):69.
- Ballou JD, Lacy RC. 1995. Identifying genetically important individuals for management of genetic variation in pedigreed populations. In: Ballou JD, Gilpin M, Foose TJ, editors. *Population management for survival and recovery. Analytical methods and strategies in small population conservation*. New York: Columbia University Press; p 76-111.
- Balmford A, Green RE, Phalan B. 2012. What conservationists need to know about farming. *Proceedings of the Royal Society of London B* 279:2714-2724.
- Barber C. 2010. The Tubney project. Laying the foundations of the RBST national gene bank. *Ark Autumn* 2010:30-31.
- Bell MJ, Wall E, Russell G, Simm G, Stott AW. 2011. The effect of improving cow productivity, fertility and longevity on the global warming potential of dairy systems. *Journal of Dairy Science* 94:3662-3678.
- Berry DP et al. 2011. The integration of "omic" disciplines and systems biology in cattle breeding. *Animal* 5:493-505.
- Berry D et al. 2013. Development of a custom genotyping panel for dairy and beef cattle breeding and research. In: *Innovation from animal science – a necessity not an option. Advances in Animal Biosciences*. *Animal* 4:249.
- Bertaglia M, Joost S, Roosen J, Econogene Consortium. 2007. Identifying European marginal areas in the context of local sheep and goat breeds conservation: a geographic information system approach. *Agricultural Systems* 94:657-670.

- Richard M. 2002. Genetic improvement in dairy cattle - an outsider's perspective. *Livestock Production Science* 75:1-10.
- Bishop SC, Axford RFE, Nicholas FW, Owen JB. 2010. Breeding for disease resistance in farm animals, 3rd edition. Wallingford, UK: CABI.
- Bishop SC, Russel AJF. 1994. Cashmere production from feral and imported cashmere goat kids. *Animal Production* 58:135-144.
- Bishop SC, Woolliams JA. 2004. Genetic approaches and technologies for improving the sustainability of livestock production. *Journal of the Science of Food and Agriculture* 84:911-919.
- Blesbois E, Grasseau I, Seigneurin F, Mignon-Grasteau S, Saint Jalme M, Mialon-Richard MM. 2008. Predictors of success of semen cryopreservation in chickens. *Theriogenology* 69:252-61.
- Bluhm W. 2009. The role of crossbreeding in UK dairy breeding Access via <http://www.afmp.co.uk>: Arla Foods Milk Partnership / International Agri-Technology Centre.
- Boe-Hansen GB, Ersbøll AK, Greve T, Christensen P. 2005. Increasing storage time of extended boar semen reduces sperm DNA integrity. *Theriogenology* 63:2006-2019.
- Boettcher PJ, Tixier-Boichard M, Toro MA, Simianer H, Eding H, Gandini GC et al. 2010. Objectives, criteria and methods for using molecular genetic data in priority setting for conservation of animal genetic resources. *Animal Genetics* 41 (suppl. 1), 64-77.
- Bomcke E, Gengler N. 2009. Combining microsatellite and pedigree data to estimate relationships among Skyros ponies. *Journal of Applied Genetics* 50:133-143.
- Bonneau M, Antoine-Ilari E, Phatsara C, Brinkmann D, Hviid M, Christiansen MG, Fàbrega E, Rodríguez P, Rydhmer L, Enting I, de Greef K, Edge H, Dourmad J-Y, Edwards S. 2011. Diversity of pig production systems at farm level in Europe. *Journal on Chain and Network Science* 11:115-135.
- Boogard BK, Oosting SJ, Bock BB, Wiskerke JSC. 2011. The sociocultural sustainability of livestock farming: an inquiry into social perceptions of dairy farming. *Animal* 5:1458-1466.
- Boon SE. 2006. The opportunity for composite flocks within the UK sheep industry http://www.nuffieldinternational.org/rep_pdf/1226660319Boon_Samuel.pdf. Nuffield Farming Scholarships Trust / Central Region Farmers Trust Award.
- Bowles D, Gilmartin P, Holt W, Leese H, Mylne J, Picton H, Robinson J, Simm G. 2004. Evolution of Heritage GeneBank into the Sheep Trust: conservation of native traditional breeds that are commercially farmed, environmentally adapted and contribute to the economy of rural communities. In: Simm G, Villanueva B, Sinclair KD, Townsend S, editors. *Farm animal genetic resources*. Nottingham: Nottingham University Press; p 45-55.
- Bowles D, Gilmartin P, Holt W et al. 2004. Evolution of Heritage GeneBank into the Sheep Trust: conservation of native traditional sheep breeds that are commercially farmed, environmentally adapted and contribute to the economy of rural communities. In: Simm G, Villanueva B, Sinclair KD, Townsend S, editors. *Farm animal genetic resources*. Nottingham: Nottingham University Press; p 45-55.
- Bowman JC, Hocking PM. 1974. The development of a new red and white breed of cattle in the United Kingdom. *Livestock Production Science* 1:401-409.
- Bray TC. 2009. Detecting and managing suspected admixture and genetic drift in domestic livestock: modern Dexter cattle - a case study. Unpublished PhD dissertation, University of Cardiff.
- Bray TC, Chikhi L, Sheppy AJ, Bruford MW. 2009. The population genetic effects of ancestry and admixture in a subdivided cattle breed. *Animal Genetics* 40:393-400.
- Bruck I, Anderson GA, Hyland JH. 1993. Reproductive performance of Thoroughbred mares on six commercial stud farms. *Australian Veterinary Journal* 70:299-303.
- Caballero A, Toro MA. 2000. Interrelations between effective population size and other pedigree tools for the management of conserved populations. *Genetical Research* 75:331-343.
- Calder A. 1927. The role of inbreeding in the development of the Clydesdale breed of horses. *Proceedings of the Royal Society of Edinburgh* 47:118-140.
- Campo JL, Gil MG, Davila SG, Torres O.. 2000. Conservation of genetic diversity in Spanish chicken: 25 years of a conservation program (1975-2000). *World Poultry Congress August 20-24; Madrid*.
- Canali G, Econogene Consortium. 2006. Common agricultural policy reform and its effects on sheep and goat market and rare breeds conservation. *Small Ruminant Research* 62:207-213.
- Carson A, Elliott M, Groom J, Winter A, Bowles D. 2009. Geographical isolation of native sheep breeds in the UK - evidence of endemism as a risk factor to genetic resources. *Livestock Science* 123:288-299. <http://archive.defra.gov.uk/fangr/documents/sheeptrustrpt-090205.pdf>
- Caughley G. 1994. Directions in conservation biology. *Journal of Animal Ecology* 63,215-244.

- Cervantes I, Molina A, Goyache F, Gutiérrez JP, Valera M. 2008. Population history and genetic variability in the Spanish Arab horse assessed via pedigree analysis. *Journal of Animal Breeding and Genetics* 113:24-33.
- Cheng H. 2010. Viral diseases in chickens. In: Bishop SC, Axford RFE, Nicholas FW, Owen JB, editors. *Breeding for disease resistance in farm animals*. 3rd ed. Wallingford, UK: CAB International; p 70-87.
- Chikhi L, Goossens B, Treanor A, Bruford MW. 2004. Population genetic structure and inbreeding in an insular cattle breed, the Jersey, and its implications for genetic resource management. *Heredity* 92:396-401.
- Clarke SW, Tucker EM, Hall SJG. 1989. Genetic polymorphisms and their relationships with inbreeding and breed structure in rare British sheep: the Portland, Manx Loghtan, and Hebridean. *Conservation Biology* 3:381-388.
- Clutton-Brock J. 1999. *A natural history of domesticated mammals*. Second edition. Cambridge: Cambridge University Press.
- Coffey M, Krzyzelewski T, Roughsedge T, Mrode RA. 2007. EGENES and BASCO. National beef evaluations in the UK. *Interbull Bulletin* 36 [Proceedings of the International Technical Workshop, Paris, March 9-10, 2006]:1-6. <http://www-interbull.slu.se/bulletins/bulletin36/Coffey.pdf>
- Conington J, Moore K, Glasgow A, Dwyer CM. 2013. Including lamb survival as a breeding goal in extensive sheep breeding programmes. In: *Innovation from animal science – a necessity not an option*. *Advances in Animal Biosciences*. Animal 4:167.
- Cothran EG, MacCluer JW, Weitkamp LR, Bailey E. 1987. Genetic differentiation associated with gait within American Standardbred horse. *Animal Genetics* 18:285-296.
- Danchin-Burge C, Palhière I, Francois D, Bibé B, Leroy G, Verrier E. 2010. Pedigree analysis of seven small French sheep populations and implications for the management of rare breeds. *Journal of Animal Science* 88:505-516.
- Danchin-Burge C, Hiemstra SJ, Blackburn H. 2011. Ex situ conservation of Holstein-Friesian cattle: comparing the Dutch, French and US germplasm collections. *Journal of Dairy Science* 94:4100-4108.
- De Marchi M, Cassandro M, Targhetta C, Baruchello M, Notter DR. 2005. Conservation of poultry genetic resource in the Veneto region of Italy. *Animal Genetic Resources Information* 37:63-74.
- Defra. 2010. *Poultry in the United Kingdom. The genetic resources of the national flocks*. <http://www.defra.gov.uk/publications/files/pb13451-uk-poultry-faw-101209.pdf> London: Department for Environment, Food and Rural Affairs.
- Dell AC. 2010. Genetic analysis and breed management of the endangered Cleveland Bay horse. Unpublished PhD dissertation, University of Lincoln, UK. <http://www.mediafire.com/?3dk403r7aq0r6ze>
- Druml T, Baumung R, Sölkner J. 2008. Morphological analysis and effect of selection for conformation in the Noriker draught horse population. *Livestock Science* 115:118-128.
- Ducrocq V. 2010. Sustainable dairy cattle breeding: illusion or reality? <http://www.kongressband.de/wcgalp2010/assets/pdf/0066.pdf>. Leipzig, Germany.
- Dunner S, Checa ML, Gutiérrez JP, Martin JP, Cañon J. 1998 Genetic analysis and management in small populations: the Asturcón pony as an example. *Genetics Selection Evolution* 30:397-405.
- Eggen A. 2012. The development and application of genomic selection as a new breeding paradigm. *Animal Frontiers* 2:10-15.
- Engelsma KA, Veerkamp RF, Calus MPL, Windig JJ. 2011. Consequences for diversity when prioritizing animals for conservation with pedigree or genomic information. *Journal of Animal Breeding and Genetics* 128:473-481.
- Evans N, Yarwood R. 2000 The politicization of livestock: rare breeds and countryside conservation. *Sociologia Ruralis* 40:228-248.
- Fabuel E, Barragán C, Silió L, Rodríguez MC, Toro MA. 2004. Analysis of genetic diversity and conservation priorities in Iberian pigs based on microsatellite markers. *Heredity* 93:104-113.
- Fair S, Hanrahan JP, O'Meara CM, Duffy P, et al. 2005. Differences between Belclare and Suffolk ewes in fertilization rate, embryo quality and accessory sperm number after cervical or laparoscopic artificial insemination. *Theriogenology* 63:1995-2005.
- FAO. 1998. Secondary guidelines for development of national farm animal genetic resources management plans. Management of small populations at risk. Rome: Food and Agricultural Organization of the United Nations. <http://www.fao.org/ag/againfo/programmes/es/lead/toolbox/indust/sml-popn.pdf>
- Fernández A, Meuwissen THE, Toro MA, Mäki-Tanila A. 2011. Management of genetic diversity in small farm animal populations. *Animal* 5:1684-1698.
- Fikse WF, Philipsson J. 2007. Development of international genetic evaluations of dairy cattle for sustainable breeding programs. *Animal Genetic Resources Information* 41:29-43.

- Fina M, Casellas J, Tarrés J, Bartolomé J, Plaixats J, Such X, Jiménez N, Sánchez A, Piedrafita J. 2008. Characterisation and conservation programme of the Alberes cattle breed in Catalonia (Spain). *Animal Genetic Resources Information* 43:1-14.
- Fouvez V. 2008. The Villard de Lans bovine breed - historical evolution Doctoral dissertation, Ecole Nationale vétérinaire d'Alfort. <http://theses.vet-alfort.fr/telecharger.php?id=897>
- Fox-Clipsham LY. 2009. Focus article: test launched for foal immunodeficiency syndrome AHT/BEVA/Defra *Equine Quarterly Disease Surveillance Report* 5(4, October-December 2009):20-21. http://www.aht.org.uk/skins/Default/pdfs/equine_vol5_4_focus3.pdf
- Fox-Clipsham LY, Carter SD, Goodhead I, Hall N, Knottenbelt DC, May PDF, Ollier WE, Swinburne JE. 2011. Identification of a mutation associated with fatal foal immunodeficiency syndrome in the Fell and Dales Pony. *PLoS Genetics* 7:e1002133.
- Frankham R, Ballou JD, Briscoe DA. 2002. *Introduction to conservation genetics*. Cambridge: Cambridge University Press.
- Fuglie KO, Heisey PW, King JL, Pray CE, Day-Rubenstein K, Schimmelpfennig D, Wang SL, Karmarkar-Deshmukh R. 2011. Research investments and market structure in the food processing, agricultural input, and biofuel industries worldwide. *USDA Economic Research Report* 130. <http://www.ers.usda.gov/publications/err130/>
- Gandini GC, Oldenbroek JK. 2007. Strategies for moving from conservation to utilisation. In: Oldenbroek JK, editor. *Utilisation and conservation of farm animal genetic resources*. Wageningen, The Netherlands: Wageningen Academic Publishers; p 29-54.
- Gandini GC, Pizzi F, Stella A, Boettcher PJ. 2007. The costs of breed reconstruction from cryopreserved material in mammalian livestock species. *Genetics Selection Evolution* 39:465-479.
- Gandini GC, et al. 2010. Motives and values in farming local cattle breeds in Europe: a survey on 15 breeds. *Animal Genetic Resources* 47:45-58.
- Gauly M, Bollwein H, Breves G, et al. 2012. Future consequences and challenges for dairy cow production systems arising from climate change in central Europe - a review. *Animal First View* posted online 20 December 2012.
- Gautier M, Laloë D, Moazami-Goudarzi K. 2010. Insights into the genetic history of French cattle from dense SNP data on 47 worldwide breeds. *PLoS One* 5[9], e13038.
- Gibbs D, Holloway L, Gilna B, Morris C. 2009. Genetic techniques for livestock breeding: restructuring institutional relationships in agriculture. *Geoforum* 40:1041-1049.
- Gómez MD, Azor PJ, Alonso ME, Jordana J, Valera M. 2012. Morphological and genetic characterization of Spanish heavy horse breeds: implications for their conservation. *Livestock Science* 144:57-66.
- Gough M. 2012. Feral goat *Capra hircus*. *Northumbrian Naturalist (Transactions of the Natural History Society of Northumbria)* 73:56-59.
- Gourdine JL, Sorensen AC, Rydhmer L. 2012. There is room for selection in a small local pig breed when using optimum contribution selection: a simulation study. *Journal of Animal Science* 90:76-84.
- Green RD. 2009. Future needs in animal breeding and genetics. *Journal of Animal Science* 87:793-800.
- Groeneveld E, Huu Tinh N, Kues W, Thi Vien N. 2008. A protocol for the cryoconservation of breeds by low-cost emergency cell banks - a pilot study. *Animal* 2:1-8.
- Groeneveld E, van der Westhuizen B, Maiwashe A, Voordewind F, Ferraz JBS. 2009. POPREP: a generic report for population management. *Genetics and Molecular Research* 8:1158-1178.
- Groeneveld LF, Lenstra JA, Eding H, Toro MA, Scherf B, Pilling D et al. 2010. Genetic diversity in farm animals - a review. *Animal Genetics* 41(suppl. 1):6-31.
- Groombridge B. 1992. *Global biodiversity. Status of the Earth's living resources*. London, UK: Chapman and Hall.
- Gura S. 2008. Livestock breeding in the hands of corporations. *Seedling (January 2008)*:2-9. <http://www.grain.org/article/entries/651-livestock-breeding-in-the-hands-of-corporations>
- Gutiérrez JP, Marmi J, Goyache F, Jordana J. 2005. Pedigree information reveals moderate to high levels of inbreeding and a weak population structure in the endangered Catalanian donkey breed. *Journal of Animal Breeding and Genetics* 122:378-386.
- Guy SZY, Thomson PC, Hermes S. 2012. Selection of pigs for improved coping with health and environmental challenges: breeding for resistance or tolerance? *Frontiers in Genetics* 2 (article 281):1-9. <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3522143/pdf/fgene-03-00281>
- Habier D, Götz K-U, Dempfle L. 2009. Breeding programme for Piétrain pigs in Bavaria with an estimation of genetic trends and effective population size. *Livestock Science* 123:187-192.

- Hall SJG. 1986. Genetic conservation of rare British sheep: the Portland, Manx Loghtan and Hebridean breeds. *Journal of Agricultural Science, Cambridge* 107:133-144.
- Hall SJG. 1989a. Breed structures of rare pigs: implications for conservation of the Berkshire, Tamworth, Middle White, Large Black, Gloucester Old Spot, British Saddleback, and British Lop. *Conservation Biology* 3:30-38.
- Hall SJG. 1989b. Conserving and developing minority British breeds of sheep: the example of the Southdown. *Journal of Agricultural Science, Cambridge* 112, 39-45.
- Hall SJG. 2009. Farm animal genetic resources: safeguarding national livestock biodiversity. *Journal of the Royal Agricultural Society of England* 170:48-54.
- Hall SJG. 2011. Number of females in cattle, sheep, pig, goat and horse breeds predicted from a single year's registration data. *Animal* 5: 980-985.
- Hall SJG, Hall JG. 1988. Inbreeding and population dynamics of the Chillingham cattle (*Bos taurus*). *Journal of Zoology, London* 216:479-493.
- Hall SJG, Henderson R. 2000. Rare and minority British sheep for meat production: the Shropshire and Ryeland as sires, and the Cotswold and primitive breeds as dams. *Small Ruminant Research* 35:55-63.
- Hambrook D. 2008. What merit is there in being unique? British Cattle Breeders Club Annual Conference, p 51-56. BCBC, Holsworthy, Devon.
- Handley LJJ, Byrne K, Santucci F, Townsend S, Taylor M, Bruford MW, Hewitt GM. 2007. Genetic structure of European sheep breeds. *Heredity* 99:620-631.
- Hansen LB. 2006. Monitoring the worldwide genetic supply for dairy cattle with emphasis on managing crossbreeding and inbreeding. 8th World Congress on Genetics applied to Livestock Production. Belo Horizonte, Brazil.
- Hart, E. 1999a. The Traditional Hereford. *Ark* 27 (2 Summer 1999):64-65.
- Hart, E. 1999b. Traditional Aberdeen Angus. *Ark* 27 (3 Autumn 1999):110-111.
- Hasler H, Flury C, Menet S et al. 2011. Genetic diversity in an indigenous horse breed – implications for mating strategies and the control of future inbreeding. *Journal of Animal Breeding and Genetics* 128:394-406.
- Hattam C. 2006. Modelling agricultural systems: applications to livestock breeding. Land Economy Working Paper Series no. 11 Edinburgh: Land Economy Research Group, SAC.
http://www.sruc.ac.uk/downloads/file/385/11_modelling_agricultural_systems_applications_to_livestock_breeding
- Hazary RC, Staines HJ, Wishart GJ. 2001. Assessing the effect of mating ratio on broiler breeder performance by quantifying sperm:egg interaction. *Journal of Applied Poultry Research* 10:1-4.
- Hazeleger W, Kemp B. 1999. State of the art in pig embryo transfer. *Theriogenology* 51:81-90.
- Heywood VH, Watson RT. 1995. Global biodiversity assessment. Cambridge, UK: United Nations Environment Programme/Cambridge University Press.
- Hiemstra S J, de Haas Y, Mäki-Tanila A, Gandini GC. 2010. Local cattle breeds in Europe. Towards policies and strategies for self-sustaining breeds
<http://www.regionalcattlebreeds.eu/publications/publications.html> Wageningen: Wageningen Academic Press.
- Hill WG. 1979. A note on effective population size with overlapping generations. *Genetics* 92:317-322.
- Hill WG, Brotherstone S, Visscher PM. 1995. Current and future developments in dairy cattle breeding: a research viewpoint. Occasional Publication, British Society of Animal Science 19:1-7.
- Hillel J, et al. 2003. Biodiversity of 52 chicken populations assessed by microsatellite typing of DNA pools. *Genetics Selection Evolution* 35:533-557.
- Holt WV, Watson PF. 2004. Role of new and current methods in semen technology for genetic resource conservation. In: Simm G, Villanueva B, Sinclair KD, Townsend S, editors. *Farm animal genetic resources*. Nottingham: Nottingham University Press; p 191-205.
- Hudson G, Wilson I, Payne BIA, et al. 2012. Unique mitochondrial DNA in highly inbred feral cattle. *Mitochondrion* 12:438-440.
- IEEP, Ecologic, GHK. 2012. Study to analyse legal and economic aspects of implementing the Nagoya Protocol on ABS in the European Union. Final report for the European Commission, DG Environment – annexes (sectoral sheet: animal breeding industry). Brussels and London: Institute for European Environmental Policy.
<http://ec.europa.eu/environment/biodiversity/international/abs/pdf/ABS%20FINAL%20REPORT%20-%20Annexes.pdf>
- Jewell PA. 1980. The Soay sheep - Parts 1 and 2. *Ark* 7:51-57;87-93.

- Jones MB, Donnelly A. 2004. Carbon sequestration in temperate grassland ecosystems and the influence of management, climate and elevated CO₂. *New Phytologist* 164:423-439.
- Jones S, Bowles D. 2006. Genetic resources of heritage sheep breeds across Europe: their value and conservation. European Regional Focal Point.
- Juodka R, Kiskiėne A, Skurdeniėne I et al. 2012. Lithuanian Vishtines goose breed. *World's Poultry Science Journal* 68:51-62.
- Kanis E, de Greef KH, Hiemstra A, van Arendonk JAM. 2005. Breeding for societally important traits in pigs *Journal of Animal Science* 83:948-957.
- Kasai J, Izumo A et al. 2000. Assessment of fresh and stored duck spermatozoa quality via in vitro sperm-egg interaction assay. *Theriogenology* 54:283-290.
- Katila T. 2001. In vitro evaluation of frozen-thawed stallion semen: a review. *Acta veterinaria Scandinavica* 42:201-217.
- Kavar T, Habe F, Brem G, Dovč P. 1999. Mitochondrial D-loop sequence variation among the 16 maternal lines of the Lipizzan horse breed. *Animal Genetics* 30:423-430.
- Kearney JF, Wall E, Villanueva B, Coffey MP. 2004. Inbreeding trends and application of optimized selection in the UK Holstein population. *Journal of Dairy Science* 87:3503-3509.
- Kijas J, van der Werf J, Ferdosi M, Bell A, Gill S, Gore K, Driver F, Maddox J. 2012. P 4026 SNP-based parentage assignment in sheep: application in Australian flocks. Proceedings, International Society for Animal Genetics 33rd Conference, Cairns, Australia, July 15-20 2012. <http://www.isag.us/proceedings.asp>
- Kinghorn BP, Meszaros S, Woolliams JA. 2002. Development and commercialization of software for genetic improvement programmes: a case study. In: Rothschild MF, Newman S, editors. Intellectual property rights in animal breeding and genetics. Wallingford, UK: CABI Publishing; p 247-261.
- Kirkpatrick JF, Lyda RO, Frank KM. 2011. Contraceptive vaccines for wildlife: a review. *American Journal of Reproductive Immunology* 66:40-50.
- Kristensen TN, Sørensen AC. 2005. Inbreeding - lessons from animal breeding, evolutionary biology and conservation genetics. *Animal Science* 80:121-133.
- Kubbinga B, Hoffmann I, Scherf B. 2007. Passing on the fire - to further inspire people to contribute to the management of animal genetic resources. *Animal Genetic Resources Information* 41:1-7.
- Kuehn LA, Notter DR, Nieuwhof GJ, Lewis RM. 2008. Changes in connectedness over time in alternative sheep sire referencing schemes. *Journal of Animal Science* 86:536-544.
- Lassen J, Gjerris M, Sandøe P. 2006. After Dolly - ethical limits to the use of biotechnology on farm animals. *Theriogenology* 65:992-1004.
- Laughlin K. 2007. The evolution of genetics, breeding and production. Temperton Fellowship Report no. 15. Harper Adams University College. <http://pt.staging.aviagen.com/assets/sustainability/LaughlinTemperton2007.pdf>
- Lauvie A. 2007. Managing small local animal populations: study of diversity of plans of action. Doctoral dissertation AgroParisTech. http://tel.archives-ouvertes.fr/docs/00/50/07/57/PDF/these_LauvieAnne2007.pdf
- Lauvie A, Danchin-Burge C, Audiot A, Brives H, Casabianca F, Verrier E. 2008. A controversy about crossbreeding in a conservation programme: the case study of the Flemish Red cattle breed. *Livestock Science* 118:113-122.
- Lauvie A, Audiot A, Couix N, Casabianca F, Brives H, Verrier E. 2011. Diversity of rare breed management programs: between conservation and development. *Livestock Science* 140:161-170.
- Leboeuf B, Manfredi E, Boue P, et al. 1998. Artificial insemination of dairy goats in France. *Livestock Production Science* 55:193-203.
- Ligda C, Zjalic M. 2011. Conservation of animal genetic resources in Europe: overview of the policies, activities, funding and expected benefits of conservation activities. *Animal Genetic Resources* 49:75-86.
- Little K. 2010. Meat goats: sustainable livestock farming http://www.nuffieldinternational.org/rep_pdf/1292058613Kate_Little_edited.pdf. Nuffield Farming Scholarships Trust.
- Luff B. 2010. Guernsey global breeding programme. Latest developments. <http://www.worldguernseys.org/GGBP.html>.
- Luff WGD, Bichard M. 2002. The current position of the Guernsey breed <http://www.worldguernseys.org/Position%20of%20the%20Breed.html>
- Lyall J, Irvine RM, Sherman A, et al. 2011. Suppression of avian influenza transmission in genetically modified chickens. *Science* 331:223-226.

- MacKenzie K, Bishop SC. 2001. Utilizing stochastic genetic epidemiological models to quantify the impact of selection for resistance to infectious diseases in domestic livestock. *Journal of Animal Science* 79:2057-2065.
- Man W-Y, Lewis RM, Boulton K, Villanueva B. 2007. Predicting the consequences of selecting on PrP genotypes on PrP frequencies, performance and inbreeding in commercial meat sheep populations. *Genetics Selection Evolution* 39:711-729.
- Mansbridge RJ. 2004. Conservation of farm animal genetic resources – a UK national view. In: Simm G, Villanueva B, Sinclair KD, Townsend S, editors. *Farm animal genetic resources*. Nottingham: Nottingham University Press; p 37-43.
- Mara L, Casu S, Carta A, Dattena M. 2013. Cryobanking of farm animal gametes and embryos as a means of conserving livestock genetics. *Animal Reproduction Science* 138:25-38.
- Marren P. 2006. Seventeen eventful years. *British Wildlife* (April issue):230-235.
- Martyniuk E. 2004. The conservation of animal genetic resources - a European perspective. In: Simm G, Villanueva B, Sinclair KD, Townsend S, editors. *Farm animal genetic resources*. Nottingham, UK: Nottingham University Press and British Society of Animal Science; p 15-35.
- Martyniuk E, Pilling D, Scherf B. 2010. Indicators: do we have effective tools to measure trends in genetic diversity of domesticated animals? *Animal Genetic Resources* 47:31-43.
- Mead M. 2012. *British Friesian 1909-2012*. British Friesian Breeders Club.
- McPhee CP. 1965. Inbreeding, migration and structure of the pedigree Large White pig population in Australia. *Australian Journal of Experimental Agriculture and Animal Husbandry* 5:270-278.
- Melka MG, Sargolzaei M, Miglior F, Schenkel F. 2013. Genetic diversity of Guernsey population using pedigree data and gene-dropping simulations. *Animal* 7:192-201.
- Men H, Walters EM, Nagashima H, Prather RS. 2012. Emerging applications of sperm, embryo and somatic cell cryopreservation in maintenance, relocation and rederivation of swine genetics. *Theriogenology* 78:1720-1729.
- Mercer JT, Lewis RM, Alderson GLH. 1997. The adaptation of rare breeds of British livestock to different environments: a review. Penicuik, Midlothian, UK: Scottish Agricultural Colleges.
- Meuwissen THE. 2007. Operation of conservation schemes. In: Oldenbroek JK, editor. *Utilisation and conservation of farm animal genetic resources*. Wageningen, Netherlands: Wageningen Academic Publishers; p 167-93.
- Moiseyeva IG, Romanov MN et al. 2007. The Poltava chicken breed of Ukraine: its history, characterization and conservation. *Animal Genetic Resources Information* 40:71-78.
- Moore RC, Boulton K, Bishop SC. 2009. Associations of PrP genotype with lamb production traits in three commercial breeds of British lowland sheep. *Animal* 3:1688-1695.
- Moran D, Barnes A, McVittie A. 2007. The rationale for Defra investment in R&D underpinning the genetic improvement of crops and animals (IF0101) Final report to Defra. Accessible at <http://randd.defra.gov.uk/> Edinburgh: SAC Commercial Ltd. SAC Land Economy and Environment Group.
- Moula N. 2012. Les races de poules belges. *Annales de Médecine vétérinaire* 156:37-65.
- Mucha S, Windig JJ. 2009. Effects of incomplete pedigree on genetic management of the Dutch Landrace goat. *Journal of Animal Breeding and Genetics* 126:250-256.
- Mucha S, Mrode R, Coffey M, Conington J. 2013. Estimation of genetic parameters for milk yield across lactations in dairy goats. In: *Innovation from animal science – a necessity not an option*. Advances in Animal Biosciences. *Animal* 4:165.
- Muir WM, Wong GKS, Zhang J, et al. 2008. Genome-wide assessment of worldwide chicken SNP genetic diversity indicates significant absence of rare alleles in commercial breeds. *Proceedings of the National Academy of Sciences of the USA* 105:17312-17317.
- Munro J. 1962. A study of the milk yield of three strains of Scottish Blackface ewes in two environments. *Animal Production* 4:203-213.
- Neeteson-van Nieuwenhoven A-M, Knap P, Avendaño S. 2013. The role of sustainable commercial pig and poultry breeding for food security. *Animal Frontiers* 3:52-57.
- Nishijima K, Iijima S. 2013. Transgenic chickens. *Development Growth and Differentiation* 55:207-216.
- O'Brien D, Shalloo L, Grainger C, Buckley F, Horan B, Wallace M. 2010. The influence of strain of Holstein-Friesian cow and feeding system on greenhouse gas emissions from pastoral dairy farms. *Journal of Dairy Science* 93:3390-3402.
- Oldenbroek JK. 1999. *Genebanks and the conservation of farm animal genetic resources*. Lelystad, Netherlands: ID-DLO.

- Ollivier L, Labroue F, Glodek P, Gandini GC, Delgado JV. 2001. Pig genetic resources in Europe. EAAP publication no. 104. Wageningen, Netherlands: Wageningen Pers.
- Olsen HF, Meuwissen T, Klemetsdal G. 2012. Optimal contribution selection applied to the Norwegian and the North-Swedish cold-blooded trotter – a feasibility study. *Journal of Animal Breeding and Genetics* published online May 2012. DOI:10.1111/j.1439-0388.2012.01005.x
- Palhière I, Brochard M, Moazami-Goudarzi K, et al. 2008. Impact of strong selection for the PrP major gene on genetic variability of four French sheep breeds. *Genetics Selection Evolution* 40:663-680.
- Parliamentary Office of Science and Technology. 2011. Improving livestock. POSTnote 393, October 2011 http://www.parliament.uk/pagefiles/504/postpn393_improving-livestock.pdf London.
- Pisenti JM et al. 1999. Avian genetic resources at risk: an assessment and proposal for conservation of genetic stocks in the USA and Canada. Report no. 20, September 1999, Genetic Resources Conservation Program, Division of Agriculture and Natural Resources, University of California, Davis, USA.
- Pollott GE, Stone DG. 2003. The breeding structure of the British sheep industry 2003. London: Defra. <http://archive.defra.gov.uk/evidence/economics/foodfarm/reports/documents/pollott2003.pdf>
- Porter V. 2002. Mason's world dictionary of livestock breeds, types and varieties. 5th edition. Wallingford, UK: CABI Publishing.
- Rasali DP, Shrestha JNB, Crow GH. 2006. Development of composite sheep breeds in the world: a review *Canadian Journal of Animal Science* 86:1-24. <http://pubs.aic.ca/doi/pdf/10.4141/A05-073>.
- Rátky J, Brüssow K-P, Solti L, Torner H, Sarlós P. 2001. Ovarian response, embryo recovery and results of embryo transfer in a Hungarian native pig breed. *Theriogenology* 56:969-978.
- Roberts J. 2008. Geneped works. *Ark* 38(3 Autumn 2008):30-31.
- Rodriguez-Ledesma A, Waterhouse A, Morgan-Davies C, Bruelisauer F. 2011. Structural assessment of the Scottish stratified sheep production system. *Small Ruminant Research* 100:79-88.
- Roper M. 2004. The UK Government policy on farm animal genetic resource conservation. In: Simm G, Villanueva B, Sinclair KD, Townsend S, editors. *Farm animal genetic resources*. Nottingham: Nottingham University Press; p 57-65.
- Rothschild MF, Newman S, editors. 2002. *Intellectual property rights in animal breeding and genetics*. Wallingford, UK: CABI Publishing
- Royal MD, Darwash AO, Flint APF, Webb R, Woolliams JA, Lamming GE. 2000. Declining fertility in dairy cattle: changes in traditional and endocrine parameters of fertility. *Animal Science* 70:487-501.
- SAC Commercial Ltd. 2010. Determining strategies for delivering environmentally sustainable production in the UK ruminant industry through genetic improvement. Final report IF0149. Accessible through <http://randd.defra.gov.uk/> SAC Edinburgh.
- Sairanen J, Nivola K, Katila T, Virtala A-M, Ojala M. 2009. Effects of inbreeding and other genetic components on equine fertility. *Animal* 3:1662-1672.
- Santiago E, Caballero A 1995. Effective size of populations under selection. *Genetics* 139:1013-1030.
- Schaeffer LR. 2006. Strategy for applying genome-wide selection in dairy cattle. *Journal of Animal Breeding and Genetics* 123:218-223.
- Schmutz SM, Buchanan FC, Winkelman-Sim DC, et al. 2001. Development of the Canadian beef reference herd for gene mapping studies. *Theriogenology* 55:963-972.
- Silversides FG, Purdy PH, Blackburn HD. 2012. Comparative costs of programmes to conserve chicken genetic variation based on maintaining living populations or storing cryopreserved material. *British Poultry Science* 53:599-607.
- Silversides FG, Shaver DMcQ, Song Y. 2007. Pure line laying chickens at the Agassiz Research Centre. *Animal Genetic Resources Information* 40:79-85.
- Simm G. 1998. *Genetic improvement of cattle and sheep*. Ipswich, UK: Farming Press.
- Siudzińska A, Łukaszewicz E. 2008. The effect of breed on freezability of semen of fancy fowl. *Animal Science Papers and Reports, Institute of Genetics and Animal Breeding, Jastrzębiec, Poland* 26:331-340.
- Small R, Hosking J. 2010. Rural development programme funding for farm animal genetic resources: a questionnaire survey. Unpublished report to Defra. <http://www.defra.gov.uk/fangr/documents/nsc-survey.pdf> Defra.
- Small RW. 2010 Conservation grazing: delivering habitat management for conservation with livestock. *Journal of the Royal Agricultural Society of England* 171:38-44.
- Small RW. 2013b. Review of policy governing FAnGR conservation strategies and breeding programmes. Unpublished report, Defra Research Contract GC0146. Livestock Diversity Ltd, Lincoln, UK.

- Smith J. 2005. Plan for the management of feral goats in the North Cheviots Northumberland National Park. Unpublished report. Stroud, UK: Wildworks Ecology.
- Soames B. 1980. Keeping domestic geese. Blandford Press, Poole, Dorset.
- Spalona A, Ranvig H, Cywa-Benko K, et al. 2007. Population size in conservation of local chicken breeds in chosen European countries. *Archiv für Geflügelkunde* 71:49-55.
- Squires EL, McCue PM, Vanderwall D. 1999. The current status of equine embryo transfer. *Theriogenology* 51:91-104.
- Stennett A. 1999. An old breed looks to the new millennium. *Ark* 27(4 Winter 1999):146.
- Sweeney T, Hanrahan JP. 2008. The evidence of associations between prion protein genotype and production, reproduction and health traits in sheep doi: 10.1051/vetres:2008004. *Veterinary Research* 39:28.
- Tholen E, Staack J, Müller P, Ingwersen J. 2010. Degree of endangerment of different German pig herdbook populations. *World Congress on Genetics applied to Livestock Production*. <http://www.kongressband.de/wcgalp2010/assets/pdf/0264.pdf>. Leipzig, Germany.
- Thornton PK. 2010. Livestock production: recent trends, future prospects. *Philosophical Transactions of the Royal Society of London B* 365:2853-2867.
- Tixier-Boichard M, Bordas A, Rognon X. 2009. Characterisation and monitoring of poultry genetic resources. *World's Poultry Science Journal* 65:272-284.
- Todd DL, Woolliams JA, Roughsedge T. 2011. Gene flow in a national cross-breeding beef population. *Animal* 5:1874-1886.
- Toro MA, Meuwissen THE, Fernandez J, et al. 2011. Assessing the genetic diversity in small farm animal populations. *Animal* 5:1669-1683.
- Toro MA, Rodrigañez J, Sillio L, Rodríguez C. 2000. Genealogical analysis of a closed herd of black hairless Iberian pigs. *Conservation Biology* 14:1843-1851.
- Townsend SJ. 2003a. Scrapie news. *Ark* 31(3 Autumn 2003):28.
- Townsend SJ. 2003b. GENIPED launched. *Ark* 31(3 Autumn 2003):29.
- Townsend SJ, Warner R, Dawson M. 2005. PrP genotypes of rare breeds of sheep in Great Britain. *Veterinary Record* 156:131-134.
- Townsend SJ, Warren S, Wilson H. 2002. FMD - how the disease has impacted on different sectors of the rare breeds' world. *Ark* 30:65-67.
- Uimari P, Tapio M. 2011. Extent of linkage disequilibrium and effective population size in Finnish Landrace and Finnish Yorkshire pig breeds. *Journal of Animal Science* 89:609-614.
- van Eldik P, van der Waaij EH, Ducro B, Kooper AW, Stout TAE, Colenbrander B. 2006. Possible negative effects of inbreeding on semen quality in Shetland pony stallions. *Theriogenology* 65:1159-1170.
- vanRaden PM, Null DJ, Olson KM, Hutchison JL. 2011. Reporting of haplotypes with recessive effects on fertility. *Interbull Bulletin Stavanger, Norway, August 26-29, 2011*[no. 44]:117-121.
- vanRaden PM, Smith LA. 1999. Selection and mating considering expected inbreeding of future progeny. *Journal of Dairy Science* 82:2771-2778.
- Vega JL, Molina A, Valera M, Rodriguez-Gallardo PP. 1997. Conservation of an equine feral breed: the Asturcón pony. *Animal Genetic Resources Information* 22:29-42.
- Verrier E, Tixier-Boichard M, Bernigaud R, Naves M. 2005. Conservation and value of local livestock breeds: usefulness of niche products and/or adaptation to specific environments. *Animal Genetic Resources Information* 36:21-31.
- Villanueva B, Pong-Wong R, Woolliams JA, Avendaño S. 2004. Managing genetic resources in selected and conserved populations. In: Simm G, Villanueva B, Sinclair KD, Townsend S, editors. *Farm animal genetic resources*. Nottingham, UK: Nottingham University Press and British Society of Animal Science; p 113-32.
- Villanueva B, Sawalha RM, Roughsedge T, Rius-Vilarassa E, Woolliams JA. 2010. Development of a genetic indicator of biodiversity for farm animals. *Livestock Science* 129:200-207.
- Visscher PM, Smith D, Hall SJG, Williams JL. 2001. A viable herd of genetically uniform cattle. *Nature* 409, 303.
- Walters R. 2012. Genetic analyses of traditional breeds - the British experience. *Agricultural Genetics and Breeding Unit, University of New England, Armidale, NSW, Australia*. http://agbu.une.edu.au/pig_genetics/workshop2012.html
- Wall E, Simm G, Moran D. 2010. Developing breeding schemes to assist mitigation of greenhouse gas emissions. *Animal* 4:366-376.
- Wang J. 1997. More efficient breeding systems for controlling inbreeding and effective size in animal populations. *Heredity* 79:591-599.

- Weigend S, Stricker K, Rohrssen FG. 2009. Establishing a conservation flock for "Vorwerkhuhn" chicken breed - a case study of in-situ conservation of local chicken breeds in Germany. *Animal Genetic Resources Information* 44:87-88.
- Wells DN, Misica PM, Tervit HR, Vivanco WH. 1998. Adult somatic cell nuclear transfer is used to preserve the last surviving cow of the Enderby Island cattle breed. *Reproduction Fertility and Development*:369-78.
- Welsh CS, Stewart TS, Schwab C, Blackburn HD. 2010. Pedigree analysis of 5 swine breeds in the United States and the implications for genetic conservation. *Journal of Animal Science* 88:1610-1618.
- Wężyk S. 2009. The poultry gene resources preservation program in Poland - reason and aims http://www.cabi.org/animalscience/Uploads/File/AnimalScience/additionalFiles/WPSABedlewo2009/1_wezyk_genetics2009.pdf.
- Whittingham MJ. 2011. The future of agri-environment schemes: biodiversity gains and ecosystem service delivery? *Journal of Applied Ecology* 48:509-513.
- Wiener P, Burton D, Williams JL. 2004. Breed relationships and definition in British cattle: a genetic analysis. *Heredity* 93:597-602.
- Wilkinson S. 2011. Genetic diversity and structure of livestock breeds. PhD dissertation, University of Edinburgh <http://lac-repo-live7.is.ed.ac.uk/bitstream/1842/6488/2/Wilkinson2012.pdf>
- Wilkinson S, Haley C, Alderson L, Wiener P. 2011. An empirical assessment of individual-based population genetic statistical techniques: application to British pig breeds. *Heredity* 106:261-269.
- Wilkinson S, Wiener P, Teverson D, Haley CS, Hocking PM. 2012. Characterization of the genetic diversity, structure and admixture of British chicken breeds. *Animal Genetics* 43:552-563.
- Windig JJ, Kaal L. 2008. An effective rotational mating scheme for inbreeding reduction in captive populations illustrated by the rare sheep breed Kempisch Heideschaap. *Animal* 2:1733-1741.
- Windig JJ, Meuleman H, Kaal L. 2007. Selection for scrapie resistance and simultaneous restriction of inbreeding in the rare sheep breed "Mergellander". *Preventive Veterinary Medicine* 78:161-171.
- Winton CL, Hegarty MJ et al. 2013. Genetic diversity and phylogenetic analysis of native mountain ponies of Britain and Ireland reveals a novel rare population. *Ecology and Evolution* 3:934-947.
- Woelders H, Hiemstra SJ. 2012. Latest developments in cryobiology and reproductive technologies. Report to European Regional Focal Point http://www.rfp-europe.org/fileadmin/SITE_ERFP/AdHoc/May2012/ERFP_AdHoc-exsitu_May2012_Report-Netherlands.pdf
- Woelders H, Kaal L. 2008. Survey of organisation, actual stocks, and procedures of ex situ conservation of heritage sheep breeds. WP3 Deliverable 15. Report 153, Animal Sciences Group, Wageningen UR, Netherlands. ISSN 1570-8616. <http://www.heritagesheep.eu/Annex-9.pdf>
- Woelders H, Windig JJ, Hiemstra SJ. 2012. How developments in cryobiology, reproductive technologies and conservation genomics could shape gene banking strategies for (farm) animals. *Reproduction in Domestic Animals* 47 (Suppl.4):264-273.
- Woolliams JA, 2004. Managing populations at risk. In: Simm G, Villanueva B, Sinclair KD, Townsend S, editors. *Farm animal genetic resources*. Nottingham: Nottingham University Press; p 85-106.
- Woolliams JA. 2007. Genetic contributions and inbreeding. In: Oldenbroek JK, editor. *Utilisation and conservation of farm animal genetic resources*. Wageningen, The Netherlands: Wageningen Academic Publishers; p 147-165.
- Woolliams JA, Toro MA. 2007. What is genetic diversity? In: Oldenbroek JK, editor. *Utilisation and conservation of farm animal genetic resources*. Wageningen, The Netherlands: Wageningen Academic Publishers; p 55-74.
- Woolliams JA, Matika O, Pattison J. 2008. Conservation of animal genetic resources: approaches and technologies for in situ and ex situ onservation. *Animal Genetic Resources Information* 42:71-89.
- Wrathall AE, Simmons HA. 2004. Biosecurity strategies for conservation of farm animal genetic resources. In: Simm G, Villanueva B, Sinclair KD, Townsend S, editors. *Farm animal genetic resources*. Nottingham: Nottingham University Press; p 243-261.
- Wright IA, Dalziel AJI, Ellis RP, Hall SJG. 2002. The status of traditional Scottish animal breeds and plant varieties and the implications for biodiversity. Edinburgh: Scottish Executive Social Research. <http://www.scotland.gov.uk/Publications/2002/12/15947/15114>
- Wright S. 1977. *Evolution and the genetics of populations*. Volume 3. Experimental results and evolutionary deductions. Chicago: University of Chicago Press.
- Young GB, Purser AF. 1962. Breed structure and genetic analysis of Border Leicester sheep. *Animal Production* 4:379-389.

Zehetmeier M, Baudracco J, Hoffmann H, Heissenhuber A. 2012. Does increasing milk yield per cow reduce greenhouse gas emissions? A system approach. *Animal* 6:154-166.

Zmihorski M, Dziarska-Palac J, Sparks TH, Tryjanowski P. 2013. Ecological correlates of the popularity of birds and butterflies in Internet information resources. *Oikos* 122:183-190.

Zuckerman S. 1994. Historical address. *Ark* 21(5):168-181.