Review: Assessing available genetic diversity estimates of rare breeds of livestock

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Abstract

The United Kingdom is home to many local and rare livestock breeds. The local breed populations are highly adapted to specific environments in the United Kingdom and these and other rare breeds provide solutions to niche needs. Rare breeds often contribute more than expected to overall species genetic diversity, which is important because genetic variation is needed for adapting to new challenges. It is therefore very important from both United Kingdom and global perspectives to maintain genetic diversity of rare livestock breeds in the United Kingdom, and to do this, we need to evaluate the monitoring of genetic diversity to identify gaps in our knowledge and prioritise resources reserved for conservation purposes. The objectives of this study were to survey the literature to: (1) summarise genetic/genomic characterisation (effective population size (**N_e**) and inbreeding) of domestic populations (livestock and equine) in the United Kingdom and Ireland; (2) compare number of populations on

the United Kingdom's Rare Breeds Survival Trust watch list and the number of United Kingdom and Irish populations in the peer-reviewed literature with inbreeding, genetic diversity and/or N_e estimates; and (3) compare annually reported (census-based) estimates of N_e with (inbreeding- and DNA-based) estimates from peer-reviewed literature. We found a total of 37 publications with N_e or inbreeding estimates for United Kingdom or Ireland livestock populations, published from 1975 to 2024. While many (42%) of the breeds on the Rare Breeds Survival Trust watchlist have been included in publications, there are still many breeds, and a few species (turkey, duck and geese) with no publicly available pedigree- or DNA-based genetic diversity measures. We found census-based N_e estimates were, on average, higher than DNA-based estimates, likely due to violated assumptions when estimating N_e with census-based data because of the way livestock mating systems are designed. Most peer-reviewed papers estimated genetic diversity measures using pedigree, microsatellite markers, or single nucleotide polymorphisms (**SNP**) markers. To identify breed-unique variants responsible for adaptive traits in rare breeds, more studies using whole-genome sequencing will be needed. Altogether, we have summarised genetic diversity estimates of United Kingdom livestock populations, identifying gaps in knowledge.

Keywords: Inbreeding, effective population size, census data, genomic data, conservation

Implications

Maintaining genetic diversity in livestock helps safeguard against future challenges to our food production systems. We surveyed publicly available measures of genetic diversity for farm animal populations in the United Kingdom (including government, Rare Breeds Survival Trust, and peer-reviewed scientific publications) to identify any gaps. We found census-based estimates of genetic diversity, which are used to inform and prioritise resources for conservation efforts, on average, are likely overestimating available genetic diversity. Additionally, most farm animal breeds had only these census-based estimates. Genetic diversity estimates could be improved using pedigree or DNA information, more accurately identifying endangered breeds.

Introduction

Livestock populations in the United Kingdom originated in centres of domestication in Southwest Asia, East Asia, and Mesoamerica, with the first domesticated species arriving to the British Isles during the Neolithic transition to agriculture (Larson et al., 2014; Whittle et al., 2011). Through this process, livestock populations have become highly adapted to many niche environments (Zeder, 2008). Those populations today are called local breeds and are often maintained by breed associations for their unique qualities and nostalgia. These breeds can be described as hardy, many of which can thrive on low-quality feed not appropriate for human consumption and habitat in areas and weather conditions where other breeds cannot. Rare breeds have lost their historic popularity because commercial breeds are more productive (Canali, 2006). As a consequence of decreasing population sizes, rare breed societies do not have the resources to support breeding programmes, unlike contemporary commercial populations that can use genomic selection to inform

mating decisions (DEFRA, 2021). However, there are several roles that rare breeds fill in the modern world. In the United Kingdom and European Union, niche products, like cheese and meat, from local breeds are sold with a geographical indicator (protected designation of origin, and protected geographical indication) (‘Geographical indications and quality schemes explained’, n.d.; ‘Protected geographical food and drink names: UK GI schemes’, 2024). Local breeds in the United Kingdom are used for conservation grazing to maintain numerous habitats (grassland, heathland, wood pasture, coastal and floodplains, fen, scrub and scrub mosaics, saltmarsh and sand dunes habitats) (‘Graze with livestock to maintain and improve habitats’, n.d.) and are used in organic farming (Van Diepen et al., 2007). Local breeds also play an intangible cultural role in their communities providing a glimpse into the past, including domestication processes and the Neolithic transition to agriculture, all the way up to modern times. Finally, in an ever-changing world, these historic breeds can play an important role as reservoirs of genetic variation, providing the variation needed for sustainable agriculture systems with animals that can adapt to future challenges, which has been recognised by the United Nations (UN environment programme, 2022; United Nations General Assembly, 2015).

There are many other important roles for local breeds to play in modern society, besides maintaining total livestock species genetic diversity. To highlight a few examples from the United Kingdom, we present breeds with unique traits and their current and historic uses. The North Ronaldsay sheep, found primarily in the Orkneys has adapted to primarily eat seaweed, mainly composed of brown kelp, after they were mostly contained to the shore in the 19th century to protect cultivated land from being grazed (RBST, n.d.; Porter, 2002). Many modern breeds struggle with

some functional traits as a result of a focus on improving production traits (Rauw et al., 1998). In contrast, local breeds are prized for these functional traits, and Shetland cattle are an example of this with their excellent calving ease (Schwabe and Hall, 1989), they can be bred with larger continental breeds without calving issues (RBST, n.d.). Local breeds can provide unique animal products that cannot be provided by commercial breeds. One of the first protected animal products in the European Union was the Gloucestershire Old Spots pig (RBST, n.d.). In the application for this status, it was indicated that texture, and flavour of these pigs are distinguishable from commercial pigs (The Gloucestershire Old Spots Pig Breeders' Club, 2006). There were some traditional functions of local breeds that may not be in their current usage, but could inspire more sustainable practices. Before the use of pesticides to control parasites Shetland geese were traditionally grazed in pastures after sheep were grazed to manage parasites like liver fluke (RBST, n.d.). Finally, many of the local breeds can thrive and forage in any climate, like the Scots Grey, a traditional Scottish chicken breed traced back to the 16th century (RBST, n.d.). This ability to thrive outdoors is particularly useful for conservation grazing. Many iconic landscapes in the United Kingdom, like meadows and grasslands that harbour a third of British flora, were created from traditional farming practices (Peach, 2019). In the Great Trossachs Forest, grazing allows for a more diverse environment for wild birds, and opportunities for less competitive grass species to seed and germinate, among other benefits (The Great Trossachs Forest, 2025). They use a combination of Luing cattle, Hebridean sheep and Scottish Blackface sheep, each providing different grazing patterns to contribute to the park's diversity (The Great Trossachs Forest, 2025).

Local breeds from the British Isles have played an outsized role in global commercial agriculture today. Breeds from the United Kingdom have had widespread popularity, for example, purebred and crossbred Angus, Jersey, and Guernsey cattle can be found in many countries around the world, many global commercial pig companies have developed lines based on Large White and Yorkshire breeds, and the Leicester Longwool was widely used in crossbreeding schemes to improve the carcass and fleece of sheep breeds in Europe, Australia, Canada, New Zealand, and the US (Porter, 2002). The Leicester Longwool was the product of a new type of breeding, “in-and-in”, developed by English farmer Robert Bakewell in the 18th century, where inbreeding was used to fix traits in a population (Wykes, 2004). This is believed to be the first implementation of systematic selective breeding, when in comparison, many famers to this point had been randomly mating livestock (Wykes, 2004).

The United Kingdom government recognises the importance of maintaining the genetic diversity of its local breeds and has several national and international obligations to conserve rare breeds, including the 2011 England Biodiversity Strategy, the United Nation’s Food and Agriculture Organisation’s “Global Plan of Action”, the United Nation’s Convention on Biological Diversity “Strategic Plan for Biodiversity 2011-2020”, and for input to the European Farm Animal Biodiversity Information System and Food and Agriculture Organisation’s Global Information System (Beale, 2024). To fulfil these obligations, the Department for Environment, Food and Rural Affairs in the United Kingdom monitors the number of active sires and dams for livestock populations by breed to inform and prioritise resources for conservation efforts (with data for cattle, equine, sheep, goat and pig publically available as far back as 2000, and for poultry available from 2021) (Beale, 2024).

The Department for Environment, Food and Rural Affairs collects this census data through collaboration with breed organisations and the Rare Breeds Survival Trust, a charity established in 1973 that conserves and promotes native livestock and equine breeds in the United Kingdom (RBST, n.d.). Census data is used to estimate effective population size (**N_e**), which is the number of individuals in an idealised population that would generate the same rate of inbreeding as found in the population of interest (Falconer and Mackay, 1996), allowing for interpretation and comparison of N_e values across populations and species.

Additionally, several research groups have studied the genetic diversity and inbreeding of local and rare breeds, publishing their results in peer-reviewed literature. These studies were standalone projects or part of global consortia (Bovine HapMap (The Bovine HapMap Consortium et al., 2009), Sheep Hapmap, Adaptmap (for goats) (Stella et al., 2018), etc.). The objectives of this study were to survey the literature to: (1) summarise genetic/genomic characterisation (genetic diversity, N_e and inbreeding) of domestic populations (livestock and equine) in the United Kingdom and Ireland; (2) compare number of populations on the Rare Breeds Survival Trust list and the number of populations in the United Kingdom and Ireland in the peer-reviewed literature with inbreeding, genetic diversity and/or N_e estimates; and (3) compare annually reported (census-based) estimates of N_e with (DNA-based) estimates from peer-reviewed literature. By systematically reviewing the peer-reviewed genetic diversity literature for livestock populations in the United Kingdom, we can identify gaps, which will help with prioritising research areas.

Material and methods

We used Web of Science (https://www.webofscience.com) to search (on 2025-01-13) using the following search term:

(inbreeding OR diversity OR "effective population size") AND (cattle OR cow* OR bull* OR pig* OR chicken* OR sheep* OR goat* OR horse* OR duck* OR turkey* OR geese) AND ("UK" OR "United Kingdom" OR "Britain" OR "Scotland" OR "England" OR "Wales" OR "Northern Ireland" OR "Ireland") AND ("genomic" or "genetic" or "pedigree").

We searched for inbreeding, diversity and N_e estimates for all species identified on the Rare Breeds Survival Trust's 2024-2025 watchlist for breeds in the United Kingdom ('RBST watchlist 2024', 2024). Irish populations were included due to the shared border between Northern Ireland and Ireland, making some livestock and equine populations to likely be well-connected. Values were extracted from articles, tables, and figures (using WebPlotDigitizer (Rohatgi, 2024)). The Rare Breeds Survival Trust watchlist ('RBST watchlist 2024', 2024) is annually published and used to prioritise breeds for conservation by considering genetic diversity and number of breeding females.

Every year the Department for Environment, Food and Rural Affairs collects census numbers (they can be number of animals registered or an estimate of total number) from breed organisations and the Rare Breeds Survival Trust, and publishes them (Beale, 2024). We have used the 2023 release of census and effective population estimates (Beale, 2024). This data is used to monitor numbers of animals over the

years to help with prioritisation of conservation efforts. The Department for Environment, Food and Rural Affairs uses the following formula to estimate N_e:

$$N_e = \frac{4N_m N_f}{N_m + N_f}$$

Where $\boldsymbol{N_m}$ is the number of breeding males, and $\boldsymbol{N_f}$ is the number of breeding females) (Wright, 1931). N_e is the number of individuals that would be needed for the inbreeding estimate to be true in an idealised population (Falconer and Mackay, 1996). An idealised population has the following conditions: (1) mating is restricted to a population with no migration, (2) generations are discrete, (3) number of breeding individuals are the same for every generation, (4) mating is random and includes self-fertilisation, (5) there is no selection, and (6) mutation is disregarded (Falconer and Mackay, 1996). The effective population estimate is standardised and comparable between populations, and can be used to estimate the rate of inbreeding (Wright, 1931). The United Nation's Food and Agriculture Organisation's guidance indicates N_e should be 50 animals per generation, or more, as an N_e of 50 corresponds to 1% inbreeding rate per generation (when number of breeding males and females are equal) (FAO Commission on Genetic Resources for Food and Agriculture, 2015).

Study design

We have summarised the peer-reviewed literature on genetic diversity in livestock populations in the United Kingdom by counting the number of published papers per species, population, data type (pedigree, mitochondrial DNA, microsatellite, single nucleotide polymorphisms (**SNP**), or whole genome sequencing) and number of populations both in the literature and on the Rare Breeds Survival Trust 2024 watchlist.

Additionally, for all inbreeding- and DNA-based N_e estimates found for populations in the United Kingdom in the literature, we compared this with census-based N_e estimates published by the Department for Environment, Food and Rural Affairs. To make the closest comparisons, we compared census-based estimates from the same year of DNA sampling that was used in the DNA-based estimates. If the year of sampling was not available, year of publication was used as a proxy. If there was no census-based estimate for the year of sampling/year of publication of DNA-based estimates, the closest year with an estimate was used. If the sampling occurred over a period of years, census-based N_e estimates from those years were averaged. We used a paired t-test to determine if census-based and DNA-based N_e estimates were significantly different.

Results

Summary of literature search

In total, we have included 36 peer-reviewed publications and one report written for the Rare Breeds Survival Trust, published between 1975 and 2024, all of which have estimates of genetic diversity, including inbreeding coefficients, nucleotide diversity or N_e of livestock or equine populations in the United Kingdom or Ireland (see **Supplementary Table S1** for information on publications and diversity estimates included in this study). The 37 publications are summarised in **Table 1**, including sources of data for each study (original data from a total of 50 publications). **Figure 1** shows our workflow, including total number of papers found through the Web of

Science search, number of papers removed due to not meeting certain criteria, and number of papers included that were not identified in the Web of Science search.

Summary of counts

Of the publications included in our analyses, there were 14 papers on equine populations, 11 on cattle, ten on sheep, one on pig, one on goat and one on chicken. Information on breeds studied, and data type are included in **Table 1**. The number of populations in both the literature and the Rare Breeds Survival Trust 2024 watchlist are plotted by conservation priority status in **Figure 2**. Notably, there were no goat, turkey, duck, or geese populations on the Rare Breeds Survival Trust 2024 watchlist that have estimates of genetic inbreeding, diversity or N_e in the literature.

Comparing genomic-based diversity estimates with census data

Of the N_e estimates from genomic data with census estimates available, 43 (of 53) census estimates were greater than inbreeding- or linkage disequilibrium (**LD**)-based estimates. The paired t-test for census-based and inbreeding or LD-based N_e was significant ($p=0.0009$). The median difference between the two was 391 (maximum difference was 24,068). All census-based N_e estimates with their corresponding inbreeding- or LD-based N_e estimates from the Department for Environment, Food and Rural Affairs are plotted in **Figure 3**.

Discussion

It is important to maintain rare breeds to adapt to future challenges, to serve niche markets, for conservation grazing, and to maintain cultural identity and contribute to sustainable agriculture. However, there are finite resources available for conservation of these breeds, and they are not immediately profitable in the larger economy, so it is important to identify gaps, and prioritise certain aspects of livestock conservation. In this sense, we discuss: (1) work already done in these areas and compare census-based N_e estimates with DNA-based estimates, (2) potential value of whole genome sequence data for rare breeds, (3) usage of N_e estimates to guide conservation strategies, (4) limitations of our study design and (5) future actions.

Effective population size estimates

The well-established threshold of concern for population conservation is a N_e of 50 (FAO Commission on Genetic Resources for Food and Agriculture, 2015). Franklin (1980) first proposed a short-term aim of a N_e of 50 for small populations (with livestock populations particularly in mind) as this corresponds to a 1% rate of inbreeding ($\Delta F = \frac{1}{2N_e}$) (Wright, 1931), which is considered a tolerable level of inbreeding, considering the negative effect of inbreeding depression. This was part of the 50/500 rule, where Franklin also proposed a long-term minimum value for N_e of 500 (where mutation offsets the loss of genetic variation through drift) (Franklin, 1980). There have been more recent discussions on updating the 50/500 rule, which is needed as our knowledge on genome biology has evolved in the following 45 years, however there has been no clear consensus on changing the recommended minimum N_e (Waples, 2025; Pérez-Pereira et al., 2022; Frankham et al., 2014; Jamieson and Allendorf, 2012).

The N_e threshold of concern may need to be updated, but N_e estimates as a measure of genetic diversity also needs to be revisited. We compared census-based and inbreeding- or LD-based N_e estimates using annually reported census-based estimates from the Department for Environment, Food and Rural Affairs and inbreeding- or LD-based estimates from the literature. Census-based N_e estimates were, on average, higher than inbreeding- or LD-based estimates (with a median difference of 391), and ~11% (6 of 53) of paired estimates had an inbreeding or LD-based N_e estimate < 50, with a corresponding census-based N_e > 50. This could indicate that several populations without LD-based N_e estimates but with census-based estimates appear to have an N_e > 50 but may actually need conservation prioritisation.

We have observed very different N_e estimates based on data and methodology. Estimating and publishing census-based estimates has been valuable as a low-cost method for estimating N_e and observing trends over time. However, inbreeding and LD-based methods are estimates based on the genome, the diversity of which we are trying to conserve. The difference between estimates could be expected due to the assumptions of the methods used. In the census-based methods, there is an assumption of an idealised population, which does not reflect the reality of livestock breeding. LD-based methods for estimating N_e also have assumptions, for example, an assumption is that LD is produced solely from the finite population size, and non-random mating and population structure are absent (Waples, 2025). Additionally, any method using microsatellite or SNP arrays will also contend with ascertainment bias of those DNA markers, where those markers have been identified usually using

animals not from the population of interest – which is especially problematic for monitoring rare breeds with unique variants that we are interested in conserving.

The census-based N_e estimates in this study showed that more common breeds in the United Kingdom had higher estimates. An extreme example of this is the Holstein-Friesian breed. The United Kingdom census-based N_e estimate for 2023 was 13 154 (Beale, 2024). Holstein-Friesian is a globally popular commercial breed, and populations in different countries are well-connected to each other, particularly through similar genetics (global use of artificial insemination with elite bulls' semen). Therefore, we would expect N_e estimates across countries to be somewhat similar to the United Kingdom estimate. N_e estimates from the Netherlands (one of the countries where this breed originated from), Canada, France, Ireland, Italy, and the United States of America range from 18 to 150 (Ablondi et al., 2022; Makanjuola et al., 2020; Harmen P. Doekes et al., 2018; H.P. Doekes et al., 2018; Rodríguez-Ramilo et al., 2015; Danchin-Burge et al., 2011; Mc Parland et al., 2007a; Weigel, 2001). These estimates came from a variety of inbreeding- and LD-based methods (but not the census-based method). This highlights how estimating and comparing N_e estimates can be challenging (even the difference between 18 and 150 has vastly different implications for conservation), and that the census-based United Kingdom estimate is unrealistic. The footnotes of Table 1 demonstrate the wide range of diversity estimates, and even methodologies within diversity estimate type, all with certain assumptions and strengths, rendering meaningful comparisions and intrepretation of results challenging. In the case of census-based N_e estimates for livestock populations there is often higher selection intensity in males (fewer active breeding males than active breeding females), which can be accounted for in

Wright's estimate (Wright, 1931). However, the definition of "active breeding males" could contribute to unreasonable N_e estimates. For example, some of the active breeding males (e.g., elite bulls) likely have thousands of offspring, while many active males only have a very small number of offspring, and this variation in family size is not accounted for in the census-based estimate.

Whole-genome sequencing

While genotyping strategies are becoming more affordable, especially SNP arrays, typically rare breeds are raised as a hobby, and it is not financially feasible to have continual producer-investment in routine genotyping. For producers raising rare breeds for conservation purposes, SNP arrays are not ideal because they likely will not contain unique breed-specific variants (due to ascertainment bias, as seen in Geibel et al. (2021)), which are the main interest of conservation programmes. Next generation sequencing technologies would be better for conservation studies, however, they can be more expensive. Whole genome sequencing costs are decreasing, and there are strategies to reduce those costs even further, including using low-pass sequencing and imputation, but this requires an initial investment to establish high coverage genotyping of a reference population to identify breed-unique variants.

Only one publication included in this study used 15X coverage Illumina 150 base pair paired-end whole genome sequence data (Lindsay-McGee et al., 2023). Due to the study design which also used available genotypes from populations genotyped with an Affymetrix array, only 400K SNPs remained for analyses. In contrast, to give an idea of the magnitude of the number of variants we could expect from sequencing,

from a publication in 2019 from the 1000 Bull Genome Project where a total of 429 animals from 14 breeds were sequenced, they identified 29.1 million single nucleotide variants, and 1.7 million insertions-deletions (Hayes et al., 2014). We could expect that there is a lot of unexplored data from the Lindsay-McGee et al. (2023) study, and that it would be valuable for further investment in generating whole genome sequence data for other rare breeds in the United Kingdom, allowing for information on breed-unique variants to be included in management plans.

Conservation management

As we previously mentioned, monitoring and follow-up conservation strategies are mainly based on the Food and Agriculture Organisation's guidance (N_e of 50 per generation, equivalent to 1% inbreeding rate per generation (FAO Commission on Genetic Resources for Food and Agriculture, 2015)). Current census-based estimates of N_e should be replaced by inbreeding-based estimates of N_e. For the census-based estimates of N_e, the Department for Environment, Food and Rural Affairs is using the number of active sires and dams, which is known because pedigree information is collected and available. An immediate improvement would be to use pedigree information to estimate rates of inbreeding, which could then be used to calculate annual inbreeding-based N_e estimates. In the long-term, developing a national strategy to regularly collect DNA samples for breeds on the Rare Breeds Survival Trust watchlist, would allow for DNA-based estimates of genetic diversity measures.

Having DNA-based contemporary N_e estimates is critical to prioritise breeds/populations for conservation activities. Furthermore, having genomic (especially whole genome sequence) data on these breeds would not only allow for better N_e estimates but would also lead to a better understanding of the general population structure. This would add value for cost-effective decision making, particularly linked to choosing the most optimal conservation system (*in situ*, *ex situ in vivo*, *ex situ in vitro*), optimising the number of individuals within the breed to keep in the chosen conservation system, as well as opening the door for future activities (e.g., precise introgression, genome editing, etc.). Conservation activities and systems based on genomic data were systematically reviewed in Oldenbroek et al. (2017), the algorithms for selection and optimisation of the number of individuals are available and can be easily adapted for conservation purposes, e.g., Pocrnic et al., (2022); Yu et al., (2014), and for a recent review of the genome editing concepts applied to livestock populations, including conservation applications, see Clark, (2020). We particularly mention genome editing technology as there is potential to introduce breed-unique causal variants into other populations (Leroy et al., 2016). Alternatively, variants could be introduced by genome editing to make local populations more resistant to disease or improve their fertility (traits that may suffer from inbreeding depression), only changing traits to improve the survival of the breed while maintaining the breed standards/definitions. Finally, a more complex application of genome editing that could be considered is surrogate sire technology. Surrogate sires are made sterile by CRISPR-Cas9 editing of *NANOS2* in mammals (Park et al., 2017) or *DDX4* in chicken (Taylor et al., 2017), and donor-derived stem cells are transplanted into the gonads (Taylor et al., 2017). The surrogate sire could then disseminate the donor's sperm through natural breeding. The potential to exploit

surrogate sire technology in commercial livestock breeding was discussed by Gottardo et al. (2019), but similarly, we could use it in a conservation context to disseminate local breed sperm. Finally, novel technologies like gene drives are emerging and could find their application in conservation strategies to help spread desired alleles in a population (e.g., Faber et al. (2021); Webber et al. (2015); Esvelt et al. (2014)).

Limitations of this study

Many of the results included in this study either came from or benefitted from international research consortiums. These consortiums build capacity through the training of individuals, building databases and sharing resources. However, from these consortium publications there were several breeds that originated in the United Kingdom, that were not included in the current study because of uncertainty of sampling locations. Additionally, breeds originating in the United Kingdom with populations in other countries, may no longer reflect the current United Kingdom population anymore due to the use of crossbreeding. Therefore, we did not include populations unless we were certain that they were United Kingdom or Ireland samples and if there was a proportion of samples included from another country, there was some evidence that these populations were well-connected with the corresponding population in the United Kingdom.

There are more peer-reviewed publications that analyse genotypes from livestock populations in the United Kingdom than we have included in this publication. We tried to keep only those publications with some genetic diversity measure, inbreeding or

N_e estimate. This means papers looking at population structure and signatures of selections, while related, were not included. Sometimes the data from those studies were used in other publications where the measures we were interested in were estimated, and we tried to cite both the original source of data and the publication with the analyses of interest.

From systematically reviewing literature for genetic diversity, inbreeding and N_e estimates for livestock and equine populations in the United Kingdom and Ireland, one recommendation for other researchers is clear: include detailed information on populations analysed, including sampling year, number of herds sampled from and sampling criteria. This additional information will be helpful for future studies (for publicly available data eventually used in other studies) and can be used to inform conservation decisions.

Future actions

This study was designed to identify gaps in our knowledge of the genetic diversity of livestock populations in the United Kingdom. Most breeds on the Rare Breeds Survival Trust watchlist do not have DNA-based studies, and for those with estimates, many are outdated. Most notably missing were any estimates on duck, geese, goat and turkey breeds. These populations should be prioritised for generating genomic data, and they need to remain on the Rare Breeds Survival Trust watchlist and the Department for Environment, Food and Rural Affairs monitoring programmes, potentially even reassessing conservation categories based on DNA-based metrics when available. The creation of a centralised database for all rare

livestock breeds in the United Kingdom, integrating the Department for Environment, Food and Rural Affairs, Rare Breeds Survival Trust and academic sources, would help with implementing a systematic approach to monitor genetic diversity, and fund the generation of genomic data to update diversity estimates. Publicly funded genetic estimates and resulting publications should be open access and allow for data sharing. Through the standardisation and sharing of data, joint conservation programmes for transboundary breeds can be developed, and breed connectedness and genetic diversity measures can be jointly assessed.

Ethics approval

Ethics approval was not needed for this study.

Data and model availability statement

The data were not deposited in an official repository. All data are available in the supplemental information.

Declaration of generative AI and AI-assisted technologies in the writing process

We declare that no generative AI or AI-assisted technologies were used in the writing process.

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Declaration of interest

We declare that we have no conflicts of interest.

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Tables

Table 1: Publications characterising genetic diversity of United Kingdom and/or Irish livestock and equine populations

Species	Populations	Data	Methods	Publication	Data from
Cattle	Aberdeen Angus	20 SSR	H_O, H_E	1	
		mtDNA	ND	2	3
		30 SSR	H_O, H_E	4	
	Angus	Pedigree	F_{PED}	5	
	Ancient Irish samples	mtDNA	ND	2	
	Ayrshire	30 SSR	H_O, H_E	4	
	Belted Galloway	50K SNP	$N_{e\text{-}LD}$, F_{ROH}, H_O	6	7
	Charolais	Pedigree	F_{PED}	5	
	Chillingham	777K SNP	F_{IS}, F_{ROH}	8	
		777K SNP	F_{IS}	9	
	Devon	50K SNP	H_O	6	7
	Dexter	30 SSR	H_O, H_E	4	
		50K SNP	$N_{e\text{-}LD}$, F_{ROH}, H_O	6	7
	English Longhorn	50K SNP	H_O	6	7
	Galloway	50K SNP	H_O	6	7
	Guernsey	30 SSR	H_O, H_E	4	
		50K SNP	F_{ROH}, H_O	6	7 & 10
	Hereford	20 SSR	H_O, H_E	1	
		mtDNA	ND	2	3
		30 SSR	H_O, H_E	4	
		Pedigree	$N_{e\text{-}F}$, F_{PED}	5	
	Highland	30 SSR	H_O, H_E	4	
		50K SNP	H_O	6	7
	Holstein-Friesian	Pedigree	F_{PED}	11	
		Pedigree	F_{PED}	12	
		Pedigree	$N_{e\text{-}F}$, F_{PED}	7 & 13	
	Friesian	30 SSR	H_O, H_E	4	
	Jersey	20 SSR	H_O, H_E	1	
		mtDNA	ND	2	3
		30 SSR	H_O, H_E	4	
	Kerry	20 SSR	H_O, H_E	1	
		mtDNA	ND	2	
		50K SNP	$N_{e\text{-}LD}$, F_{ROH}, H_O	6	This study, 1 & 14
	Limousin	Pedigree	F_{PED}	5	
	Simmental	Pedigree	$N_{e\text{-}F}$, F_{PED}	5	
	South Devon	50K SNP	H_O	6	7
	Sussex	50K SNP	H_O	6	7
	Welsh Black	50K SNP	H_O	6	7
	White Park	777K SNP	F_{IS}	9	
		50K SNP	H_O	6	7
Chicken	Appenzeller	30 SSR	F_{IS}, H_O, H_E	15	
	Araucana	30 SSR	F_{IS}, H_O, H_E	15	
	Brahma	30 SSR	F_{IS}, H_O, H_E	15	
	Buff Orpington	30 SSR	F_{IS}, H_O, H_E	15	
	Cochin	30 SSR	F_{IS}, H_O, H_E	15	
	Croad Langshan	30 SSR	F_{IS}, H_O, H_E	15	

	Derbyshire Redcap	30 SSR	F_{IS}, H_O, H_E	15	
	Dorking	30 SSR	F_{IS}, H_O, H_E	15	
	Hamburgh	30 SSR	F_{IS}, H_O, H_E	15	
	Indian Game	30 SSR	F_{IS}, H_O, H_E	15	
	Ixworth	30 SSR	F_{IS}, H_O, H_E	15	
	Leghorn (coloured)	30 SSR	F_{IS}, H_O, H_E	15	
	Light Sussex	30 SSR	F_{IS}, H_O, H_E	15	
	Lincolnshire Buff	30 SSR	F_{IS}, H_O, H_E	15	
	Maran	30 SSR	F_{IS}, H_O, H_E	15	
	Marsh Daisy	30 SSR	F_{IS}, H_O, H_E	15	
	Norfolk Grey	30 SSR	F_{IS}, H_O, H_E	15	
	Old English Pheasant Fowl	30 SSR	F_{IS}, H_O, H_E	15	
	Rhode Island Red	30 SSR	F_{IS}, H_O, H_E	15	
	Scots Dumpy	30 SSR	F_{IS}, H_O, H_E	15	
	Scots Grey	30 SSR	F_{IS}, H_O, H_E	15	
	Silkie	30 SSR	F_{IS}, H_O, H_E	15	
	Spanish	30 SSR	F_{IS}, H_O, H_E	15	
	Sussex	30 SSR	F_{IS}, H_O, H_E	15	
Equine	Carneddau pony	50K SNP	H_O, H_E	16	
		17 SSR	H_O, H_E	16	
		mtDNA	ND	16	
		17 SSR	F_{IS}, H_O, H_E	17	16
		mtDNA	ND	17	16
	Cleveland Bay horse	10 SSR	H_O	18	
		15 SSR	$N_{e\text{-}F}$, H_O, H_E	19	This study & 20-22
		Pedigree	$N_{e\text{-}F}$, F_{PED}	23	
		15 SSR	H_O, H_E	23	
	Clydesdale horse	10 SSR	H_O	18	
		15 SSR	$N_{e\text{-}F}$, H_O, H_E	19	This study & 20-22
	Connemarra pony	394 SSR	H_O	24	
		50K SNP	H_O, H_E	16	
		17 SSR	H_O, H_E	16	
		mtDNA	ND	16	
		17 SSR	F_{IS}, H_O, H_E	17	16
		mtDNA	ND	17	16
		400K SNP	F_{ROH}	25	
	Dales pony	10 SSR	H_O	18	
		15 SSR	H_O, H_E	23	26
		15 SSR	$N_{e\text{-}F}$, H_O, H_E	19	This study & 20-22
	Dartmoor pony	17 SSR	F_{IS}, H_O, H_E	17	
		mtDNA	ND	17	
	Eriskay pony	10 SSR	H_O	18	
		15 SSR	$N_{e\text{-}F}$, H_O, H_E	19	This study & 20-22
	Exmoor pony	10 SSR	H_O	18	
		50K SNP	$N_{e\text{-}LD}$, F_{IS}	27	
		600K SNP	F_{ROH}	28	
		15 SSR	H_O, H_E	23	29
		15 SSR	$N_{e\text{-}F}$, H_O, H_E	19	This study & 20-22
	Fell pony	10 SSR	H_O	18	
		50K SNP	$N_{e\text{-}LD}$, F_{IS}	27	
		17 SSR	F_{IS}, H_O, H_E	17	

	mtDNA	ND	17	
	15 SSR	H_O, H_E	23	26
	15 SSR	N_{e-F}, H_O, H_E	19	This study & 20-22
Hackney horse	15 SSR	N_{e-F}, H_O, H_E	19	This study & 20-22
Hackney pony	15 SSR	N_{e-F}, H_O, H_E	19	This study & 20-22
Highland pony	10 SSR	H_O	18	
	50K SNP	H_O, H_E	16	
	17 SSR	H_O, H_E	16	
	mtDNA	ND	16	
	17 SSR	F_{IS}, H_O, H_E	17	16
	mtDNA	ND	17	16
	15 SSR	N_{e-F}, H_O, H_E	19	This study & 20-22
Irish Draught horse	10 SSR	H_O	18	
	15 SSR	H_O, H_E	23	30
Kerry Bog pony	15 SSR	N_{e-F}, H_O, H_E	19	This study & 20-22
New Forest pony	50K SNP	N_{e-LD}, F_{IS}	27	
	17 SSR	F_{IS}, H_O, H_E	17	
	mtDNA	ND	17	
	15 SSR	N_{e-F}, H_O, H_E	19	This study & 20-22
Shetland pony	13 SSR	H_O, H_E	31	
	17 SSR	F_{IS}, H_O, H_E	17	
	mtDNA	ND	17	
	15 SSR	H_O, H_E	23	32
	15 SSR	N_{e-F}, H_O, H_E	19	This study & 20-22
Shire horse	10 SSR	H_O	18	
	15 SSR	N_{e-F}, H_O, H_E	19	This study & 20-22
Suffolk Punch horse	10 SSR	H_O	18	
	15 SSR	N_{e-F}, H_O, H_E	19	This study & 20-22
Thoroughbred horse	Pedigree	F_{PED}	33	
	13 SSR	F_{IS}, H_O, H_E	31	
	Pedigree	F_{PED}	31	
	10 SSR	H_O	18	
	15 SSR	H_O, H_E	34	
	394 SSR	H_O	24	
	30K SNP	N_{e-LD}	35	
	50K SNP	N_{e-LD}, F_{IS}	27	
	15 SSR	H_O, H_E	23	24
	15 SSR	N_{e-F}, H_O, H_E	19	This study & 20-22
	30K SNP	F_{ROH}	36	
Warmblood horse	400K SNP	F_{ROH}	25	
	400K SNP	F_{ROH}	25	
Welsh pony	15 SSR	N_{e-F}, H_O, H_E	19	This study & 20-22
Section A Welsh pony	50K SNP	H_O, H_E	16	
	17 SSR	H_O, H_E	16	
	mtDNA	ND	16	
	17 SSR	H_O, H_E	17	16
	mtDNA	ND	17	16
Section B Welsh pony	17 SSR	F_{IS}, H_O, H_E	17	
	mtDNA	ND	17	
Section C Welsh pony	17 SSR	F_{IS}, H_O, H_E	17	

		mtDNA	ND	17	
	Section D Welsh pony	50K SNP	H_O, H_E	16	
		17 SSR	H_O, H_E	16	
		mtDNA	ND	16	
		17 SSR	F_{IS}, H_O, H_E	17	16
		mtDNA	ND	17	16
Goat	Bilberry	50K SNP	F_{ROH}, H_O, H_E	37	38
	Old Irish Goat	50K SNP	F_{ROH}, H_O, H_E	37	38
	Traditional Aran	50K SNP	F_{ROH}, H_O, H_E	37	38
Pig	British Lop	60K SNP	$N_{e\text{-}F}$, $N_{e\text{-}LD}$, F_{PED}, F_{ROH}	39	
Sheep	Badger Faced Welsh Mountain	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
	Balwen	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
	Belclare	50K SNP	$N_{e\text{-}LD}$, F_{ROH}	41	
		600K SNP	F_{IS}, H_O, H_E	42	
		Pedigree	$N_{e\text{-}F}$, F_{PED}	43	
	Beltex	50K SNP	$N_{e\text{-}LD}$, F_{ROH}	41	
	Beulah	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
	Black Welsh Mountain	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
	Blue-faced Leicester	600K SNP	$N_{e\text{-}LD}$, F_{IS}, H_O, H_E	42	
	Border Leicester	50K SNP	$N_{e\text{-}LD}$, F_{IS}, H_E	44	
		50K SNP	$N_{e\text{-}LD}$, F_{IS}, F_{ROH}, H_O	45	44
		600K SNP	$N_{e\text{-}LD}$, F_{IS}, H_O, H_E	42	46
		50K SNP	$N_{e\text{-}F}$, F_{ROH}, H_O	47	
	Boreray	50K SNP	F_{IS}, H_E	44	
	Brecknock Hill Cheviot	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
	Charolais	50K SNP	$N_{e\text{-}LD}$, F_{ROH}	41	
		Pedigree	$N_{e\text{-}F}$, F_{PED}	43	
	Cheviot (commercial)	50K SNP	F_{ROH}, H_O	47	
	Clun Forest	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
	Dolgellau Welsh Mountain	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
	Dorset Horn	50K SNP	$N_{e\text{-}LD}$, F_{IS}, H_E	44	
		50K SNP	$N_{e\text{-}LD}$, F_{IS}, F_{ROH}, H_O	45	44
	EasyCare	50K SNP	F_{ROH}, H_O	47	
	Exmoor Horn	31 SSR	$N_{e\text{-}F}$, H_O, H_E	48	
	Galway	Pedigree	F_{PED}	49	
		50K SNP	$N_{e\text{-}LD}$, F_{IS}, H_E	44	
		50K SNP	$N_{e\text{-}LD}$, F_{IS}, F_{ROH}, H_O	45	
		Pedigree	$N_{e\text{-}F}$, F_{PED}	43	
	Greyface Dartmoor	50K SNP	$N_{e\text{-}F}$, F_{ROH}, H_O	47	
	Hill Flock Welsh Mountain	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
	Hill Radnor	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
	Improved Welsh Mountain	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
	Kerry Blackface	600K SNP	$N_{e\text{-}LD}$, F_{IS}, H_O, H_E	42	
	Kerry Hill	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
	Lincoln Longwool	50K SNP	F_{ROH}, H_O	47	
	Llandovery White Faced	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
	Llanwenog	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
	Lleyn	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
		600K SNP	$N_{e\text{-}LD}$, F_{IS}, H_O, H_E	42	
		50K SNP	F_{ROH}, H_O	47	
	Norfolk Horn	50K SNP	$N_{e\text{-}F}$, F_{ROH}, H_O	47	
	North Ronaldsay	50K SNP	$N_{e\text{-}LD}$, F_{ROH}	50	
	Oxford Down	50K SNP	$N_{e\text{-}F}$, F_{ROH}, H_O	47	

Poll Dorset	50K SNP	F_{ROH}, H_O	47	
Ryeland	50K SNP	F_{ROH}, H_O	47	
Scottish Blackface	31 SSR	$N_{e\text{-}F}$, H_O, H_E	48	
	50K SNP	$N_{e\text{-}LD}$, F_{IS}, H_E	44	
	50K SNP	$N_{e\text{-}LD}$, F_{IS}, F_{ROH}, H_O	45	44
	50K SNP	$N_{e\text{-}F}$, F_{ROH}, H_O	47	
Soay	50K SNP	$N_{e\text{-}LD}$, F_{IS}, H_E	44	
	50K SNP	$N_{e\text{-}LD}$, F_{IS}, F_{ROH}, H_O	45	44
South Wales Welsh Mountain	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
Southdown sheep	600K SNP	FI_S, H_O, H_E	42	
Suffolk	50K SNP	$N_{e\text{-}LD}$, F_{IS}, H_E	44	
	50K SNP	$N_{e\text{-}LD}$, F_{ROH}	41	
	50K SNP	$N_{e\text{-}LD}$, F_{IS}, F_{ROH}, H_O	45	
	Pedigree	$N_{e\text{-}F}$, F_{PED}	43	
	50K SNP	F_{ROH}, H_O	47	
Swaledale	31 SSR	$N_{e\text{-}F}$, H_O, H_E	48	
Talybont Welsh Mountain	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
Texel	50K SNP	$N_{e\text{-}LD}$, F_{IS}, H_E	44	
	50K SNP	$N_{e\text{-}LD}$, F_{ROH}	41	
	Pedigree	$N_{e\text{-}F}$, F_{PED}	43	
Tregaron Welsh Mountain	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
Vendeen	50K SNP	$N_{e\text{-}LD}$, F_{ROH}	41	
	Pedigree	$N_{e\text{-}F}$, F_{PED}	43	
Waterford Blackface	600K SNP	$N_{e\text{-}LD}$, F_{IS}, H_O, H_E	42	
Welsh Hardy Speckled Faced	50K SNP	$N_{e\text{-}LD}$, F_{IS}	40	
Welsh Mountain	31 SSR	$N_{e\text{-}F}$, H_O, H_E	48	
Whiteface Woodland	50K SNP	F_{ROH}, H_O	47	
Wicklow Cheviot	600K SNP	$N_{e\text{-}LD}$, F_{IS}, H_O, H_E	42	
Wiltshire Horn	50K SNP	$N_{e\text{-}LD}$, F_{IS}, H_E	44	
	50K SNP	$N_{e\text{-}LD}$, F_{IS}, F_{ROH}, H_O	45	44
	50K SNP	$N_{e\text{-}F}$, F_{ROH}, H_O	47	

Abbreviations: H_O = Observed heterozygosity; H_E = expected heterozygosity; ND = nucleotide diversity using (Tajima, 1983), (Arlequin v.3.5 (Excoffier and Lischer, 2010; Nei, 1987)), or (DnaSP (Librado and Rozas, 2009; Nei, 1987)); F_{PED} = pedigree-based inbreeding coefficient using (Meuwissen and Luo, 1992), (Henderson, 1976), (Wright and McPhee, 1925), (Gutiérrez and Goyache, 2005; Wright, 1931), (ABTK (Golden et al., 1991; Henderson, 1976)), or an unknown pedigree-based method; F_{IS} = inbreeding coefficient using (Wright, 1950), (PLINK (Purcell et al., 2007; Wright, 1950)), or an unknown method likely based on (Wright, 1950); F_{ROH} = runs of homozygosity inbreeding coefficient; $N_{e\text{-}LD}$ = Linkage disequilibrium (LD)-based effective population size using (Barbato et al., 2015), (Tenesa et al., 2007), (Weir and Hill, 1980), (Hayes et al., 2003), or (Kijas et al., 2012); $N_{e\text{-}F}$ = Inbreeding (F)-based effective population size, with F estimates from (Hill, 1972), (Weir and Cockerham, 1984), (ENDOG (Gutiérrez and Goyache, 2005; Wright, 1950)), (Jorde and Ryman, 1995); SSR = single sequence repeats, also known as microsatellites; SNP = single nucleotide polymorphism; mtDNA = mitochondrial DNA.

[1] MacHugh et al., 1998

[2] MacHugh et al., 1999

[3] Bradley et al., 1996

[4] Wiener et al., 2004

[5] Mc Parland et al., 2007

[6] Browett et al., 2018

[7] Decker et al., 2009

[8] Williams et al., 2016

[9] Orozco-terWengel et al., 2015

[10] The Bovine HapMap Consortium et al., 2009

[11] Roughsedge et al., 1999

[12] Wall et al., 2005

[13] Mc Parland et al., 2007

[14] MacHugh et al., 1997

[15] Wilkinson et al., 2012

[16] Winton et al., 2013

[17] Winton et al., 2020

[18] Alderson (Bodo et al., 2005)

[19] Funk et al., 2020

[20] Khanshour et al., 2013

[21] Khanshour et al., 2015

[22] Juras et al., 2003

[23] Dell et al., 2020

[24] Gu et al., 2009

[25] Lindsay-McGee et al., 2023

[26] Fox-Clipsham et al., 2011

[27] Petersen et al., 2013

[28] Grilz-Seger et al., 2019

[29] Prystupa et al., 2012

[30] McGahern et al., 2006

[31] Cunningham et al., 2001

[32] Brinkmann et al., 2012

[33] Mahon and Cunningham, 1982

[34] Cunningham (Bodo et al., 2005)

[35] Corbin et al., 2010

[36] Hill et al., 2022

[37] Manunza et al., 2023

[38] Stella et al., 2018

[39] Banos et al., 2022

[40] Beynon et al., 2015

[41] Purfield et al., 2017

[42] Cao et al., 2021

[43] Rafter et al., 2022

[44] Kijas et al., 2012

[45] McHugo et al., 2019

[46] Kijas et al., 2014

[47] Kerr et al., 2024

[48] Peter et al., 2007

[49] Martin, 1975

[50] Banos, 2023

Figures

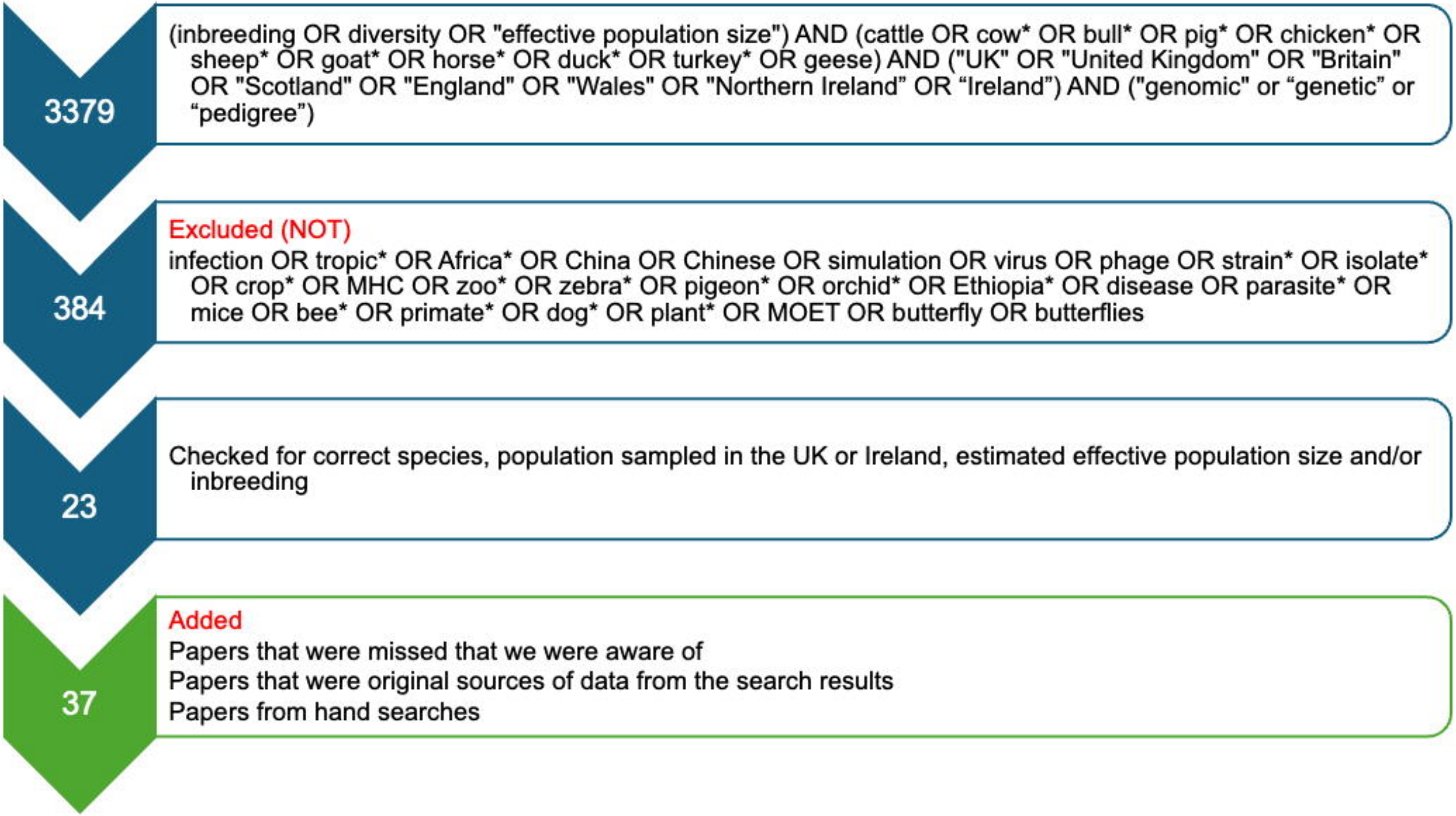
Figure 1: Literature search terms and number of results from Web of Science, for a search of genetic diversity measures of cattle, chicken, duck, equine, geese, goat, pig, sheep, and turkey populations in the United Kingdom and Ireland.

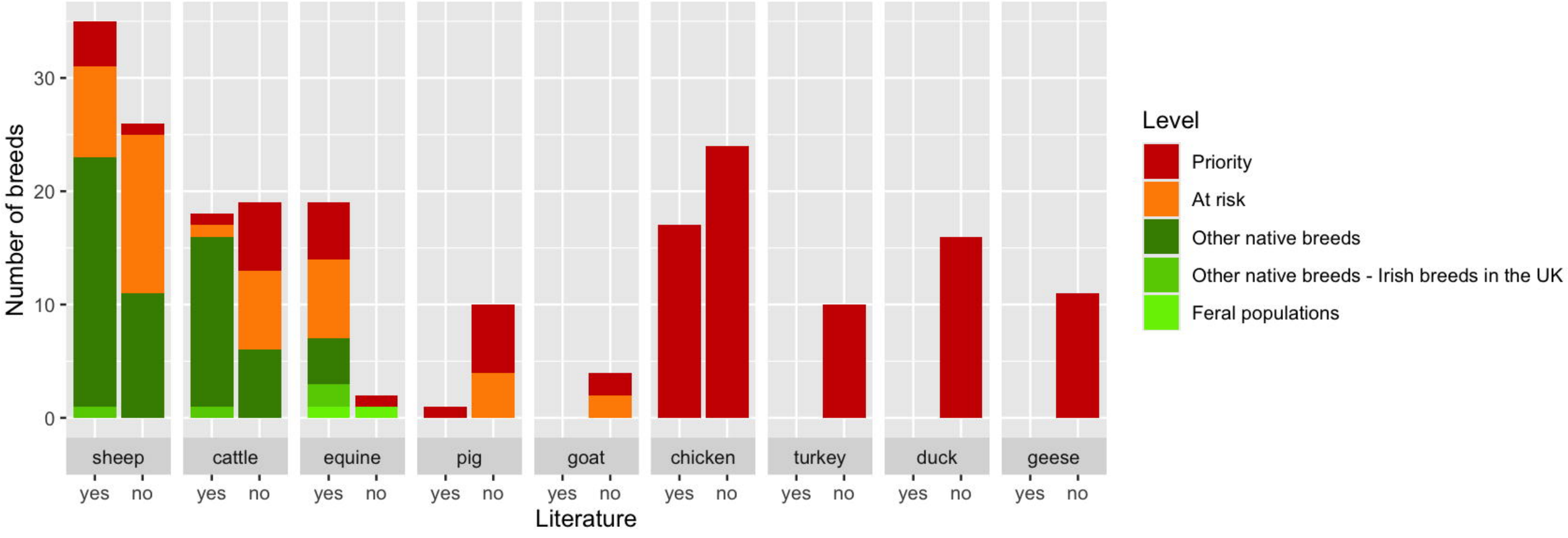
Figure 2: Clustered stacked bar plot of the number of United Kingdom and Irish livestock populations on the Rare Breeds Survival Trust's watchlist with estimates of inbreeding, diversity or effective population size estimated using pedigree or molecular markers available ("yes") or not ("no").

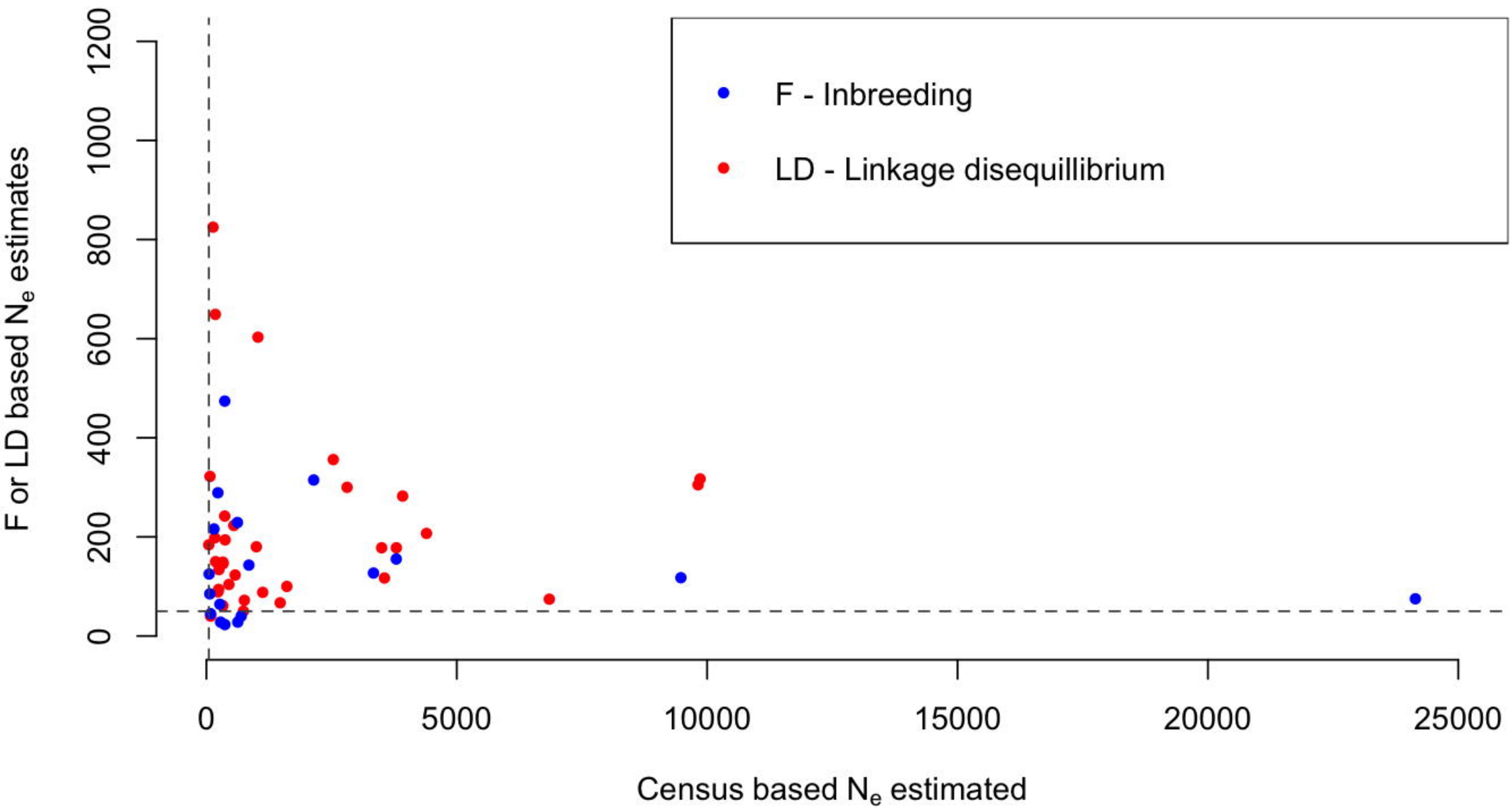
Figure 3: Inbreeding (F)- and linkage disequilibrium (LD)-based effective population size (N_e) estimates of cattle, equine, pig, and sheep breeds. N_e of 50 are indicated on both axes with grey dashed lines.

Supplementary files

Supplementary Table S1: Supplementary_file_1.xlsx – Effective population size, inbreeding, observed and expected heterozygosity, and nucleotide diversity of United Kingdom and Irish livestock and equine populations


3379
(inbreeding OR diversity OR "effective population size") AND (cattle OR cow* OR bull* OR pig* OR chicken* OR sheep* OR goat* OR horse* OR duck* OR turkey* OR geese) AND ("UK" OR "United Kingdom" OR "Britain" OR "Scotland" OR "England" OR "Wales" OR "Northern Ireland" OR "Ireland") AND ("genomic" or "genetic" or "pedigree")
384
Excluded (NOT)
infection OR tropic* OR Africa* OR China OR Chinese OR simulation OR virus OR phage OR strain* OR isolate* OR crop* OR MHC OR zoo* OR zebra* OR pigeon* OR orchid* OR Ethiopia* OR disease OR parasite* OR mice OR bee* OR primate* OR dog* OR plant* OR MOET OR butterfly OR butterflies
23
Checked for correct species, population sampled in the UK or Ireland, estimated effective population size and/or inbreeding
37
Added
Papers that were missed that we were aware of
Papers that were original sources of data from the search results
Papers from hand searches


Number of breeds
30
20
10
0
sheep
cattle
equine
pig
goat
chicken
turkey
duck
geese
yes
no
Literature
Level
Priority
At risk
Other native breeds
Other native breeds - Irish breeds in the UK
Feral populations


F - Inbreeding
LD - Linkage disequillibrium
F or LD based N_e estimates
0
200
400
600
800
1000
1200
0
5000
10000
15000
20000
25000
Census based N_e estimated