

UK Biodiversity Indicators 2023

This document supports
C9a. Animal genetic resources:
Effective population size of Native Breeds at Risk

Technical background document:

For further information on C9a. Animal genetic resources –
Effective population size of Native Breeds at Risk
visit <https://jncc.gov.uk/ukbi-C9a>

For further information on the UK Biodiversity Indicators
visit <https://jncc.gov.uk/ukbi>

Technical Background Document:

Calculation of UK Biodiversity Indicator C9a – Effective Population Size of Native Breeds at Risk.

Obtaining Data

The UK Farm Animal Genetic Resources (FAnGR) Committee [breed inventory](#) was first published in 2014 with information for pigs, goats and horses, and was expanded in 2015 to include sheep and cattle. From the 2016 inventory publication (published annually), the available data has been extended.

Data in the inventory is sourced from individual breed society records. As all pedigree animals need to be registered with their respective society to receive their pedigree certificate, the breed society records are comprehensive. To maximise efficiency in data collection, central database suppliers who maintain the breed society databases supply the data to the Defra FAnGR team. Breed societies have given their permission for these companies to supply the data every year for this exercise.

In previous versions of this indicator, the last three years of data were considered provisional, as finalisation of the data was carried out using the results of a 3-yearly survey of breed societies. This survey is no longer carried out, with all data now being collected annually and considered final when published, and this is reflected in the 2023 version of the indicator.

The figures in the indicator are based on the inventory published on 11 May 2023.

Calculating average effective population size

The indicator was calculated in 3 steps:

1. The effective population size (N_e) for each breed in the inventory was calculated using Sewell Wright's formula:

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

where M = number of sires and F = number of dams

2. Data for breeds flagged as Native Breeds at Risk (NBAR) were selected; and
3. The geometric mean of the N_e for NBAR breeds within a species was calculated.

Data for each breed within a species have been combined using a geometric mean rather than an arithmetic mean, as this reduces the influence of very common or very rare breeds on the overall number calculated. This technique is used for a number of other UK biodiversity indicators – such as for birds, bats and butterflies.

Wright's formula makes a number of assumptions; it usually produces an estimate of N_e that is higher than would be produced by a calculation using breed by breed pedigree information. However, such information is not readily available, and the indicator could not be calculated if it relied on such a methodology. Wright's formula has the advantage of being simple to calculate, and importantly, can be applied to the data available.

For many other UK Biodiversity Indicators, the variability in the data is presented through confidence intervals, and the number of species increasing or decreasing within the trend lines shown. Given that it is necessary to register offspring as pedigree before they can themselves be used to produce pedigree offspring, the data in the inventory are census rather than sample data, and therefore confidence intervals are not necessary – the value is what the value is. In bringing the data together as an average, that is itself the only value that can be calculated, so unlike most averages which are based on sampling data, it is not appropriate to calculate confidence intervals. The datasheet contains the values from which the geometric means have been calculated – this will allow users to see the range of values combined within the geometric means.

It is noted that there may be a delay in registering pedigree offspring, such that the data for a year in the inventory may actually partly represent individuals born in the previous year.

Graphical presentation

Three graphs are drawn.

1. The average effective population size of native breeds at risk as a line graph, which incorporates a dotted line for $N_e=50$ to show where the average is relative to the threshold considered to be a minimum by the United Nations Food and Agriculture Organisation. Colours have been chosen to be tonally discrete in both black and white and for someone who is red-green colour-blind
2. Column graphs, per species, to show the number of breeds per year which have $N_e \leq 50$. These are all with the same vertical axis to aid comparability.
3. A line graph showing the number of breeds for each species which contribute to the indicator is included in this Technical Document. This uses the same colour scheme as Figure C9ai to aid cross referencing and consistency.

The datasheet provides the values for each of these graphs, plus a list of the breeds which are within Figure C9aii.

Indicator description

Simply defined, a breed can be taken to mean a specific group of animals that, through selection and breeding, have similar characteristics (including, for example, appearance and behaviour) that are passed on to their offspring and which distinguish them from other animals of the same species. However, worldwide use of the term 'breed' and the various breed categories (for example 'autochthonous', 'native', 'indigenous', 'heritage', 'patrimonial', 'naturalised', or 'locally adapted') does not guarantee that these terms are defined in the same way. The UK has adopted some of these terms; definitions are provided in Appendix 1 of the [2012 UK Country Report on Farm Animal Genetic Resources](#).

Effective population size is a calculation which takes account of the total number of animals in a population. A low effective population size signifies a greater likelihood of inbreeding and risk of loss of genetic diversity. A larger effective population size implies a lower risk of inbreeding and higher genetic diversity.

The indicator shows the change in the average effective population sizes (N_e) for breeds of goats, pigs, horses, sheep and cattle classified by the UK Farm Animal Genetic Resources Committee as Native Breeds at Risk (NBAR). In the inventory published in 2023, all 5 native breeds of goats, all 11 native breeds of pigs, 13 of 19 native horse breeds, 48 of 61 native sheep breeds, and 23 of 30 native cattle breeds were classified as NBAR (for definitions of native breeds, and native breeds at risk, see Appendix 1 of the [UK Country Report on Farm Animal Genetic Resources 2012](#)).

For pigs, data to calculate effective population size is available for all years for all breeds included in the indicator (from 2000 to 2020 for 11 breeds). However, for goats, horses, sheep and cattle, the number of breeds contributing to the indicator increases over time as more data becomes available.

Table C9ai provides information on the number of breeds in the indicator published in 2023 (latest data 2022), and context of the total number classified as NBAR.

Table C9ai. The number of breeds contributing to the indicator in 2020

Species	Number of breeds in the indicator*	Total number of native breeds at risk	Percentage coverage by the indicator
Goats	5	5	100
Pigs	11	11	100
Horses	13	13	100
Sheep	36	48	75
Cattle	20	23	87

* Data represents 86 of the 101 UK breeds (85%) classified as NBAR within these species.

Table C9aii provides information on the maximum number of breeds in the indicator over the complete data series, and context of the total number classified as NBAR.

Table C9aii. The maximum number of breeds contributing to the indicator

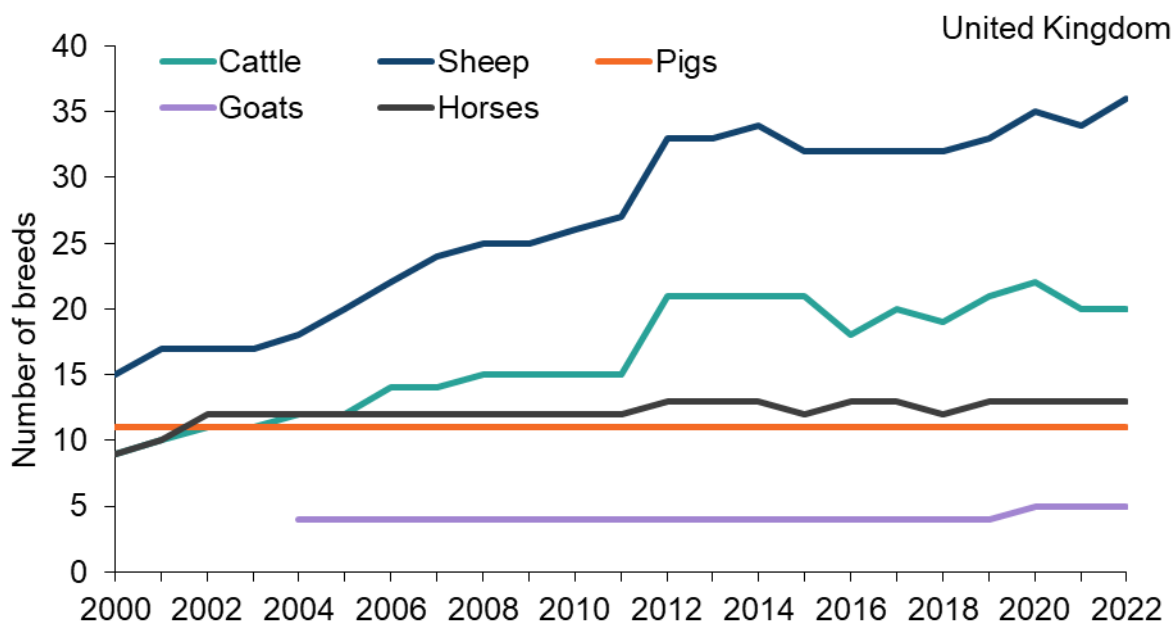
Species	Maximum number of breeds in the indicator*	Total number of native breeds at risk	Percentage coverage by the indicator
Goats	5	5	100
Pigs	11	11	100
Horses	13	13	100
Sheep	36	48	75
Cattle	22	23	96

* Data represents 86 of the 101 UK breeds (85%) classified as NBAR within these species.

The calculations in this indicator are for the breeds for which there are currently data; this is a subset of the native breeds at risk. Figure C9aiii shows the number of native

breeds at risk for which it was possible to calculate effective population size in a year, and thus contribute to the indicator.

Figure C9aiii. The number of NBAR breeds contributing to the indicator.



Notes:

1. Based on data in the UK Farm Animal Genetic Resources Breed Inventory published on 11 May 2023. <https://www.gov.uk/government/statistics/uk-farm-animal-genetic-resources-fangr-breed-inventory-results>.
2. Over the course of time, data for some breeds has been revised. In 2021, four breeds of NBAR cattle (Aberdeen Angus (Original Population); British Friesian (Original); Dairy Shorthorn (Original Population); and Hereford Traditional / Original) were merged with their associated larger non-NBAR populations, this was to ensure there was no duplication of data for these breeds. In addition, one sheep breed Badger Face Welsh (Torddu and Torwen) was split into two separate breeds, resulting in a recalculation of the entire data series. In the latest inventory, data for one NBAR goat breed, Cheviot (Feral), have been omitted while the data are under assessment. Therefore, this indicator is not directly comparable with previous publications. The Breed Inventory Excel datasheet provides information on revisions.

Source: British Pig Association, Defra, Grassroots Systems Ltd., Rare Breeds Survival Trust, and participating breed societies.

There is an increase in the number of breeds in the indicator for 2012 to 2014 as a result of incorporating the data from the triennial data collection exercise that was formerly carried out. The datasheet provides information on the number of breeds included in the indicator each year under the tabs 'Data - C9aiii', and 'Ne values for NBAR'.

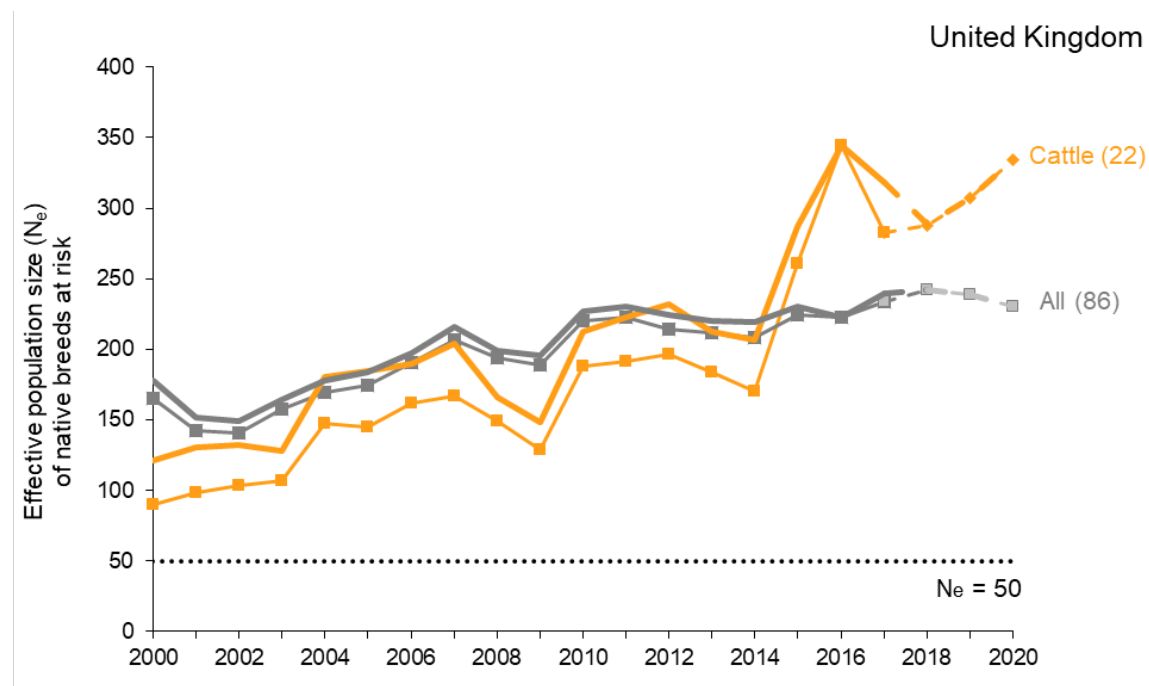
Changes to the Indicator Published in 2021

In 2021, the FAnGR Committee took the decision to merge four breeds of NBAR cattle (Aberdeen Angus (Original Population); British Friesian (Original); Dairy

Shorthorn (Original Population); and Hereford Traditional / Original) with their associated larger non-NBAR populations, this was to ensure there was no duplication of data for these breeds. It was determined that the merging of these breeds was only for the purpose of the national inventory, should be applied to the entire indicator data series and does not represent removal of these populations from the BAR or NBAR lists. Furthermore, in the 2021 Breed Inventory, the NBAR sheep breed, Badger Face Welsh (Torddu and Torwen), has been split into two separate breeds (Badger Face Welsh (Torddu) and Badger Face Welsh (Torwen)). The original combined version has been removed, and the two split breeds added to the indicator. As a consequence of these changes to cattle and sheep, the entire data series has been recalculated and the 2021 version of the indicator is not directly comparable with previously published versions. These revisions are documented in the Breed Inventory Results (Excel datasheet) published on 23 June 2021: <https://www.gov.uk/government/statistics/uk-farm-animal-genetic-resources-fangr-breed-inventory-results>.

The splitting of the Badger Face Welsh (Torddu and Torwen) sheep breed has had minimal impact on the trend of the sheep component of the indicator as shown in Figure C9ai. The merge within the 4 cattle breeds has affected the trend of the cattle component of the indicator, by slightly shifting this 'upwards' in Figure C9ai. This means that the effective population size (N_e) of cattle has increased slightly over the entire data series, and this has also resulted in a very slight increase in the trend line for all breeds. This is illustrated in Figure C9aiv, which shows the cattle trend line as included in Figure C9ai in the 2021 publication, with the historical trend line for cattle shown with square markers. The 2021 and historical trend lines for all breeds are also included, with the historical trend line similarly shown with square markers. In terms of the cattle trend line, the largest impact is over the period 2000 to 2017. This is due to the Dairy Shorthorn population with which is the only one of the 4 merged breeds for which data has been consistently available. Dairy Shorthorn (Original Population) consistently recorded low N_e values, never rising above an N_e of 30 in the 17 years for which it was included in the indicator.

Figure C9aiv. Comparison of recalculated N_e and original N_e following merging of 4 cattle breeds, 2000 to 2020.



Notes:

1. Based on data in the UK Farm Animal Genetic Resources Breed Inventory published on 23 June 2021. <https://www.gov.uk/government/statistics/uk-farm-animal-genetic-resources-fangr-breed-inventory-results>.
2. In 2021, four breeds of NBAR cattle (Aberdeen Angus (Original Population); British Friesian (Original); Dairy Shorthorn (Original Population); and Hereford Traditional / Original) were merged with their associated larger non-NBAR populations, this was to ensure there was no duplication of data for these breeds. The graph shows the average effective population (N_e) for cattle and all breeds following this merge. Recalculation of complete series are shown in solid lines. Corresponding historical series prior to the merge are shown in solid lines with square markers. Some of the breed data were collected through a 3-yearly survey that was formerly carried out, so in this analysis the last part of the lines was considered provisional ahead of the next survey that was to be published, and therefore shown as 'dashed'.

Source: British Pig Association, Defra, Grassroots Systems Ltd., Rare Breeds Survival Trust, and participating breed societies.

Previous indicator

A [previous UK biodiversity indicator](#) for animal genetic resources presented the change in genetic diversity in native breeds of cattle and sheep in the UK for 2001 and 2007, as measured by their effective population size calculated from population statistics and rates of change of inbreeding over time. The indicator was based upon a research contract undertaken in 2008 to 2009 which calculated effective population size for a set of sheep and cattle breeds for which full pedigree data were made available by breed societies. While the measure developed was state of the art at that time, it was not possible to repeat the work subsequently, nor is it likely that resources

will be available to repeat the work in the future. In addition, the indicator only covered 2 species, and therefore omitted much of the breadth of UK domesticated animal resources. The indicator was replaced in 2015 with the current indicator, based on the UK Farm Animal Genetic Resources breed inventory.