THE KENNEL CLUB
*Making a difference for dogs*

June 2020

**Population analysis of the *Bernese Mountain Dog* breed**

Genetic analysis of the Kennel Club pedigree records of the UK ***Bernese Mountain Dog*** population has been repeated with the aim of updating estimates the rate of loss of genetic diversity within the breed. The population statistics summarised provide a picture of trends in census size, the number of animals used for breeding, the rate of inbreeding and the estimated effective population size. The rate of inbreeding and estimated effective population size indicate the rate at which genetic diversity is being lost within the breed. The analysis also calculates the average relationship (kinship) among all individuals of the breed born per year and is used to determine the level of inbreeding that might be expected if matings were made among randomly selected dogs from the population (the expected rate of inbreeding). Please note that figures for the latter years covered in previous reports may have changed slightly, as ancestors of dogs imported to the UK are added to the Kennel Club pedigree (thus the pedigree may not be exactly the same).

**Summary of results**

The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered ***Bernese Mountain Dog*** population, and statistics were calculated for the period 1980-2019.

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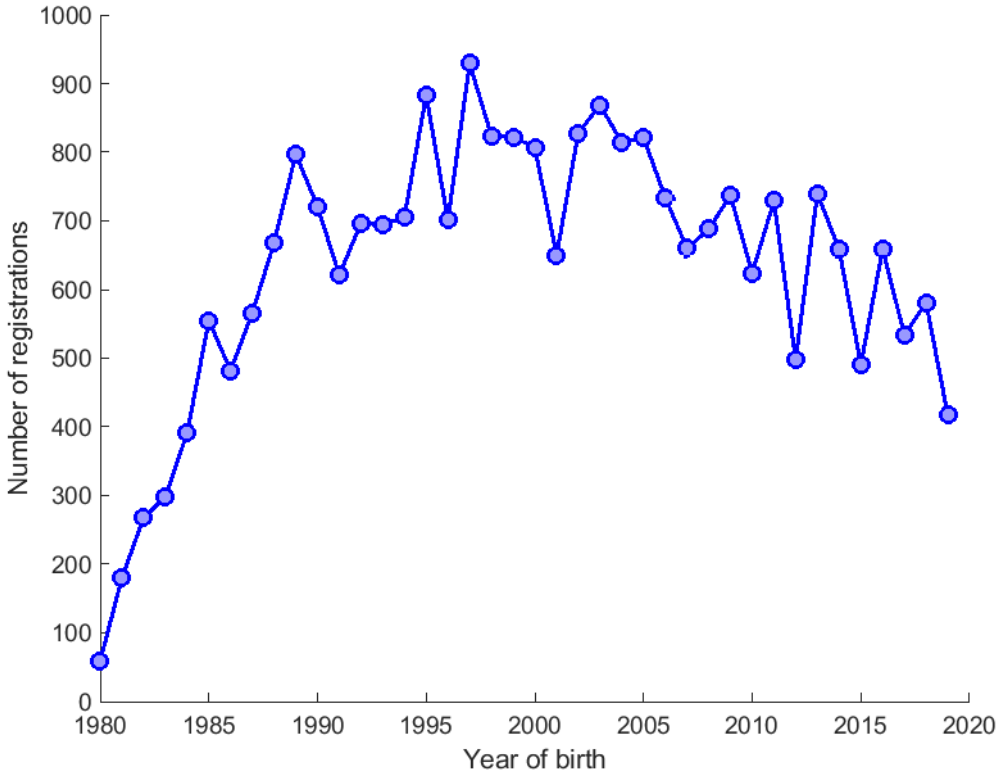
**Figure 1:** a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

**Breed:** ***Bernese Mountain Dog***

Figure 1: Number of registrations by year of birth




**Trend of registrations over year of birth (1980-2019) = 5.75 per year (with a 95% confidence interval of 0.61 to 10.90).**

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**Table 1:** census statistics by year, including sire use statistics.

Table 1: by year (1980-2019), the number of registered puppies born, by the number of unique dams and sires; maximum, median, mode, mean and standard deviation of number of puppies per sire; and the percentage of all puppies born to the most prolific 50%, 25%, 10% and 5% of sires.

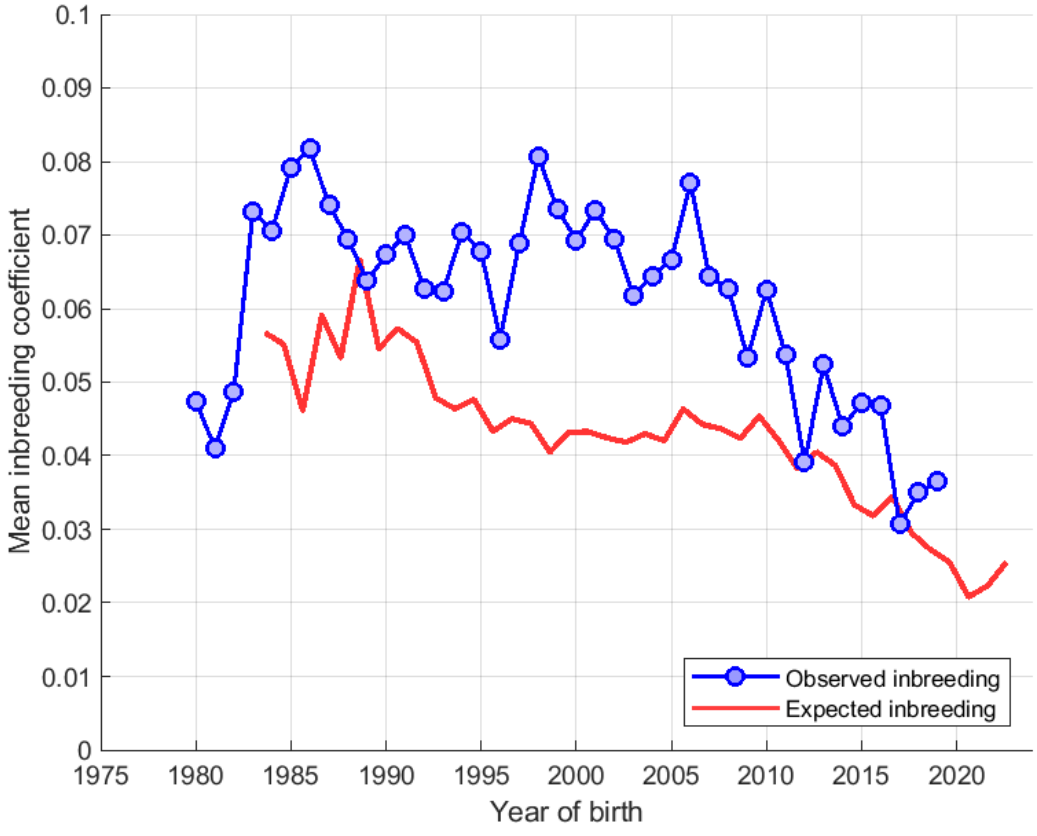
| year | nborn | ndams | nsires | puppies per sire | | | | | % puppies sired by most prolific sires | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | max | median | mode | mean | sd | 50% sires | 25% sires | 10% sires | 5%sires |
| 1980 | 59 | 32 | 21 | 10 | 2 | 1 | 2.81 | 2.25 | 79.66 | 49.15 | 27.12 | 16.95 |
| 1981 | 180 | 36 | 23 | 29 | 5 | 4 | 7.83 | 7.4 | 81.67 | 60.56 | 28.33 | 16.11 |
| 1982 | 268 | 52 | 29 | 27 | 8 | 3 | 9.24 | 7.11 | 79.48 | 51.12 | 27.99 | 10.07 |
| 1983 | 298 | 59 | 35 | 43 | 7 | 7 | 8.51 | 7.68 | 75.84 | 54.36 | 33.22 | 20.81 |
| 1984 | 391 | 82 | 40 | 34 | 7 | 1 | 9.78 | 9.93 | 85.42 | 63.43 | 32.99 | 16.88 |
| 1985 | 555 | 107 | 48 | 88 | 6 | 1 | 11.56 | 15.37 | 89.01 | 67.75 | 40.9 | 24.5 |
| 1986 | 482 | 100 | 57 | 50 | 5 | 4 | 8.46 | 9.18 | 81.12 | 59.75 | 37.97 | 23.86 |
| 1987 | 566 | 120 | 64 | 71 | 6 | 8 | 8.84 | 11.32 | 83.04 | 61.13 | 40.28 | 26.33 |
| 1988 | 668 | 124 | 69 | 71 | 7 | 7 | 9.68 | 10.86 | 80.84 | 57.93 | 35.48 | 22.31 |
| 1989 | 797 | 149 | 83 | 51 | 7 | 1 | 9.6 | 9.7 | 81.05 | 57.97 | 34.13 | 21.71 |
| 1990 | 721 | 132 | 78 | 33 | 7 | 7 | 9.24 | 7.37 | 77.39 | 54.92 | 28.85 | 16.64 |
| 1991 | 621 | 121 | 69 | 35 | 6 | 1 | 9 | 8.49 | 81 | 58.13 | 33.98 | 16.59 |
| 1992 | 697 | 125 | 80 | 46 | 6.5 | 1 | 8.71 | 8.88 | 81.06 | 57.25 | 34.86 | 22.96 |
| 1993 | 694 | 122 | 70 | 56 | 7 | 5 | 9.91 | 10.69 | 79.11 | 58.5 | 37.03 | 26.22 |
| 1994 | 706 | 129 | 76 | 41 | 7 | 10 | 9.29 | 8.56 | 80.17 | 55.67 | 33.57 | 20.68 |
| 1995 | 883 | 162 | 82 | 57 | 8 | 8 | 10.77 | 10.26 | 79.05 | 56.4 | 32.5 | 20.95 |
| 1996 | 701 | 121 | 65 | 58 | 7 | 1 | 10.78 | 11.52 | 82.03 | 58.2 | 37.95 | 21.97 |
| 1997 | 929 | 158 | 76 | 94 | 7 | 7 | 12.22 | 14.83 | 82.99 | 63.83 | 39.83 | 25.83 |
| 1998 | 824 | 156 | 74 | 40 | 8 | 6 | 11.14 | 8.83 | 78.52 | 54.98 | 26.7 | 16.63 |
| 1999 | 822 | 147 | 80 | 47 | 7 | 9 | 10.28 | 9.96 | 81.02 | 58.39 | 33.45 | 20.68 |
| 2000 | 807 | 153 | 85 | 42 | 7 | 1 | 9.49 | 9.68 | 81.66 | 59.6 | 37.79 | 19.08 |
| 2001 | 650 | 131 | 69 | 61 | 7 | 1 | 9.42 | 9.61 | 81.85 | 56.62 | 32.92 | 19.54 |
| 2002 | 828 | 157 | 76 | 89 | 6.5 | 1 | 10.89 | 14.81 | 86.35 | 64.49 | 42.03 | 29.59 |
| 2003 | 869 | 162 | 74 | 60 | 6 | 1 | 11.74 | 12.23 | 87.11 | 63.52 | 31.76 | 20.25 |
| 2004 | 814 | 164 | 98 | 34 | 6.5 | 1 | 8.31 | 7.76 | 83.54 | 60.32 | 31.45 | 17.44 |
| 2005 | 821 | 164 | 85 | 62 | 7 | 1 | 9.66 | 10.79 | 88.19 | 62.85 | 37.15 | 20.71 |
| 2006 | 734 | 140 | 73 | 43 | 7 | 1 | 10.05 | 10.78 | 86.1 | 61.72 | 35.97 | 22.34 |
| 2007 | 660 | 142 | 81 | 48 | 6 | 1 | 8.15 | 9.05 | 86.82 | 62.12 | 36.67 | 21.82 |
| 2008 | 688 | 144 | 83 | 40 | 6 | 1 | 8.29 | 8.67 | 88.23 | 64.24 | 32.7 | 18.46 |
| 2009 | 737 | 151 | 78 | 75 | 5.5 | 1 | 9.45 | 11.74 | 88.87 | 67.3 | 38.4 | 23.74 |
| 2010 | 624 | 138 | 84 | 42 | 4.5 | 1 | 7.43 | 8.75 | 89.1 | 65.22 | 37.34 | 22.92 |
| 2011 | 729 | 167 | 100 | 36 | 5 | 1 | 7.29 | 7.58 | 87.24 | 62.41 | 34.84 | 19.07 |
| 2012 | 498 | 130 | 86 | 38 | 3 | 1 | 5.79 | 6.94 | 88.96 | 64.86 | 38.55 | 23.9 |
| 2013 | 740 | 158 | 101 | 36 | 3 | 1 | 7.33 | 8.89 | 90.95 | 68.11 | 40 | 22.7 |
| 2014 | 658 | 156 | 102 | 41 | 2 | 1 | 6.45 | 8.08 | 91.19 | 70.06 | 39.82 | 23.71 |
| 2015 | 491 | 127 | 93 | 34 | 2 | 1 | 5.28 | 6.24 | 88.8 | 66.8 | 36.05 | 24.64 |
| 2016 | 659 | 165 | 113 | 37 | 3 | 1 | 5.83 | 7.31 | 90.29 | 68.13 | 40.36 | 26.4 |
| 2017 | 534 | 132 | 99 | 28 | 3 | 1 | 5.39 | 5.73 | 87.27 | 62.55 | 35.39 | 20.79 |
| 2018 | 581 | 138 | 89 | 59 | 3 | 1 | 6.53 | 8.99 | 89.85 | 68.85 | 42 | 25.3 |
| 2019 | 417 | 92 | 66 | 32 | 5.5 | 1 | 6.32 | 5.98 | 84.17 | 56.83 | 32.61 | 17.99 |

**Generation interval:** the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

**Mean generation interval (years) = 3.53**

**Figure 2:** a plot of the annual mean observed inbreeding coefficient (showing changes in genetic diversity), and mean expected inbreeding coefficient (from simulated 'random mating') over the period 1980-2019. 'Expected inbreeding' is staggered by the generation interval and, where >2000 animals are born in a single year, the 95% confidence interval is indicated.

Figure 2: Annual mean observed and expected inbreeding coefficients



**Estimated effective population size:** the rate of inbreeding (slope or steepness of the observed inbreeding in Figure 2) is used to estimate the effective population size of the breed. The effective population size is the number of breeding animals in an idealised, hypothetical population that would be expected to show the same rate of loss of genetic diversity (rate of inbreeding) as the breed in question. It may be thought of as the size of the 'gene pool' of the breed.

Below an effective population size of 100 (inbreeding rate of 0.50% per generation) the rate of loss of genetic diversity in a breed/population increases dramatically (Food & Agriculture Organisation of the United Nations, "Monitoring animal genetic resources and criteria for prioritization of breeds", 1992). An effective population size of below 50 (inbreeding rate of 1.0% per generation) indicates the future of the breed many be considered to be at risk (Food & Agriculture Organisation of the United Nations, "Breeding strategies for sustainable management of animal genetic resources", 2010).

Where the rate of inbreeding is negative (implying *increasing* genetic diversity in the breed), effective population size is denoted 'n/a'.

**Estimated effective population size = n/a**

*NB - this estimate is made using the rate of inbreeding over the whole period 1980-2019*

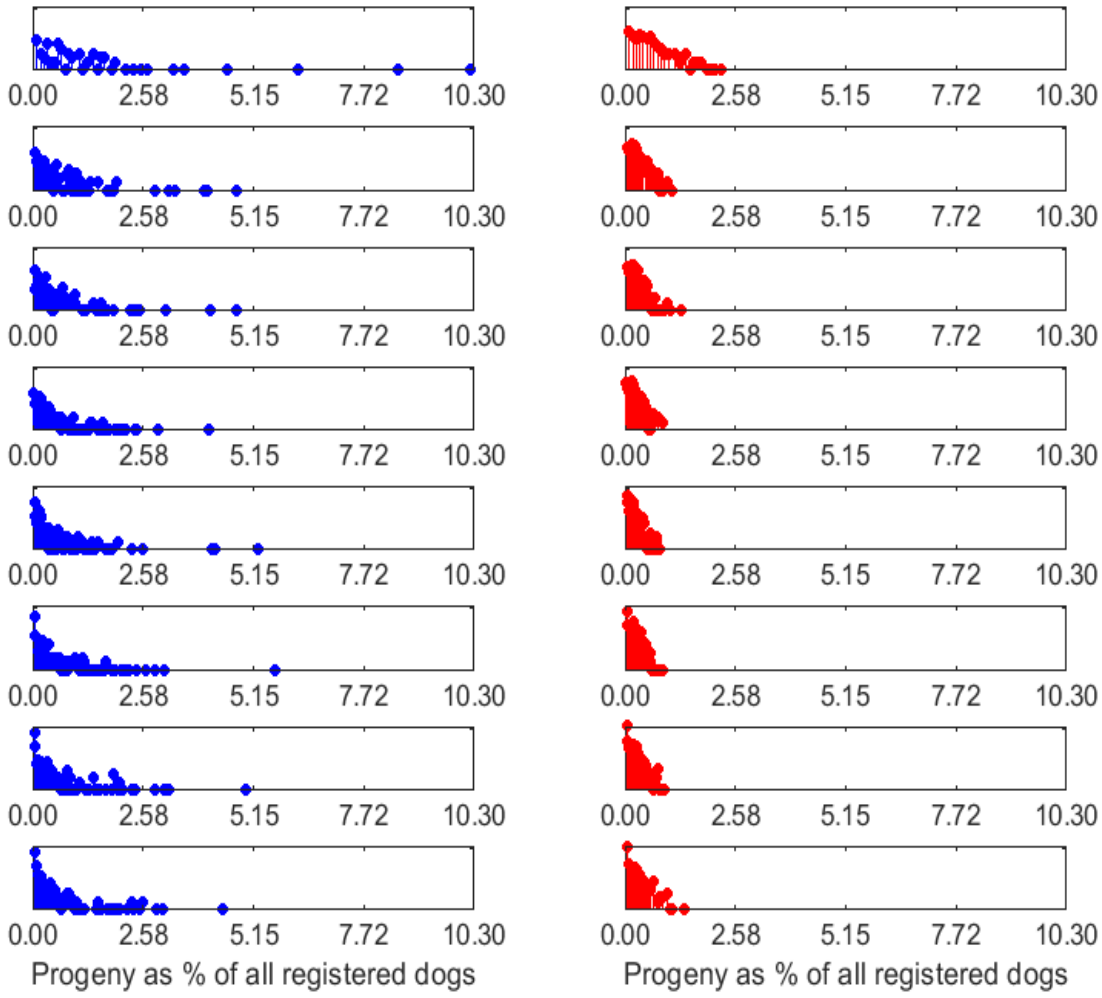
**Table 2:** a breakdown of census statistics, sire and dam usage and indicators of the rate of loss of genetic diversity over 5 year periods (1980-4, 1985-9, 1990-4, 1995-9, 2000-4, 2005-9, 2010-14, 2015-19). Rate of inbreeding and estimated effective population size for each 5-year block can be compared with the trend in observed inbreeding in Figure 2.

Table 2: by 5-year blocks, the mean number of registrations; for sires the total number used, maximum, mean, median, mode, standard deviation and skewness (indicative of the size of the 'tail' on the distribution) of number of progeny per sire; for dams the total number used, maximum, mean, median, mode, standard deviation and skewness of number of progeny per dam; rate of inbreeding per generation (as a decimal, multiply by 100 to obtain as a percentage); mean generation interval; and estimated effective population size.

| years | 1980-84 | 1985-89 | 1990-94 | 1995-99 | 2000-04 | 2005-09 | 2010-14 | 2015-19 |
|---|---|---|---|---|---|---|---|---|
| **Mean registrations** | 239.2 | 613.6 | 687.8 | 831.8 | 793.6 | 728 | 649.8 | 536.4 |
| **Total sires** | 86 | 184 | 208 | 210 | 249 | 240 | 306 | 305 |
| **Max n progeny** | 122 | 146 | 164 | 171 | 209 | 206 | 161 | 119 |
| **Mean n progeny** | 13.907 | 16.674 | 16.534 | 19.805 | 15.936 | 15.167 | 10.618 | 8.7934 |
| **Median n progeny** | 8 | 8 | 9 | 9 | 7 | 6 | 2 | 2 |
| **Mode n progeny** | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| **SD n progeny** | 19.504 | 23.591 | 22.187 | 26.755 | 25.668 | 23.854 | 19.26 | 15.289 |
| **skew n progeny** | 3.5598 | 3.1683 | 3.3407 | 2.7776 | 4.0015 | 3.4755 | 3.5324 | 3.4022 |
| **Total dams** | 176 | 402 | 433 | 512 | 562 | 549 | 587 | 510 |
| **Max n progeny** | 27 | 34 | 45 | 37 | 31 | 32 | 29 | 37 |
| **Mean n progeny** | 6.7955 | 7.6318 | 7.9423 | 8.123 | 7.0605 | 6.6302 | 5.5349 | 5.2588 |
| **Median n progeny** | 5 | 6 | 6 | 7 | 6 | 6 | 4 | 3 |
| **Mode n progeny** | 1 | 5 | 5 | 6 | 1 | 1 | 1 | 1 |
| **SD n progeny** | 5.5491 | 5.8479 | 6.1489 | 6.2934 | 5.5928 | 5.4968 | 5.3747 | 5.5022 |
| **skew n progeny** | 1.3906 | 1.4511 | 1.7867 | 1.5656 | 1.3646 | 1.2688 | 1.6059 | 1.894 |
| **Rate of inbreeding** | 0.0285 | -0.0162 | -0.0005 | 0.0143 | -0.0084 | -0.0160 | -0.0157 | -0.0121 |
| **Generaton interval** | 3.4309 | 3.4626 | 3.7121 | 3.6434 | 3.6803 | 3.6276 | 3.84 | 3.5077 |
| **Effective pop size** | 17.55 | n/a | n/a | 35.003 | n/a | n/a | n/a | n/a |

**Figure 3:** a histogram ('tally' distribution) of progeny as a percent of all registered dogs per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number of offspring, known to be a major contributor to a high rate of inbreeding).

Figure 3: Distribution of progeny per sire (blue) and per dam (red) over 5-year blocks (1980-4 top, 2015-19 bottom). Vertical axis is a logarithmic scale.



**Comments**

The rate of inbreeding for this breed over the entire period 1980 and 2019 remains negative due to a continuing negative rate of inbreeding determined over 2015-19. This means that genetic variation within the breed appears to be increasing (most probably through the use of imported animals).

There appears to be extensive use of popular dogs as sires in this breed (the 'tail' of the blue distribution in figure 3).

It should be noted that, while animals imported from overseas may appear completely unrelated, this is not always the case. Often the pedigree available to the Kennel Club is limited in the number of generations, hampering the ability to detect true, albeit distant, relationships.