



THE KENNEL CLUB

Making a difference for dogs

September 2015

Population analysis of the *Greyhound* breed

Genetic analysis of the Kennel Club pedigree records of the UK ***Greyhound*** population has been carried out with the aim of estimating the rate of loss of genetic diversity within the breed and providing information to guide a future sustainable breeding strategy. 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. However, the number of animals of this breed registered with the Kennel Club per year has not been consistently high enough to allow all intended features of the report to be presented.

Summary of results

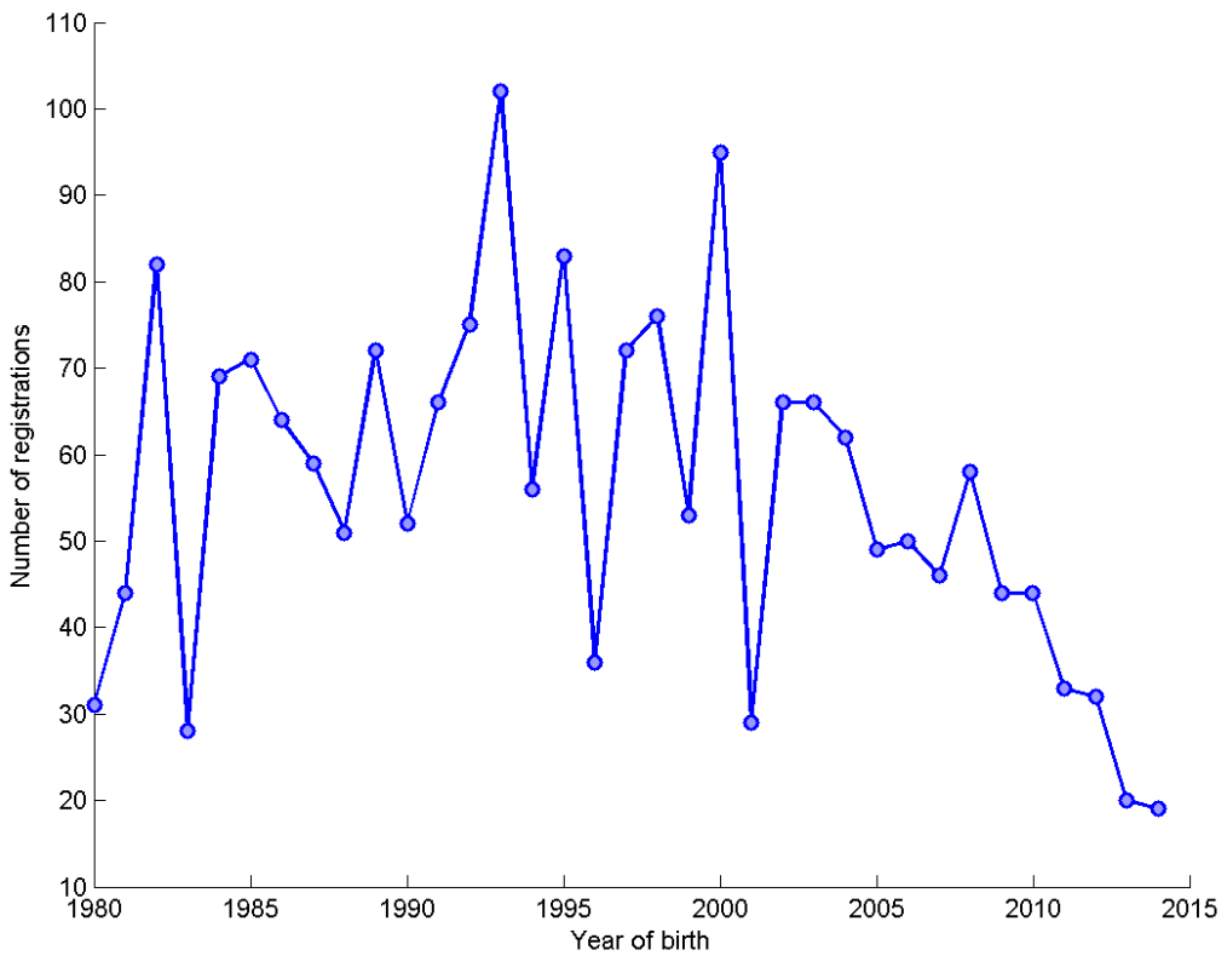
The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered ***Greyhound*** population, and statistics were calculated for the period 1980-2014.



Figure 1: a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed.

Breed: *Greyhound*

Figure 1: Number of registrations by year of birth





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

Table 1: by year (1980–2014), 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	#born	#dams	#sires	puppies per sire					%puppies sired by most prolific sires			
				max	median	mode	mean	sd	50% sires	25% sires	10% sires	5% sires
1980	31	16	13	13	1	1	2.38	3.28	80.65	61.29	41.94	41.94
1981	44	13	12	9	3	1	3.67	2.57	77.27	47.73	20.45	20.45
1982	82	21	17	16	3	1	4.82	4.97	87.8	62.2	36.59	19.51
1983	28	14	15	5	1	1	1.87	1.41	75	53.57	35.71	17.86
1984	69	17	16	14	4.5	1	4.31	3.7	84.06	52.17	31.88	20.29
1985	71	21	18	11	1.5	1	3.94	3.76	87.32	63.38	29.58	15.49
1986	64	17	15	14	2	1	4.27	3.99	85.94	59.38	35.94	21.88
1987	59	22	20	7	1.5	1	2.95	2.35	83.05	54.24	23.73	11.86
1988	51	17	18	7	1.5	1	2.83	2.2	82.35	56.86	27.45	13.73
1989	72	22	19	11	3	1	3.79	2.9	81.94	52.78	27.78	15.28
1990	52	17	14	8	3	1	3.71	2.95	84.62	57.69	15.38	15.38
1991	66	20	18	10	2.5	1	3.67	3.22	83.33	62.12	28.79	15.15
1992	75	24	16	14	3.5	1	4.69	4.38	84	58.67	36	18.67
1993	102	28	26	20	1	1	3.92	5.11	87.25	73.53	47.06	19.61
1994	56	18	14	12	2	1	4	4.08	85.71	69.64	21.43	21.43
1995	83	26	25	12	2	1	3.32	3.15	84.34	59.04	34.94	14.46
1996	36	16	15	8	1	1	2.4	2.44	80.56	63.89	41.67	22.22
1997	72	22	20	9	1	1	3.6	3.27	86.11	55.56	25	12.5
1998	76	22	20	14	2	1	3.8	3.65	85.53	57.89	28.95	18.42
1999	53	24	22	8	1	1	2.41	2.3	79.25	66.04	28.3	15.09
2000	95	27	21	19	2	1	4.52	5.63	88.42	71.58	35.79	20
2001	29	23	23	5	1	1	1.26	0.86	62.07	41.38	24.14	17.24
2002	66	33	29	11	1	1	2.28	2.75	78.79	65.15	42.42	16.67
2003	66	28	28	9	1	1	2.36	2.71	78.79	66.67	37.88	13.64
2004	62	29	29	8	1	1	2.14	2.2	77.42	61.29	37.1	12.9
2005	49	28	25	9	1	1	1.96	1.88	75.51	55.1	38.78	18.37
2006	50	26	23	16	1	1	2.17	3.3	78	66	46	32
2007	46	19	17	10	2	1	2.71	2.66	82.61	58.7	39.13	21.74
2008	58	24	23	20	1	1	2.52	4.25	81.03	67.24	51.72	34.48
2009	44	21	18	8	1.5	1	2.44	2.31	79.55	61.36	36.36	18.18
2010	44	17	16	13	1	1	2.75	4.02	81.82	68.18	59.09	29.55
2011	33	20	18	7	1	1	1.83	1.47	72.73	51.52	30.3	21.21
2012	32	13	13	9	1	1	2.46	2.93	81.25	62.5	28.13	28.13
2013	20	11	11	3	2	2	1.82	0.6	65	35	15	15
2014	19	11	9	9	1	1	2.11	2.67	78.95	63.16	47.37	n/a



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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) = 4.33

Estimated effective population size: the rate of inbreeding 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 may 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 1980-2014



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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). Rate of inbreeding and estimated effective population size for each 5-year block can be observed.

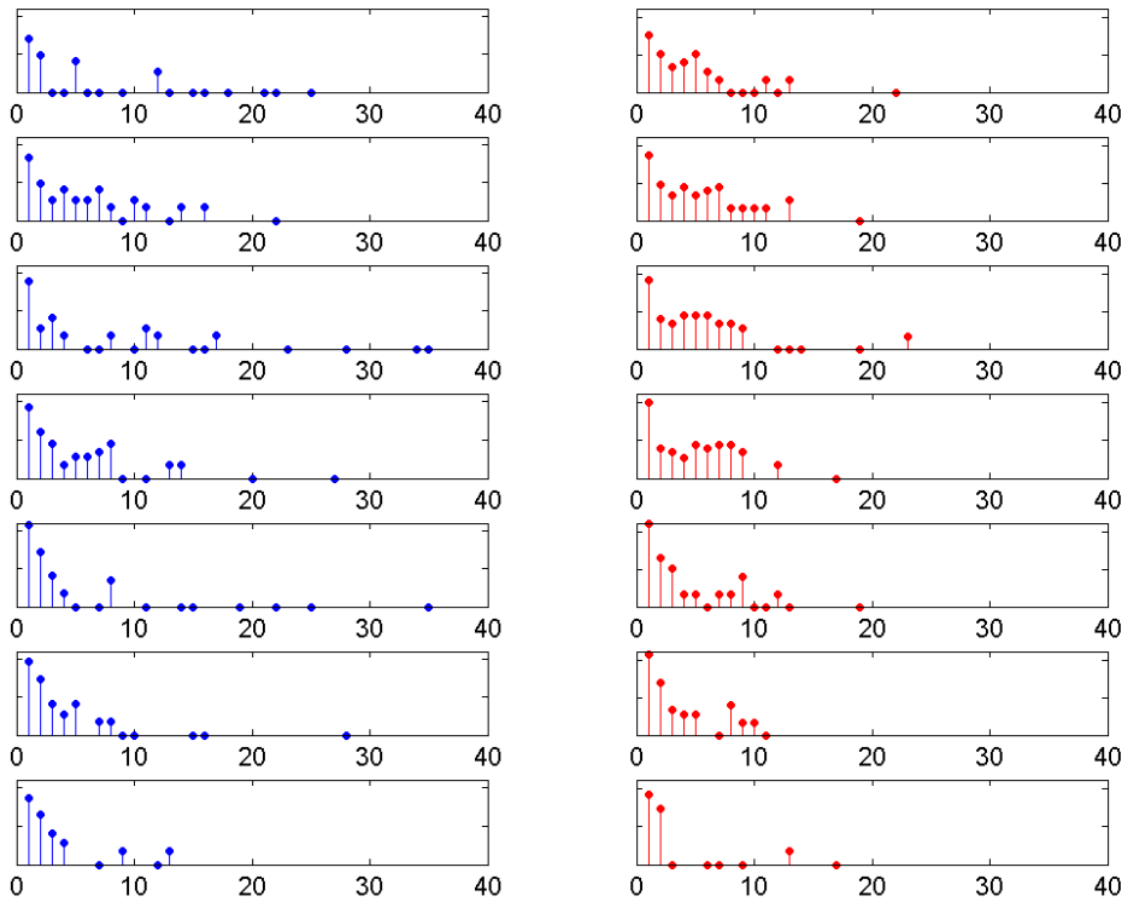
Table 2: by 5-year blocks, the mean number of registrations; for sires the total number used, maximum, mean, median, mode, standard deviation and skewness (indicative of the size of the 'tail' on the distribution) of number of progeny per sire; for dams the total number used, maximum, mean, median, mode, 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	1980-1984	1985-1989	1990-1994	1995-1999	2000-2004	2005-2009	2010-2014
mean #registrations	50.8	63.4	70.2	64	63.6	49.4	29.6
Total #sires	44	67	62	83	111	89	58
Max #progeny	25	22	35	27	35	28	13
Mean #progeny	5.7045	4.6269	5.5484	3.8313	2.8559	2.764	2.5345
Median #progeny	2	2	1	2	1	1	1
Mode #progeny	1	1	1	1	1	1	1
SD #progeny	6.6212	4.7092	8.028	4.6534	5.1201	3.8935	2.9512
Skew #progeny	1.4478	1.4923	2.1696	2.4879	4.0251	4.08	2.5243
Total #dams	61	78	85	99	131	115	67
Max #progeny	22	19	23	17	19	11	17
Mean #progeny	4.1148	3.9744	4.0471	3.2121	2.4198	2.1391	2.194
Median #progeny	3	2	2	1	1	1	1
Mode #progeny	1	1	1	1	1	1	1
SD #progeny	4.0747	3.8409	4.616	3.271	3.0858	2.3504	3.0063
Skew #progeny	1.9807	1.4702	2.2797	1.5405	2.7241	2.3157	3.4732
Rate of inbreeding	-0.06018	-0.02555	0.014757	0.038213	0.020033	-0.02843	0.012808
Generation interval	5.1646	4.1946	4.6696	4.4551	4.958	3.9722	1.9199
Effective pop size	n/a	n/a	33.882	13.085	24.959	n/a	39.038



Figure 3: a histogram ('tally' distribution) of number of progeny 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 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, 2010-14 bottom). Vertical axis is a logarithmic scale.





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Comments

As can be seen from figure 1, the number of animals of this breed registered with the Kennel Club is consistently small. The small population size and possible use of migrant animals mean there may be large fluctuations in the rate of inbreeding and effective population size.

There appears to be evidence of only modest use of popular 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.