



THE KENNEL CLUB

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September 2015

Population analysis of the *Collie (Smooth)* breed

Genetic analysis of the Kennel Club pedigree records of the UK ***Collie (Smooth)*** 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. 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).

Summary of results

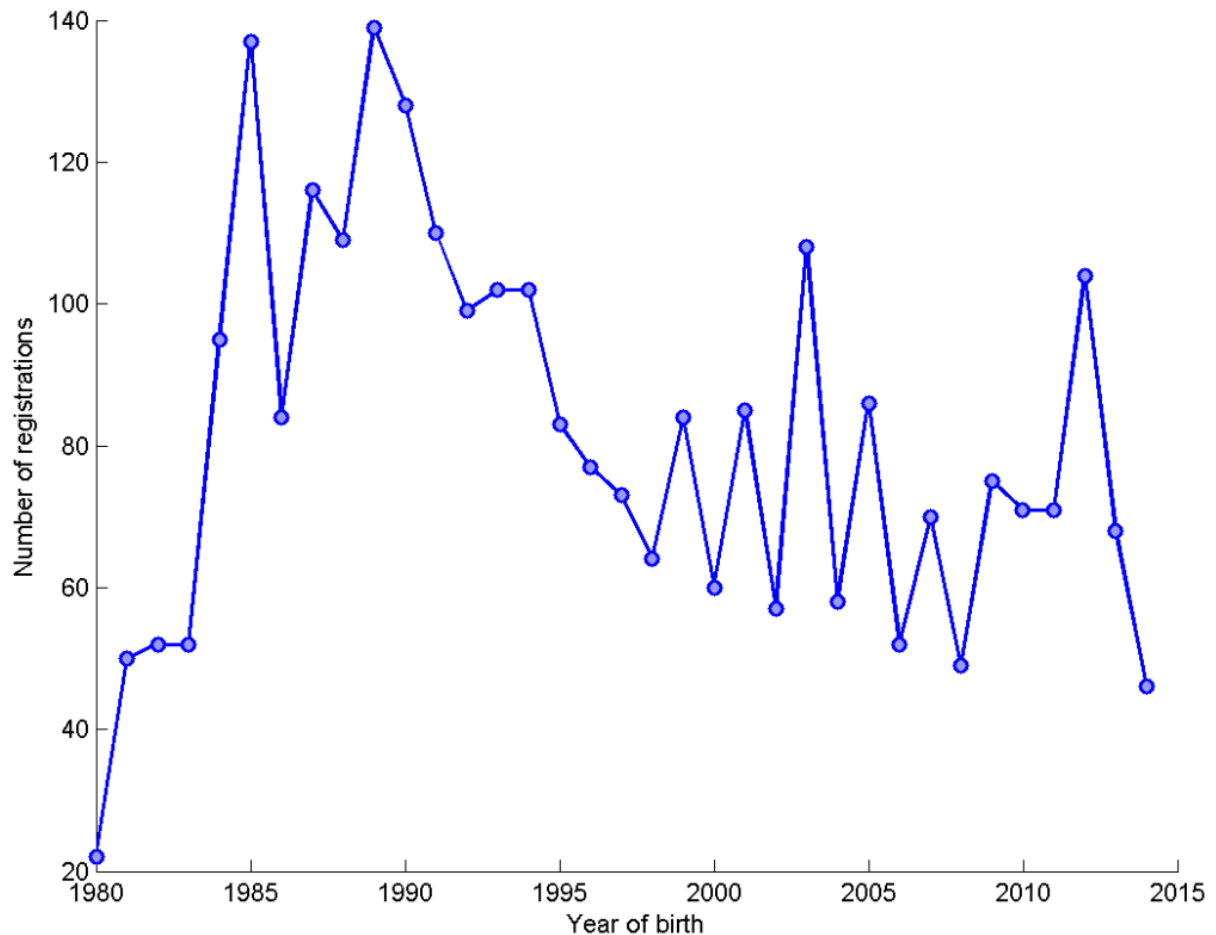
The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered ***Collie (Smooth)*** population, and statistics were calculated for the period 1980-2014.



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

Breed: Collie (Smooth)

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = -0.56 per year (with a 95% confidence interval of -1.50 to 0.37).



Table 1: census statistics by year, 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	22	13	13	4	2	1	1.69	0.85	72.73	36.36	18.18	18.18
1981	50	17	21	6	1	1	2.38	1.86	80	52	24	12
1982	52	16	13	10	3	3	4	2.61	76.92	44.23	19.23	19.23
1983	52	24	18	7	3	1	2.89	1.81	75	50	23.08	13.46
1984	95	29	13	22	3	1	7.31	7.89	91.58	62.11	23.16	23.16
1985	137	43	33	19	3	1	4.15	4.36	86.86	60.58	32.85	24.82
1986	84	23	17	16	5	1	4.94	3.77	79.76	46.43	29.76	19.05
1987	116	33	28	15	3	1	4.14	3.49	81.9	54.31	28.45	12.93
1988	109	33	25	16	4	3	4.36	3.12	74.31	46.79	29.36	14.68
1989	139	41	39	14	3	1	3.56	2.82	81.29	51.8	27.34	15.83
1990	128	33	35	24	2	1	3.66	4.23	84.38	59.38	36.72	25.78
1991	110	30	28	15	2	1	3.93	4.12	83.64	60.91	39.09	13.64
1992	99	31	34	11	1	1	2.91	2.76	82.83	61.62	29.29	21.21
1993	102	25	26	16	2	1	3.92	3.91	85.29	63.73	35.29	15.69
1994	102	27	26	9	4	4	3.92	2.24	71.57	48.04	24.51	8.82
1995	83	22	16	12	4.5	1	5.19	3.83	81.93	50.6	27.71	14.46
1996	77	16	11	21	5	2	7	6.07	83.12	59.74	27.27	27.27
1997	73	23	15	13	4	3	4.87	3	73.97	46.58	28.77	17.81
1998	64	17	12	11	5.5	1	5.33	3.6	76.56	46.88	17.19	17.19
1999	84	23	21	9	4	1	4	2.79	82.14	45.24	20.24	10.71
2000	60	15	12	16	5	1	5	4.05	75	48.33	26.67	26.67
2001	85	25	18	22	1.5	1	4.72	6.54	89.41	75.29	49.41	25.88
2002	57	16	11	18	4	6	5.18	4.85	84.21	56.14	31.58	31.58
2003	108	25	20	16	4	1	5.4	4.35	78.7	52.78	28.7	14.81
2004	58	19	14	11	2.5	1	4.14	3.42	82.76	60.34	18.97	18.97
2005	86	21	17	22	3	1	5.06	5.9	86.05	62.79	45.35	25.58
2006	52	16	13	13	1	1	4	3.94	88.46	55.77	25	25
2007	70	19	15	22	2	1	4.67	5.6	87.14	65.71	47.14	31.43
2008	49	18	17	8	2	1	2.88	2.32	81.63	51.02	32.65	16.33
2009	75	14	10	17	6.5	5	7.5	4.55	72	52	22.67	22.67
2010	71	21	19	13	2	1	3.74	3.36	83.1	57.75	32.39	18.31
2011	71	20	16	16	3	1	4.44	4.1	83.1	54.93	35.21	22.54
2012	104	23	15	31	1	1	6.93	10.36	93.27	78.85	59.62	29.81
2013	68	14	10	12	8	9	6.8	3.61	70.59	44.12	17.65	17.65
2014	46	9	7	9	7	7	6.57	1.51	n/a	n/a	n/a	n/a

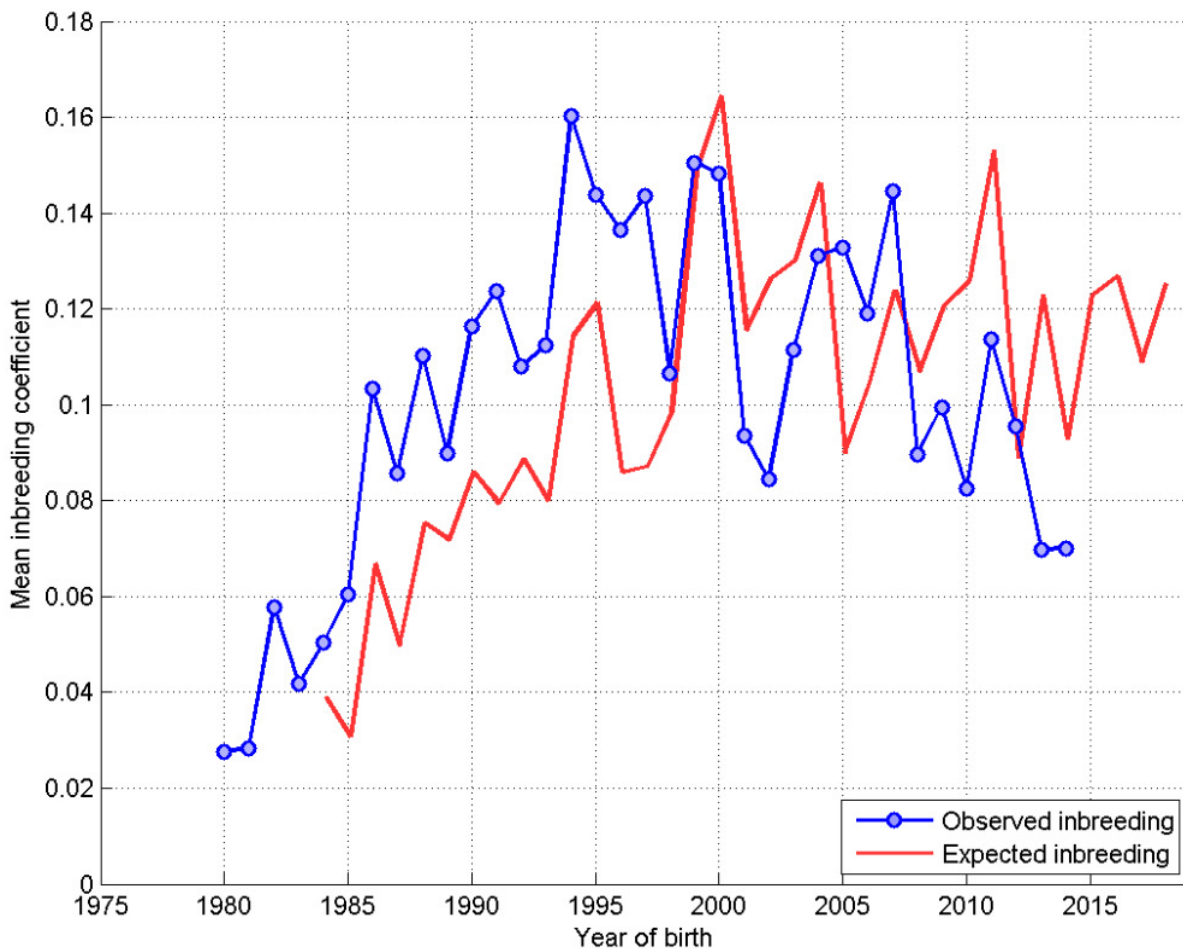


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 4.10

Figure 2: a plot of the annual mean observed inbreeding coefficient (showing loss of genetic diversity), and mean expected inbreeding coefficient (from 'random mating') over the period 1980-2014. '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





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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 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 = 90.0

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 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	1980-1984	1985-1989	1990-1994	1995-1999	2000-2004	2005-2009	2010-2014
Mean #registrations	54.2	117	108.2	76.2	73.6	66.4	72
Total #sires	57	97	121	53	59	49	51
Max #progeny	29	53	29	46	38	39	49
Mean #progeny	4.7193	6.0206	4.4628	7.1698	6.2203	6.7551	7.0392
Median #progeny	2	3	2	5	4	3	5
Mode #progeny	1	1	1	1	1	1	1
SD #progeny	6.3267	7.8062	5.6746	8.5726	6.6516	8.807	8.9643
Skew #progeny	2.2692	3.3135	2.5192	2.5143	2.3525	2.1585	2.7226
Total #dams	82	135	119	84	82	73	77
Max #progeny	13	20	16	14	17	21	15
Mean #progeny	3.2805	4.3185	4.4958	4.5238	4.4756	4.5342	4.6623
Median #progeny	3	4	4	4	4	3	5
Mode #progeny	1	1	1	1	1	1	1
SD #progeny	2.4559	3.4655	3.417	3.1373	3.3673	4.1636	3.2992
Skew #progeny	1.4139	1.6469	1.3296	0.86043	0.96938	1.6813	0.72101
Rate of inbreeding	0.02106	0.028258	0.034602	-0.0092367	-0.0074345	-0.053585	-0.02762
Generation interval	3.4598	3.9742	3.9172	4.9711	3.6763	4.9202	3.6677
Effective pop size	23.741	17.694	14.45	n/a	n/a	n/a	n/a



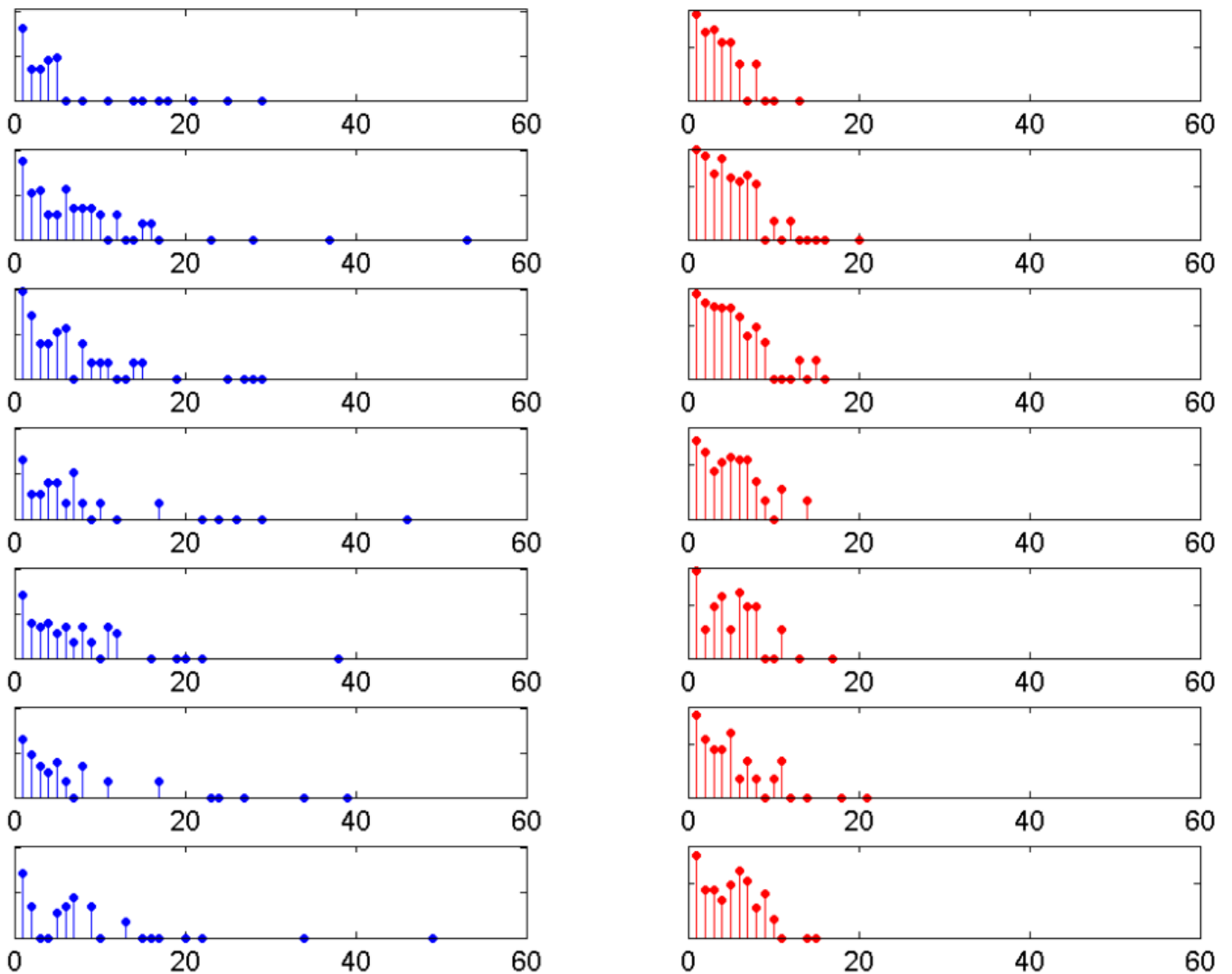
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number 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, 2010-14 bottom). Vertical axis is a logarithmic scale.





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Comments

As with most breeds, the rate of inbreeding was at its highest in this breed in the 1980s and 1990s. This represents a 'genetic bottleneck', with genetic variation lost from the population. However, since the late 1990s the rate of inbreeding has been negative, implying moderate restoration of genetic diversity (possibly through the use of imported animals). The small population size and possible influence of migrant animals mean there may be large fluctuations in the rate of inbreeding and effective population size.

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.