THE KENNEL CLUB
Making a difference for dogs

September 2015

Population analysis of the *Spaniel (Field)* breed

Genetic analysis of the Kennel Club pedigree records of the UK ***Spaniel (Field)*** 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).

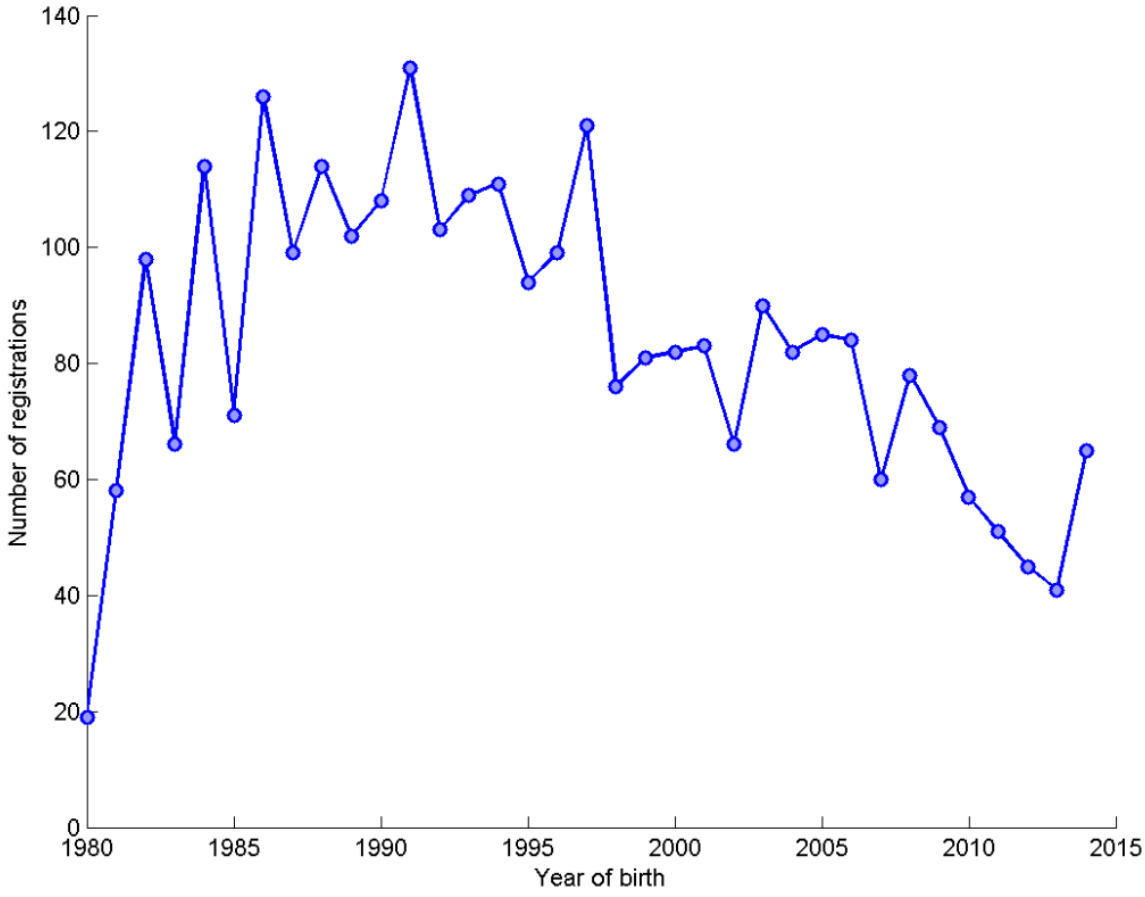
Summary of results

The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered ***Spaniel (Field)*** 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: ***Spaniel (Field)***

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = -0.96 per year (with a 95% confidence interval of -1.79 to -0.14).

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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.

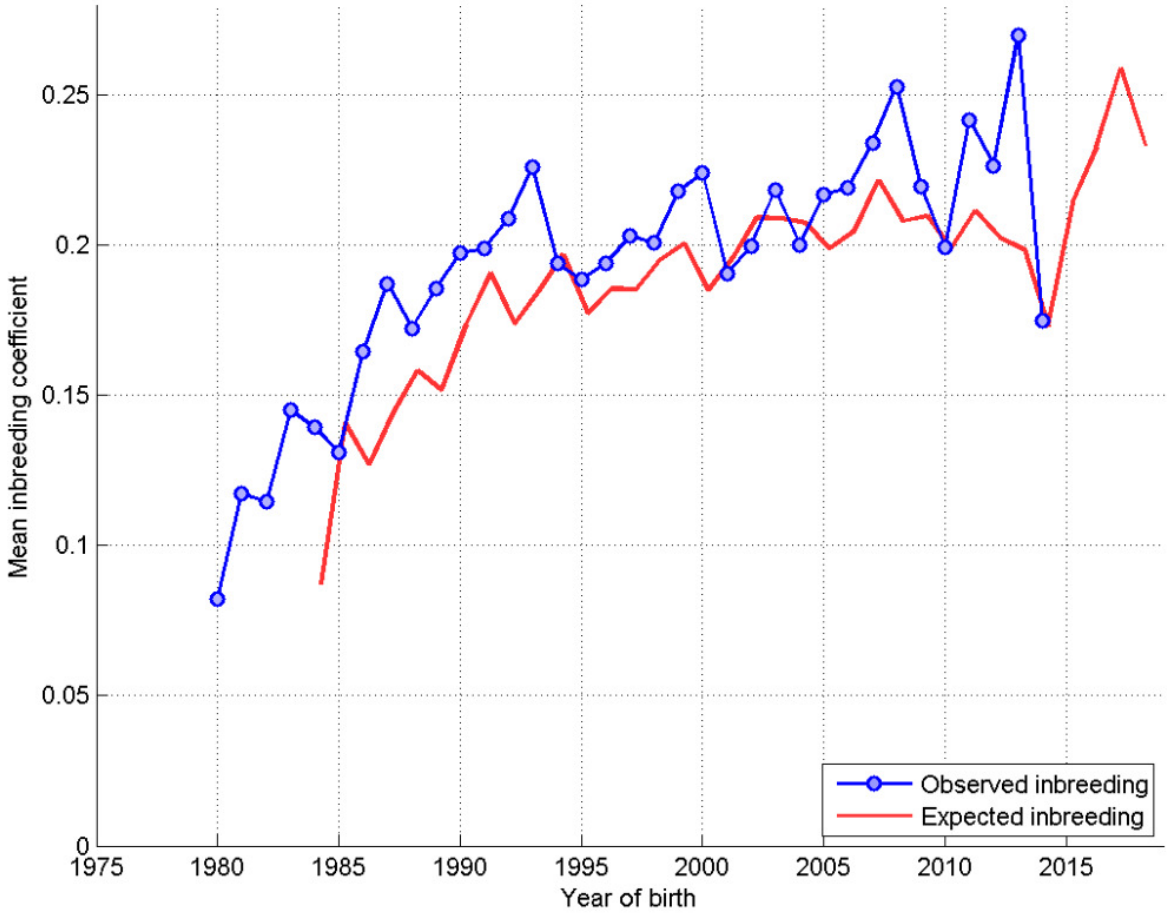
year	#born	#dams	#sires	puppies per sire					%puppies sired by most prolific sires			
				max	median	mode	mean	sd	50% sires	25% sires	10% sires	5% sires
1980	19	14	10	5	1.5	1	1.9	1.29	73.68	52.63	26.32	26.32
1981	58	13	10	16	3.5	3	5.8	4.92	79.31	63.79	27.59	27.59
1982	98	24	16	20	4	1	6.13	5.91	83.67	60.2	37.76	20.41
1983	66	14	13	10	5	1	5.08	2.96	77.27	40.91	15.15	15.15
1984	114	30	19	12	5	3	6	3.71	78.07	48.25	20.18	10.53
1985	71	17	15	14	4	4	4.73	3.08	71.83	46.48	29.58	19.72
1986	126	25	16	21	6.5	9	7.88	5.06	73.81	46.83	27.78	16.67
1987	99	22	17	20	5	2	5.82	4.8	80.81	50.51	32.32	20.2
1988	114	27	23	12	4	3	4.96	3.01	73.68	49.12	20.18	10.53
1989	102	22	18	12	5	5	5.67	2.66	65.69	45.1	21.57	11.76
1990	108	25	19	17	4	2	5.68	4.57	79.63	54.63	30.56	15.74
1991	131	28	22	15	5	3	5.95	3.95	77.1	50.38	21.37	11.45
1992	103	22	20	10	5.5	6	5.15	2.78	71.84	41.75	18.45	9.71
1993	109	23	19	17	5	5	5.74	3.97	75.23	49.54	26.61	15.6
1994	111	25	17	21	6	7	6.53	4.67	74.77	45.05	29.73	18.92
1995	94	20	15	16	6	3	6.27	4.53	82.98	52.13	29.79	17.02
1996	99	21	18	10	6	6	5.5	2.77	69.7	44.44	20.2	10.1
1997	121	22	19	14	6	1	6.37	4.11	77.69	47.93	23.14	11.57
1998	76	16	11	15	5	4	6.91	4.18	76.32	50	19.74	19.74
1999	81	21	17	13	4	5	4.76	3.31	77.78	48.15	28.4	16.05
2000	82	21	16	15	5	1	5.13	4.03	80.49	50	31.71	18.29
2001	83	19	16	16	4	2	5.19	4.04	77.11	51.81	33.73	19.28
2002	66	18	13	11	4	4	5.08	3.35	78.79	45.45	16.67	16.67
2003	90	18	13	15	6	2	6.92	5.16	85.56	45.56	16.67	16.67
2004	82	17	16	11	5.5	1	5.13	3.3	75.61	43.9	25.61	13.41
2005	85	19	16	15	4.5	1	5.31	4.17	81.18	51.76	30.59	17.65
2006	84	18	14	16	4.5	1	6	4.79	80.95	58.33	19.05	19.05
2007	60	15	14	12	2.5	2	4.29	3.58	81.67	60	20	20
2008	78	20	19	11	4	1	4.11	3.16	84.62	52.56	25.64	14.1
2009	69	17	14	14	4.5	2	4.93	3.36	73.91	52.17	20.29	20.29
2010	57	21	17	11	2	1	3.35	2.94	84.21	54.39	31.58	19.3
2011	51	15	13	9	3	1	3.92	3.07	84.31	49.02	17.65	17.65
2012	45	11	10	10	4.5	1	4.5	3.31	80	55.56	22.22	22.22
2013	41	8	7	13	5	1	5.86	4.63	n/a	n/a	n/a	n/a
2014	65	10	6	21	11	1	10.83	6.55	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) = 4.12

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



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 = 32.0

NB - this estimate is made using the rate of inbreeding over the whole period 1980-2014

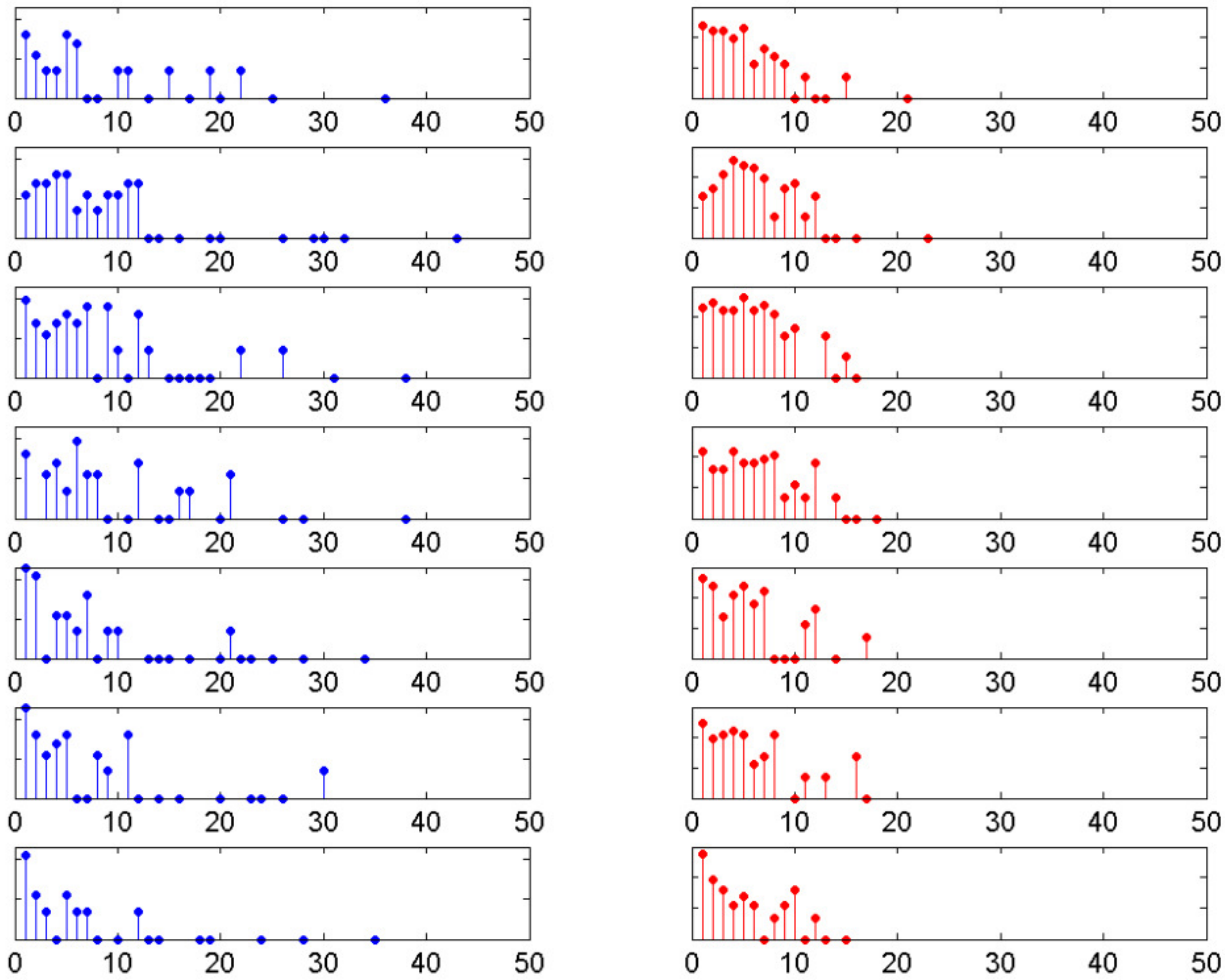
Table 2: a breakdown of census statistics, sire and dam usage and indicators of the rate of loss of genetic diversity over 5 year periods (1980-4, 1985-9, 1990-4, 1995-9, 2000-4, 2005-9, 2010-14). Rate of inbreeding and estimated effective population size for each 5-year block can be compared with the 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	71	102.4	112.4	94.2	80.6	75.2	51.8
Total #sires	38	52	61	46	49	48	32
Max #progeny	36	43	38	38	34	30	35
Mean #progeny	9.3158	9.7692	9.1803	10.109	8.2041	7.8125	8.0625
Median #progeny	6	7.5	7	7	5	5	5
Mode #progeny	1	4	1	6	1	1	1
SD #progeny	8.24	8.7663	7.7942	8.1	8.3641	7.9054	8.6246
Skew #progeny	1.2455	1.8453	1.5537	1.3067	1.314	1.4633	1.5505
Total #dams	69	81	99	73	77	69	54
Max #progeny	21	23	16	18	17	17	15
Mean #progeny	5.1304	6.3086	5.6566	6.411	5.2208	5.4348	4.7778
Median #progeny	4	5	5	6	5	4	3
Mode #progeny	1	4	5	1	1	1	1
SD #progeny	3.9702	3.8067	3.5604	4.0887	3.9022	4.2478	3.97
Skew #progeny	1.5163	1.413	0.85938	0.65409	1.0792	1.2076	0.79061
Rate of inbreeding	0.063824	0.053016	0.011361	0.039484	-0.01008	0.02096	-0.00785
Generation interval	4.0033	3.841	4.4685	4.8386	3.8864	4.0964	3.6235
Effective pop size	7.8341	9.431	44.011	12.663	n/a	23.854	n/a

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.



Comments

As can be seen from figure 1, the number of animals of this breed registered with the Kennel Club is very small. 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. 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 mid-1990s the rate of inbreeding has declined implying a slowdown in the rate of loss of genetic diversity (possibly through the use of imported animals).

There appears to be moderate 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.