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September 2015

Population analysis of the *Spaniel (Clumber)* breed

Genetic analysis of the Kennel Club pedigree records of the UK *Spaniel (Clumber)* 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 (Clumber)* population, and statistics were calculated for the period 1980-2014.



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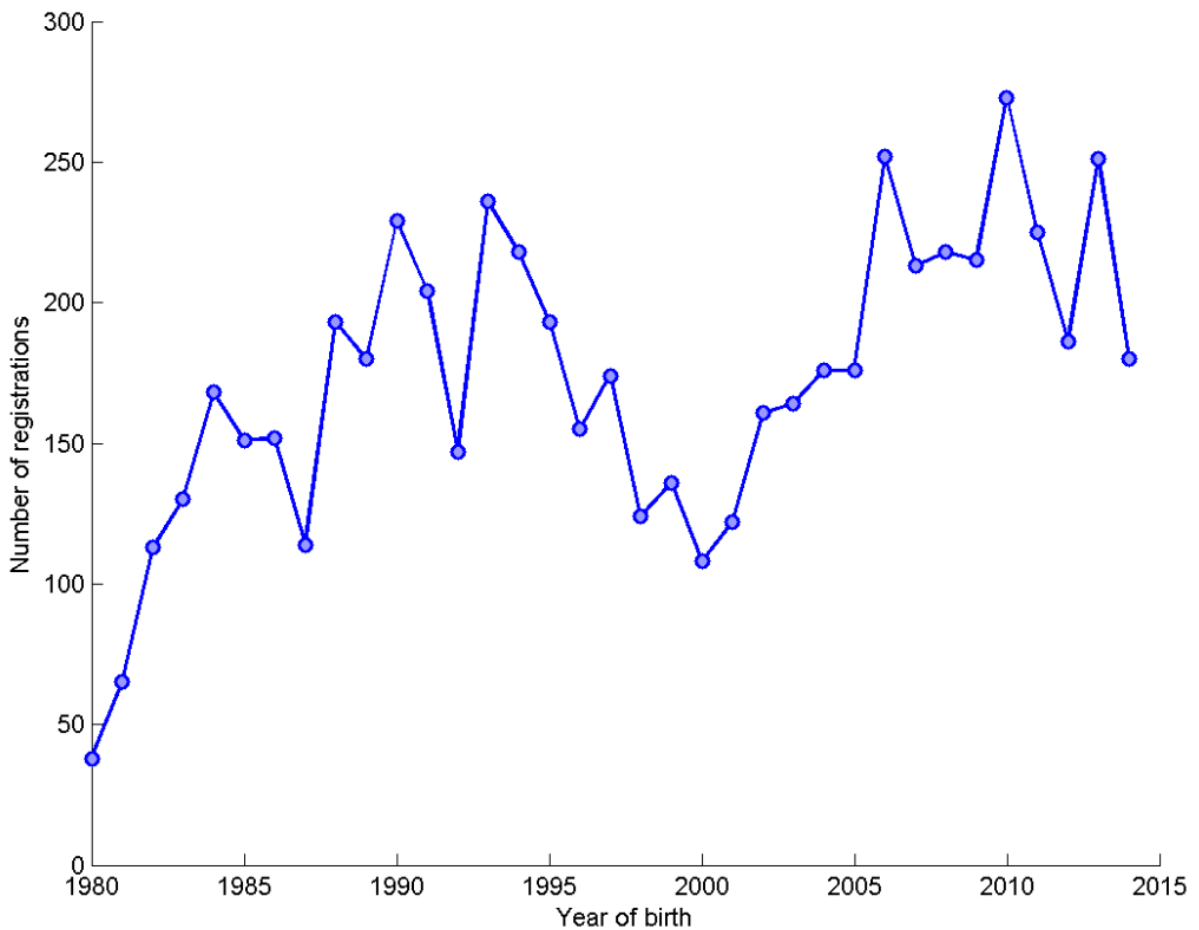
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Figure 1: a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

Breed: *Spaniel (Clumber)*

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = 2.99 per year (with a 95% confidence interval of 1.53 to 4.46).



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	38	20	15	5	2	2	2.53	1.19	71.05	42.11	23.68	13.16
1981	65	15	12	15	4.5	1	5.42	3.9	75.38	49.23	23.08	23.08
1982	113	24	13	30	5	3	8.69	8.16	84.07	54.87	26.55	26.55
1983	130	28	19	24	5	1	6.84	6	80.77	56.92	33.08	18.46
1984	168	31	21	14	7	3	8	3.78	72.02	38.69	16.67	8.33
1985	151	29	16	35	7	1	9.44	8.85	82.78	56.29	35.76	23.18
1986	152	26	18	32	6	4	8.44	7.41	75	55.92	35.53	21.05
1987	114	29	18	19	5	1	6.33	5.51	84.21	60.53	29.82	16.67
1988	193	38	22	45	6	2	8.77	9.51	78.24	59.59	35.23	23.32
1989	180	34	22	21	7	7	8.18	5.7	75	52.78	22.22	11.67
1990	229	40	24	48	6.5	6	9.54	10.1	76.86	57.64	31	20.96
1991	204	36	17	48	8	4	12	11.78	81.86	58.82	35.78	23.53
1992	147	28	20	16	7.5	4	7.35	4.33	73.47	44.22	21.09	10.88
1993	236	44	22	42	7.5	5	10.73	9.66	76.27	57.2	31.78	17.8
1994	218	40	25	30	8	6	8.72	6.41	75.23	48.17	30.73	13.76
1995	193	40	18	39	7	6	10.72	8.72	74.09	54.4	32.64	20.21
1996	155	32	25	15	6	7	6.2	3.85	75.48	45.16	26.45	9.68
1997	174	33	20	22	7	6	8.7	6.1	75.29	51.15	24.71	12.64
1998	124	28	27	9	5	2	4.59	2.78	78.23	45.97	21.77	7.26
1999	136	30	19	34	5	1	7.16	7.83	87.5	61.03	35.29	25
2000	108	21	17	20	5	5	6.35	5.05	76.85	51.85	33.33	18.52
2001	122	30	21	17	5	1	5.81	4.74	82.79	51.64	27.05	13.93
2002	161	35	23	19	6	2	7	5.52	81.99	54.66	22.98	11.8
2003	164	32	22	26	7	1	7.45	5.85	75.61	51.22	27.44	15.85
2004	176	32	24	27	5.5	1	7.33	7.15	84.66	60.8	27.27	15.34
2005	176	36	23	32	5	1	7.65	7.44	83.52	60.8	28.98	18.18
2006	252	47	32	27	6	1	7.88	7.33	80.56	56.75	31.75	21.43
2007	213	43	30	27	5	1	7.1	6.6	83.57	61.5	30.05	22.07
2008	218	42	27	31	7	2	8.07	7.11	83.03	56.42	32.11	14.22
2009	215	47	31	26	6	2	6.94	6.1	81.86	54.42	30.7	23.26
2010	273	54	37	23	7	7	7.38	5.08	77.29	47.99	25.64	14.65
2011	225	54	43	23	5	1	5.23	4.26	79.56	51.56	25.33	15.56
2012	186	39	33	17	6	1	5.64	4.29	79.57	48.39	25.81	17.74
2013	251	53	34	22	5.5	3	7.38	6.07	80.88	56.97	25.1	17.13
2014	180	35	24	26	5.5	5	7.5	6.08	78.33	52.78	25.56	14.44

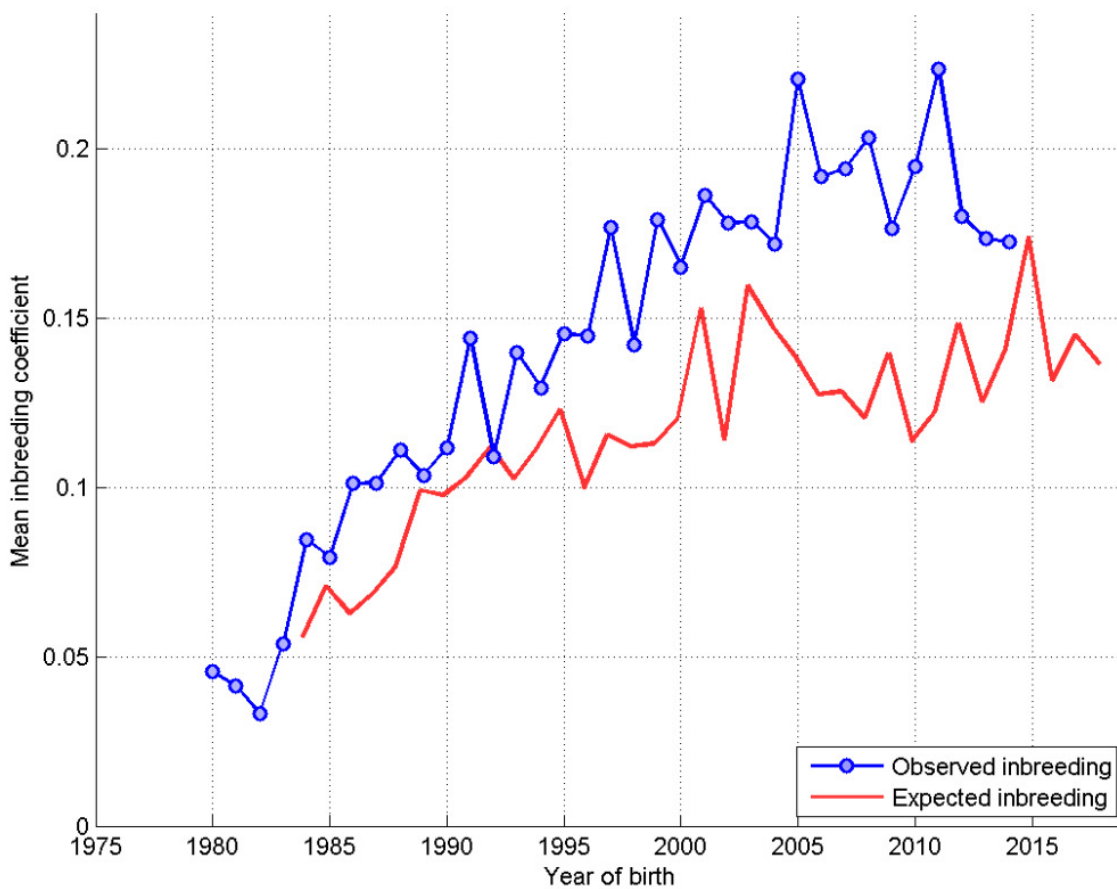


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 3.85

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 = 24.5

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	102.8	158	206.8	156.4	146.2	214.8	223
Total #sires	46	62	68	66	67	83	106
Max #progeny	64	115	83	59	63	63	57
Mean #progeny	11.174	12.742	15.206	11.848	10.91	12.94	10.519
Median #progeny	7	8	8	7.5	7	8	6
Mode #progeny	3	6	6	7	1	1	1
SD #progeny	12.351	17.648	17.419	11.328	11.615	16.092	11.429
Skew #progeny	2.5791	3.8887	2.126	1.7924	2.1403	1.9401	1.7598
Total #dams	88	118	143	124	111	151	185
Max #progeny	21	20	34	23	21	25	20
Mean #progeny	5.8409	6.6949	7.2308	6.3065	6.5856	7.1126	6.027
Median #progeny	5	6	6	6	6	6	5
Mode #progeny	3	6	6	1	1	1	5
SD #progeny	4.0255	4.5451	4.9967	4.3602	5.1088	5.2884	4.0839
Skew #progeny	1.4364	1.0138	1.8347	1.2198	0.98811	1.1092	1.1249
Rate of inbreeding	0.032063	0.022045	0.011472	0.027537	0.003048	-0.03993	-0.05784
Generation interval	3.339	3.4398	3.3138	3.5674	4.4384	4.1499	4.9066
Effective pop size	15.594	22.681	43.583	18.158	164.04	n/a	n/a



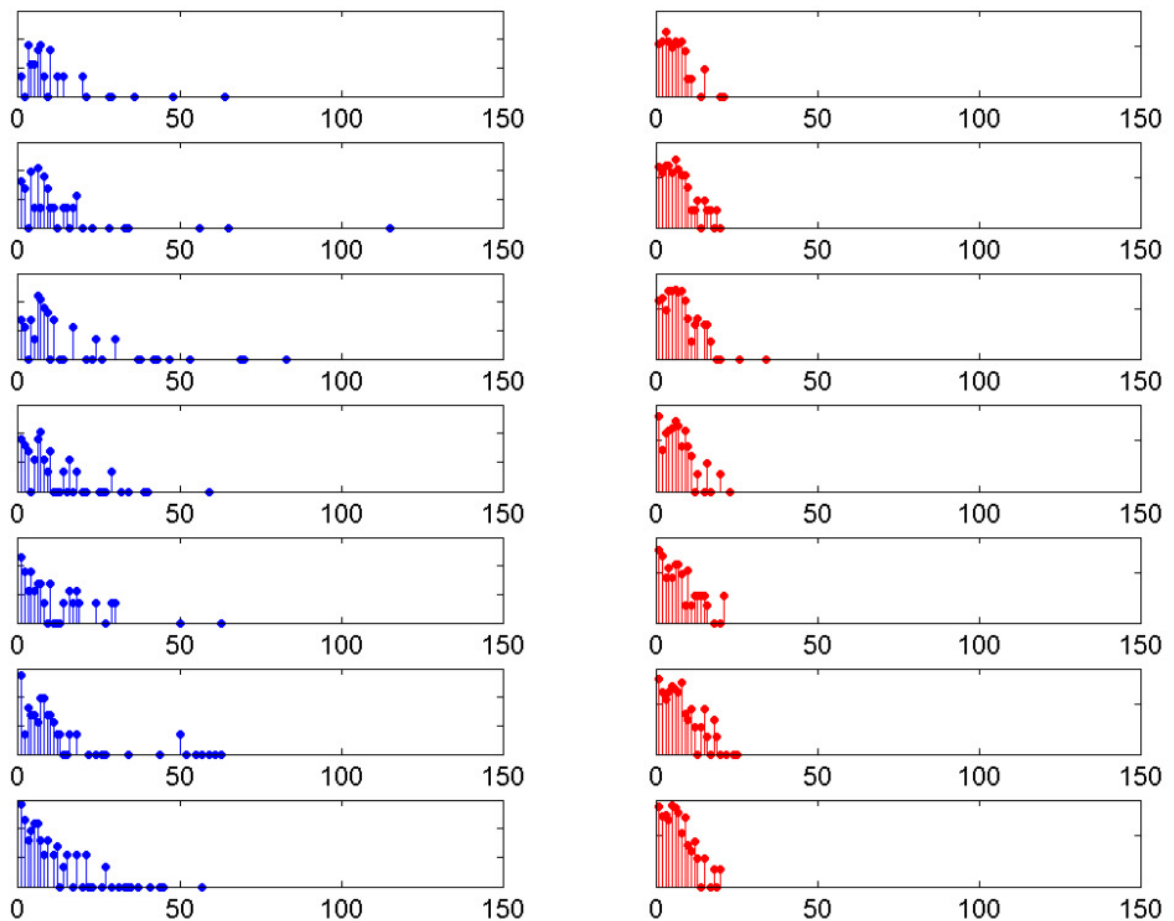
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number 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 2000 the rate of inbreeding has decreased, implying a slowdown in the rate of loss of genetic diversity (possibly through the use of imported animals).

It appears that the extensive use of popular dogs as sires has eased a little (the 'tail' of the blue distribution shortening 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.