Population analysis of the *Cavalier King Charles Spaniel* breed

Genetic analysis of the Kennel Club pedigree records of the UK *Cavalier King Charles Spaniel* 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 *Cavalier King Charles Spaniel* population, and statistics were calculated for the period 1980-2014.

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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: *Cavalier King Charles Spaniel*

Figure 1: Number of registrations by year of birth

Trend of registrations over year of birth (1980-2014) = -64.06 per year (with a 95% confidence interval of -172.36 to 44.24).

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	2006	1455	722	2.44	49	2	1	2.78	3.19	79.51	57.43	34.9
1981	7121	3109	1104	0.73	52	4	1	6.45	7.62	86.01	65.33	39.28
1982	9509	3660	1170	0.88	84	4	1	8.13	9.99	86.04	65.92	40.03
1983	10261	3931	1311	1	103	4	1	7.83	9.89	85.67	65.53	40.04
1984	10120	4017	1375	0.98	99	4	1	7.36	8.85	85.18	64.16	39.39
1985	9925	3969	1418	0.93	92	4	1	7	8.79	84.98	64.72	39.99
1986	9533	3830	1406	0.68	65	4	1	6.78	7.82	84.28	63.44	38.42
1987	9117	3572	1392	0.82	75	4	1	6.55	8.09	84.27	63.67	39.27
1988	9637	3603	1400	0.74	71	4	2	6.88	8.17	84.23	63.3	38.12
1989	15833	4105	1464	0.97	153	7	5	10.81	12.51	83.66	62.07	36.9
1990	15687	3832	1426	1.26	197	6	4	11	13.25	83.55	62.52	38.17
1991	15084	3683	1405	0.89	135	6	3	10.74	12.51	83.34	62.38	38.33
1992	13516	3344	1329	1.29	175	6	4	10.17	11.87	83.05	62.39	37.19
1993	13456	3269	1268	0.91	123	6	4	10.61	12.11	83.15	62.02	36.79
1994	14132	3496	1282	1.03	146	6	4	11.02	13.27	84.02	62.96	38.19
1995	14234	3480	1265	0.97	138	7	3	11.25	13.31	83.75	62.29	37.74
1996	14139	3479	1300	1.25	177	6	4	10.88	12.8	83.36	61.67	37
1997	13074	3285	1288	0.98	128	6	4	10.15	11.52	82.68	61.21	36.26
1998	12378	3079	1249	0.71	88	6	4	9.91	10.56	82.81	61.08	35.83
1999	11738	2906	1175	0.66	77	6	4	9.99	10.28	81.99	59.5	34.77
2000	10495	2706	1128	0.98	103	6	4	9.3	10.31	81.89	60.26	35.84
2001	10097	2524	1090	1.38	139	6	3	9.26	10.68	82.08	60.85	36.45
2002	10091	2575	1057	1	101	6	4	9.55	10.54	82.66	60.84	36.19
2003	10807	2694	1102	0.84	91	6	4	9.81	10.88	82.59	61.37	37.24
2004	10520	2635	1079	1.19	125	6	4	9.75	11.48	82.8	62.21	38.45
2005	11503	2793	1107	0.89	102	6	5	10.39	11.56	82.41	61.25	36.69
2006	11372	2839	1133	0.82	93	6	4	10.04	10.88	83.14	61.73	36.44
2007	11464	2842	1179	0.81	93	6	4	9.72	10.56	81.83	59.74	36.34
2008	10520	2655	1148	0.85	89	6	3	9.16	10.07	82.23	60.87	36.33
2009	8958	2265	1013	1.13	101	6	5	8.84	9.76	81.37	59.59	36.03
2010	7900	2019	914	1.11	88	5	4	8.64	9.81	82.49	61.49	36.85
2011	7048	1825	867	0.94	66	5	3	8.13	8.61	81.99	59.86	36.01
2012	5753	1424	700	1.55	89	5	4	8.22	8.61	79.75	58.07	35.04
2013	5218	1334	613	1.69	88	5	4	8.51	9.03	80.76	58.95	34.78
2014	4259	1046	486	1.88	80	6	4	8.76	9.36	80.84	60.06	36.3

> **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) = 3.50

> **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
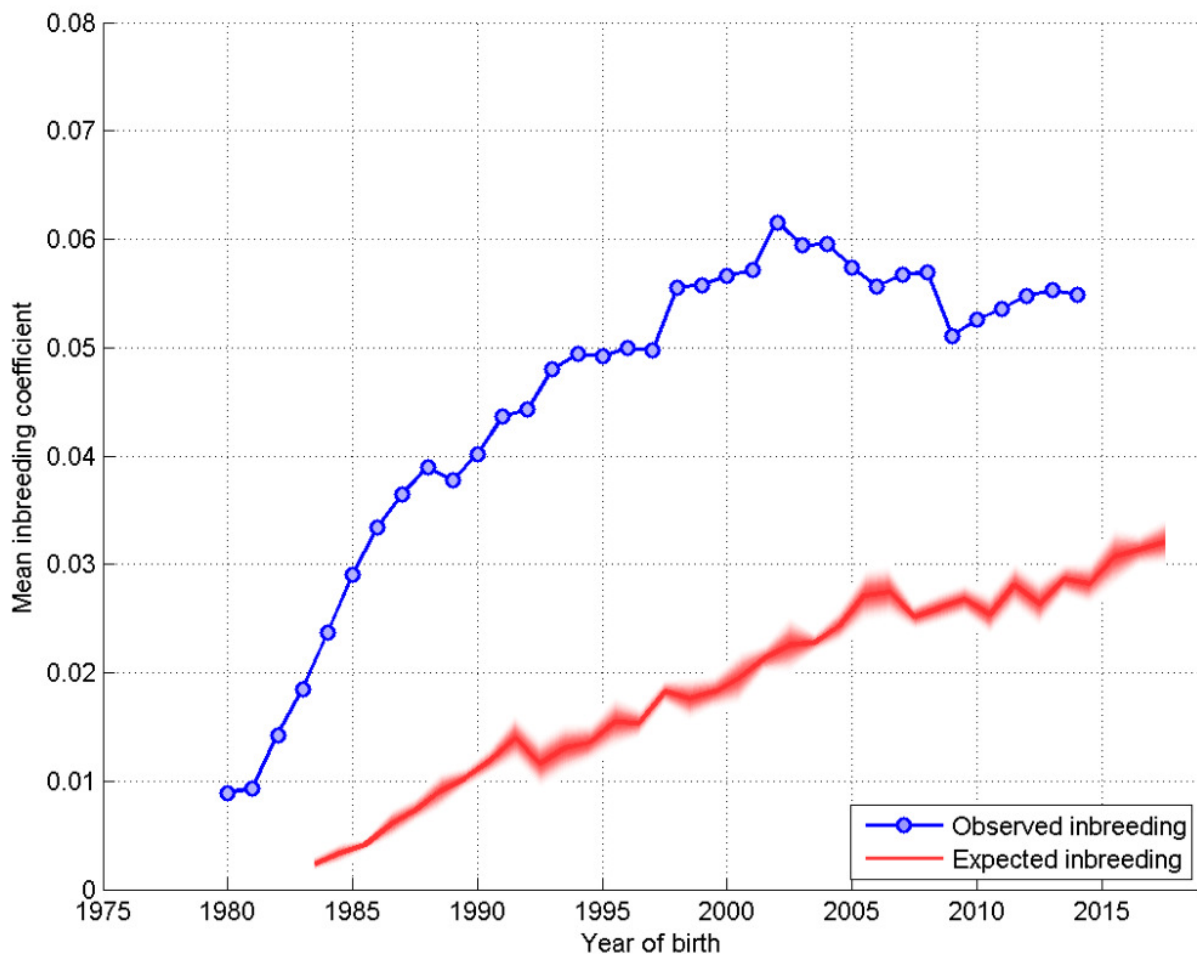
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Estimated effective population size: the rate of inbreeding (slope or steepness of the observed inbreeding in Figure 2) is used to estimate the effective population size of the breed. The effective population size is the number of breeding animals 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 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 = 111.2
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	7803.4	10809	14375	13113	10402	10763	6035.6
Total #sires	2816	3496	3390	3144	2763	2827	1905
Max #progeny	297	260	398	419	354	283	217
Mean #progeny	13.836	15.459	21.202	20.851	18.823	19.036	15.822
Median #progeny	5	6	9	9	9	9	7
Mode #progeny	1	1	4	4	4	4	4
SD #progeny	23.98	24.374	33.946	32.3	27.859	27.9	22.603
Skew #progeny	4.0512	3.7388	3.8646	4.2979	4.0259	3.55	3.474
Total #dams	10497	12269	11114	10134	8693	8751	5250
Max #progeny	28	28	43	44	34	32	28
Mean #progeny	3.7118	4.4049	6.467	6.4695	5.9829	6.1497	5.741
Median #progeny	3	4	5	5	5	5	5
Mode #progeny	1	2	4	4	4	4	4
SD #progeny	2.9901	3.327	4.8198	4.7142	4.1583	4.2729	3.9919
Skew #progeny	1.8445	1.5846	1.7554	1.5929	1.4984	1.3684	1.4382
Rate of inbreeding	0.011587	0.00762	0.008477	0.007093	0.003239	-0.00424	0.002554
Generation interval	2.9617	3.2372	3.5574	3.5719	3.7331	3.5636	3.8616
Effective pop size	43.15	65.62	58.986	70.495	154.39	n/a	195.79

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.
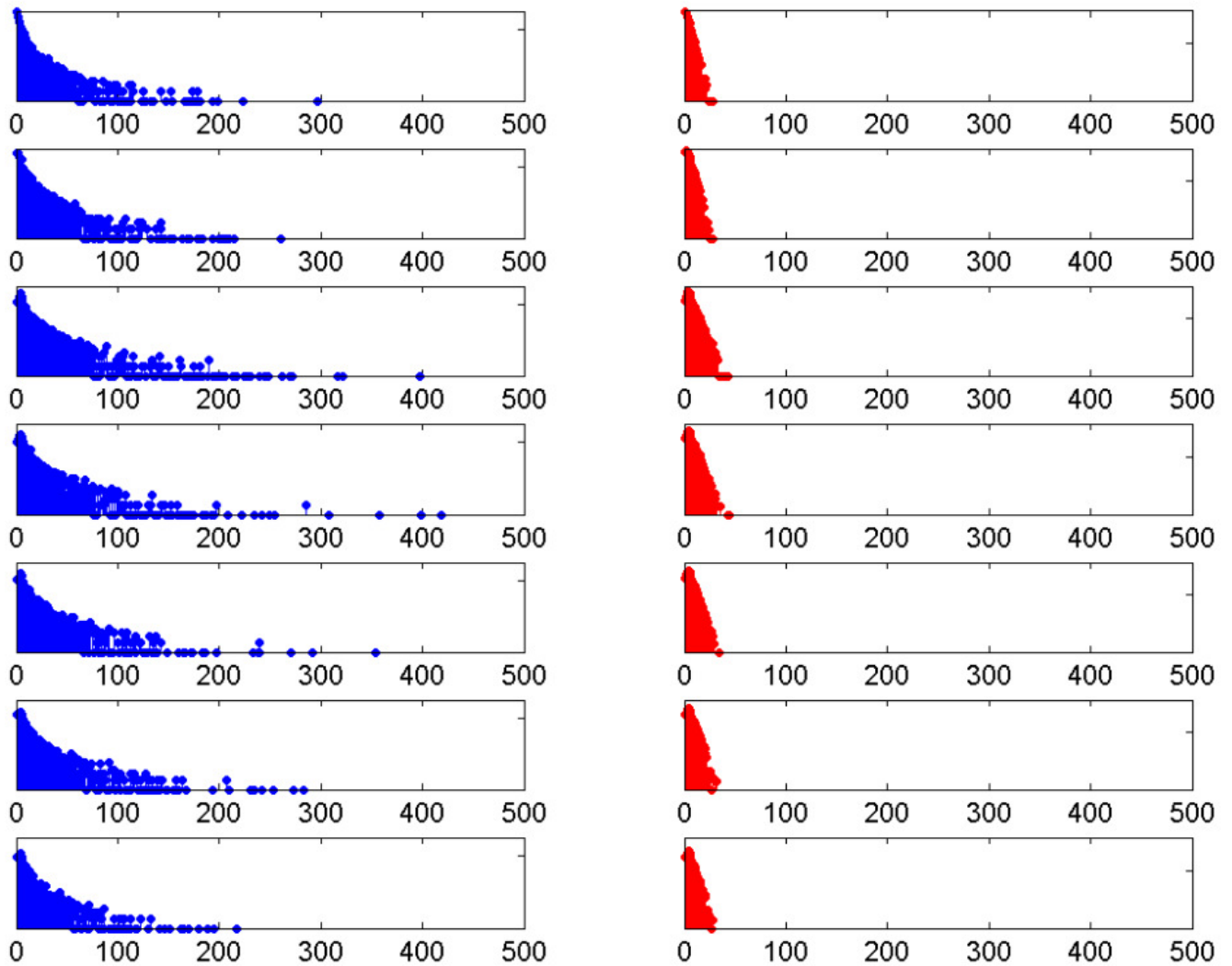
Comments

As 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.