Population analysis of the *Bearded Collie* breed

Genetic analysis of the Kennel Club pedigree records of the UK ***Bearded Collie*** 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 ***Bearded Collie*** population, and statistics were calculated for the period 1980-2014.

THE KENNEL CLUB
Making a difference for dogs

> **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: *Bearded Collie*

Figure 1: Number of registrations by year of birth
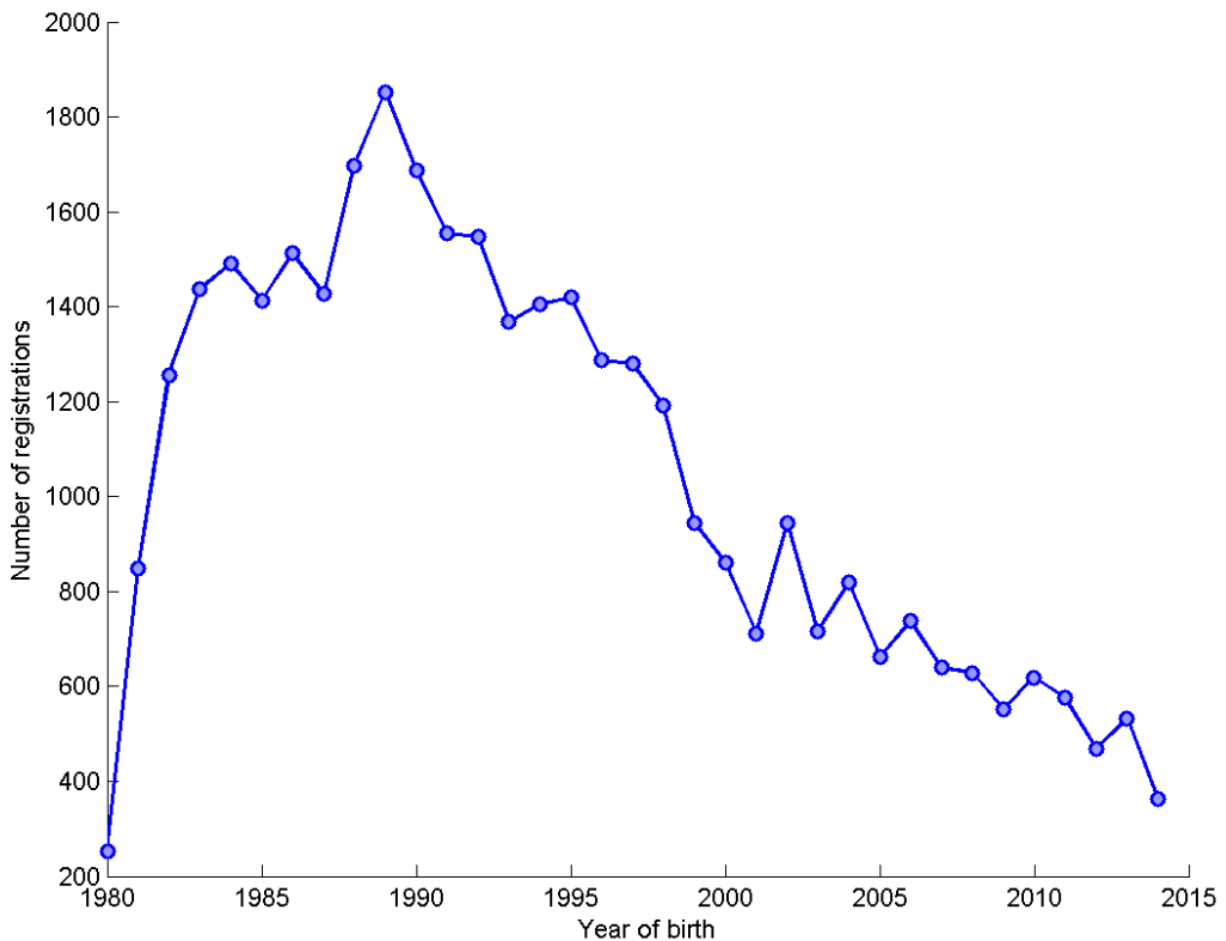
Trend of registrations over year of birth (1980-2014) = -29.09 per year (with a 95% confidence interval of -40.43 to -17.76).

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	253	156	94	13	2	1	2.69	2.39	79.45	56.13	30.43	19.76
1981	848	236	127	54	4	1	6.68	7.39	82.67	59.32	36.44	23
1982	1256	265	137	76	6	1	9.17	10.3	83.6	61.23	36.46	23.33
1983	1437	302	156	57	7	6	9.21	8.44	78.36	56.02	32.15	19.62
1984	1491	320	154	57	7	6	9.68	8.53	80.35	56.07	29.64	17.91
1985	1413	300	138	49	6	5	10.24	9.67	82.02	59.24	32.27	19.6
1986	1513	307	149	67	7	5	10.15	9.77	80.44	55.58	32.52	19.83
1987	1427	289	149	53	7	4	9.58	8.75	79.26	54.31	30.9	19.2
1988	1698	320	151	105	7	5	11.25	12.47	81.1	58.95	35.1	23.67
1989	1852	309	152	54	8	6	12.18	10.24	78.51	55.4	29.16	18.25
1990	1687	268	142	50	8	6	11.88	10.29	77.12	56.31	31.54	17.72
1991	1554	256	129	44	9	7	12.05	8.77	76.77	50.26	26.83	14.54
1992	1547	246	139	67	8	8	11.13	8.9	75.24	52.49	28.18	16.81
1993	1368	221	131	51	7	6	10.44	8.24	75.58	52.56	27.85	18.2
1994	1405	227	131	54	8	7	10.73	8.45	76.73	52.74	27.62	17.3
1995	1419	223	128	63	8	8	11.09	8.51	75.05	50.67	27.27	15.5
1996	1287	209	113	47	8	6	11.39	8.65	77.62	52.21	26.42	16.01
1997	1280	214	122	44	8	6	10.49	8.05	77.27	52.34	27.03	15.86
1998	1193	199	111	49	8	7	10.75	9.51	79.46	55.49	31.52	19.7
1999	945	163	96	67	7	6	9.84	10.02	78.73	56.83	35.03	23.07
2000	860	140	77	67	8	7	11.17	11.74	81.28	60.12	36.4	22.91
2001	712	130	90	50	7	6	7.91	7.34	75.98	52.39	32.02	22.75
2002	945	156	88	79	8	1	10.74	10.58	78.31	54.5	31.96	18.73
2003	717	129	80	42	7	1	8.96	7.88	79.08	54.67	30.54	18.69
2004	819	155	93	49	7	1	8.81	9.24	83.27	58.61	34.8	23.44
2005	662	128	82	36	6	1	8.07	7.62	80.36	58.91	32.18	18.43
2006	738	138	82	31	7	1	9	7.57	80.89	55.69	28.73	15.72
2007	639	127	85	74	6	1	7.52	9.38	85.29	59.94	36.78	22.85
2008	629	120	76	38	6	1	8.28	8.2	80.76	58.03	36.09	22.1
2009	552	112	70	28	7	1	7.89	6.8	81.7	56.7	29.35	19.02
2010	619	124	95	64	6	1	6.52	7.27	79.81	53.31	31.66	21.32
2011	576	124	81	33	6	1	7.11	7.01	85.94	59.55	32.81	18.23
2012	469	96	67	43	6	1	7	6.74	83.37	56.08	30.49	17.48
2013	532	109	82	28	6	1	6.49	5.48	80.83	53.57	28.01	16.92
2014	364	72	53	27	6	1	6.87	5.77	81.59	52.47	28.02	19.23

> **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) = 5.04

> **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
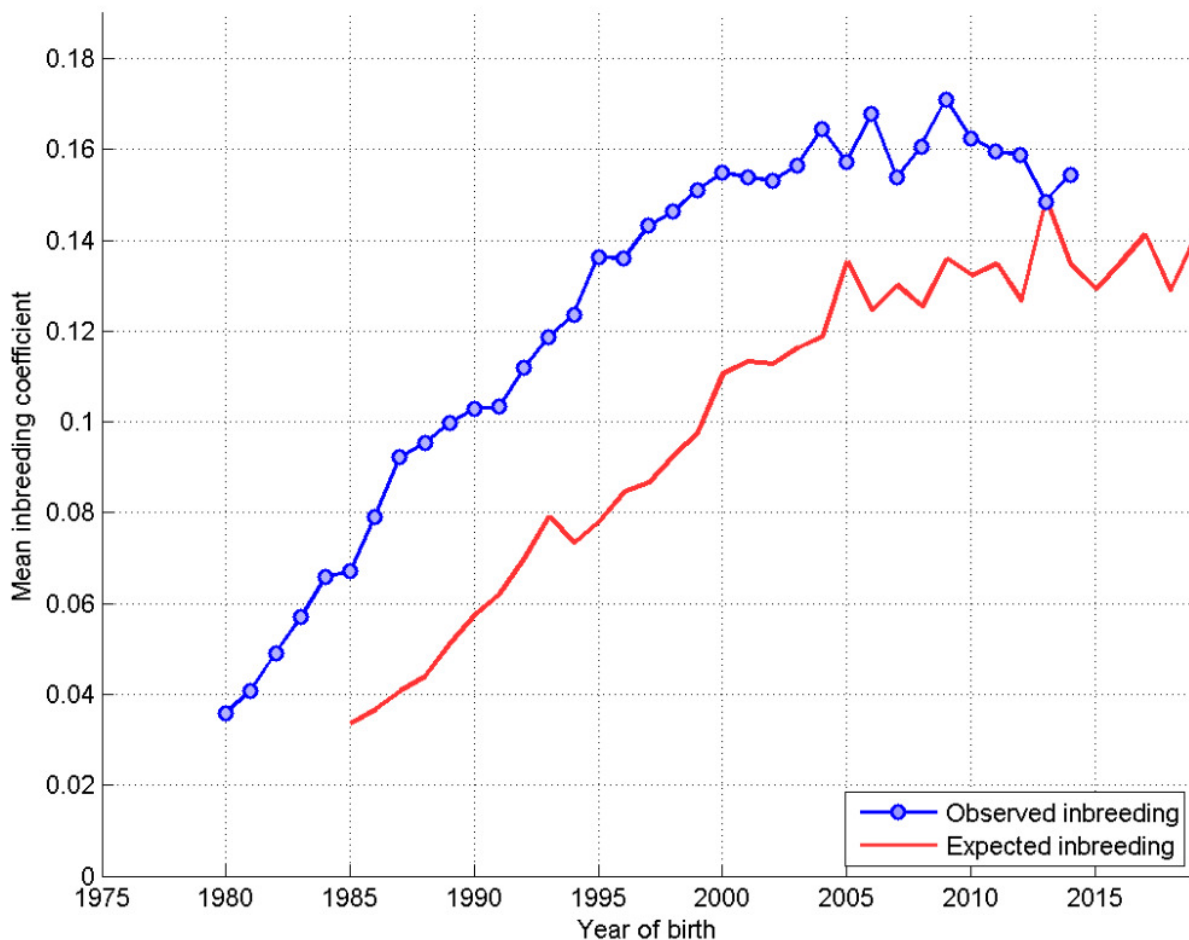
> **Estimated effective population size:** the rate of inbreeding (slope or steepness of the observed inbreeding in Figure 2) is used to estimate the effective population size of the breed. The effective population size is the number of breeding animals in an idealised, hypothetical population that would 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 = 23.9
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	1057	1580.6	1512.2	1224.8	810.6	644	512
Total #sires	345	367	342	300	242	241	232
Max #progeny	222	229	151	138	256	112	175
Mean #progeny	15.296	21.52	22.085	20.377	16.744	13.34	11.026
Median #progeny	7	10	11	11	8	6	6
Mode #progeny	1	6	7	7	1	1	1
SD #progeny	23.324	29.234	26.426	23.121	27.047	17.542	17.293
Skew #progeny	3.9318	3.0839	2.3167	2.1648	4.323	2.3954	4.8669
Total #dams	873	1058	837	720	525	468	416
Max #progeny	40	36	48	39	27	26	31
Mean #progeny	6.0447	7.4622	9.0251	8.5042	7.7162	6.8697	6.149
Median #progeny	5	6	7	7	7	6	6
Mode #progeny	1	7	7	7	7	1	1
SD #progeny	4.7566	5.3462	5.9413	5.6811	5.2569	5.2568	4.8128
Skew #progeny	1.6901	1.638	1.6513	1.4544	1.0378	1.1078	1.2867
Rate of inbreeding	0.035703	0.039773	0.032819	0.024548	0.013642	0.012755	-0.01777
Generation interval	4.473	4.4872	5.1285	5.2558	5.2206	5.2632	5.5349
Effective pop size	14.005	12.571	15.235	20.368	36.651	39.201	n/a

THE KENNEL CLUB
Making a difference for dogs

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.
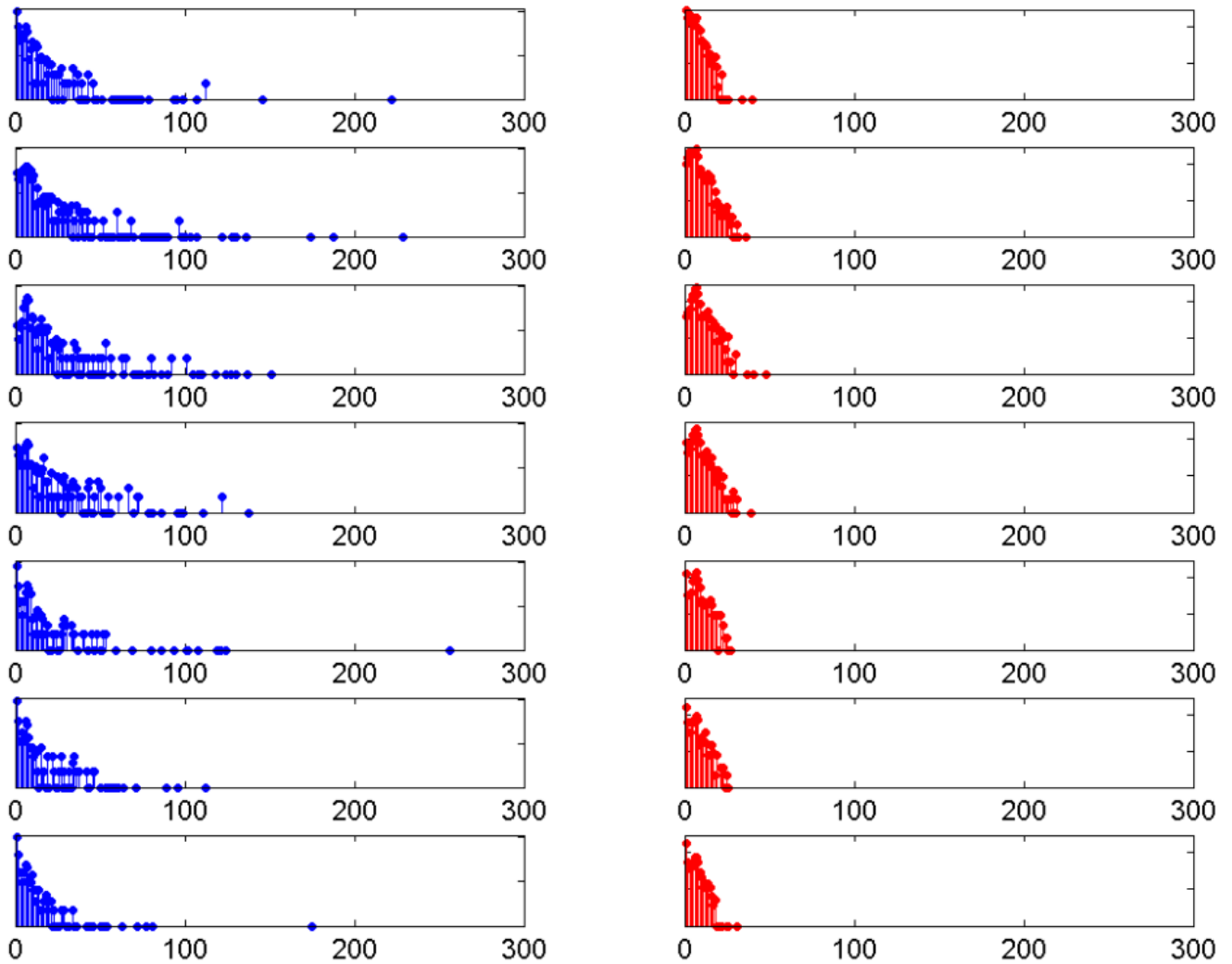
Comments

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).

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.