



**THE KENNEL CLUB**

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September 2015

### **Population analysis of the *Collie (Rough)* breed**

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

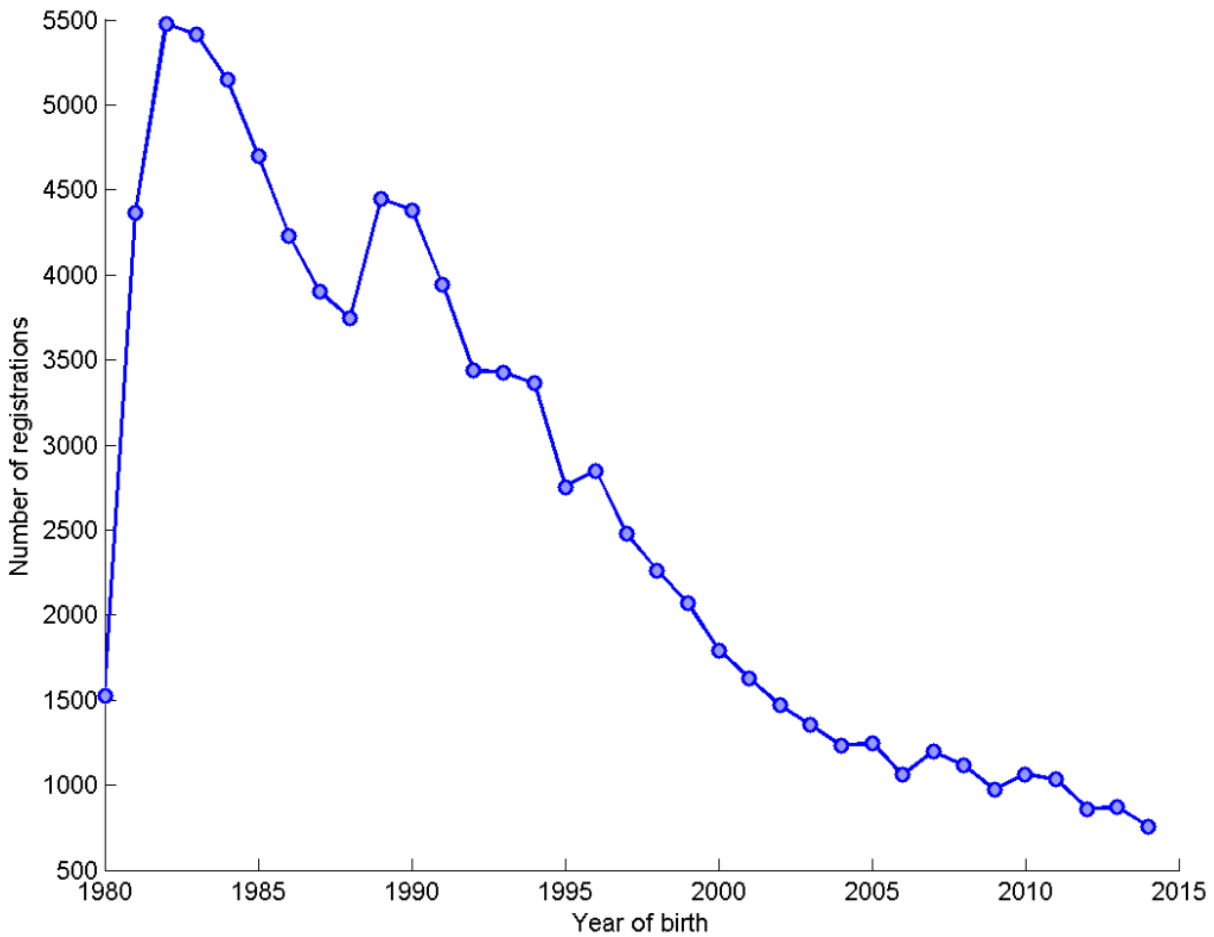
The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered ***Collie (Rough)*** population, and statistics were calculated for the period 1980-2014.



**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 (Rough)**

Figure 1: Number of registrations by year of birth



**Trend of registrations over year of birth (1980-2014) = -131.55 per year (with a 95% confidence interval of -156.44 to -106.66).**



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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	1523	1056	522	49	2	1	2.92	4.18	81.88	62.97	40.64	28.17
1981	4366	1670	728	171	3	1	6	10.68	85.71	67.59	46.01	32.52
1982	5476	1806	739	151	4	1	7.41	12.66	85.79	67.7	47.01	33.75
1983	5417	1715	713	134	4	1	7.6	11.99	86.49	67.09	44.82	32.43
1984	5146	1664	711	93	4	1	7.24	10.78	86.34	66.83	43.94	30.92
1985	4697	1509	694	78	4	2	6.77	8.96	84.25	65.21	42.18	28.25
1986	4232	1310	616	82	4	1	6.87	9.02	84.1	63.87	40.38	27.17
1987	3901	1213	540	106	4	2	7.22	10.49	85.47	66.14	42.86	29.43
1988	3744	1071	512	93	4	2	7.31	10.56	85.26	65.87	44.34	31.09
1989	4447	1036	505	102	6	6	8.81	11.24	81.81	61.68	40	26.85
1990	4381	946	465	94	6	5	9.42	10.74	82.13	61.7	36.98	23.76
1991	3942	838	401	66	6	5	9.83	9.96	80.59	58.37	34.2	21.99
1992	3440	731	378	63	6.5	5	9.1	9.16	80.38	57.59	34.07	22.15
1993	3423	729	378	65	6	5	9.06	9.44	80.22	59.48	36.05	22.58
1994	3365	702	349	75	6	5	9.64	9.42	80.56	58.04	33.31	19.76
1995	2753	587	309	63	6	5	8.91	9.13	80.06	58.37	35.2	21.07
1996	2850	605	326	113	6	7	8.74	10.49	79.96	58.53	35.23	23.51
1997	2478	539	311	72	6	3	7.97	8.8	79.14	56.42	34.06	23.65
1998	2261	478	258	93	6	4	8.76	10.25	79.88	58.96	36.71	24.68
1999	2068	430	235	54	6	6	8.8	8.98	78.87	57.83	35.44	23.16
2000	1794	396	212	70	6	6	8.46	8.72	78.82	56.02	33.67	22.69
2001	1625	351	191	44	6	1	8.51	7.56	80.8	56.68	30.28	18.65
2002	1469	319	179	41	6	1	8.21	7.37	80.26	56.77	31.38	18.45
2003	1355	295	168	43	6.5	1	8.07	6.75	78.82	53.65	28.86	16.75
2004	1231	271	165	36	6	6	7.46	6.47	78.8	54.51	31.36	18.12
2005	1246	290	166	42	5	1	7.51	7.1	81.78	58.91	32.34	18.46
2006	1061	256	159	65	5	1	6.67	7.61	83.22	59.85	35.53	22.71
2007	1198	285	151	94	5	1	7.93	10.15	84.97	63.44	37.23	25.63
2008	1115	250	138	55	6	1	8.08	8.12	83.86	60.36	33.27	19.37
2009	971	229	128	30	5	1	7.59	7.33	85.07	60.97	32.54	16.89
2010	1065	254	131	37	5	1	8.13	7.64	82.72	59.34	32.02	19.44
2011	1034	233	140	32	5.5	1	7.39	6.71	83.17	59.09	30.08	16.25
2012	861	220	131	45	5	1	6.57	6.66	84.2	57.84	32.98	22.18
2013	871	211	125	40	5	1	6.97	6.53	83.24	58.21	31.8	16.88
2014	758	168	107	32	5	1	7.08	6.43	81.4	56.6	32.06	18.21

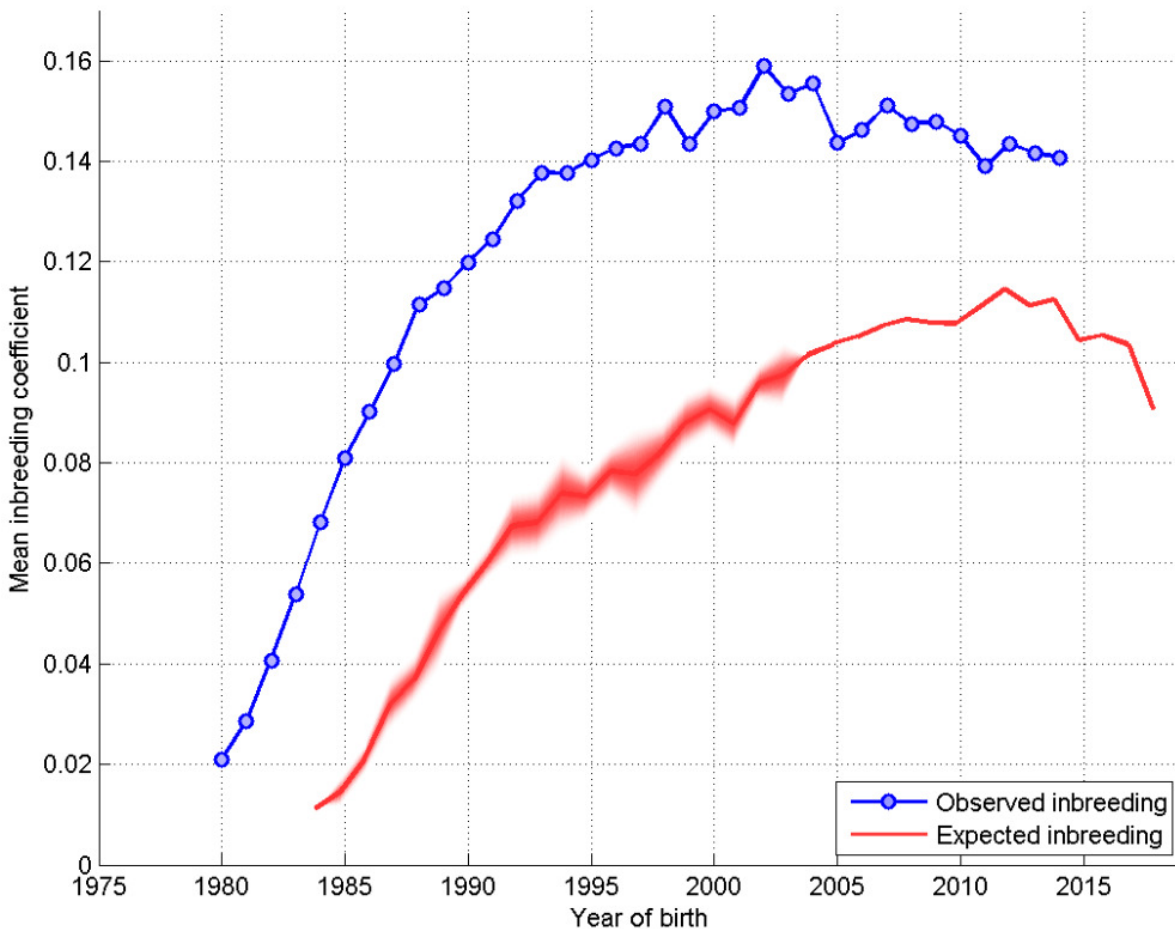


**Generation interval:** the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

**Mean generation interval (years) = 3.80**

**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 = 39.4**

*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.

<b>years</b>	<b>1980-1984</b>	<b>1985-1989</b>	<b>1990-1994</b>	<b>1995-1999</b>	<b>2000-2004</b>	<b>2005-2009</b>	<b>2010-2014</b>
Mean #registrations	4385.6	4204.2	3710.2	2482	1494.8	1118.2	917.8
Total #sires	1929	1589	1092	780	523	439	364
Max #progeny	470	379	259	327	134	206	133
Mean #progeny	11.348	13.228	16.987	15.908	14.289	12.733	12.604
Median #progeny	4	6	7	8	7	6	6
Mode #progeny	1	2	5	1	1	1	1
SD #progeny	27.792	26.95	26.475	24.784	19.667	19.537	17.45
Skew #progeny	8.5028	6.5268	3.9245	5.7357	3.0807	4.3834	2.7453
Total #dams	5834	4577	2882	1939	1270	980	846
Max #progeny	26	32	35	27	27	26	24
Mean #progeny	3.7521	4.5925	6.4365	6.3992	5.8843	5.7041	5.4232
Median #progeny	3	4	6	6	5	5	5
Mode #progeny	1	2	5	6	5	1	1
SD #progeny	2.9896	3.5309	4.4873	4.1514	3.9087	4.3536	3.9372
Skew #progeny	1.8006	1.6422	1.7102	1.3805	1.2834	1.3674	1.2895
Rate of inbreeding	0.038729	0.034559	0.022722	0.006593	0.006731	0.00476	-0.00266
Generation interval	3.1193	3.5252	4.0831	3.9006	4.0979	4.1001	3.7522
Effective pop size	12.91	14.468	22.005	75.836	74.281	105.05	n/a



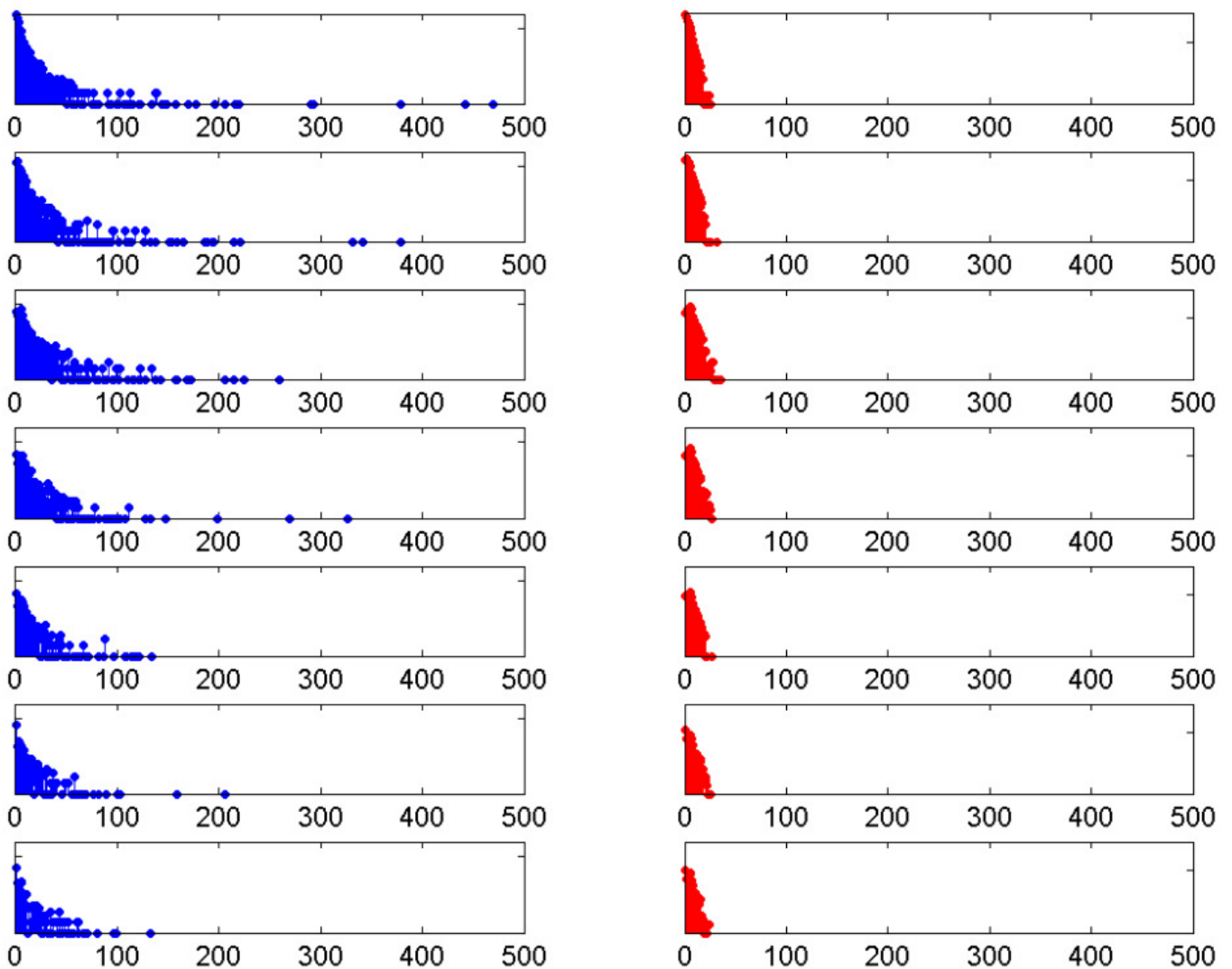
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**Figure 3:** a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large 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 slowed and even declined slightly, implying maintenance and even some possible replenishment 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.