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September 2015

### **Population analysis of the *Retriever (Curly Coated)* breed**

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



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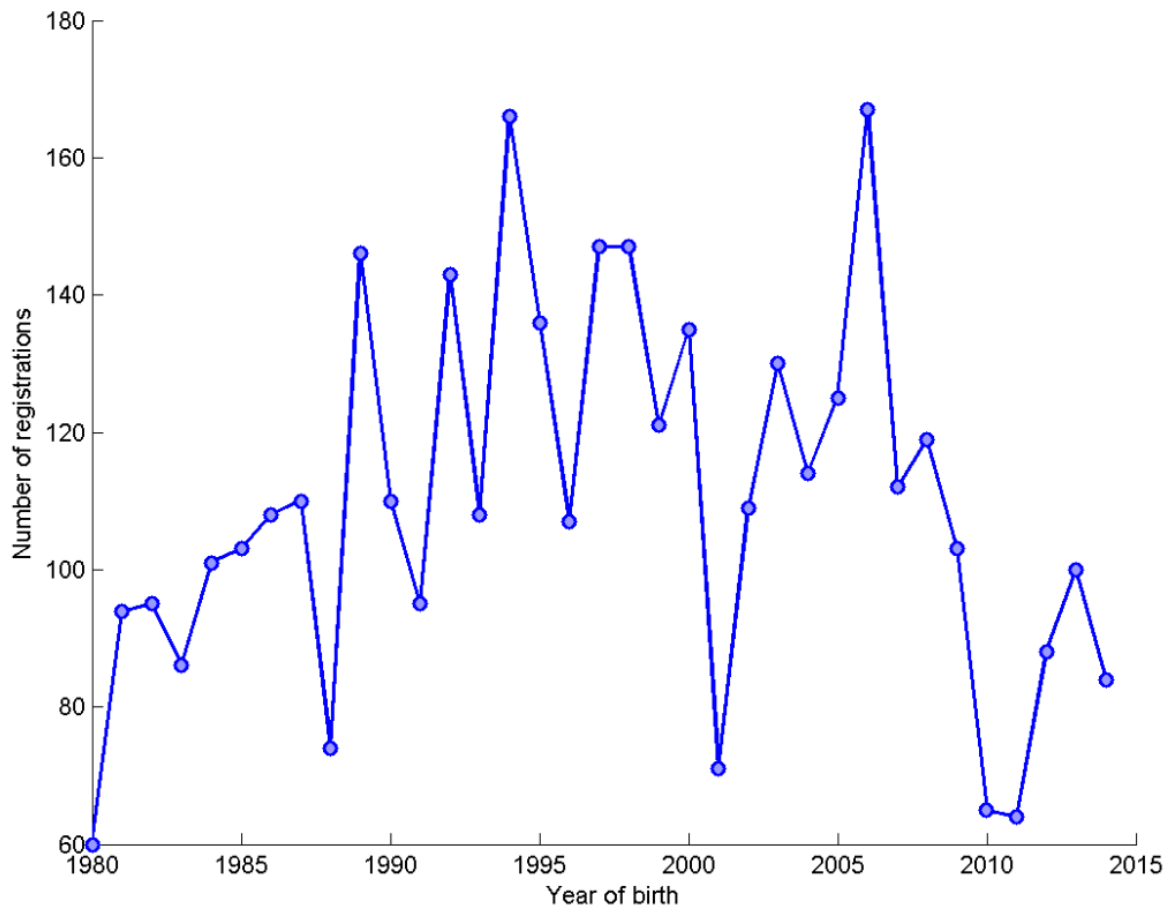
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September 2015

**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: Retriever (Curly Coated)**

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = 0.08 per year (with a 95% confidence interval of -0.88 to 1.03).



**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	60	17	12	17	4	2	5	4.37	76.67	53.33	28.33	28.33
1981	94	22	16	20	3.5	8	5.88	5.44	84.04	54.26	37.23	21.28
1982	95	19	16	13	5	5	5.94	3.64	72.63	46.32	26.32	13.68
1983	86	15	10	26	5.5	3	8.6	7.43	77.91	62.79	30.23	30.23
1984	101	22	17	13	5	5	5.94	3.47	74.26	44.55	24.75	12.87
1985	103	22	16	13	6.5	3	6.44	3.6	73.79	42.72	24.27	12.62
1986	108	20	13	31	5	4	8.31	8	83.33	52.78	28.7	28.7
1987	110	21	17	30	5	5	6.47	7.11	83.64	58.18	40.91	27.27
1988	74	19	16	12	3	2	4.63	3.76	82.43	55.41	31.08	16.22
1989	146	24	15	31	7	1	9.73	8.52	82.19	58.9	36.3	21.23
1990	110	18	12	20	8	1	9.17	6.07	75.45	46.36	18.18	18.18
1991	95	18	13	21	5	1	7.31	6.66	87.37	55.79	22.11	22.11
1992	143	24	21	13	8	9	6.81	4.04	78.32	41.96	17.48	9.09
1993	108	21	15	24	5	3	7.2	5.85	80.56	53.7	34.26	22.22
1994	166	24	19	31	8	9	8.74	5.91	69.88	43.98	26.51	18.67
1995	136	25	19	23	6	1	7.16	5.52	77.94	51.47	30.15	16.91
1996	107	19	13	22	8	1	8.23	5.93	80.37	43.93	20.56	20.56
1997	147	23	17	20	8	1	8.65	6.15	80.27	46.94	26.53	13.61
1998	147	25	19	28	8	1	7.74	6.23	79.59	50.34	28.57	19.05
1999	121	21	14	24	7.5	1	8.64	7.09	82.64	59.5	19.83	19.83
2000	135	22	15	21	8	1	9	6.6	81.48	54.07	30.37	15.56
2001	71	13	10	25	6	2	7.1	6.97	78.87	60.56	35.21	35.21
2002	109	22	14	13	9	9	7.79	3.72	66.97	42.2	11.93	11.93
2003	130	25	18	29	4	1	7.22	7.56	86.92	64.62	36.15	22.31
2004	114	22	14	22	5.5	1	8.14	7.22	82.46	64.04	19.3	19.3
2005	125	24	22	12	5.5	1	5.68	3.51	76.8	48	18.4	9.6
2006	167	29	21	24	7	1	7.95	5.87	79.04	47.9	23.95	14.37
2007	112	22	17	19	6	1	6.59	5.8	85.71	53.57	33.04	16.96
2008	119	22	18	14	8	1	6.61	4.33	75.63	47.06	22.69	11.76
2009	103	20	16	23	4.5	1	6.44	6.17	85.44	58.25	35.92	22.33
2010	65	13	11	13	7	1	5.91	4.46	87.69	50.77	20	20
2011	64	14	12	14	3	1	5.33	5.05	89.06	57.81	21.88	21.88
2012	88	16	12	22	7.5	1	7.33	6.01	79.55	48.86	25	25
2013	100	18	12	36	5	1	8.33	9.78	86	62	36	36
2014	84	13	13	12	6	1	6.46	4.05	77.38	41.67	14.29	14.29

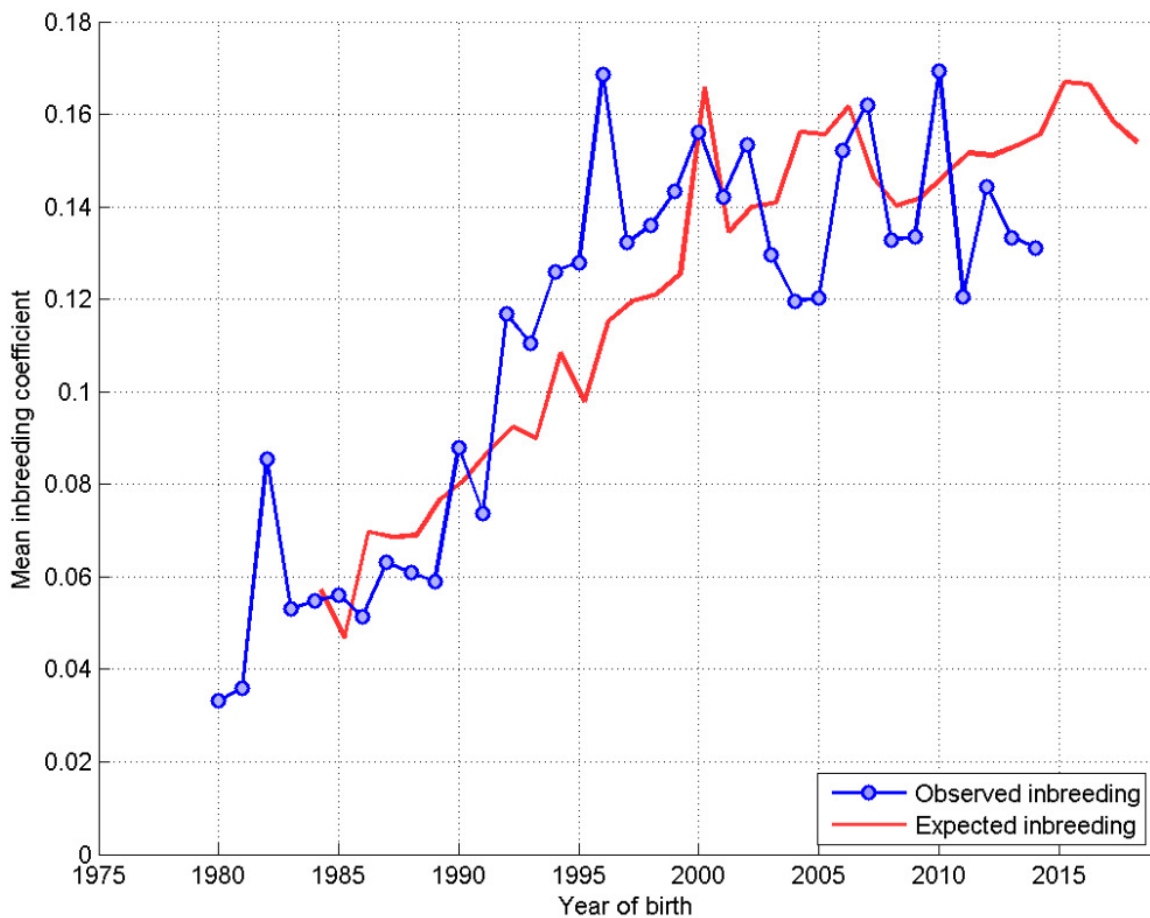


**Generation interval:** the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

**Mean generation interval (years) = 4.24**

**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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September 2015

**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 = 32.7**

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



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September 2015

**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	87.2	108.2	124.4	131.6	111.8	125.2	80.2
Total #sires	45	45	49	50	47	67	38
Max #progeny	29	53	55	52	48	55	50
Mean #progeny	9.6667	12	12.673	13.12	11.872	9.3284	10.526
Median #progeny	7	6	9	12.5	8	7	7.5
Mode #progeny	4	2	1	1	1	1	1
SD #progeny	7.9943	14.142	10.264	10.528	12.247	10.738	11.145
Skew #progeny	1.1143	1.796	1.6192	1.2083	1.5749	2.1373	1.8361
Total #dams	67	76	73	79	87	92	59
Max #progeny	32	35	29	25	21	24	29
Mean #progeny	6.4925	7.1053	8.5068	8.3038	6.4138	6.6304	6.7797
Median #progeny	4	6	8	8	6	6	6
Mode #progeny	4	2	9	9	7	1	1
SD #progeny	6.0236	5.7447	6.3358	5.8449	4.4344	5.3385	5.6723
Skew #progeny	1.8026	2.0572	1.4444	1.044	1.109	1.0773	1.533
Rate of inbreeding	0.024948	0.0063414	0.049243	-0.0012484	-0.043926	0.0033965	-0.040747
Generation interval	3.9775	3.8461	3.9395	4.2561	4.4096	4.3287	5.393
Effective pop size	20.042	78.847	10.154	n/a	n/a	147.21	n/a



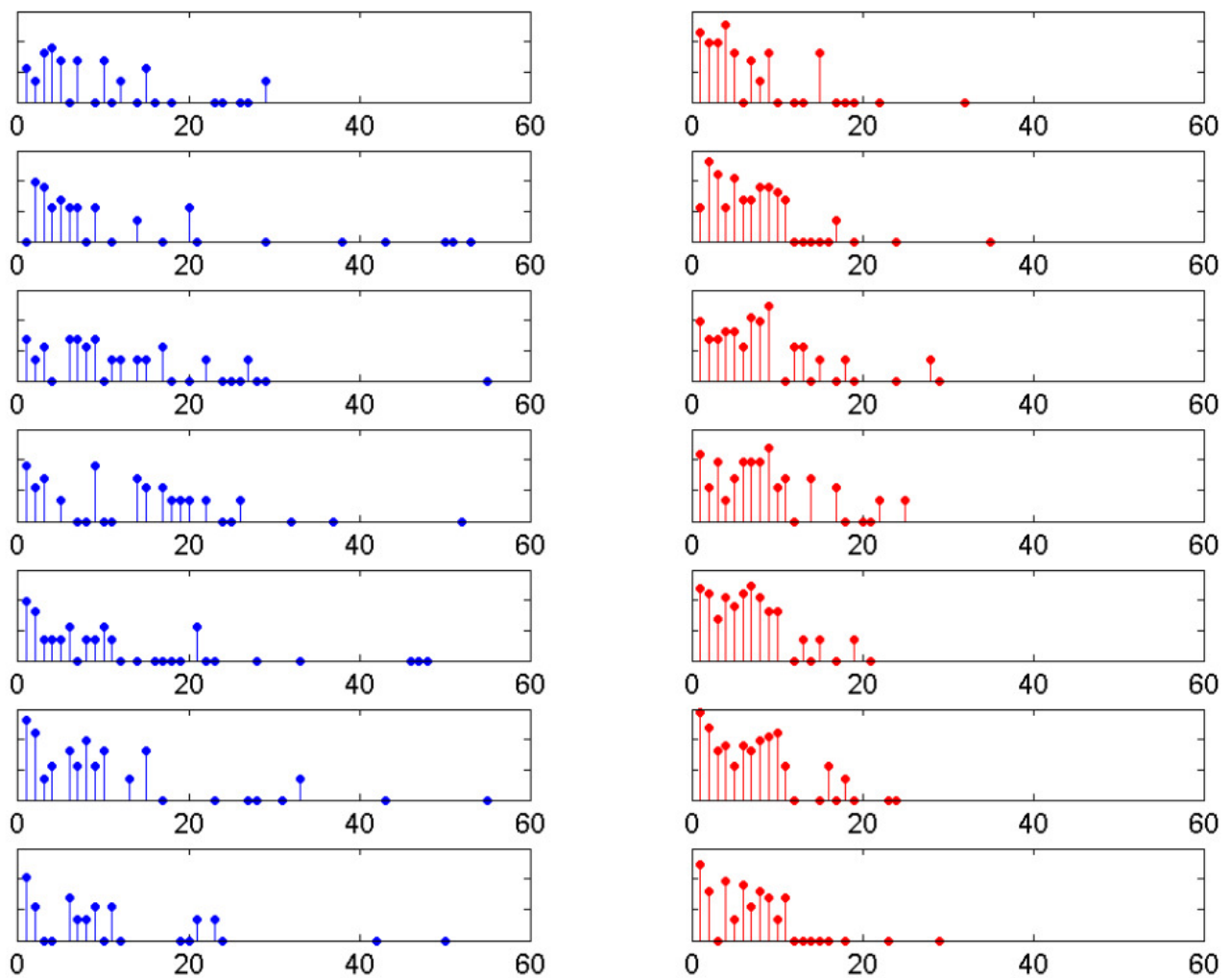
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**Figure 3:** a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large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