Population analysis of the *Retriever (Flat Coated)* breed

Genetic analysis of the Kennel Club pedigree records of the UK ***Retriever (Flat 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 (Flat Coated)*** 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: *Retriever (Flat Coated)*

Figure 1: Number of registrations by year of birth
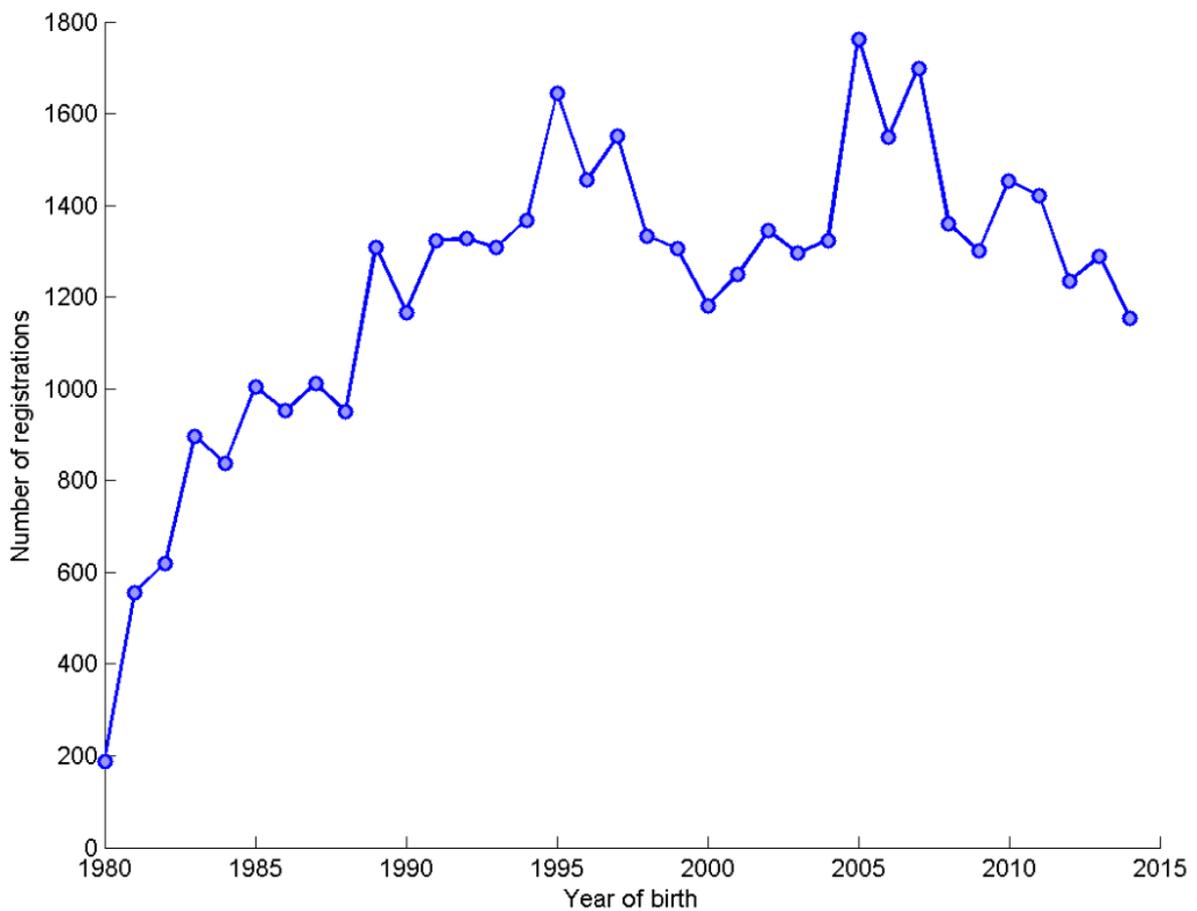
Trend of registrations over year of birth (1980-2014) = 21.30 per year (with a 95% confidence interval of 13.01 to 29.59).

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	187	85	57	21	2	1	3.28	3.8	85.03	63.1	38.5	25.13
1981	556	121	77	44	5	3	7.22	7.83	81.83	58.81	37.41	23.92
1982	620	111	67	36	8	1	9.25	7.53	79.19	52.74	29.84	15.81
1983	897	167	86	65	7	4	10.43	10.57	81.49	59.75	35.12	19.51
1984	837	145	83	44	8	8	10.08	8.18	78.73	53.88	27.96	16.01
1985	1003	179	98	49	7	4	10.23	9.53	78.27	56.53	34.1	20.64
1986	953	179	99	86	6	4	9.63	11.35	81.64	60.55	37.57	24.45
1987	1011	176	96	60	7.5	6	10.53	9.68	80.32	55.79	30.86	19.29
1988	950	169	90	59	7	3	10.56	11.14	82.42	62	35.89	23.68
1989	1309	195	111	73	8	7	11.79	11.43	78.76	56.76	33.23	22.31
1990	1167	178	119	52	8	10	9.81	8.78	76.69	52.78	32.31	20.22
1991	1322	183	110	71	8	7	12.02	11.77	76.4	56.81	34.11	23.45
1992	1328	183	108	79	9	9	12.3	12.9	75.6	55.87	37.05	22.89
1993	1309	178	96	70	10	9	13.64	12.14	77.31	54.09	31.86	20.7
1994	1368	195	109	50	10	6	12.55	9.91	78.36	51.83	28.22	15.72
1995	1644	221	118	66	9	9	13.93	12.58	77.25	57.73	32.06	18.49
1996	1455	192	110	102	9	6	13.23	13.94	77.53	57.46	35.53	23.99
1997	1550	212	127	79	9	9	12.2	11.7	78.19	56.77	33.03	19.42
1998	1333	185	109	58	9	1	12.23	11.9	80.65	58.21	35.11	18.3
1999	1305	187	113	43	9	9	11.55	8.89	77.24	52.87	26.36	15.94
2000	1181	161	105	51	9	9	11.25	8.85	74.51	51.48	29.64	17.02
2001	1249	180	108	54	8	1	11.56	12	82.55	60.45	37.07	20.26
2002	1344	197	121	51	9	1	11.11	9.49	80.06	54.76	28.79	16.96
2003	1295	184	114	88	9	7	11.36	11.54	76.14	52.59	30.35	22.24
2004	1324	196	121	58	9	1	10.94	11.35	82.85	59.21	35.88	21.75
2005	1763	251	136	70	9	1	12.96	12.89	81.34	59.56	34.54	21.21
2006	1549	221	137	64	9	1	11.31	9.93	80.12	54.29	29.76	18.66
2007	1699	235	143	72	9	1	11.88	10.88	78.99	55.86	30.61	18.89
2008	1360	200	139	39	8	1	9.78	8.18	79.78	55.22	29.19	16.69
2009	1300	188	119	52	9	10	10.92	10.55	79.77	57	34.15	21.31
2010	1453	216	135	45	8	1	10.76	9.72	81.21	56.99	31.73	19.55
2011	1420	215	132	93	8	1	10.76	11.84	80.63	57.82	34.3	23.66
2012	1234	192	123	64	7	1	10.03	11.18	84.68	62.32	36.14	22.93
2013	1288	184	110	55	9	1	11.71	10.21	80.98	55.9	29.97	18.17
2014	1154	165	107	56	9	1	10.79	8.47	75.74	50.87	28.34	15.6

> **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) = 4.58

> **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
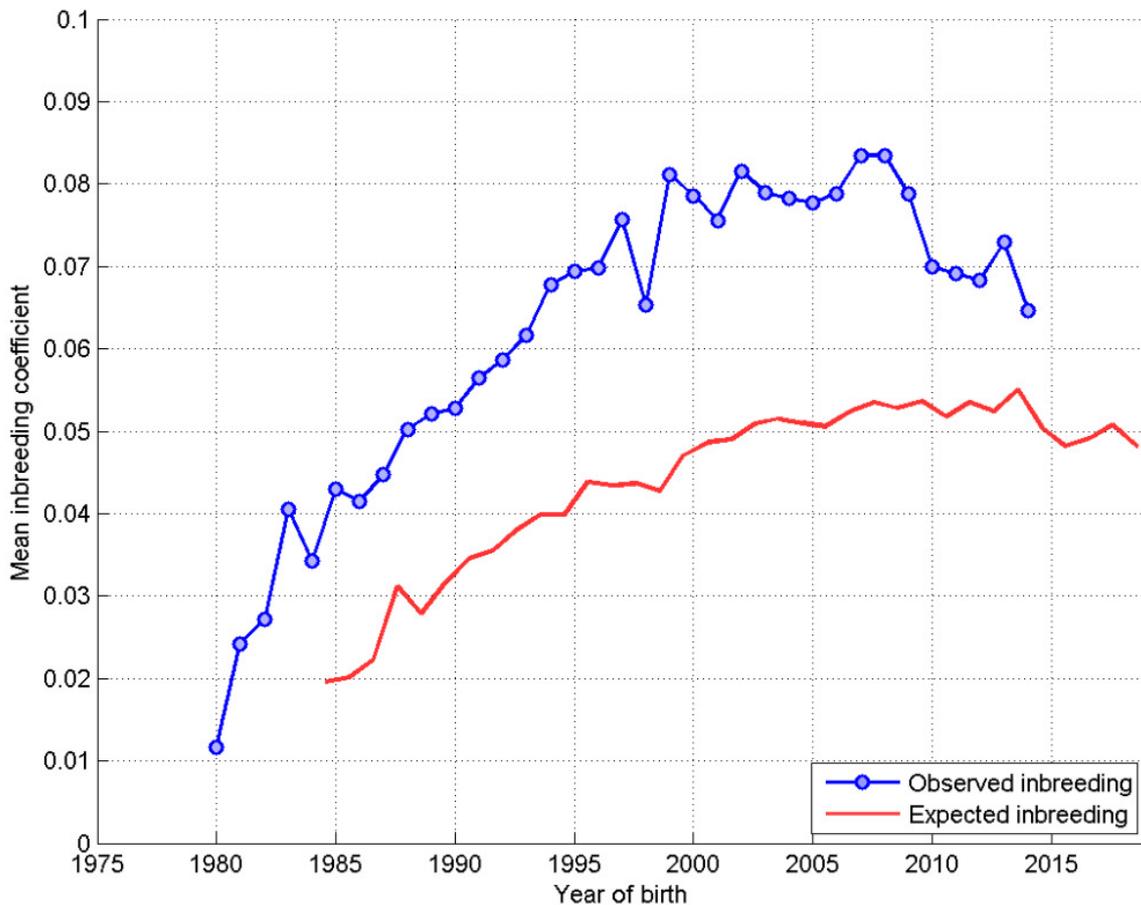
> **Estimated effective population size:** the rate of inbreeding (slope or steepness of the observed inbreeding in Figure 2) is used to estimate the effective population size of the breed. The effective population size is the number of breeding animals in an idealised, hypothetical population that would 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).

Estimated effective population size = 67.9
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	619.4	1045.2	1298.8	1457.4	1278.6	1534.2	1309.8
Total #sires	214	295	317	327	343	389	357
Max #progeny	188	228	209	202	245	187	230
Mean #progeny	14.416	17.712	20.467	22.281	18.627	19.717	18.331
Median #progeny	7	9	10	10	10	10	9
Mode #progeny	1	4	10	1	1	1	1
SD #progeny	21.186	26.088	28.019	30.854	27.284	26.194	27.565
Skew #progeny	3.7632	3.9644	3.3338	2.738	3.8687	2.841	3.6907
Total #dams	492	699	693	783	731	846	765
Max #progeny	37	35	40	38	38	45	31
Mean #progeny	6.2703	7.4678	9.3694	9.3052	8.7442	9.0662	8.5542
Median #progeny	5	6	8	8	8	8	8
Mode #progeny	1	6	9	9	8	1	1
SD #progeny	5.0422	5.0861	5.842	5.7055	5.7146	6.2725	5.6867
Skew #progeny	1.8215	1.5296	1.3072	1.3508	1.33	1.3705	0.90344
Rate of inbreeding	0.026309	0.012895	0.017143	0.010074	0.001502	0.003463	-0.00317
Generation interval	4.1879	4.5153	4.6034	4.8736	4.7115	4.6889	4.4171
Effective pop size	19.005	38.774	29.167	49.634	332.93	144.39	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.
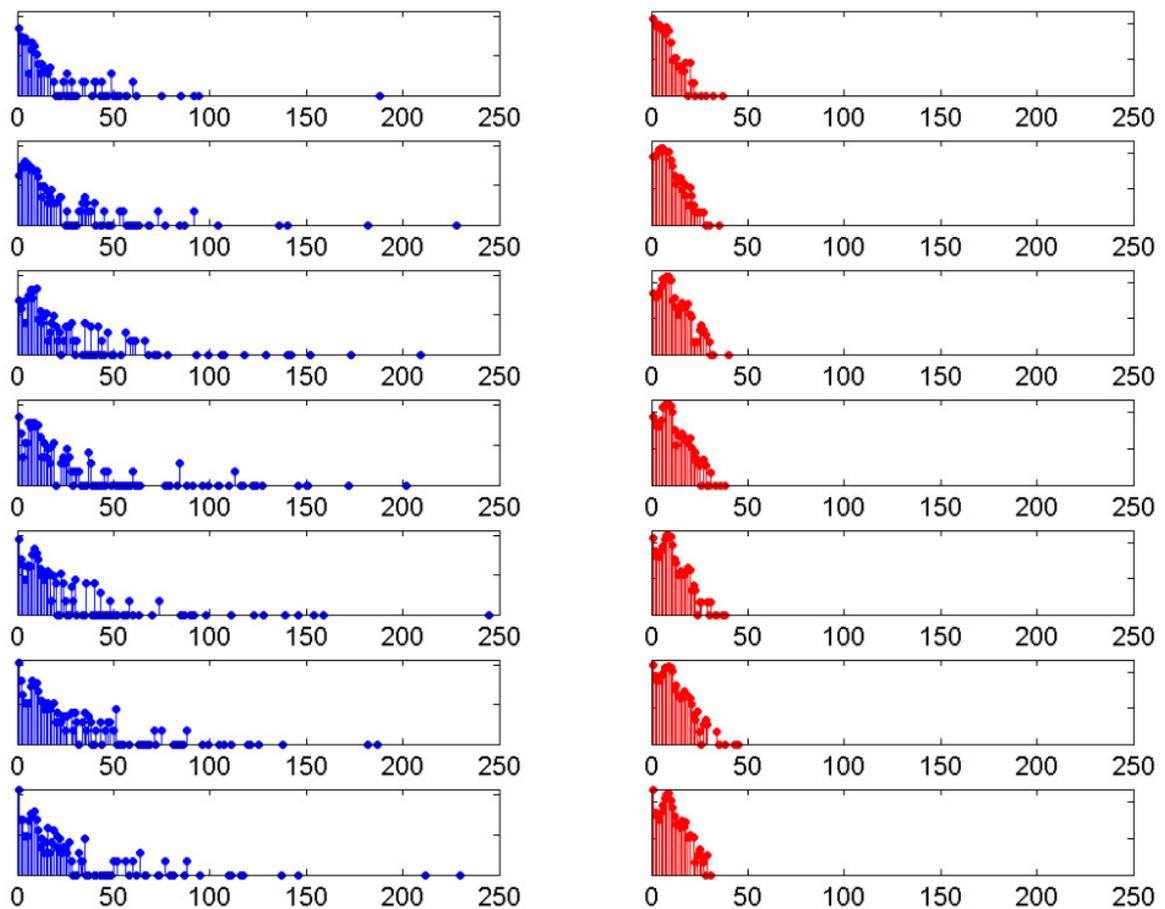
Comments

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 flattened, 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.