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September 2015

Population analysis of the *Retriever (Labrador)* breed

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



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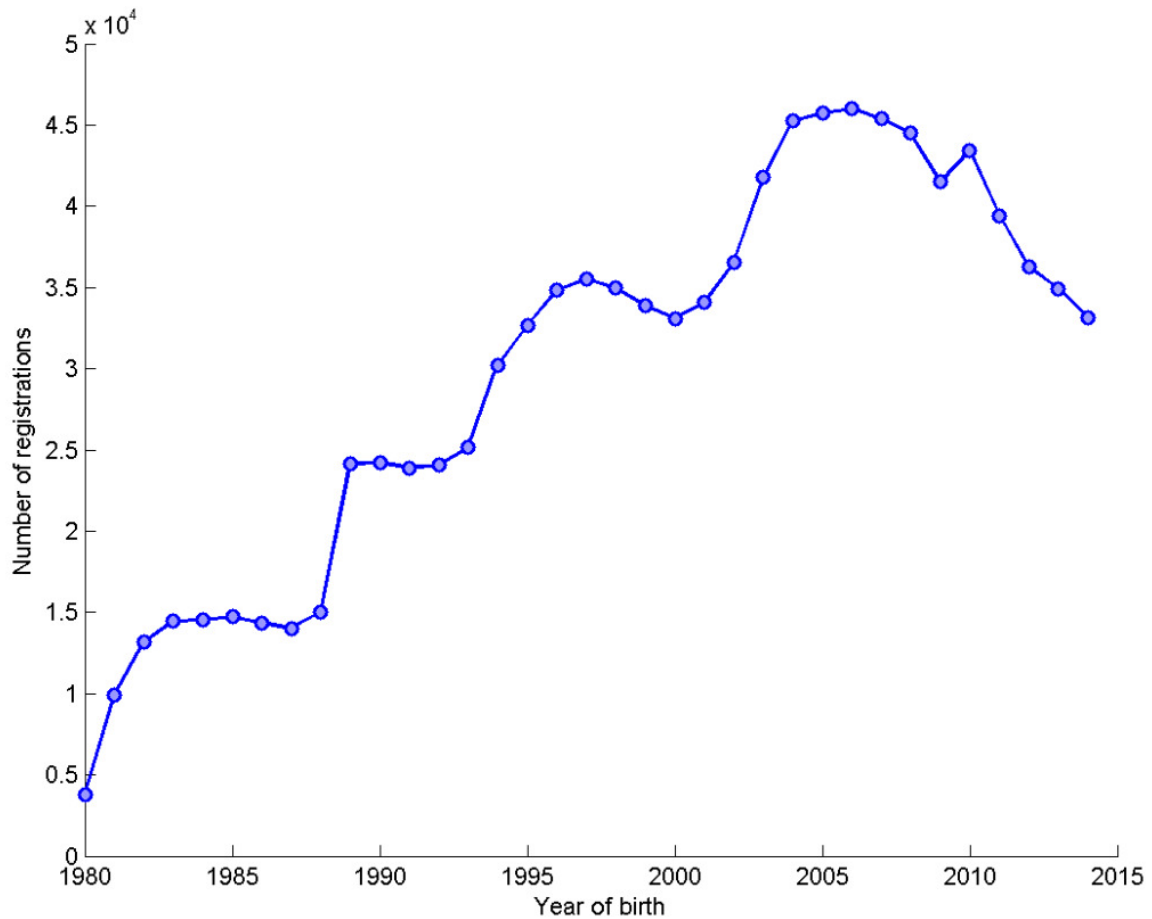
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Figure 1: a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

Breed: Retriever (Labrador)

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = 1051.01 per year (with a 95% confidence interval of 864.25 to 1237.77).



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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	3807	2222	1215	46	2	1	3.13	4.24	80.93	61.2	39.74	27.58
1981	9935	3245	1587	130	3	1	6.26	10.02	86.03	67.9	46.59	32.85
1982	13170	3596	1678	128	4	1	7.85	12.34	85.86	67.6	46.22	32.48
1983	14450	3907	1762	146	4	3	8.2	13.78	86.06	68.81	48.02	34.65
1984	14532	3987	1840	177	4	1	7.9	13.39	86.21	68.63	47.85	34.24
1985	14736	4064	1882	173	4	2	7.83	12.78	85.3	67.57	46.47	32.88
1986	14362	3878	1846	206	4	1	7.78	13.1	85.11	67.32	47.05	33.87
1987	14022	3658	1890	212	4	3	7.42	12.69	83.99	65.6	45.84	33.69
1988	15030	3641	1786	209	5	3	8.42	13.93	84.56	65.97	45.05	31.56
1989	24129	3940	1876	253	8	8	12.86	18.25	81.48	63.06	41.33	28.06
1990	24246	3718	1908	217	8	8	12.71	17.39	80.19	61.98	41.24	28.18
1991	23900	3652	1882	247	8	6	12.7	18.49	80.37	61.65	40.9	28.77
1992	24057	3684	1905	305	8	7	12.63	18.32	79.8	61.26	41.41	28.76
1993	25176	3806	1878	233	8	8	13.41	18.92	80.35	62.31	41.62	29.08
1994	30212	4495	2163	237	8	7	13.97	20.67	81.26	64.09	43.83	30.93
1995	32679	4805	2275	229	8	7	14.36	20.9	81.53	64.48	44.15	31.19
1996	34827	5146	2470	262	8	7	14.1	19.77	81.07	63.3	41.8	29.06
1997	35508	5216	2537	351	8	7	14	20.38	80.73	63.16	42.58	30.02
1998	34992	5160	2534	261	8	7	13.81	19.1	80.5	62.59	41.71	28.97
1999	33885	4912	2425	288	8	7	13.97	19.11	80.6	62.68	41.71	28.43
2000	33090	4910	2350	251	8	7	14.08	19.64	80.24	62.23	41.83	28.82
2001	34078	5033	2443	253	8	8	13.95	19.07	79.88	61.47	40.61	28.32
2002	36577	5421	2565	364	8	8	14.26	20.98	81.28	63.42	42.6	29.49
2003	41771	6110	2802	412	9	7	14.91	20.61	81.03	63.16	41.25	27.92
2004	45271	6566	2911	293	9	8	15.55	21.43	82	64.26	42.1	28.52
2005	45729	6669	3115	282	9	8	14.68	19.15	80.62	62.44	41.16	27.7
2006	46001	6633	3164	224	9	8	14.54	18.73	80.4	61.73	40.13	27.22
2007	45378	6554	3294	252	8	8	13.78	17.74	79.52	60.8	39.61	27.05
2008	44484	6445	3308	194	8	8	13.45	16.16	79.06	59.76	38.28	25.55
2009	41505	6090	3202	264	8	8	12.96	16.3	79.54	60.29	38.7	26.11
2010	43411	6366	3279	228	8	8	13.24	16.91	79.23	60.06	38.85	26.7
2011	39431	5781	3074	236	8	7	12.83	16.1	78.75	59.3	37.97	26.07
2012	36260	5262	2884	227	8	8	12.57	16.07	78.02	58.92	38.42	26.66
2013	34945	5053	2734	181	8	8	12.78	15.99	78.45	59.21	38.41	26.78
2014	33157	4703	2383	328	9	7	13.91	18.47	78.9	60.15	39.36	27.35

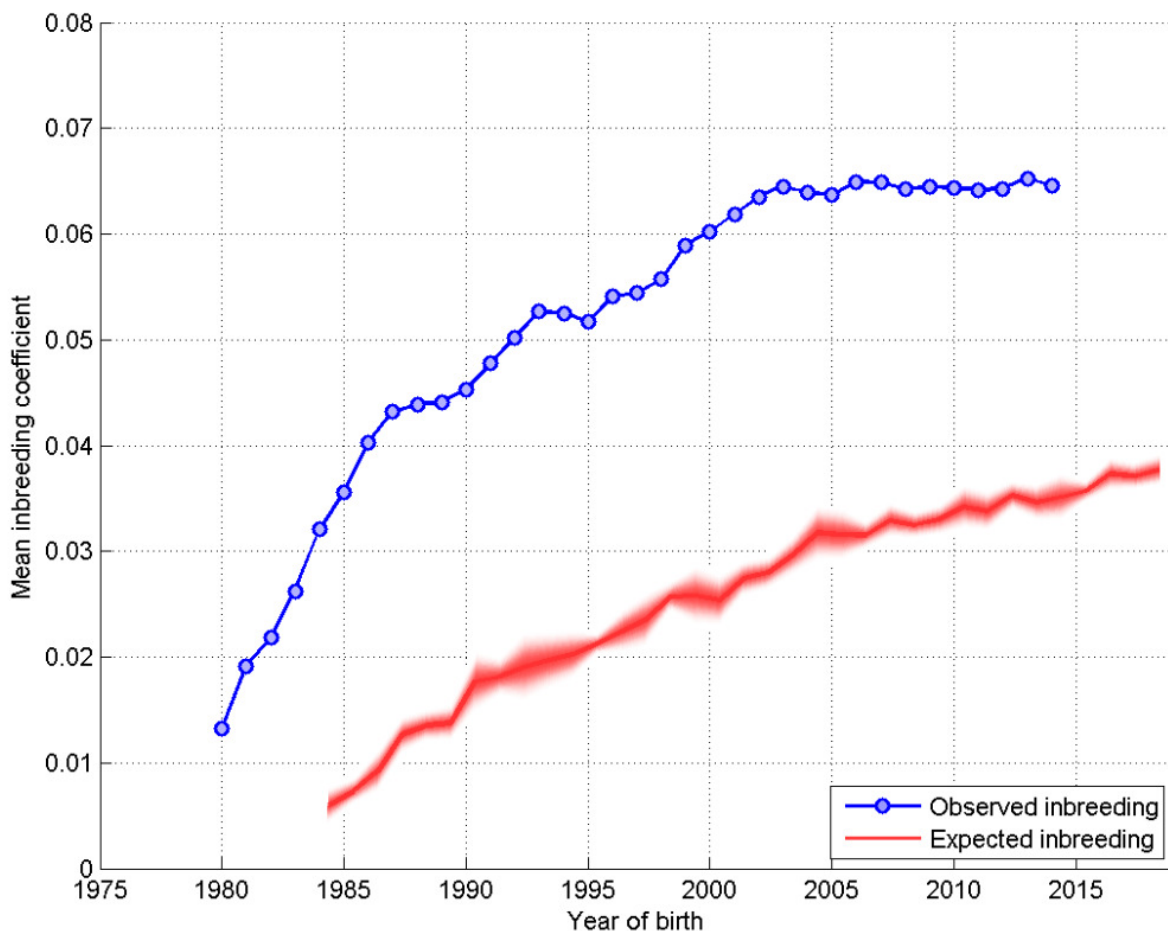


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 4.39

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 = 81.7

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	11179	16456	25518	34378	38157	44619	37441
Total #sires	4996	5737	5982	7500	7793	9461	8582
Max #progeny	488	685	1106	1286	1097	872	736
Mean #progeny	11.173	14.341	21.329	22.919	24.481	23.579	21.784
Median #progeny	4	6	9	9	9	9	9
Mode #progeny	1	3	7	7	8	8	7
SD #progeny	28.564	34.816	48.905	50.268	53.131	46.153	42.309
Skew #progeny	7.6431	8.86	8.9437	8.1383	7.6914	6.4622	7.1666
Total #dams	12666	14307	13976	17774	19612	22785	19770
Max #progeny	40	40	53	60	51	60	46
Mean #progeny	4.4072	5.7508	9.1292	9.6709	9.7278	9.7907	9.4563
Median #progeny	3	5	8	8	8	8	8
Mode #progeny	1	3	7	7	8	8	8
SD #progeny	3.7996	4.4958	6.3284	6.6355	6.3968	6.5769	5.9654
Skew #progeny	2.3035	1.9107	1.8729	1.8499	1.582	1.6695	1.5601
Rate of inbreeding	0.018247	0.0089828	0.0091693	0.0075289	0.0048176	0.0003947	0.000716
Generation interval	3.9897	4.1755	4.4899	4.4034	4.4989	4.4604	4.7168
Effective pop size	27.402	55.662	54.53	66.411	103.79	1266.8	698.28



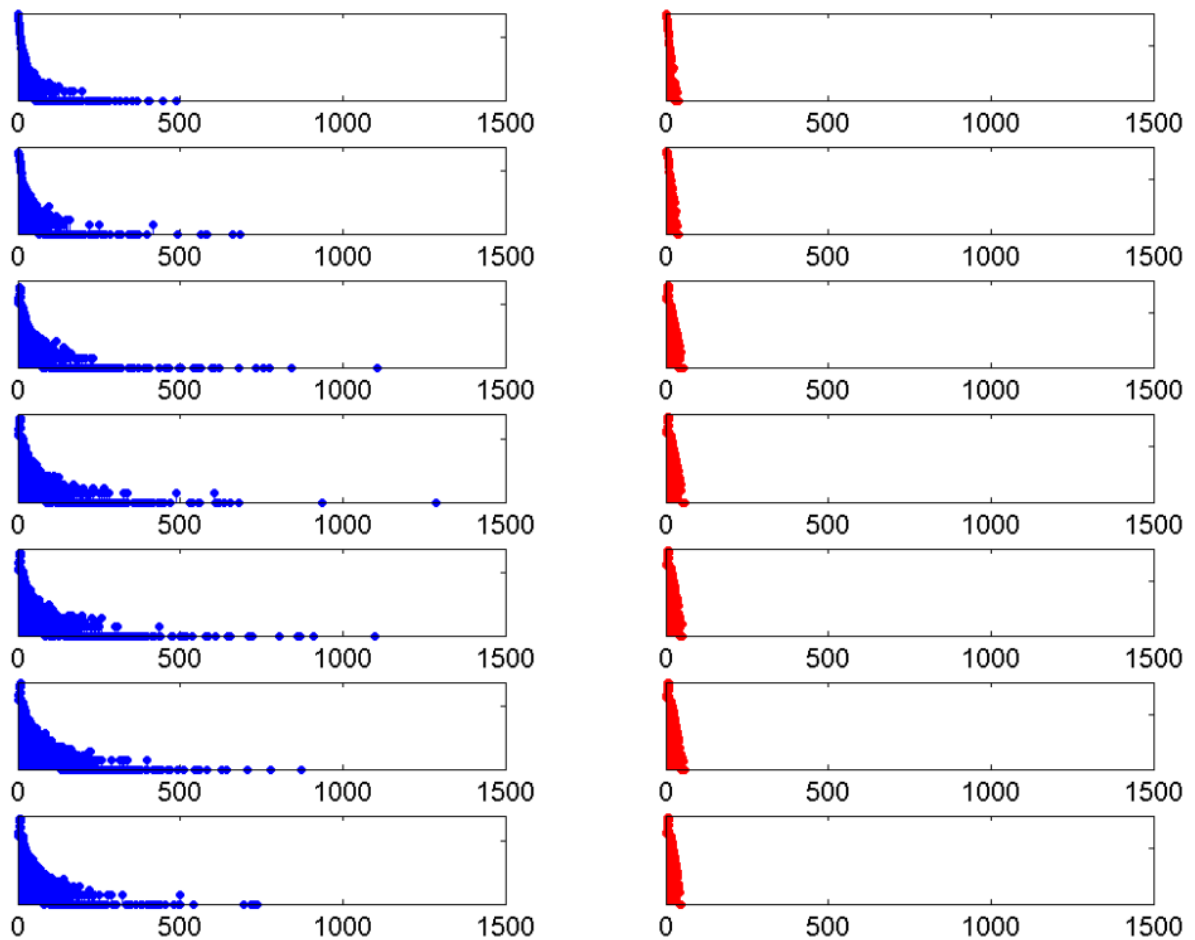
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number 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 early 2000s 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.