



THE KENNEL CLUB

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September 2015

Population analysis of the *English Setter* breed

Genetic analysis of the Kennel Club pedigree records of the UK ***English Setter*** 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

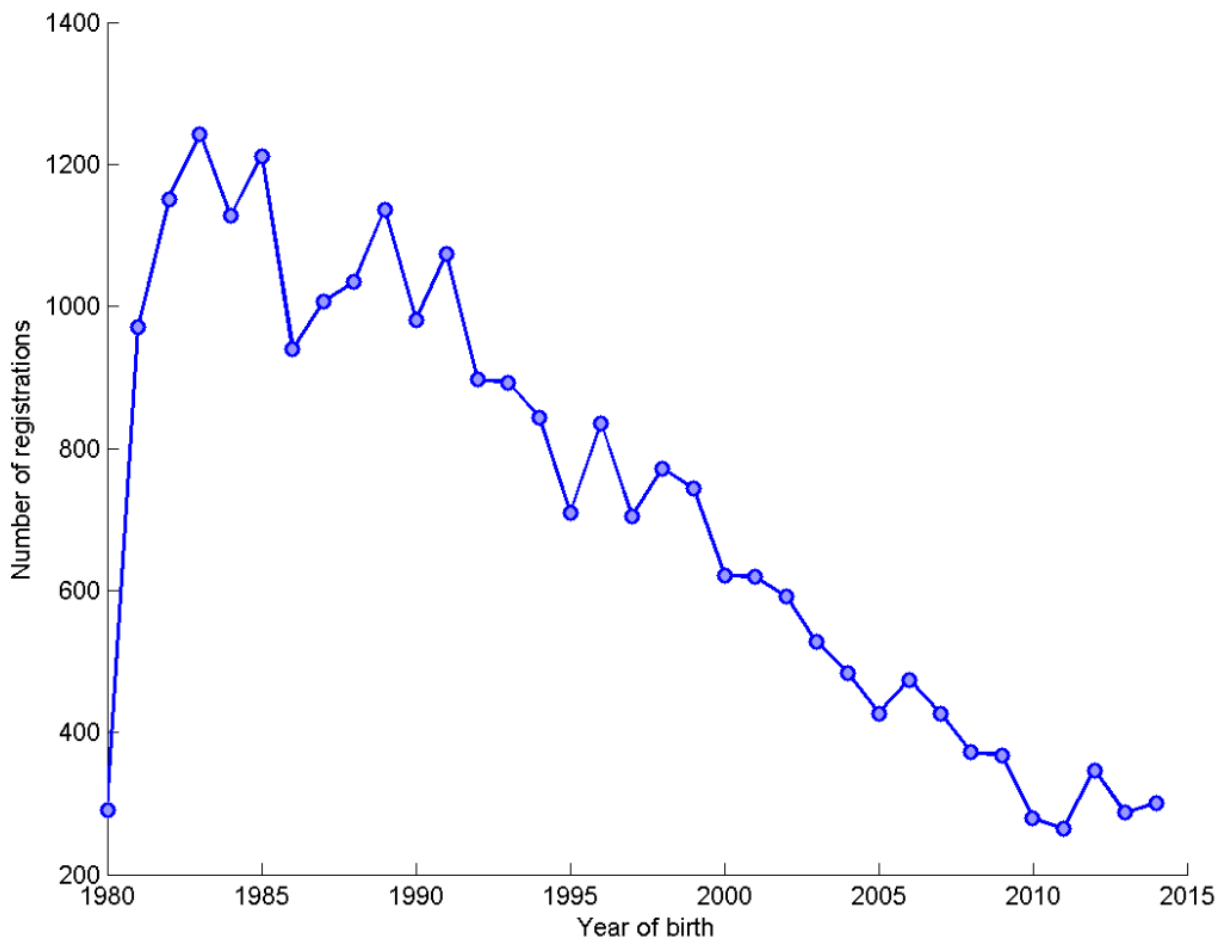
The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered ***English Setter*** population, and statistics were calculated for the period 1980-2014.



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: English Setter

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = -25.33 per year (with a 95% confidence interval of -31.31 to -19.34).



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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	290	170	102	17	2	1	2.84	3.25	80.69	62.41	39.66	24.14
1981	971	253	131	83	5	2	7.41	9.56	83.42	62.41	39.03	26.88
1982	1151	259	137	52	6	1	8.4	8.7	83.41	60.47	35.53	21.55
1983	1242	266	137	51	6	4	9.07	9.19	83.66	61.35	34.46	20.53
1984	1127	244	127	68	5	4	8.87	10.14	81.72	61.93	38.6	23.43
1985	1211	267	130	79	6	2	9.32	10.67	82.66	61.6	37.08	25.02
1986	939	212	116	89	5	1	8.09	10.25	82.22	58.57	38.13	25.99
1987	1007	210	109	57	6	6	9.24	9.48	80.44	58.99	34.66	20.56
1988	1034	222	118	63	6	2	8.76	9.14	81.82	59.86	35.11	21.57
1989	1136	216	122	76	6	4	9.31	11.11	80.19	60.12	37.68	25.18
1990	980	190	115	41	6	6	8.52	7.06	77.14	54.29	30.41	18.37
1991	1074	191	104	65	8	8	10.33	9.94	79.33	57.08	30.91	19.74
1992	897	164	100	64	7	7	8.97	9.17	76.7	55.41	33.78	22.41
1993	893	167	93	69	7	5	9.6	10.44	78.95	57.22	34.6	25.64
1994	844	171	99	59	7	1	8.53	8.38	79.62	55.69	33.65	20.62
1995	709	145	84	46	6	5	8.44	8.45	79.13	57.55	34.56	20.87
1996	835	155	85	44	8	1	9.82	8.79	80.36	55.45	32.22	17.96
1997	705	138	83	51	6	4	8.49	8.38	80.99	58.16	33.05	19.72
1998	772	144	76	57	7	6	10.16	9.77	79.66	56.99	34.72	21.11
1999	744	136	81	56	7	1	9.19	9.52	80.78	57.66	35.22	22.04
2000	621	120	72	34	8	1	8.63	7.07	80.03	52.98	28.02	18.04
2001	619	120	65	50	8	1	9.52	9.62	82.88	57.84	35.86	19.87
2002	592	126	80	46	6	1	7.4	7.72	82.09	58.78	34.63	22.47
2003	527	106	67	35	6	1	7.87	7.01	80.08	56.17	32.83	16.51
2004	484	94	57	40	7	1	8.49	8.57	83.26	57.64	35.74	22.11
2005	427	84	43	60	7	4	9.93	11.03	81.73	60.66	36.3	21.78
2006	474	98	52	37	7	1	9.12	9	81.43	58.23	34.6	22.78
2007	427	90	47	37	7	1	9.09	9.05	81.5	59.25	37.24	16.86
2008	372	79	49	34	5	1	7.59	8.07	84.68	61.56	36.56	17.74
2009	368	83	45	25	7	1	8.18	6.34	80.98	51.63	28.26	12.77
2010	279	62	37	33	6	5	7.54	6.86	77.06	51.61	33.69	22.58
2011	265	66	43	41	4	1	6.16	6.75	83.02	56.98	32.45	21.51
2012	347	76	47	37	5	1	7.38	7.45	84.73	59.65	35.45	18.16
2013	287	63	39	32	6	1	7.36	6.08	79.44	52.96	27.87	17.07
2014	301	60	33	52	7	6	9.12	9.01	75.75	52.16	30.56	25.25

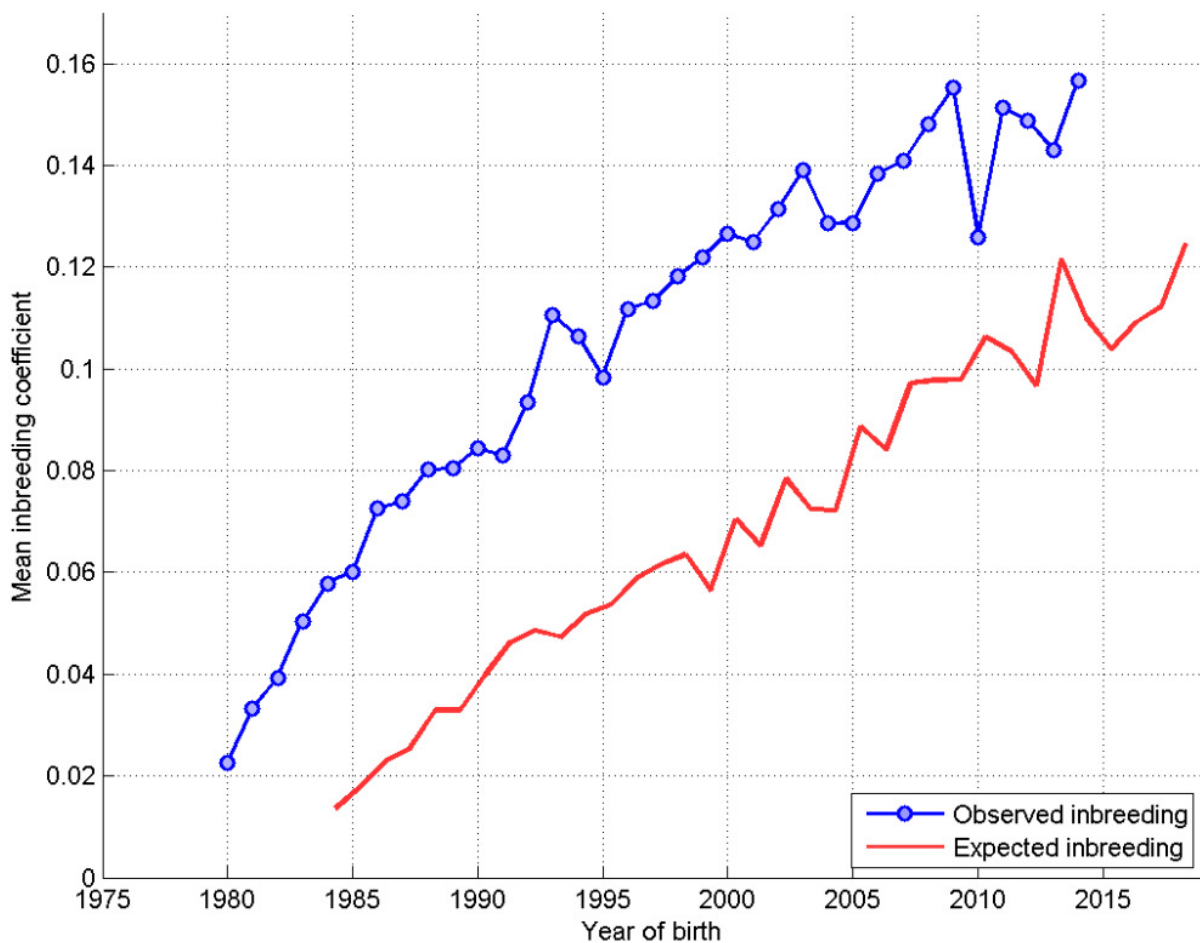


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 4.32

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 = 29.8

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	956.2	1065.4	937.6	753	568.6	413.6	295.8
Total #sires	350	346	293	249	199	140	121
Max #progeny	128	354	211	179	133	124	113
Mean #progeny	13.62	15.393	15.997	15.116	14.281	14.757	12.215
Median #progeny	6	7	9	7	8	7	7
Mode #progeny	1	2	7	1	1	1	1
SD #progeny	22.033	27.122	24.343	22.323	19.674	21.736	16.141
Skew #progeny	3.1112	6.9923	4.6164	3.5843	2.807	3.0046	3.4034
Total #dams	929	886	699	557	437	338	252
Max #progeny	27	25	26	33	29	24	25
Mean #progeny	5.1313	6.0113	6.701	6.7576	6.5034	6.1154	5.8651
Median #progeny	4	5	6	6	6	5	6
Mode #progeny	1	2	7	7	1	1	6
SD #progeny	4.2685	3.8891	4.3031	4.6962	4.7209	4.2714	3.8937
Skew #progeny	1.7148	1.2252	1.3229	1.5919	1.2903	1.2149	1.1459
Rate of inbreeding	0.034779	0.020602	0.033214	0.026385	0.009213	0.031238	0.032731
Generation interval	3.8247	3.9999	4.2087	4.3756	4.4155	4.2619	5.3216
Effective pop size	14.377	24.27	15.054	18.95	54.274	16.006	15.276



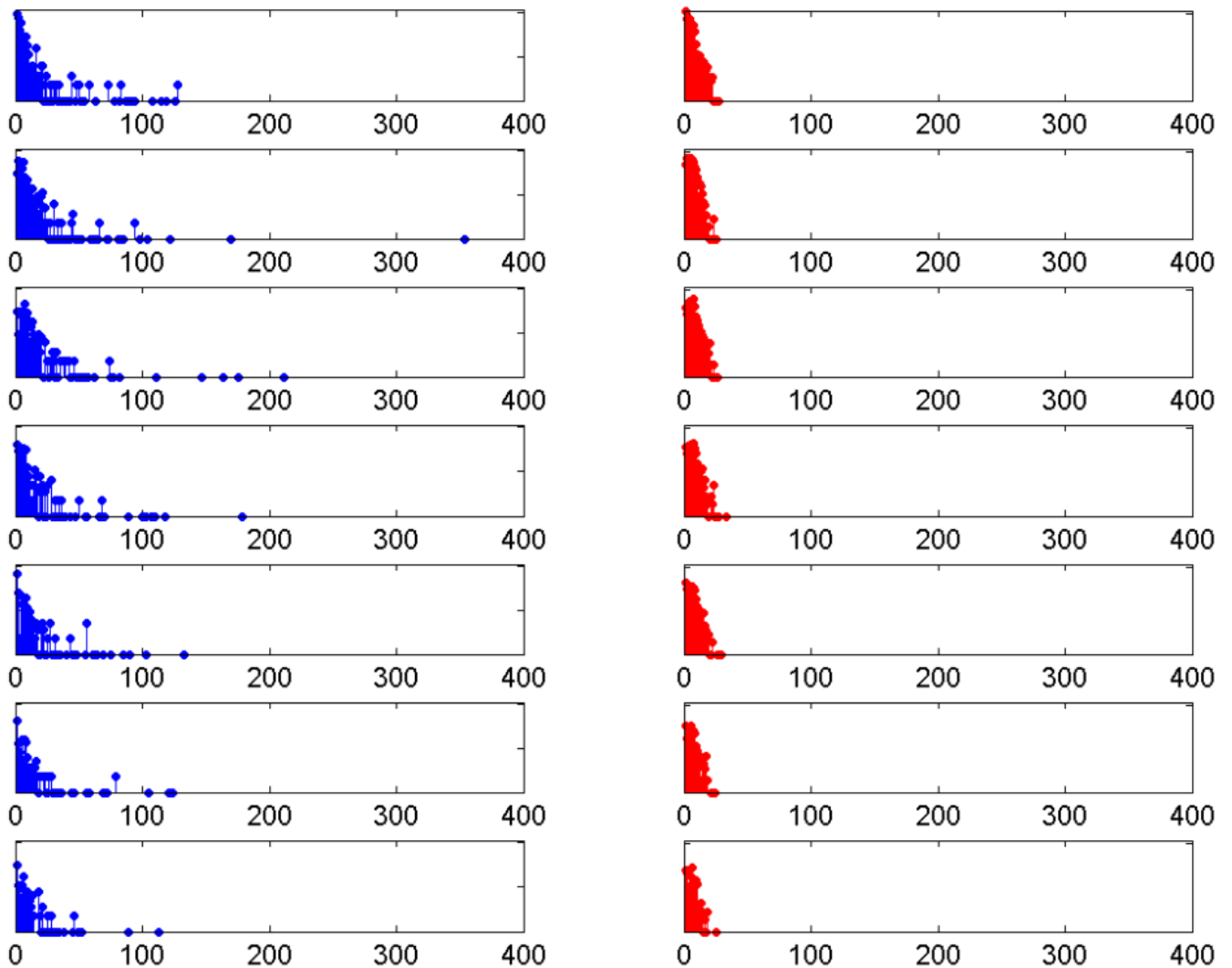
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number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

The rate of inbreeding in this breed has remained relatively steady but high over the whole period.

This implies genetic variation is steadily being lost from the population.

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.