THE KENNEL CLUB
Making a difference for dogs

September 2015

Population analysis of the *Staffordshire Bull Terrier* breed

Genetic analysis of the Kennel Club pedigree records of the UK ***Staffordshire Bull Terrier*** 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).

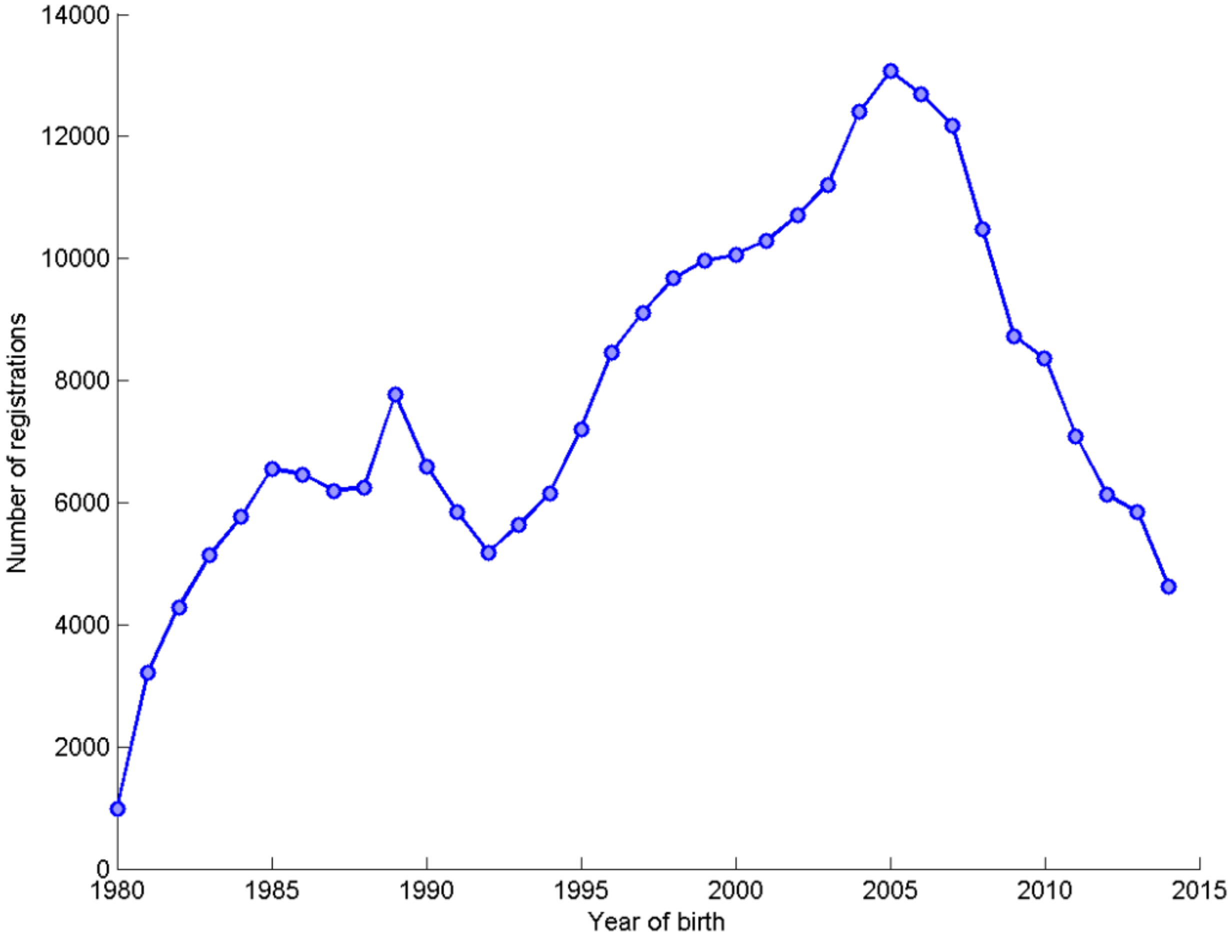
Summary of results

The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered ***Staffordshire Bull Terrier*** 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: *Staffordshire Bull Terrier*

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = 157.19 per year (with a 95% confidence interval of 75.40 to 238.97).

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.

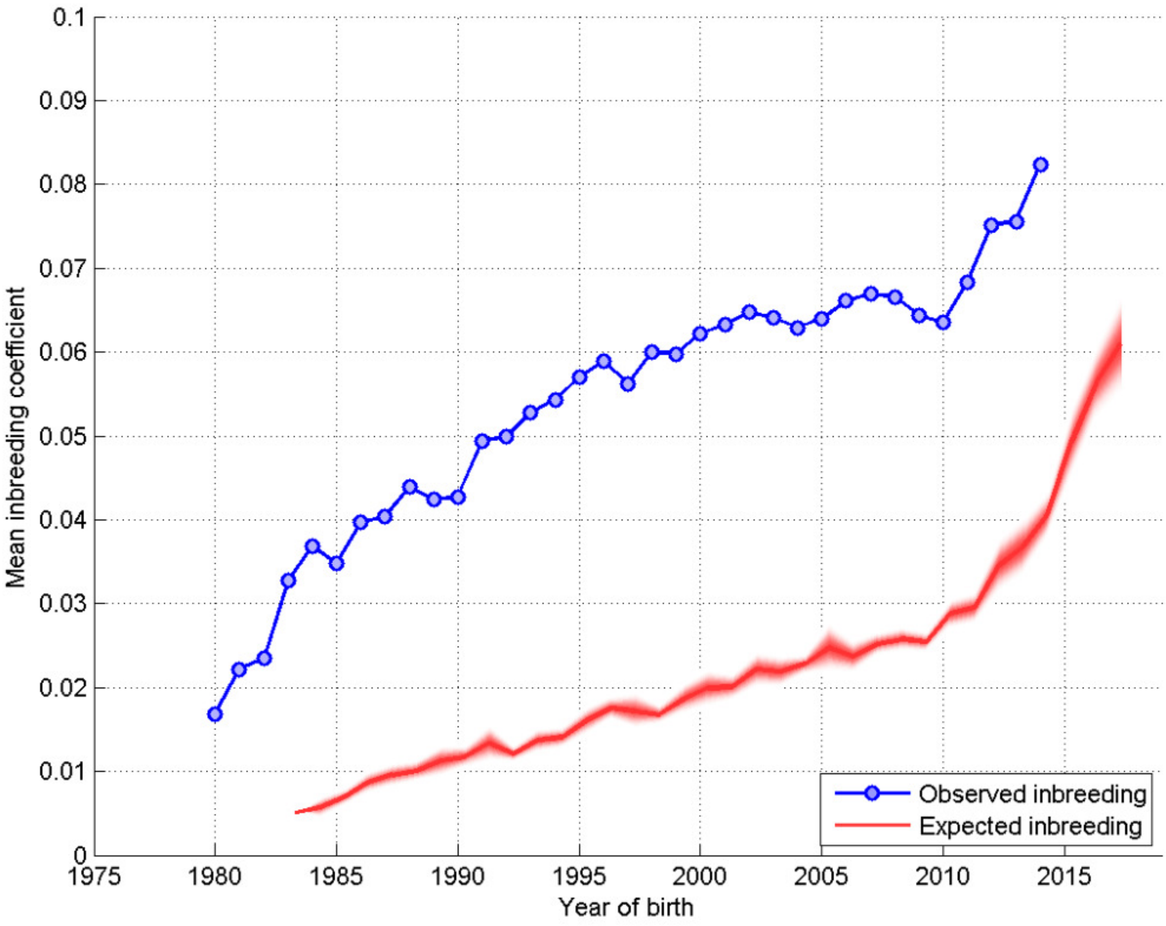
year	#born	#dams	#sires	puppies per sire					%puppies sired by most prolific sires			
				max	median	mode	mean	sd	50% sires	25% sires	10% sires	5% sires
1980	984	603	364	26	2	1	2.7	2.8	79.88	58.23	34.55	21.75
1981	3222	1057	572	70	3	1	5.63	7.72	83.4	62.63	41.46	29.27
1982	4287	1266	675	70	4	4	6.35	8.16	82.04	61.91	40.19	27.6
1983	5136	1477	819	91	4	3	6.27	8.3	81.83	62.11	40.38	27.82
1984	5761	1738	980	71	4	3	5.88	7.68	82.02	61.57	40.15	27.77
1985	6558	2056	1200	74	4	2	5.46	6.91	80.97	59.99	38.93	26.62
1986	6458	2072	1282	111	3	2	5.04	6.55	80.85	59.68	37.97	26.32
1987	6196	1974	1238	101	3	2	5	6.23	80.7	59.12	37.36	25.52
1988	6248	1941	1229	96	3	3	5.08	6.96	80.52	59.22	39.34	27.94
1989	7767	1754	1153	65	5	5	6.74	6.85	76.12	53.11	32.77	22.36
1990	6590	1452	996	63	5	5	6.62	6.55	75.78	53.2	32.85	21.88
1991	5850	1262	890	71	5	4	6.57	6.29	75.69	52.75	31.79	21.06
1992	5184	1111	777	65	5	5	6.67	5.92	74.71	51.45	31.02	20.14
1993	5629	1183	802	69	5	5	7.02	6.88	75.93	53.26	32.65	21.67
1994	6159	1320	854	58	5	5	7.21	6.83	76.81	54.18	32.57	20.96
1995	7198	1474	951	78	6	5	7.57	7.71	76.69	54.47	33.7	23.16
1996	8461	1693	1036	111	6	5	8.17	9	76.91	55.79	34.77	23.37
1997	9114	1800	1127	92	6	6	8.09	8.74	76.7	55.09	34.74	23.66
1998	9677	1884	1192	104	6	5	8.12	8.16	76.39	54.69	33.55	22
1999	9957	1935	1246	75	6	6	7.99	8.42	77.14	55.81	35.24	23.51
2000	10068	1985	1248	122	6	5	8.07	8.78	76.31	54.65	34.17	22.95
2001	10292	2007	1307	92	6	6	7.87	7.6	75.1	52.65	31.9	21.09
2002	10708	2070	1319	193	6	6	8.12	9.65	76.37	54.88	34.41	23.52
2003	11215	2163	1323	153	6	5	8.48	9.68	76.94	55.41	34.94	23.87
2004	12399	2302	1405	175	6	6	8.82	10.48	76.41	55.18	34.72	24.01
2005	13074	2445	1493	123	6	5	8.76	10.06	77.4	56.4	36.01	24.59
2006	12699	2348	1484	130	6	6	8.56	10.14	76.45	54.97	35	24.32
2007	12181	2239	1362	161	6	6	8.94	11.66	78.17	57.68	37.09	25.91
2008	10484	1955	1244	136	6	5	8.43	9.8	76.86	55.22	35.05	24.12
2009	8733	1625	1027	180	6	6	8.5	11.38	77.37	56.48	36.56	25.92
2010	8366	1578	969	147	6	6	8.63	12.52	78.54	58.28	38.57	27.87
2011	7093	1385	839	139	6	5	8.45	11.94	80.69	60.03	39.74	28.65
2012	6137	1194	742	127	6	6	8.27	11.24	80.22	59.39	40.08	28.97
2013	5840	1123	676	232	6	6	8.64	13.56	81.03	60.86	41.51	29.9
2014	4626	863	540	128	6	6	8.57	12.92	78.6	58.82	41.07	30.42

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) = 3.30

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).

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 = 97.7

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

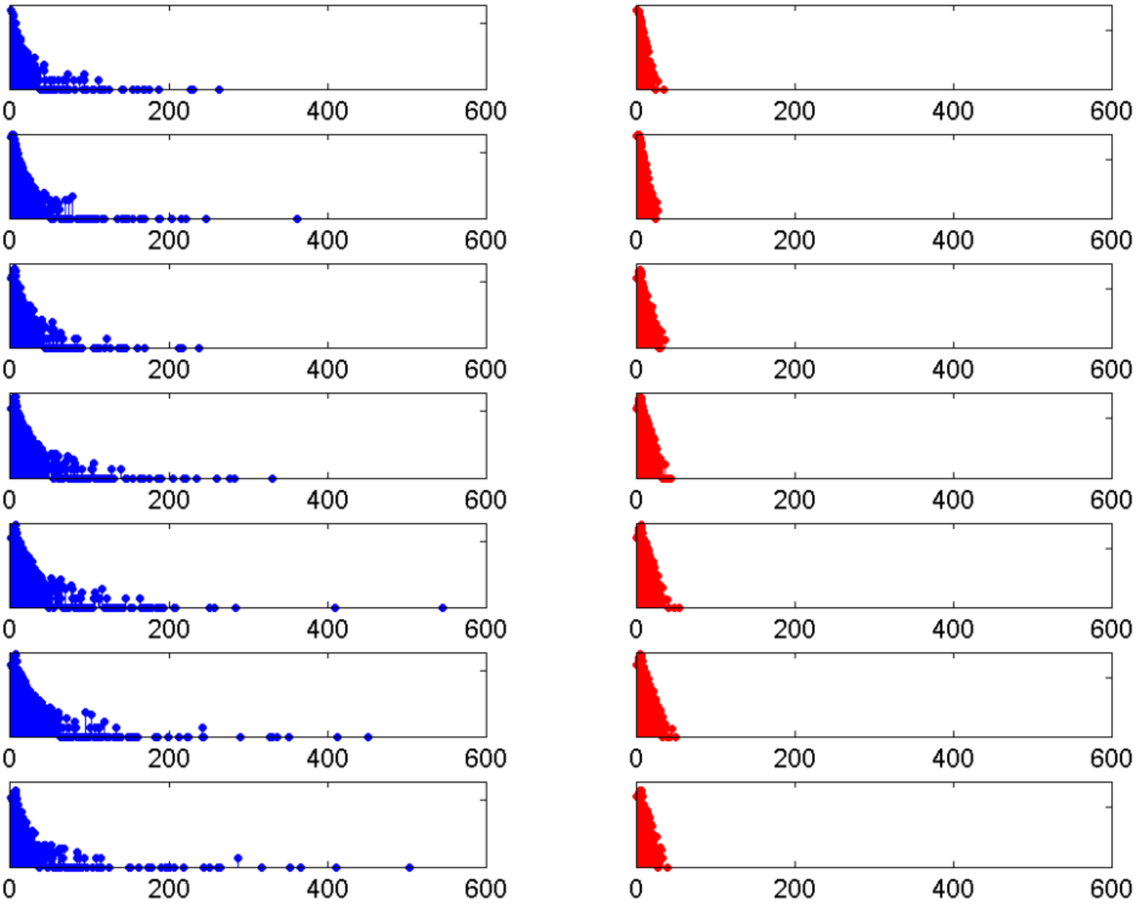
Table 2: a breakdown of census statistics, sire and dam usage and indicators of the rate of loss of genetic diversity over 5 year periods (1980-4, 1985-9, 1990-4, 1995-9, 2000-4, 2005-9, 2010-14). Rate of inbreeding and estimated effective population size for each 5-year block can be compared with the 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	3878	6645.4	5882.4	8881.4	10936	11434	6412.4
Total #sires	2175	3984	2951	3637	4203	4371	2517
Max #progeny	264	362	238	330	545	451	504
Mean #progeny	8.9085	8.3396	9.9665	12.209	13.01	13.079	12.732
Median #progeny	4	4	6	7	7	7	6
Mode #progeny	1	2	5	6	6	6	6
SD #progeny	18.244	16.135	15.195	20.402	22.166	23.844	28.289
Skew #progeny	6.755	8.8088	6.4092	6.6906	8.5941	8.3024	8.6592
Total #dams	4510	7425	4741	6295	7495	7803	4657
Max #progeny	35	27	36	44	54	50	39
Mean #progeny	4.2962	4.4749	6.2035	7.0542	7.2957	7.3267	6.8815
Median #progeny	3	4	5	6	6	6	6
Mode #progeny	1	3	5	5	6	5	5
SD #progeny	3.3747	3.2516	4.4117	4.9343	5.0254	5.2133	4.8885
Skew #progeny	1.9797	1.8405	1.9372	1.8274	1.8501	1.9948	1.6709
Rate of inbreeding	0.016291	0.006316	0.009828	0.002389	0.000744	0.000473	0.015633
Generation interval	3.1446	3.1284	3.53	3.4139	3.4061	3.2335	3.2589
Effective pop size	30.692	79.163	50.878	209.31	672.3	1057.1	31.985

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

The rate of inbreeding in this breed has remained relatively steady over the whole period. However, this appears to be close to the level thought to be sustainable.

It appears that the extensive use of popular dogs as sires has increased (the ‘tail’ of the blue distribution increasing 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.