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September 2015

Population analysis of the *Border Terrier* breed

Genetic analysis of the Kennel Club pedigree records of the UK ***Border 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 ***Border Terrier*** population, and statistics were calculated for the period 1980-2014.



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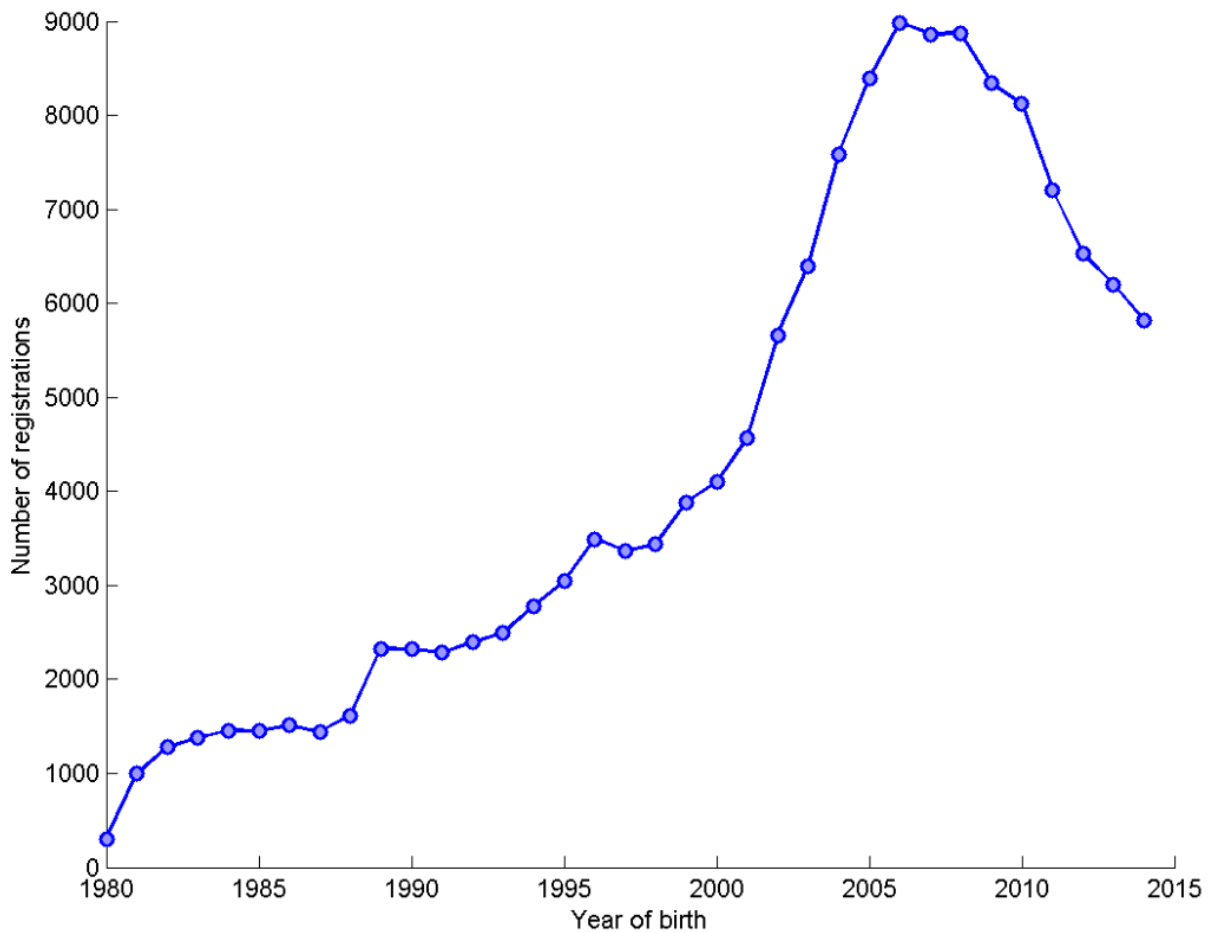
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Figure 1: a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

Breed: Border Terrier

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = 243.24 per year (with a 95% confidence interval of 203.25 to 283.23).



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	301	198	117	17	2	1	2.57	2.49	80.4	56.15	32.89	20.93
1981	1001	393	193	46	3	1	5.19	5.93	83.42	61.64	36.86	23.98
1982	1281	455	214	50	4	2	5.99	6.94	83.06	61.28	37.47	25.53
1983	1383	446	229	40	4	2	6.04	6.74	82	60.52	37.67	24.08
1984	1459	500	254	50	4	1	5.74	6.64	82.25	61.82	37.08	24.06
1985	1447	500	284	34	3	1	5.1	5.33	81.69	59.85	35.59	21.63
1986	1515	504	270	38	4	2	5.61	5.8	79.93	58.88	34.79	23.1
1987	1442	460	253	73	4	2	5.7	7.11	80.86	60.06	38.35	25.87
1988	1616	512	277	53	4	3	5.83	6.54	81.62	60.46	37.75	23.7
1989	2327	603	319	48	5	2	7.29	7.16	80.92	57.97	33.3	20.54
1990	2322	558	314	52	5	5	7.39	6.83	77.86	55.17	31.09	20.16
1991	2283	566	304	83	5	4	7.51	8.72	80.07	59.48	36.84	24
1992	2394	576	325	40	5	5	7.37	6.68	78.4	56.39	32.25	19.13
1993	2495	601	338	60	5	5	7.38	7.26	77.88	55.51	33.15	21.56
1994	2779	647	330	80	6	5	8.42	9.01	78.99	57.79	35.05	23.75
1995	3046	726	365	68	6	4	8.35	8	79.84	57.75	32.34	19.37
1996	3493	819	416	77	5	5	8.4	8.82	79.13	58.49	35.47	22.53
1997	3367	795	411	52	6	3	8.19	7.81	79.15	56.96	32.4	20.97
1998	3435	796	415	66	5	4	8.28	8.22	78.98	57.15	33.25	21.46
1999	3886	863	449	63	6	5	8.65	8.78	80.39	58.96	35.46	21.49
2000	4101	948	491	68	6	5	8.35	8.03	78.35	55.3	32.07	21.36
2001	4566	1048	526	59	6	5	8.68	8.72	79.85	58.43	34.56	21.38
2002	5663	1252	557	65	6	5	10.17	10.69	80.73	59.4	36.5	23.13
2003	6399	1402	627	93	7	4	10.21	10.46	80.25	58.15	34.54	22.05
2004	7587	1663	758	86	6	4	10.01	10.44	81.09	59.94	35.28	21.96
2005	8390	1796	832	71	7	5	10.08	10.13	79.99	57.87	34.6	21.87
2006	8985	1915	934	88	6	5	9.62	9.87	79.74	57.53	33.91	22.18
2007	8863	1927	951	134	6	5	9.32	9.81	79.7	58.34	34.58	21.49
2008	8874	1898	977	96	6	5	9.08	9.22	78.75	57	33.75	21.61
2009	8346	1809	946	95	6	5	8.82	9.08	78.83	57.34	34.9	21.84
2010	8118	1762	932	82	6	5	8.71	8.72	78.65	56.96	33.62	21.37
2011	7203	1618	867	84	6	5	8.31	8.48	78.83	57.14	34.67	21.96
2012	6529	1447	773	71	6	4	8.45	8.86	78.79	58	35.46	22.94
2013	6199	1352	730	83	6	5	8.49	8.03	77.22	55.64	32.94	20.63
2014	5824	1245	649	70	6	4	8.97	8.74	78.37	56.83	33.5	21.14

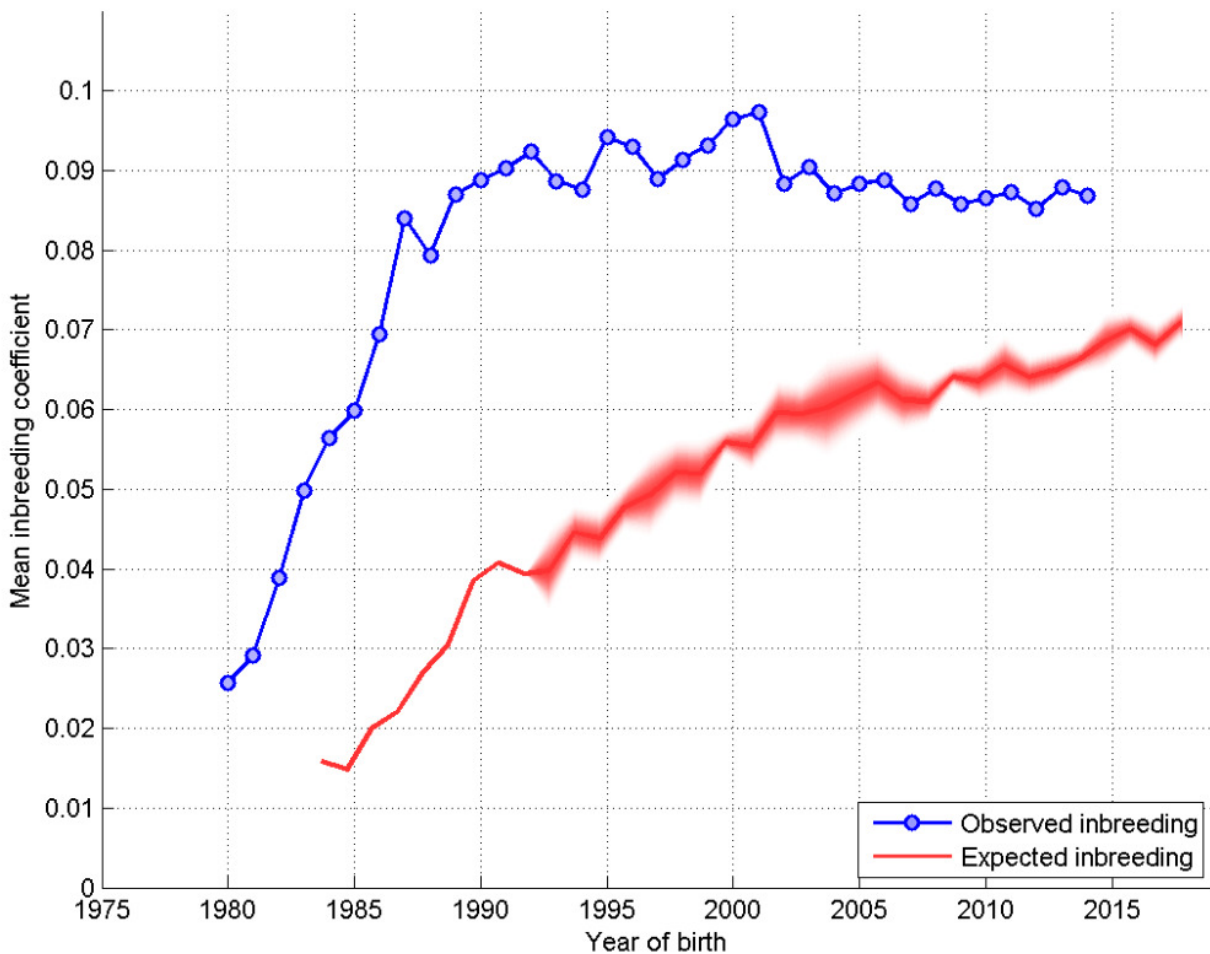


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 3.71

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 = 106.1

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	1085	1669.4	2454.6	3445.4	5663.2	8691.6	6774.6
Total #sires	546	747	881	1099	1535	2362	2101
Max #progeny	118	194	201	240	285	375	258
Mean #progeny	9.9231	11.167	13.926	15.674	18.446	18.398	16.119
Median #progeny	4	5	7	8	9	9	8
Mode #progeny	1	2	5	4	5	5	5
SD #progeny	15.316	17.054	19.692	22.968	26.98	27.426	23.709
Skew #progeny	3.7137	4.541	3.909	4.1655	3.5901	4.2266	4.0209
Total #dams	1360	1724	1991	2641	4082	5981	5039
Max #progeny	27	28	30	36	32	42	29
Mean #progeny	3.9838	4.8411	6.1637	6.5225	6.9366	7.2658	6.7208
Median #progeny	3	4	5	5	6	6	5
Mode #progeny	1	2	5	5	5	5	4
SD #progeny	3.3706	3.6859	4.4022	4.6802	4.6553	5.1565	4.4716
Skew #progeny	2.0651	1.5958	1.6523	1.6217	1.3551	1.6144	1.3741
Rate of inbreeding	0.028539	0.025163	-0.0017	-0.00145	-0.01041	-0.00258	0.000457
Generation interval	3.3432	3.6515	3.8335	3.7449	3.6858	3.7704	4.0301
Effective pop size	17.52	19.871	n/a	n/a	n/a	n/a	1094.9



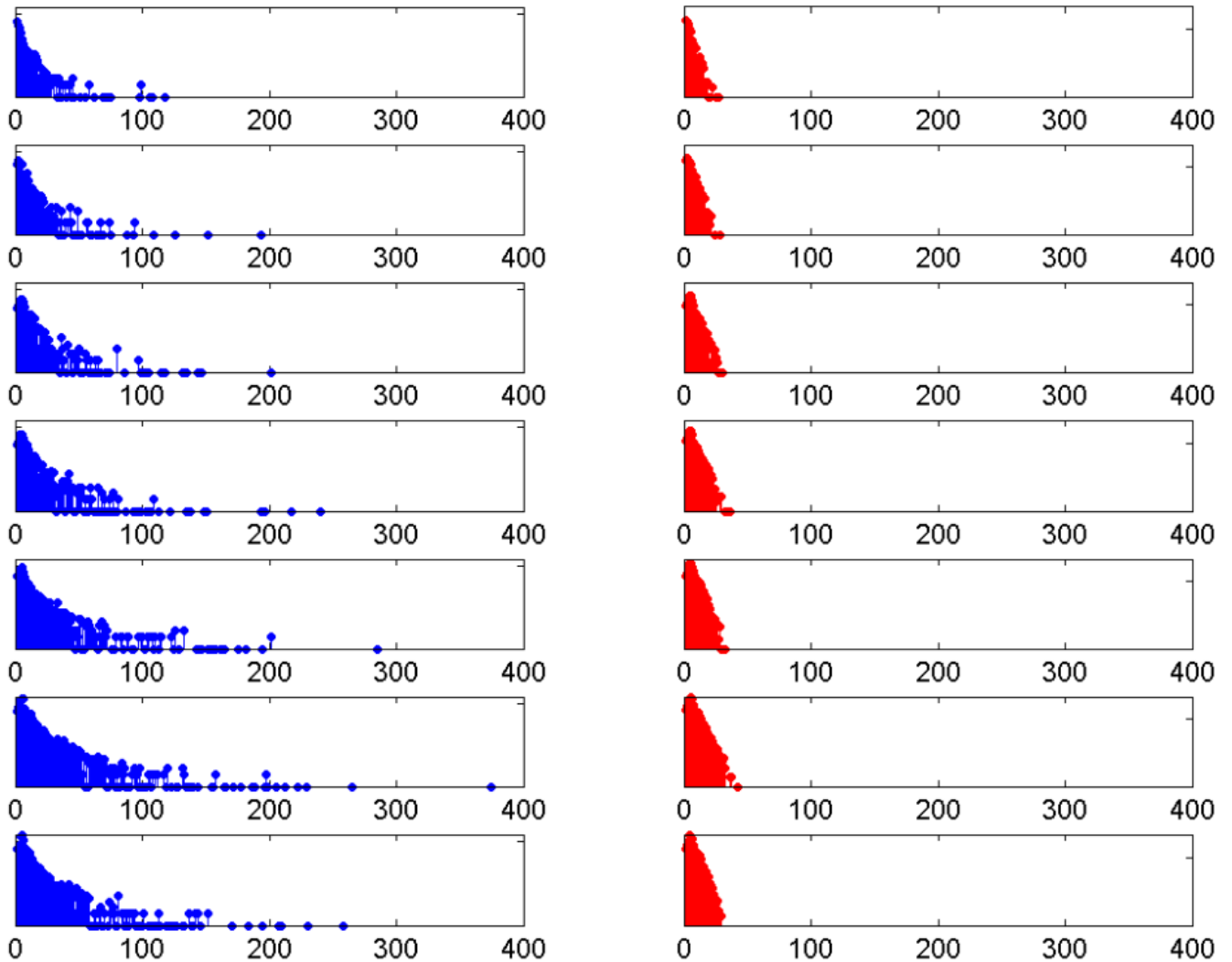
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number 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. This represents a 'genetic bottleneck', with genetic variation lost from the population. However, since the 1990s the rate of inbreeding has slowed and even declined slightly, implying maintenance of genetic diversity (possibly through the use of imported animals).

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.