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September 2015

Population analysis of the *Bedlington Terrier* breed

Genetic analysis of the Kennel Club pedigree records of the UK *Bedlington 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

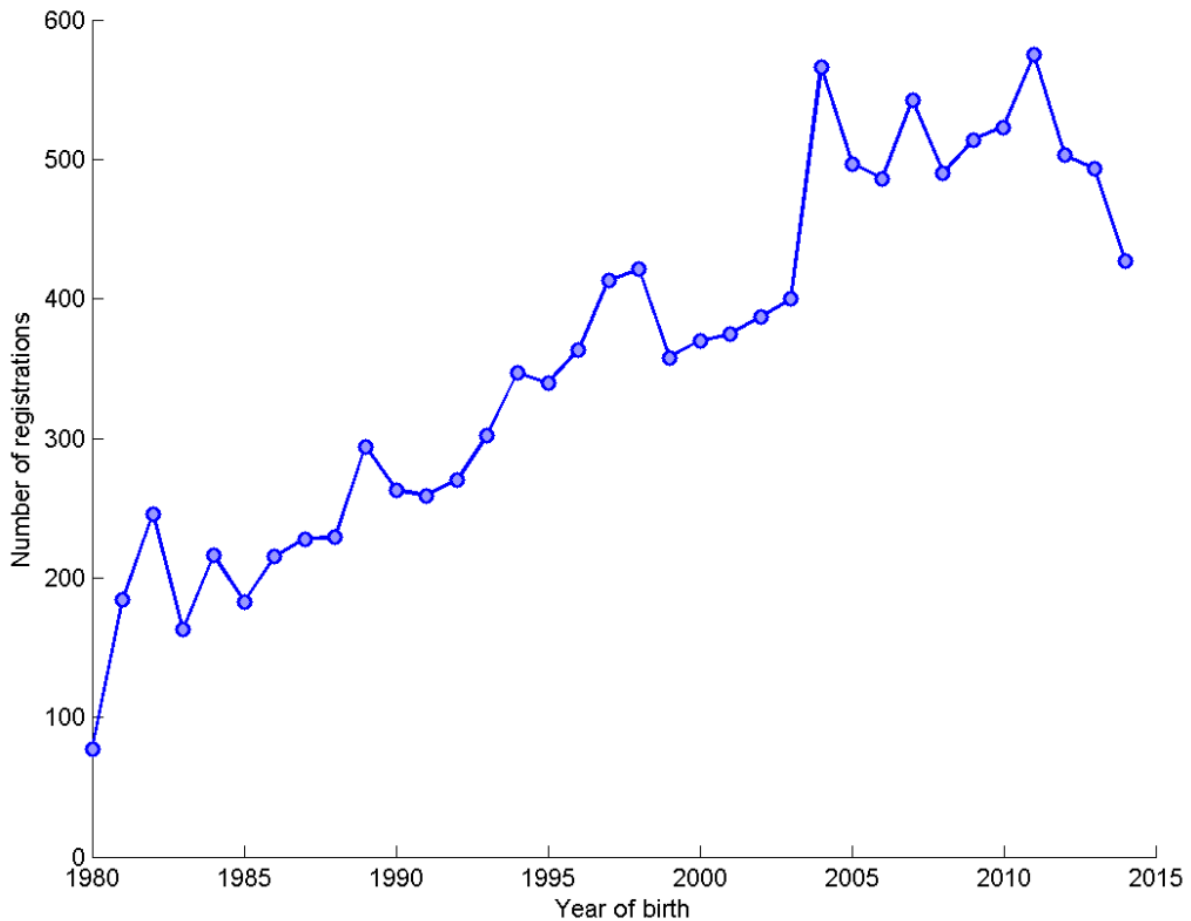
The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered *Bedlington Terrier* population, and statistics were calculated for the period 1980-2014.



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: *Bedlington Terrier*

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = 11.93 per year (with a 95% confidence interval of 10.32 to 13.54).



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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	77	50	36	12	1	1	2.14	2.21	76.62	55.84	36.36	25.97
1981	184	81	51	12	2	1	3.61	2.78	80.43	53.8	25.54	16.85
1982	246	77	51	23	3	1	4.82	4.79	82.52	60.57	33.74	22.36
1983	163	58	39	14	3	2	4.18	3.28	78.53	54.6	28.83	15.95
1984	216	79	52	22	3	3	4.15	3.87	76.39	52.78	31.94	23.15
1985	183	62	42	28	3	1	4.36	4.69	80.87	57.92	32.79	22.4
1986	215	72	53	16	3	2	4.06	3.22	76.28	52.09	27.91	19.07
1987	228	77	55	24	3	3	4.15	4.03	77.63	52.63	33.33	23.68
1988	229	73	47	34	4	4	4.87	5.22	78.17	56.33	33.62	20.09
1989	294	84	60	39	4	3	4.9	5.2	75.85	51.02	30.95	21.77
1990	263	64	45	30	5	3	5.84	5.32	76.43	51.71	34.22	19.01
1991	259	75	43	20	4	1	6.02	4.91	80.69	55.6	26.25	14.67
1992	270	71	40	19	5	3	6.75	4.99	77.04	52.96	25.56	13.33
1993	302	79	57	20	4	5	5.3	4.4	77.81	52.32	31.46	18.87
1994	347	88	59	21	4	4	5.88	4.94	75.79	54.76	31.99	17.87
1995	340	87	61	22	5	5	5.57	3.84	73.82	48.53	25	14.41
1996	363	91	64	21	4.5	3	5.67	4.2	74.1	49.31	27	15.98
1997	413	99	66	21	5	5	6.26	4.07	71.67	48.18	26.88	13.32
1998	421	100	67	25	6	2	6.28	4.55	77.2	50.36	26.37	13.3
1999	358	91	74	14	4	4	4.84	2.97	73.18	47.49	21.79	13.41
2000	370	97	67	17	5	4	5.52	3.54	75.68	47.84	23.78	11.62
2001	375	98	74	23	4	3	5.07	3.85	73.6	48.27	26.67	18.93
2002	387	96	62	25	4	4	6.24	5.51	78.81	57.36	30.75	17.57
2003	400	95	62	23	5	3	6.45	4.58	74.25	51.5	25.75	14.5
2004	566	136	83	42	5	4	6.82	6.21	77.39	54.42	30.74	18.9
2005	497	125	85	15	5	4	5.85	3.54	73.24	46.88	23.94	11.27
2006	486	118	90	25	4.5	4	5.4	3.99	74.9	50.41	26.54	17.28
2007	542	134	94	31	5	1	5.77	4.67	76.57	50.74	27.12	18.27
2008	490	126	82	31	4.5	4	5.98	5.53	77.96	54.9	32.65	20.41
2009	514	121	87	28	5	4	5.91	5.18	78.21	54.09	31.91	18.29
2010	523	124	87	32	5	4	6.01	5.08	75.91	51.63	30.4	18.55
2011	575	129	86	22	6	6	6.69	4.66	73.57	49.91	27.48	14.43
2012	503	104	74	23	6	6	6.8	4.53	72.37	48.91	24.65	15.51
2013	493	113	78	27	5	4	6.32	4.79	74.04	51.52	28.19	17.44
2014	427	96	60	26	6	5	7.12	5.05	74.47	49.18	25.29	15.46

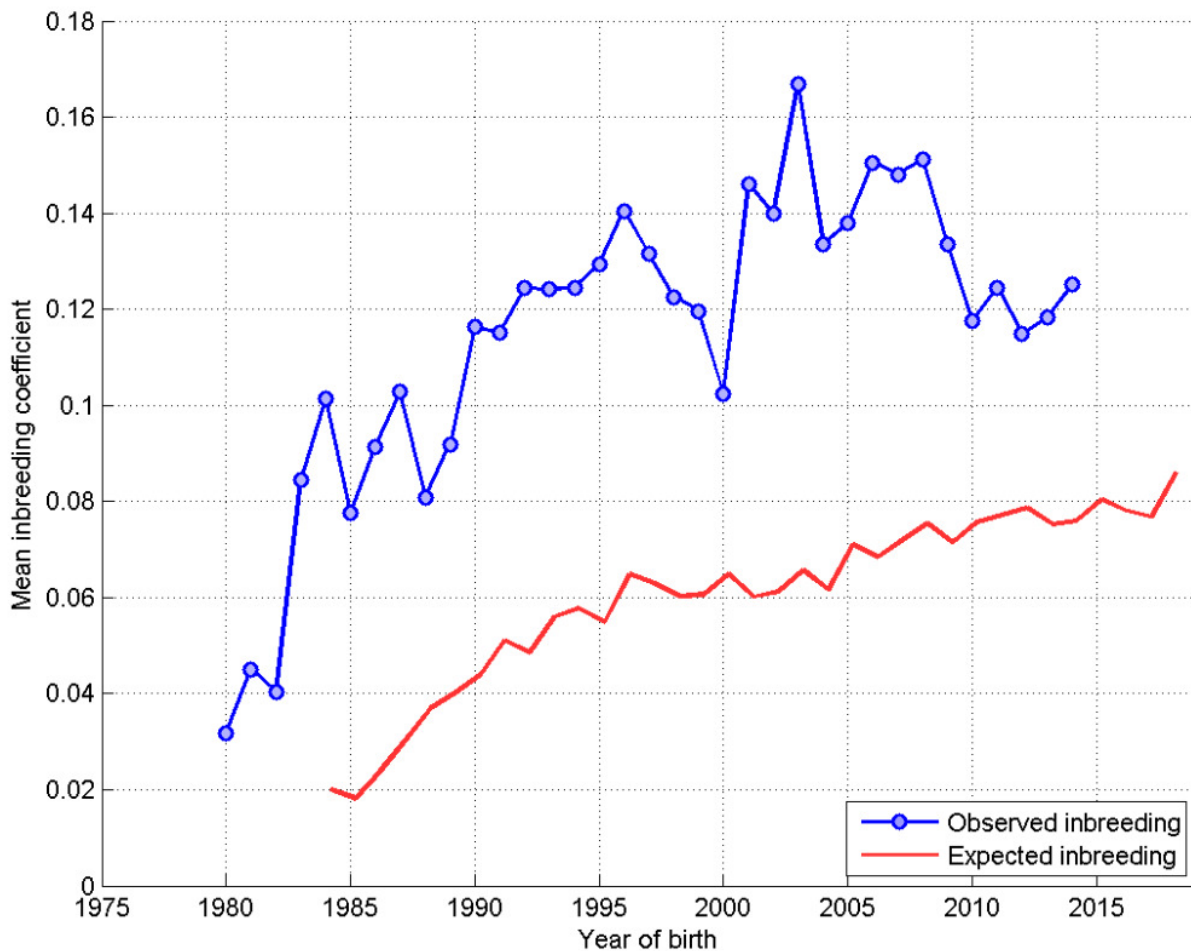


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 4.21

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 = 48.3

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	177.2	229.8	288.2	379	419.6	505.8	504.2
Total #sires	127	141	136	187	206	248	207
Max #progeny	56	107	93	61	108	85	73
Mean #progeny	6.9213	8.1348	10.324	10.128	10.18	10.194	12.174
Median #progeny	4	5	6	6	6	6	7
Mode #progeny	1	4	5	4	6	4	4
SD #progeny	9.0199	11.264	12.89	10.607	12.897	11.54	12.681
Skew #progeny	3.0528	5.4036	3.3325	2.4042	3.6107	2.7341	2.0855
Total #dams	241	251	240	327	358	443	405
Max #progeny	22	16	21	27	25	45	22
Mean #progeny	3.6473	4.5737	6	5.792	5.8575	5.7065	6.2222
Median #progeny	3	4	5	5	5	5	5
Mode #progeny	1	2	3	4	4	4	4
SD #progeny	3.273	3.3961	4.1297	4.0366	4.182	4.6613	4.3086
Skew #progeny	2.4636	1.2531	1.2366	1.6475	1.5333	2.7333	1.4504
Rate of inbreeding	0.080099	0.007992	0.012034	-0.01776	0.040334	-0.00406	0.004305
Generation interval	4.228	4.131	4.1941	4.1479	4.225	4.2839	4.2738
Effective pop size	6.2423	62.564	41.548	n/a	12.397	n/a	116.15



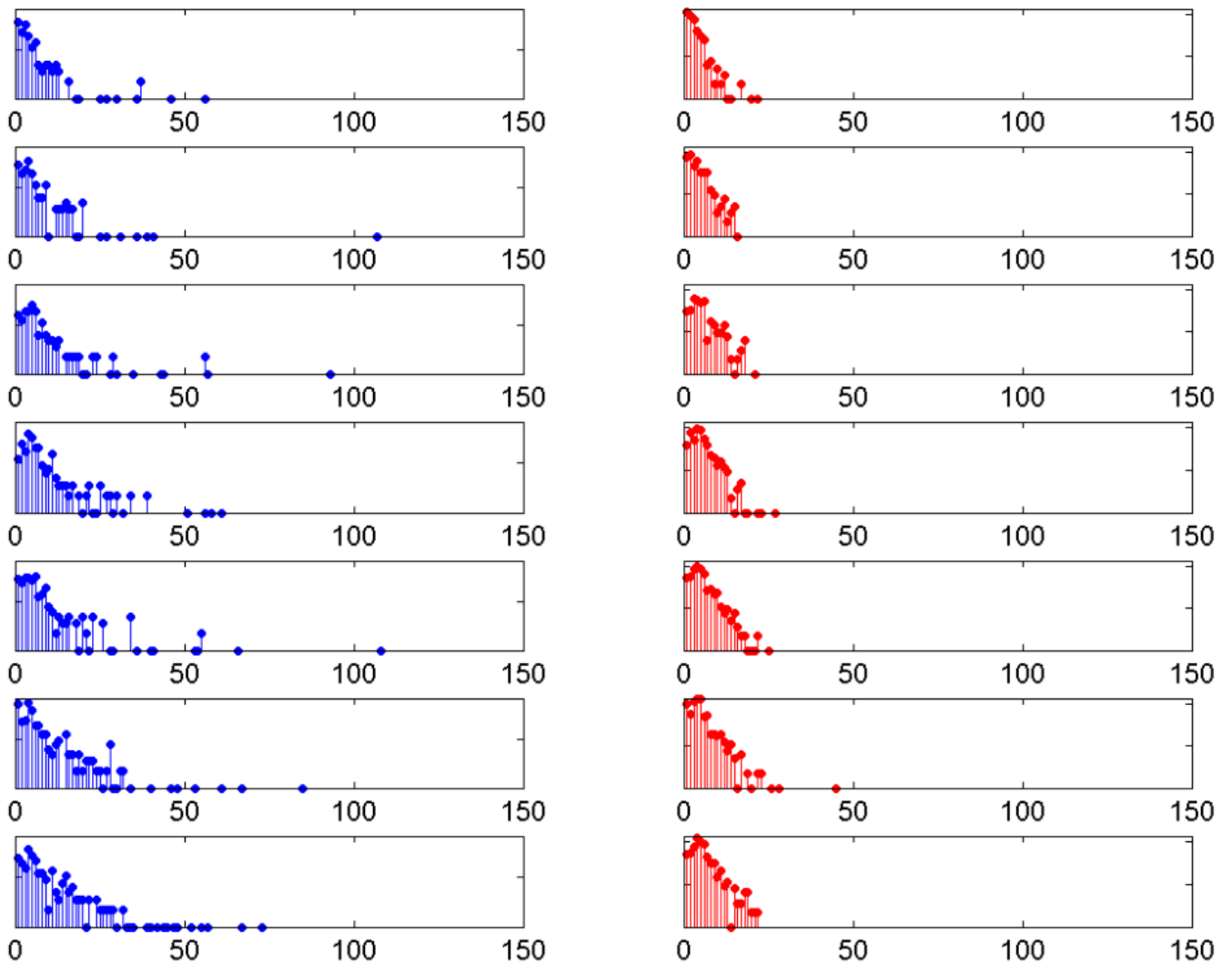
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number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