



THE KENNEL CLUB

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September 2015

Population analysis of the *Glen of Imaal Terrier* breed

Genetic analysis of the Kennel Club pedigree records of the UK *Glen of Imaal 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

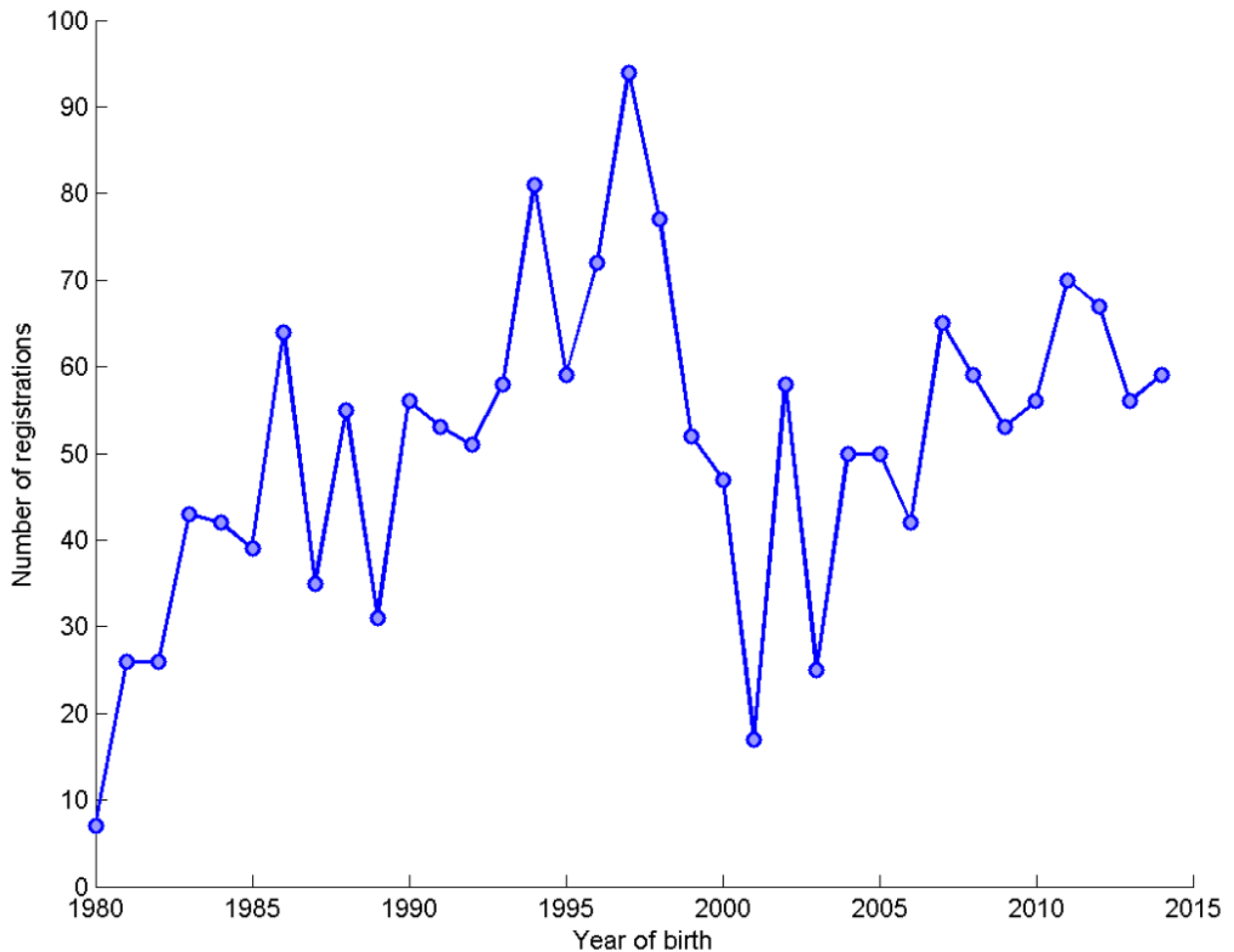
The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered *Glen of Imaal Terrier* population, and statistics were calculated for the period 1980-2014.



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: Glen of Imaal Terrier

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = 0.71 per year (with a 95% confidence interval of 0.13 to 1.29).



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	7	5	5	2	1	1	1.4	0.55	n/a	n/a	n/a	n/a
1981	26	10	8	14	1	1	3.25	4.5	n/a	n/a	n/a	n/a
1982	26	9	7	8	3	1	3.71	2.69	n/a	n/a	n/a	n/a
1983	43	12	10	12	3.5	1	4.3	3.3	76.74	55.81	27.91	27.91
1984	42	14	12	16	2	1	3.5	4.52	83.33	66.67	38.1	38.1
1985	39	13	12	8	2.5	1	3.25	2.56	82.05	53.85	20.51	20.51
1986	64	18	10	16	5	1	6.4	5.27	79.69	62.5	25	25
1987	35	10	9	7	5	1	3.89	2.57	n/a	n/a	n/a	n/a
1988	55	15	12	10	4	2	4.58	3.15	80	47.27	18.18	18.18
1989	31	8	6	12	4	2	5.17	3.82	n/a	n/a	n/a	n/a
1990	56	14	12	12	4.5	1	4.67	3.52	78.57	50	21.43	21.43
1991	53	12	9	15	5	1	5.89	4.46	n/a	n/a	n/a	n/a
1992	51	12	9	15	2	2	5.67	5.43	n/a	n/a	n/a	n/a
1993	58	17	15	10	4	4	3.87	2.45	75.86	48.28	29.31	17.24
1994	81	20	15	15	5	6	5.4	4.07	79.01	50.62	34.57	18.52
1995	59	14	8	14	6.5	6	7.38	4.34	n/a	n/a	n/a	n/a
1996	72	18	15	8	5	1	4.8	2.57	75	43.06	22.22	11.11
1997	94	18	12	33	6	8	7.83	8.47	78.72	55.32	35.11	35.11
1998	77	20	11	16	6	1	7	5.29	84.42	53.25	20.78	20.78
1999	52	14	11	16	3	3	4.73	4.78	82.69	65.38	30.77	30.77
2000	47	10	8	12	5	3	5.88	3.91	n/a	n/a	n/a	n/a
2001	17	9	7	6	1	1	2.43	1.99	n/a	n/a	n/a	n/a
2002	58	15	9	17	4	1	6.44	5.81	n/a	n/a	n/a	n/a
2003	25	5	4	14	5	1	6.25	5.56	n/a	n/a	n/a	n/a
2004	50	14	11	17	2	1	4.55	5.3	90	70	34	34
2005	50	15	10	15	3.5	1	5	4.76	86	64	30	30
2006	42	10	8	11	5.5	1	5.25	4.03	n/a	n/a	n/a	n/a
2007	65	13	9	12	7	11	7.22	3.6	n/a	n/a	n/a	n/a
2008	59	13	9	17	5	5	6.56	4.61	n/a	n/a	n/a	n/a
2009	53	13	9	20	3	1	5.89	6.95	n/a	n/a	n/a	n/a
2010	56	14	10	16	5	1	5.6	4.45	76.79	57.14	28.57	28.57
2011	70	13	9	19	6	6	7.78	5.78	n/a	n/a	n/a	n/a
2012	67	15	11	15	4	1	6.09	5.38	88.06	61.19	22.39	22.39
2013	56	13	8	15	8	1	7	5.18	n/a	n/a	n/a	n/a
2014	59	10	7	20	5	5	8.43	6.45	n/a	n/a	n/a	n/a

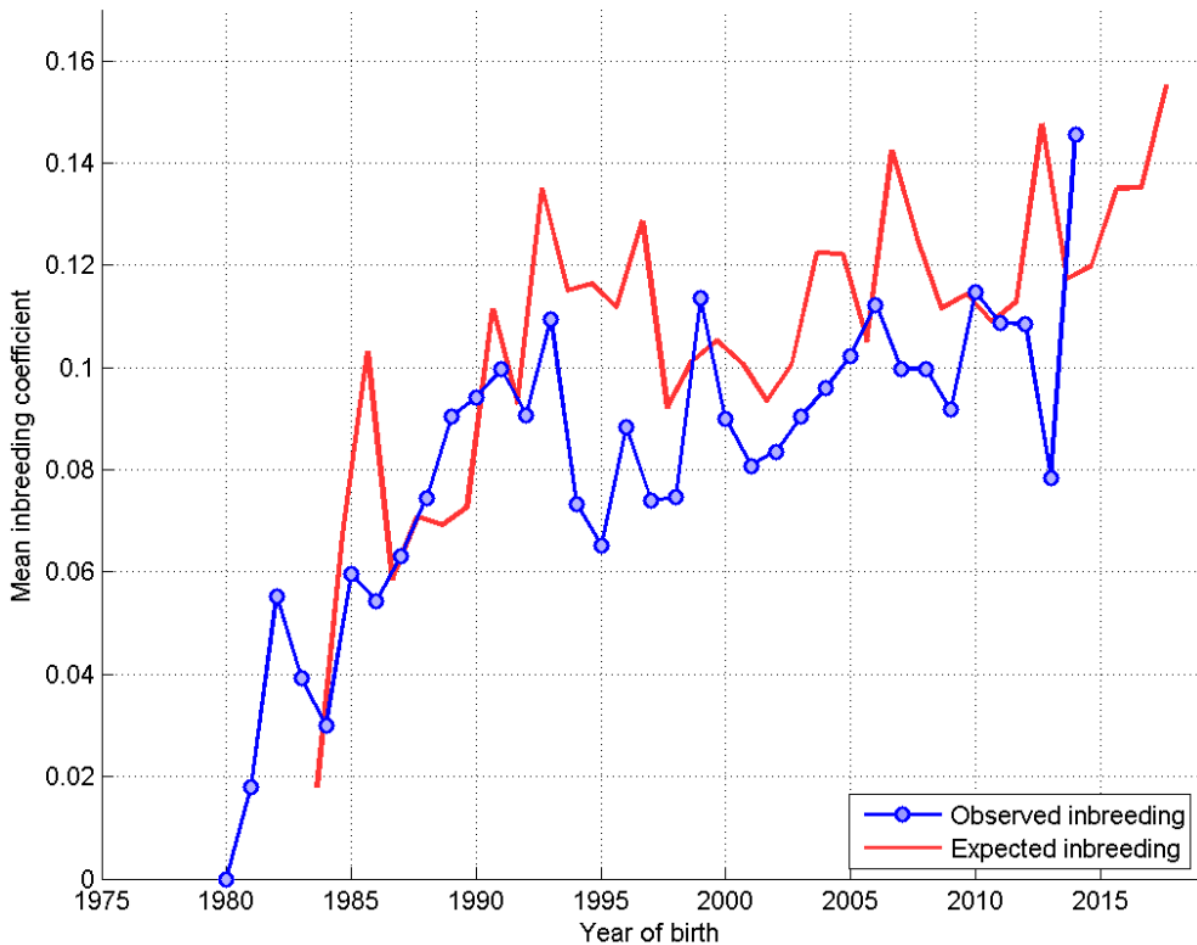


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 3.65

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 = 57.2

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	28.8	44.8	59.8	70.8	39.4	53.8	61.6
Total #sires	26	29	38	36	30	27	33
Max #progeny	20	37	45	69	25	41	31
Mean #progeny	5.3077	7.6897	7.7105	9.8056	6.5333	9.9259	9.303
Median #progeny	3	5	5	7	3	6	6
Mode #progeny	1	2	1	1	1	1	1
SD #progeny	5.9516	7.8427	8.5611	11.926	7.3425	11.337	9.019
Skew #progeny	1.493	1.9955	2.4855	3.5504	1.3348	1.4506	1.0089
Total #dams	37	46	54	65	46	48	55
Max #progeny	18	16	27	15	15	19	19
Mean #progeny	3.7297	4.8478	5.5185	5.4308	4.2174	5.5833	5.5818
Median #progeny	2	4	4	5	3	4.5	5
Mode #progeny	1	2	1	1	1	1	1
SD #progeny	3.7539	3.8642	4.9858	3.6656	3.4891	4.9026	4.3363
Skew #progeny	2.0092	1.4462	2.3067	0.74924	1.314	1.1918	1.1582
Rate of inbreeding	0.016659	0.027599	-0.012139	0.040906	0.011467	-0.013129	0.015545
Generation interval	2.0238	3.1558	3.5279	4.5073	4.8543	3.5115	4.1549
Effective pop size	30.015	18.116	n/a	12.223	43.603	n/a	32.164



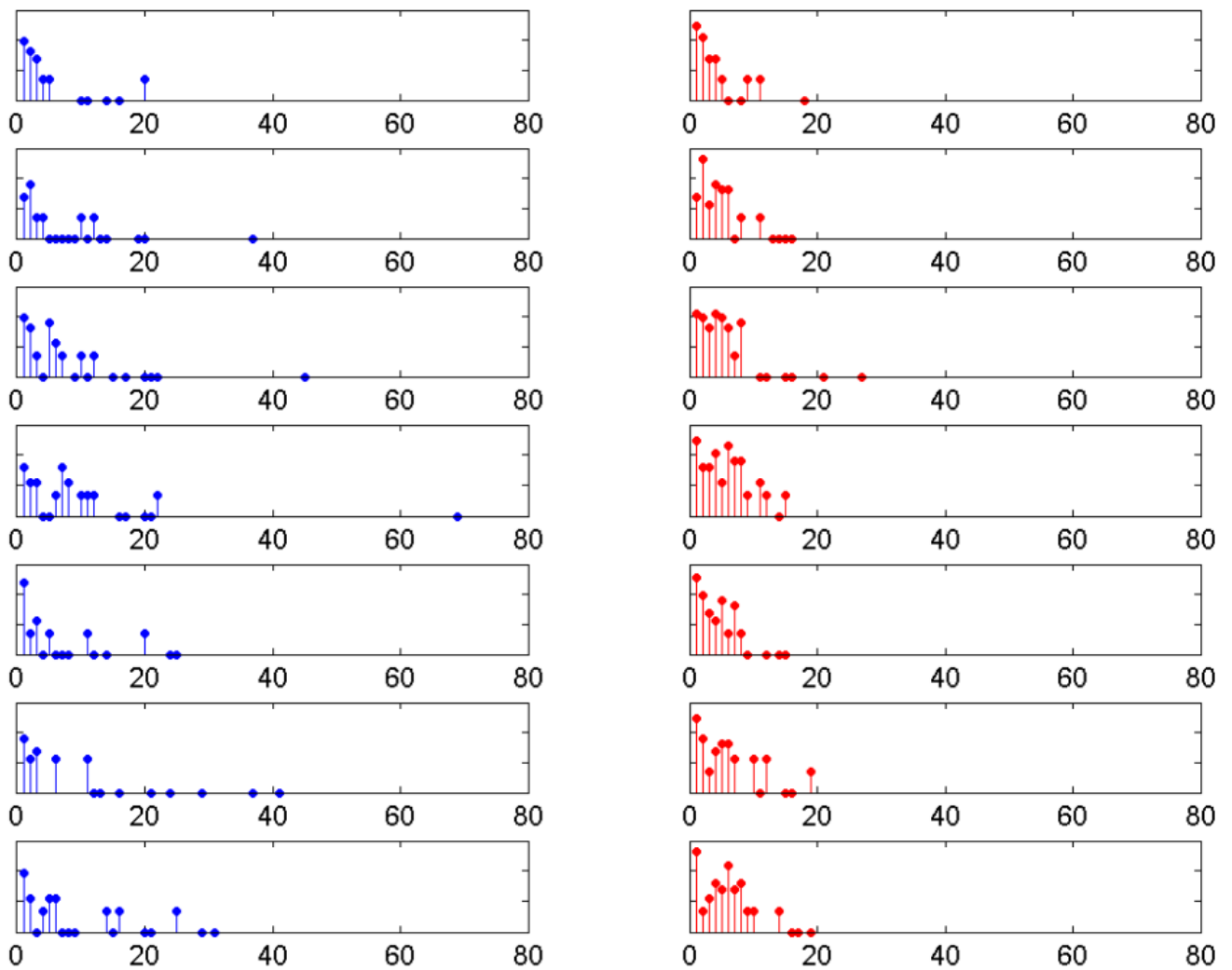
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number 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 can be seen from figure 1, the number of animals of this breed registered with the Kennel Club is fairly small. The small population size and possible influence of migrant animals mean there may be large fluctuations in the rate of inbreeding and effective population size. However, the rate of inbreeding in this breed has remained relatively steady but rather high over the whole period.

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.