THE KENNEL CLUB
Making a difference for dogs

September 2015

Population analysis of the *Newfoundland* breed

Genetic analysis of the Kennel Club pedigree records of the UK ***Newfoundland*** 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).

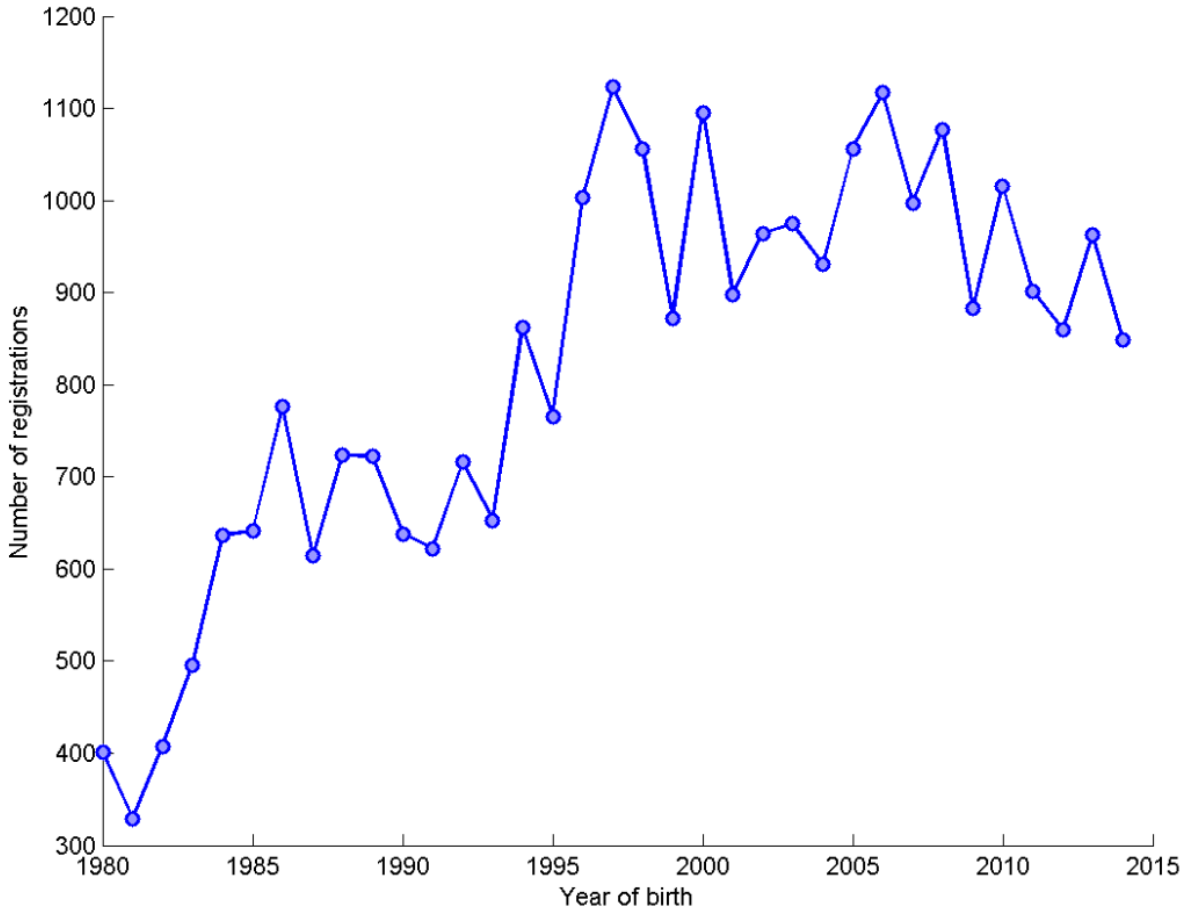
Summary of results

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

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = 16.46 per year (with a 95% confidence interval of 11.85 to 21.07).

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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.

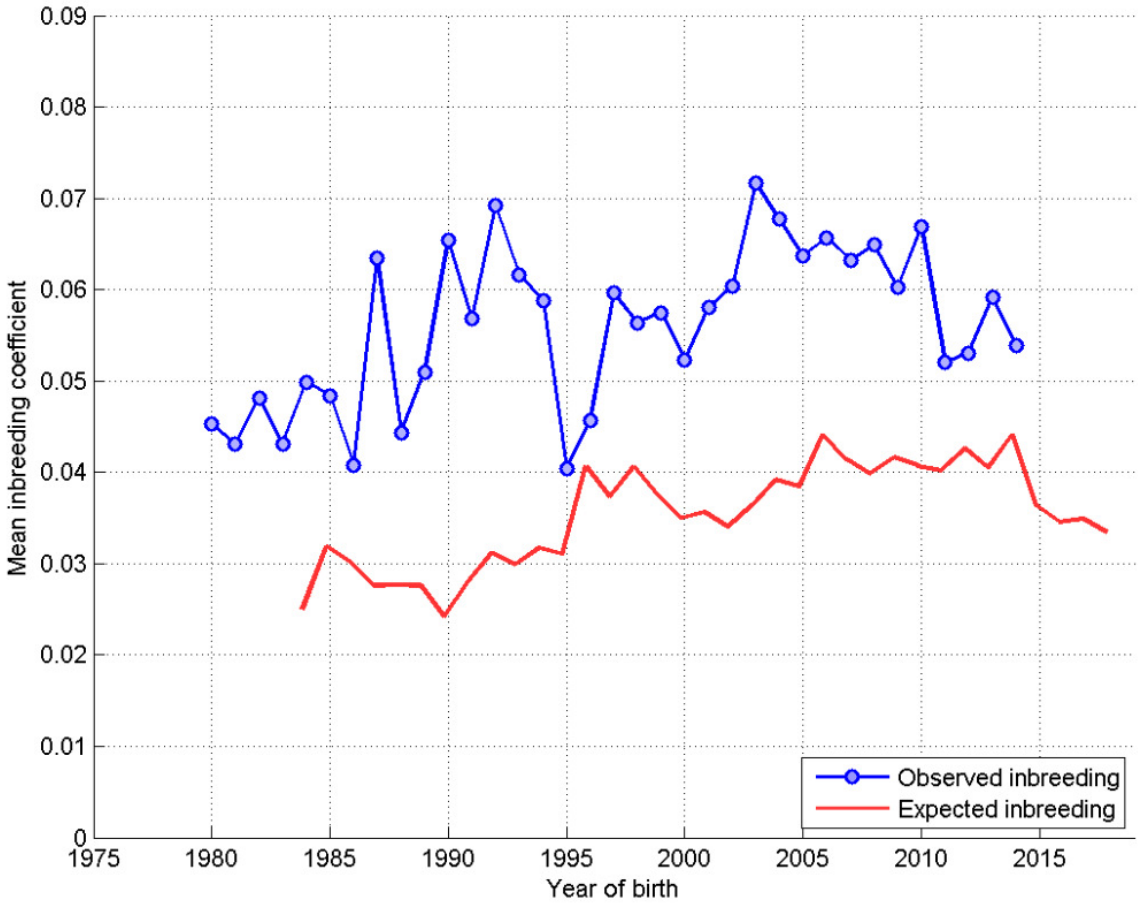
year	#born	#dams	#sires	puppies per sire					%puppies sired by most prolific sires			
				max	median	mode	mean	sd	50% sires	25% sires	10% sires	5% sires
1980	401	83	52	38	6	1	7.71	6.76	79.55	52.62	28.93	19.95
1981	329	65	56	44	4	1	5.88	7.24	87.84	62.61	39.51	26.44
1982	407	72	58	40	6	1	7.02	6.69	79.36	55.04	32.68	20.88
1983	496	89	52	32	6.5	1	9.54	8.81	82.46	60.08	29.44	18.95
1984	637	109	65	40	8	1	9.8	9.02	82.73	56.99	33.44	17.27
1985	641	107	64	47	6.5	5	10.02	9.79	81.75	60.69	31.51	18.41
1986	776	134	78	61	7.5	3	9.95	10.01	81.44	57.99	35.05	21.65
1987	614	105	73	38	7	1	8.41	7.3	81.43	54.56	28.83	18.73
1988	724	112	71	54	8	7	10.2	8.89	78.45	54.28	30.11	20.17
1989	722	105	64	48	8.5	5	11.28	10.35	78.39	56.23	31.3	19.39
1990	638	94	62	42	8	6	10.29	8.18	76.02	53.92	28.06	16.3
1991	622	103	72	47	8	8	8.64	7.17	76.53	51.61	27.01	18.33
1992	716	107	66	31	9	9	10.85	7.43	75.7	50.42	26.12	12.29
1993	653	88	57	36	10	10	11.46	7.94	74.43	48.39	26.95	15.47
1994	862	135	68	102	8	1	12.68	17.05	86.66	66.36	43.27	25.87
1995	765	127	68	83	7	7	11.25	13.01	83.14	61.44	37.12	22.09
1996	1003	151	78	70	9	1	12.86	14.32	83.95	62.91	38.38	23.93
1997	1123	155	77	91	10	1	14.58	16.5	83.7	60.82	38.38	25.2
1998	1056	157	79	99	9	6	13.37	15.8	84.09	61.36	37.31	25.57
1999	872	138	83	67	7	1	10.51	11.64	85.55	62.84	35.67	21.67
2000	1095	162	84	86	9	1	13.04	13.61	83.56	60.55	32.05	18.72
2001	898	141	81	50	7	7	11.09	11.38	82.41	59.13	35.41	21.38
2002	964	156	95	72	8	1	10.15	10.57	80.39	56.12	34.34	23.13
2003	975	152	73	78	9	1	13.36	13.5	84.21	58.36	32.51	21.54
2004	931	167	99	39	7	1	9.4	8.95	85.61	59.61	31.58	17.51
2005	1056	183	101	47	7	1	10.46	10.71	85.98	61.17	33.81	20.64
2006	1117	185	101	49	8	1	11.06	10.47	84.96	59.09	30.08	17.99
2007	997	175	100	44	7.5	1	9.97	9.33	81.85	57.67	32.3	19.46
2008	1077	186	109	51	8	1	9.88	9.9	85.61	59.8	33.98	18.29
2009	883	166	95	49	6	1	9.29	9.97	86.41	63.08	36.58	22.65
2010	1016	177	98	64	7	1	10.37	11.31	84.15	61.52	35.43	22.93
2011	902	170	96	66	7	1	9.4	10.11	85.59	61.09	34.26	22.17
2012	860	153	94	61	6.5	1	9.15	9.69	85.12	62.33	32.44	21.74
2013	963	181	107	61	6	1	9	10.88	86.92	64.17	41.02	24.09
2014	849	136	77	49	8	1	11.03	10.68	83.98	57.95	34.04	20.61

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) = 3.83

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 = 276.3

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

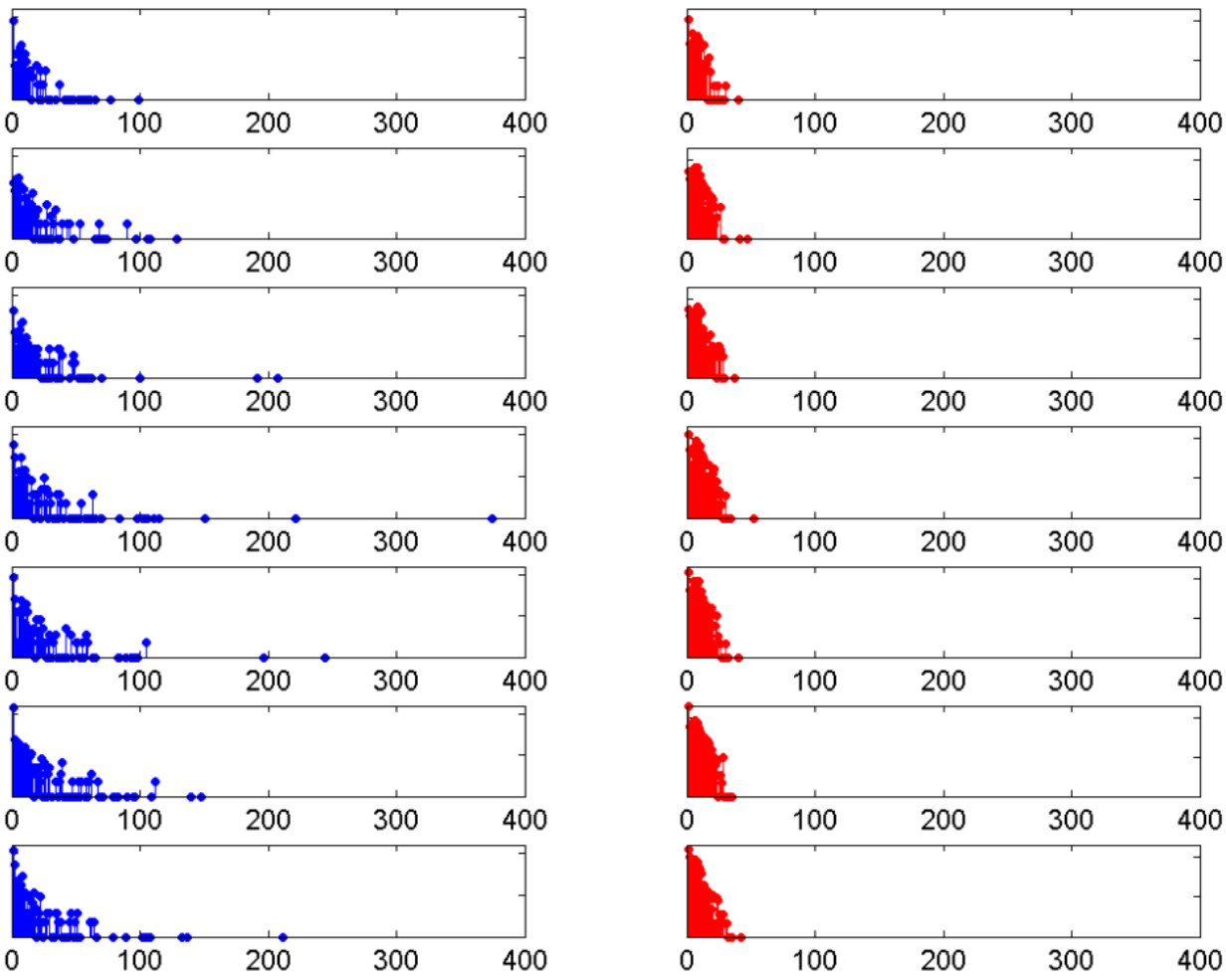
Table 2: a breakdown of census statistics, sire and dam usage and indicators of the rate of loss of genetic diversity over 5 year periods (1980-4, 1985-9, 1990-4, 1995-9, 2000-4, 2005-9, 2010-14). Rate of inbreeding and estimated effective population size for each 5-year block can be compared with the 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	454	695.4	698.2	963.8	972.6	1026	918
Total #sires	184	208	195	228	253	288	292
Max #progeny	99	129	207	375	244	148	211
Mean #progeny	12.332	16.712	17.887	21.132	19.217	17.809	15.712
Median #progeny	7	9	9	10	9	8	7
Mode #progeny	1	5	1	1	1	1	1
SD #progeny	15.933	21.424	24.839	36.051	28.165	24.398	24.458
Skew #progeny	2.471	2.6011	4.4604	5.5444	3.8215	2.3629	3.6031
Total #dams	305	391	383	526	569	613	588
Max #progeny	40	47	37	52	40	35	42
Mean #progeny	7.4393	8.89	9.1123	9.1578	8.5448	8.367	7.8027
Median #progeny	6	8	8	8	8	7	6
Mode #progeny	1	6	8	1	1	1	1
SD #progeny	6.1036	6.3189	6.4154	6.7989	6.2282	6.6363	6.5549
Skew #progeny	1.5329	1.5814	1.1447	1.3388	1.1313	1.0988	1.534
Rate of inbreeding	0.003289	0.003347	-0.00374	0.016888	0.019355	-0.00343	-0.00747
Generation interval	3.4167	3.6828	4.1671	3.5779	4.0842	4.1458	3.7231
Effective pop size	152.03	149.4	n/a	29.607	25.834	n/a	n/a

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 but over the whole period and within levels thought to be sustainable. This means that genetic variation within the breed appears to be being maintained.

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.