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September 2015

Population analysis of the *Basenji* breed

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



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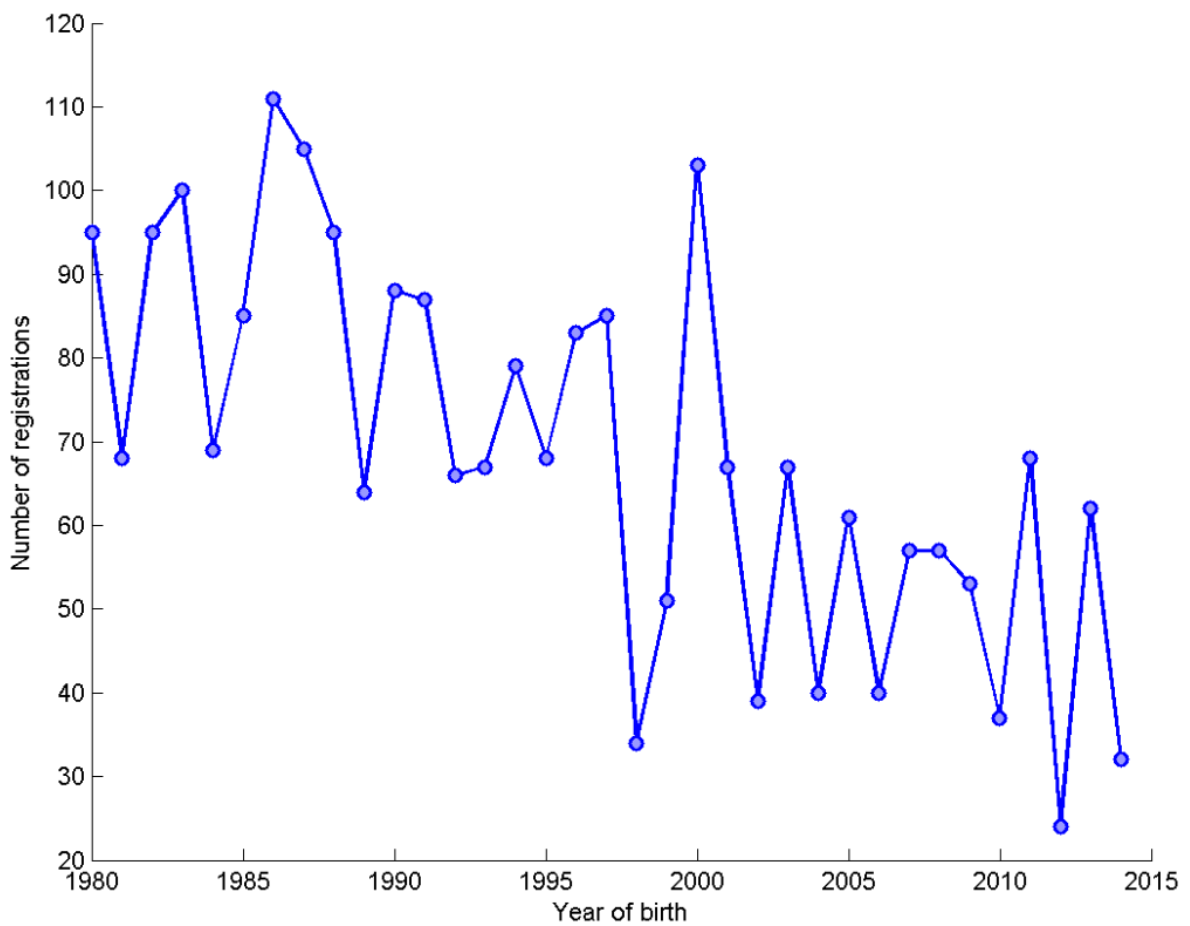
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Figure 1: a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

Breed: Basenji

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = -1.59 per year (with a 95% confidence interval of -2.15 to -1.03).



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	95	29	23	15	3	2	4.13	3.43	78.95	54.74	26.32	15.79
1981	68	21	17	9	4	4	4	2.18	72.06	41.18	25	13.24
1982	95	26	19	23	3	3	5	5.44	81.05	61.05	40	24.21
1983	100	29	25	14	4	4	4	2.53	70	42	27	14
1984	69	18	17	10	4	5	4.06	2.3	73.91	40.58	24.64	14.49
1985	85	25	23	9	3	3	3.7	1.87	69.41	43.53	18.82	10.59
1986	111	27	24	22	4	4	4.63	3.97	67.57	45.95	27.03	19.82
1987	105	28	21	20	4	4	5	4.02	73.33	47.62	28.57	19.05
1988	95	26	18	14	4.5	9	5.28	3.59	76.84	52.63	24.21	14.74
1989	64	17	14	9	4.5	5	4.57	1.91	65.63	42.19	14.06	14.06
1990	88	23	16	13	4.5	4	5.5	2.97	69.32	44.32	26.14	14.77
1991	87	23	20	8	4	4	4.35	1.76	64.37	36.78	18.39	9.2
1992	66	17	16	10	4	4	4.13	2	65.15	39.39	24.24	15.15
1993	67	18	18	6	4	5	3.72	1.67	68.66	40.3	17.91	8.96
1994	79	20	17	11	5	5	4.65	2.4	70.89	39.24	24.05	13.92
1995	68	19	15	12	4	2	4.53	2.85	75	48.53	29.41	17.65
1996	83	22	20	10	4	5	4.15	2.39	72.29	43.37	21.69	12.05
1997	85	25	22	10	4	4	3.86	2.42	71.76	48.24	22.35	11.76
1998	34	11	10	8	3.5	1	3.4	2.46	79.41	55.88	23.53	23.53
1999	51	19	17	8	3	1	3	2.06	80.39	45.1	27.45	15.69
2000	103	31	27	9	4	1	3.81	2.5	77.67	47.57	25.24	8.74
2001	67	25	23	9	3	1	2.91	2.09	79.1	49.25	23.88	13.43
2002	39	18	16	10	1	1	2.44	2.5	79.49	61.54	38.46	25.64
2003	67	21	21	7	3	1	3.19	1.89	77.61	41.79	19.4	10.45
2004	40	14	13	7	2	1	3.08	2.43	85	50	17.5	17.5
2005	61	21	21	6	2	1	2.9	1.97	80.33	47.54	19.67	9.84
2006	40	13	13	6	3	1	3.08	2.06	82.5	45	15	15
2007	57	17	15	11	3	1	3.8	3.28	84.21	57.89	36.84	19.3
2008	57	23	17	14	2	1	3.35	3.67	85.96	61.4	40.35	24.56
2009	53	18	17	14	2	1	3.12	3.28	84.91	54.72	37.74	26.42
2010	37	9	8	10	5	1	4.63	3.46	n/a	n/a	n/a	n/a
2011	68	30	28	8	1	1	2.43	2.13	79.41	58.82	29.41	11.76
2012	24	13	13	5	1	1	1.85	1.34	75	50	20.83	20.83
2013	62	19	18	13	2.5	1	3.44	3.2	83.87	59.68	32.26	20.97
2014	32	8	8	6	4	4	4	1.77	n/a	n/a	n/a	n/a

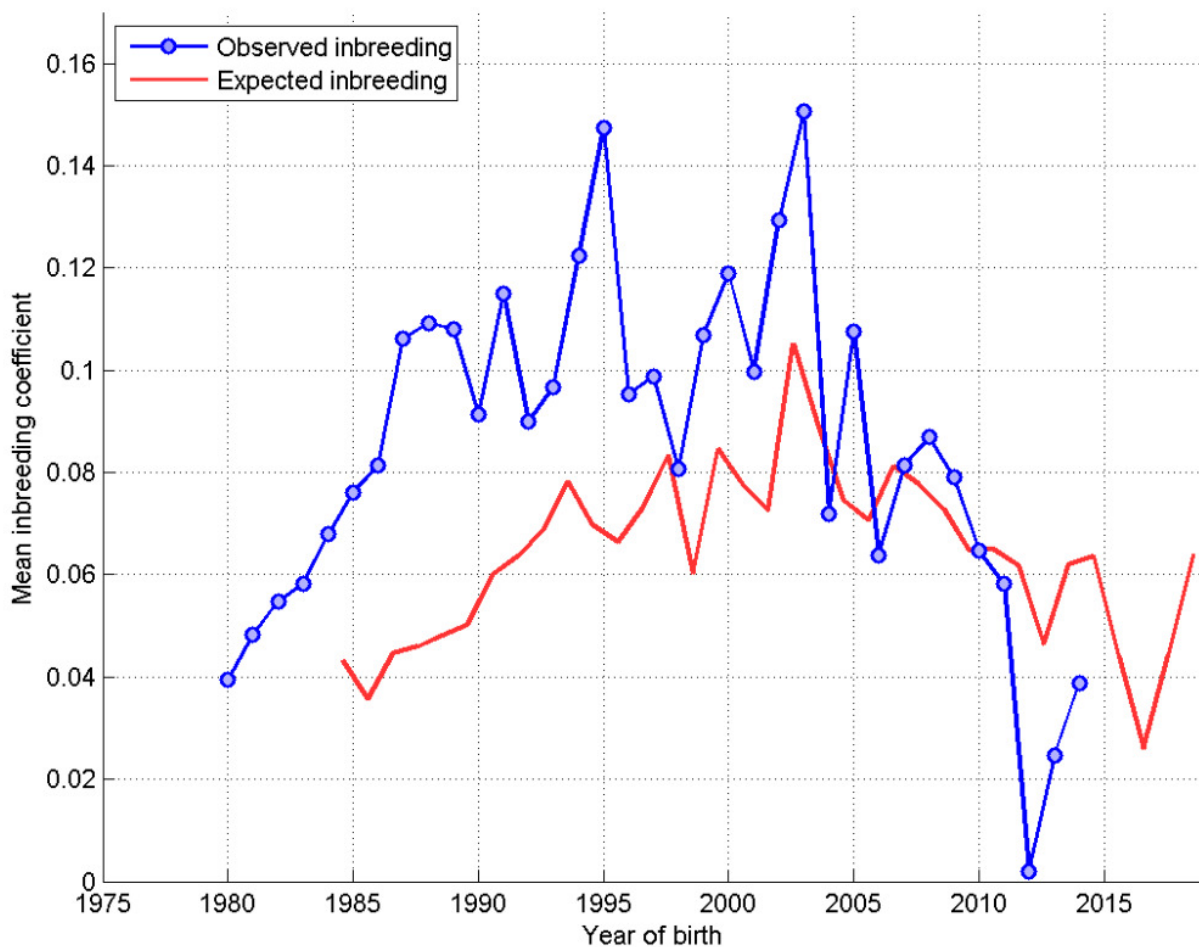


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 4.57

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 = n/a

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.

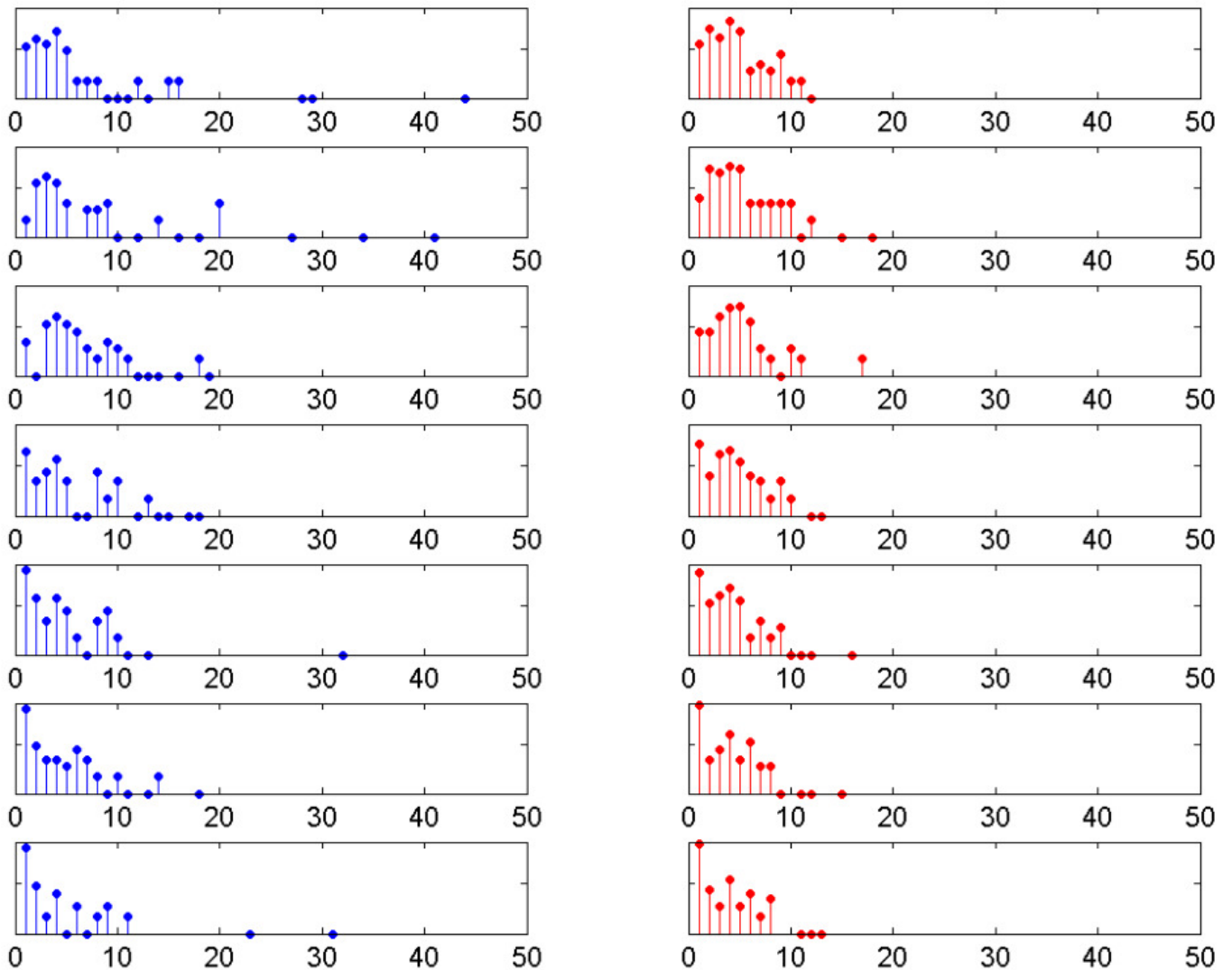
Table 2: by 5-year blocks, the mean number of registrations; for sires the total number used, maximum, mean, median, mode, standard deviation and skewness (indicative of the size of the 'tail' on the distribution) of number of progeny per sire; for dams the total number used, maximum, mean, median, mode, 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	85.4	92	77.4	64.2	63.2	53.6	44.6
Total #sires	69	59	59	58	80	69	60
Max #progeny	44	41	19	18	32	18	31
Mean #progeny	6.1449	7.7797	6.5254	5.5172	3.9375	3.8696	3.6833
Median #progeny	4	4	5	4	2	2	1
Mode #progeny	4	3	4	1	1	1	1
SD #progeny	7.1974	8.1623	4.3046	4.4416	4.4362	3.8878	5.2545
Skew #progeny	3.1209	2.1438	1.2458	1.0238	3.4806	1.5542	3.3472
Total #dams	97	94	78	77	87	80	72
Max #progeny	12	18	17	13	16	15	13
Mean #progeny	4.3711	4.883	4.9487	4.1558	3.6207	3.3375	3.0694
Median #progeny	4	4	4.5	4	3	2	1
Mode #progeny	4	4	5	1	1	1	1
SD #progeny	2.5873	3.1447	3.0147	2.8241	2.9422	2.9551	2.8989
Skew #progeny	0.97184	1.5434	1.8471	0.9622	1.5745	1.4855	1.52
Rate of inbreeding	0.024388	0.044208	0.021154	-0.057909	-0.023735	-0.017212	-0.043967
Generation interval	3.4609	4.3791	4.351	5.2964	5.1768	4.5148	4.8937
Effective pop size	20.502	11.31	23.636	n/a	n/a	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.





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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.

It appears that there has been moderate use of popular sires in this breed (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.