



THE KENNEL CLUB

Making a difference for dogs

September 2015

Population analysis of the *Schipperke* breed

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



THE KENNEL CLUB

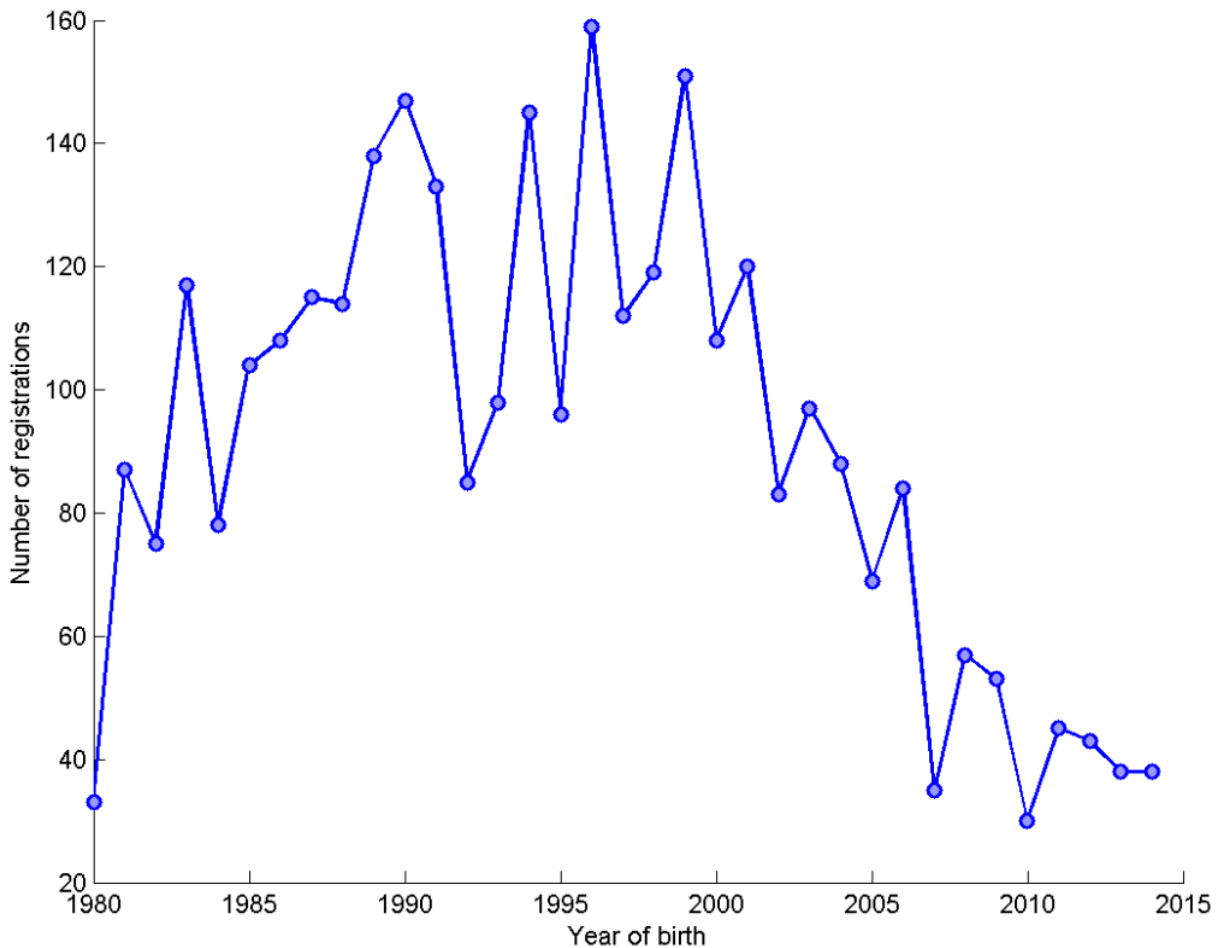
Making a difference for dogs

September 2015

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: *Schipperke*

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = -1.74 per year (with a 95% confidence interval of -2.86 to -0.61).



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	33	24	17	6	1	1	1.94	1.48	75.76	48.48	33.33	18.18
1981	87	37	30	6	3	1	2.9	1.58	72.41	43.68	19.54	13.79
1982	75	32	20	9	3.5	1	3.75	2.57	76	49.33	24	12
1983	117	46	30	14	3	1	3.9	3.06	77.78	52.99	27.35	20.51
1984	78	30	23	9	2	2	3.39	1.97	73.08	47.44	19.23	11.54
1985	104	41	32	12	2	2	3.25	2.77	75.96	54.81	29.81	22.12
1986	108	34	27	10	4	2	4	2.54	76.85	49.07	25	9.26
1987	115	40	25	18	3	2	4.6	4.07	80	54.78	34.78	15.65
1988	114	36	21	13	4	3	5.43	3.49	77.19	45.61	21.93	11.4
1989	138	39	26	19	3.5	3	5.31	4.97	78.99	60.14	36.96	13.77
1990	147	50	33	17	4	5	4.45	3.14	74.83	45.58	23.13	17.69
1991	133	35	22	27	4	2	6.05	6.34	81.95	61.65	35.34	20.3
1992	85	26	19	11	4	4	4.47	2.72	72.94	47.06	24.71	12.94
1993	98	31	23	10	4	4	4.26	2.43	73.47	45.92	19.39	10.2
1994	145	40	21	31	4	4	6.9	7.62	80.69	57.93	39.31	21.38
1995	96	32	20	19	4	4	4.8	4.42	79.17	56.25	31.25	19.79
1996	159	48	35	18	3	1	4.54	4.02	80.5	55.35	32.7	22.01
1997	112	37	28	20	4	4	4	3.51	72.32	46.43	28.57	17.86
1998	119	36	27	19	4	4	4.41	3.44	73.11	47.9	28.57	15.97
1999	151	42	29	26	4	4	5.21	4.95	76.16	52.98	33.77	17.22
2000	108	35	26	10	4	1	4.15	2.52	74.07	46.3	23.15	9.26
2001	120	37	24	16	5	1	5	3.95	79.17	51.67	24.17	13.33
2002	83	30	24	12	3	1	3.46	2.41	74.7	45.78	21.69	14.46
2003	97	34	26	14	3	3	3.73	2.68	71.13	48.45	29.9	14.43
2004	88	30	24	10	3	1	3.67	2.48	75	48.86	20.45	11.36
2005	69	27	23	9	2	1	3	2.45	81.16	55.07	26.09	13.04
2006	84	28	24	12	3	2	3.5	2.8	75	50	27.38	14.29
2007	35	16	15	4	2	1	2.33	1.18	74.29	42.86	22.86	11.43
2008	57	18	17	8	3	4	3.35	1.77	71.93	38.6	22.81	14.04
2009	53	19	16	7	3	2	3.31	2.02	73.58	47.17	26.42	13.21
2010	30	11	10	5	3	1	3	1.49	70	46.67	16.67	16.67
2011	45	18	14	14	2	1	3.21	3.64	82.22	64.44	31.11	31.11
2012	43	13	11	10	4	2	3.91	2.47	76.74	48.84	23.26	23.26
2013	38	17	17	5	2	1	2.24	1.39	78.95	44.74	23.68	13.16
2014	38	13	13	5	3	4	2.92	1.44	73.68	34.21	13.16	13.16

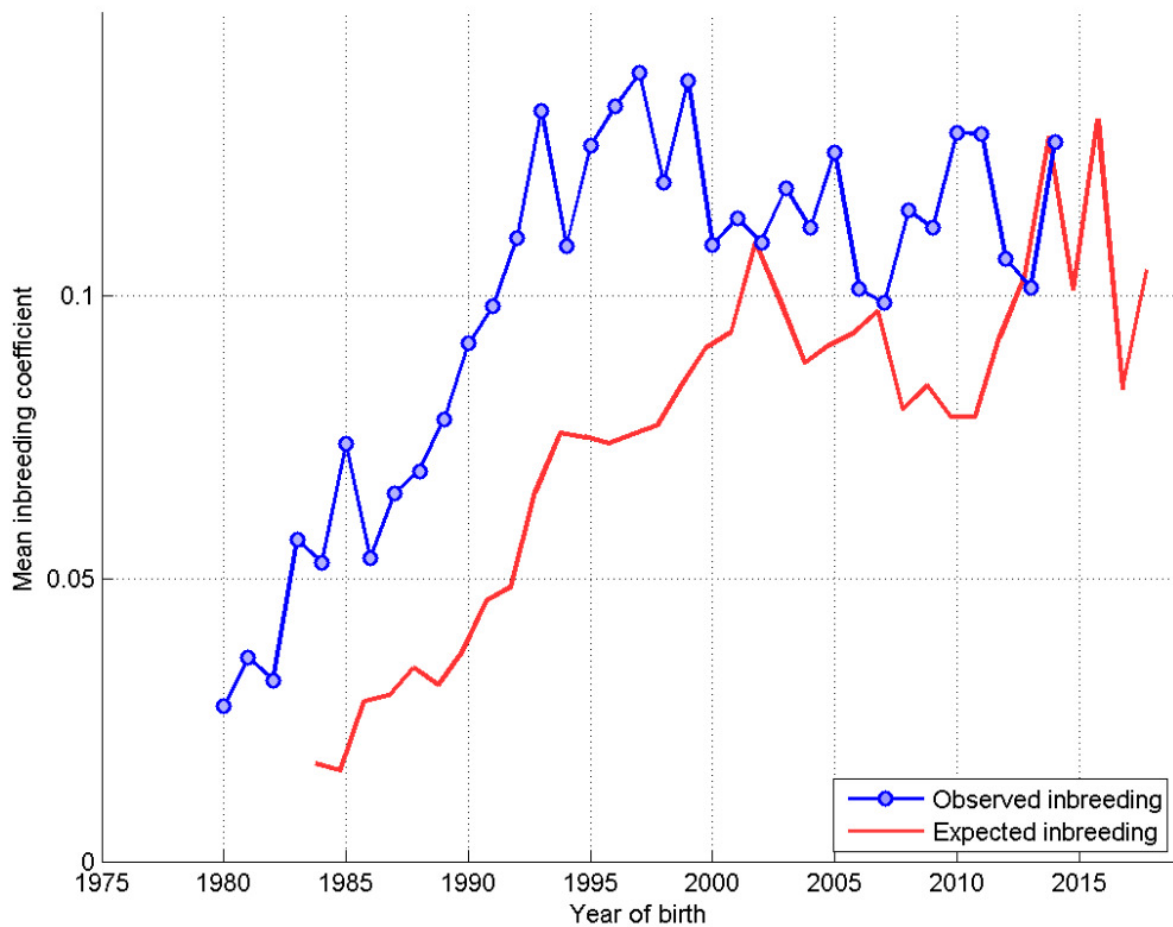


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 3.76

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





THE KENNEL CLUB

Making a difference for dogs

September 2015

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 = 53.3

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.

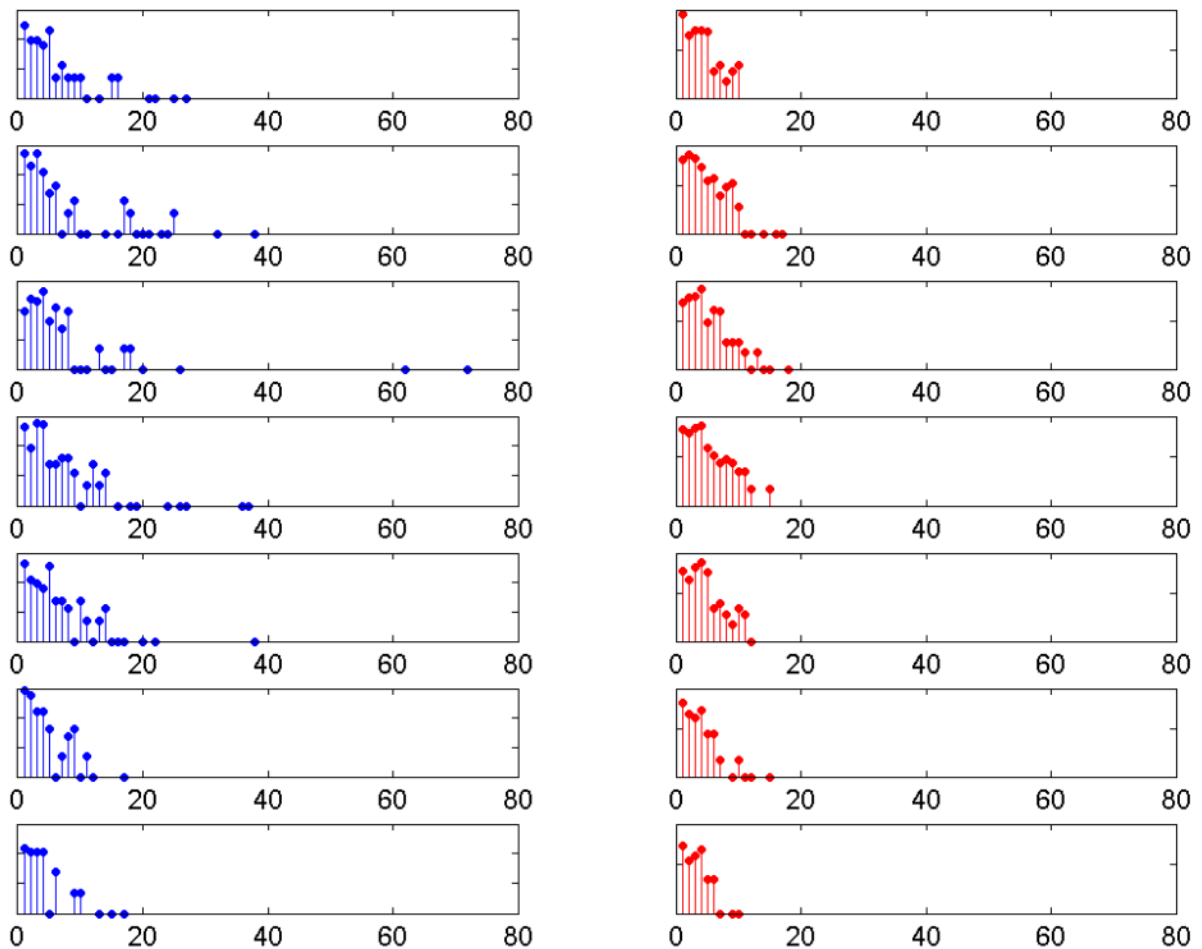
Table 2: by 5-year blocks, the mean number of registrations; for sires the total number used, maximum, mean, median, mode, standard deviation and skewness (indicative of the size of the 'tail' on the distribution) of number of progeny per sire; for dams the total number used, maximum, mean, median, mode, 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	78	115.8	121.6	127.4	99.2	59.6	38.8
Total #sires	63	81	81	93	78	75	45
Max #progeny	27	38	72	37	38	17	17
Mean #progeny	6.1746	7.1235	7.4938	6.8065	6.3462	3.96	4.2889
Median #progeny	4	4	4	4	5	3	3
Mode #progeny	1	1	4	3	1	1	1
SD #progeny	6.0736	8.0006	10.761	7.0715	6.0428	3.3428	3.7757
Skew #progeny	1.7652	1.7686	4.4251	2.2994	2.3833	1.4599	1.756
Total #dams	113	135	133	144	121	84	61
Max #progeny	10	17	18	15	12	15	10
Mean #progeny	3.4425	4.2741	4.5639	4.4167	4.0909	3.5357	3.1639
Median #progeny	3	3	4	4	4	3	3
Mode #progeny	1	2	4	4	4	1	1
SD #progeny	2.4088	3.1845	3.1727	3.0782	2.543	2.7483	1.9932
Skew #progeny	1.0276	1.4258	1.5385	1.1663	1.11	1.7603	1.1089
Rate of inbreeding	0.031811	0.009443	0.025569	0.003546	0.004974	-0.00587	-0.01334
Generation interval	4.2604	3.6982	3.3143	3.2982	3.865	4.0368	3.8695
Effective pop size	15.718	52.951	19.555	141.02	100.52	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.





THE KENNEL CLUB

Making a difference for dogs

September 2015

Comments

As with most breeds, the rate of inbreeding was at its highest in this breed in the 1980s and early 1990s. This represents a 'genetic bottleneck', with genetic variation lost from the population. However, since the mid-1990s the rate of inbreeding has slowed and even declined slightly, implying maintenance and even some replenishment of genetic diversity (possibly through the use of imported animals).

It appears that the extensive use of popular dogs as sires has eased a little (the 'tail' of the blue distribution shortening 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.