THE KENNEL CLUB
Making a difference for dogs

September 2015

Population analysis of the *Pomeranian* breed

Genetic analysis of the Kennel Club pedigree records of the UK ***Pomeranian*** 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 ***Pomeranian*** 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: ***Pomeranian***

Figure 1: Number of registrations by year of birth

Trend of registrations over year of birth (1980-2014) = -12.36 per year (with a 95% confidence interval of -20.29 to -4.43).

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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.

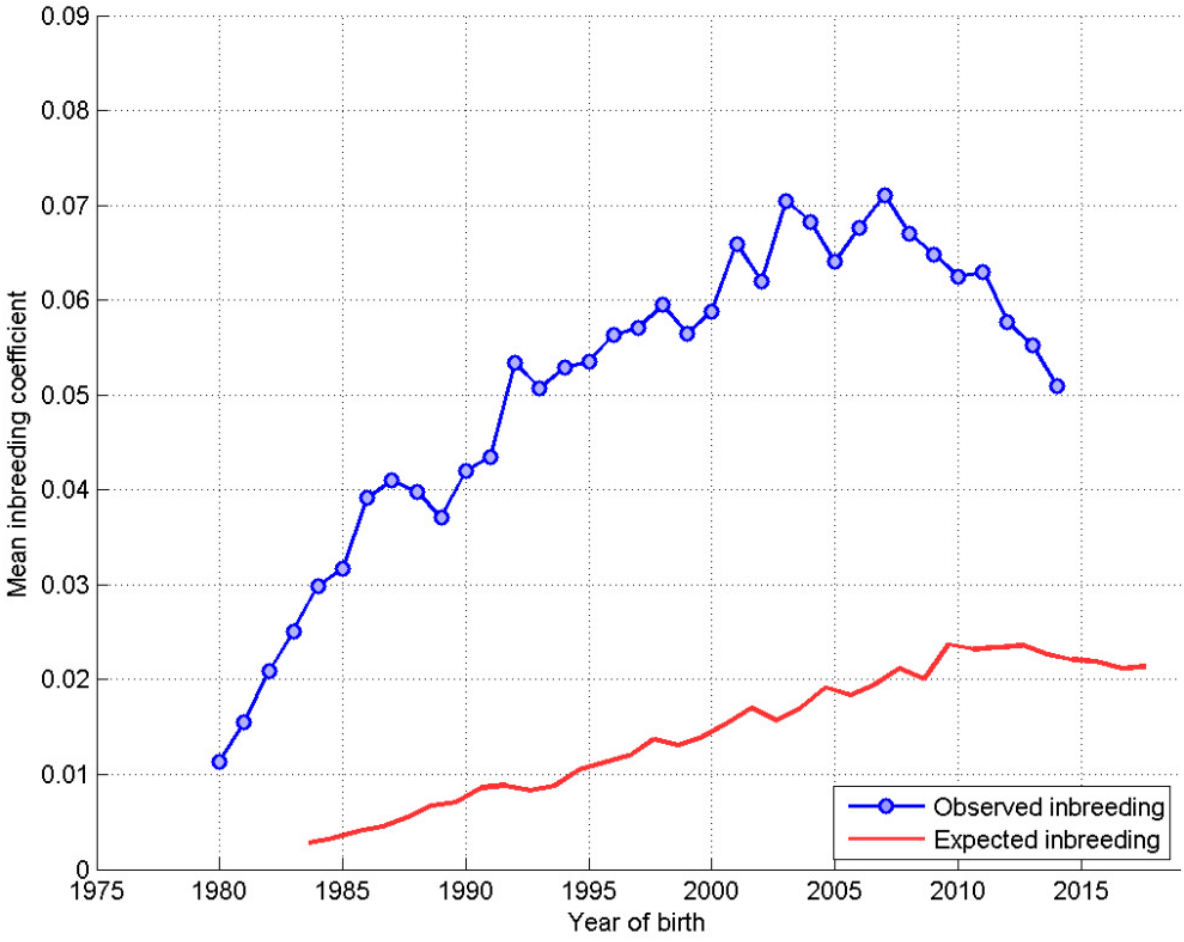
year	#born	#dams	#sires	puppies per sire					%puppies sired by most prolific sires			
				max	median	mode	mean	sd	50% sires	25% sires	10% sires	5% sires
1980	274	218	160	12	1	1	1.71	1.35	70.8	48.91	27.37	17.15
1981	865	506	282	20	2	1	3.07	2.75	78.15	55.03	31.68	19.08
1982	1073	621	320	39	2	1	3.35	3.41	79.31	55.92	31.41	19.94
1983	1175	644	320	21	3	1	3.67	3.25	79.91	55.74	30.72	18.64
1984	1126	610	330	17	3	1	3.41	2.75	77.53	52.58	28.69	17.76
1985	1066	583	313	20	2	1	3.41	2.87	78.33	53.75	29.74	18.39
1986	996	556	309	12	2	1	3.22	2.5	77.41	53.31	28.01	15.46
1987	982	534	303	18	2	2	3.24	2.73	77.7	54.38	30.04	17.31
1988	1025	549	297	18	3	2	3.45	2.7	77.56	52.2	27.9	16.78
1989	1456	660	348	24	3	1	4.18	3.97	79.95	57.01	32.97	19.92
1990	1441	635	338	22	3	2	4.26	3.54	77.79	53.85	29.77	17.9
1991	1341	594	333	21	3	1	4.03	3.54	78.75	54.44	31.17	19.61
1992	1335	594	334	22	3	2	4	3.46	77.15	53.41	30.64	19.25
1993	1210	536	297	35	3	2	4.07	4.22	79.75	57.93	34.79	21.82
1994	1231	522	302	28	3	2	4.08	3.77	78.15	55.81	31.76	19.82
1995	1107	486	292	28	3	1	3.79	3.67	79.58	56.46	33.42	21.23
1996	997	443	245	22	3	2	4.07	3.64	77.83	54.96	32.7	18.96
1997	973	443	257	18	3	1	3.79	3.26	78.42	54.68	31.04	18.81
1998	931	438	252	20	3	1	3.69	3.28	79.27	55.53	31.36	19.76
1999	810	359	234	22	2	2	3.46	3.03	78.4	54.07	30.25	19.26
2000	725	343	211	16	3	2	3.44	2.61	76.69	51.45	27.03	16.83
2001	661	312	174	16	3	2	3.8	3.26	78.82	55.82	30.11	18.76
2002	664	309	185	24	3	2	3.59	3.25	76.51	53.01	31.63	20.18
2003	638	284	183	24	3	1	3.49	3.06	77.43	53.76	29.31	18.34
2004	699	299	172	26	3	3	4.06	3.73	76.11	53.22	31.19	21.17
2005	738	319	192	38	3	2	3.84	3.88	78.73	54.74	30.76	20.73
2006	795	340	202	33	3	2	3.94	3.88	80.63	57.23	31.82	19.37
2007	763	324	195	21	3	1	3.91	3.37	78.64	54	30.41	18.35
2008	799	328	200	32	3	2	4	3.81	78.97	55.07	31.91	20.03
2009	788	324	195	28	3	1	4.04	3.5	78.68	54.31	29.95	18.02
2010	756	328	206	18	3	1	3.67	2.94	77.78	53.44	28.7	16.53
2011	746	323	207	23	2	1	3.6	3.49	80.29	57.1	33.11	20.51
2012	733	314	219	19	2	1	3.35	2.86	79.13	54.3	29.6	18.14
2013	724	324	222	30	2	1	3.26	3.13	78.87	55.39	31.35	19.48
2014	668	273	187	20	3	1	3.57	3.36	79.49	55.99	32.34	20.21

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) = 3.62

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 = 99.1

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

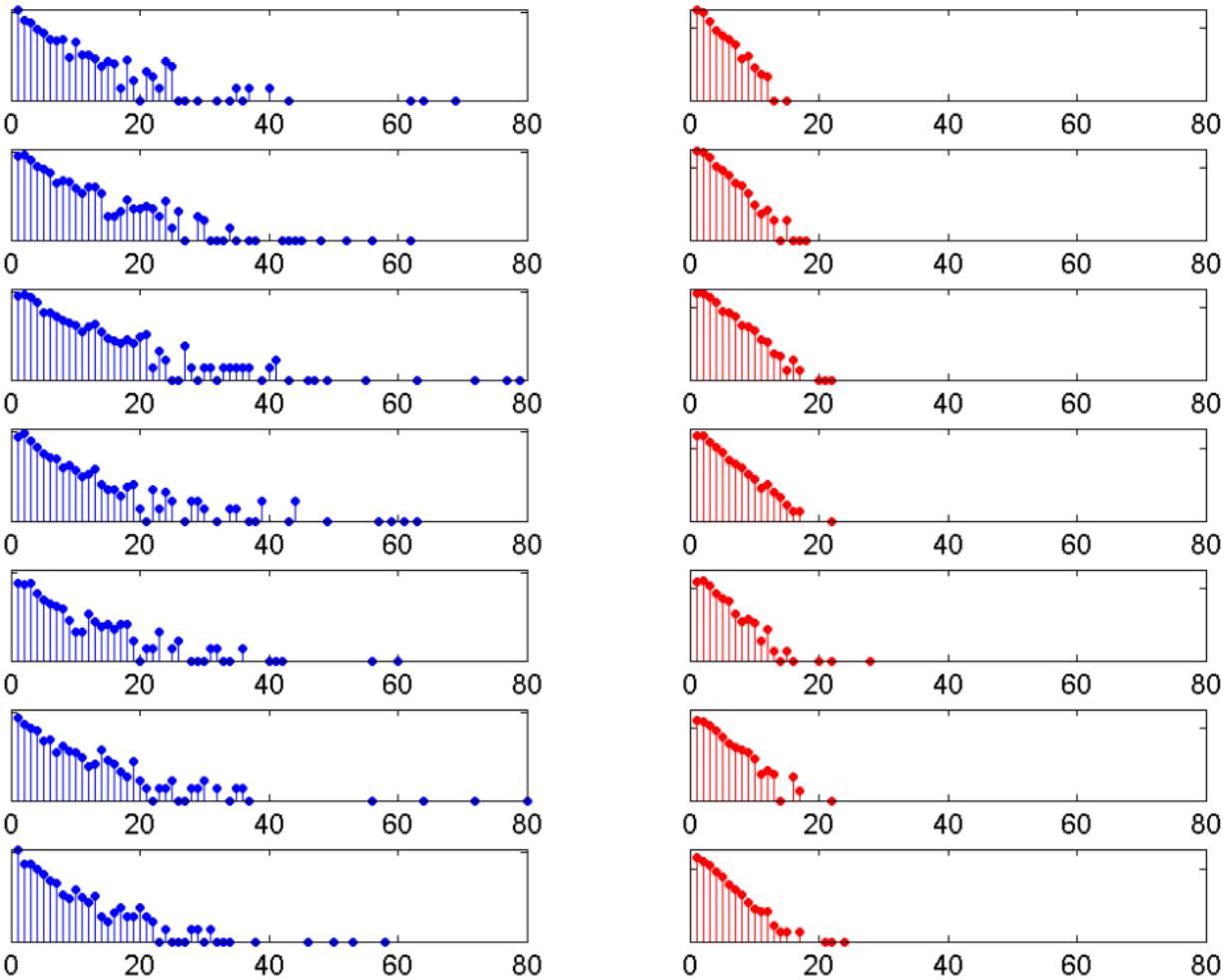
Table 2: a breakdown of census statistics, sire and dam usage and indicators of the rate of loss of genetic diversity over 5 year periods (1980-4, 1985-9, 1990-4, 1995-9, 2000-4, 2005-9, 2010-14). Rate of inbreeding and estimated effective population size for each 5-year block can be compared with the 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	902.6	1105	1311.6	963.6	677.4	776.6	725.4
Total #sires	711	782	846	708	509	550	625
Max #progeny	69	62	79	63	60	80	58
Mean #progeny	6.3305	7.0639	7.7494	6.8037	6.6523	7.0582	5.7936
Median #progeny	4	4	4	4	4	4	3
Mode #progeny	1	2	2	2	1	1	1
SD #progeny	7.7661	7.9906	9.2592	8.4891	7.8036	8.6994	7.1592
Skew #progeny	3.2592	2.605	3.1046	3.0541	2.7569	3.5446	3.0451
Total #dams	1636	1767	1820	1399	1017	1088	1112
Max #progeny	15	18	22	22	28	22	24
Mean #progeny	2.7512	3.1262	3.6022	3.4432	3.3294	3.5671	3.2563
Median #progeny	2	2	3	3	3	3	2
Mode #progeny	1	1	1	2	2	1	1
SD #progeny	2.0976	2.3856	2.7932	2.7355	2.6696	2.8051	2.6904
Skew #progeny	1.7303	1.826	1.7924	1.8793	2.6019	1.8261	2.377
Rate of inbreeding	0.014758	0.004253	0.011283	0.003449	0.009853	0.000421	-0.01118
Generation interval	3.1035	3.5985	3.7003	3.6721	3.9262	3.8352	3.4421
Effective pop size	33.879	117.55	44.314	144.96	50.745	1186.4	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

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, since the mid-2000s 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).

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.