



THE KENNEL CLUB

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September 2015

Population analysis of the *Japanese Chin* breed

Genetic analysis of the Kennel Club pedigree records of the UK *Japanese Chin* 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

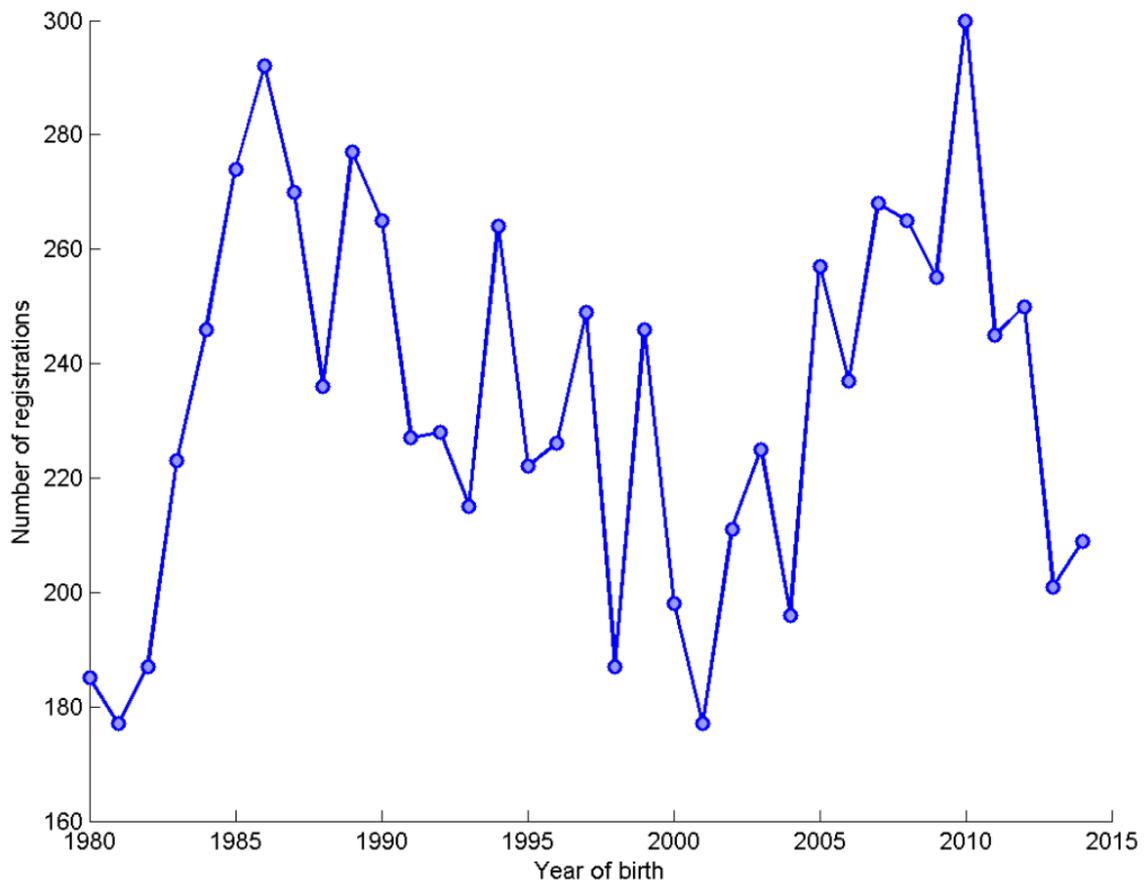
The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered *Japanese Chin* population, and statistics were calculated for the period 1980-2014.



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: Japanese Chin

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = 0.32 per year (with a 95% confidence interval of -0.83 to 1.46).



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	185	89	56	12	3	1	3.3	2.53	77.3	52.43	29.19	16.22
1981	177	83	60	11	2	1	2.95	2.18	77.4	50.28	26.55	15.25
1982	187	83	56	10	3	1	3.34	2.04	72.73	44.92	23.53	14.44
1983	223	94	59	12	3	2	3.78	2.77	77.13	51.57	27.35	15.25
1984	246	94	61	19	3	1	4.03	3.43	78.46	52.85	30.08	17.48
1985	274	109	71	16	3	3	3.86	3.04	75.91	51.46	28.1	18.98
1986	292	122	73	12	3	2	4	2.95	78.08	52.74	24.66	15.07
1987	270	116	79	22	2	1	3.42	3.26	79.26	54.81	30.74	20.37
1988	236	96	65	24	2	2	3.63	3.53	79.24	53.81	32.63	19.92
1989	277	107	65	12	3	2	4.26	3.15	77.26	52.35	27.8	12.27
1990	265	98	69	16	3	1	3.84	3.14	78.49	52.83	29.43	15.09
1991	227	91	62	10	3	2	3.66	2.2	73.57	47.14	22.03	11.89
1992	228	82	58	15	3	3	3.93	2.79	74.56	50.88	26.32	15.35
1993	215	82	60	11	3	2	3.58	2.53	75.81	51.16	25.58	13.95
1994	264	105	64	21	3	2	4.13	3.5	75.38	51.52	29.17	18.56
1995	222	86	60	12	3	4	3.7	2.59	74.32	48.65	26.58	15.32
1996	226	84	53	17	3	1	4.26	3.48	78.76	53.98	26.99	18.58
1997	249	87	60	15	4	4	4.15	2.67	73.09	46.18	23.29	14.06
1998	187	76	56	13	3	2	3.34	2.47	74.87	49.2	28.88	17.65
1999	246	96	62	12	3	2	3.97	2.77	75.61	51.63	24.8	13.41
2000	198	78	55	9	3	3	3.6	2.21	73.74	47.98	23.74	13.13
2001	177	76	54	11	3	1	3.28	2.67	77.4	53.67	28.25	18.08
2002	211	85	56	13	3	1	3.77	2.67	76.78	49.29	26.07	14.69
2003	225	91	61	18	3	1	3.69	3.06	78.22	51.11	28.44	17.78
2004	196	82	56	14	3	2	3.5	2.59	77.04	50	27.04	16.84
2005	257	104	63	13	3	2	4.08	2.99	77.43	52.92	24.9	13.62
2006	237	102	71	12	3	1	3.34	2.38	78.06	50.21	24.89	16.03
2007	268	106	80	12	3	2	3.35	2.29	75.75	48.88	25	14.55
2008	265	102	80	16	3	1	3.31	2.74	76.6	52.45	29.43	17.74
2009	255	100	70	16	3	1	3.64	3.23	80.78	58.43	29.8	20
2010	300	116	76	19	3	3	3.95	2.94	75	49	27.33	16.33
2011	245	105	76	18	2	1	3.22	2.96	77.96	53.47	32.65	21.22
2012	250	100	75	12	3	1	3.33	2.4	76.8	49.6	26.8	16.4
2013	201	83	59	14	3	2	3.41	2.26	73.13	46.27	24.88	15.42
2014	209	84	58	21	3	1	3.6	3.35	77.51	55.02	32.06	19.62

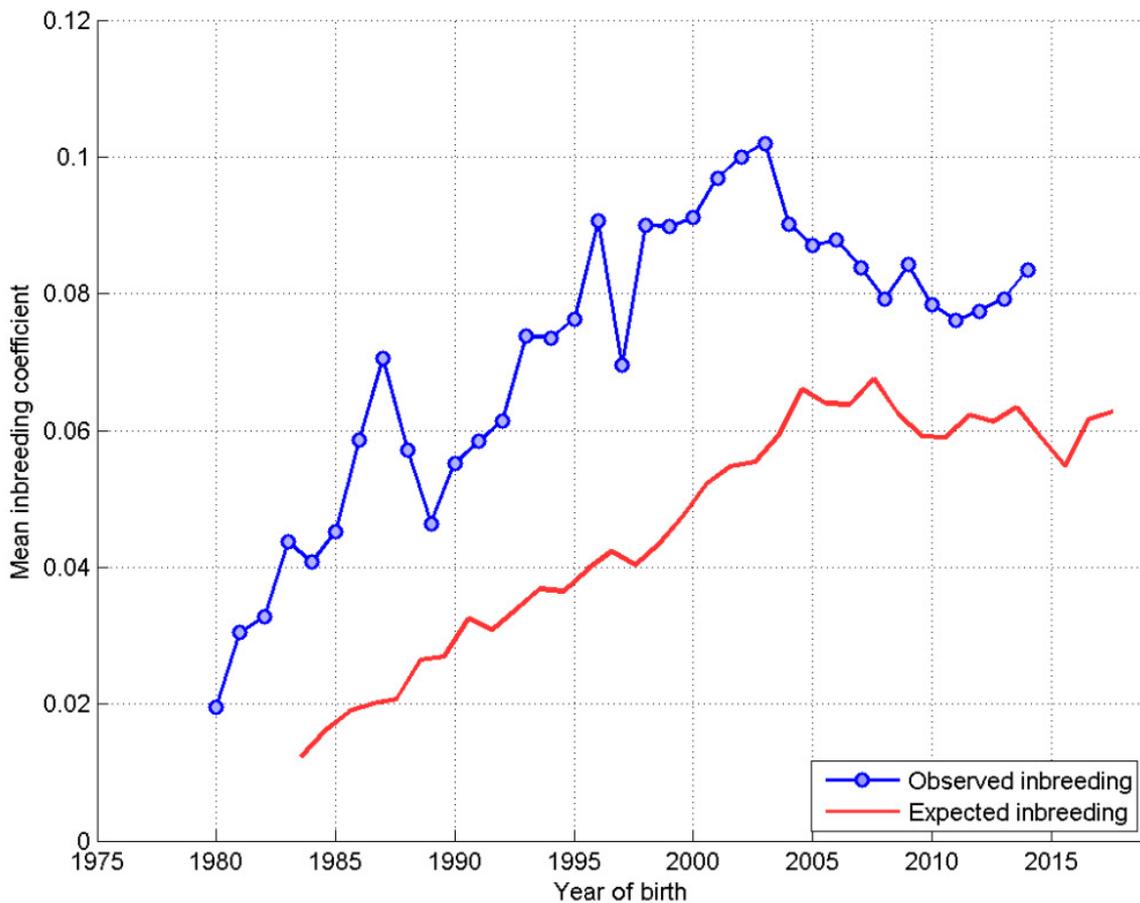


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 3.56

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 = 81.4

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	203.6	269.8	239.8	226	201.4	256.4	241
Total #sires	171	196	184	170	170	226	226
Max #progeny	26	54	37	40	36	41	37
Mean #progeny	5.9357	6.8724	6.5109	6.6294	5.9176	5.6681	5.323
Median #progeny	3	4	4	5	4	4	4
Mode #progeny	1	1	2	1	1	1	1
SD #progeny	5.8753	7.855	6.3254	6.8196	5.8849	6.3204	5.8854
Skew #progeny	1.4116	2.9462	2.0322	2.4077	2.0782	2.6387	2.88
Total #dams	283	341	304	287	278	352	352
Max #progeny	17	27	16	15	13	20	16
Mean #progeny	3.5866	3.9501	3.9408	3.899	3.6187	3.6392	3.4176
Median #progeny	3	3	3	3	3	3	3
Mode #progeny	1	1	3	1	1	1	2
SD #progeny	2.8188	3.1456	2.8055	3.0658	2.5218	2.7118	2.4919
Skew #progeny	1.7282	2.1402	1.4808	1.5316	1.1538	1.9024	1.6296
Rate of inbreeding	0.019326	0.000276	0.01969	0.010479	0.001395	-0.0058	0.004788
Generation interval	3.3683	3.444	3.5383	3.6602	3.8414	3.7366	3.2623
Effective pop size	25.872	1808.5	25.394	47.714	358.31	n/a	104.43



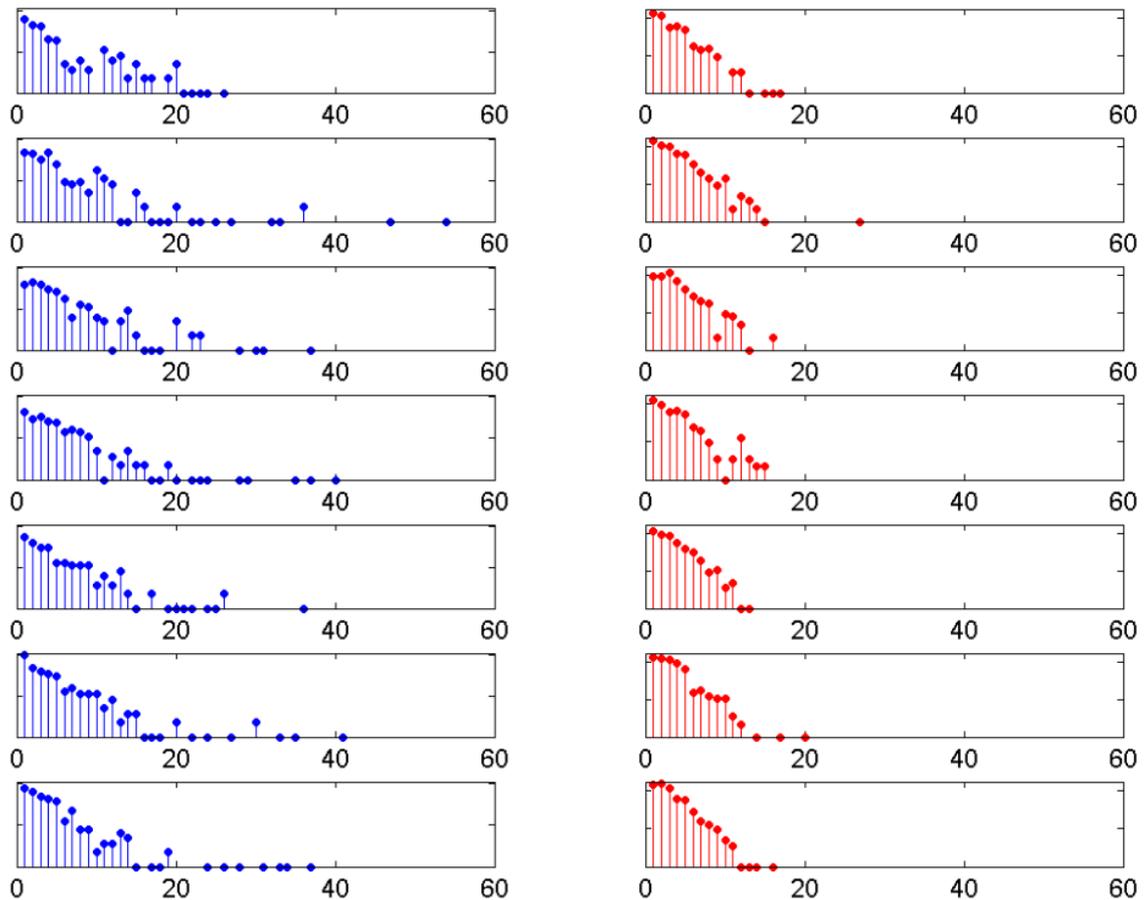
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number 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 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 early 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.