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September 2015

Population analysis of the *Papillon* breed

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



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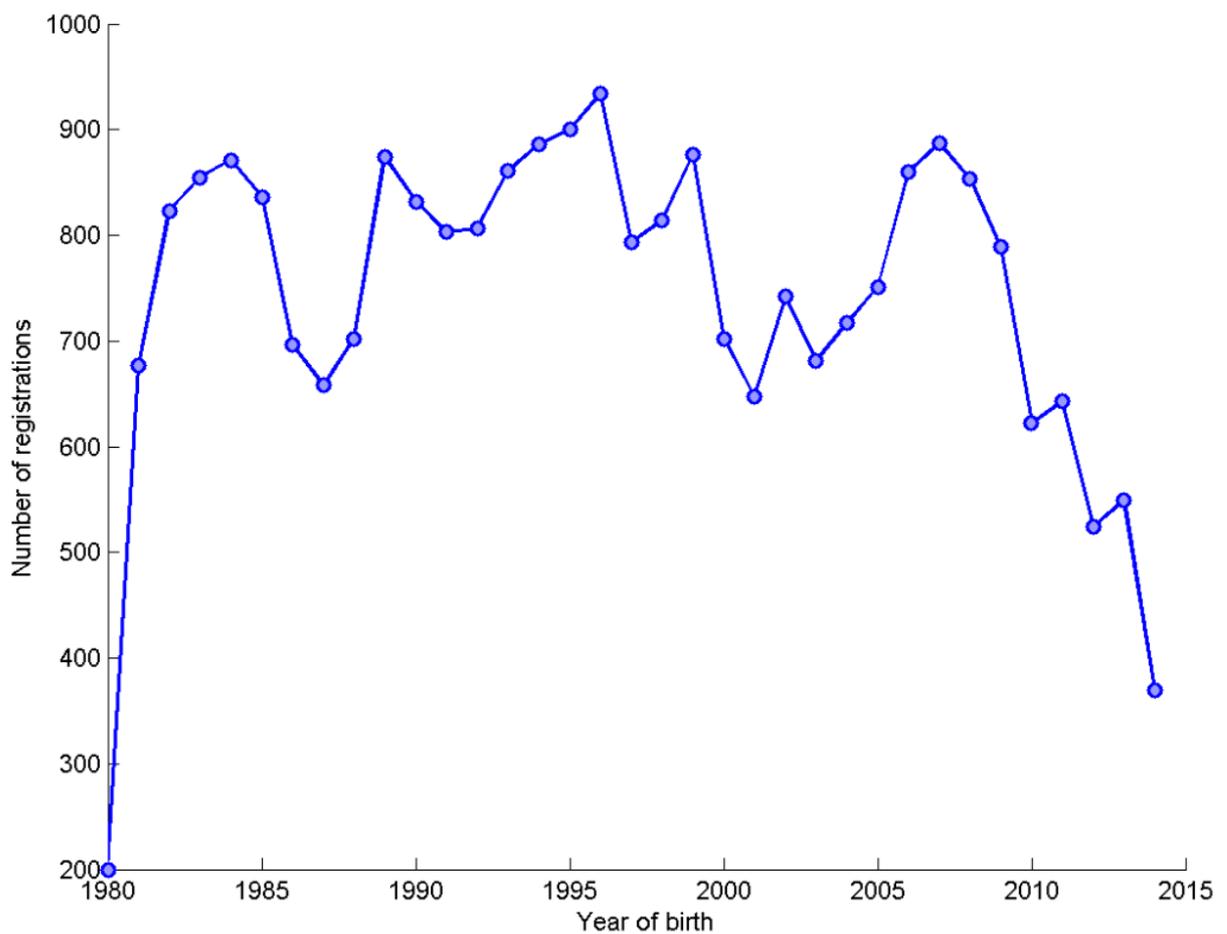
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Figure 1: a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

Breed: Papillon

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = -2.63 per year (with a 95% confidence interval of -7.92 to 2.66).



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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	200	161	123	7	1	1	1.63	1.2	69.5	49	27	17.5
1981	677	361	208	21	2	1	3.25	2.74	77.7	53.18	29.84	17.13
1982	823	397	224	26	3	1	3.67	3.18	77.52	53.1	29.53	18.59
1983	855	411	240	29	2	2	3.56	3.17	78.25	53.68	29.94	18.48
1984	871	416	245	30	2	2	3.56	3.65	79.22	56.26	33.98	21.58
1985	836	394	239	35	3	1	3.5	3.51	78.59	54.55	32.3	20.93
1986	697	330	228	20	2	1	3.06	2.73	76.9	53.95	30.85	19.23
1987	658	313	201	18	2	1	3.27	2.92	79.48	54.86	30.85	19.15
1988	702	324	217	20	3	1	3.24	2.67	76.21	50.57	29.49	18.09
1989	874	330	204	24	3	2	4.28	3.89	79.41	55.72	31.35	19.34
1990	832	321	194	26	3	3	4.29	3.35	75.6	50.96	27.4	17.31
1991	803	312	205	15	3	1	3.92	3.02	77.21	52.18	28.77	15.69
1992	806	333	202	31	3	1	3.99	4.02	80.02	57.82	34.12	21.09
1993	861	324	207	28	3	2	4.16	3.68	76.89	53.19	30.66	18.47
1994	886	326	210	26	3	2	4.22	3.6	76.64	53.5	30.25	19.64
1995	900	348	226	20	3	2	3.98	3.23	76.22	52.56	29.22	17.56
1996	934	342	219	25	3	3	4.26	3.64	77.09	54.28	30.41	18.31
1997	793	318	211	17	3	3	3.76	2.81	75.66	51.07	27.49	16.39
1998	814	306	206	21	3	3	3.95	3.29	76.78	53.81	30.1	17.08
1999	876	334	220	22	3	3	3.98	2.87	75.23	49.77	25.8	14.95
2000	702	283	190	19	3	2	3.69	2.79	74.93	51	26.92	17.09
2001	647	274	180	18	3	3	3.59	2.56	74.5	49.46	25.66	15.15
2002	742	302	212	18	3	1	3.5	2.65	77.09	51.48	26.82	16.04
2003	681	273	194	21	3	3	3.51	2.76	73.57	49.34	28.05	18.36
2004	717	283	198	15	3	3	3.62	2.73	74.76	50.21	27.89	17.29
2005	751	292	207	30	3	2	3.63	3.15	74.97	51.26	29.43	17.98
2006	860	331	231	25	3	1	3.72	3.01	77.33	52.44	27.67	17.21
2007	887	339	221	36	3	1	4.01	3.96	79.26	55.69	31.34	20.18
2008	853	323	229	31	3	2	3.72	3.01	76.2	50.18	26.03	15.12
2009	789	293	205	29	3	3	3.85	3.32	76.3	51.71	29.78	18
2010	622	239	167	16	3	1	3.72	3.08	79.26	54.18	29.26	16.56
2011	643	250	180	17	3	1	3.57	2.85	76.05	52.1	28.93	17.42
2012	524	221	166	15	3	1	3.16	2.55	78.44	51.91	28.24	17.37
2013	549	209	151	14	3	2	3.64	2.49	76.32	49.36	24.77	14.75
2014	370	133	108	14	3	2	3.43	2.58	74.86	50	28.38	16.22

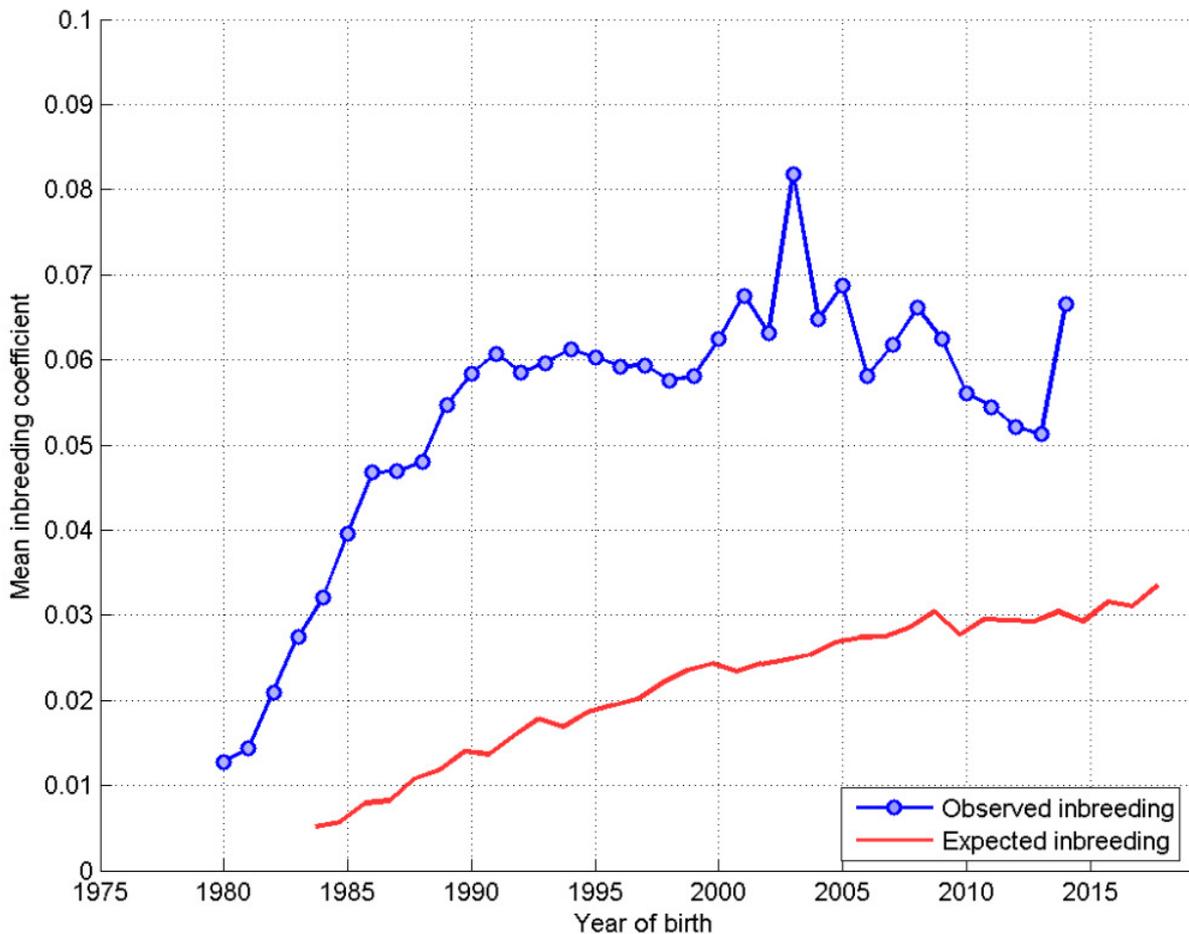


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 3.71

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 = 123.6

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	685.2	753.4	837.6	863.4	697.8	828	541.6
Total #sires	547	619	569	603	558	627	485
Max #progeny	106	112	100	61	43	80	48
Mean #progeny	6.2468	6.0775	7.3515	7.1575	6.2491	6.5997	5.5753
Median #progeny	3	4	5	4	4	4	4
Mode #progeny	1	1	1	1	1	1	1
SD #progeny	7.9754	8.1919	8.6252	7.6909	6.2964	7.7059	5.646
Skew #progeny	4.8463	6.1841	3.7392	2.5578	2.2875	3.8611	2.4773
Total #dams	1083	1085	1002	1010	944	1035	724
Max #progeny	20	19	25	21	29	22	18
Mean #progeny	3.1551	3.47	4.1786	4.2733	3.6949	3.9981	3.7348
Median #progeny	2	3	3	3	3	3	3
Mode #progeny	1	1	1	1	2	2	1
SD #progeny	2.558	2.7591	3.2191	3.2917	2.8066	3.3259	2.8901
Skew #progeny	1.9188	1.7871	1.6464	1.5522	2.1365	1.9999	1.5883
Rate of inbreeding	0.017111	0.011289	0.001687	-0.00241	0.008384	-0.00193	0.007897
Generation interval	3.2471	3.4116	3.5183	3.7706	4.0992	3.8575	4.1472
Effective pop size	29.221	44.291	296.33	n/a	59.637	n/a	63.316



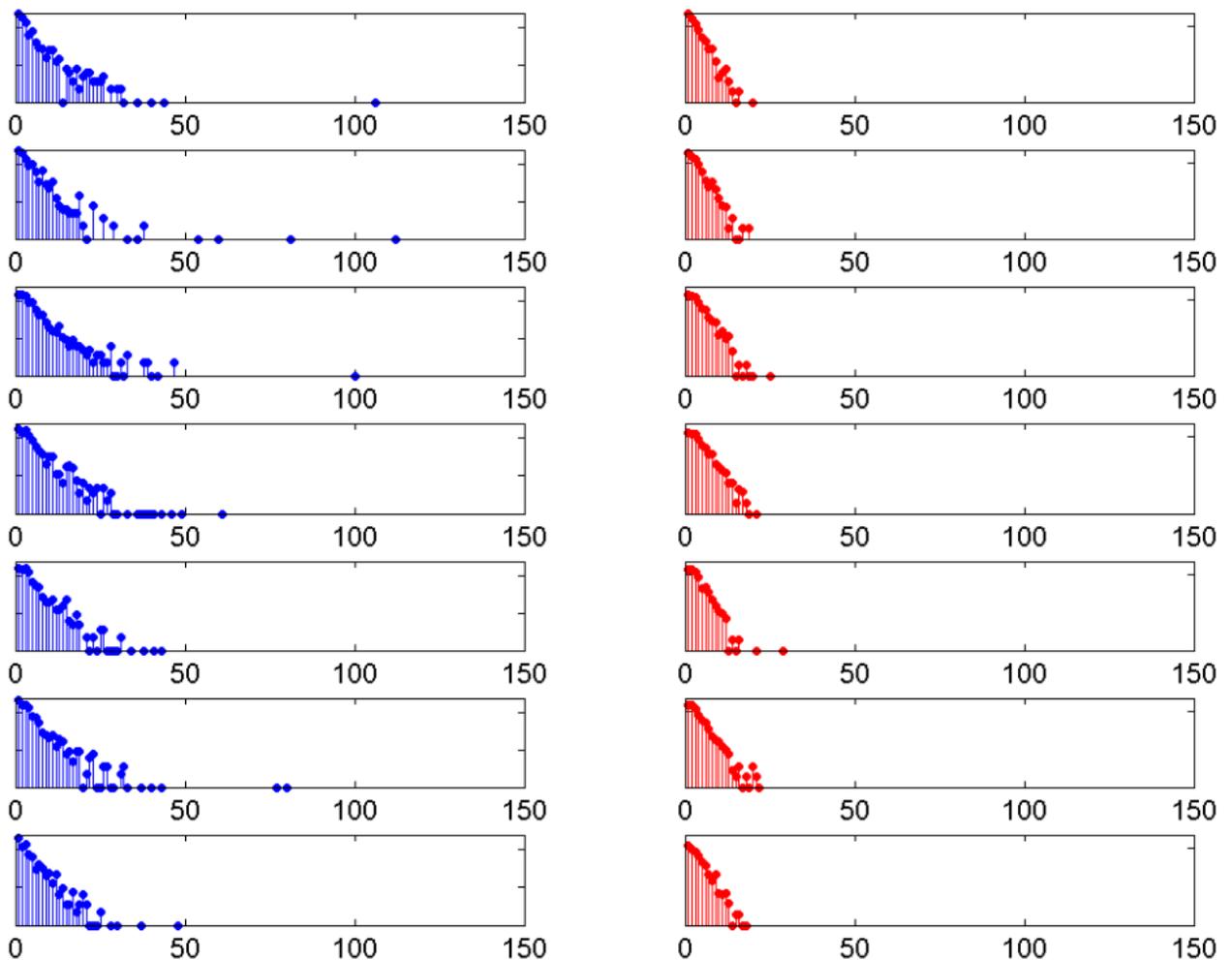
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number 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. This represents a 'genetic bottleneck', with genetic variation lost from the population. However, during the 1990s the rate of inbreeding flattened off, implying maintenance of genetic diversity (possibly through the use of imported animals). Since the turn of the century there have been more noticeable fluctuations in the rate of inbreeding and effective population size.

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.