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September 2015

### **Population analysis of the *Pug* breed**

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



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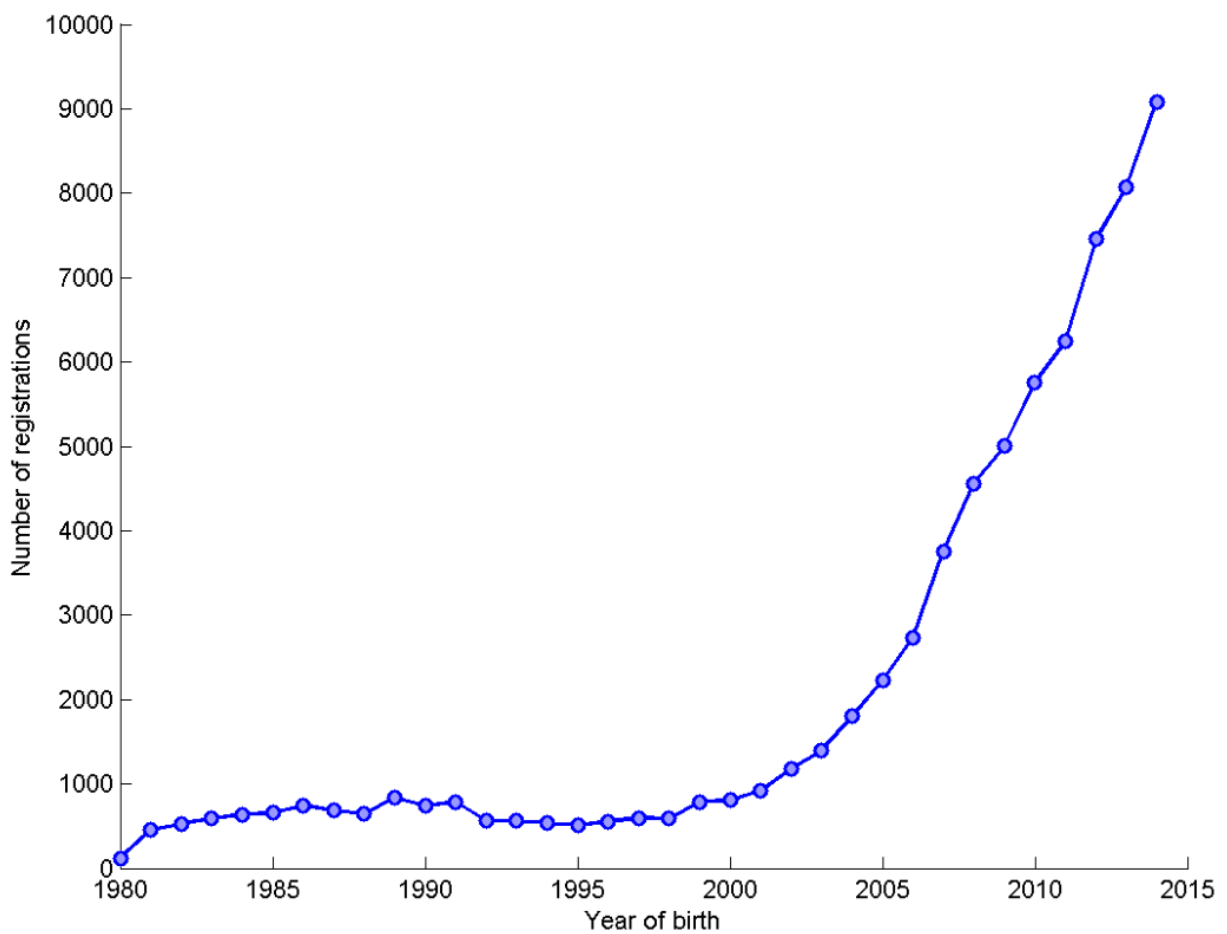
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**Figure 1:** a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

**Breed: Pug**

Figure 1: Number of registrations by year of birth



**Trend of registrations over year of birth (1980-2014) = 194.77 per year (with a 95% confidence interval of 143.33 to 246.21).**



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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	121	81	51	36	3	1	5.18	6.46	89.12	65.61	41.05	26.67
1981	455	177	91	28	5	1	6.53	6	81.18	54.3	30.38	18.01
1982	529	167	86	53	7	4	10.61	10.97	80.96	58.23	35.3	26.06
1983	592	187	102	46	7	5	9.18	9.61	79.08	57.3	37.47	26.8
1984	638	218	106	61	7	4	9.17	9.61	79.87	55.03	35.57	22.32
1985	658	209	105	47	5	4	8.12	9.05	79.87	59.4	36.94	27.45
1986	746	228	102	48	6	4	7.89	7.47	78.02	55.25	30.5	19.21
1987	684	218	110	47	6	7	7.57	7.4	79	54.33	32.68	20.78
1988	646	216	118	80	7	6	10.5	14	81.27	61.43	41.75	29.37
1989	833	235	117	48	7	4	9.73	9.26	77.25	55.6	35.23	22.57
1990	738	210	101	39	6	6	8.73	7.48	78.63	54.01	30.53	18.32
1991	789	225	112	39	7	7	9.2	7.77	73.44	53.12	30.38	20.32
1992	563	164	96	61	8	8	9.65	10.2	75.82	55.28	33.78	26.49
1993	559	167	95	49	7.5	8	9.24	8.29	75.26	54.38	29.38	19.33
1994	538	161	89	29	7	6	8.32	5.86	74.6	47.17	25.4	17.23
1995	505	148	74	59	8	1	11.13	11.63	80.71	58.8	34.46	21.16
1996	558	164	78	26	8	1	9.21	6.83	78.96	51.81	25.11	11.76
1997	598	164	95	51	8	9	9.54	9.11	79.03	54.84	33.33	20.7
1998	587	175	96	56	7	6	9.95	10.4	80.37	58.45	32.65	21.69
1999	778	217	111	53	5	1	7.42	9.31	84.4	62.41	40.07	26.95
2000	815	220	117	39	8	6	9.55	7.75	76.84	51.22	30.51	16.04
2001	922	250	132	34	6	1	7.68	7.41	80.82	56.85	34.25	22.26
2002	1180	317	148	44	6	1	7.43	8.51	85.09	58.18	39.64	25.82
2003	1391	379	168	40	7	1	8.17	6.98	76.06	51.6	31.65	16.76
2004	1800	478	208	68	7	1	9.62	11.41	82.4	59.73	35.73	25.33
2005	2224	581	265	20	6	9	6.43	4.11	74.66	45.61	23.99	12.5
2006	2738	708	334	22	8	9	7.85	5.3	75.6	46.95	25.2	11.41
2007	3750	952	431	30	7	1	7.61	6.53	80.3	52.84	28.66	16.42
2008	4559	1123	529	36	7	1	7.1	6.11	78.3	51.61	29.03	15.54
2009	5000	1292	613	22	6	1	5.74	4.37	79.1	49.25	27.36	16.92
2010	5755	1485	728	30	6	1	6.87	5.98	83.82	53.07	30.1	15.21
2011	6244	1619	789	25	8.5	1	8.4	5.63	73.81	48.02	24.6	17.46
2012	7458	1859	919	37	3.5	1	7.44	8.78	88.66	64.29	38.66	27.31
2013	8071	2003	925	31	8	1	9.11	7.56	80.56	55.49	31.35	18.18
2014	9076	2170	944	23	7	1	7.95	6.06	80.24	50.3	25.15	13.77

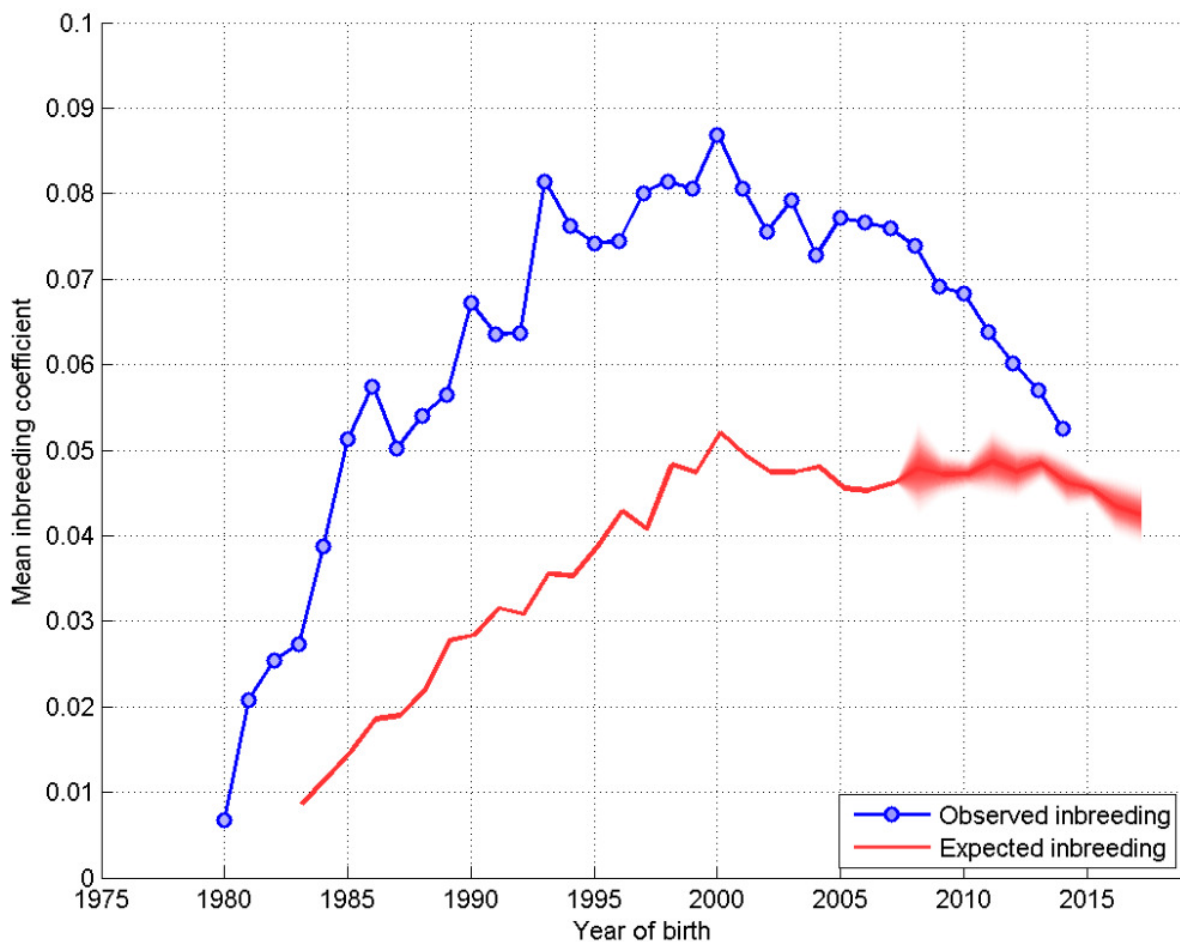


**Generation interval:** the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

**Mean generation interval (years) = 3.14**

**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 = 133.9**

*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	467	713.4	637.4	605.2	1221.6	3654.2	7320.8
Total #sires	243	296	275	244	435	1190	2382
Max #progeny	116	133	86	129	221	147	388
Mean #progeny	9.5761	12.047	11.585	12.393	14.039	15.353	15.364
Median #progeny	4	6	6	6	6	7	7
Mode #progeny	1	1	2	1	1	1	1
SD #progeny	15.559	17.179	14.719	17.826	20.667	20.73	24.368
Skew #progeny	3.9444	3.7805	2.4295	3.3991	3.9682	2.5618	4.9707
Total #dams	605	770	652	606	1125	3121	6419
Max #progeny	21	23	23	26	21	28	33
Mean #progeny	3.8463	4.6299	4.885	4.9917	5.4284	5.8539	5.7015
Median #progeny	3	4	4	4	5	5	5
Mode #progeny	1	2	4	3	3	4	4
SD #progeny	3.1346	3.3689	3.3834	3.7068	3.7613	4.1048	3.806
Skew #progeny	1.7166	1.5175	1.4582	1.6288	1.1478	1.3845	1.3595
Rate of inbreeding	0.02298	0.002252	0.013327	0.007492	-0.00973	-0.00591	-0.01183
Generation interval	3.197	3.029	3.4498	3.526	3.0168	2.9023	2.8726
Effective pop size	21.758	222.06	37.517	66.739	n/a	n/a	n/a



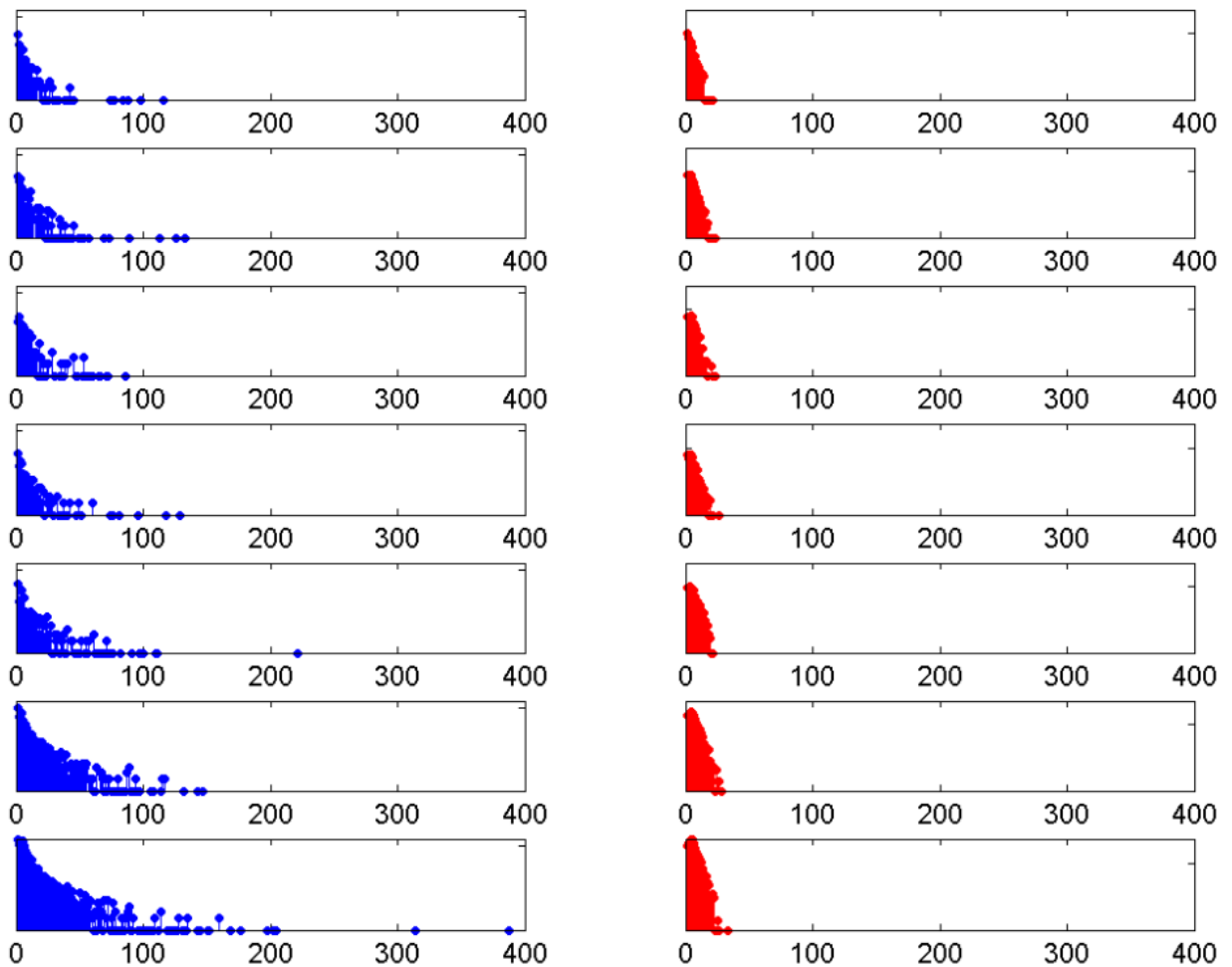
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**Figure 3:** a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large 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 2000 the rate of inbreeding has been negative, implying moderate restoration 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.