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September 2015

### **Population analysis of the *Whippet* breed**

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



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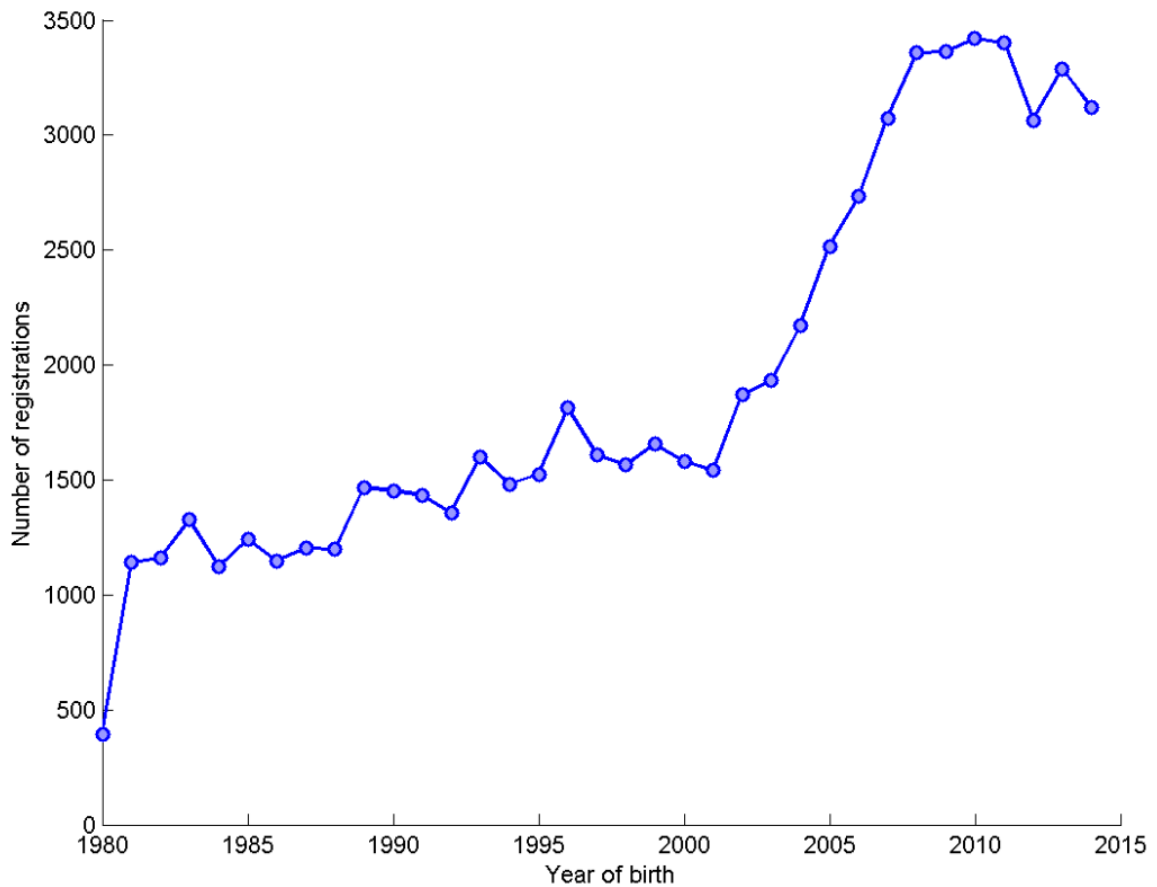
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**Figure 1:** a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

**Breed: Whippet**

Figure 1: Number of registrations by year of birth



**Trend of registrations over year of birth (1980-2014) = 75.49 per year (with a 95% confidence interval of 63.84 to 87.14).**



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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	395	236	173	10	2	1	2.28	1.81	77.47	52.91	28.35	16.96
1981	1141	361	243	36	4	1	4.7	4.37	78.97	54.25	30.76	20.16
1982	1161	344	241	36	4	1	4.82	4.95	80.02	55.21	32.99	22.22
1983	1327	369	245	62	4	3	5.42	5.73	78.15	54.86	32.55	21.25
1984	1123	314	213	31	4	4	5.27	4.47	77.38	53.52	29.3	18.43
1985	1241	329	213	43	4	2	5.83	6.27	80.1	57.05	35.46	24.42
1986	1148	310	219	34	4	2	5.24	4.61	78.31	53.57	29.97	18.9
1987	1204	306	206	39	4	1	5.84	5.68	79.9	56.73	33.39	20.68
1988	1198	283	199	36	5	3	6.02	5.02	78.38	53.67	29.38	17.2
1989	1468	308	209	34	6	6	7.02	5.59	74.73	50.89	29.5	17.64
1990	1453	290	200	43	6	5	7.26	5.98	74.12	50.79	30.01	18.38
1991	1433	294	196	38	6	6	7.31	5.51	73.62	50.24	28.19	17.17
1992	1357	272	187	49	6	6	7.26	5.89	74.36	50.77	28.81	17.17
1993	1600	311	220	30	6	7	7.27	5.55	74.13	49.38	28.38	17.88
1994	1481	291	199	51	6	5	7.44	6.16	74.41	51.32	28.63	18.37
1995	1524	287	190	73	6	6	8.02	7.24	73.29	50.13	28.87	20.08
1996	1813	338	226	44	6	5	8.02	6.43	73.75	50.91	30.01	18.04
1997	1609	295	210	37	6.5	7	7.66	5.76	73.96	49.47	27.84	17.59
1998	1565	291	205	40	6	6	7.63	6.63	76.36	53.04	32.4	18.72
1999	1655	306	222	72	6	6	7.45	6.57	74.14	50.63	28.22	17.82
2000	1581	294	196	40	6	6	8.07	6.53	75.52	51.93	29.85	18.15
2001	1543	302	205	57	6	5	7.53	7.55	76.93	53.92	33.25	21.84
2002	1871	360	254	46	6	6	7.37	6.23	76.27	52.43	28.54	18.55
2003	1933	356	224	71	6	6	8.63	8.2	77.86	54.79	31.51	19.92
2004	2171	383	247	66	7	6	8.79	8.34	75.73	53.48	32.15	21.05
2005	2517	446	284	43	7	7	8.86	6.95	74.57	50.89	27.41	17.44
2006	2734	480	294	68	7	6	9.3	8.46	75.49	53.44	30.8	20.41
2007	3075	525	335	58	7	6	9.18	7.16	74.8	50.5	28.62	17.5
2008	3358	568	370	92	7	6	9.08	7.76	74.66	51.82	28.77	17.87
2009	3362	571	381	68	7	6	8.82	7.23	75.19	51.31	28.41	17.43
2010	3420	577	394	37	7	6	8.68	6.3	74.33	51.08	26.7	15.94
2011	3400	583	380	57	7	7	8.95	7.57	76.15	52.44	29.97	18.88
2012	3065	549	347	74	7	5	8.83	8.23	77.72	54.52	31.55	19.48
2013	3288	567	349	58	7	6	9.42	8.38	77.22	54.35	31.63	18.92
2014	3120	513	338	56	8	8	9.23	7.3	73.69	50.58	28.78	18.17

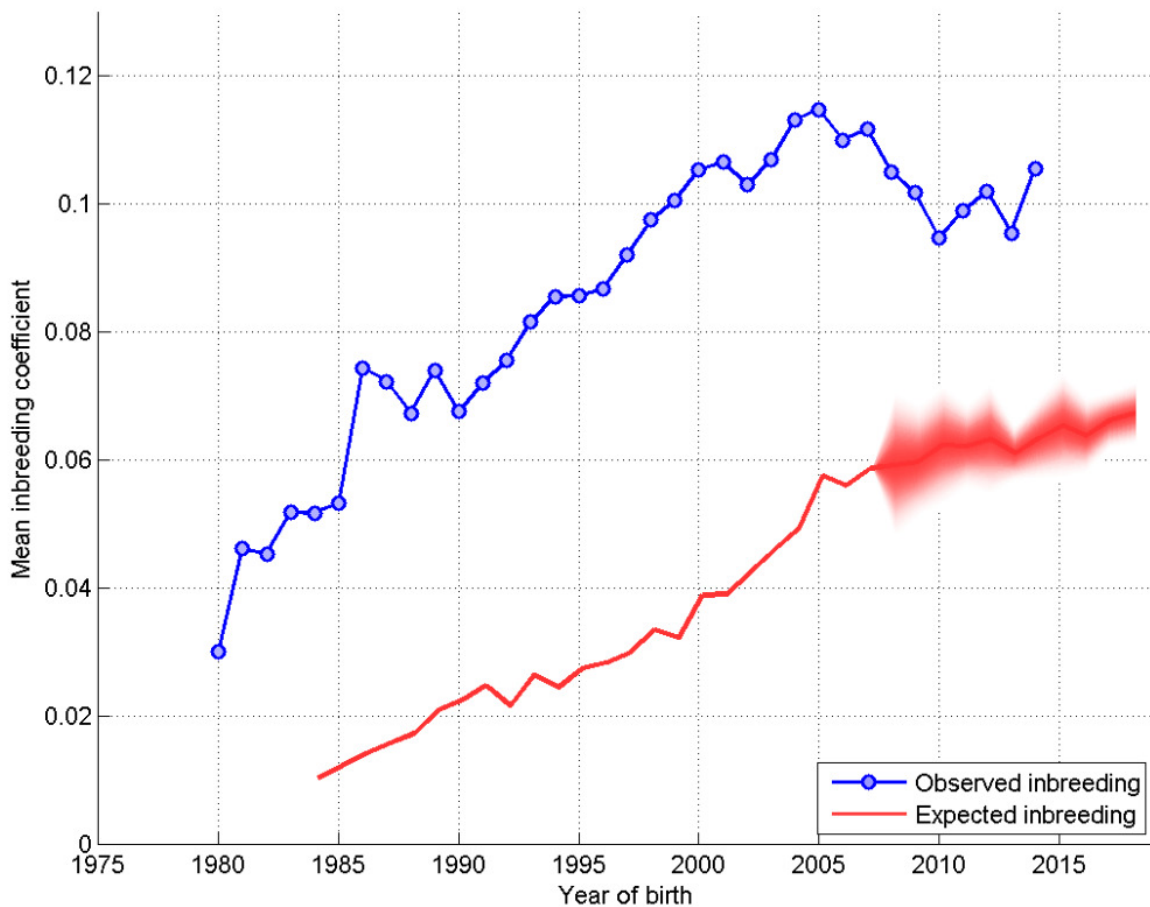


**Generation interval:** the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

**Mean generation interval (years) = 4.15**

**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 = 56.4**

*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	1029.4	1251.8	1464.8	1633.2	1819.8	3009.2	3258.6
Total #sires	703	649	604	664	702	1002	1110
Max #progeny	131	96	149	179	184	307	191
Mean #progeny	7.3144	9.6425	12.124	12.297	12.96	15.015	14.674
Median #progeny	4	5	7	7	8	9	8
Mode #progeny	1	3	6	6	5	6	6
SD #progeny	10.554	12.784	14.847	15.891	17.424	19.441	18.498
Skew #progeny	5.5328	3.2066	3.8799	4.43	4.7119	5.4847	3.5979
Total #dams	1253	1170	1105	1151	1277	1891	2118
Max #progeny	23	28	35	30	30	36	39
Mean #progeny	4.1038	5.3444	6.6271	7.0921	7.1245	7.9561	7.6903
Median #progeny	3	5	6	6	6	7	7
Mode #progeny	1	4	5	6	6	6	6
SD #progeny	3.0455	3.7905	4.2548	4.3719	4.5115	5.3013	4.8347
Skew #progeny	1.5925	1.9498	1.8012	1.6244	1.3687	1.5338	1.5025
Rate of inbreeding	0.020538	0.01514	0.021955	0.019017	0.007595	-0.01361	0.007863
Generation interval	4.0228	4.1463	4.4766	4.2903	4.2507	3.9172	3.9125
Effective pop size	24.345	33.025	22.774	26.292	65.829	n/a	63.588



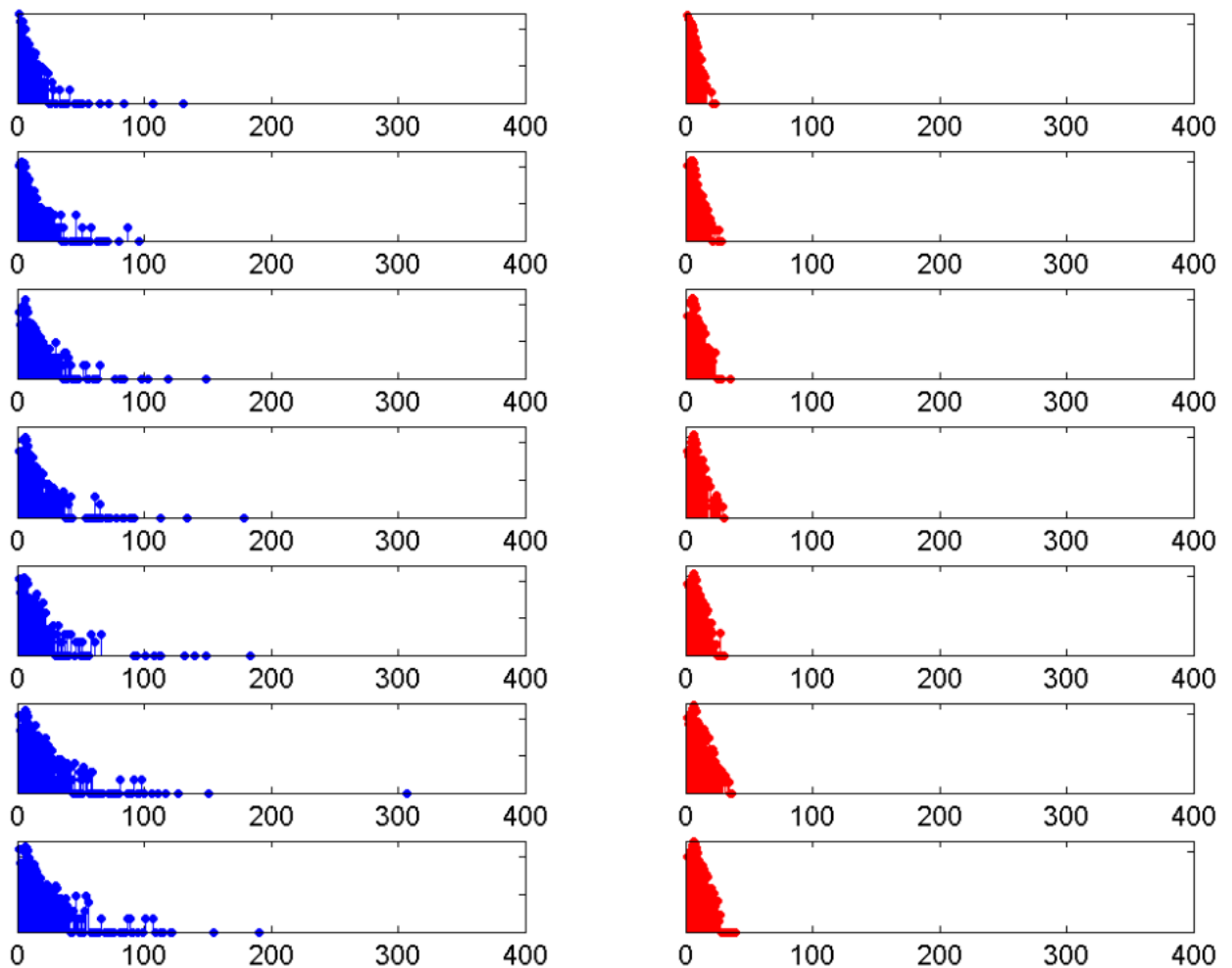
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**Figure 3:** a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large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