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September 2015

### **Population analysis of the *Soft-Coated Wheaten Terrier* breed**

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



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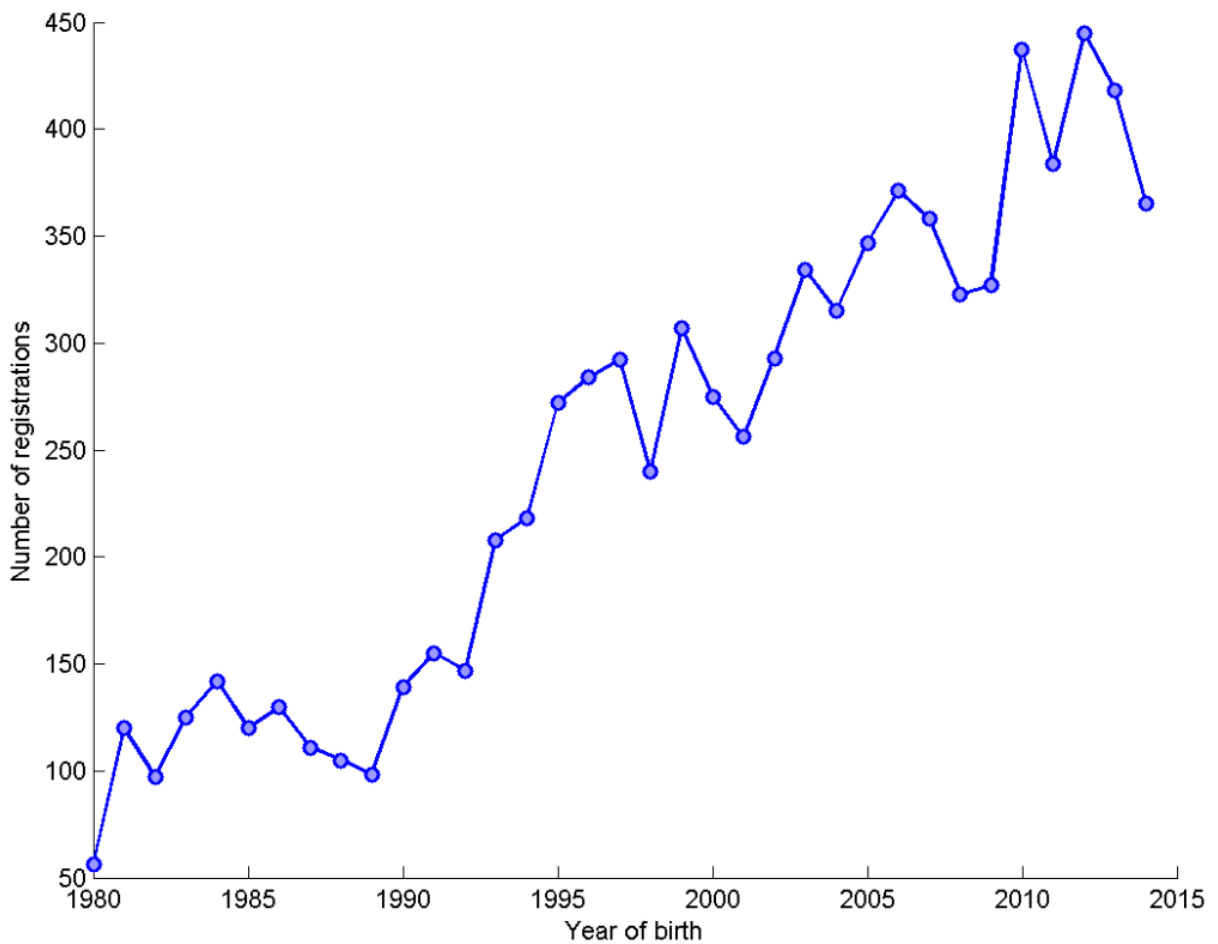
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**Figure 1:** a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

**Breed: *Soft-Coated Wheaten Terrier***

Figure 1: Number of registrations by year of birth



**Trend of registrations over year of birth (1980-2014) = 10.53 per year (with a 95% confidence interval of 9.37 to 11.69).**



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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	56	22	16	9	3	1	3.5	2.78	80.36	55.36	30.36	16.07
1981	120	31	17	21	6	1	7.06	6.17	86.67	52.5	31.67	17.5
1982	97	24	19	15	5	1	5.11	3.65	79.38	48.45	24.74	15.46
1983	125	26	18	25	6	1	6.94	6.25	80	57.6	33.6	20
1984	142	31	23	15	5	4	6.17	4.14	77.46	50	21.13	10.56
1985	120	26	18	17	6	6	6.67	3.5	66.67	44.17	22.5	14.17
1986	130	30	14	33	8	10	9.29	7.78	75.38	53.08	25.38	25.38
1987	111	22	13	24	7	4	8.54	5.88	76.58	45.05	21.62	21.62
1988	105	19	16	12	7	7	6.56	3.05	66.67	39.05	21.9	11.43
1989	98	22	19	17	5	1	5.16	4.5	83.67	54.08	32.65	17.35
1990	139	31	20	24	5	1	6.95	6.36	81.29	58.27	30.94	17.27
1991	155	31	23	26	6	1	6.74	6.62	82.58	55.48	32.9	16.77
1992	147	33	20	27	6	1	7.35	6.3	79.59	53.06	28.57	18.37
1993	208	33	20	34	8	8	10.4	7.8	72.12	50.96	27.4	16.35
1994	218	40	27	30	6	5	8.07	7.46	79.82	57.34	34.86	13.76
1995	272	51	29	72	6	1	9.38	13.73	87.13	63.97	45.59	26.47
1996	284	53	34	38	6.5	1	8.35	7.41	79.93	55.99	26.06	20.07
1997	292	54	34	32	7	1	8.59	7.41	79.45	56.51	28.08	20.89
1998	240	42	30	32	6	1	8	7.68	79.17	59.17	33.33	25.42
1999	307	57	42	64	6	1	7.31	10.35	84.69	62.21	40.07	28.66
2000	275	50	33	38	6	1	8.33	8.42	82.18	58.91	32.36	24.36
2001	256	50	37	28	7	1	6.92	5.91	81.64	52.34	30.08	18.36
2002	293	55	39	22	7	1	7.51	6	81.23	54.61	27.65	15.02
2003	334	61	42	32	6	1	7.95	6.83	80.84	56.89	27.25	16.17
2004	315	64	43	24	6	1	7.33	5.93	80.95	54.29	26.67	14.29
2005	347	63	42	50	7	1	8.26	8.39	78.67	56.48	31.99	20.46
2006	371	73	51	32	6	1	7.27	6.76	83.29	57.41	30.73	21.02
2007	358	70	51	25	6	1	7.02	6.07	81.56	56.15	29.61	18.72
2008	323	66	42	26	5.5	1	7.69	7.37	86.69	63.78	27.55	15.79
2009	327	65	47	36	5	1	6.96	7.33	81.04	58.1	36.7	21.71
2010	437	78	49	31	8	1	8.92	7.62	83.75	55.15	27.69	13.27
2011	384	67	41	40	7	1	9.37	9.03	86.2	57.03	31.25	18.23
2012	445	78	50	32	7	7	8.9	7.15	77.75	55.06	28.31	19.33
2013	418	72	48	32	6.5	1	8.71	8.16	83.25	58.85	32.78	15.07
2014	365	53	35	31	7	6	10.43	7.79	76.71	53.7	30.41	16.16

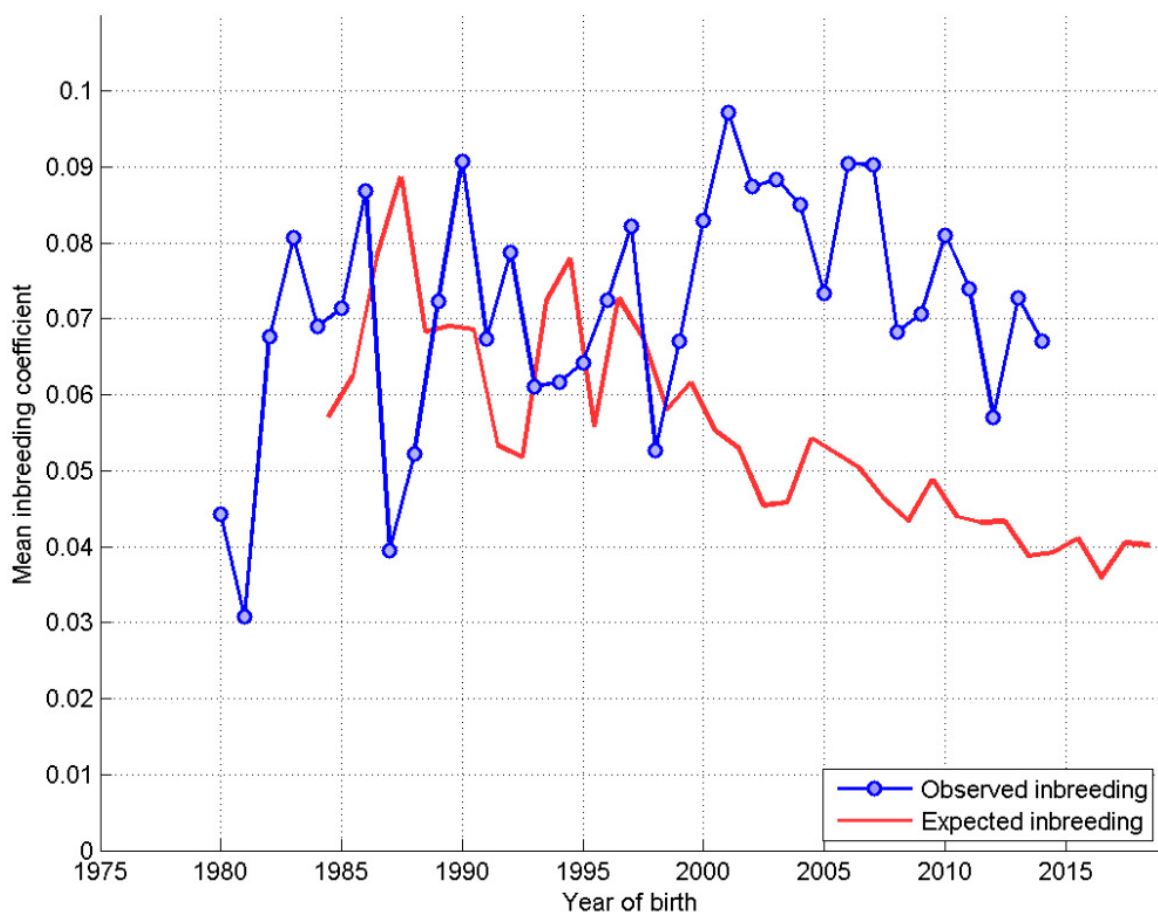


**Generation interval:** the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

**Mean generation interval (years) = 4.47**

**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 = 193.7**

*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	108	112.8	173.4	279	294.6	345.2	409.8
Total #sires	56	48	70	99	110	137	133
Max #progeny	51	74	89	154	93	111	85
Mean #progeny	9.6071	11.375	12.371	14.081	13.364	12.584	15.376
Median #progeny	7	7	6.5	7	8	6	8
Mode #progeny	1	7	1	1	1	1	1
SD #progeny	10.29	14.248	18.069	22.4	16.357	17.977	18.633
Skew #progeny	1.7155	2.7055	2.6415	3.7046	2.2013	2.6504	1.9064
Total #dams	89	80	120	181	196	248	251
Max #progeny	20	20	33	30	23	32	36
Mean #progeny	6.0449	6.95	7.2167	7.7017	7.5102	6.9516	8.1474
Median #progeny	5	6	6	7	7	6	7
Mode #progeny	1	7	1	1	1	1	1
SD #progeny	4.8568	4.8206	5.7675	5.8423	5.4833	5.5006	6.2115
Skew #progeny	0.97436	0.84481	1.3922	1.0125	0.75512	1.6587	1.2446
Rate of inbreeding	0.04111	-0.01566	-0.02938	-0.00688	-0.00238	-0.01315	-0.0163
Generation interval	3.9275	4.4664	4.2076	4.5592	4.6662	4.4191	5.1856
Effective pop size	12.163	n/a	n/a	n/a	n/a	n/a	n/a



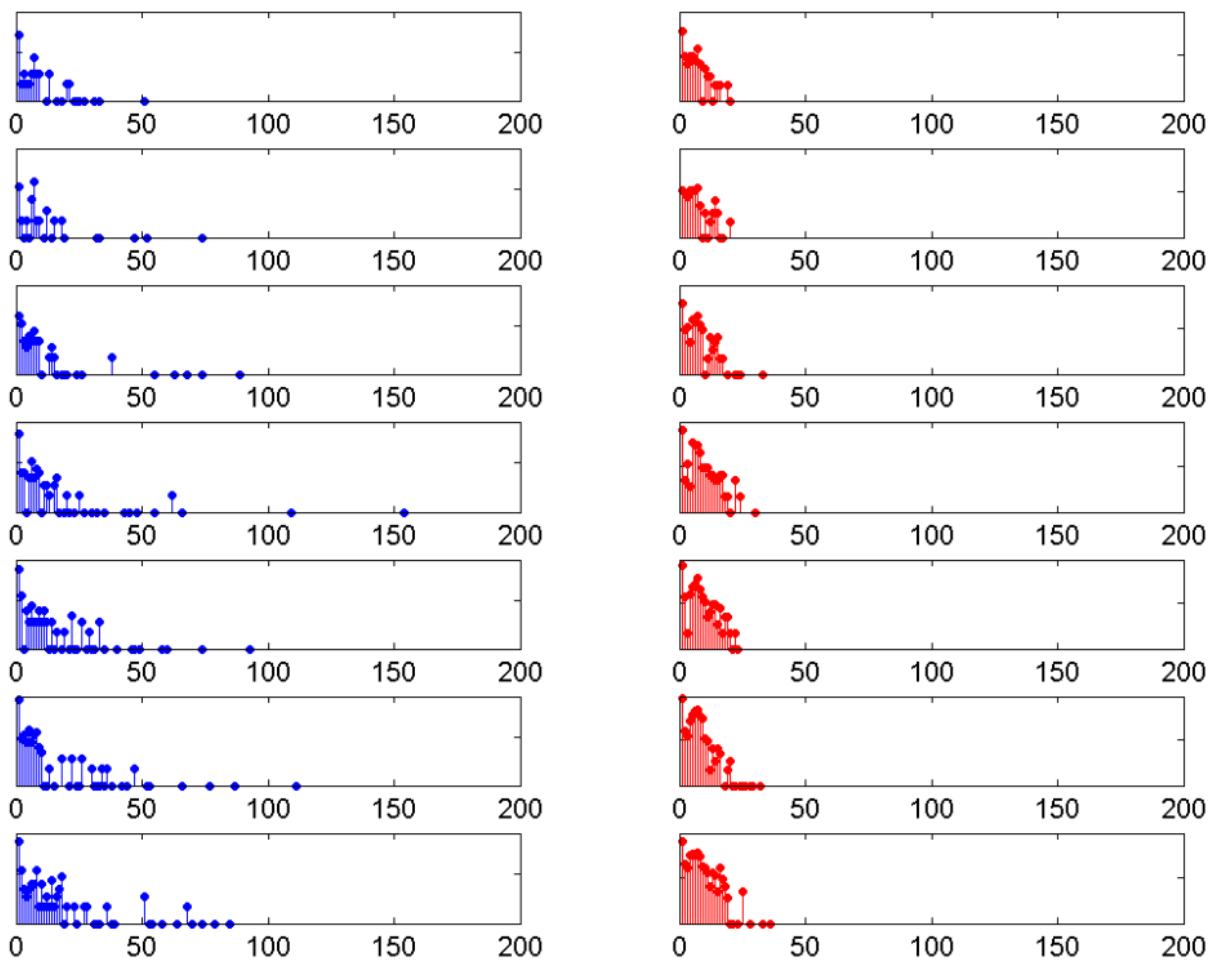
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**Figure 3:** a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large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

There appears to have been significant fluctuations in the rate of inbreeding between 1980-2014. While this has resulted in no overall apparent loss of genetic diversity, the breed will have seen diversity contract and then be replenished (possibly through the use of imported animals).

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.