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September 2015

### **Population analysis of the *Yorkshire Terrier* breed**

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



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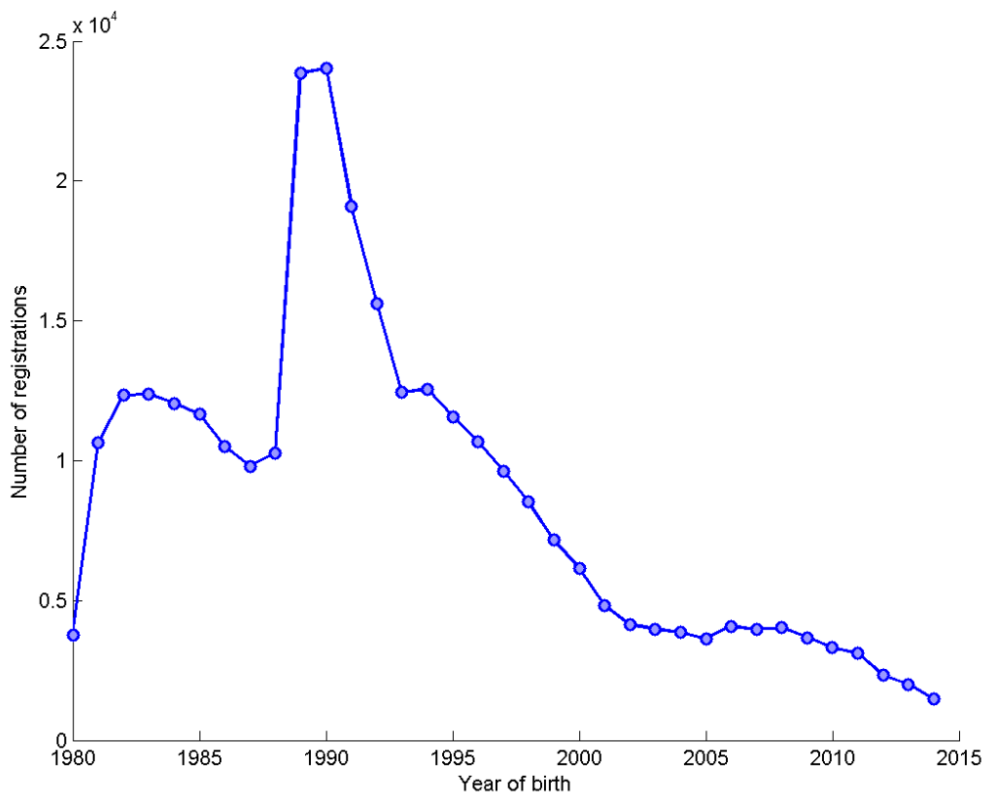
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**Figure 1:** a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

**Breed: Yorkshire Terrier**

Figure 1: Number of registrations by year of birth



**Trend of registrations over year of birth (1980-2014) = -381.77 per year (with a 95% confidence interval of -530.33 to -233.20).**



**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	3754	2923	1574	72	1.5	1	2.39	2.91	79.04	56.9	33.86	22.38
1981	10634	6175	2558	62	2	1	4.16	5.15	84.02	63.85	40.2	26.16
1982	12344	6581	2682	64	3	1	4.6	5.6	84.07	63.82	39.22	25.45
1983	12371	6492	2681	71	3	1	4.61	5.74	84.21	63.89	39.71	25.97
1984	12047	6324	2599	69	3	1	4.64	5.9	84.54	64.58	40.23	26.41
1985	11650	6074	2597	84	3	1	4.49	5.62	83.59	62.9	38.54	25.55
1986	10508	5470	2498	79	2	1	4.21	5.27	83.34	62.82	39.47	26.15
1987	9803	5149	2360	82	3	1	4.15	5.28	82.86	61.95	38.36	25.39
1988	10274	5134	2253	119	3	1	4.56	6.09	83.39	62.68	38.83	25.77
1989	23861	6547	2545	214	5	4	9.38	15.37	85.31	67.28	45.14	31.99
1990	24015	6046	2337	379	5	3	10.28	17.99	85.85	68.38	46.45	32.88
1991	19089	4941	2100	238	5	3	9.09	14.39	84.28	65.81	43.5	30.33
1992	15605	4124	1868	175	5	3	8.35	11.58	84.01	65.07	42.42	28.47
1993	12436	3453	1655	104	5	3	7.51	9.3	82.33	62.17	39.1	25.97
1994	12556	3357	1557	115	5	3	8.06	10.27	82.47	62.53	39.61	26.12
1995	11571	3125	1495	102	5	3	7.74	9.99	82.28	62.25	40	26.77
1996	10685	2914	1410	71	5	4	7.58	9.03	81.69	61.7	38.63	25.65
1997	9624	2642	1332	61	5	3	7.23	7.96	81.55	60.25	36.8	23.76
1998	8522	2318	1135	95	5	3	7.51	8.87	81.72	61.21	38.21	24.84
1999	7155	1946	1026	112	4	3	6.97	8.54	81.34	60.68	38.29	25.41
2000	6135	1731	884	92	4	3	6.94	8.53	81.42	60.78	38.32	26.1
2001	4825	1355	756	87	4	3	6.38	7.53	79.92	57.74	35.96	24.46
2002	4141	1240	665	81	4	3	6.23	7.26	80.95	59.09	35.98	23.76
2003	3984	1179	634	59	4	2	6.28	7.09	81.15	60.14	36.57	24.25
2004	3863	1110	579	85	4	3	6.67	7.38	80.9	57.99	35.36	23.69
2005	3639	1037	547	56	4	1	6.65	7.15	81.64	59.63	35.5	22.78
2006	4083	1079	536	89	5	2	7.62	8.76	82.1	61.08	37.42	24.1
2007	3959	1064	536	56	5	2	7.39	7.22	80.8	57.74	33.32	20.71
2008	4028	1063	582	59	5	3	6.92	7	80.61	58.42	33.89	21.1
2009	3677	1025	550	44	5	4	6.69	6.66	80.12	57.95	34.57	21.65
2010	3309	935	528	44	4	3	6.27	5.9	79.81	56.78	32.82	19.82
2011	3112	869	488	45	4.5	3	6.38	6.06	79.82	56.65	32.94	20.31
2012	2319	663	432	45	4	2	5.37	5	78.44	55.28	32.34	20.14
2013	2006	592	352	39	4	4	5.7	5.16	77.17	54.89	31.41	19.69
2014	1480	400	258	58	4	2	5.74	5.7	78.11	55.27	32.43	20.61

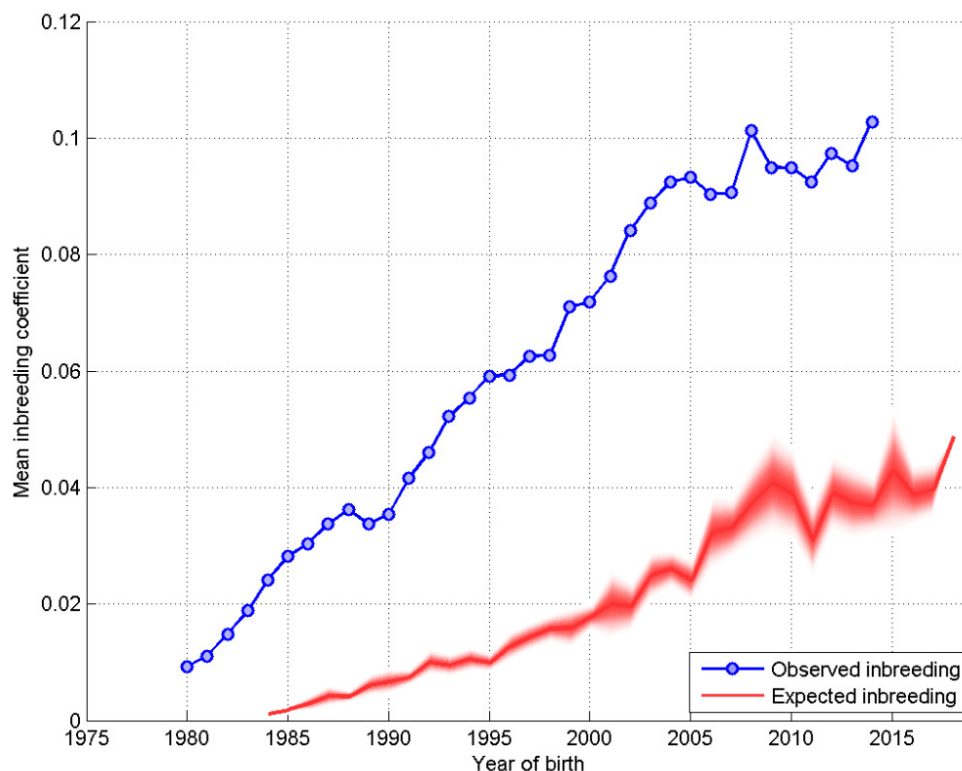


**Generation interval:** the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

**Mean generation interval (years) = 4.06**

**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 = 40.2**

*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	10230	13219	16740	9511.4	4589.6	3877.2	2445.2
Total #sires	6194	6260	4829	3258	1870	1420	1127
Max #progeny	231	420	750	291	247	224	135
Mean #progeny	8.2452	10.558	17.333	14.597	12.271	13.65	10.846
Median #progeny	3	4	7	6	6	6	6
Mode #progeny	1	1	3	3	3	1	3
SD #progeny	14.37	20.151	36.461	23.977	19.768	19.788	14.313
Skew #progeny	4.8685	7.1519	7.8502	4.6477	5.1375	3.7651	3.5177
Total #dams	18298	17771	13597	7963	4473	3421	2398
Max #progeny	28	26	40	37	30	30	29
Mean #progeny	2.7911	3.7191	6.1558	5.972	5.1299	5.6659	5.0976
Median #progeny	2	3	5	5	4	4	4
Mode #progeny	1	1	3	3	3	4	3
SD #progeny	2.2107	2.9889	4.9126	4.7637	3.7597	4.3206	3.6593
Skew #progeny	1.9712	1.8227	1.7125	1.6846	1.7142	1.4955	1.5287
Rate of inbreeding	0.011907	0.006565	0.021865	0.012295	0.02633	0.006996	0.008757
Generation interval	3.1249	3.7588	4.1292	4.2708	4.5195	4.4168	4.2504
Effective pop size	41.992	76.16	22.868	40.668	18.99	71.465	57.098



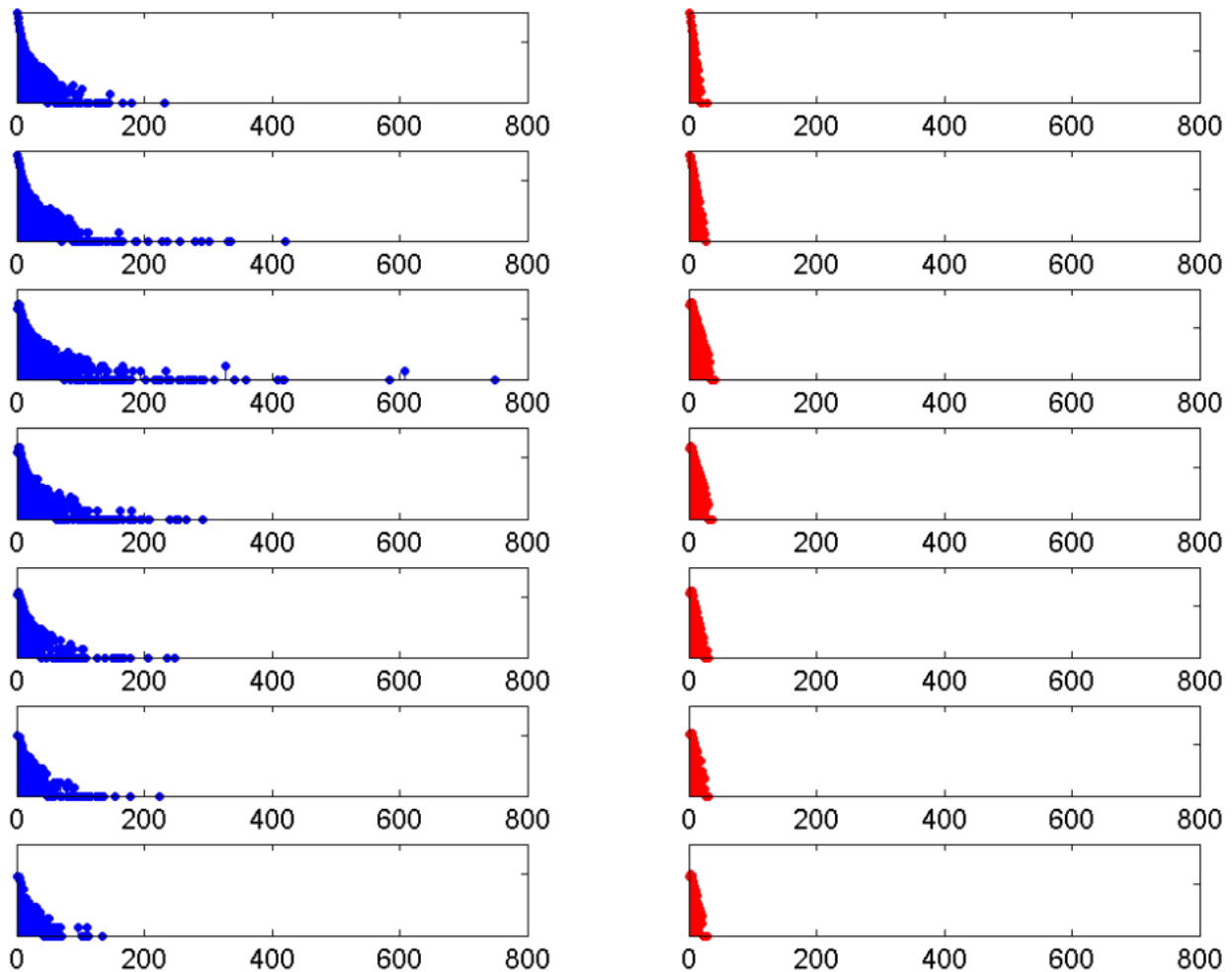
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**Figure 3:** a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large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

The rate of inbreeding in this breed has remained steady but consistently high over the whole period. This implies genetic variation is steadily being lost from the population.

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.