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September 2015

Population analysis of the *Cairn Terrier* breed

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



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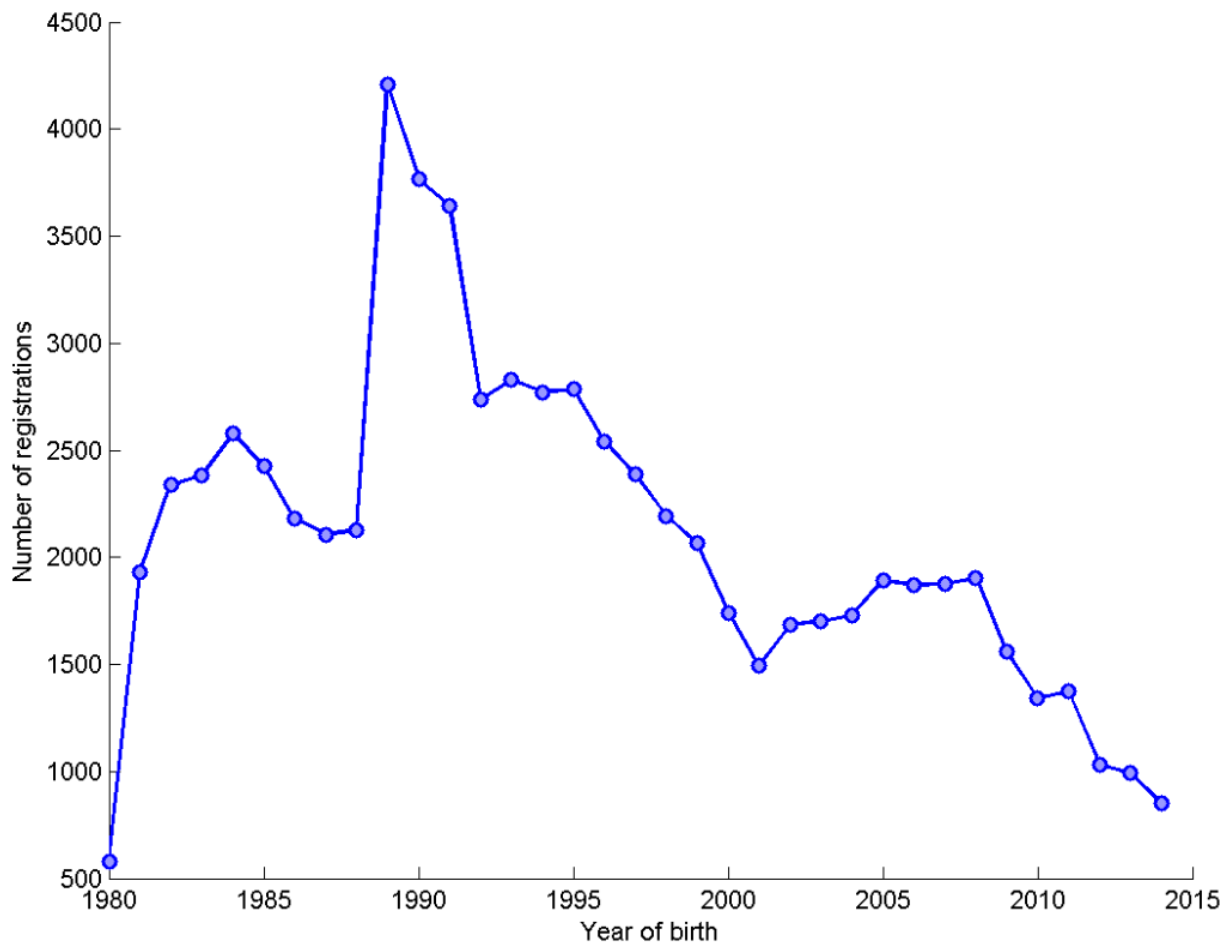
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Figure 1: a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

Breed: Cairn Terrier

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = -38.69 per year (with a 95% confidence interval of -62.17 to -15.21).



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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	578	461	257	18	2	1	2.25	2.03	76.82	52.08	29.76	19.38
1981	1932	1036	451	47	3	1	4.28	4.46	82.87	59.47	33.28	21.17
1982	2340	1116	461	43	3	1	5.08	5.47	83.29	60.77	35.73	22.56
1983	2382	1091	472	36	3	1	5.05	5.31	82.91	60.71	34.63	21.79
1984	2578	1174	483	40	4	1	5.34	5.51	83.13	58.96	34.21	21.8
1985	2424	1086	454	52	3	2	5.34	5.41	82.67	59.65	32.92	20.42
1986	2179	970	430	33	3	1	5.07	5.2	83.02	59.89	34.69	22.12
1987	2106	980	422	34	3	2	4.99	4.9	81.05	58.97	33.95	20.42
1988	2128	918	406	31	4	1	5.24	4.94	80.31	56.16	32.57	20.25
1989	4208	1088	432	96	6	4	9.74	10.79	82.06	59.34	35.72	24.14
1990	3768	928	393	151	6	3	9.59	12.48	82.38	59.69	36.12	24.95
1991	3641	864	382	111	6	3	9.53	12.12	82.64	61.85	40.46	27.63
1992	2738	693	320	53	5.5	5	8.56	8.77	81.23	59.06	35.1	22.17
1993	2828	729	319	64	5	4	8.87	10.06	83.8	62.66	37.91	24.36
1994	2771	691	308	75	6	4	9	9.78	81.88	60.23	35.26	21.94
1995	2784	678	294	84	6	3	9.47	10.97	82.61	62.36	36.89	24.5
1996	2542	638	277	64	6	4	9.18	9.62	81.94	59.17	34.93	22.54
1997	2387	575	246	60	6	3	9.7	9.2	80.94	57.56	32.38	19.86
1998	2194	557	252	55	6	4	8.71	8.19	81.31	56.97	31.45	19.83
1999	2066	523	240	39	6	1	8.61	7.32	80.78	56.24	28.94	16.51
2000	1741	448	224	48	6	4	7.77	6.99	80.18	56.4	30.27	17.75
2001	1494	405	199	37	6	1	7.51	6.51	80.72	55.35	29.99	17.54
2002	1683	428	205	47	5	4	8.21	7.91	81.16	57.75	33.04	19.9
2003	1702	451	213	61	6	1	7.99	7.97	80.67	56.58	33.08	21.74
2004	1731	454	210	38	6	1	8.24	7.43	80.94	57.19	31.43	19.06
2005	1892	478	224	59	6	1	8.45	8.46	82.19	58.35	33.35	20.77
2006	1872	463	207	73	6	4	9.04	8.6	80.88	55.77	31.52	19.02
2007	1874	462	229	82	6	4	8.18	8.54	81	57.47	33.56	20.49
2008	1905	445	240	35	6	1	7.94	6.9	80.89	56.54	29.76	17.22
2009	1559	358	201	54	5	4	7.76	7.33	79.92	56.83	32.07	19.69
2010	1343	327	189	54	6	1	7.11	6.42	79.6	53.91	30.01	17.57
2011	1373	319	188	43	5	1	7.3	6.64	80.34	56.37	31.25	17.99
2012	1033	237	131	58	6	1	7.89	8.33	81.8	58.86	33.69	22.75
2013	991	233	133	47	6	1	7.45	7.04	80.83	54.49	30.47	20.99
2014	852	174	95	32	6	6	8.97	6.96	78.64	53.99	28.05	15.85

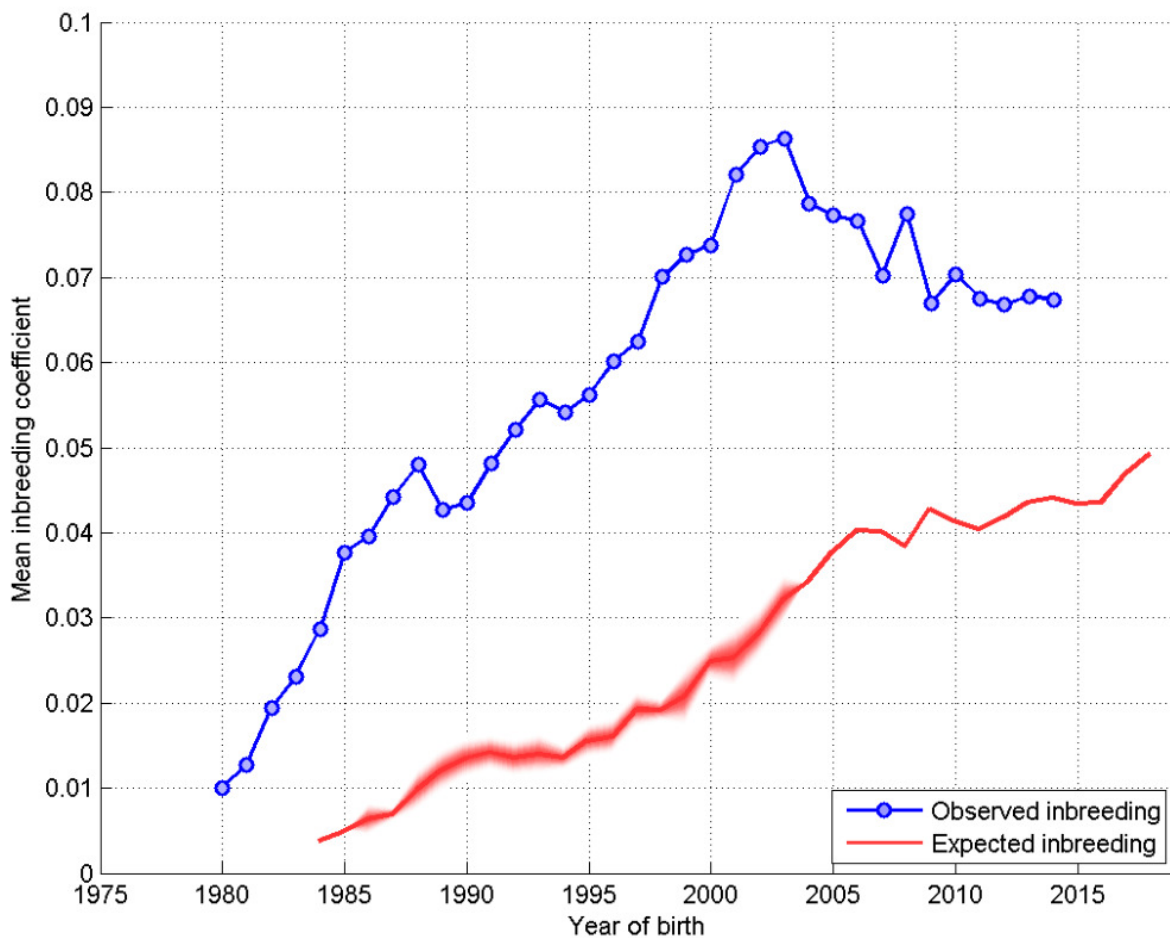


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 3.93

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 = 70.3

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	1962	2609	3149.2	2394.6	1670.2	1820.4	1118.4
Total #sires	1007	993	803	630	534	552	397
Max #progeny	131	131	400	272	151	175	173
Mean #progeny	9.7239	13.136	19.608	19.003	15.637	16.487	14.073
Median #progeny	4	6	9	9	7	9	7
Mode #progeny	1	2	4	3	1	1	1
SD #progeny	13.624	17.54	31.014	27.79	20.3	20.544	18.299
Skew #progeny	3.4492	2.8209	5.305	3.8204	2.6028	2.6962	3.4584
Total #dams	3147	3144	2416	1821	1449	1449	867
Max #progeny	23	22	37	35	32	30	30
Mean #progeny	3.1115	4.1489	6.517	6.5744	5.7626	6.2809	6.4441
Median #progeny	2	3	5	5	5	5	5
Mode #progeny	1	1	3	4	4	4	4
SD #progeny	2.6013	3.2652	5.1514	5.0719	4.3885	4.7229	4.9274
Skew #progeny	1.9962	1.5308	1.7327	1.5017	1.7466	1.4856	1.4134
Rate of inbreeding	0.017373	0.007103	0.012528	0.018635	0.006354	-0.00827	-0.00234
Generation interval	3.5786	3.7475	4.1344	4.0742	4.2025	3.8943	3.8887
Effective pop size	28.78	70.398	39.91	26.831	78.693	n/a	n/a



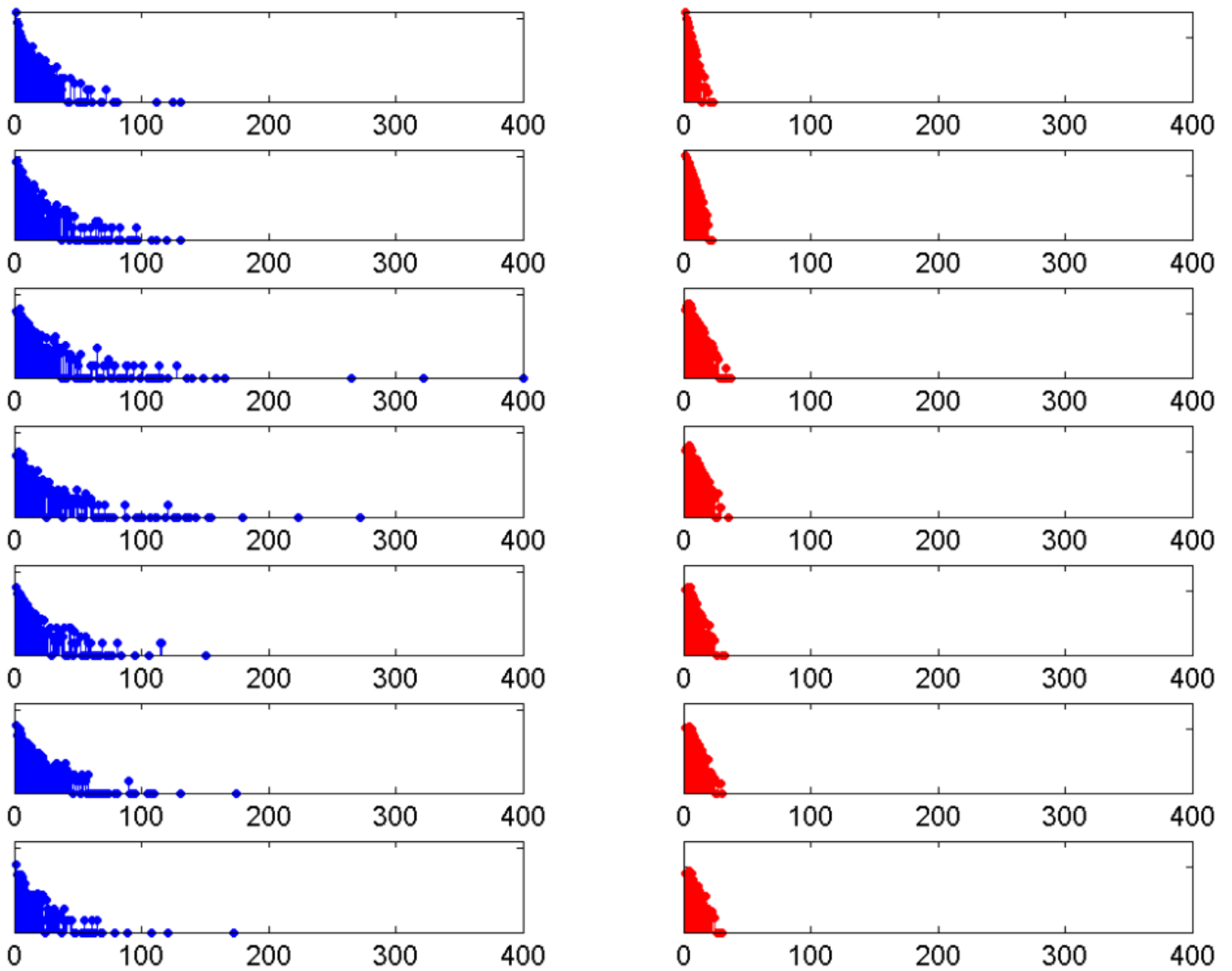
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number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