Population analysis of the *Cesky Terrier* breed

Genetic analysis of the Kennel Club pedigree records of the UK *Cesky 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. However, the number of animals of this breed registered with the Kennel Club per year has not been consistently high enough to allow all intended features of the report to be presented.

Summary of results

The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered *Cesky Terrier* population, and statistics were calculated for the period 1980-2014.

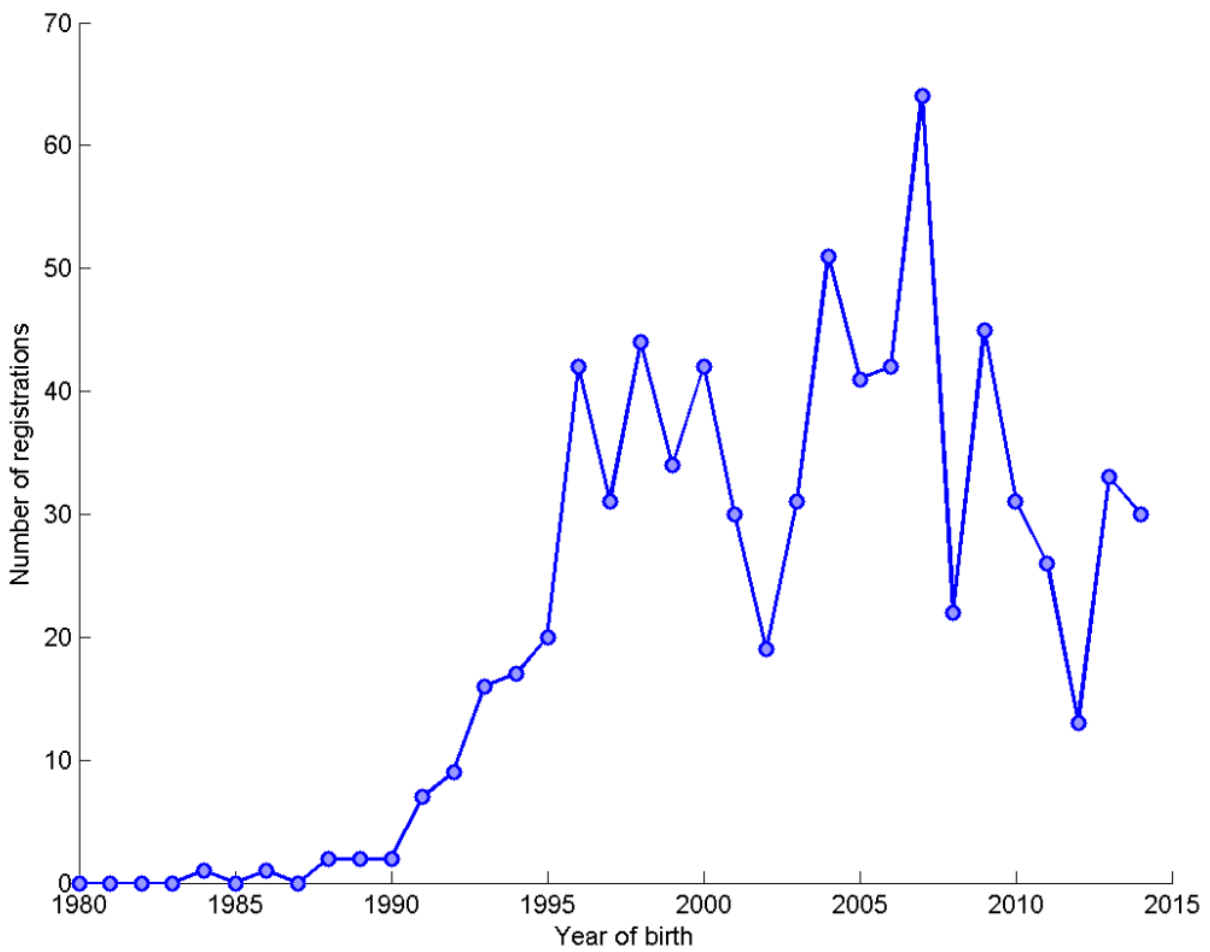> **Figure 1:** a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed.

Breed: *Cesky Terrier*

Figure 1: Number of registrations by year of birth

Table 1: census statistics by year where available, 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	0	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
1981	0	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
1982	0	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
1983	0	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
1984	1	1	1	1	1	1	1	0	n/a	n/a	n/a	n/a
1985	0	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
1986	1	1	1	1	1	1	1	0	n/a	n/a	n/a	n/a
1987	0	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
1988	2	2	2	1	1	1	1	0	n/a	n/a	n/a	n/a
1989	2	2	2	1	1	1	1	0	n/a	n/a	n/a	n/a
1990	2	2	2	1	1	1	1	0	n/a	n/a	n/a	n/a
1991	7	4	4	4	1	1	1.75	1.5	n/a	n/a	n/a	n/a
1992	9	4	2	8	4.5	1	4.5	4.95	n/a	n/a	n/a	n/a
1993	16	6	4	6	4	2	4	1.83	n/a	n/a	n/a	n/a
1994	17	6	6	6	2	1	2.83	2.23	n/a	n/a	n/a	n/a
1995	20	8	7	8	1	1	2.86	2.73	n/a	n/a	n/a	n/a
1996	42	13	10	10	4	1	4.2	2.78	73.81	52.38	23.81	23.81
1997	31	10	7	12	5	1	4.43	3.99	n/a	n/a	n/a	n/a
1998	44	14	10	15	2	1	4.4	4.65	88.64	68.18	34.09	34.09
1999	34	12	10	9	3	1	3.4	2.67	82.35	55.88	26.47	26.47
2000	42	11	8	14	4	1	5.25	4.56	n/a	n/a	n/a	n/a
2001	30	8	8	6	5	1	3.75	2.31	n/a	n/a	n/a	n/a
2002	19	9	7	11	1	1	2.71	3.73	n/a	n/a	n/a	n/a
2003	31	15	14	8	1	1	2.21	2.01	77.42	61.29	25.81	25.81
2004	51	17	14	6	4	6	3.64	2.37	80.39	47.06	11.76	11.76
2005	41	14	10	12	2	1	4.1	4.07	82.93	70.73	29.27	29.27
2006	42	16	11	14	1	1	3.82	4.17	88.1	66.67	33.33	33.33
2007	64	17	11	16	5	2	5.82	4.35	81.25	53.13	25	25
2008	22	7	5	13	2	1	4.4	5.08	n/a	n/a	n/a	n/a
2009	45	14	14	9	2	1	3.21	2.83	82.22	64.44	20	20
2010	31	14	12	8	2	1	2.58	2.15	77.42	54.84	25.81	25.81
2011	26	10	9	5	3	1	2.89	1.62	n/a	n/a	n/a	n/a
2012	13	6	5	6	2	1	2.6	2.07	n/a	n/a	n/a	n/a
2013	33	11	9	7	4	2	3.67	1.87	n/a	n/a	n/a	n/a
2014	30	9	9	5	4	2	3.33	1.32	n/a	n/a	n/a	n/a

> **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) = 3.30

> **Estimated effective population size:** the rate of inbreeding 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 many 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 = 17.1
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 observed.

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	0.2	1	10.2	34.2	34.6	42.8	26.6
Total #sires	1	5	13	30	35	36	31
Max #progeny	1	1	14	20	28	38	19
Mean #progeny	1	1	3.9231	5.7	4.9429	5.9444	4.2903
Median #progeny	1	1	1	3.5	2	3	4
Mode #progeny	1	1	1	1	1	1	1
SD #progeny	0	0	4.1525	5.2532	6.6152	8.1589	3.7876
Skew #progeny	n/a	n/a	1.2558	1.1535	2.3732	2.4899	2.2183
Total #dams	1	5	16	46	46	56	42
Max #progeny	1	1	16	12	14	12	9
Mean #progeny	1	1	3.1875	3.7174	3.7609	3.8214	3.1667
Median #progeny	1	1	2.5	3	3	3	3
Mode #progeny	1	1	1	1	1	1	1
SD #progeny	0	0	3.7098	2.9864	3.1985	3.0398	1.8989
Skew #progeny	n/a	n/a	2.7521	0.90964	1.402	1.355	0.73152
Rate of inbreeding	n/a	n/a	0.034087	-0.03576	0.078004	0.013309	-0.04203
Generation interval	n/a	n/a	2.5553	3.168	3.834	4.3323	4.7342
Effective pop size	n/a	n/a	14.668	n/a	6.4099	37.568	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 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.
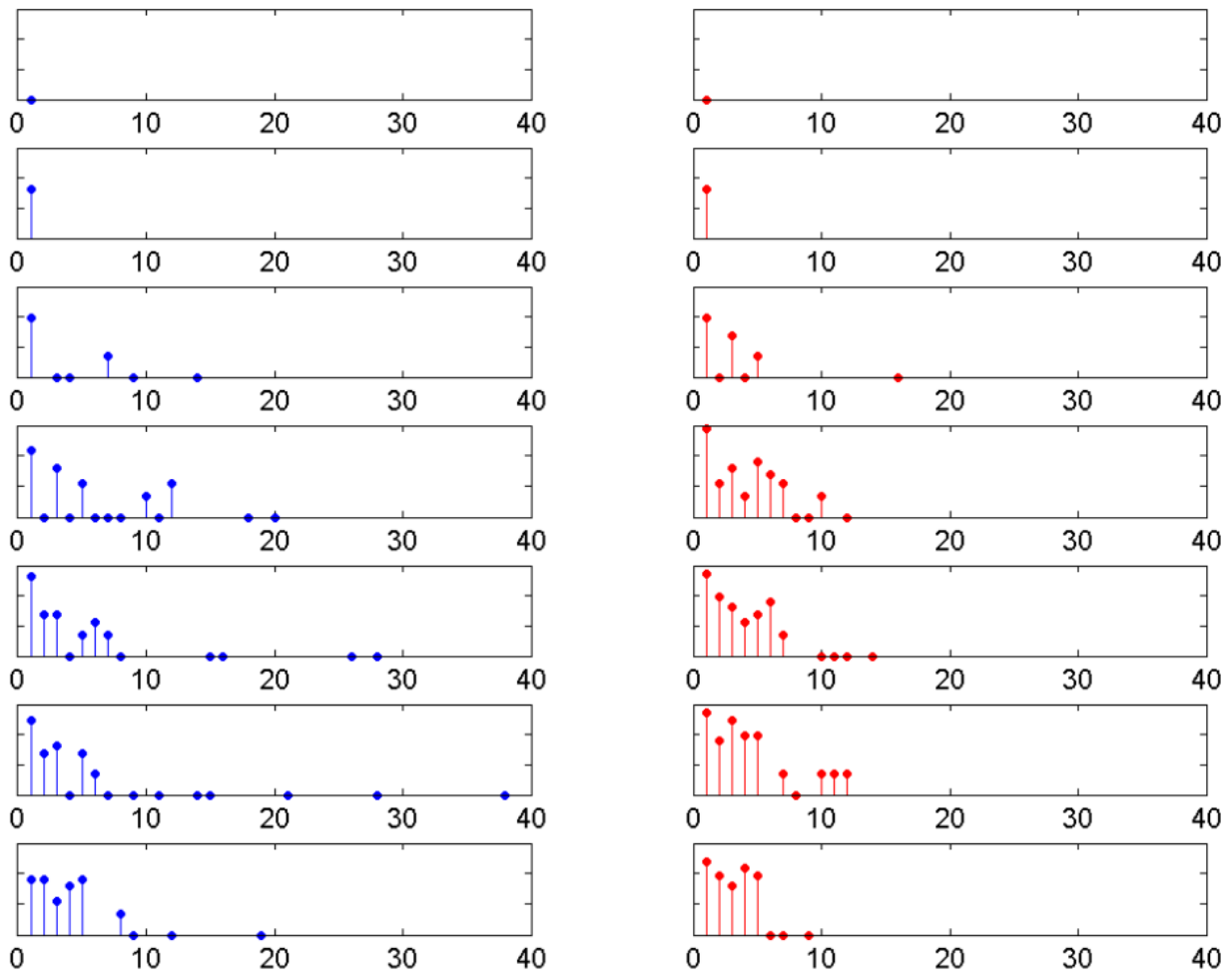
Comments

As can be seen from figure 1, the number of animals of this breed registered with the Kennel Club is consistently small. The small population size and possible use of migrant animals mean there may be large fluctuations in the rate of inbreeding and effective population size.

There appears to be evidence of popular dogs used 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.