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September 2015

Population analysis of the *Otterhound* breed

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



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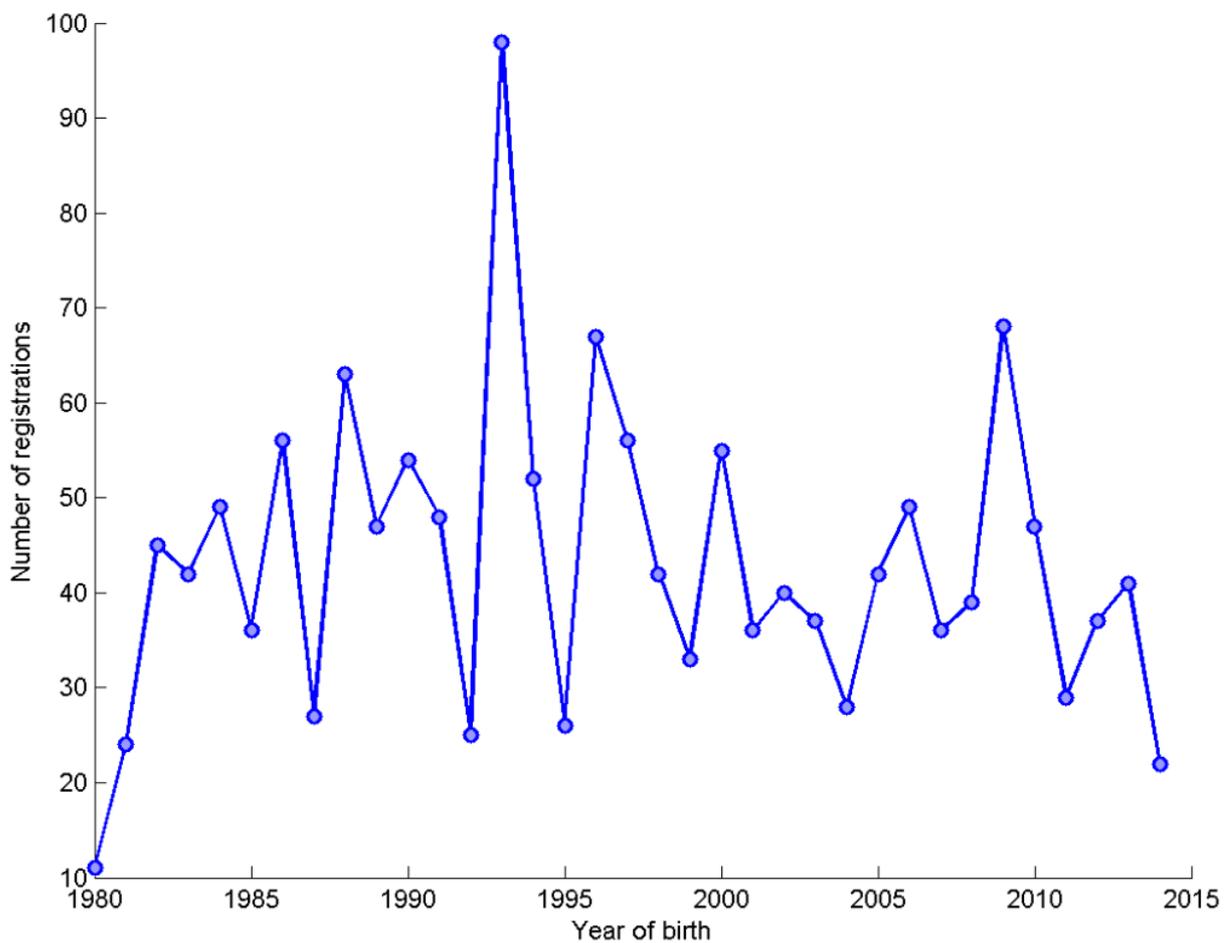
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Figure 1: a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

Breed: Otterhound

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = -0.05 per year (with a 95% confidence interval of -0.61 to 0.51).



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	11	6	6	4	1.5	1	1.83	1.17	n/a	n/a	n/a	n/a
1981	24	6	6	10	2.5	1	4	3.69	n/a	n/a	n/a	n/a
1982	45	8	7	11	7	2	6.43	3.26	n/a	n/a	n/a	n/a
1983	42	8	8	8	5.5	4	5.25	2.31	n/a	n/a	n/a	n/a
1984	49	10	9	17	4	4	5.44	4.72	n/a	n/a	n/a	n/a
1985	36	8	7	10	5	1	5.14	3.34	n/a	n/a	n/a	n/a
1986	56	10	8	11	8.5	9	7	3.82	n/a	n/a	n/a	n/a
1987	27	5	4	10	7.5	2	6.75	3.4	n/a	n/a	n/a	n/a
1988	63	9	9	17	6	3	7	4.39	n/a	n/a	n/a	n/a
1989	47	9	8	15	5	1	5.88	4.94	n/a	n/a	n/a	n/a
1990	54	10	9	9	5	5	6	2.12	n/a	n/a	n/a	n/a
1991	48	7	7	10	6	6	6.86	2.61	n/a	n/a	n/a	n/a
1992	25	5	5	7	7	7	5	2.83	n/a	n/a	n/a	n/a
1993	98	16	16	10	6.5	8	6.13	2.33	65.31	34.69	18.37	10.2
1994	52	9	9	13	6	6	5.78	3.99	n/a	n/a	n/a	n/a
1995	26	5	4	10	7.5	1	6.5	3.87	n/a	n/a	n/a	n/a
1996	67	13	13	15	5	1	5.15	4.22	85.07	49.25	22.39	22.39
1997	56	12	10	10	6	6	5.6	2.59	66.07	44.64	17.86	17.86
1998	42	8	8	10	6	2	5.25	3.28	n/a	n/a	n/a	n/a
1999	33	7	7	9	4	2	4.71	2.56	n/a	n/a	n/a	n/a
2000	55	10	7	25	4	1	7.86	8.95	n/a	n/a	n/a	n/a
2001	36	7	6	10	7.5	1	6	4	n/a	n/a	n/a	n/a
2002	40	7	7	9	6	1	5.71	2.69	n/a	n/a	n/a	n/a
2003	37	6	6	11	7	9	6.17	4.12	n/a	n/a	n/a	n/a
2004	28	6	6	11	4	1	4.67	4.03	n/a	n/a	n/a	n/a
2005	42	6	5	10	9	10	8.4	1.82	n/a	n/a	n/a	n/a
2006	49	6	5	20	8	6	9.8	5.85	n/a	n/a	n/a	n/a
2007	36	8	6	13	6	1	6	5.02	n/a	n/a	n/a	n/a
2008	39	8	8	9	4.5	4	4.88	2.23	n/a	n/a	n/a	n/a
2009	68	12	10	19	5.5	3	6.8	4.92	75	54.41	27.94	27.94
2010	47	8	7	16	4	4	6.71	5.06	n/a	n/a	n/a	n/a
2011	29	4	4	10	7	7	7.25	2.06	n/a	n/a	n/a	n/a
2012	37	6	6	10	5.5	3	6.17	2.79	n/a	n/a	n/a	n/a
2013	41	5	5	10	8	8	8.2	1.1	n/a	n/a	n/a	n/a
2014	22	4	4	8	5.5	3	5.5	2.08	n/a	n/a	n/a	n/a

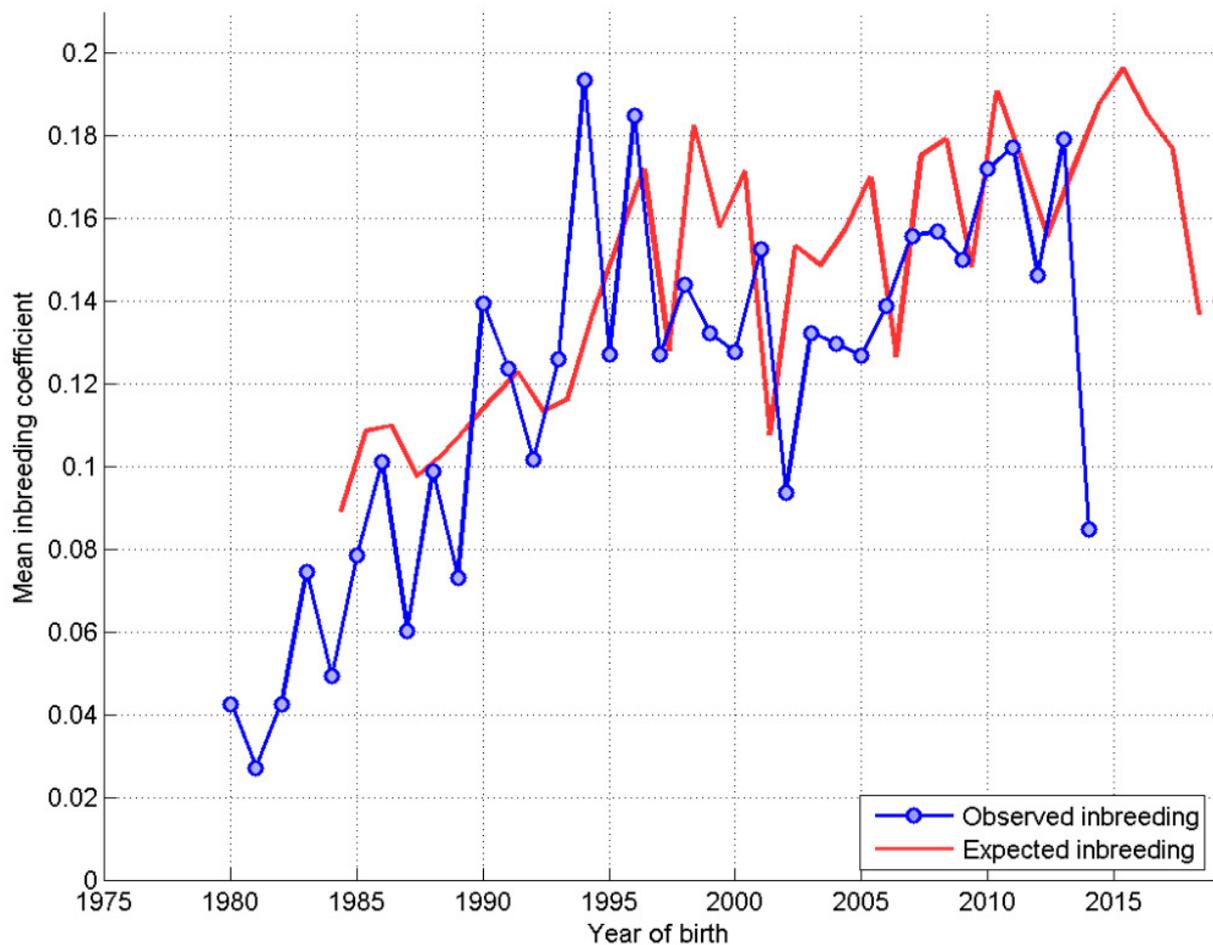


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 4.36

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 = 33.9

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	34.2	45.8	55.4	44.8	39.2	46.8	35.2
Total #sires	24	28	34	35	26	25	23
Max #progeny	27	42	25	17	25	25	16
Mean #progeny	6.9167	7.8929	7.4118	6.2	7.5	8.96	7.3043
Median #progeny	5.5	6	6	6	7	7	8
Mode #progeny	2	1	5	1	1	4	8
SD #progeny	5.8675	7.9458	5.1881	4.0424	6.015	7.0739	3.4959
Skew #progeny	1.8174	2.9343	1.4948	0.67642	1.6156	1.133	0.37949
Total #dams	29	27	39	36	29	29	25
Max #progeny	19	22	17	17	27	18	18
Mean #progeny	5.8621	8.3333	6.9744	6.1944	6.5172	7.8276	6.84
Median #progeny	5	7	7	6	5	9	7
Mode #progeny	6	1	8	5	1	9	4
SD #progeny	4.7863	5.5262	4.3799	3.7631	6.2998	4.045	3.3749
Skew #progeny	1.4013	0.68141	0.66095	0.81868	1.6341	0.54923	1.2095
Rate of inbreeding	0.025369	-0.00628	0.062303	-0.01799	-0.00812	0.030396	-0.08005
Generation interval	3.9688	4.3837	4.7467	4.8598	4.3016	4.069	3.9987
Effective pop size	19.709	n/a	8.0252	n/a	n/a	16.449	n/a



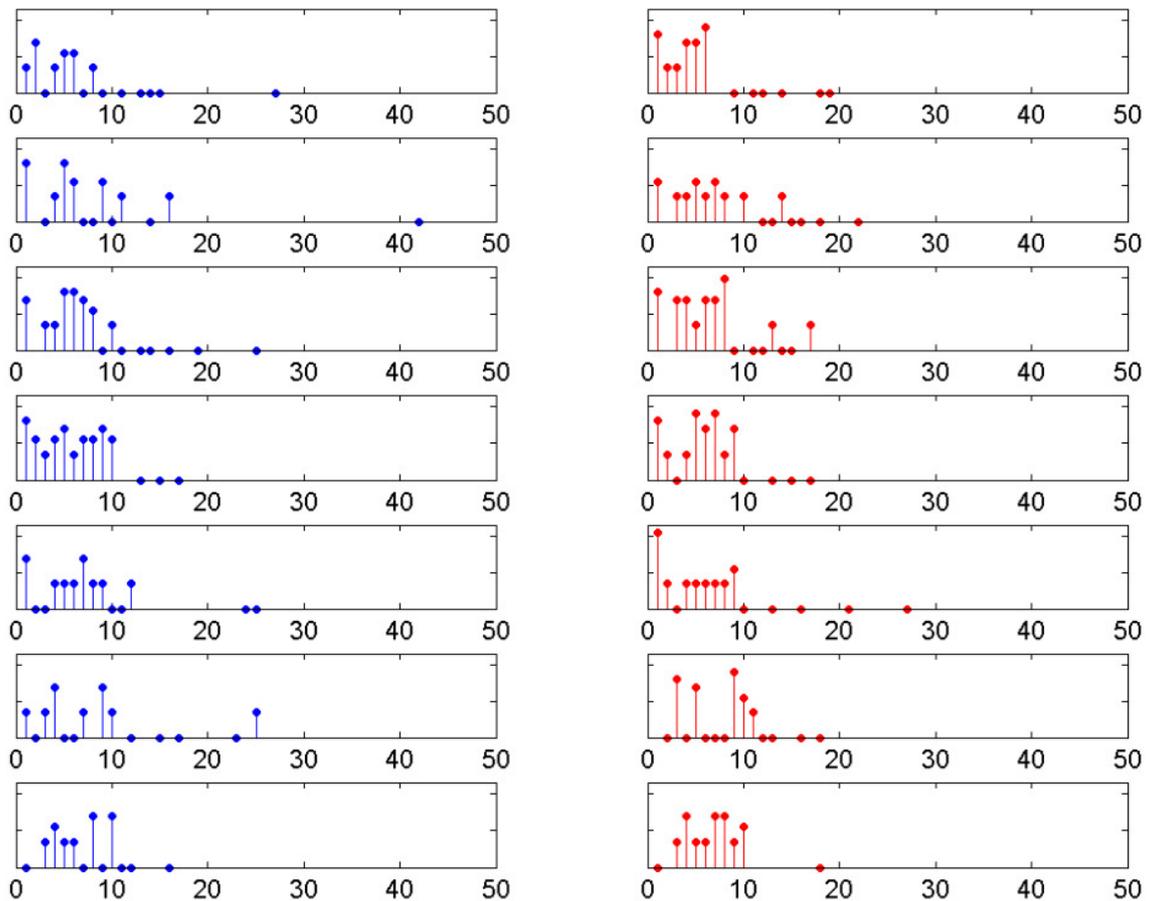
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number 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 can be seen from figure 1, the number of animals of this breed registered with the Kennel Club is very small. The small population size and possible influence of migrant animals mean there may be large fluctuations in the rate of inbreeding and effective population size. Over the whole period the rate of inbreeding in this breed has remained relatively steady but high.

There appears to be little 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.