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September 2015

Population analysis of the *Basset Hound* breed

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



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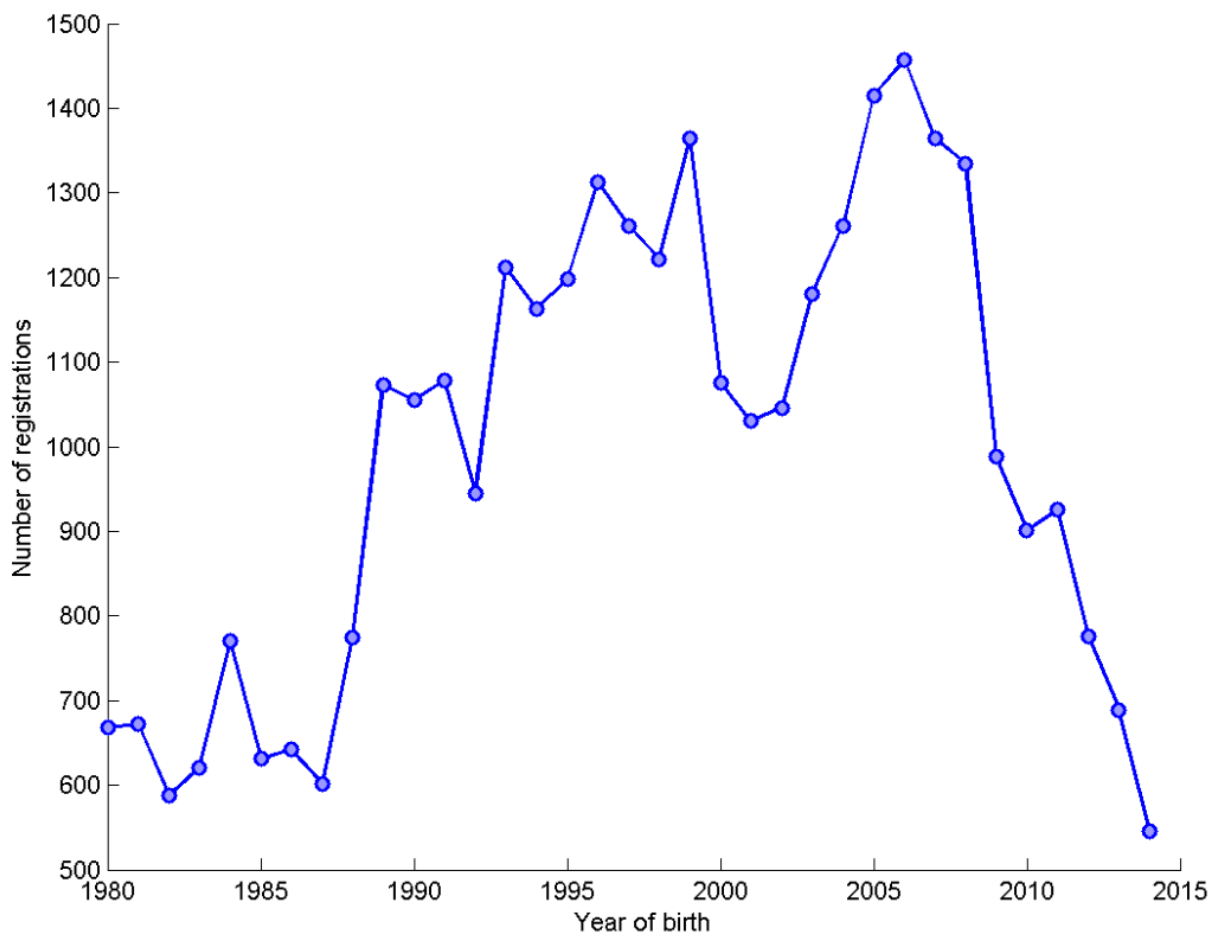
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Figure 1: a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

Breed: *Basset Hound*

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = 10.43 per year (with a 95% confidence interval of 1.53 to 19.32).



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	668	205	113	30	4	1	5.91	6.17	87.87	63.17	33.08	19.91
1981	672	187	96	60	5	2	7	8.49	84.08	62.2	39.58	25.89
1982	588	163	93	28	5	1	6.32	5.85	81.8	53.74	31.12	21.94
1983	620	140	73	52	5	3	8.49	9.35	85	60.32	35.97	25.48
1984	770	174	81	64	6	1	9.51	11.91	86.1	64.16	41.04	27.14
1985	631	151	71	86	5	1	8.89	14.28	86.21	68.46	47.07	36.61
1986	642	148	61	64	7	1	10.52	12.71	87.23	63.55	38.94	25.23
1987	602	136	73	53	5	3	8.25	9.24	83.55	59.14	36.71	25.75
1988	774	172	72	48	7	3	10.75	9.72	80.88	57.49	29.97	19.64
1989	1073	179	88	76	9	8	12.19	12.78	79.78	57.97	36.44	21.25
1990	1055	183	81	87	8	1	13.02	14.09	82.37	58.29	33.55	23.22
1991	1079	180	81	83	8	8	13.32	14.32	81.28	59.41	34.48	22.15
1992	945	161	75	75	8	8	12.6	13.92	83.07	60.53	37.99	25.19
1993	1212	201	84	142	8	8	14.43	19.34	83.5	63.94	38.78	26.4
1994	1163	195	74	97	8.5	5	15.72	19.99	84.69	66.04	41.27	29.66
1995	1198	205	90	121	7.5	1	13.31	18.55	84.97	66.78	42.57	31.64
1996	1313	223	88	105	9	7	14.92	17.16	82.94	60.62	36.86	23.15
1997	1261	223	106	74	8	6	11.9	13.2	83.58	61.7	36.48	22.84
1998	1222	214	114	70	7	8	10.72	11.77	81.34	61.05	37.64	23.98
1999	1365	230	108	78	8	1	12.64	13.79	84.25	62.12	37	20.88
2000	1075	198	103	70	8	10	10.44	10.88	80.47	58.14	34.51	21.77
2001	1030	186	97	63	7	1	10.62	10.93	82.23	58.16	34.76	22.23
2002	1046	187	104	60	7	1	10.06	10.37	82.6	59.46	33.46	21.03
2003	1181	198	102	100	8	6	11.58	13.11	82.05	60.97	34.55	22.44
2004	1261	232	109	77	7	1	11.57	12.69	84.77	59.08	34.58	21.49
2005	1415	237	111	91	8	6	12.75	14.58	82.26	62.19	38.16	25.58
2006	1457	243	117	57	8	1	12.45	12.81	84.28	62.66	35.14	20.32
2007	1364	245	137	50	7	1	9.96	9.65	81.96	57.4	33.72	21.19
2008	1335	238	128	46	7.5	1	10.43	9.54	82.7	57.23	31.31	17.68
2009	988	179	106	53	7	2	9.32	8.6	80.36	57.79	32.09	17.51
2010	901	171	113	39	6	1	7.97	7.11	80.8	56.6	29.41	19.31
2011	926	175	108	40	7	1	8.57	7.97	81.21	57.02	32.29	18.36
2012	776	157	105	41	6	1	7.39	7.57	82.86	58.89	36.21	21.01
2013	689	124	80	47	6	1	8.61	7.84	81.71	56.46	29.75	17.85
2014	546	94	52	58	8	7	10.5	9.54	78.39	54.03	29.12	20.51

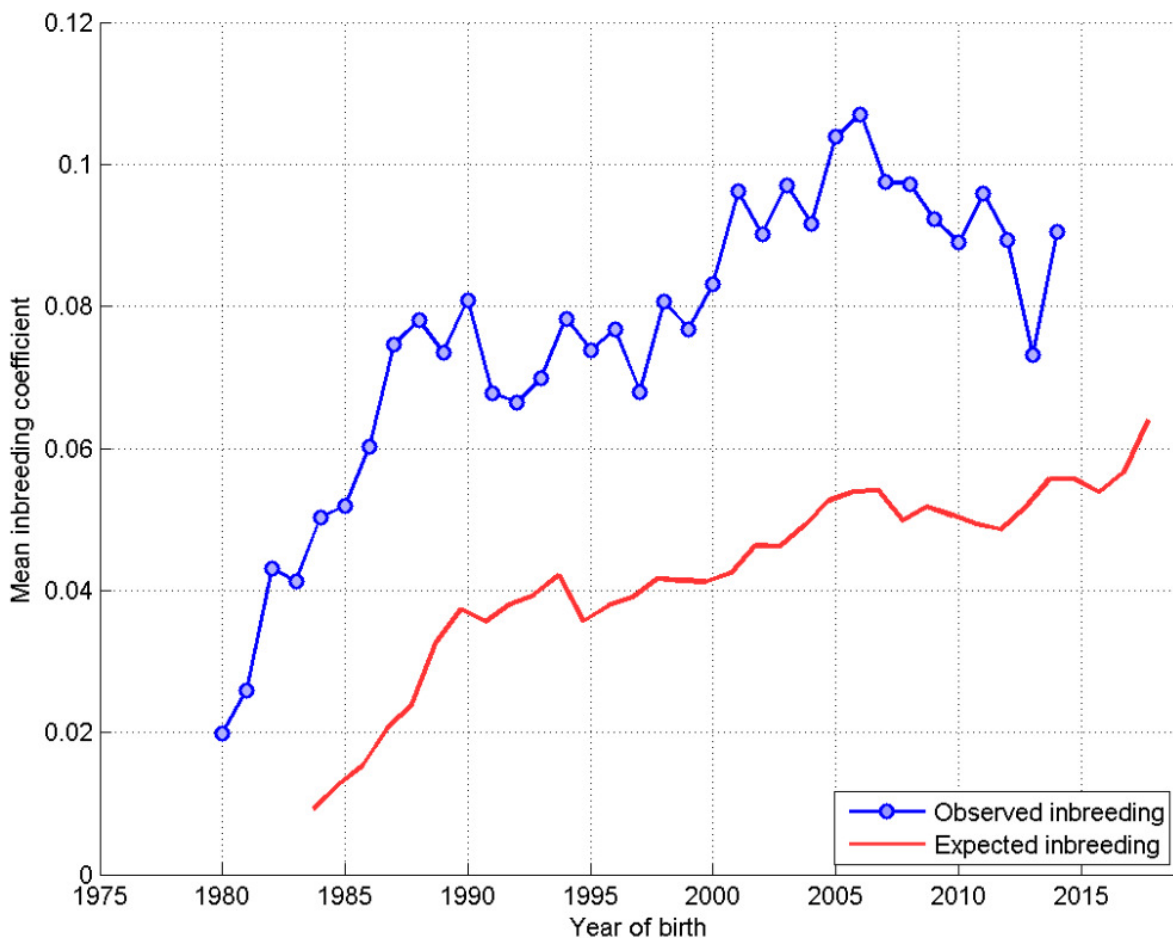


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 3.72

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 = 74.2

NB - this estimate is made using the rate of inbreeding over the whole period 1980-2014



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	663.6	744.4	1090.8	1271.8	1118.6	1311.8	767.6
Total #sires	270	199	204	283	279	344	266
Max #progeny	127	264	314	386	229	235	125
Mean #progeny	12.274	18.693	26.73	22.466	20.043	19.064	14.406
Median #progeny	5	8	11	10	9	9	8
Mode #progeny	1	1	1	1	1	1	1
SD #progeny	19.457	32.6	42.485	38.969	28.576	28.138	18.647
Skew #progeny	3.1697	4.7511	3.7669	4.8536	3.6469	3.3981	2.8754
Total #dams	670	559	613	735	732	817	562
Max #progeny	30	32	44	45	33	43	29
Mean #progeny	4.9463	6.6565	8.8956	8.6503	7.638	8.0269	6.8185
Median #progeny	4	6	7	7	7	7	6
Mode #progeny	1	7	5	7	7	7	1
SD #progeny	4.1637	4.7734	6.7525	6.1626	5.3679	5.7547	5.0547
Skew #progeny	1.6866	1.5861	1.7432	1.4657	1.2714	1.4262	1.4562
Rate of inbreeding	0.028006	0.024559	-0.0012048	0.0036419	0.0078279	-0.014166	-0.0083355
Generation interval	3.5709	3.7872	3.5919	3.4323	3.9372	3.8536	3.8633
Effective pop size	17.853	20.359	n/a	137.29	63.874	n/a	n/a



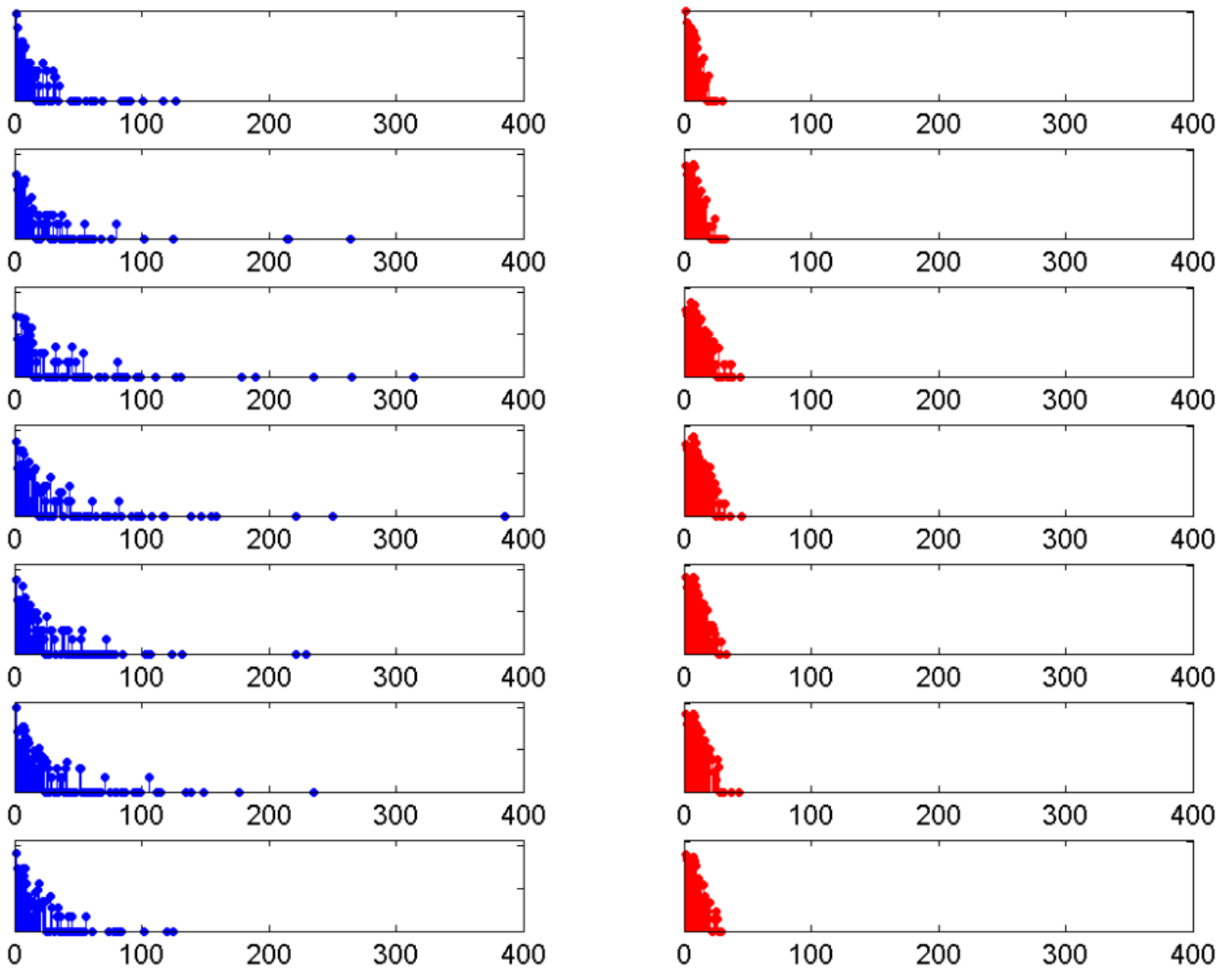
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number 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. This represents a 'genetic bottleneck', with genetic variation lost from the population. However, since the mid-2000s the rate of inbreeding has been negative, implying moderation restoration 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.