



THE KENNEL CLUB

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September 2015

Population analysis of the *Great Dane* breed

Genetic analysis of the Kennel Club pedigree records of the UK ***Great Dane*** 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

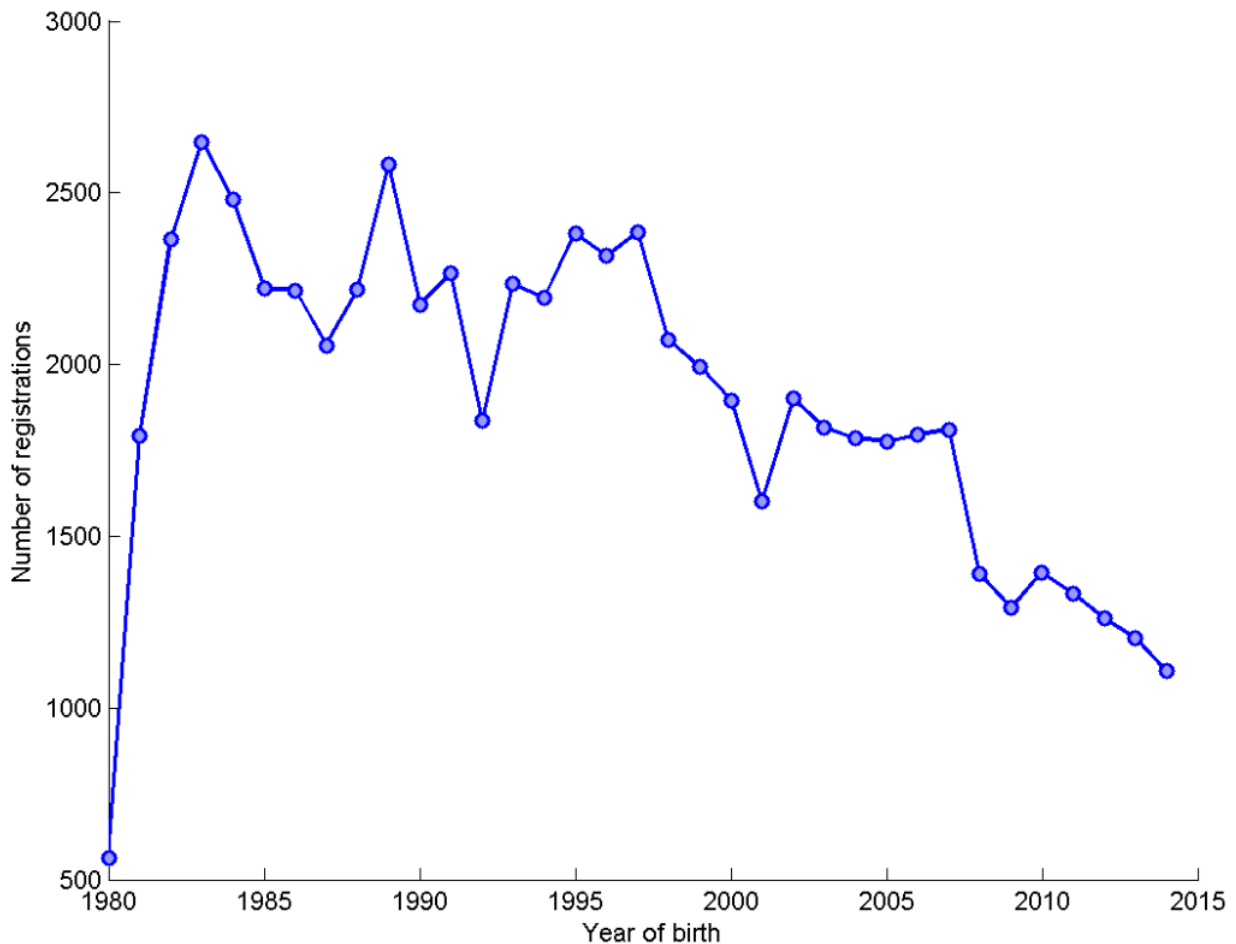
The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered ***Great Dane*** population, and statistics were calculated for the period 1980-2014.



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

Breed: Great Dane

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = -25.69 per year (with a 95% confidence interval of -39.35 to -12.03).



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	562	323	195	31	2	1	2.88	4.09	82.03	63.7	44.13	31.85
1981	1793	466	273	96	4	1	6.57	9.4	85.83	64.75	41.77	28.78
1982	2364	507	294	65	6	2	8.04	8.75	82.23	59.6	36	23.43
1983	2648	526	294	76	7	3	9.01	9.08	80.32	56.87	33.23	21.6
1984	2479	559	316	127	5	1	7.84	10.47	84.07	61.84	38.44	26.18
1985	2223	524	310	66	5	3	7.17	8.42	81.87	59.65	37.74	25.96
1986	2216	523	326	56	5	1	6.8	7.24	81	57.9	35.47	22.52
1987	2055	460	264	59	5	2	7.78	8.23	81.56	58.15	34.89	22.34
1988	2218	474	288	50	5	4	7.7	8.03	82.55	58.93	35.26	22.41
1989	2583	445	277	81	7	4	9.32	8.84	78.71	54.74	32.33	20.17
1990	2173	386	239	41	7	6	9.09	7.33	78.65	53.43	28.67	16.94
1991	2266	372	230	46	7	6	9.85	8.28	78.16	54.41	29.57	18.14
1992	1837	329	227	65	7	1	8.09	7.79	78.33	53.24	31.74	20.41
1993	2234	354	212	82	8	7	10.54	10.33	78.6	55.73	32.81	21.71
1994	2193	355	216	77	8	9	10.15	9.78	78.61	55.08	32.24	20.16
1995	2382	383	220	110	8	1	10.83	10.81	79.3	55.5	31.07	19.82
1996	2316	353	217	54	8	6	10.67	9.76	78.54	56.52	33.2	19.43
1997	2384	363	227	46	9	6	10.5	8.04	76.51	51.05	27.85	16.57
1998	2071	343	219	49	8	4	9.46	8.15	79.19	53.79	30.03	18.88
1999	1994	323	217	63	8	5	9.19	7.72	76.93	51.2	28.39	17.75
2000	1895	310	199	63	8	1	9.52	8.79	78.94	53.98	31.66	19.74
2001	1602	261	169	50	7	6	9.48	8.59	79.84	55.81	32.27	18.23
2002	1902	299	189	51	8	8	10.06	8.79	78.97	54.57	31.07	18.09
2003	1815	278	170	48	8	7	10.68	8.69	78.18	53.72	28.65	17.69
2004	1786	271	168	54	7	1	10.63	10.09	80.57	58.12	33.15	19.09
2005	1777	282	196	43	8	1	9.07	7.47	78.28	51.94	29.26	18.29
2006	1797	266	191	38	8	1	9.41	7.56	78.13	52.87	28.55	17.75
2007	1810	266	177	51	8	8	10.23	9.01	78.23	54.25	31.93	19.39
2008	1389	228	161	32	7	1	8.63	6.72	78.19	52.05	27.79	15.91
2009	1291	211	146	54	7	1	8.84	7.95	79.09	54.22	31.37	18.98
2010	1395	222	156	52	7	1	8.94	8.63	79.93	55.56	33.33	21.65
2011	1332	189	140	33	8	1	9.51	6.74	76.5	49.4	25.38	14.94
2012	1262	196	145	59	7	1	8.7	8.49	82.25	55.23	32.57	20.29
2013	1203	181	126	47	8	1	9.55	7.82	77.72	51.37	29.59	17.21
2014	1107	147	96	53	9	7	11.53	9.59	77.96	52.66	30.44	18.61

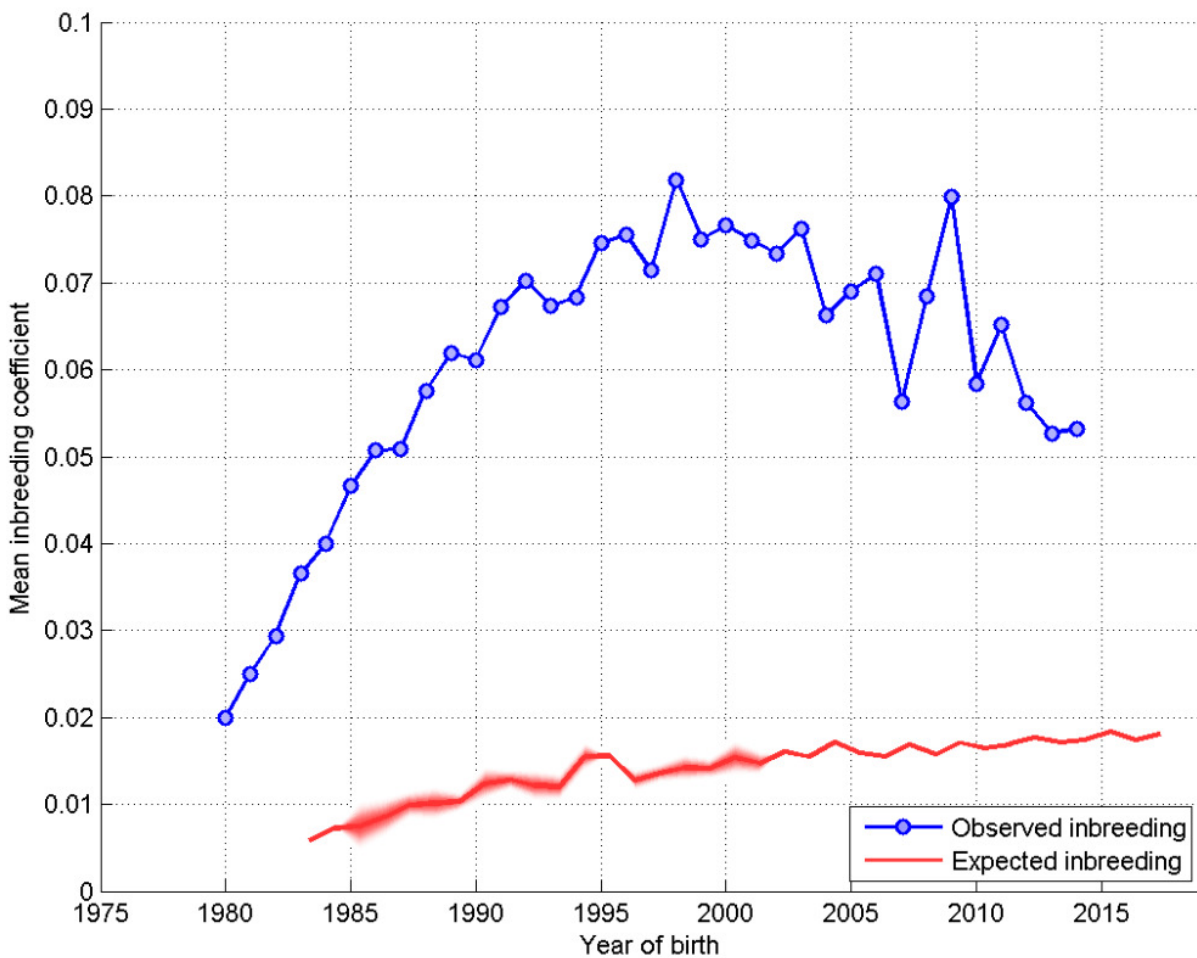


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 3.34

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 = 166.8

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	1969.2	2259	2140.6	2229.4	1800	1612.8	1259.8
Total #sires	867	943	717	690	580	567	414
Max #progeny	200	210	185	185	176	121	108
Mean #progeny	11.331	11.977	14.926	16.154	15.516	14.208	15.198
Median #progeny	5	7	9	9	9	9	9
Mode #progeny	1	2	1	6	1	1	1
SD #progeny	19.096	18.412	19.25	19.133	19.55	16.668	17.179
Skew #progeny	4.67	4.7203	4.1574	3.0581	3.2871	2.6305	2.3186
Total #dams	1748	1746	1273	1282	1063	952	698
Max #progeny	37	33	36	37	43	54	41
Mean #progeny	5.6201	6.4685	8.3943	8.6942	8.4657	8.4695	9.0143
Median #progeny	4	5	7	7	7	7	8
Mode #progeny	1	3	4	7	7	1	1
SD #progeny	4.8295	5.0788	5.9857	6.2848	5.9436	6.0843	6.6505
Skew #progeny	1.8817	1.6988	1.3708	1.4564	1.3769	1.4511	1.1446
Rate of inbreeding	0.016028	0.012895	0.005489	0.002462	-0.00705	0.007047	-0.00876
Generation interval	3.0201	3.2469	3.5478	3.2365	3.3721	3.4061	3.6388
Effective pop size	31.196	38.776	91.089	203.07	n/a	70.955	n/a



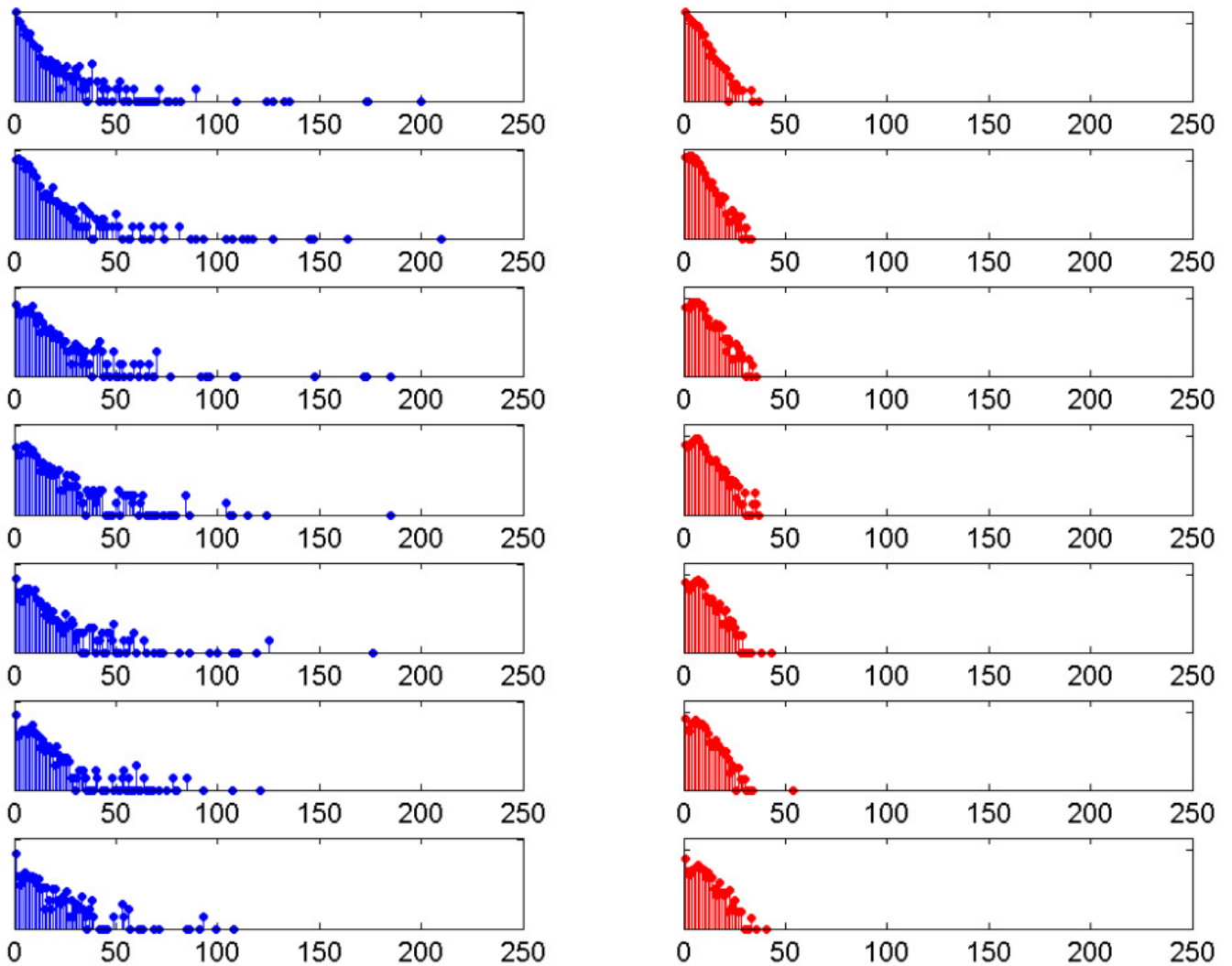
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number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