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September 2015

Population analysis of the *Dobermann* breed

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



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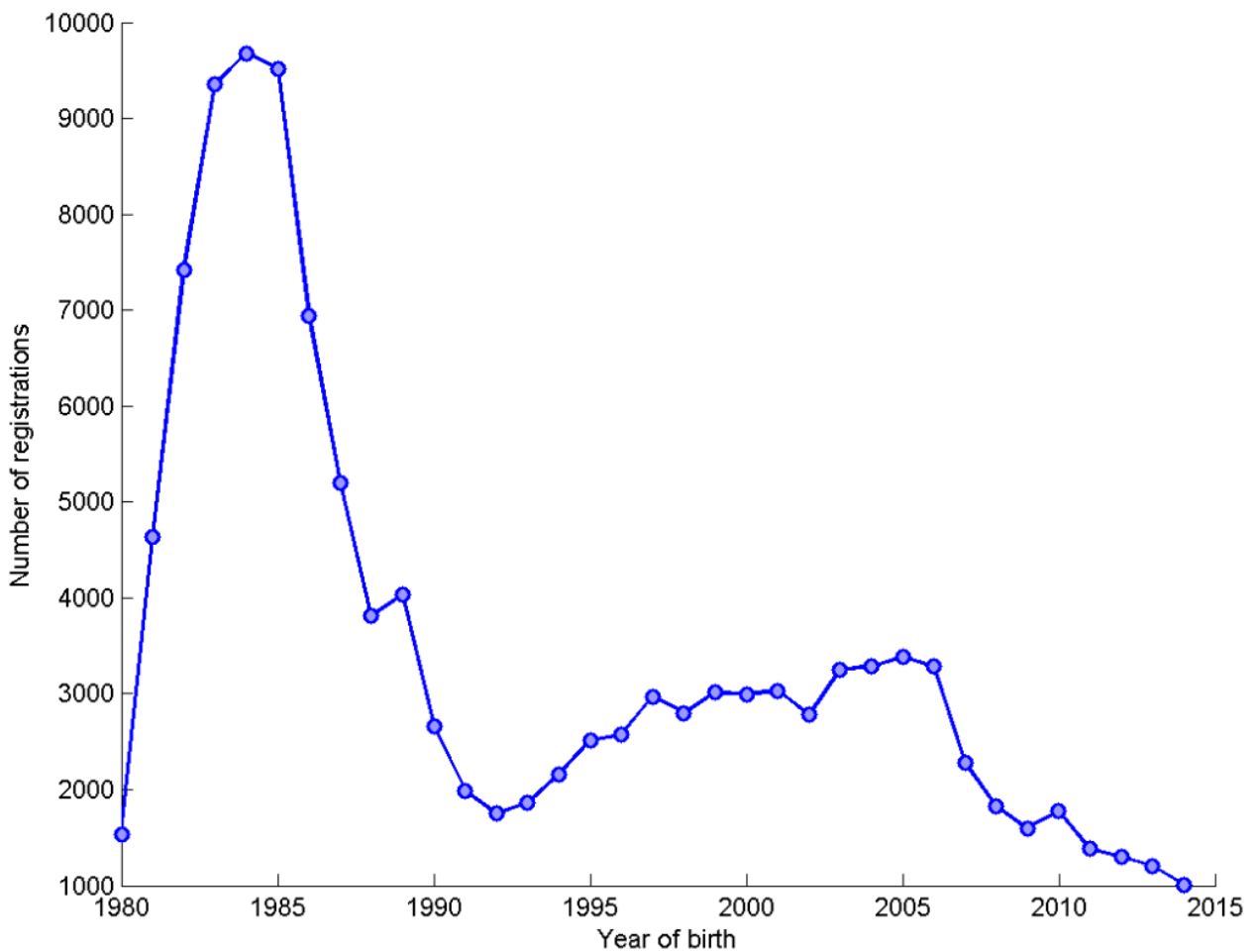
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Figure 1: a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

Breed: *Dobermann*

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = -149.75 per year (with a 95% confidence interval of -212.02 to -87.49).



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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	1529	768	424	32	2	1	3.61	4.54	83.26	63.83	40.16	26.42
1981	4638	1092	585	65	5	1	7.93	9.63	85.04	64.38	41.05	25.7
1982	7420	1577	795	85	6	4	9.33	11.11	83.36	62.36	39.76	25.47
1983	9353	2064	1035	174	5	3	9.04	12.35	84.51	65.1	42.48	28.27
1984	9678	2389	1229	117	4	3	7.87	10.78	84.67	65.09	42.61	28.84
1985	9520	2619	1459	128	4	1	6.53	9.22	83.73	64.31	42.27	29.17
1986	6945	2007	1272	74	3	1	5.46	6.85	82.66	61.4	38.29	26.09
1987	5195	1531	1003	86	3	1	5.18	7.14	83	62.77	39.88	27.35
1988	3816	1028	741	77	3	1	5.15	6.08	81.79	59.85	35.22	23.72
1989	4037	706	496	62	6	7	8.14	8.46	77.46	53.95	34.01	23.41
1990	2661	442	297	64	7	7	8.96	8.84	77.3	54.27	33.67	22.1
1991	1988	324	238	71	7	4	8.35	7.72	76.41	51.91	30.63	19.57
1992	1752	286	169	83	8	7	10.37	10.97	79.28	57.13	35.84	22.43
1993	1860	301	183	69	7	3	10.16	10.11	78.71	56.99	34.19	21.88
1994	2161	333	192	118	8	8	11.26	13.78	79.41	59.23	38.82	27.35
1995	2509	375	195	83	8	7	12.87	12.61	80.47	58.63	34.52	20.69
1996	2577	382	209	90	8	7	12.33	13.09	79.24	57.66	35.55	22.97
1997	2972	420	233	113	8	8	12.76	14.9	80.22	60.2	39.2	25.84
1998	2800	407	214	115	9	7	13.08	14.11	78.5	58.32	35.29	23.11
1999	3014	417	226	89	9	8	13.34	13.75	79.63	59.19	36.6	21.53
2000	2998	431	243	108	9	9	12.34	14.3	79.02	58.31	37.36	24.75
2001	3035	435	254	115	9	9	11.95	11.3	76.61	53.87	30.35	20.07
2002	2782	402	230	81	8	6	12.1	13.14	79.55	58.95	35.95	25.13
2003	3246	477	278	94	9	9	11.68	10.95	78.31	55.55	32.32	20.02
2004	3292	474	271	107	8	8	12.15	13	79.74	58.14	36.24	23.72
2005	3381	481	283	140	9	8	11.95	12.94	79.21	57.08	33.48	21.65
2006	3290	465	272	196	9	8	12.1	14.78	76.96	55.2	33.47	22.52
2007	2279	327	232	57	8	9	9.82	8.68	75.47	51.82	30.72	20.27
2008	1828	272	192	62	8	7	9.52	9.03	77.46	52.95	30.42	20.95
2009	1598	248	172	81	8	1	9.29	10.11	78.72	54.44	33.85	24.47
2010	1778	282	181	73	7	1	9.82	10.72	82.85	59.67	36.73	22.22
2011	1385	229	154	65	7	1	8.99	10.05	82.45	57.91	35.02	24.91
2012	1302	234	156	47	6	1	8.35	8.21	81.64	56.84	34.02	21.35
2013	1208	200	139	42	7	1	8.69	7.89	80.22	55.13	31.46	19.87
2014	1012	141	90	71	9	1	11.24	10.17	78.95	55.14	29.55	19.96

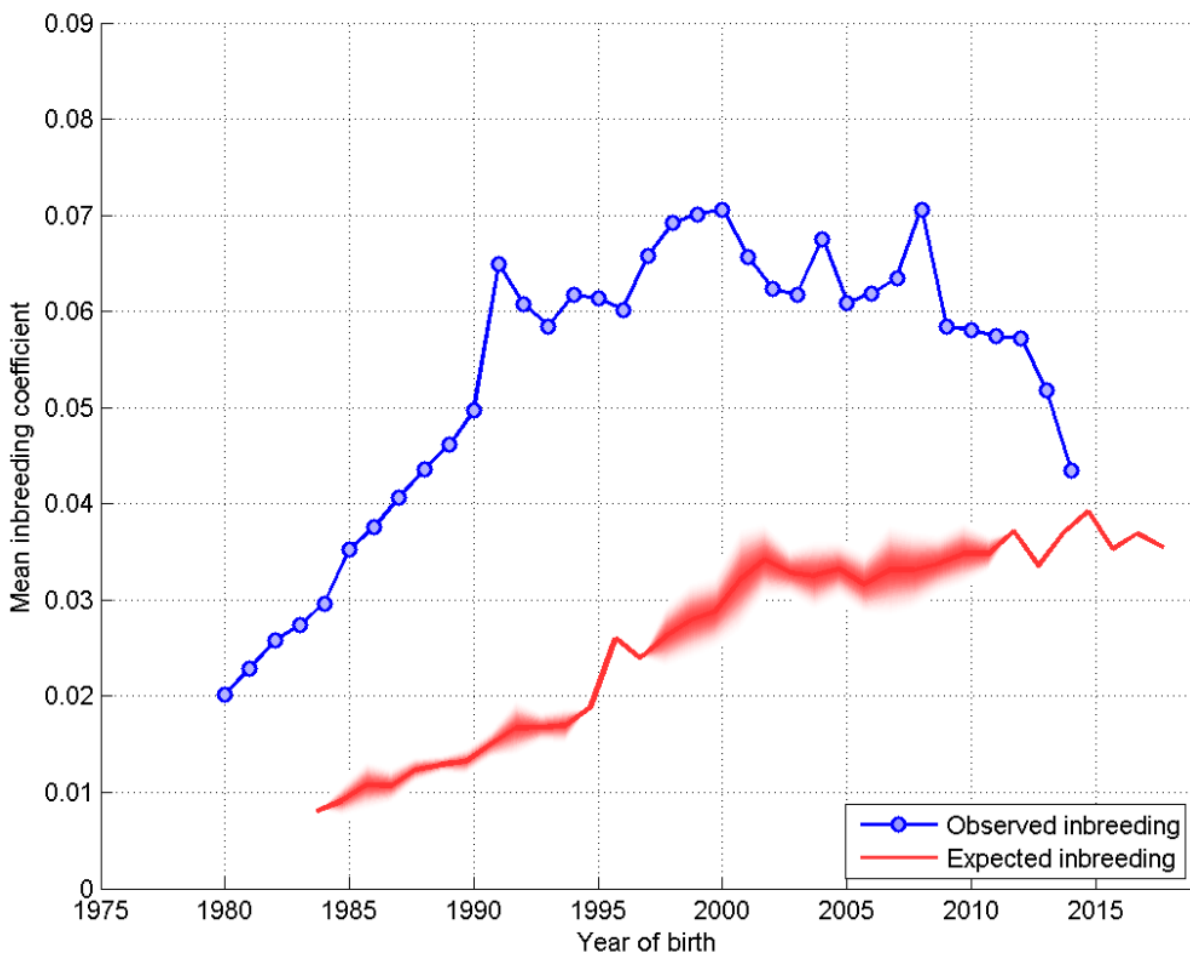


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 3.69

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 = 133.4

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	6523.6	5902.6	2084.4	2774.4	3070.6	2475.2	1337
Total #sires	2501	3430	720	629	773	726	485
Max #progeny	350	312	319	379	320	456	203
Mean #progeny	13.03	8.6041	14.474	22.052	19.86	17.045	13.781
Median #progeny	6	4	8	10	10	10	8
Mode #progeny	1	1	8	8	1	9	1
SD #progeny	24.767	16.535	23.662	34.547	30.604	27.109	20.486
Skew #progeny	5.1233	7.1016	5.5343	4.5469	4.6767	7.6845	4.2886
Total #dams	5421	6318	1253	1397	1560	1366	835
Max #progeny	44	37	39	51	43	40	50
Mean #progeny	6.0116	4.6708	8.3152	9.9291	9.841	9.0593	8.0048
Median #progeny	5	4	7	8	9	8	7
Mode #progeny	1	1	8	7	9	9	1
SD #progeny	4.9794	3.924	5.7315	6.6326	6.7453	5.9981	6.5001
Skew #progeny	1.7814	2.2355	1.6173	1.445	1.2729	1.2282	1.6323
Rate of inbreeding	0.007628	0.009964	0.007758	0.010964	-0.00398	0.001526	-0.01399
Generation interval	3.176	3.459	4.1878	3.8625	3.7276	3.635	3.7931
Effective pop size	65.551	50.181	64.452	45.602	n/a	327.71	n/a



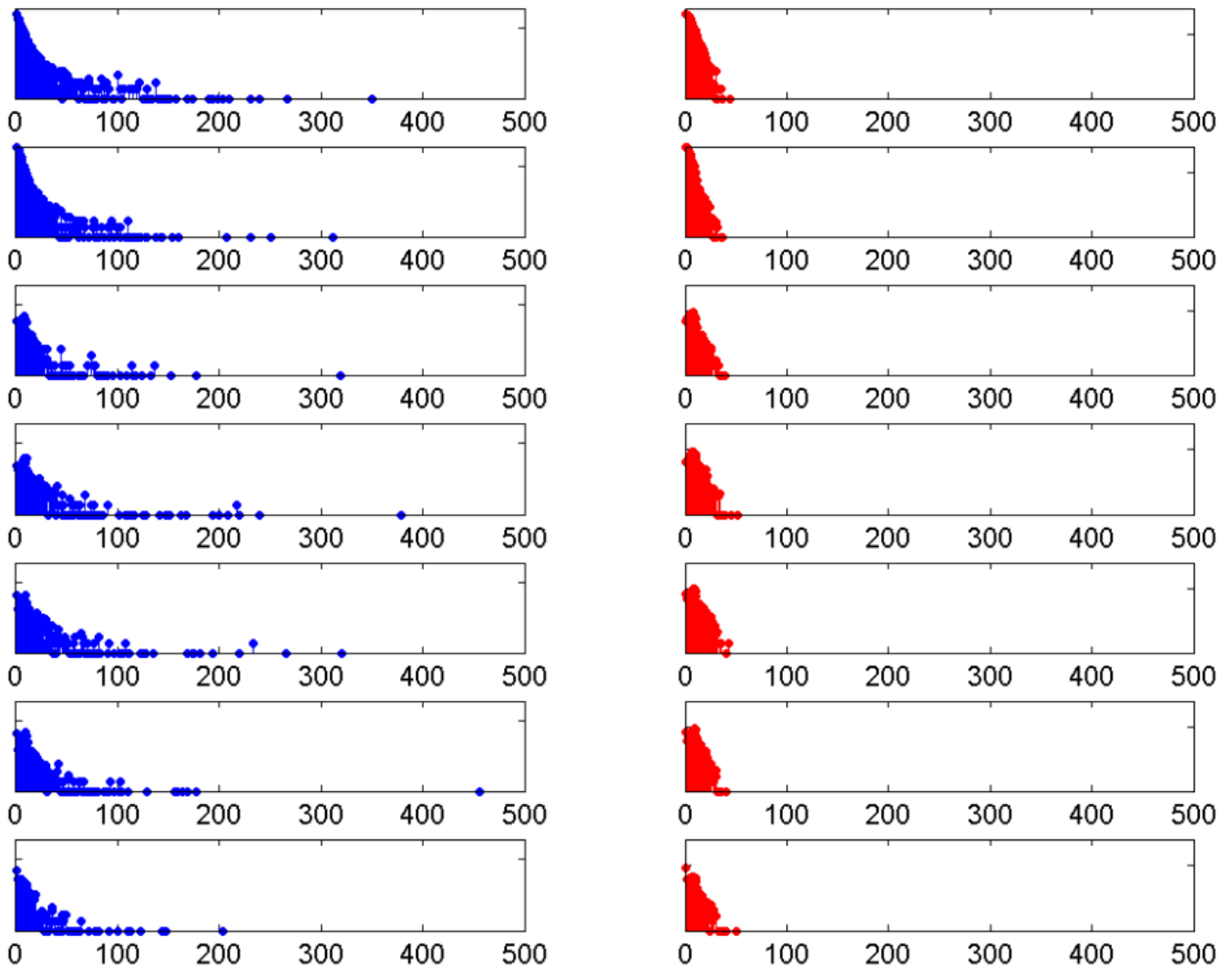
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number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