

Population analysis of the Dalmatian breed

Genetic analysis of the Kennel Club pedigree records of the UK **Dalmatian** 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 *Dalmatian* 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: Dalmatian

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = 27.66 per year (with a 95% confidence interval of -2.17 to 57.50).



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	167	123	95	8	1	1	1.76	1.41	71.86	52.69	31.14	17.96
1981	566	183	117	47	2	1	4.84	6.04	86.4	65.02	38.87	23.85
1982	679	194	123	35	4	1	5.52	5.05	82.18	56.55	29.31	17.53
1983	726	189	105	37	5	3	6.91	6.44	81.13	55.37	33.47	18.73
1984	782	203	112	32	5	1	6.98	6.22	80.69	55.63	30.43	19.57
1985	862	225	121	42	5	1	7.12	6.53	80.86	56.26	30.74	18.56
1986	756	196	125	35	5	2	6.05	5.21	78.7	52.65	31.22	17.59
1987	767	204	115	49	5	2	6.67	6.62	80.57	55.93	33.77	21.38
1988	936	209	122	41	6	4	7.67	6.4	77.56	54.06	29.17	17.09
1989	1338	222	116	72	8	7	11.53	11.79	77.88	56.35	35.28	23.17
1990	1350	209	106	124	8	7	12.74	16.63	80.22	60.44	40.74	27.11
1991	1600	238	127	124	9	6	12.6	15.97	79.56	57.81	35.88	24.56
1992	1922	276	132	150	9	8	14.56	18.71	80.91	60.04	38.03	27.16
1993	2341	326	159	124	8	7	14.72	16.71	81.72	62.41	37.89	23.62
1994	2855	394	176	101	10	9	16.22	18.3	82.31	61.79	39.68	24.45
1995	3393	479	216	178	10	7	15.71	19.25	80.78	59.45	37.46	25.52
1996	3786	517	244	169	10	9	15.52	16.84	79.56	58.37	34.31	22.24
1997	3656	514	271	83	9	9	13.49	12.64	77.71	56.51	33.62	20.43
1998	3011	432	257	73	9	9	11.72	10.27	75.82	53.94	31.25	18.93
1999	2676	380	241	96	9	9	11.1	10.04	75.75	53.14	30.98	19.06
2000	2520	352	223	77	9	8	11.3	9.49	74.96	52.38	29.56	17.82
2001	1987	291	194	50	8	8	10.24	7.49	73.02	49.62	27.18	16.66
2002	2089	317	207	47	8	7	10.09	8.05	76.02	51.94	29.2	17.33
2003	2294	327	206	54	9	7	11.14	8.94	76.07	52.4	29.25	16.91
2004	2193	315	186	76	9	6	11.79	10.91	78.52	56.32	32.83	19.15
2005	2007	282	180	54	9	9	11.15	8.96	75.73	51.07	28.5	18.09
2006	1998	294	172	63	8	8	11.62	10.99	78.63	56.71	32.93	21.22
2007	1578	228	140	58	9	6	11.27	8.64	74.08	50.13	27.88	17.11
2008	1485	211	134	73	8	1	11.08	11.14	79.06	56.97	33.74	22.42
2009	1342	193	129	51	8	6	10.4	8.93	78.32	54.32	30.77	17.21
2010	1551	221	145	40	8	9	10.7	8.5	77.89	53.32	29.46	15.93
2011	1559	210	127	100	9	1	12.28	12.14	79.03	55.23	32.07	19.5
2012	1361	195	120	51	9	7	11.34	9.67	78.91	54.81	30.2	17.78
2013	1132	156	103	57	9	9	10.99	8.96	73.41	50.09	28.09	18.37
2014	1034	132	80	76	9	7	12.93	13.33	77.76	57.25	34.72	23.21



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) = 4.14

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.







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 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 = 142.4

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 ofgenetic 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 comparedwith 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	584	931.8	2013.6	3304.4	2216.6	1682	1327.4
Total #sires	316	336	370	721	605	447	346
Max #progeny	100	111	450	401	153	203	227
Mean #progeny	9.2278	13.863	27.208	22.914	18.317	18.812	19.171
Median #progeny	5	8	11	11	10	10	10
Mode #progeny	1	2	7	9	8	1	1
SD #progeny	12.936	17.65	46.852	34.982	21.771	24.482	25.683
Skew #progeny	2.9193	2.8645	5.3885	4.3678	2.5983	3.2675	3.906
Total #dams	671	766	983	1652	1169	899	691
Max #progeny	29	39	57	55	42	45	44
Mean #progeny	4.3458	6.0809	10.241	10.001	9.4799	9.3537	9.5991
Median #progeny	3	5	8	8	8	8	8
Mode #progeny	1	4	7	9	8	7	7
SD #progeny	3.5534	4.5468	7.4	6.8743	6.413	6.5947	6.4072
Skew #progeny	1.9031	1.9274	1.6967	1.893	1.5787	1.6736	1.2461
Rate of inbreeding	0.029919	0.005052	0.002451	-0.00238	0.003676	-0.00321	-0.01193
Generation interval	4.3979	3.9731	4.0145	3.8244	4.2765	4.2336	4.3109
Effective pop size	16.712	98.975	203.97	n/a	136.01	n/a	n/a



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.





Comments

The rate of inbreeding was at its highest in this breed in the early 1980s. This represents a 'genetic bottleneck', with genetic variation lost from the population. From the mid-1980s the rate of inbreeding has slowed and even declined slightly since the mid-2000s, implying a slowdown in the rate of loss and even some replenishment of genetic diversity (possibly through the use of imported animals).

There appears to be extensive use of popular dogs as sires in this breed (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.