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September 2015

Population analysis of the *Bouvier Des Flandres* breed

Genetic analysis of the Kennel Club pedigree records of the UK *Bouvier Des Flandres* 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

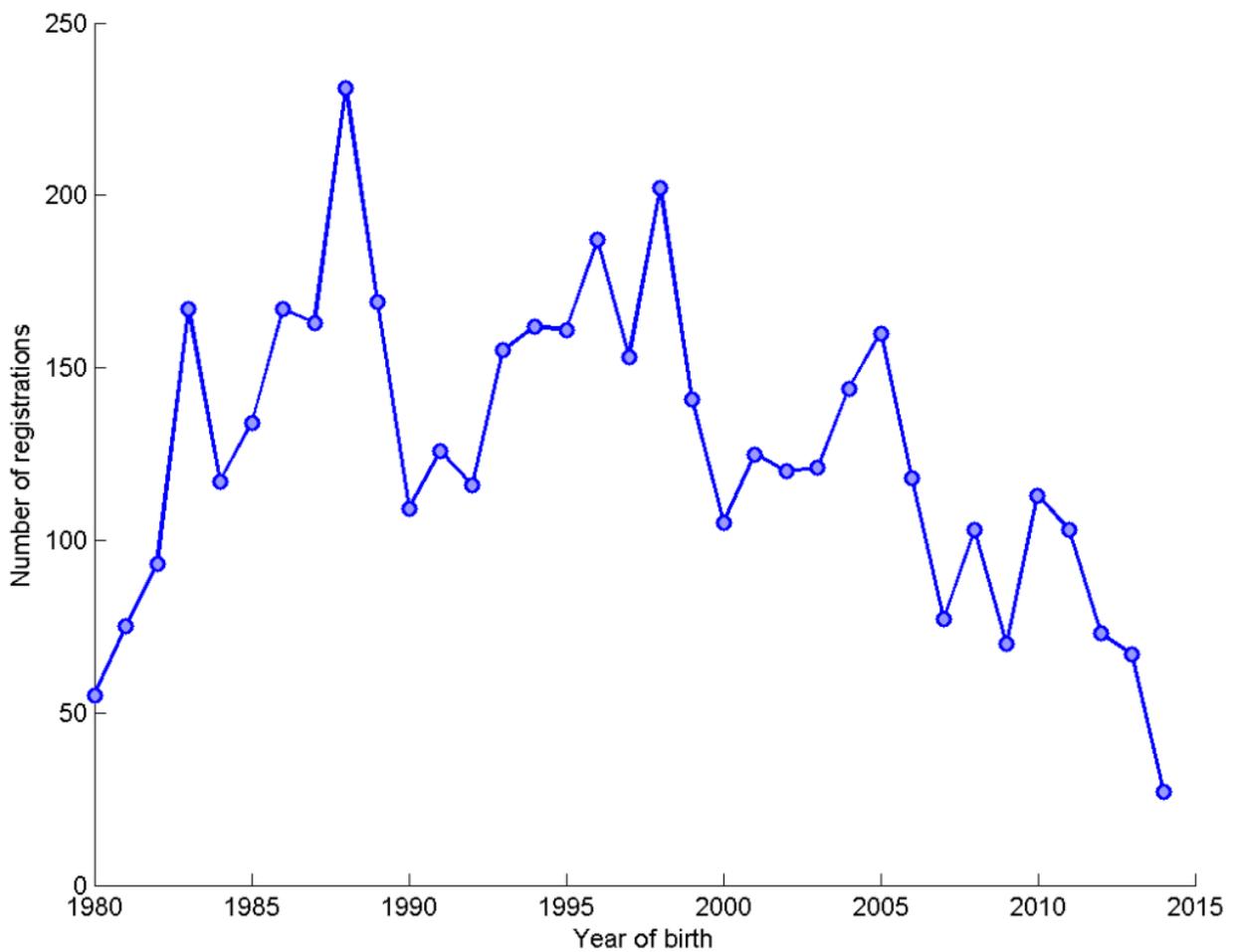
The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered *Bouvier Des Flandres* population, and statistics were calculated for the period 1980-2014.



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: *Bouvier Des Flandres*

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = -1.50 per year (with a 95% confidence interval of -2.92 to -0.08).



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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	55	16	17	11	1	1	3.24	3.49	85.45	65.45	38.18	20
1981	75	21	15	20	1	1	5	5.74	90.67	68	45.33	26.67
1982	93	16	13	22	6	1	7.15	6.08	83.87	50.54	23.66	23.66
1983	167	31	17	35	5	1	9.82	10.44	89.22	61.08	38.92	20.96
1984	117	23	17	27	6	1	6.88	6.15	80.34	49.57	34.19	23.08
1985	134	28	25	15	5	1	5.36	3.7	79.1	45.52	27.61	11.19
1986	167	33	19	30	7	3	8.79	7.81	83.23	58.68	31.74	17.96
1987	163	29	23	16	6	9	7.09	4.33	75.46	46.01	19.02	9.82
1988	231	42	30	20	7	7	7.7	4.9	73.59	50.65	23.38	16.02
1989	169	34	24	27	6	1	7.04	5.93	78.7	52.66	24.85	15.98
1990	109	23	19	12	6	6	5.74	3.46	76.15	46.79	21.1	11.01
1991	126	20	19	16	7	1	6.63	4.6	80.95	49.21	24.6	12.7
1992	116	21	18	17	6	1	6.44	4.48	77.59	50.86	25.86	14.66
1993	155	26	10	40	14	1	15.5	11.94	79.35	57.42	25.81	25.81
1994	162	33	22	40	5.5	1	7.36	8.64	83.95	62.35	36.42	24.69
1995	161	32	20	22	7	1	8.05	6.49	79.5	54.04	26.71	13.66
1996	187	35	22	31	6	6	8.5	8.1	80.21	58.29	32.62	16.58
1997	153	24	18	26	7	6	8.5	6.66	73.86	53.59	32.68	16.99
1998	202	35	24	40	6.5	1	8.42	8.87	81.68	60.4	30.69	19.8
1999	141	25	17	22	6	1	8.29	6.92	83.69	53.19	30.5	15.6
2000	105	22	16	22	5.5	1	6.56	5.56	80	52.38	34.29	20.95
2001	125	28	15	31	7	1	8.33	8.26	88.8	60	38.4	24.8
2002	120	22	19	11	6	6	6.32	3.43	75	44.17	18.33	9.17
2003	121	28	16	50	2	1	7.56	12.4	91.74	76.03	53.72	41.32
2004	144	28	20	31	4.5	1	7.2	8.24	89.58	64.58	36.11	21.53
2005	160	27	21	23	6	1	7.62	6.05	83.75	50.63	24.38	14.38
2006	118	27	17	24	5	1	6.94	7.15	89.83	59.32	38.14	20.34
2007	77	18	17	11	3	1	4.53	3.71	88.31	49.35	25.97	14.29
2008	103	23	18	16	5.5	1	5.72	4.2	77.67	53.4	27.18	15.53
2009	70	17	14	13	3.5	3	5	3.78	78.57	58.57	18.57	18.57
2010	113	19	16	18	7	1	7.06	6.01	84.96	53.98	31.86	15.93
2011	103	20	17	17	5	1	6.06	5.25	88.35	50.49	32.04	16.5
2012	73	16	14	13	5	1	5.21	3.89	82.19	53.42	17.81	17.81
2013	67	16	12	11	6	1	5.58	3.4	76.12	43.28	16.42	16.42
2014	27	8	7	8	5	1	3.86	2.85	n/a	n/a	n/a	n/a

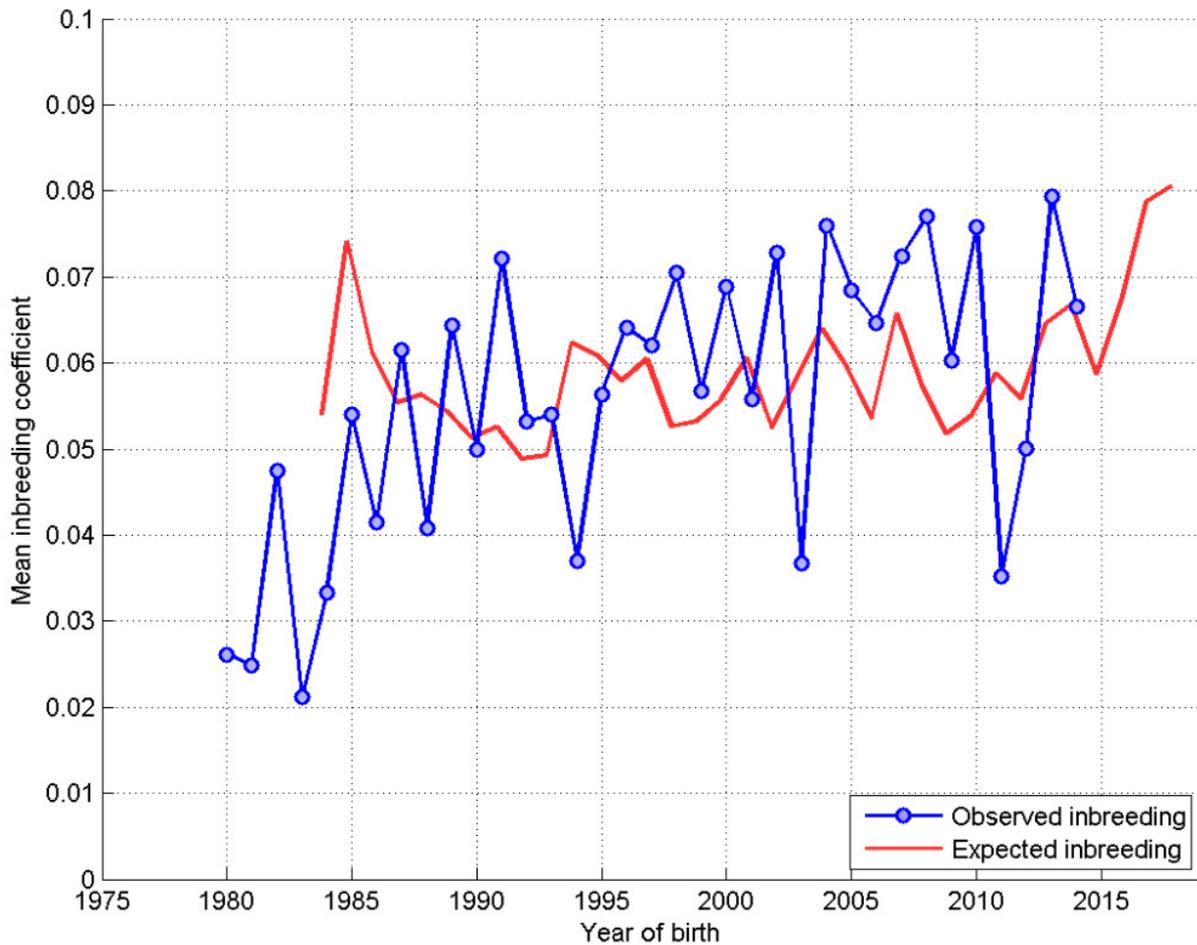


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 3.80

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 = 133.1

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	101.4	172.8	133.6	168.8	123	105.6	76.6
Total #sires	56	75	56	61	58	62	41
Max #progeny	66	47	62	71	76	74	57
Mean #progeny	9.0357	11.427	11.911	13.82	10.586	8.5	9.2927
Median #progeny	4	7	6	7	6	4	8
Mode #progeny	1	1	1	1	1	1	1
SD #progeny	12.977	11.546	15.983	17.74	13.737	12.005	10.036
Skew #progeny	2.5854	1.6089	2.0331	1.9733	2.579	3.2785	2.8187
Total #dams	78	127	93	111	101	85	64
Max #progeny	30	22	24	35	22	31	21
Mean #progeny	6.4872	6.7717	7.172	7.5946	6.0792	6.2	5.9531
Median #progeny	5	6	6	6	6	6	5
Mode #progeny	1	1	1	1	1	1	1
SD #progeny	6.3711	4.6088	5.6734	6.1841	4.3144	5.855	4.8776
Skew #progeny	1.5738	1.0075	0.93246	1.5519	0.83542	1.7587	1.0767
Rate of inbreeding	0.003422	0.00746	-0.01799	0.003322	-0.00195	-0.00169	0.011336
Generation interval	3.0754	3.5238	3.8603	4.2848	4.0251	3.8423	4.2291
Effective pop size	146.1	67.02	n/a	150.5	n/a	n/a	44.107



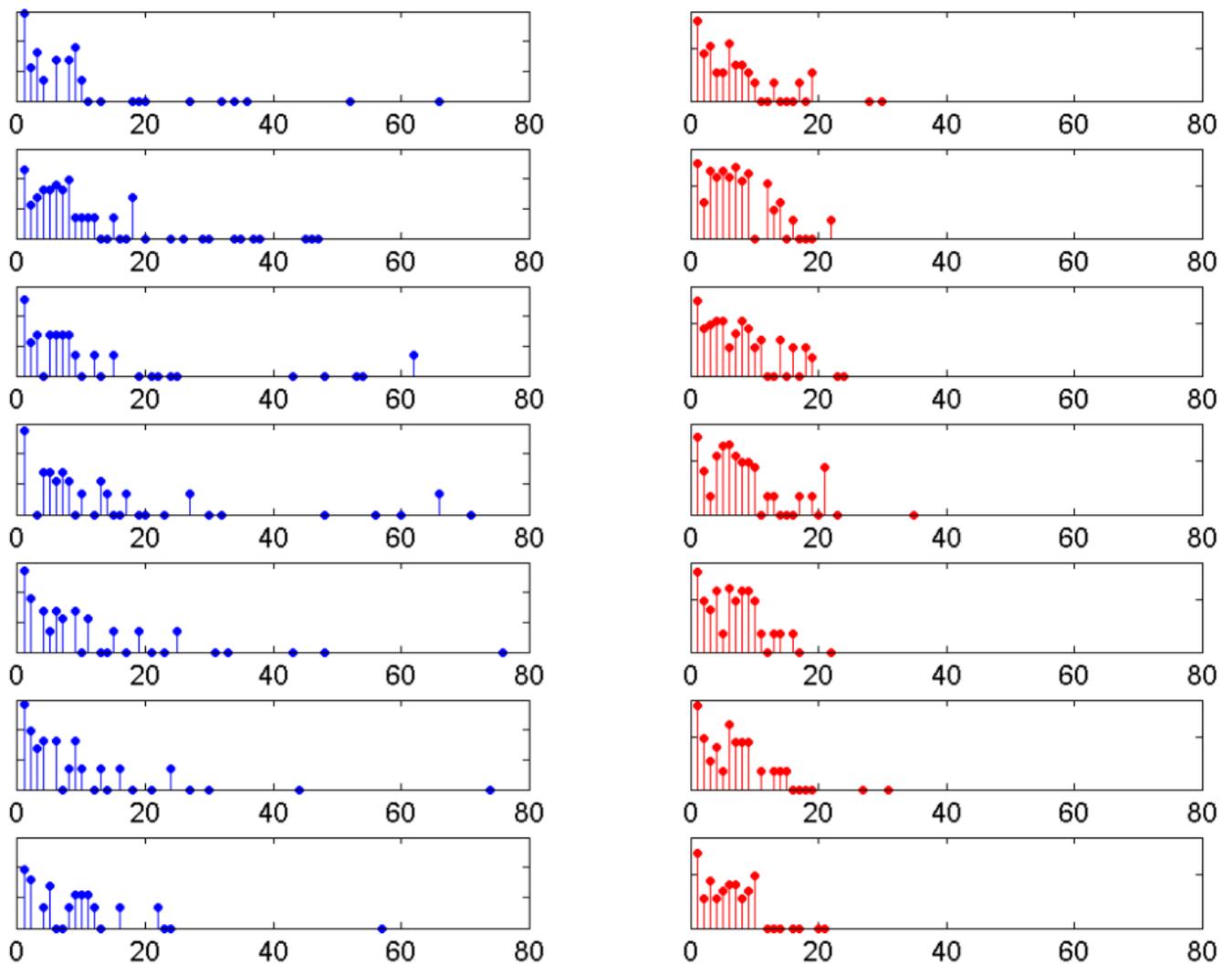
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number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

It appears that there has been moderate use of popular sires in this breed (the 'tail' of the blue distribution increasing 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.