



THE KENNEL CLUB

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September 2015

Population analysis of the *Hungarian Vizsla* breed

Genetic analysis of the Kennel Club pedigree records of the UK *Hungarian Vizsla* 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

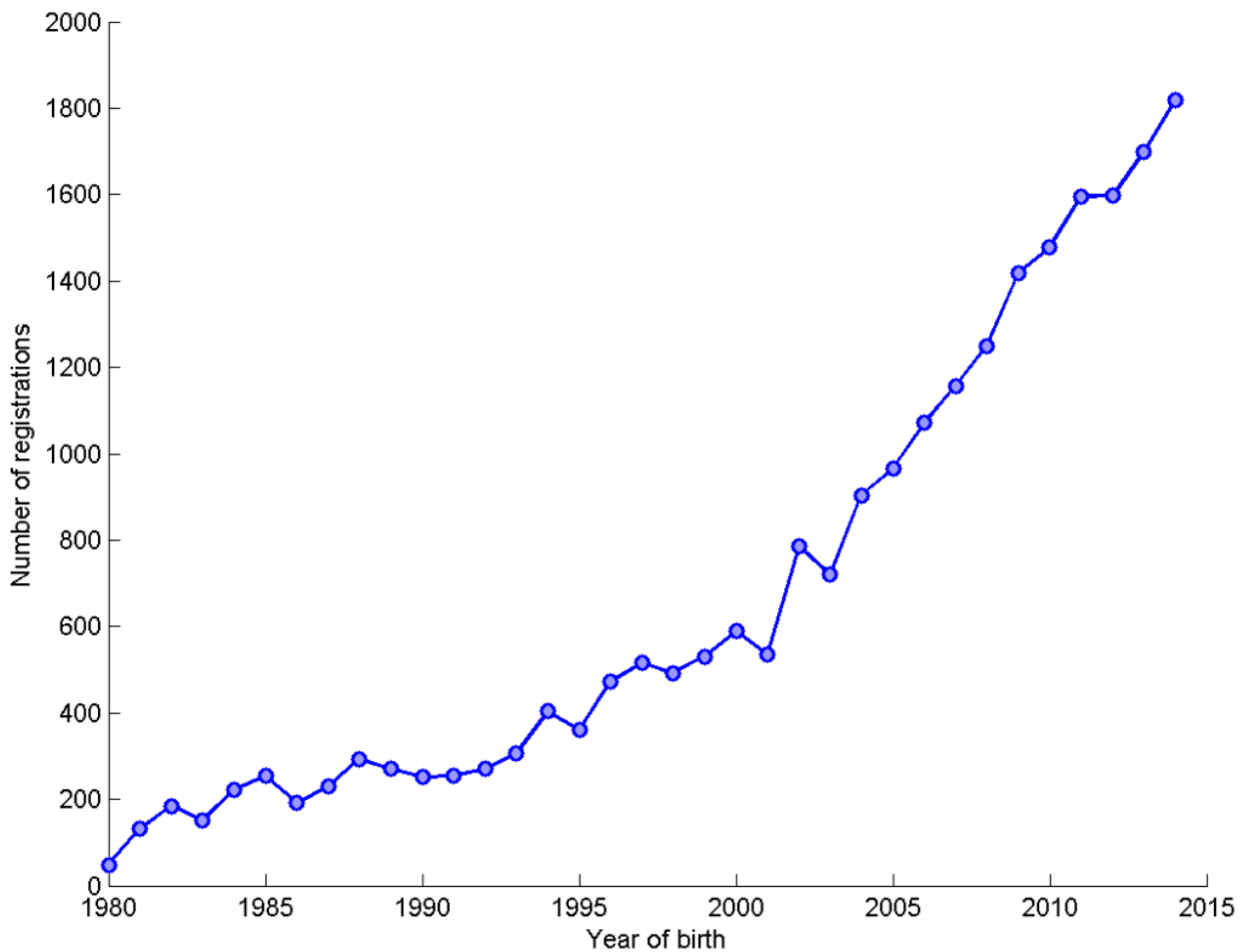
The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered *Hungarian Vizsla* population, and statistics were calculated for the period 1980-2014.



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: Hungarian Vizsla

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = 48.21 per year (with a 95% confidence interval of 41.92 to 54.49).



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	49	26	16	10	2	2	3.06	2.46	71.43	51.02	36.73	20.41
1981	133	22	13	21	10	4	10.23	5.97	75.94	42.86	15.79	15.79
1982	185	33	27	29	5	1	6.85	7.65	86.49	63.24	42.16	15.68
1983	150	32	23	22	5	5	6.52	5.36	78	53.33	28	14.67
1984	222	37	26	32	7	7	8.54	6.9	74.77	53.6	32.88	14.41
1985	254	50	29	49	7	2	8.76	9.16	79.92	53.54	34.65	19.29
1986	191	36	28	19	6	2	6.82	4.24	73.3	46.07	24.08	9.95
1987	230	37	27	33	7	6	8.52	6.38	73.91	50.43	28.26	14.35
1988	294	55	34	38	6	6	8.65	8.84	80.95	62.59	31.63	23.81
1989	272	45	29	34	7	7	9.38	7.63	76.1	51.84	30.88	12.5
1990	251	41	30	23	7	7	8.37	5.14	71.31	48.21	23.11	16.73
1991	254	44	24	53	6	6	10.58	11.54	81.89	62.2	30.71	20.87
1992	271	45	31	35	7	6	8.74	7.11	75.28	51.66	29.15	21.77
1993	306	51	28	29	8.5	1	10.93	8.17	80.72	50.65	26.14	9.48
1994	404	66	38	32	8	3	10.63	8.83	81.19	57.18	29.46	15.84
1995	361	72	41	33	6	1	8.8	8.57	83.38	58.17	33.8	17.73
1996	473	84	42	51	8	8	11.26	11.08	79.07	59.41	32.98	20.3
1997	517	77	47	47	8	8	11	10.14	79.69	59.19	32.88	17.02
1998	493	78	46	44	7	5	10.72	9.47	79.51	57.81	32.05	16.63
1999	530	82	50	36	8	5	10.6	8.5	77.36	56.04	28.49	19.06
2000	589	87	53	44	9	8	11.11	7.86	72.84	48.05	25.64	17.66
2001	535	84	56	39	7	6	9.55	7.63	77.38	54.77	28.04	16.07
2002	786	127	75	41	8	6	10.48	8.37	78.5	54.07	29.39	16.41
2003	720	115	72	42	8	7	10	8.29	77.92	54.44	28.47	18.61
2004	904	144	86	109	7	7	10.51	12.99	78.65	58.08	36.28	22.79
2005	966	158	97	49	7	6	9.96	9.51	79.71	57.45	35.2	20.08
2006	1071	168	82	194	7	1	13.06	22.67	85.34	65.27	41.74	30.53
2007	1158	179	108	104	7.5	1	10.72	13.04	81.09	59.07	37.39	24.35
2008	1250	187	96	99	8	6	13.02	15.61	82.64	63.04	40.4	26.32
2009	1417	214	112	99	8	8	12.65	14.45	81.79	61.04	35.99	25.12
2010	1478	218	119	82	8	5	12.42	13.18	79.84	58.86	36.2	23.21
2011	1596	230	124	69	8	8	12.87	13.73	80.83	61.72	35.71	22.62
2012	1598	247	131	68	8	1	12.2	12.48	82.67	59.01	34.23	23.59
2013	1698	238	124	73	9	6	13.69	13.55	80.04	58.36	33.98	20.79
2014	1819	257	129	135	9	8	14.1	17.47	81.75	59.98	38.32	24.74

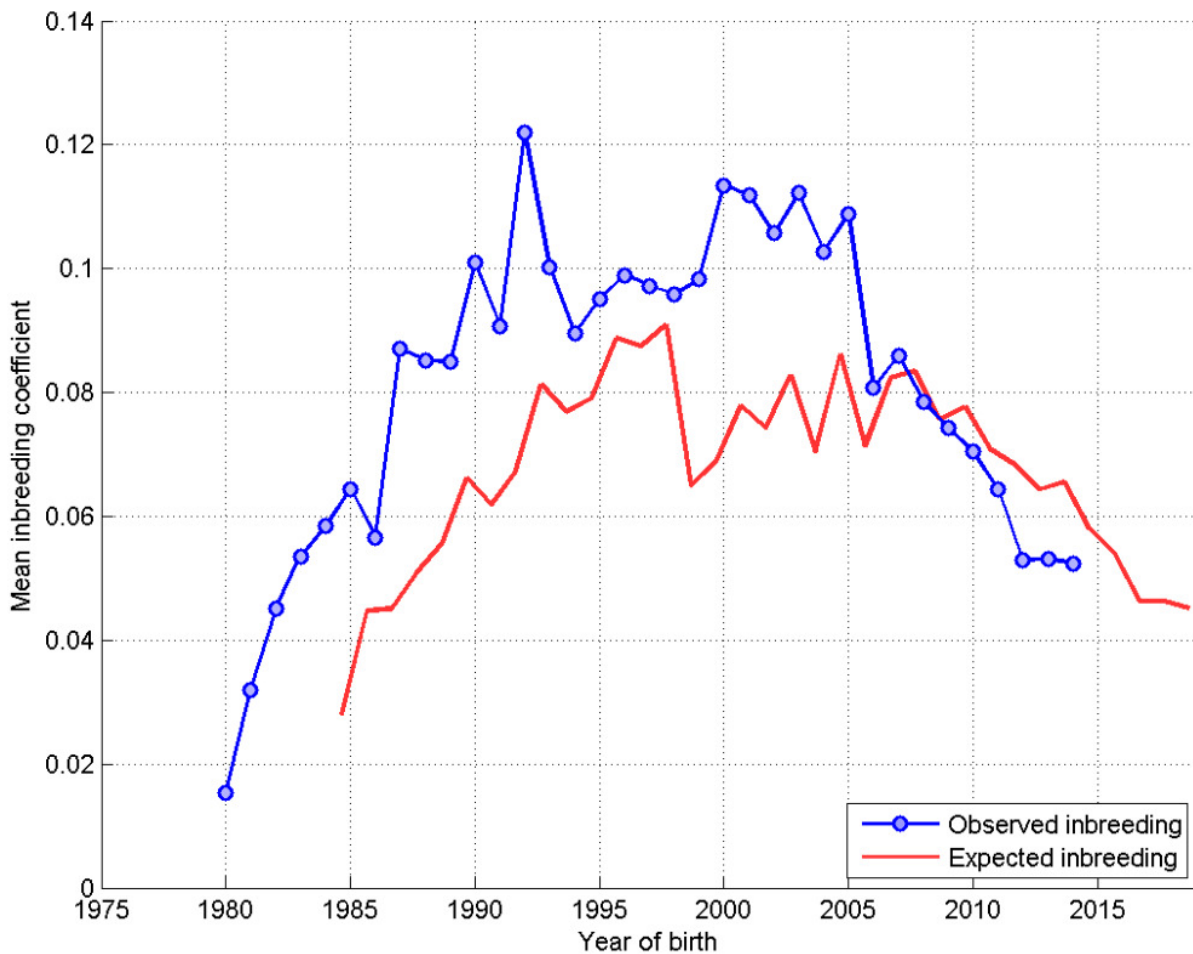


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 4.66

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 = 173.9

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	147.8	248.2	297.2	474.8	706.8	1172.4	1637.8
Total #sires	66	83	89	137	203	278	347
Max #progeny	103	94	96	148	164	533	282
Mean #progeny	11.167	14.94	16.685	17.321	17.404	21.083	23.597
Median #progeny	6.5	8	8	8	9	9	10
Mode #progeny	1	2	7	1	1	1	1
SD #progeny	15.264	20.059	20.016	26.44	22.528	41.757	37.033
Skew #progeny	3.7942	2.4229	2.0183	2.9911	3.0089	7.643	3.8768
Total #dams	121	177	186	302	413	637	856
Max #progeny	24	28	30	33	34	45	39
Mean #progeny	6.0909	7	7.9839	7.8576	8.5545	9.2009	9.5654
Median #progeny	5	6	7	7	8	8	8
Mode #progeny	1	6	7	8	8	8	8
SD #progeny	4.6476	4.9681	5.2643	5.4605	5.373	6.8715	6.3789
Skew #progeny	1.4179	1.7353	1.2106	1.3019	1.3055	1.705	1.2993
Rate of inbreeding	0.058764	0.032376	-0.00695	0.001814	-0.01087	-0.03375	-0.02279
Generation interval	5.2684	4.3159	4.647	4.9674	4.6246	4.2911	4.4967
Effective pop size	8.5085	15.444	n/a	275.7	n/a	n/a	n/a



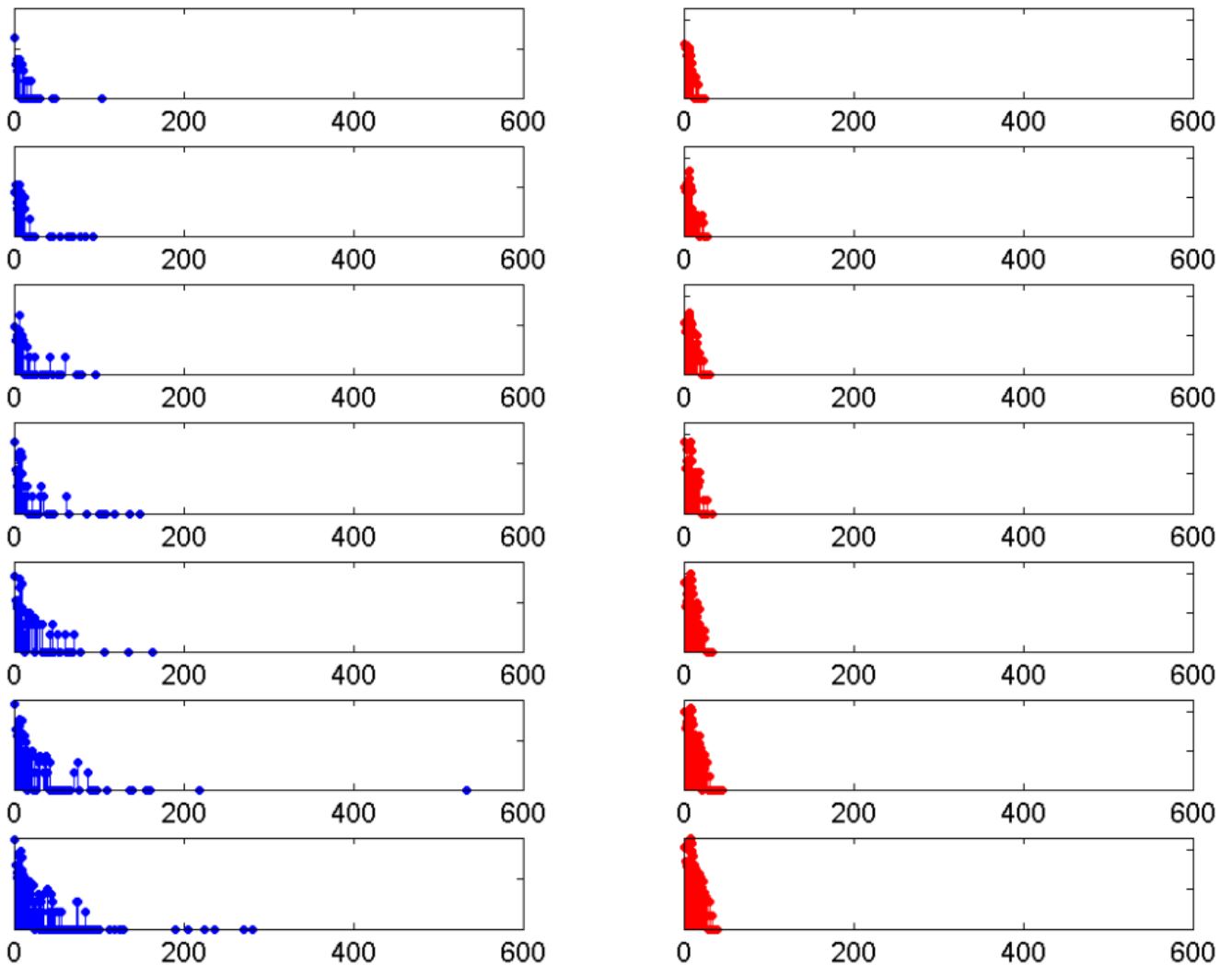
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number 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, during the 1990s the rate of inbreeding has slowed and since the mid-2000s even declined slightly, implying maintenance and even some replenishment of genetic diversity (possibly through the use of imported animals).

It appears that the extensive use of popular dogs as sires has increased (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.