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Heritability and epidemiology of canine hip-dysplasia score and its components in Labrador retrievers in the United Kingdom

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Abstract

Hip-dysplasia (malformation of the coxofemoral joint) in dogs is a major health problem. Under the British Veterinary Association/Kennel Club's voluntary hip-dysplasia scheme, dog-owners/breeders submit radiographs from animals >1-year-old, to ensure adequate skeletal maturity. An overall hip score quantifies the degree of malformation in the hip joints of these animals, by summing the scores for nine components of the radiographs of both the left and right joints. The hip score data for 29,610 Labrador retrievers (registered with The Kennel Club, UK) were merged with the Kennel Club pedigree database for 472,435 Labrador retrievers. The merged data included the animal's identity, date of birth, sex and hip score and similar records for the dog's relatives, including the hip score if the relative had been tested.

In recent years, breeding had been increasingly from tested parents. The mean hip score for male Labradors was significantly higher than that for females. Regression modelling showed a significant, positive dependence of the hip score of the offspring upon the hip scores of its sire, dam and grandparents. Genetic heritability (using data from 13,382 Labrador retrievers comprising 718 litters) was highly significant: 0.34 from the two parents, 0.41 from sire alone and 0.30 from dam alone. Using components data from 2038 offspring Labrador retrievers comprising 1248 litters, three similar estimates of heritability were significant for three major components (Norberg angle, cranial acetabular edge and subluxation); for other components, heritability was significant from the sire but not from the dam. Offspring hip score could be reduced substantially by using only parents with zero hip score.

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1. Introduction

1.1. Background

Recent similar studies on hip-dysplasia scores in Flat Coated retrievers, Newfoundlands and Gordon Setters (Wood et al., 2000a,b) contain detailed background on hip-dysplasia in canine pedigree breeds. For completeness, we include most of it here.

Malformation of the coxofemoral joint in dogs or canine hip-dysplasia (CHD) is a major canine health problem. The hip joint consists of a rounded femoral head lying in a cup-shaped socket, the acetabulum. Surrounding soft tissues holds the bones together, and the looseness of these tissues may result in the dislocation or partial dislocation (subluxation) of the joint. Schnelle (1937) described the condition in 1937—he found that several large breeds of dogs had defective hip joints. However, the high prevalence of this condition was recognised only after the Second World War (Schales, 1956; Henricson and Olsson, 1959) and control schemes were set up in Sweden, Great Britain, America and Germany to combat the problem. The British Veterinary Association (BVA) and the Kennel Club (KC) run the British scheme. It is based on the scoring of radiographs of both hip joints by a panel of scrutineers. Nine radiographic features of each hip joint are scored separately for each hip joint and the dog's hip score is obtained as the sum of the 18 scores (BVA/KC, 1991; Gibbs, 1997; Willis, 1997; Dennis, 1998, Wood et al., 2000a,b). The pathological changes in defective joints in young dogs, in which incompletely ossified bony structures might be subjected to undue stresses, often lead to osteoarthritis in later life (Dennis, 1998).

1.2. Clinical information on the breeds

The current BVA/KC scheme is voluntary and depends upon co-operation by dog-owners/breeders. The scheme relies on submission of radiographs from animals that are >1-year-old (to ensure adequate skeletal maturity). The control scheme and the scoring of radiographs are described fully by Gibbs (1997), Willis (1997) and Dennis (1998). Briefly, under this scheme, nine specific radiographic features (components of the radiograph)—which are considered collectively to define the condition of the coxofemoral joint—are examined by a panel of veterinarians for each joint and awarded a numerical score. These components are acetabular fossa (AF), cranial acetabular edge (CAE), caudal acetabular edge (CDAE), cranial effective acetabular rim (CEAR), dorsal acetabular edge (DAE), femoral head and neck exostosis (FHNE), femoral head recontouring (FHR), Norberg angle (NA) and subluxation (SUBL). All components are scored on a scale from 0 (ideal) to 6 (worst) except for CDAE, which is scored on a scale from 0 to 5. Hence, the score for each hip ranges from 0 to 53, and the total score over both hips (hip score) ranges from 0 to 106. By early 1998, over 108,000 dogs (representing 97 breeds) had been examined and scored (Dennis, 1998).

The clinical condition of hip-dysplasia is likely to be caused by a combination of genetic and environmental factors—but for selective breeding, the interest is in the genetic factor. The severity of hip-dysplasia is a continuous variable which is difficult to measure—our measure, hip score, is ordinal. Hip-dysplasia can manifest later in life if the hip joint had

failed to be satisfactory at birth (early in life). In contrast, the hip score is obtained at an early age (but ≥ 1 year) and is designed to provide a quantitative assessment of the radiographic condition of the joint. Hence, it is likely to be correlated positively with the probability of occurrence and the severity of hip-dysplasia. This is supported by various studies (Smith et al., 1995; Swenson et al., 1997; Cardinet and Lust, 1997; Lust, 1997; Fluckiger et al., 1998).

This paper is based on detailed statistical analyses of hip scores from 29,610 Labrador retrievers (registered with The Kennel Club in the United Kingdom) and of all nine components that were recorded for 8628 Labradors retrievers.

1.3. Objectives

One objective of the study was to assess how the BVA/KC control scheme was performing—but the main objective of this research was to study the effects of the individual's different attributes (including the hip scores of its relatives) on the individual's hip score. An understanding of such relationships was clearly necessary to provide scientific evidence-based selective-breeding policies intended to prevent or reduce hip-dysplasia in the breed.

These goals identified the following specific needs:

- (a) to estimate summary statistics for hip scores in LRs;
- (b) to examine whether the observed values of hip scores have declined over the years since the BVA/KC scheme started;
- (c) to examine whether (since the BVA/KC scheme started) puppies have been increasingly from sires and dams which had been tested under the scheme;
- (d) to assess the effects of the animal's gender on its hip score;
- (e) to develop mathematical models that predict offspring hip scores given the parental hip scores, and—a key need—to estimate the heritability of hip score.

2. Materials and methods

2.1. Data

The hip score data for this study were from 29,610 registered Labrador retrievers (21,854 females and 7754 males; gender not recorded for two animals) born during 1965–1999 of which 29,312 (99%) were born from 1980 onwards. The data for the nine components were from 8628 Labradors (6255 females and 2373 males) born during 1973–1996 (98.5% of these were born during 1980–1990). All dogs were registered with the Kennel Club in the UK. The Kennel Club registration number was recorded for every tested dog and so the clinical data could be collated with the breed-pedigree database. The resulting database consisted of 472,435 registered Labrador retrievers by 1999. These data included the dog's identity, date of birth, sex and (for tested animals) hip-dysplasia scores, and similar records for the animal's sire, dam and grandparents. The pedigree information made it possible to take into account the likely positive correlation in the hip score data from dogs from

the same litter and to assess the heritability of hip-dysplasia. There were 13,382 tested Labrador retrievers from 7185 litters (incomplete litters) for which the hip scores were recorded for the offspring as well as both parents.

2.2. Statistical checks and methods

The hip score for each dog was defined as the sum of its left- and right-hip scores. Checks were made to ensure that these pairs of scores were similar by comparing percentiles, checking that the correlation between left- and right-hip scores was high and checking that the slope of the regression of left-hip score on right-hip score was ≈ 1.0 .

As argued by Wood et al. (2000a), although the hip score and component scores take only integral values, these scores measure a condition (quality of the joint) which—if it were measurable—would be on a continuous scale. The situation is to some extent similar to measuring temperature using an inexact thermometer that records temperature at best to the nearest degree (or 2).

The variation in hip scores between genders was examined by comparing percentiles and testing the null hypothesis of equal median hip scores using Mann–Whitney *U*-test. The dependence of the offspring hip score on parental scores was studied by computing the mean, median and other percentiles of the hip score of offspring from sires and dams with known hip scores. Multiple regression models relating offspring score (three models: one each for all offspring, for male offspring and for female offspring) to the score for parents and grandparents were developed. Enlarged regression models that included the interactions between the sire's hip score and dam's hip score also were examined.

Heritability of hip score was estimated using the slope in the regression of mean hip score values of offspring in a litter on parental scores (Falconer, 1989). Thus, the estimate of the slope in the linear regression of the mean of the offspring hip scores for each litter on the mid-parent score (i.e. the mean of the two parental hip scores) provided a direct estimate of heritability. Heritability from sires and dams separately was estimated by regressing the offspring mean score on the hip score of each parent separately. (In this case, twice the regression slope estimated the heritability.) The standard errors of the estimated regression slopes were used to obtain the standard errors for the estimates of heritability. All calculations were done using SAS/STAT (1989).

3. Results

3.1. Statistical checks: left- and right-hip scores

Out of 29,610 dogs, many (7849 = 27%) had identical left and right scores. The five percentiles (5, 25, 50, 75, 95) for the left- and right-hip scores were (2, 4, 6, 8 and 27) and (2, 4, 5, 8 and 26), respectively. The correlation between the left- and right-hip score was 0.81 ($P < 0.0001$) and the regression slope of left-hip score on right-hip score was 0.94 ± 0.03 (S.E.).

Table 1

Number of male and female Labrador retrievers born (and registered in the UK) each year and the percentage tested, i.e. hip score obtained from radiographs

Year of birth	Male offspring		Female offspring	
	Number born	Percent tested	Number born	Percent tested
<1980	2,959	0.95	4,256	1.08
1980	1,417	1.62	2,348	2.56
1981	4,330	1.32	5,596	2.23
1982	5,756	2.15	7,406	4.94
1983	6,446	3.10	8,009	7.75
1984	6,500	3.83	8,004	9.85
1985	6,713	4.68	8,021	10.57
1986	6,616	5.20	7,736	12.42
1987	6,537	5.77	7,470	12.64
1988	7,042	4.93	7,973	11.80
1989	12,065	3.69	12,062	9.99
1990	12,242	4.06	11,991	11.51
1991	11,844	4.75	11,769	13.53
1992	11,578	5.08	11,548	14.17
1993	12,583	4.78	12,586	15.59
1994	15,145	4.55	15,049	15.07
1995	16,427	4.59	16,238	13.27
1996	17,439	3.89	17,331	11.41
1997	17,875	3.23	17,561	7.81
1998	17,561	1.33	17,113	2.62

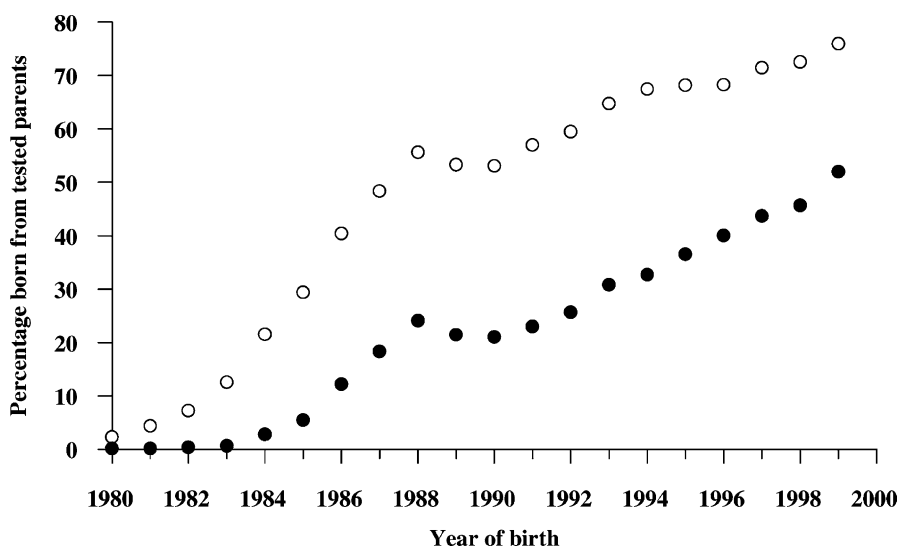


Fig. 1. Percentage of Labrador retrievers born in different years from parents where at least one parent was tested (○) and from parents who were both tested (●) (UK).

Table 2

Number of Labrador retrievers born and registered each year, with number born from four categories of parents: sire and dam both untested (UU), sire untested and dam tested (UT), sire tested and dam untested (TU) and both parents tested (TT)^a

Year	Number born	Number from parental category				P1	P2
		UU	UT	TU	TT		
<1980	7,215	7,130	9	75	1	1.2	0.0
1980	3,765	3,679	13	66	7	2.3	0.2
1981	9,926	9,489	91	329	17	4.4	0.2
1982	13,162	12,206	193	711	52	7.3	0.4
1983	14,455	12,637	424	1,301	93	12.6	0.6
1984	14,504	11,377	729	1,994	404	21.6	2.8
1985	14,734	10,401	1,142	2,383	808	29.4	5.5
1986	14,352	8,554	1,231	2,815	1,752	40.4	12.2
1987	14,007	7,234	1,212	2,995	2,566	48.4	18.3
1988	15,015	6,666	1,201	3,528	3,620	55.6	24.1
1989	24,127	11,270	1,657	6,023	5,177	53.3	21.5
1990	24,233	11,373	1,896	5,864	5,100	53.1	21.0
1991	23,613	10,159	1,942	6,083	5,429	57.0	23.0
1992	23,126	9,377	2,083	5,733	5,933	59.5	25.7
1993	25,169	8,875	2,252	6,284	7,758	64.7	30.8
1994	30,194	9,821	2,532	7,967	9,874	67.5	32.7
1995	32,665	10,395	2,773	7,565	11,932	68.2	36.5
1996	34,770	11,027	2,621	7,204	13,918	68.3	40.0
1997	35,436	10,118	2,465	7,367	15,486	71.4	43.7
1998	36,474	9,527	2,136	7,174	15,837	72.524	54.674
1999	16,668	4,013	905	3,089	8,661	75.9	52.0
Total	425,810	195,328	29,507	86,550	114,425		

^a The table also shows the percent of offspring with at least one parent tested (P1) and with both parents tested (P2) (UK).

3.2. Recent trends

In the early years of the control scheme, only a small percent of the dogs born each year were tested (i.e. radiographed) for hip score (Table 1). The percentage of Labrador retrievers tested shows an increasing trend. The declining trend in these figures since 1993 is probably because the radiograph results for recently born animals had not been completed.

Most offspring could result from tested parents if animals selected for breeding were more often those that had been tested. Recently, there has been a steady increase in the percentage of offspring born from such parents (Table 2; Fig. 1). The initial change after the control scheme began was an increased use of one tested parent. Thus, the percentage of Labrador retrievers born from a mating in which at least one parent was tested was 12.5% in 1983; in that year <1% were from matings in which both parents were tested. These figures were 75.9 and 51.9%, respectively, in 1999. It is important to note that these figures are based upon the entire population of Kennel Club registered Labrador retrievers, and so, are free from sampling errors.

3.3. Variation in hip scores between genders

The 5th, 25th, 50th, 75th and 95th percentiles for hip scores of 7754 male Labrador retrievers were 3, 8, 11, 16 and 45, respectively; for 21,854 females, these percentiles were 4, 8, 11, 17 and 51, respectively. Although these percentiles appear similar for the two genders, the null hypothesis of equal median hip scores for the two genders was rejected using the non-parametric Mann–Whitney U -test (χ^2 with 1 d.f. = 72.9, $P < 0.0001$).

3.4. Dependence of offspring hip score on parental hip scores

As we expected, the offspring hip score increased with the parental hip scores (Table 3) and the offspring hip score was lowest when *both parents* had very-low hip scores. Although there were 5028 offspring from sires with very-low hip scores (0–5), there were only 2290 offspring from dams with very-low hip scores. At the upper end of the range,

Table 3
Dependence of hip score in Labrador retriever offspring upon the hip score of sires, dams and both parents^a

Hip score of sire or dam or both parents	Number of offspring	Offspring hip score (percentile)		
		25 th	50 th	75 th
<i>Sire</i>				
0–2	2060	7	10	14
3–5	2968	7	10	14
6–10	7455	8	11	16
11–20	5587	8	11	17
21–30	633	9	12	22
31–40	194	10	13	26
>40	191	10	15	32
<i>Dam</i>				
0–2	863	6	9	13
3–5	1427	7	10	13
6–10	6583	8	10	15
11–20	5842	8	12	17
21–30	1000	9	12	18
31–40	405	9	12	21
>40	323	10	16	29
<i>Sire and dam</i>				
0–2	121	5	8	12
3–5	191	6	8	12
6–10	2147	8	11	15
11–20	1451	9	12	17
21–30	31	9	13	29
>30	195	10	15	32
31–40 ^b	4	9	17	28
>40 ^b	191	10	15	32

^a Parental scores are grouped into convenient ranges (1980–1998, UK).

^b For the range 31–40 the sample size of 4 is too small: the ranges 31–40 and >40 were pooled.

Table 4
Male and female UK Labrador retrievers (both genders; 1980–1998)^a

Model number	Model terms	Sample size	b_i	S.E.	t	P
1	Intercept	19,088	13.42	0.158	84.9	<0.0001
	Sirehip		0.20	0.013	15.7	<0.0001
2	Intercept	16,443	12.84	0.170	75.6	<0.0001
	Damhip		0.18	0.011	16.24	<0.0001
3	Intercept	13,382	13.21	0.144	91.6	<0.0001
	S&Dhip		0.014	0.001	16.8	<0.0001
4	Intercept	13,382	10.90	0.238	45.8	<0.0001
	Sirehip		0.21	0.016	13.2	<0.0001
	Damhip		0.16	0.013	12.3	<0.0001
5	Intercept	13,382	11.19	0.311	35.9	<0.0001
	Sirehip		0.18	0.027	6.8	<0.0001
	Damhip		0.13	0.021	6.3	<0.0001
	S&Dhip		0.003	0.002	1.4	0.15
6 (stepwise)	Intercept	4,054	7.89	0.549	14.4	<0.0001
	Sirehip		0.21	0.031	6.8	<0.0001
	Damhip		0.16	0.022	7.3	<0.0001
	SShip		0.08	0.029	2.7	0.0068
	DShip		0.07	0.020	3.2	0.0013
	SDhip		0.08	0.023	3.4	0.0007

^a Linear regressions of hip scores on the hip scores of the animal's Sire (Sirehip), Dam (Damhip), derived product variable Sirehip \times Damhip (S&Dhip: interaction) and hip scores of grandparents: Sire of Sire (SShip), Sire of Dam (SDhip), Dam of Sire (DShip) and Dam of Dam (DDhip).

there were 385 offspring from sires with hip score >30—but 728 offspring from dams with hip score >30.

3.5. Relationship between offspring and parental and grandparental hip scores

Linear regression models (Tables 4–6) related the hip score of the animal to the hip scores of its Sire (Sirehip), Dam (Damhip), derived product variable Sirehip \times Damhip (S&Dhip = interaction) and hip scores of grandparents: Sire of Sire (SShip), Sire of Dam (SDhip), Dam of Sire (DShip) and Dam of Dam (DDhip). The univariable Models 1–3 (intercept \approx 13) and the bivariable Model 4 (intercept \approx 11) were significant, but in Model 5 the extra interaction term (compared with Model 4) was not significant. Model 6 (intercept \approx 8) used the parental scores as well as grand-parental scores; stepwise Model 7 (intercept \approx 8), which allowed all variables to enter the model, agreed with the findings of Model 6. As expected, the intercepts in the models (the intercept estimates the hip score of the offspring if the hip scores of its relatives were 0) declined as the number of terms in the models increased.

Tables 5 and 6 (results for male and female offspring separately) indicated that the hip score of male offspring depended more upon the hip score of the sire's parents (not the dam's parents); for female offspring, the dam's parents had a greater effect.

Table 5

Male Labrador retrievers (UK; 1980–1999): regressions of hip scores on the hip scores of animal's parents and grandparents as in Table 4

Model number	Model terms	Sample size	b_i	S.E.	t	P
1	Intercept	5146	12.21	0.280	43.5	<0.0001
	Sirehip		0.23	0.023	10.1	<0.0001
2	Intercept	4527	12.08	0.307	39.4	<0.0001
	Damhip		0.17	0.021	8.4	<0.0001
3	Intercept	3696	12.49	0.251	49.8	<0.0001
	S&Dhip		0.013	0.001	9.4	<0.0001
4	Intercept	3696	10.22	0.426	24.0	<0.0001
	Sirehip		0.19	0.030	6.2	<0.0001
	Damhip		0.17	0.024	7.3	<0.0001
5	Intercept	3696	10.92	0.546	20.0	<0.0001
	Sirehip		0.11	0.047	2.3	0.019
	Damhip		0.12	0.035	3.4	0.0008
	S&Dhip		0.006	0.003	2.0	0.041
6	Intercept	1424	7.27	0.878	8.29	<0.0001
	Sirehip		0.18	0.055	3.3	<0.0001
	Damhip		0.24	0.042	5.8	<0.0001
	SShip		0.12	0.049	2.4	0.016
	DShip		0.08	0.033	2.5	0.012
7	Intercept	1395	6.89	0.837	8.23	<0.0001
	Sirehip		0.24	0.057	4.3	<0.0001
	Damhip		0.20	0.041	4.8	<0.0001
	SShip		0.11	0.033	3.2	0.0012
	DShip		0.07	0.038	1.8	0.073

3.6. Heritability of hip-dysplasia

For Labrador retrievers, the estimate of heritability by regressing the litter mean score for offspring upon the mean score of the two parents was 0.34 ± 0.02 (S.E.) (Table 7) and highly significant ($P < 0.0001$). There was significant heritability from sire alone (heritability = 0.41 ± 0.04 , $P < 0.0001$) and also from dam alone (heritability = 0.30 ± 0.03 , $P < 0.0001$). Table 8 shows the estimates of heritability of the nine component variables; again, heritability was estimated from regression of offspring litter mean hip score on indicated parental score and its significance using the t -test. All three estimates of heritability were clearly significant for NA, CAE and SUBL. For the other six components, heritability was significant from sire but not from dam.

4. Discussion

Our results show the extent to which the hip-dysplasia scheme in the UK is being followed for Labrador retrievers. Because hip score is likely to be correlated positively with

Table 6

Female UK Labrador retrievers (1980–1999): regressions of hip scores on the hip scores of animal's parents and grandparents as in Table 4

Model number	Model terms	Sample size	b_i	S.E.	t	P
1	Intercept	13,942	13.88	0.190	73.1	<0.0001
	Sirehip		0.19	0.015	12.3	<0.0001
2	Intercept	11,916	13.15	0.203	64.7	<0.0001
	Damhip		0.18	0.013	13.8	<0.0001
3	Intercept	9,686	13.48	0.175	76.9	<0.0001
	S&Dhip		0.014	0.001	13.9	<0.0001
4	Intercept	9,686	11.20	0.286	39.2	<0.0001
	Sirehip		0.22	0.019	11.6	<0.0001
	Damhip		0.15	0.015	9.9	<0.0001
5	Intercept	9,686	11.33	0.380	29.8	<0.0001
	Sirehip		0.21	0.032	6.3	<0.0001
	Damhip		0.14	0.026	5.3	<0.0001
	S&Dhip		0.001	0.002	0.5	0.61
6	Intercept	4,163	9.41	0.526	17.9	<0.0001
	Sirehip		0.20	0.031	6.4	<0.0001
	Damhip		0.17	0.021	8.0	<0.0001
	SShip		0.08	0.030	2.6	0.010
	DShip		0.04	0.021	2.0	0.051
7	Intercept	4,086	10.06	0.540	18.6	<0.0001
	Sirehip		0.20	0.030	6.9	<0.0001
	Damhip		0.12	0.022	5.2	<0.0001
	SShip		0.06	0.031	2.0	0.044
	DDhip		0.06	0.025	2.2	0.025
8	Intercept	3,826	9.61	0.516	18.6	<0.0001
	Sirehip		0.17	0.030	5.6	<0.0001
	Damhip		0.14	0.023	6.1	<0.0001
	DShip		0.05	0.020	2.5	0.012
	SDhip		0.10	0.025	3.8	0.0001
9	Intercept	4,057	8.93	0.525	17.0	<0.0001
	Sirehip		0.25	0.029	8.5	<0.0001
	Damhip		0.16	0.026	6.2	<0.0001
	SDhip		0.07	0.027	2.7	0.0073
	DDhip		0.05	0.020	2.6	0.011

Table 7

Heritability (h^2) of hip score in Labrador retriever estimated from regression of offspring litter mean hip score on indicated parental score and its significance using t -test^a

Parental score	Intercept	S.E.	b	S.E.	h^2	S.E.	t	P
Mid-parental scores	11.46	0.29	0.34	0.02	0.34	0.02	14.4	<0.0001
Sire's score	13.18	0.23	0.21	0.02	0.41	0.04	10.8	<0.0001
Dam's score	13.31	0.23	0.15	0.02	0.30	0.03	9.9	<0.0001

^a The data consisted of 7185 litters which comprised of 13,382 offspring Labrador retrievers in the UK. Heritability, $h^2 = b$ or $2b$ depending upon whether b is the regression slope of offspring score on mid-parental score or the score of one parent.

Table 8
Heritability (h^2) of the component variables^a

Parental score	Intercept	S.E.	Slope		Heritability			
			<i>b</i>	S.E.	h^2	S.E.	<i>t</i>	<i>P</i>
<i>Norberg angle</i>								
Mid-parental scores	2.55	0.13	0.29	0.05	0.29	0.05	5.6	<0.0001
Sire's score	2.78	0.10	0.21	0.04	0.42	0.08	5.2	<0.0001
Dam's score	2.91	0.11	0.10	0.03	0.20	0.07	3.0	<0.0030
<i>Cranial acetabular edge</i>								
Mid-parental scores	3.45	0.12	0.17	0.04	0.17	0.04	4.5	<0.0001
Sire's score	3.72	0.09	0.09	0.03	0.17	0.05	3.4	0.0008
Dam's score	3.66	0.11	0.09	0.03	0.18	0.06	3.2	0.0015
<i>Dorsal acetabular edge</i>								
Mid-parental scores	1.00	0.06	0.16	0.06	0.16	0.06	2.7	0.0081
Sire's score	1.02	0.05	0.16	0.05	0.33	0.10	3.2	0.0014
Dam's score	1.05	0.05	0.04	0.04	0.07	0.08	1.0	0.33
<i>Cranial effective acetabular rim</i>								
Mid-parental scores	1.08	0.06	0.07	0.05	0.07	0.05	1.4	0.17
Sire's score	1.08	0.05	0.10	0.04	0.19	0.09	2.2	0.027
Dam's score	1.12	0.06	0.001	0.03	0.002	0.07	0.02	0.98
<i>Acetabular fossa</i>								
Mid-parental scores	0.72	0.05	0.17	0.06	0.17	0.06	3.0	0.0030
Sire's score	0.74	0.05	0.17	0.05	0.33	0.09	3.6	0.0004
Dam's score	0.76	0.05	0.04	0.04	0.07	0.07	1.0	0.31
<i>Caudal acetabular edge</i>								
Mid-parental scores	0.54	0.04	0.08	0.06	0.08	0.06	1.4	0.16
Sire's score	0.54	0.04	0.08	0.04	0.17	0.09	1.9	0.058
Dam's score	0.55	0.04	0.01	0.04	0.02	0.08	0.2	0.85
<i>Femoral head and neck exostosis</i>								
Mid-parental scores	0.99	0.06	0.14	0.05	0.14	0.05	2.9	0.0042
Sire's score	1.01	0.05	0.13	0.04	0.25	0.08	3.3	0.0010
Dam's score	1.06	0.06	0.03	0.03	0.06	0.06	1.0	0.30
<i>Femoral-head recontouring</i>								
Mid-parental scores	0.45	0.04	0.15	0.05	0.15	0.05	2.8	0.0047
Sire's score	0.45	0.04	0.19	0.04	0.38	0.09	4.5	<0.0001
Dam's score	0.48	0.04	0.001	0.04	0.002	0.07	0.04	0.97
<i>Subluxation</i>								
Mid-parental scores	3.54	0.14	0.26	0.04	0.26	0.04	6.8	<0.0001
Sire's score	3.99	0.10	0.14	0.03	0.29	0.06	5.3	<0.0001
Dam's score	3.98	0.11	0.12	0.03	0.24	0.05	4.3	<0.0001
<i>Hip score = HIPSC2 using 1248 litters</i>								
Mid-parental scores	11.81	0.70	0.26	0.05	0.26	0.05	4.8	<0.0001
Sire's score	14.62	0.55	0.21	0.04	0.43	0.09	5.0	<0.0001
Dam's score	15.71	0.59	0.07	0.04	0.14	0.07	2.0	0.047

^a Heritability was estimated from regression of offspring litter mean hip score on indicated parental score and its significance using *t*-test. The data consisted of 1248 litters which comprised of 2038 offspring Labrador retrievers from the UK. Heritability, $h^2 = b$ or $2b$ depending upon whether *b* is the regression slope of offspring score on mid-parental score or the score of one parent.

the probability of occurrence and the severity of hip-dysplasia (see Section 1.2 and Smith et al., 1995; Swenson et al., 1997; Cardinet and Lust, 1997; Lust, 1997; Fluckiger et al., 1998), our results also confirm the benefits of breeding from tested animals with low scores for the reduction of hip score and hence the extent of hip-dysplasia in the Labrador retriever breed.

Our regression models (Tables 4–6) are from analysing observations on dogs whose hip scores depended upon the hip scores of relatives (Table 4). Clearly, observations within litters might be correlated. In contrast, the estimation of the heritability (Tables 7 and 8) used litters (and not dogs) as sampling units, and in these analyses the problem of correlated scores does not arise. Most canine research workers have ignored this statistical complication of possibly correlated data in simple regressions—it is generally accepted that the failure of the implied assumption of statistical independence is unlikely to greatly affect the magnitude of various parameter estimates, but the standard errors of the estimates could be underestimated. Our results support this. Thus, for example, the intercept estimate in Model 1 in Table 4, based upon sire score, is 13.42, which is comparable to the intercept 13.18 in the heritability results based upon sire's score in Table 7. Tables 4 and 7 show similar comparable intercept estimates in models based upon dam's score or upon scores of both parents.

Section 3.4 pointed out that the intercepts in Tables 4–6 provide predictions. For example, the intercept 13.42 in Model 1 (Table 4) shows that if a sire with no hip-dysplasia ($Sire_{hip} = 0$) were to mate with a random dam, then the ensuing Labrador offspring will be expected to have a hip score of about 14. Similarly, if both parents had no hip-dysplasia ($Sire_{hip} = 0$ and $Dam_{hip} = 0$), then Model 4 (intercept = 10.9) shows that the expected value of the offspring hip score will be about 11. The intercept 7.6 in Model 6 indicates that the expected hip score of offspring from a mating where both parents and all four grandparents had no hip-dysplasia will be about 8. These predictions are of the “expected” hip score—for any particular offspring, the hip score could be higher or lower because the offspring and parental hip scores are all stochastic variables. As pointed out by Wood et al. (2000a), these predictions can be based upon linear *structural* relationships between offspring and parental hip scores (see Kendall and Stuart, 1963) instead of the regression relationships. If, as here, the relationship between offspring and ancestral variables is positive, then the regression relationship overestimates the intercept. Thus, the benefits by breeding from healthy parents might be greater than those predicted using these least-squares regressions.

Swenson et al. (1997) found that the estimates of heritability for male and female Labrador retrievers were 0.54 ± 0.21 and 0.60 ± 0.13 and significantly different from 0. Our estimates of heritability of hip score and some of the components are significant but lower (Tables 7 and 8).

In Sweden, dog owners have agreed that the Swedish Kennel Club (SKC) registers the results of the evaluation of coxofemoral joint conformation and, since 1983, breeders have been able to obtain this information as well as further pedigree information. Since 1984, it has been mandatory that coxofemoral joint status be known for the sire and the dam if the offspring are to be registered by the SKC. Swenson et al. (1997) point out that these measures have led to a shift towards using only those potential sires and dams that do not have hip-dysplasia, and this has been accompanied by a decreased prevalence of hip-dysplasia in most breeds. Because all results in the UK have been published since 1991, similar benefits should occur in the UK as well.

Kealy et al. (1997) compared the effect of diet on osteoarthritis in Labrador retrievers—from pairs of otherwise comparable animals, one member was allowed 75% of the diet taken by the other member. They found greater frequency and more severity of osteoarthritis in the group on unlimited diet. With no data on environmental variables such as diet, weight or exercise, our study has been restricted to the genetic variables.

Leppanen and Saloniemi (1999) analysed records of hip-dysplasia screening of 69,349 dogs in 22 breeds that were born in 1988–1995 and compared the prevalence of dysplasia in data prior to 1988. They found that, in most breeds, there was no significant change in prevalence. The *testingscreening* of potential parents should be followed by a *selection* for breeding (from those screened) only those potential sires and dams that were free from hip-dysplasia. Clearly, such a recommendation must be based upon a scientific demonstration of positive relationship between offspring and parents (Tables 3–7).

Our results summarised in the conclusions below suggest the recommendation that all future breeding should be from sires and dams *both* with zero or very-low hip scores. If this is done then, in time, future Labrador retriever population will be from parents, grandparents and earlier parental ancestors all free of hip-dysplasia with low hip scores. The hip scores in such future populations will be expected to be much smaller.

5. Conclusions

The main conclusions which apply to Labrador retrievers are:

- (1) The genetic heritability of this condition was significant from both sires and dams, with higher heritability from sires.
- (2) Hip-dysplasia scores were higher in males than in females.
- (3) Breeding tends to be from sires and dams that have been tested, but there was no strong selection of only those potential parents who had very low scores.
- (4) The expected hip score of the offspring born can be predicted from the hip scores of the sire and dam using the intercept estimates in the regression models presented. Because the relationship between offspring and parental hip scores is likely to be structural, the true expected score for the offspring might be even less than that predicted.

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