Hip-Dysplasia (HD) and Hip-Quality (HQ) in Norwegian Breton

Preliminary Report!!

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Introduction

Hip Dysplasia is one of the most severe skeletal abnormalities and a problem in many dog breeds. Traditionally veterinarian radiologists grade the dysplasia subjectively, using a standardized x-ray and following the guidelines of the Federation Cynologique International (FCI). Official grading is limited to members of a national panel. Unfortunately there are great differences between countries, panelists and time periods over years, which make modern breeding difficult. Modern breeding strategies use data across countries and from all relatives, also from ancestors from years ago, and therefore the trait of interest should be defined constantly.

There are different attempts to use objective measurements from the x-ray to characterize the dysplasia objectively. A new method is to apply a Selection Index approach to predict the genotype of the animal by a function of phenotypic measurements from the joint. The prediction includes 6 points to characterize the conformation differences of the joints

The numerical value from the function is called Hip Quality (HQ) instead of Hip Dysplasia (HD). These values are standardized to a Variation in a way, that the best dogs of the first evaluated breeds (Berger des Pyrenees and Hovawart) reached the value 1 (100%). The HQ formula in its generalized form, not breed specific, was also applied to the Breton breed of Norway.

Material and method

The Bretons of Norway are stored in a database. In total 3392 dogs are registered. From 1509 dogs the hips are graded (HD). There are generally 5 classes, A to E, which represent hips with no signs of dysplasia up to severe dysplasia. In some cases the classes were subdivided in two subclasses, e.g. A1, A2, B1, B2 etc. To use this nominal figures as a numerical trait, the classes were translated to numerical equivalents: A=10, B=20, C=30, D=40 and E=50. In the case of subdivision of the classes, the value is lowered or altered by 3, e.g. A1=7, A2=13, B1=17 etc.

The HQ values were estimated for the Norwegian dogs from which an x-ray was archived in the Norwegian Kennel Club (NKK). In total 381 dogs were classified by HQ.

Results and Discussion

The frequency of HQ estimates is given in Fig.1. HQ, here multiplied by 100, ranges from 0.79 to 1.01. The population mean is 0.927. with a standard deviation of 0.029. The variable is normal distributed and close to the biological variation. The HD-classifications, shown in Fig. 2, are mostly in category A, partly subdivided in A1 and A2. The higher grades get lower in frequency. The skew distribution does not fit the underlying biological Variation.

Fig.1: Frequencies of HQ Estimates (n=373)

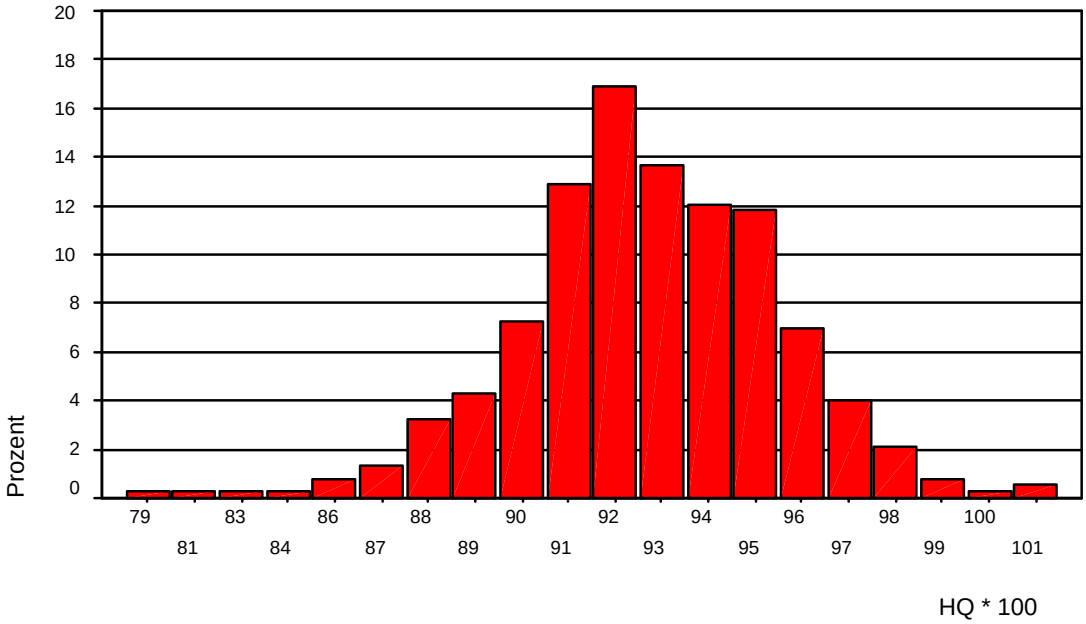
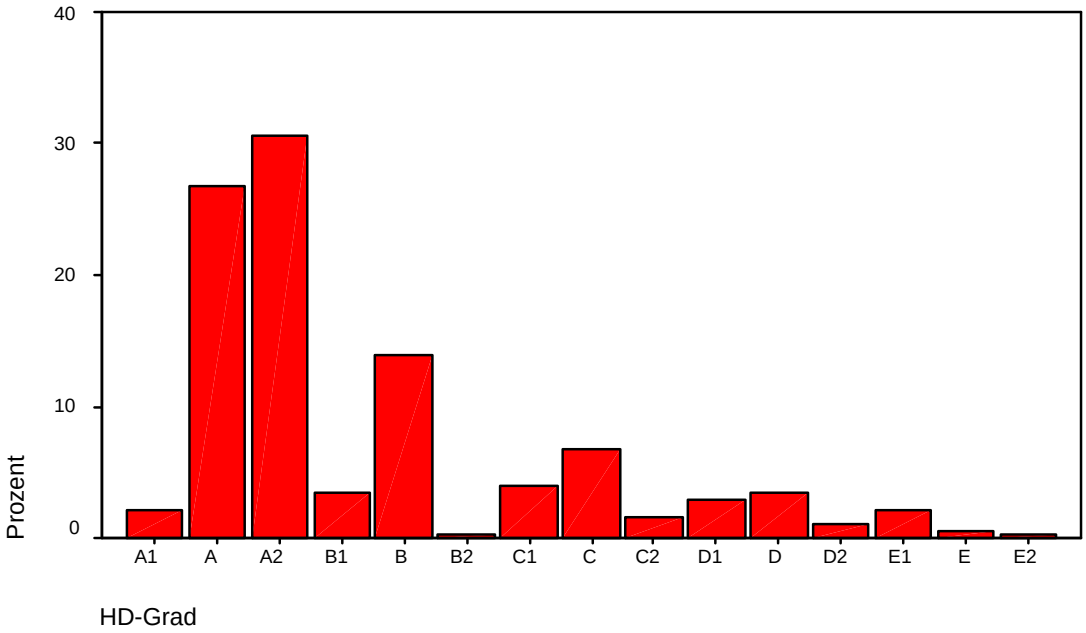


Fig. 2: Frequencies of HD-Classes (n=373) of dogs with HQ-estimates



As shown in Fig.3 the Hip-Quality is decreasing with higher degree of dysplasia, but there is still a wide variation of HQ within the same HD-class, which may be caused by different factors. One factor may be a conflict between the veterinarian's and the breeder's point of view. HQ is optimized in respect to inherited measurements to predict the genotype, which is

equal to HD of the progeny, while HD-grading is also used to characterize the health state of the dog and therefore HD has to include non genetic reasons. In Fig. 3 HQ is plotted against HD-classes. Fig. 4 shows the average HQ within HD classes. The average must be seen in context with the number of observations, which are presented in Fig. 2.

Fig. 3: Hip-Quality (HQ) in different HD-Classes

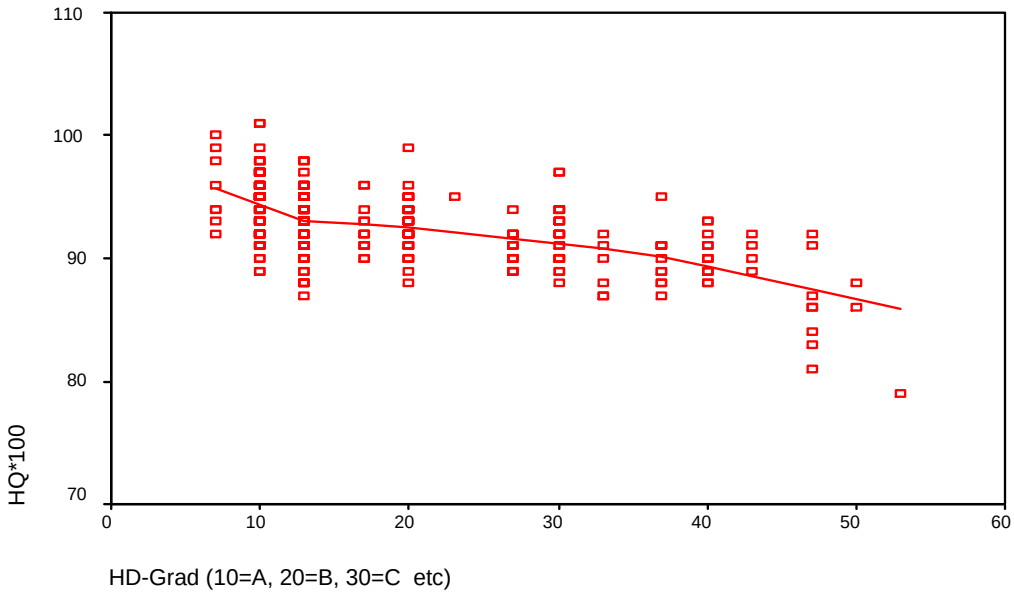
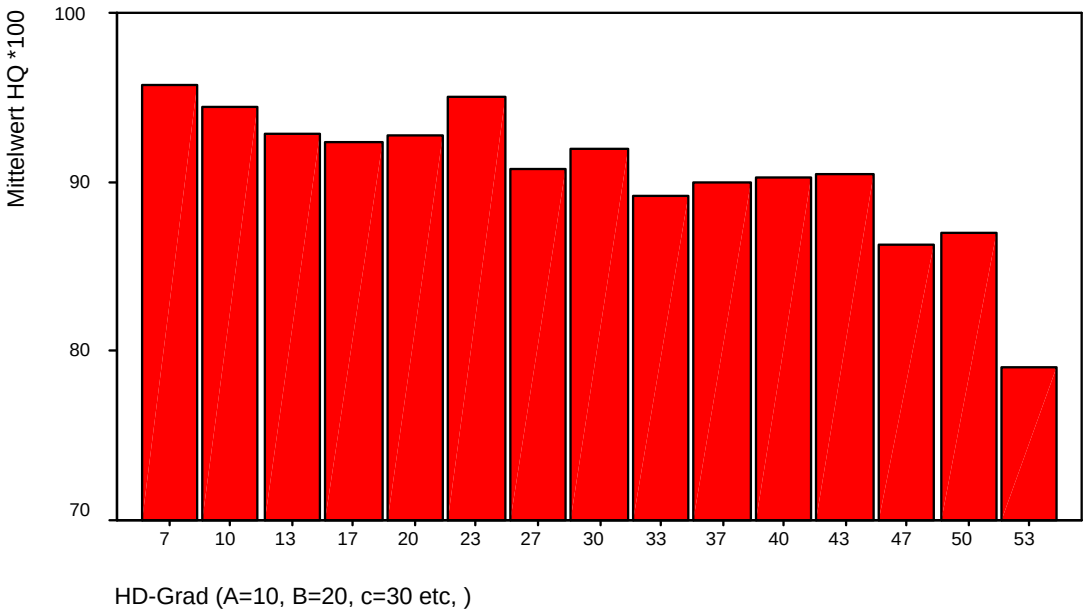


Fig. 4: Level of HQ in different HD-Classes



The correlation between HD and HQ is –0.579, where the negative sign indicates that quality and dysplasia are defined antagonistically. The highest quality has the lowest grade.

Genetic aspects

One statistical method to compare the genetic background of two traits is the Analysis of Variance (ANOVA). This analysis is testing, how much the variance (variation between animals) is caused by a specified factor. In our case it can be tested, how much the father or the mother influences the HD or HQ of the dogs. The data used are limited to those where HD and HQ is present simultaneously.

HQ

	Quadratsumme	df	Mittel der Quadrate	F	Signifikanz
Zwischen den Vätern	1251,691	68	18,407	3,059	,000
Innerhalb der Vätergruppen	1877,259	312	6,017		
Gesamt	3128,950	380			

HD

	Quadratsumme	df	Mittel der Quadrate	F	Signifikanz
Zwischen den Vätern	10924,126	66	165,517	1,776	,001
Innerhalb der Vatergruppen	28518,158	306	93,197		
Gesamt	39442,284	372			

The comparison shows a much higher F-Value for HQ (3.059 versus 1.776) for the father s influence on HQ than on HD, which indicates higher heritability for HQ than for HD.

The influence of the mother is given in the following tables. The F-Value is also higher for HQ than for HD (2.27 versus 1.66).

HQ

	Quadratsumme	df	Mittel der Quadrate	F	Signifikanz
Zwischen den Müttern	1379,913	98	14,081	2,270	,000
Innerhalb der Muttergruppen	1749,038	282	6,202		
Gesamt	3128,950	380			

HD

	Quadratsumme	df	Mittel der Quadrate	F	Signifikanz
Zwischen den Müttern	14455,122	96	150,574	1,663	,001
Innerhalb der Muttergruppen	24987,163	276	90,533		
Gesamt	39442,284	372			

The results show clearly, that sires and dams can be characterized much clearer by measuring HQ instead of grading HD of the progeny.

The common way to estimate heritability of different traits and genetic correlation between traits is to estimate variance components by the *restricted maximum likelihood* method (REML). In this method it is necessary to define a model, how the trait Y, HD or HQ in this case, is influenced by different factors. The model used here is

Y= Population mean + effect of animal's genotype + maternal environmental effect + effect of gender + unknown residual environmental effects.

Heritability finally is defined as the variance component caused by the genetic effects divided by (or in relation to) the total Variance (genetic plus residual environmental). 1128 dogs were graded for HD only, 8 were characterized for HQ without knowledge about HD and 373 dogs have HD and HQ values, derived from the same x-ray. So in total 1509 HD- and 381 HQ-results were processed. The following table shows the final results with standard errors from a bivariate analysis, where HD and HQ were analyzed simultaneously.

	Genetic component	Maternal componenet	Standard errors genetic/maternal
Hip Dysplasia (HD)	0.204	0.077	0.043 / 0.021
Hip-Quality (HQ)	0.654	0.013	0.070 / 0.029
Correlation between HD and HQ	-0.837	-0.966	0.081 / 0.597

The heritability of HD is comparable with estimations in the most breeds. There is no doubt that a successful breeding is possible, when -by breeding value estimation- additional information from relatives is included.

The heritability of HQ is much higher. To reach that accuracy of 0.65, the dog itself must be graded for HD and additionally about 25 offspring from 25 different partners. This is impossible for a female and seldom for a male in a small population. Simply testing a dog for HQ has more accuracy than any breeding value estimation on the base of HD-scores ever can reach in the Breton breed.

The genetic correlation between HD and HQ is -.837, which shows an high but incomplete agreement of both genotypes. If two traits correlate genetically not completely one can argue, that HD-grades do not cover all genetic effects which are important for HQ or HQ does not cover all genes which are important for HD-grading. The real validation of both traits is only possible, if clinical symptoms (CS) are defined as the target trait and HD and HQ are used as predictors for the genotype of CS. However, as long as no data are available for CS, lameness and handicaps, the most heritable trait should be preferred.

Conclusions

The estimation of HD and HQ showed clearly, that the measured hip quality is preferable in dog breeding to combat hip dysplasia. Some main points are to mention: HQ is objectively measurable and by this independent from personal opinions. HQ is comparable over years and countries. Furthermore HQ is a continuous trait, which simply describes the conformation characteristic of the joint. There is no need to classify dogs into certain categories. Finally it must be stated, that the heritability of HQ is very high. This means, that the HQ-value describes the genetic expectation of a dog much better than the HD-grading in the classical way. Especially young dogs, before they are used in breeding, can be selected with more accuracy.

Literature

Beuing, R. (2002) HQ, eine neue Methode zur Bestimmung der Hüftqualität : Link: www.hundezucht-aktuell.de