New Zealand Veterinary Journal

ISSN: 0048-0169 (Print) 1176-0710 (Online) Journal homepage: https://www.tandfonline.com/loi/tnzv20

Heritabilities and genetic trends for elbow score as recorded by the New Zealand Veterinary Association Elbow Dysplasia Scheme (1992–2013) in four breeds of dog

M Soo, N Lopez-Villalobos & AJ Worth

To cite this article: M Soo, N Lopez-Villalobos & AJ Worth (2018) Heritabilities and genetic trends for elbow score as recorded by the New Zealand Veterinary Association Elbow Dysplasia Scheme (1992–2013) in four breeds of dog, New Zealand Veterinary Journal, 66:3, 154-161, DOI: 10.1080/00480169.2018.1440652

To link to this article: https://doi.org/10.1080/00480169.2018.1440652

Published online: 08 Mar 2018.

Scientific Article

Heritabilities and genetic trends for elbow score as recorded by the New Zealand Veterinary Association Elbow Dysplasia Scheme (1992–2013) in four breeds of dog

M Soo*, N Lopez-Villalobos † and AJ Worth‡§

Abstract

AIM: To estimate the heritability of the New Zealand Veterinary Association (NZVA) elbow phenotype, obtain estimated breeding values (EBV) for the worst-elbow score and estimate the genetic trends for this trait in four populous breeds of dogs, using the records from the NZVA Canine Elbow Dysplasia Scheme database (1992–2013).

METHODS: Overall, 4,070 elbow records from a pedigree of 11,311 dogs were available for animals scored between 1992 and 2013. The worst elbow score between the left and right elbows was identified for each dog and used for EBV analysis. Estimates of heritability and EBV for the elbow score of dogs from German Shepherd dog, Labrador Retriever, Golden Retriever and Rottweiler breeds were obtained using restricted maximum likelihood procedures with a within-breed linear animal model. The model included the fixed effects of sex and birth year, with age at scoring as a covariable, and the random effect of animal. Genetic trends for the worst-elbow score were calculated as the regression coefficient of the EBV, weighted by reliabilities, on year of birth.

RESULTS: The estimates of heritability for worst-elbow score were 0.25 (SE 0.06) in German Shepherd dogs, 0.46 (SE 0.06) in Labrador Retrievers, 0.18 (SE 0.07) in Golden Retrievers and 0.29 (SE 0.11) in Rottweilers. The genetic trend for German Shepherd dogs was −0.0082 (SE 0.0015), for Labrador Retrievers was −0.0016 (SE 0.0016), for Golden Retrievers was −0.0033 (SE 0.0010) and for Rottweilers was −0.0070 (SE 0.0023) units per annum, which were different from zero (p<0.01) in all breeds except Labrador Retrievers.

CONCLUSIONS AND CLINICAL RELEVANCE: A small but favourable response to selection was achieved by three of the four breeds in the study period; during which selection for elbow traits has been largely voluntary. While the magnitude of genetic change in terms of elbow units per annum may appear small, it must be remembered that elbow scoring grades only range from 0–3. Greater improvement may be possible if compulsory screening was a requirement for pedigree breeding stock, and if greater selection pressure were applied on the basis on an individual's EBV, rather than the worst-elbow score alone. The maintenance of an open registry, with transparency of EBV information made available to all breeders, may enhance selection intensity opportunities and potentially assist with the process and progress of breeding selection.

KEY WORDS: *Canine elbow dysplasia, estimated breeding values, genetic trend, heritability, International Elbow Working Group*

Introduction

Canine elbow dysplasia (CED) is recognised as a common debilitating developmental orthopaedic disease primarily affecting large- and giant-breed dogs. The lesions associated with CED, as defined by the International Elbow Working Group (IEWG), are fragmented medial coronoid process, ununited anconeal process, osteochondrosis dessicans of the medial aspect of the humeral condyle and incongruity of the elbow joint (Flückiger 2011). A combination of osteochondrosis, joint incongruity and abnormal biomechanical forces occurring across the elbow joint are thought to precede and contribute to the development of the CED lesions in genetically-predisposed individuals. All four CED lesions are manifested clinically as elbow joint pain, forelimb lameness or stiffness. The peak onset of clinical signs can be observed as early as 6–8 months of age; however some dogs present later in life at 6 years of age or older with little or no history of early-age lameness (Temwichitr *et al.* 2010; Michelsen 2013).

The inheritance of CED is considered polygenic or multifactorial, meaning that its expression is influenced by the effect of multiple genes and environmental factors (Guthrie and Pidduck 1990;

* Cahill Animal Hospital, Palmerston North, 4414, New Zealand
† Institute of Fundamental Sciences, Massey University, Private Bag 11222, Palmerston North, 4442, New Zealand
‡ Massey University Veterinary Teaching Hospital, Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Private Bag 11222, Palmerston North, 4442, New Zealand
§ Author for correspondence. Email: a.j.worth@massey.ac.nz

https://doi.org/10.1080/00480169.2018.1440652

CED	Canine elbow dysplasia
EBV	Estimated breeding value
h^2	Estimated heritability
IEWG	International Elbow Working Group
NZKC	New Zealand Kennel Club
NZVA	New Zealand Veterinary Association

Maki *et al.* 2002; Stock *et al.* 2011). Some researchers have suggested that each CED lesion may be inherited independently (Padgett *et al.* 1995; Ubbink *et al.* 1999; Janutta and Distl 2008) or that a major gene may exist for CED (Mäki *et al.* 2004), and the mode of inheritance is still the subject of ongoing research (Michelsen 2013). Environmental factors such as trauma to the elbow joint, over-exercise and excessive caloric intake leading to rapid weight gain during developmental ages are thought to contribute to the expression of CED in the genetically-predisposed dog (Sallander *et al.* 2006; Temwichitr *et al.* 2010; Michelsen 2013). Due to the multifactorial nature of the inheritance of CED, there is currently a lack of readily-available genomic tests for routine clinical use. In the absence of feasible methods for direct clinical assessment of CED, that is a diagnosis of CED cannot be made on the basis of physical examination alone, radiological elbow scoring or grading methods have been developed and are widely used to identify dogs phenotypically affected by the disease.

The New Zealand Veterinary Association (NZVA) introduced the Elbow Dysplasia Scheme in 1992 as a method for identifying dogs with the disease (Anonymous 1992a). In co-operation with the New Zealand Kennel Club (NZKC), the NZVA elbow scoring records were maintained in a national computerised database from 1992 (Anonymous 1992b). Phenotypic screening for elbow dysplasia under the NZVA Elbow Dysplasia Scheme is based on the IEWG protocol using a single fully-flexed (45°) mediolateral radiograph of each elbow in dogs aged 1 year or older (Flückiger 2011). The flexed mediolateral elbow projection was chosen to be the primary radiographic view for differentiating individuals with and without CED because it highlights the non-articular aspect of the anconeal process, a reliable location for identifying early osteophytosis indicative of CED (Keller *et al.* 1997). A score of 0, 1, 2 or 3 is assigned to each elbow, based on the evidence of any primary CED lesions, extent of elbow incongruity, size of osteophytes (if present) and presence of any bony sclerosis (Worth *et al.* 2010). Under the NZVA Elbow Dysplasia Scheme, the accreditation panel assigns each elbow one of six possible grades: 0, borderline, 1a, 1b, 2 and 3 (Worth *et al.* 2010). The final score is based on the worst of the left or right elbow, and does not represent the combined score of both elbows (Flückiger 2011).

In order to reduce the prevalence of CED via selective breeding, the trait being selected for or against must be genetically-influenced (heritable) and directly measurable on live animals. The higher the heritability, the greater the influence of genetic effects on the trait and thus the greater the response to selection. Recognition of the heritable nature of CED and the use of effective selective breeding techniques are critical to achieve a reduction in the prevalence of the disease (Keller *et al.* 2011). To date, numerous studies have demonstrated that CED has sufficient heritability to manipulate the prevalence of the disease through selective breeding (Lavrijsen *et al.* 2012; Hou *et al.* 2013; Lewis *et al.* 2013). In New Zealand, a phenotypic study was conducted to assess the efficacy of the NZVA Elbow Dysplasia Scheme in improving elbow conformation (Worth *et al.* 2010). However, to our knowledge, heritability estimation and genetic trend analysis of the elbow scoring data held by the NZVA have not been previously reported.

Based on the phenotypic trend of the NZVA elbow scores of the German Shepherd dog, Labrador Retriever, Golden Retriever and Rottweiler breeds, Worth *et al.* (2010) reported that there was a significant reduction in the incidence of CED over the period between 1991 and 2008. As it was only based on the phenotypic trend of the individual animal NZVA elbow scores, the analysis by Worth *et al.* (2010) may have inaccurately estimated the genetic improvement made in the four breeds. The genetic response (trend) can be determined by the regression coefficient of estimated breeding values (EBV) on year of birth of animals. The EBV is a measure of the genetic superiority of an animal as compared to its contemporaries and is calculated from the phenotypes of the individual and its relatives, and pedigree data (Nicholas 2010). Therefore an analysis of the genetic trend calculated using EBV provides more accurate indication of the amount of genetic progress attained by the respective breeds towards better elbow conformation, as compared to using the phenotypic trend.

The aims of this study were to estimate the heritability of the NZVA elbow phenotype for overall dysplasia status, left elbow score, right elbow score and worst elbow, obtain EBV for the NZVA worst-elbow score and estimate the genetic trends for this trait in four breeds of dogs scored under the NZVA Elbow Dysplasia Scheme. The breeds considered in this study were German Shepherd dog, Labrador Retriever, Golden Retriever and Rottweiler.

Materials and methods

Elbow score data extracted from the NZVA database

The database of the NZVA Elbow Dysplasia Scheme was made available for the aims of this study. Records of the four most populous breeds in the NZVA database (German Shepherd dog, Labrador Retriever, Golden Retriever and Rottweiler) were selected for analysis. Data were collated by breed consisting of each dog's unique NZKC registration number, date of birth, sex, date of radiography, age at radiographic scoring, left elbow score, right elbow score, worst-elbow score and overall dysplasia status. Dysplasia status is a nominal trait; with a dog determined to have elbow dysplasia or not after the consideration of both elbow scores. All dogs scored at 12-months of age or older were included; for dogs that were re-scored at a later date only the most recent elbow score was evaluated in this study. The NZVA elbow dysplasia scores are ordinal, where each elbow is assigned one of six possible grades (0, borderline, 1a, 1b, 2 and 3) by the NZVA Elbow Dysplasia accreditation panel. The borderline score was introduced by the NZVA and is not part of the IEWG guidelines. According to the NZVA guidelines dogs with both elbows scored as borderline or one elbow scored as borderline with the contralateral elbow scored as 0 are classified as non-dysplastic and all others are classified as dysplastic. For the purposes of statistical and genetic analyses, the grades 0 and borderline were combined as Grade 0, and the grades 1a and 1b were classified as Grade 1, resulting in a total of four elbow grades (0, 1, 2 and 3). The worst score between the left and right elbow was also identified for each dog.

If a dog's sex or date of birth was missing, the data were obtained from NZKC records. Under the rules of the NZVA Elbow Dysplasia Scheme, a dog must be at least 12 months of age to be eligible for scoring. Although many breeders present dogs for elbow scoring at 12 months of age, some dogs are not scored until they are much older. Age at scoring (in days) was determined by subtracting the date of birth from date of scoring, and was then divided by 30.4 to give an age at scoring in months.

Pedigree data extracted from the NZKC database

In order to generate breeding values, pedigree information on all animals scored under the NZVA Elbow Dysplasia Scheme were obtained from the NZKC and sorted by breed. The pedigree file was created by extracting the names of animal, sire and dam and tracked back to the founding generation where the first animal was recorded. The unique NZKC identification number for each named individual allowed the generation of a pedigree database. Missing parents or grandparents were denoted as 0 to indicate unknown individuals. The NZKC pedigree information was sorted and cleaned using the Structured Query Language procedure of SAS (version 9.3, SAS Institute Inc., Cary NC, USA, 2011). All phenotyped animals included in the study were elbow scored between 1992 and 2013 inclusive. After the removal of dogs with inconsistent or incomplete NZVA elbow scoring data, a total of 4,070 elbow scoring records from a pedigree of 11,311 dogs were available for genetic evaluation. The pedigree data were further sub-categorised into smaller pedigrees for each of the four breeds studied, and this is presented in Table 1. For German Shepherd dogs, 165 dogs were identified as having been bred or owned by the New Zealand Police Dog Breeding Centre (Trentham, New Zealand). The EBV analysis was performed on this subset of German Shepherd police dogs and also the remaining pedigree file without the police dogs.

Genetic analysis

The NZVA elbow scoring data were not normally distributed, on the basis of the Sharpiro-Wilk, Kolmogorov-Smirnov, Cramer-von Mises or Anderson-Darling tests; but performing logarithmic-transformation of the data did not improve the normality of the ordinal data. Therefore, it was decided that the original untransformed data were to be used for genetic analysis.

Estimates of variance components and EBV for the NZVA worst-elbow score were obtained using the ASReml software program release 3.0 (VSN International Ltd, Hemel Hempstead, UK) with a single trait linear animal model within-breed, similar to that described in Soo *et al.* (2015). The model included the fixed effects of sex and year of birth, with the age at elbow scoring as a co-variable, the random animal effect and residual error for each observation.

Estimates of the animal and residual variances and the solution of the random animals effects (vector u), were obtained using restricted maximum likelihood analysis. The estimated heritability (h^2) for the NZVA elbow score was calculated for the right elbow score, left elbow score, worst-elbow score and overall elbow dysplasia status as follows:

$$h^2 = \sigma_a^2/(\sigma_a^2 + \sigma_e^2).$$

The estimate of animal variance is equal to the additive genetic variance, and therefore phenotypic variance (σ_p^2) is estimated as $\sigma_p^2 = \sigma_a^2 + \sigma_e^2$. Based on the worst-elbow score, the EBV for each animal (i) was obtained as $EBV_i = u_i$ where u_i is the estimate of animal effect from the mixed model. The reliability of EBV was estimated as

$$\text{Reliability} = \left(1 - \left(\frac{SE}{\sigma_a}\right)^2\right) \times 100$$

where SE is the standard error of the estimate of animal effect and σ_a is the root square of the animal variance for the NZVA elbow score (Ufford *et al.* 1979).

A negative EBV is interpreted as the animal having favourable (lower) worst-elbow score compared to the mean of the breed population. A positive EBV is interpreted as the animal having unfavourable (higher) worst-elbow score compared to the mean of the breed population. Therefore, a negative EBV is the goal for selection.

Statistical analysis

The genetic trend of the NZVA worst-elbow score for each of the four breeds was estimated as the weighted regression line of EBV on year of birth, obtained by performing regression analysis. The EBV were weighted by their reliabilities. A favourable genetic trend (improvement in the elbow phenotype within a breed over time) would be represented by a negative regression line of EBV on birth year. This regression analysis can be considered as a measure of the genetic trend over time to evaluate the efficiency of a breeding programme. However, this is regression analysis is not an attempt to use birth year as a predictor of animal EBV.

Within the German Shepherd breed, 165 dogs were identified as having been bred by the New Zealand Police Dog Breeding Centre. Genetic trends were obtained for police and non-police dogs, and compared using the least squares method in a GLM. All statistical analyses were carried out using SAS version 9.3 (SAS Institute Inc.).

Table 1. Numbers of dogs with scoring records in the New Zealand Veterinary Association (NZVA) Canine Elbow Dysplasia database from 1992–2013, and with pedigree information from the New Zealand Kennel Club for German Shepherd, Labrador Retriever, Golden Retriever, and Rottweiler dog breeds.

	German Shepherd	Labrador Retriever	Golden Retriever	Rottweiler
NZVA elbow scoring records (n)	1,254	1,565	842	409
All animals in pedigree (n)	3,505	4,066	2,229	1,511
Generations (n)	14	14	14	13
Sires (n)	1,013	1,201	1,033	528
Sires of sires (n)	459	546	561	261
Dams of sires (n)	611	713	368	304
Dams (n)	1,588	1,833	627	694
Sires of dams (n)	577	683	395	304
Dams of dams (n)	813	974	281	364

Results

Estimates of heritability

Table 2 presents the estimates of phenotypic, additive genetic and residual variances, and the h^2 of the NZVA elbow scores for the four dog breeds examined in this study. Based on the genetic analysis of the worst-elbow score, the Labrador Retriever had the highest h^2 at 0.46 (SE 0.06) and the Golden Retriever had the lowest h^2 at 0.18 (SE 0.07), amongst the four breeds analysed. For the genetic analysis of the worst-elbow score, the German Shepherd dog had the largest phenotypic and residual variances in the study.

Genetic trends

Figures 1–4 show the genetic trends of worst-elbow score for each of the breeds investigated. The largest amount of genetic change was observed in German Shepherd dogs at −0.0082 (SE 0.0015) elbow units per annum, or −0.18 units over the 22 year study period, and the slope of the regression line differed from zero (p<0.001). The genetic trend for the 165 German Shepherd dogs that were bred by the New Zealand Police dog breeding programme was −0.0080 (SE 0.0033) elbow score units per annum, or −0.17 units over 22 years (p=0.016). The genetic trend for the remaining 3,340 non-police dogs was −0.0082 (SE 0.0015) elbow units per annum, or −0.18 units over 22 years (p<0.0001). The genetic trends differed between the police and non-police German Shepherds (p=0.009). The genetic trend for Golden Retrievers was −0.0033 (SE 0.0010) elbow score units per annum (p=0.002) and for Rottweilers −0.0070 (SE 0.0023) elbow score units per annum (p=0.002). The genetic trend for Labrador Retrievers was −0.0016 (SE 0.0016) elbow units per annum, but this did not differ from zero (p=0.33). The fixed effects of year of birth (p=0.21) and sex (p=0.29) were not associated with worst elbow score in our study model.

Discussion

Genetic analysis of the NZVA worst-elbow score data demonstrated low to moderate heritability in Golden Retrievers; moderate heritability in German Shepherd dogs and Rottweilers; and moderate to high heritability in Labrador Retrievers. This indicates that elbow traits as scored by the NZVA Elbow Dysplasia Scheme possess sufficient genetic influence such that selective breeding should translate to a decreased prevalence of CED over time. Heritability estimates are unique to the population and method of analysis, but the NZVA Elbow Dysplasia Scheme is in accordance with the IEWG protocol so it is reasonable to compare the h^2 values in this study to those obtained by other researchers analysing IEWG-type elbow scores in countries outside New Zealand. Heritability estimates for Golden Retrievers in other studies vary between 0.07 (SE 0.05) and 0.30 (SE 0.05) (Lavrijsen *et al.* 2012; Lewis *et al.* 2013; Oberbauer *et al.* 2017). This range includes the h^2 for Golden Retrievers in this study, however our results are on the lower end. In Labrador Retrievers, heritability estimates elsewhere vary between 0.10 (SE 0.03) and 0.19 (SE 0.03) (Lavrijsen *et al.* 2012; Lewis *et al.* 2013; Oberbauer *et al.* 2017). The h^2 for Labrador Retrievers in the present study was higher than these. We suggest our findings differ from those of other studies due to a combination of reasons such as inherent differences between study populations, different methods of h^2 calculation and transformation of data. Some researchers have transformed their elbow score data prior to genetic analysis (Malm *et al.* 2008; Lewis *et al.* 2011),

Table 2. Estimates (±SE) of heritability (h^2), and phenotypic, additive genetic and residual variances for elbow traits in German Shepherd, Labrador Retriever, Golden Retriever, and Rottweiler dog breeds recorded in the New Zealand Veterinary Association Canine Elbow Dysplasia database from 1992–2013.

Breed and trait	h^2	Phenotypic variance [a]	Additive genetic variance [b]	Residual variance [c]
German Shepherd				
Right elbow score	0.23±0.06	0.57±0.02	0.13±0.04	0.43±0.03
Left elbow score	0.20±0.06	0.54±0.02	0.11±0.03	0.43±0.03
Worst elbow score	0.25±0.06	0.65±0.03	0.17±0.04	0.48±0.03
Dysplasia status	0.17±0.05	0.24±0.01	0.42±0.01	0.20±0.01
Labrador Retriever				
Right elbow score	0.34±0.06	0.44±0.02	0.15±0.03	0.28±0.02
Left elbow score	0.37±0.06	0.43±0.02	0.16±0.03	0.27±0.02
Worst elbow score	0.46±0.06	0.47±0.02	0.21±0.03	0.25±0.02
Dysplasia status	0.30±0.05	0.21±0.01	0.06±0.01	0.15±0.01
Golden Retriever				
Right elbow score	0.16±0.07	0.41±0.02	0.07±0.03	0.34±0.03
Left elbow score	0.20±0.07	0.44±0.02	0.09±0.03	0.36±0.03
Worst elbow score	0.18±0.07	0.47±0.02	0.08±0.03	0.38±0.03
Dysplasia status	0.08±0.05	0.18±0.01	0.01±0.01	0.17±0.01
Rottweiler				
Right elbow score	0.27±0.11	0.55±0.04	0.15±0.06	0.40±0.06
Left elbow score	0.37±0.12	0.61±0.05	0.23±0.08	0.38±0.07
Worst elbow score	0.29±0.11	0.58±0.04	0.17±0.07	0.41±0.06
Dysplasia status	0.14±0.10	0.08±0.01	0.01±0.01	0.07±0.08

[a] The extent to which individuals differ in their observed trait values.
[b] The extent to which animals differ in their breeding values.
[c] The portion of the phenotypic variance unexplained by the model.

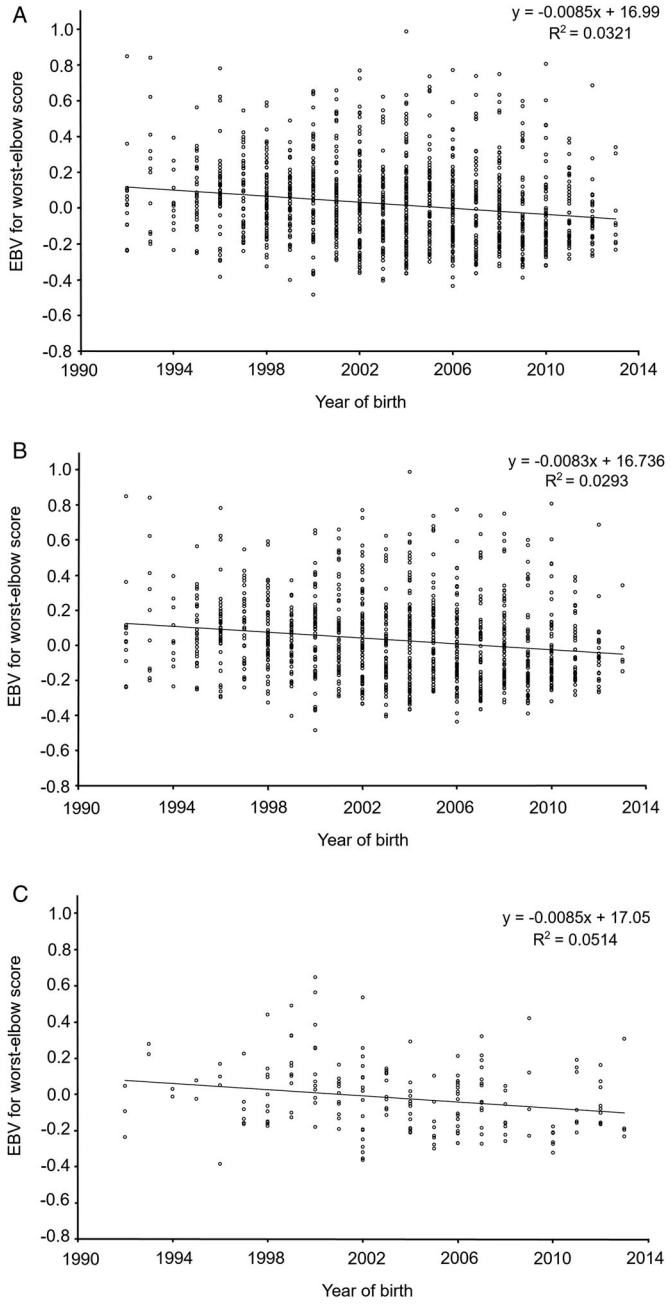

Figure 1. Genetic trends of worst-elbow score estimated breeding values (EBV) for (a) all German Shepherd dogs (n=3,505), (b) German Shepherd dogs that were not police dogs (n=3,340), and (c) German Shepherd dogs that were police dogs (n=165), recorded in the New Zealand Veterinary Association Canine Elbow Dysplasia database from 1992–2013.

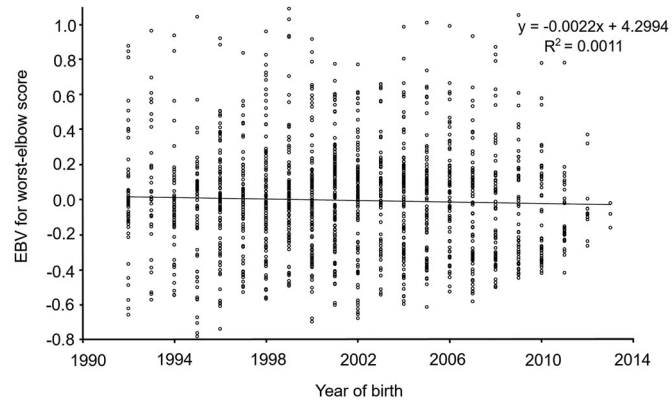

Figure 2. Genetic trend of worst-elbow score estimated breeding value (EBV) for Labrador Retrievers (n=4,066) recorded in the New Zealand Veterinary Association Canine Elbow Dysplasia database from 1992–2013.

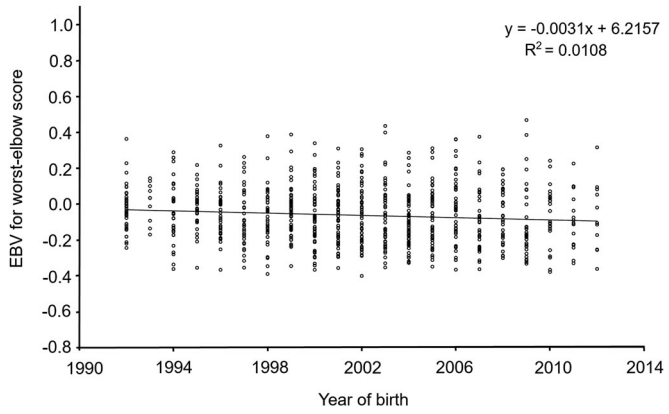

Figure 3. Genetic trend of worst-elbow score estimated breeding value (EBV) for Golden Retrievers (n=2,229) recorded in the New Zealand Veterinary Association Canine Elbow Dysplasia database from 1992–2013.

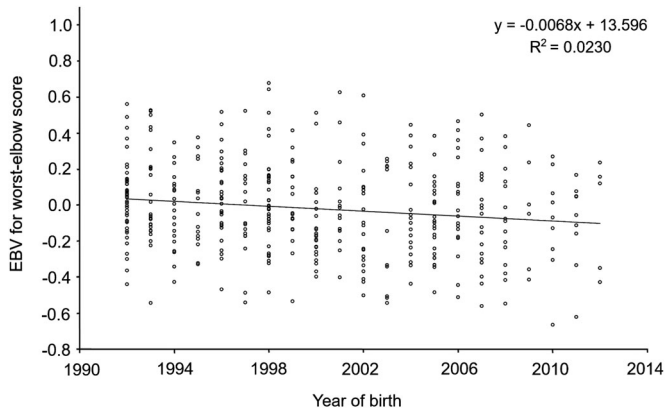

Figure 4. Genetic trend of worst-elbow score estimated breeding value (EBV) for Rottweilers (n=1,511) recorded in the New Zealand Veterinary Association Canine Elbow Dysplasia database from 1992–2013.

whereas others have not (Maki *et al.* 2002; Stock *et al.* 2011; Oberbauer *et al.* 2017). Lewis *et al.* (2011) observed that even though their worst-elbow dataset was transformed using a liability scale, the h^2 for Labrador Retrievers was only marginally greater on the untransformed scale, as compared to the transformed scores. Heritability estimates for German Shepherd dogs elsewhere varied between 0.15 (SE 0.02) and 0.3 (SE 0.02) (Janutta *et al.* 2006; Stock *et al.* 2011; Lewis *et al.* 2013; Oberbauer *et al.* 2017); and for Rottweilers, between 0.14 (SE 0.1) and 0.68 (SE 0.03) (Malm *et al.* 2008; Heine *et al.* 2009; Lewis *et al.* 2013; Oberbauer *et al.* 2017). The h^2 observed for the German Shepherd dogs and Rottweilers in our study are within the ranges reported.

The German Shepherd dogs in this study had the highest phenotypic variance for the worst-elbow score, arising from both greater additive genetic and greater residual variances, compared to the remaining three breeds. A large additive genetic variance indicates a wider selection of dogs for breeders to choose from. In theory, the larger the additive genetic variance, the greater the potential of obtaining a larger genetic response and genetic gain, if a breeding programme was implemented to decrease the prevalence CED. Due to the closely intertwined relationships between response to selection, h^2 and phenotypic variation, a large residual variance will also ultimately impact the response to selection.

Within each breed, the phenotypic and additive genetic variances of the h^2 of the left, right and worst-elbow scores were similar,

consistent with genetic equivalence of the left, right and worst-elbow scores. The overall dysplasia status was not useful as an elbow phenotype for genetic analysis as it was a nominal variable with only two possible outcomes (dysplastic or not dysplastic), which may also account for this phenotype having the lowest h^2 of all four elbow traits evaluated in this study (Table 2). It must be remembered that under IEWG protocols, a dog's final NZVA elbow score is based on the worst of the left or right elbow, and does not represent the combined score of both elbows (Flückiger 2011). It is thus the worst-elbow score that breeders have based their breeding decisions upon. Therefore we decided to use the worst-elbow score for EBV analysis and assessment of genetic progress, as it does not add bias to the genetic evaluation. Several other studies have also used the worst-elbow score for EBV analyses as typically only the worst-elbow score is publicly reported and is thus the elbow phenotype used for selective breeding (Malm *et al.* 2008; Stock *et al.* 2011; Lewis *et al.* 2013). Other studies (Maki *et al.* 2002) have elected to use the mean scores between the left and the right elbow; but it needs to be highlighted that this is effectively creates a new elbow trait for measurement, that is not in accordance with the IEWG scoring protocols.

Genetic progress was estimated by the regression coefficient of EBV on year of birth and was found to be negative and different from zero in the German Shepherd dog, Golden Retriever and Rottweiler populations. This indicates a significant genetic improvement (reduction) in the elbow phenotype (score) between 1992 and 2013. While the actual magnitude of genetic improvement was small over the study period, the negative genetic trend suggests that sufficient selection pressure has been applied to these breeds to improve elbow phenotype over time. This is consistent with the findings of Worth *et al.* (2010) who observed a significant phenotypic trend towards lower elbow scores of the worst-affected elbow and decreased prevalence of CED over time. For many of the years in this present study, the New Zealand Police Dog breeding programme utilised the NZVA Elbow Dysplasia Scheme for phenotypic scoring and selective breeding within a closed population and 165 New Zealand Police German Shepherd dogs were included in the pedigree dataset used in this study. The genetic trend for the 165 police dogs and 3,340 non-police dogs appeared similar at −0.17 and −0.18 elbow units over 22 years, respectively, but this difference was statistically significant. The non-police dog population had a higher initial EBV but exhibited a more rapid rate of genetic improvement over the study period, as compared to the police dogs. Nevertheless the difference is too small to be relevant in the context of breed improvement.

The genetic trend was favourable for the NZVA worst-elbow score for all four breeds in the study. For the German Shepherd dog, the magnitude of change of −0.0082 elbow units per annum appears very small, but it must be remembered that elbow scoring grades only range from 0–3. Using 2017 data released by the NZVA, the German Shepherd dog phenotypic average for worst-elbow score was 0.687 (Anonymous 2017). Based on the favourable genetic trend of −0.18 elbow units observed during our study period, this approximates to a decrease in the breed's phenotypic average for the worst-elbow score to 0.507, or a 26% improvement phenotypically, over a similar 22 year period. The comparable observation in the Golden Retriever, Labrador Retriever and Rottweiler breeds is an expected improvement in the phenotypic breed average of the worst-elbow scores of 8.3, 4.1 and 9.9%, respectively. However, the genetic trend of Labrador Retrievers was not significantly different from zero, suggesting that lower selection intensity may have been applied to reduce the elbow score in New Zealand Labrador Retrievers, compared to the other three breeds in this study.

Comparing genetic trends between studies is problematic because EBV analysis is very specific to the phenotype (elbow score or grade), breed and population on which the analysis is based (Nicholas 2010). Whilst the IEWG protocol is cited and utilised by several genetic analysis studies internationally, there are inconsistencies in the number of radiographic projections required for elbow assessments between countries. In New Zealand, Finland and the USA, the elbow evaluation is based on the minimum IEWG requirement of a single flexed mediolateral elbow view of both elbows (Worth *et al.* 2010; Hou *et al.* 2013; Lappalainen *et al.* 2013); the United Kingdom requires flexed and extended mediolateral elbow views (Lewis *et al.* 2011); in the Netherlands and Germany, orthogonal views are also included in the elbow assessment if available to scorers (Janutta *et al.* 2006; Lavrijsen *et al.* 2012). A comparison between the elbow dysplasia studies worldwide is still possible because they ultimately utilise the same radiographic elbow grades (phenotype), in accordance with IEWG protocol. In the few genetic analysis studies that have evaluated the IEWG-type elbow scores, researchers have observed slow but significantly improving genetic trends in similar breeds to those in our study. Our study is also in agreement with the findings of other researchers in that while there was significant genetic progress towards better elbow conformation, the actual magnitude of change per annum was very small (Maki *et al.* 2002; Lewis *et al.* 2011, 2013). Lewis *et al.* (2013) estimated that there had been a genetic improvement of −0.0018 to −0.0039 elbow units per annum in German Shepherd dogs, Labrador Retrievers, Golden Retrievers and Rottweilers in the United Kingdom, which was equivalent to only excluding the worst 4–8% of animals from the breeding pool. Given the moderate estimates of h^2, our analysis would also indicate that relatively weak selection intensity has been applied to improving the elbow conformation of these four breeds within New Zealand, which translates to the low rate of genetic progress over the 22 year study period.

A number of plausible reasons may be conjectured to explain the limited genetic improvement seen in the worst-elbow score found in this study. Between 1984 and 2008, a maximum of a quarter of any year's progeny was subjected to elbow scoring, and typically less than 10–15% of dogs born in any year was elbow scored (Worth *et al.* 2010). The low uptake of the NZVA Elbow Dysplasia Scheme was thought to likely be the result of the majority of NZKC-registered puppies being sold as pets and not retained for breeding purposes. It was also acknowledged that dogs not scored under the NZVA Elbow Dysplasia Scheme may have been scored elsewhere in alternative schemes in Australia (Worth *et al.* 2010). Hence, it is possible that if those additional elbow data and progeny information were included, different results may have been obtained in the current study.

The NZVA Elbow Dysplasia Scheme is at present a strictly voluntary scheme, intended as an advisory tool for breeders to identify breeding stock with a suitable phenotype. It is currently only optionally used by breeders because elbow dysplasia scoring is not a mandatory requirement for pedigree registration with the NZKC. It is therefore likely that some breeders may utilise Australian-based schemes, but there will also be a proportion of

breeders not currently scoring their breeding dogs. Even though the NZVA provides recommendations for selection of phenotypically-superior dogs for breeding, neither the NZVA nor the NZKC can enforce selection thresholds on breeders. Oberbauer *et al.* (2017), also observed that without mandatory participation by breeders in radiographic screening, elbow data held by the Orthopaedic Foundation for Animals in North America would continue to be incomplete thus limiting the potential for improvement by breeding selection. Similarly, without tight regulation of breeding selection within New Zealand, any possible genetic improvement can be diluted by random selection of elbow traits occurring within the population. Another factor to consider is that elbow conformation is one of the many characteristics a dog breeder has to consider when a breeding assessment is made. The low selection intensity or the apparent lack of active selection against CED may also occur when breeders are more focused on selection for or against other genetic diseases.

Pre-screening may also contribute to the loss of parental and progeny performance information required in genetic analyses. Pre-screening occurs when veterinarians or breeders fail to submit the radiographs of obviously radiologically abnormal dogs for evaluation under the NZVA Elbow Dysplasia Scheme (Worth *et al.* 2010). The pre-screening of elbow radiographs not only lowers submission rates but also falsely lowers the average phenotypic elbow scores and the accuracy of EBV for the population concerned. As a consequence, pre-screening may impact selection intensity and rate of genetic progress and this practice is strongly discouraged by the NZVA.

Breeding selection strategies also have a role in the rate of genetic improvement. It is critical to realise that throughout the period examined by this study, NZKC-registered breeders did not have EBV data available to them on which to base breeding selections. Calculation and provision of EBV information to New Zealand dog breeders would be an advantageous step forward in future breeding strategies. An EBV-based selection strategy is a more accurate indicator of an animal's genetic superiority because it provides valuable information of the genetic risk of CED being transmitted to the offspring, compared to solely using its radiographic elbow phenotype for selection. EBV can be generated and provide information on an individual's genetic merit even in the absence of elbow scores, as long as they have relatives within their pedigree that have been previously scored. By utilising the available information from relatives, the EBV of a puppy can be calculated the moment it is born, and this information can assist with future breeding decisions even before the puppy itself has been scored. Therefore, an EBV-based selection of breeding stock can still be carried out even if not all animals within the breeding population have been scored. The maintenance of an open registry, with transparency of EBV information made available to all breeders, may enhance selection intensity opportunities and potentially accelerate the process and progress of breeding selection (Hou *et al.* 2013; Lewis *et al.* 2013; Oberbauer *et al.* 2017). As the extent of genetic progress is correlated with the accuracy of breeding selection, greater genetic improvement could have been achieved with EBV-based selection compared to elbow phenotype-based selection (Hou *et al.* 2013; Lewis *et al.* 2013; Oberbauer *et al.* 2017).

It has also been proposed that inclusion of molecular genetic information into breeding selection schemes may further enhance the accuracy and achieve an even greater response to selection than EBV-selection alone (Hou *et al.* 2013). However there has only been a limited number of genomic studies conducted on identification of critical genes in CED and associated DNA markers (Mäki *et al.* 2004; Clements *et al.* 2010; Pfahler *et al.* 2012). These genomic technologies will have to be further developed and refined for routine clinical use before they can be readily employed to predict individual genetic susceptibility to CED prior to selection for breeding. Therefore, in the short term at least, it is in the authors' view that breeding selection on the basis of EBV of the phenotypic worst-elbow score remains the next best alternative to genomic selection. While the use of EBV to select against CED is still in its infancy, it carries a lot of potential if incorporated appropriately into selective breeding schemes to effectively enhance the rate of genetic gain towards better elbow conformation in dogs.

This study demonstrates that the NZVA elbow score phenotype in the four breeds studied has sufficient heritability to allow for genetic improvement through the use of selective breeding, provided that there is adequate selection intensity. A small but favourable response to selection was achieved by three of the four breeds in the study period, during which selection for elbow traits has been largely voluntary. The EBV analysis of the worst-elbow score for the Labrador Retriever showed no significant genetic change over the study period, suggesting random selection of elbow traits or very low selection intensity toward a better elbow phenotype. Greater genetic improvement could be achievable if EBV were to be used for selection against CED instead of individual phenotypic records.

Acknowledgements

The authors would like to thank the New Zealand Companion Animal Health Foundation and Massey University for their generosity in funding this study. The authors would also like to thank Trish Thorpe of NZVA and the NZKC for the extraction, provision and spread-sheeting of the data.

Declaration of interest

Andrew Worth is the current Convenor of the NZVA Hip and Elbow Dysplasia Schemes and receives an honorarium for this position.

ORCID

N Lopez-Villalobos http://orcid.org/0000-0001-6611-907X

References

*__Anonymous__. Elbow dysplasia scheme. *Vetscript* 5(10), 6–7, 1992a

*__Anonymous__. Elbow dysplasia: outline of national registry. *Vetscript* 5(6), 18–9, 1992b

*__Anonymous__. *Elbow Dysplasia – Totals by Breed*. http://c.ymcdn.com/sites/www.nzva.org.nz/resource/collection/7C465AA2-923C-40C7-803A-9A846EF7C7D9/ElbowDysplasia_March2017.pdf (accessed 17 November 2017). New Zealand Veterinary Association, Wellington, New Zealand, 2017

Clements DN, Short AD, Barnes A, Kennedy LJ, Ferguson JF, Butterworth SJ, Fitzpatrick N, Pead M, Bennett D, Innes JF *et al.* A candidate gene study of canine joint diseases. *Journal of Heredity* 101, 54–60, 2010

*Flückiger M. *Radiographic procedure and scoring of elbow dysplasia in the dog*. In Proceedings of the 26th Annual Meeting of the International Elbow Working Group, Pp 8–13 http://www.vet-iewg.org/wp-content/uploads/2017/02/proceedings2011iewg.pdf (accessed 17 November 2017). International Elbow Working Group, Amsterdam, The Netherlands, 2011

Guthrie S, Pidduck HG. Heritability of elbow osteochondrosis within a closed population of dogs. *Journal of Small Animal Practice* 31, 93–6, 1990

Heine A, Hamann H, Tellhelm B, Distl O. Estimation of population genetic parameters and breeding values for elbow dysplasia in Rottweilers. *Berliner und Munchener Tierarztliche Wochenschrift* 122, 100–7, 2009

Hou Y, Wang Y, Lu X, Zhang X, Zhao Q, Todhunter RJ, Zhang Z, Moore S. Monitoring hip and elbow dysplasia achieved modest genetic improvement of 74 dog breeds over 40 years in USA. *PLoS One* 8, e76390, 2013

Janutta V, Distl O. Review on canine elbow dysplasia: pathogenesis, diagnosis, prevalence and genetic aspects. *Deutsche Tierarztliche Wochenschrift* 115, 172–81, 2008

Janutta V, Hamann H, Klein S, Tellhelm B, Distl O. Genetic analysis of three different classification protocols for the evaluation of elbow dysplasia in German shepherd dogs. *Journal of Small Animal Practice* 47, 75–82, 2006

Keller GG, Kreeger JM, Mann FA, Lattimer JC. Correlation of radiographic, necropsy and histologic findings in 8 dogs with elbow dysplasia. *Veterinary Radiology and Ultrasound* 38, 272–6, 1997

Keller GG, Dziuk E, Bell JS. How the Orthopedic Foundation for Animals (OFA) is tackling inherited disorders in the USA: using hip and elbow dysplasia as examples. *The Veterinary Journal* 189, 197–202, 2011

Lappalainen AK, Mölsä S, Liman A, Snellman M, Laitinen-Vapaavuori O. Evaluation of accuracy of the Finnish elbow dysplasia screening protocol in Labrador Retrievers. *Journal of Small Animal Practice* 54, 195–200, 2013

Lavrijsen IC, Heuven HCM, Voorhout G, Meij BP, Theyse LFH, Leegwater PAJ, Hazewinkel HAW. Phenotypic and genetic evaluation of elbow dysplasia in Dutch Labrador Retrievers, Golden Retrievers, and Bernese Mountain dogs. *The Veterinary Journal* 193, 486–92, 2012

Lewis TW, Ilska JJ, Blott SC, Woolliams JA. Genetic evaluation of elbow scores and the relationship with hip scores in UK Labrador retrievers. *The Veterinary Journal* 189, 227–33, 2011

Lewis TW, Blott SC, Woolliams JA. Comparative analyses of genetic trends and prospects for selection against hip and elbow dysplasia in 15 UK dog breeds. *BMC Genetics* 14, 16, 2013

Maki K, Groen A, Liinamo A, Ojala M. Genetic variances, trends and mode of inheritance for hip and elbow dysplasia in Finnish dog populations. *Animal Science* 75, 197–208, 2002

Mäki K, Janss LLG, Groen AF, Liinamo A-E, Ojala M. An indication of major genes affecting hip and elbow dysplasia in four Finnish dog populations. *Journal of Heredity* 92, 402–8, 2004

Malm S, Fikse WF, Danell B, Strandberg E. Genetic variation and genetic trends in hip and elbow dysplasia in Swedish Rottweiler and Bernese Mountain Dog. *Journal of Animal Breeding and Genetics* 125, 403–12, 2008

Michelsen J. Canine elbow dysplasia: aetiopathogenesis and current treatment recommendations. *The Veterinary Journal* 196, 12–9, 2013

*Nicholas FW. *Introduction to Veterinary Genetics*. 3rd Edtn. Wiley-Blackwell, Chichester, United Kingdom, 2010

Oberbauer AM, Keller GG, Famula TR, Loor JJ. Long-term genetic selection reduced prevalence of hip and elbow dysplasia in 60 dog breeds. *PLoS One* 12, e0172918, 2017

Padgett GA, Mostosky UV, Probst CW, Thomas MW, Krecke CF. The inheritance of osteochondritis dissecans and fragmented coronoid process of the elbow joint in Labrador retrievers. *Journal of the American Animal Hospital Association* 31, 327–30, 1995

Pfahler S, Distl O, Moore S. Identification of quantitative trait loci (QTL) for canine hip dysplasia and canine elbow dysplasia in Bernese mountain dogs. *PLoS One* 7, e49782, 2012

Sallander MH, Hedhammar A, Trogen MEH. Diet, exercise, and weight as risk factors in hip dysplasia and elbow arthrosis in Labrador Retrievers. *The Journal of Nutrition* 136, 2050S–2S, 2006

Soo M, Sneddon NW, Lopez-Villalobos N, Worth AJ. Genetic evaluation of the total hip score of four populous breeds of dog, as recorded by the New Zealand Veterinary Association Hip Dysplasia Scheme (1991–2011). *New Zealand Veterinary Journal* 63, 79–85, 2015

Stock KF, Klein S, Tellhelm B, Distl O. Genetic analyses of elbow and hip dysplasia in the German shepherd dog. *Journal of Animal Breeding and Genetics* 128, 219–29, 2011

Temwichitr J, Leegwater PAJ, Hazewinkel HAW. Fragmented coronoid process in the dog: a heritable disease. *The Veterinary Journal* 185, 123–9, 2010

Ubbink GJ, Hazewinkel HA, van de Broek J, Rothuizen J. Familial clustering and risk analysis for fragmented coronoid process and elbow joint incongruity in Bernese Mountain Dogs in The Netherlands. *American Journal of Veterinary Research* 60, 1082–7, 1999

Ufford GR, Henderson CR, Van Vleck LD. An approximate procedure for determining prediction error variances of sire evaluations. *Journal of Dairy Science* 62, 621–6, 1979

Worth AJ, Bridges JP, Jones G. Reduction in the incidence of elbow dysplasia in four breeds of dog as measured by the New Zealand Veterinary Association scoring scheme. *New Zealand Veterinary Journal* 58, 190–5, 2010

Submitted 26 July 2017

Accepted for publication 6 February 2018

First published online 18 February 2018

*Non-peer-reviewed