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Review

Canine hip and elbow dysplasia in UK Labrador retrievers

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ABSTRACT

This paper examines the outcomes from recent genetic analyses of hip and elbow scores from British Veterinary Association (BVA)/UK Kennel Club (KC) screening programmes targeted at reducing the prevalence of hip dysplasia (HD) and elbow dysplasia in UK Labrador retrievers. The analyses made use of 25,243 hip scores and 3613 elbow scores. Heritabilities (± standard error) for hip score, analysed on a log scale, and for elbow score were 0.35 ± 0.02 and 0.19 ± 0.04, respectively, with a genetic correlation of 0.41 ± 0.09.

For both hip and elbow scores, there was a near perfect genetic correlation between the left and right joint; analysis of hip score showed a predictive benefit of using the total of left and right scores rather than worst score and the benefit of using all component scores rather than their aggregate score. Downward genetic trends were observed in both hip and elbow scores, although the latter was consistent with it being correlated to response to genetic change in hip score. Estimated breeding values (EBVs) offered substantial benefits in accuracy and hence genetic progress when compared to the use of phenotypes for both hip and elbow scores. There are major opportunities for improving selection against elbow dysplasia through the use of bivariate evaluations, although progress against dysplasia would be improved by more widespread elbow scoring. The studies highlighted a number of ways in which data recording for addressing complex traits may be improved in the future. Ongoing advances in genomic technology may be utilised for increasing the rate of genetic progress in selection against HD and for complex diseases in general, through the use of genomic evaluations.

Introduction

The extent of inherited disease in dog breeds has emerged as an important issue in companion animal welfare and, in the UK, concerns have been reinforced by media reports (Higgins and Nicholas, 2008). This has resulted in three reports (Rooney and Sargan, 2009; APGAW, 2009; Bateson, 2010) on the topic and the formation of a new independent Advisory Council on the Welfare Issues of Dog Breeding sponsored by the Dogs Trust, People's Dispensary for Sick Animals (PDSA) and the Royal Society for Prevention of Cruelty to Animals (RSPCA) to address the issues.[1]

Flint and Woolliams (2008) argued more directly that selection objectives recognised as promoting a higher disease burden should be considered as unethical by breeders of both livestock and companion animals. Among companion animals, reducing the prevalence of known diseases should be a priority for breeders, yet the infrastructure to assist breeders in the form of genetic information and the awareness among breeders and owners remains rudimentary. However, researchers too have been slow to make the best use of the data available to provide the tools that will enable breeders to reduce the disease burden across pedigree dog breeds effectively and to do so alongside their other selection objectives.

This review will investigate some of these issues, with particular reference to some of the latest research findings from analyses of UK data on hip dysplasia (HD) and elbow dysplasia (ED). Both conditions are important and complex genetic diseases in dogs and are observed in a range of pedigree breeds. Complex diseases result from the effects of multiple genes and environmental factors and, as such, pose particular challenges for breeders. However, these challenges need to be addressed, as it has been estimated that 72% of known canine genetic disorders are complex diseases (Online Mendelian Inheritance in Animals data base).[2] Therefore, as well as being of intrinsic importance, HD and ED serve as examples of how scientific research could improve the effectiveness of selection against complex disease in a wider context.

Both HD and ED are developmental disorders leading to malformations of their respective joints. HD is a developmental orthopaedic disorder, characterised by the development of laxity in the

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[1] See: www.dogadvisorycouncil.org.uk

[2] See: www.omia.angis.org.au

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coxofemoral (hip) joint, which exhibits varying degrees of severity. The aetiology of HD is undetermined, but the effect of hip laxity is to reduce the stability of the joint, resulting in partial or complete dislocation (subluxation and luxation) during weight bearing. Over time, this leads to abnormal wearing of the articular surfaces and the development of degenerative joint diseases, such as exostosis (abnormal bone growth) and cartilage erosions. Clinical signs of hip dysplasia may first appear in puppies as early as 5 months of age and it affects the mobility and well-being of the dog for the rest of its life. Lesions can be treated surgically, but the secondary osteoarthritis that develops is irreversible, with salvage surgery, such as hip replacement, being the only option.

Elbow dysplasia (ED) is a related disease, covering a number of distinct malformations and malfunctions of the elbow joint. As with HD, ED can also lead to osteoarthritis of the affected joint. The prevalence of HD varies among breeds from 3% to 70%, but it particularly afflicts larger breeds; a survey of dogs in Denmark found that euthanasia due to HD was the cause of death in ~5% of dogs (Proschowsky et al., 2003). The prevalence of ED is less widely documented, but historically has been as high as 60% in some Swedish breeds (Swenson et al., 1997).

Given the available epidemiological evidence on risk factors and the lack of long-term treatment options, short of drastic intervention such as joint replacement, the most effective way to improve dog welfare is to reduce the prevalence of HD and ED through the use of genetic selection. The genetic background to the risk of developing the dysplasias is well documented, with evidence arising from different prevalences between breeds and from pedigree studies within breeds. The complex nature of the inheritance of HD is confirmed by studies reporting multiple putative qualitative trait loci (QTL) for HD in various breeds (Maki, 2004; Todhunter et al., 2005), with at least 12 chromosomal regions identified in a Greyhound/Labrador retriever cross (Todhunter et al., 2005) and some of these regions being reported repeatedly in QTL scans across different breeds (Chase et al., 2004; Marschall and Distl, 2007). The evidence for the complex nature of ED is less strong, but studies of patterns of inheritance within affected families (Guthrie and Pidduck, 1990) hint that this is the case.

Background

Within the UK, the most extensive data related to HD and ED is available from the hip and elbow scoring of Labrador retrievers. This scoring is conducted as part of a scheme that was established in 1984 by the British Veterinary Association (BVA) and the UK Kennel Club (KC). The BVA/KC scheme for both dysplasias is voluntary and, to ensure skeletal maturity, is restricted to dogs over 1 year old. There is no upper age limit restricting participation, but dogs may only be scored once. Within these schemes, all dogs that are scored are recorded in a data base, so that there is no selection, apart from a voluntary decision by the owner not to submit a particular dog, which may be related to advice from the veterinary surgeon performing the radiography.

Nine features are scored from radiographs for HD: Norberg angle (NA), subluxation (SUB), cranial acetabular edge (CrAE), dorsal acetabular edge (DAE), cranial effective acetabular rim (CrEAR), acetabular fossa (AF), caudal acetabular edge (CAE), femoral head and neck exostosis (FHNE) and femoral head re-contouring (FHR). These features measure both laxity and damage. All features are scored from 0 to 6 for each hip, except for CAE, which is scored from 0 to 5 for each hip, where zero scores indicate no signs of dysplasia. The official score is the total of both hips, which can range from 0 to 106, and is considered to describe the general condition of the dog's hip joints. The nine components are scored on the basis of the detectable laxity of the joint, bone formation and the degree of any exostosis (abnormal bone growth) and wearing. A more detailed description of the scoring criteria is given by Gibbs (1997).

This scoring system is identical to that used in Australia and New Zealand, but the final quantitative score is different from the scoring system used by the Federation Cynologique Internationale (FCI), which has five subjective grades and is used in many parts of Europe, Russia and in parts of South America and Asia, and the system used by the Orthopedic Foundation for Animals, which has seven grades and is used in the USA and Canada. In the UK, the left and right sub-totals are routinely stored in the data bases, but the component scores are not, although a large subset of UK animals does have complete records through the work of Dr. M. Willis. The participation rate ranges from 8 to 10% of the annual cohort of eligible dogs.

Scoring of ED follows the International Elbow Working Group (IEWG) procedures,[3] using radiographs of extended and flexed lateral views. Scoring is from 0 to 3 for each elbow, based upon the degree of elbow incongruity, the size of osteophytes and the occurrence of sclerosis. In this case, the official score is the worst of the left or right elbow, not the total. The data bases hold both left and right values. In the UK, the scoring scheme for ED was only initiated in 1998, much later than the scheme for HD and has a lower participation rate (2.3% of dogs born in 2009).

Detailed descriptions of analyses made of these data sets have recently been published. Lewis et al. (2010a) describe the genetic analysis of left and right total HD scores for 25,243 Labradors born between 2000 and 2007, whilst Lewis et al. (2010b) describe the genetic analysis following the decomposition of the total HD score into the component scores for a subset of 11,928 dogs with full components records. Lewis et al. (2011) describe the analysis of 3613 Labradors with ED scores born from 2000 to 2008, of which 2590 also had HD scores. The methodology for these studies was to fit mixed linear models and restricted maximum likelihood (REML) to account for additive genetic, maternal and litter components of variance in the data using the extensive Kennel Club pedigree. The descriptions that follow will not attempt to report all the genetic parameters and information gleaned from these analyses, but instead will attempt to summarise what was learnt and what can be readily applied to the genetic improvement of dysplasia, as well as to other complex diseases.

Scoring systems for hip and elbow dysplasia

In this section, the systems of scoring used by BVA/KC will be examined. At the outset, it is important to recognise that there is a difference in objective between scoring as a means of diagnosis and assessing the utility of potential treatments on the one hand, and using the score as part of assessing the predisposing genetic risk on the other hand. With a complex disease, the former is a dichotomy, to make an intervention or not, although there may be a variety of treatment choices following the initial decision, whereas the latter is a quantitative assessment of a continuum of risk. In complex diseases, the genetic risk will be affected by environmental influences, which may either reduce or enhance the chance that an individual animal will develop the disease and, consequently, its need for treatment. Therefore environmental influences are an integral part of assessing the need for treatment. In contrast, the genetic risk an offspring might inherit from its parent is unchanged by environmental influences on the parent; the environmental influences hinder the genetic evaluation by reducing the 'signal-to-noise ratio'.

[3] www.iewg-vet.org/.