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Review

International and collaborative strategies to enhance genetic health in purebred dogs

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ABSTRACT

Health problems in pedigree dogs have recently been highlighted in the media worldwide and verified internationally by cynological organisations. Collaborative actions are now needed to deal with both existing and future issues. In this article, potential roles for various stakeholders are discussed and the value of national and international platforms for collaborations is stressed. Development of specific strategies for action must be based on criteria of significance, such as severity, prevalence and inheritance, as well as availability of effective preventive measures. Assessment of options should be founded on evidence from appropriate populations-at-risk and consider broader issues, such as demographics and human–animal interactions. Existing data, such as those from insurance statistics and health surveys, should be used as a reference until representative national/international population-level breed-specific data are available. Key issues and challenges, as well as possible strategies to address them, are discussed.

Introduction

The domestic dog (*Canis familiaris*) is the most morphologically diverse mammalian species (Vilà et al., 1999). There are currently more than 350 breeds recognised by the Fédération Cynologique Internationale (FCI). This large number implies breeding in many small populations, where each breed constitutes a relatively closed genetic pool (Parker et al., 2004).

Artificial selection for specific characteristics and behaviours has led to both diversity between and reduced genetic variation within breeds. In addition, many breeds originate from a small number of founders and have experienced population bottlenecks and popular sire effects, resulting in effective population sizes far smaller than census population sizes (McGreevy and Nicholas, 1999; Calboli et al., 2008; Karlsson and Lindblad-Toh, 2008). These factors have contributed to the unique genetic structure of the dog, making it a valuable resource for studying the genetic basis of quantitative traits and a model species for human diseases, especially with its relatively high rates of heritable diseases (Karlsson et al., 2007; Karlsson and Lindblad-Toh, 2008; Lequarre et al., 2011).

Recently, several problems related to genetic health in purebred dogs have been highlighted, including breed predispositions for and the proven, indicated or presumed inheritance of canine disease by organ system and by breed (CIDD, 2011; IDID, 2011; Nicholas et al., 2011; OMIA, 2011). Numerous publications have highlighted the need for action (Hedhammar, 1999, 2005; McGreevy and Nicholas, 1999; Indrebø, 2005a,b; Asher et al., 2009; Nicholas et al., 2010; Summers et al., 2010). Health problems in purebred dogs have also been highlighted in the media, for example in a BBC production in 2008, which has stimulated activity among various stakeholders (APGAW, 2009; Rooney and Sargan, 2009; Bateson, 2010). The problems can be divided into effects of (1) loss of heterogeneity; (2) accumulation of detrimental genes; and (3) exaggeration of anatomical features. The combined effects of these factors may underlie the complex nature of many health problems in dogs.

To stimulate further discussion on collaborative actions to address the problems, this paper aims to: (1) define briefly some of the key issues and challenges; (2) describe existing sources of information and tools for genetic evaluation; (3) outline the basis for actions; and (4) suggest specific collaborative strategies to address recognition of new breeds, reduction of exaggerated anatomical features, selection of breeding stock and handling of recognised or emerging diseases of suspected genetic origin.

Issues and challenges

To enhance the health and well-being of purebred dogs, genetic variation needs to be preserved, accumulation of detrimental genotypes should be discouraged and exaggerated anatomical and mental characteristics should be counteracted. Achieving these goals

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will require vision, with immediate and longer-term activities and strategies coordinated at both national and international levels.

All stakeholders must be willing to accept some responsibility for the problems that exist and to be willing to look for ways to improve the health and well-being of purebred dogs through leadership and cooperation. Although, ultimately, it is the individual breeder who chooses to breed a bitch and selects a sire, there are many others with direct or indirect influence on the selection of breeding stock (Bateson, 2010; Bonnett, 2011a). The list includes individual dog owners, breeders, veterinarians (individually and collectively), researchers, geneticists, epidemiologists, cynological organisations (local, national and international), dog show judges and governmental and humane agencies. Many individuals will be members of more than one stakeholder category, e.g. professionals involved in healthcare or research, including veterinarians and geneticists, are commonly also involved in cynological organisations or directly involved in breeding dogs. Those with an understanding of various aspects of purebred dogs may be instrumental in bridging gaps between science and cynology, e.g. to help create policies and breeding strategies that are both feasible and effective. However, it must also be recognised that most individuals bring their own history, preferences, biases and agendas to this emotionally-charged issue, adding to the challenges of achieving cooperation and collaboration.

Focus of selection and breeding of purebred dogs on physical appearance

Achieving a balance between preserving a homogenous and specific breed type and the need for strong selection for health, longevity and performance is a challenge. It has been shown repeatedly that strong artificial selection for certain phenotypic traits may not only affect the specific trait, but also other features of the breed, including health. For example, selection for the skin phenotype in the Shar Pei increases the risk of a pleiotropic mutation, predisposing these dogs to a periodic fever syndrome (Olsson et al., 2011).

Dog breeding is international

The geographical isolation of regional populations in the past has been superseded as breeds have become segregated (or interrelated) more due to rules and regulations than because of distance. Recently recognised breeds with national/regional origin are often created from very limited populations and commonly have to pass through national genetic bottlenecks when introduced to other countries. Despite extensive transportation of dogs and semen, the sometimes limited availability of unrelated breeding stock hampers the maintenance of heterogeneity in both newly recognised and many long-established breeds.

Breeding of purebred dogs is a collaborative challenge

Breeding is often performed on a small scale, by many people, with variations in objectives, competence, economic conditions and ethical concern for the long-term viability of the breed. Given the diversity of stakeholders, it will be a challenge to address their various needs, objectives and priorities.

Corrective measures to decrease the prevalence of genetic diseases must be addressed in ways that do not create new ones or exacerbate existing problems

Restrictions, with reference to specific diseases or physical characteristics, have to be balanced against potential effects on other traits or on heterogeneity within the breed. There is a risk that implementing or mandating genetic tests based primarily on availability is misguided; the easiest or earliest tests to develop may not be those that identify the most important problems. In addition, balancing the economic interests of those developing/offering genetic tests and screening programmes against the value for current and future canine genetic health will not be straightforward or uncomplicated.

Lack of information on size and structure of various breed populations, as well as on breed-specific risks for diseases in these populations

By having dogs registered only in national kennel club databases, with no linkage between them, there is no global picture. Well-validated population-level quantification of breed-specific risks of disease is not yet widely available.

Resources and tools

Information resources

Pedigree information and phenotypic records for different traits are essential for genetic evaluation and development of breeding strategies. For dogs, this kind of information is most often kept in national registries by kennel or breed clubs. Theoretically, extensive data are available at the population level, although variation in type and amount of data kept, format, regulations and lack of willingness to share data or recognise pedigrees often hampers exchange of information and, occasionally, exchange of breeding stock. Data quality issues pose challenges to the use of even well-established registries for research or comparison of findings between various sources (Egenvall et al., 2011).

Results from screening programmes and genetic tests, in registries open to the public, are important sources of information, for which cynological organisations and the veterinary profession should share responsibility. However, it should be noted that there is a difference between comprehensive, population-based screening programmes, in which the status of both affected and unaffected dogs is recorded for as many individuals as possible in a defined population, vs. recording of only known cases of a specific condition with little or no information on the rest of the population. For registries to be reliable and useful, errors or bias in data need to be minimised, e.g. selective reporting of results should be counteracted by routines for testing and recording that ensure the correct identity of the dog at testing/examination and include the submission of both positive and negative results.

In addition to kennel and breed club registries, other sources of data include insurance companies and clinical data (Bonnett et al., 1997, 2005; Egenvall et al., 2000a,b; Fleming et al., 2011). Recent reviews have highlighted the potential and limitations of such material (Egenvall et al., 2009, 2011). In Sweden, extensive analysis of insurance data from Agria Animal Animal Insurance has resulted in several publications in refereed scientific journals on overall morbidity and mortality (Bonnett et al., 1997; Egenvall et al., 2000a,b, 2005a), as well as on specific diseases (Egenvall et al., 2005b; Nødtvedt et al., 2006; Fall et al., 2007). In an effort to improve transfer of research findings to stakeholders, there has been an ongoing partnership between the Swedish Kennel Club (SKC) and Agria Animal Insurance to produce and use the Agria Dog Breed Profiles (ADBP, 2011). Statistics on morbidity and mortality in over 80 breeds were first provided for the years 1995–2002 (Fig. 1) and have now been updated to include the years 2003–2006. Efforts are underway to increase access to these data.

Health surveys performed by national breed clubs contain valuable information if they are performed on a representative sample and in a manner that produces accurate and unbiased data (e.g.

preferably not limited to one disease). Information about health and disease in birth cohorts in existing registries may form the basis for setting priorities and even for monitoring changes over time. Unfortunately, breed clubs may not always have people with the necessary expertise to design and analyse surveys. Collaboration and support from academics, especially epidemiologists, is therefore needed; funding bodies should support such efforts.

Integration of data from different sources can be used for extended analysis of health and disease in dogs. Recently, screening data on hip dysplasia from a kennel club registry were integrated with veterinary care and mortality claims from an insurance database to determine (lifetime) clinical experiences (Malm et al., 2010). This study illustrates the potential for both epidemiological and genetic analyses of heritable diseases where data can be accurately linked, based on the registration number of the dog, and also highlighted the challenges of such endeavours.

Bateson (2010) and others have suggested that data on national populations may not be relevant to populations of the same breed in other countries due to the diversity of genetic make-up between different populations. However, the evidence to support this hypothesis is uncertain. It is likely that, in spite of specific differences (e.g. in genetic characterisation of a given population/breed), there are also marked similarities (e.g. in conformation, constitution or risk of disease) and substantial sharing of genetic material. The focus should be on both consistent patterns across populations (e.g. recognition of high rates of cancer in Bernese mountain dogs and Flat coated retrievers worldwide), as well as in differences that could be informative of disease causation (e.g. anecdotally reported higher rates of haemangiosarcoma in Golden retrievers in the USA than in Europe (J. Dobson, personal communication).

Tools for genetic evaluation

Both general and specific tools are available to support evaluation of genetic health in dogs. Screening programmes for several diseases in dogs have been in place for decades (e.g. hip and elbow dysplasia). However, despite extensive examination and subsequent selection based on screening records, the magnitude of

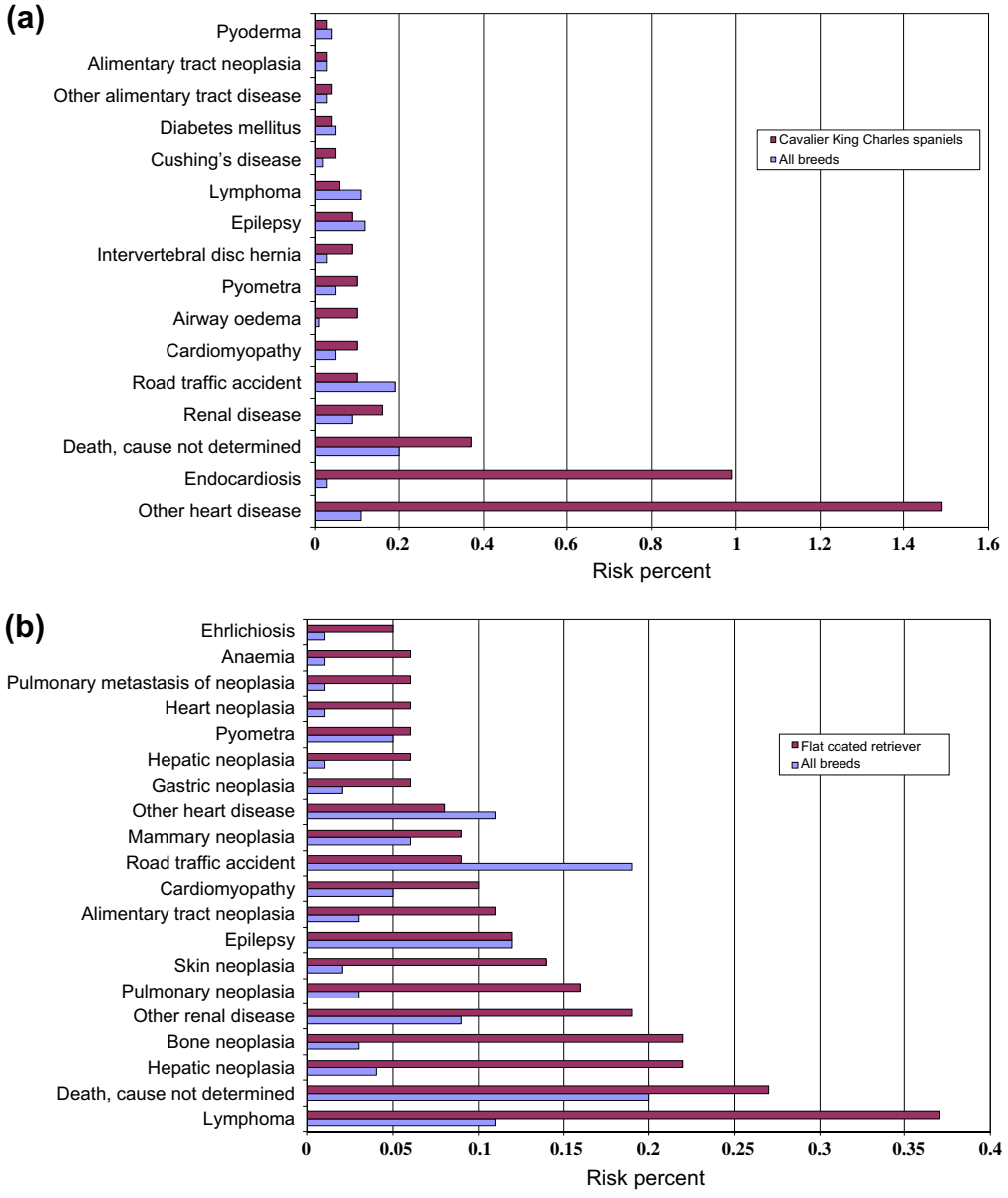

Fig. 1. Average yearly risk for the most common specific causes of death (cumulative incidence, %) in two breeds compared to all breeds using Agria Dog Breed Profiles based on approximately 200,000 dogs per year from 1998 to 2002. (a) Cavalier King Charles spaniel. (b) Flat coated retriever.

improvement has been somewhat disappointing (Willis, 1997; Leppänen and Saloniemi, 1999; Malm et al., 2008), although there has been improvement in some populations (Swenson et al., 1997a,b; Hou et al., 2010; Worth et al., 2010; Lewis et al., 2010).

One reason for the limited success of some programmes is that selection on the basis of the screening record alone is ineffective because the disease is measured as a categorical trait with a small number of broad categories. This applies especially at low disease prevalence when the proportion of dogs in the healthy category is much larger than the proportion of dogs selected for breeding (Falconer and Mackay, 1996). In many cases, screening programmes have not been designed or implemented in a way that allows a clear monitoring of any change in disease rates. There is a need for a more effective use of available information and a more comprehensive evaluation of diseases and the tools and strategies to control them.

In livestock breeding, methods for prediction of breeding values have been successfully used worldwide for many years (Simm, 2000), whereas such methods have not been widely used in dog breeding. The introduction of methods such as Best Linear Unbiased Prediction (BLUP) for breeding value prediction could result in faster genetic progress (Woolliams et al., 2011). In some countries (e.g. Germany, Finland, Denmark and Norway), this methodology is already being routinely used for genetic evaluation of hip dysplasia, based on screening records (Mäki, 2004; Stock and Distl, 2010). Another advantage of the BLUP method is that it enables calculation of the genetic trend, yielding a more accurate reflection of genetic change compared with the phenotypic trend, which is also influenced by environmental factors (Malm et al., 2008; Hou et al., 2010; Lewis et al., 2010).

Genetic tests are becoming increasingly available for single-gene disorders. The canine genome sequence and single-nucleotide polymorphism arrays enhance the possibilities for clarifying the genetic basis of several canine diseases. The development of genetic tests for different gene mutations makes it possible to accurately determine or predict the genotype of an individual dog with respect to a specific disease, i.e. to identify genetically normal, carrier and affected animals. This can be used in management of breeding programmes to decrease the frequency of a particular gene without unnecessary reduction of the overall gene pool. However, it should be emphasised that using the availability of genetic tests as the main criteria for disease control programmes is prone to the risk that other, potentially more important, diseases may be ignored.

The increased availability of genetic tests is expected to increase the complexity (and cost) of breeding programmes for many breeds. Without consistency in tests, data collection and validation, as well as a willingness to provide public access to the results, it is uncertain that there will be a concomitant major impact on genetic disease worldwide. Hence, setting priorities on the basis of the prevalence and clinical relevance of health problems will become increasingly important.

Information, education and training

Information, education and training are probably the most powerful tools to influence dog breeding. Efforts need to be coordinated and based on effective communication strategies in order to reach appropriate audiences in a way likely to enhance uptake and compliance. Recognition of the diverse interests, background and knowledge of various stakeholders will be needed in designing information transfer strategies. Ultimately, an interdisciplinary approach and collaboration among stakeholders are needed.

In the short term, enhanced transfer of knowledge about risk and occurrence of disease is needed. Even for individual owners, a preventive approach should include education as to breed-specific risks prior to acquisition of a dog, ideally fostering an appropriate and sustainable relationship. Breeders need help in accessing and understanding the evidence to support complex breeding decisions; they should also be partners in educating purchasers.

Informative sources, including web pages containing data on inherited diseases in dogs (CIDD, 2011; IDID, 2011; Nicholas et al., 2011; OMIA, 2011) and disease-specific web pages, such as those of the Orthopedic Foundation for Animals (OFA, 2011) and the International Elbow Working Group (IEWG, 2011), provide worldwide availability of information. However, both information and misinformation are widely available on the Internet. Stakeholders may need help to identify the most relevant and accurate information.

To promote a more holistic view on dog breeding and to support breeders in selection of breeding stock, the SKC initiated a task in 2001 to create a specific breeding programme for each breed. This breeding programme is meant to consolidate information on the breed, including identifying breed-specific goals, guidelines and strategies for the breed, i.e. identifying and prioritising aspects of both physical and mental health, taking into account the population structure and genetic variation. Where possible, the club is to use data from the open registry at the SKC (SKC, 2011), ADBP (ADBP, 2011) and any other sources of population-level statistics. The responsibility for developing the breed-specific breeding programmes was given to the breed clubs in Sweden and, at present, most (i.e., >300/329) have complied.

Basis for action

The basis for all actions to enhance canine genetic health should be an integrated consideration of severity, prevalence, inheritance and detection (e.g. ability to identify diseased/affected/carriers) of disorders, along with the availability of effective control or prevention programmes that can be monitored) (Bonnett, 2011b) (Fig. 2).

Severity

It is essential that the health traits on which selection is based (i.e., phenotypic or genotypic characteristics), are clinically relevant for health and well-being. There is no single over-riding definition of what constitutes the most 'important' condition. Presumably, diseases that cause death at an early age or lifelong suffering by impairment of vital functions have greater significance than, for example, degenerative processes later in life and those of lesser impact. Morbidity and mortality data should be evaluated with this in mind. The impact on the dog's and the owner's quality of life should be considered. Arman (2007) has suggested evaluating genetic conditions in the context of the widely accepted framework for assessing animal welfare originally formulated in 1965, i.e. the '5 Freedoms'. Asher et al. (2009) and Summers et al. (2010) have addressed this issue, by developing the Generic Illness Severity Index for Dogs (GISID). More recently Collins et al. (2011) developed Breed-Disorder Welfare Impact Scores (BDWIS). As better population-based incidence and risk information becomes available, disease and breed rankings may need to be re-evaluated.

Prevalence, occurrence and risk

Simple frequency counts (reported cases) of alleged 'genetic diseases' or an enumeration of the number of different conditions seen in a breed are, in general, neither appropriate nor adequate measures of the occurrence of disease. Informative measures of prevalence (existing cases) or incidence (new cases) require knowledge of both the population-at-risk (e.g. the number of dogs of a certain breed in a region, the 'denominator') and the number that experience the condition (the 'numerator'). Notwithstanding considerations of severity defined above, conditions that affect a greater proportion of a population generally are more important

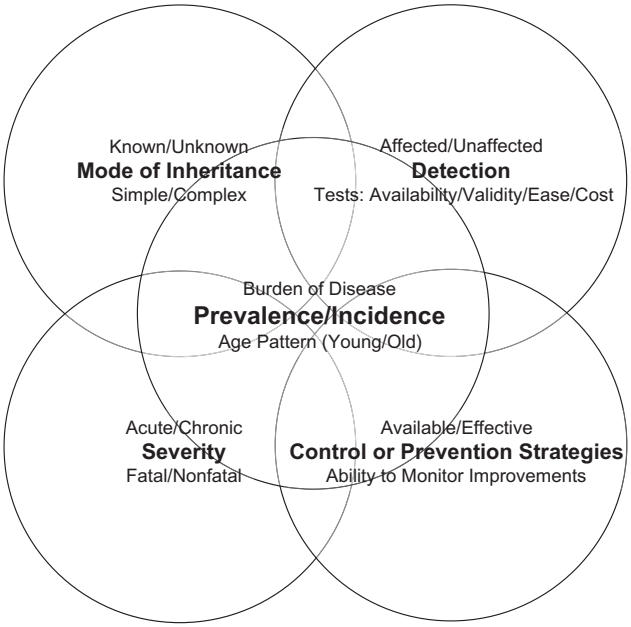

Fig. 2. Basis for actions: considerations for setting priorities for genetic health issues in dogs.

candidates for control programmes. Unfortunately, valid population-level estimates of disease occurrence are not widely available. A research project to create an electronic system for collection, analysis and reporting of data on inherited disorders in dogs and cats in the UK was recently started (RSPCA, 2010).

Fig. 1 presents examples from the ADBP (2011), with charts for the 20 most common specific causes of death (before 10 years of age) for two breeds. In each graph, the risk within the breed is presented alongside the risk for the same condition in all breeds combined. It is clear that there is a breed-specific predisposition for certain conditions. Furthermore, mortality and morbidity (claims for veterinary care) data, including information on age and gender distribution of death, as well as proportional mortalities (i.e. specific causes of death as a percentage of all deaths within a breed) are available (ADBP, 2011) and can be used in quantifying disease problems in various breeds. This visual presentation has proven effective in educating stakeholders on the relative occurrence of conditions across breeds.

Proportional mortalities are not appropriate for comparisons between breeds in terms of actual risk, but they do identify the most common, perhaps most important, causes of death or disease within a breed. For example, the actual risks of death (before 10 years of age) for Flat coated retrievers, Cavalier King Charles spaniels and French bulldogs were similar (data not shown); all three breeds had mortality rates more than twice as high as that for all purebreds (data from ADBPs, not shown). In the first two breeds, one general cause of death accounted for almost 50% of deaths (i.e. cancer in Flat-coated retrievers and heart disease in Cavalier King Charles spaniels). In French bulldogs, four separate general causes accounted for over 10% of deaths each (neurological, neoplasia, locomotor and injury) and deaths due to eye problems were among the 'top 10' causes of death. These examples of breed-specific measures at the population-level can be used to set priorities for addressing problems within a breed.

Inheritance

The mode of inheritance of specific diseases in dogs is an important feature, since it influences the development of breeding strategies. As mentioned above, genetic tests are increasingly available to inform selection of breeding stock (Mellersh, 2011). Out of about 500 heritable diseases reported in dogs (OMIA, 2011), more than 100 are known to be caused by a single mutation, but most heritable diseases are likely to be quantitative in character, i.e., influenced by several genes and environmental factors. For the majority of inherited diseases prevalent in dogs, the inheritance is still unknown. However, the varying prevalence between breeds, as well as between families, indicates a genetic background for many conditions.

Genetic analyses of certain common diseases with a quantitative background (e.g. hip and elbow dysplasia) have indicated moderate to high heritabilities (Malm et al., 2008), implying possibilities for improving health by selection. Ideally, it should be ensured that the traits (e.g. disease diagnoses) on which selection is based are both heritable and of clinical relevance for the dogs' health and well-being, e.g. that the radiographic assessment of hip status being used as the selection criterion is closely associated with the subsequent clinical problems and mortality that we wish to decrease (Malm et al., 2010; Wilson et al., 2011).

Detection

A basic requirement for an effective genetic disease control programme is that the phenotype/clinical expression used as the basis for selection is sufficiently defined, detectable and heritable. Phenotypic screening procedures, as well as individual genetic tests, preferably should be evaluated in terms of both reliability (repeatability) and accuracy (epidemiological sensitivity and specificity) for the desired outcomes before being used widely in a breeding programme.

Availability of effective control or prevention strategies

Effective control programmes must include baseline knowledge of the prevalence/incidence of disease and an ability to accurately monitor changes over time; otherwise it will be impossible to determine the effectiveness of any intervention. Any strategies must be feasible and cost-effective and compliance must be high. There are many disorders for which highly efficacious measures are available, but the procedures would not be adopted by a necessary proportion of dog breeders, reducing the effectiveness of the interventions.

For effective selection against quantitative traits, it is important that a sufficiently large proportion of the population is screened for an accurate genetic evaluation, based not only on records of prospective breeding animals, but also the records of their relatives. As an example, suggestions to reveal features of elbow dysplasia by more radiographic projections (IEWG, 2011) and the more costly and elaborative procedures of the PennHip method to measure laxity as a feature of hip dysplasia (Sondel, 2010) might be clinically relevant for the individual dog, but less useful as the basis for cost-effective screening programmes.

Specific strategies

To stimulate further discussion on collaborative actions to enhance canine genetic health, specific strategies are outlined below.

Recognising new breeds

The prime responsibility for the recognition of new breeds rests on the cynological organisations (e.g. FCI, American Kennel Club and the UK Kennel Club). More restrictive policies should be considered by these organisations (Hedhammar and Indrebø, 2011). Regional/national populations of dogs should be evaluated for relatedness to breeds already recognised and, if closely related, should be defined instead as varieties and allowed to interbreed. If the population is found to be genetically diverse from existing breeds, an extensive evaluation of whether the population size

and structure will support sustainable breeding should be made before recognising the breed.

Only after having passed this national evaluation and been assessed as sustainable should a breed be considered for international recognition. If the population is considered too small for sustainable breeding, the stud book should be left open to enable the inflow of new genes. Any rules that prohibit interbreeding between varieties based merely on colour, type of coat, regional origin or how the dog is used should be avoided.

Geneticists should participate in evaluating the possibilities for sustainable breeding with respect to population structure and genetic variation. Molecular genetic techniques may be used to evaluate genetic diversity between breeds and varieties, as well as within breeds. Veterinary advice should be used to review health status in new breed populations and in the wording of standards with reference to health issues.

Selection of breeding stock

Breeding stock should be selected with due consideration of each dog's soundness for breeding and potential contribution to the breed. Advice should be sought preferably from experienced breeders, breed clubs, judges and/or veterinarians and not based primarily on emotional attachment or personal interest. For an accurate genetic evaluation, breeders should have access to, and take advantage of, pedigree information and health records about the prospective breeding animal itself, as well as its relatives.

Collaborative actions are required to enhance the availability of data and tools for informed breeding. Registration bodies should share knowledge about the population available for breeding and their health and performance records (e.g. open availability of screening test results). Ideally, data should be available on the health and performance of any offspring already produced. Although such information has historically formed the basis for individual and breed-specific strategies, there is a need for better integration of information and establishment of priorities with reference to health and fitness.

In Sweden, on average only about 5% of male dogs and 10–20% of bitches that are potentially available are currently used in breeding (S. Malm et al., unpublished data) and the situation is likely to be similar in other countries (Calboli et al., 2008). Cynological organisations should promote the use of a larger proportion of the potential breeding stock rather than over-usage of popular sires (or dams), for example by restrictions on the maximum number of litters an individual sire is allowed to register in the stud book. The SKC has introduced limitations on the maximum number of litters in some of the Swedish scent hound breeds and many breed clubs have recommendations related to maximum number of litters per sire (SKC, 2011).

Besides promoting the wider usage of breeding stock, controlling the level of inbreeding is essential to avoid loss of genetic variation. According to the SKC ground-rules, matings between full-sibs or between father–daughter/mother–son are prohibited. Inbreeding coefficients for each dog and the ability to calculate inbreeding coefficients for offspring resulting from a planned mating are available at the SKC web site. All planned matings between dogs more related than cousins are marked with a note (SKC, 2011). Neutering of purebred dogs purchased as pets is commonly practiced in some countries and may reduce the available breeding stock. The actual impact on the population structure is unknown, but it is presumably less than that of overuse of popular sires.

Health problems related to (extreme) anatomical features

Judges at dog shows and veterinarians can have a substantial impact on the development of dog breeds with respect to anatomical features by stressing the anatomical soundness of potential breeding stock. Furthermore, cynological organisations have a responsibility to regularly evaluate and (where necessary) modify breed standards to ensure they do not compromise welfare, as well as to educate and train show judges in this aspect.

Handling 'new' diseases

A newly recognised disease may cause a disturbance that is likely to hamper coordinated, collaborative and effective measures, especially when the disease has 'emerged' in a limited or unknown proportion of a breed population. The first step in handling a 'new' disease should be to develop systems for accurate diagnosis and recording. If possible, grading of the disease in more than two categories (i.e. more than affected vs. unaffected) is desirable, because it enhances genetic evaluation (Falconer and Mackay, 1996). Accurate information about a disease underpins analyses of prevalence and mode of inheritance, which then facilitates the development of appropriate breeding strategies. The clinical relevance of the disease must also be considered. It should be emphasised that overly intense selection (i.e. excluding dogs with the 'new' disease, as well as their relatives, from breeding) may be an inappropriate way to manage the situation with respect to the improvement of overall health. Such a practice will most likely also exclude healthy animals from breeding, implying unnecessary reduction of genetic variation and the risk of more clinically relevant diseases emerging as a consequence, especially in numerically small populations.

Breed-specific overall breeding programmes

Many of the major challenges in dog breeding are related to breeding in small populations, combined with a focus on morphological characteristics (McGreevy and Nicholas, 1999). For sustainable breeding of healthy dogs, an overall breeding programme must be developed for each breed. The breeding programme should consider all traits of importance (e.g. health, behaviour and appearance), taking population structure and genetic variation into account. A broadly defined breeding goal is expected to result in a lower rate of inbreeding compared with a limited focus on only a few traits (Sørensen et al., 1999). Monitoring genetic progress and restricting the rate of inbreeding should be components of optimised breeding programmes. Breed-specific health strategies should be based on national populations, regulations and circumstances, but should also involve international collaborations.

Platforms for collaborations

There is a need to coordinate, assemble and critically appraise the information needed to address issues of genetic disease in dogs and make it available to the public in an appropriate format. For effective collaboration on, for example, producing information resources and breeding guidelines, it is essential that key stakeholders develop ongoing partnerships/platforms at national and international levels. After the intense media attention and public scrutiny of issues of disease in purebred dogs, it is important that conferences and workshops are organised where various stakeholders can meet and exchange knowledge, experience and evidence on how to enhance the genetic health of purebred dogs.

Conclusions

Increasing attention to and awareness of health problems in purebred dogs has to be followed by collaborative actions to evaluate and strategically counteract them. Actions should be based on severity, prevalence and inheritance of each problem within

breeds. Strategies regarding recognition of new breeds, health problems related to anatomical features and selection of breeding stock, need to be developed. For effective collaboration on these strategies, key stakeholders should develop platforms at national and international levels.

Conflict of interest statement

None of the authors of this paper has a financial or personal relationship with other people or organisations that could inappropriately influence or bias the content of the paper.

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