Prioritising health in pedigree dog breeding

Tom Lewis
Animal Health Trust

THE KENNEL CLUB
GENETICS CENTRE
AT THE ANIMAL HEALTH TRUST

AHT

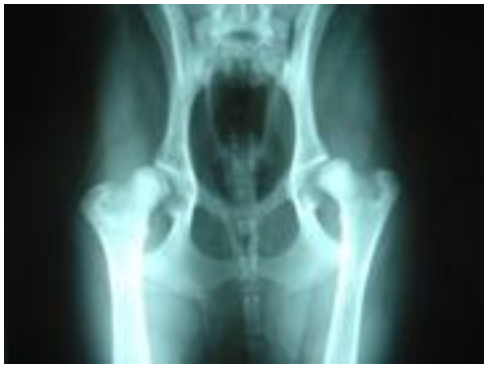
What are the health problems?

Some related to breed standard (e.g. brachycephaly)

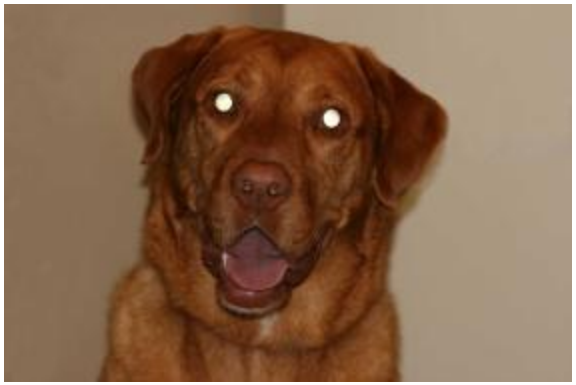
Some (apparently) unrelated to standard (e.g. deafness in sheepdogs)

What are the health problems?

Complex (HD, ED, epilepsy, bloat)



Simple (PRA, PLL, CLAD, copper toxicosis)



What are the health problems?

High levels of inbreeding

‘Line breeding’ to fix traits

Popular sire effects

Selection in dogs & other species

Short term aim → increase gain (ΔG) in selection objective traits

Long term aim → constrain the rate of inbreeding (ΔF)

$$\Delta F = \tfrac{1}{4} \Sigma r_i^2$$ Wray & Thompson, 1990

$$\Delta G = \Sigma r_i a_i$$ Woolliams & Thompson, 1994

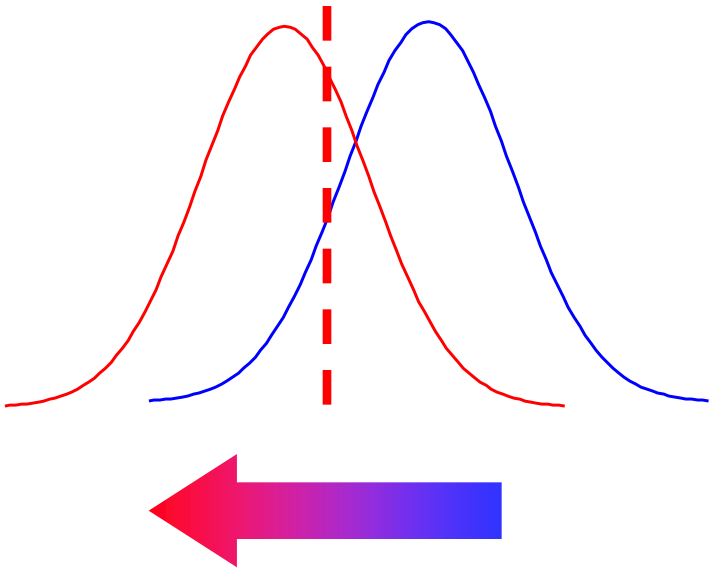
Current selection objectives

Livestock → yield, growth rates, cut costs

Dogs → show winning, field trials, function (sheepdogs, gundogs, guide / assistance dogs, sniffer dogs), pets?

Successful selection requires:

- Motivation → must want to change trait!
- Information → able to differentiate on objective traits
- Control → ability to influence or direct matings



Easy in livestock species

MOTIVATION → profit!

INFORMATION → payment linked to data

CONTROL → large number of animals per farmer

Success in achieving objective is attainable by multiple stakeholders, leading to breed-wide change…

Not so easy for dogs…

MOTIVATION → winning shows, trials, money, hobby?

INFORMATION → by eye, anecdote and experience…

CONTROL → small number of animals per breeder

If objective is showing or profit, then health is a secondary concern. Harder to achieve breed-wide change

Health vs. other breeding objectives

‘Type’

‘Health’

Motivation:	primary objective	secondary objective?
Information:	by ‘eye’?	expensive to collect
Control:	looking for one off → individual	widespread improvement → co-operation

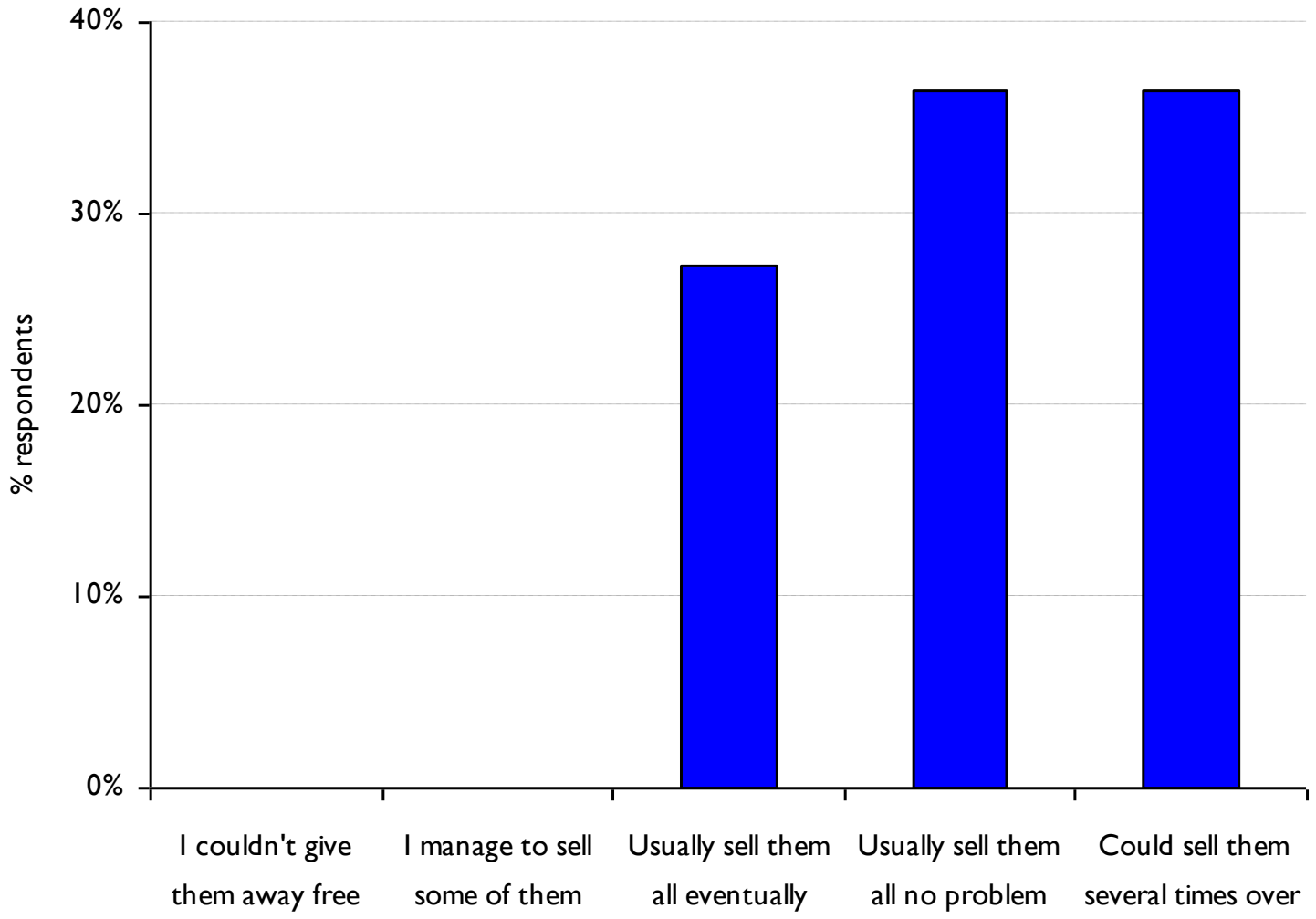
To prioritise health we need to:

1) Foster the MOTIVATION

→ demand differential across litters of puppies destined for pet homes

a) Breeder activities appear to be sensitive to selling all puppies

Breeders rely on being able to sell all puppies



To prioritise health we need to:

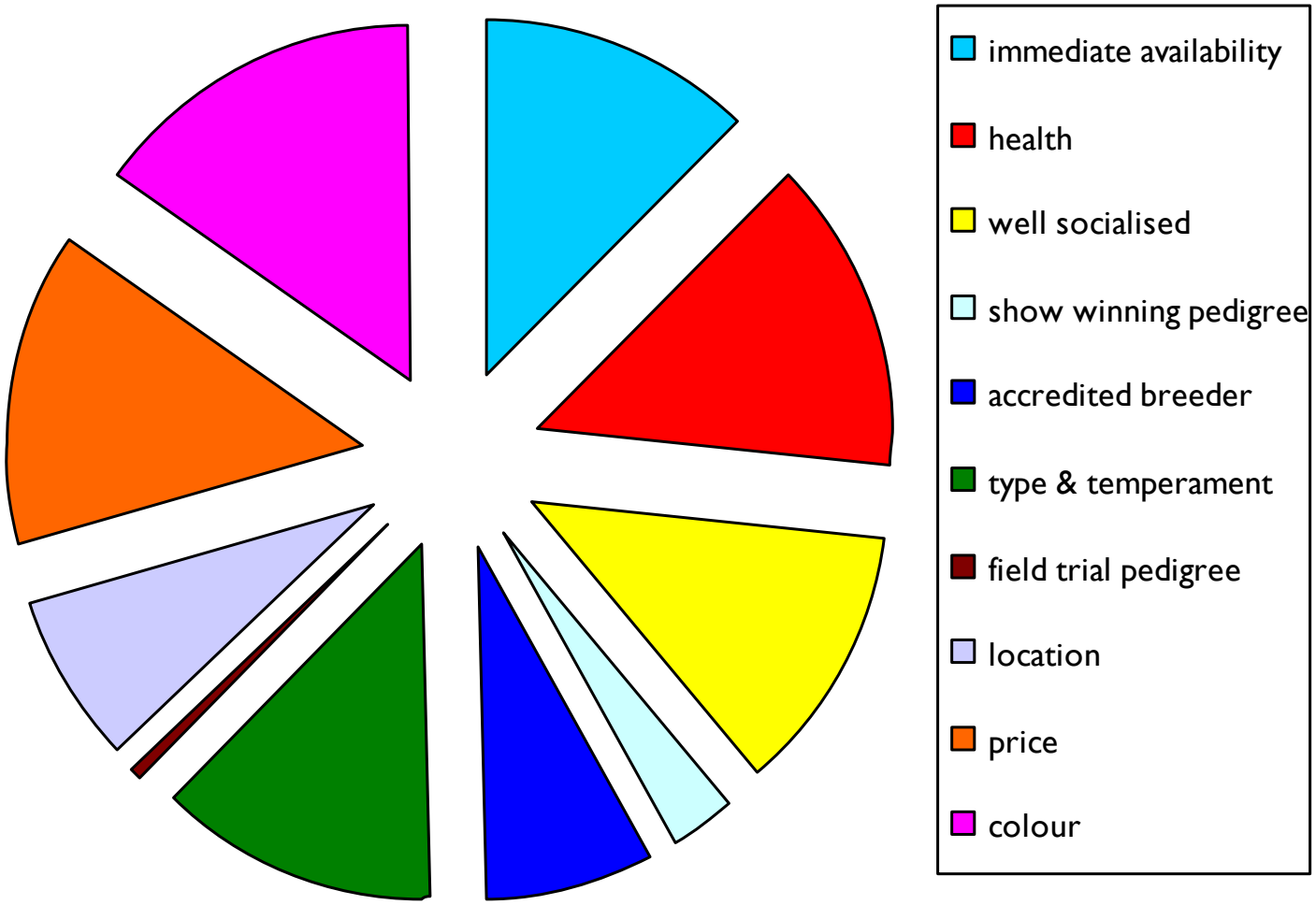
1) Foster the MOTIVATION

→ price differential across litters of puppies destined for pet homes

a) Breeder activities appear to be sensitive to selling all puppies

b) Health appears to be a consideration of puppy buyers

Health is a consideration for buyers…



To prioritise health we need to:

1) Foster the MOTIVATION

→ price differential across litters of puppies destined for pet homes

a) Breeder activities appear to be sensitive to selling all puppies

b) Health appears to be a consideration of puppy buyers

→ consider health in judging at shows

Vet checks at UK dog shows…

Breed: CLUMBER SPANIEL	Dog Name/Exhibit Number: CHERVOOD'S SNOWSUN 8961

Is the dog suffering from any visible condition which adversely affects its health or welfare?

YES ☑ NO ☐

If YES, please give details:

① BILATERAL ECTROPION - PARTICULARLY MARKED. IN ® LOWER LID LEAD TO DIAMOND EYE CONFORMATION. HAS A SECONDARY CONJUNCTIVITIS. RIGHT EYE.

Additional Comments:

UNILATERAL OTITIS EXTERNA RIGHT EAR. - CAUSING ONLY MILD CLINICAL SIGNS NOT SUFFICIENT TO DISQUALIFY

Veterinary Health Check: PASS ☐ FAIL ☑

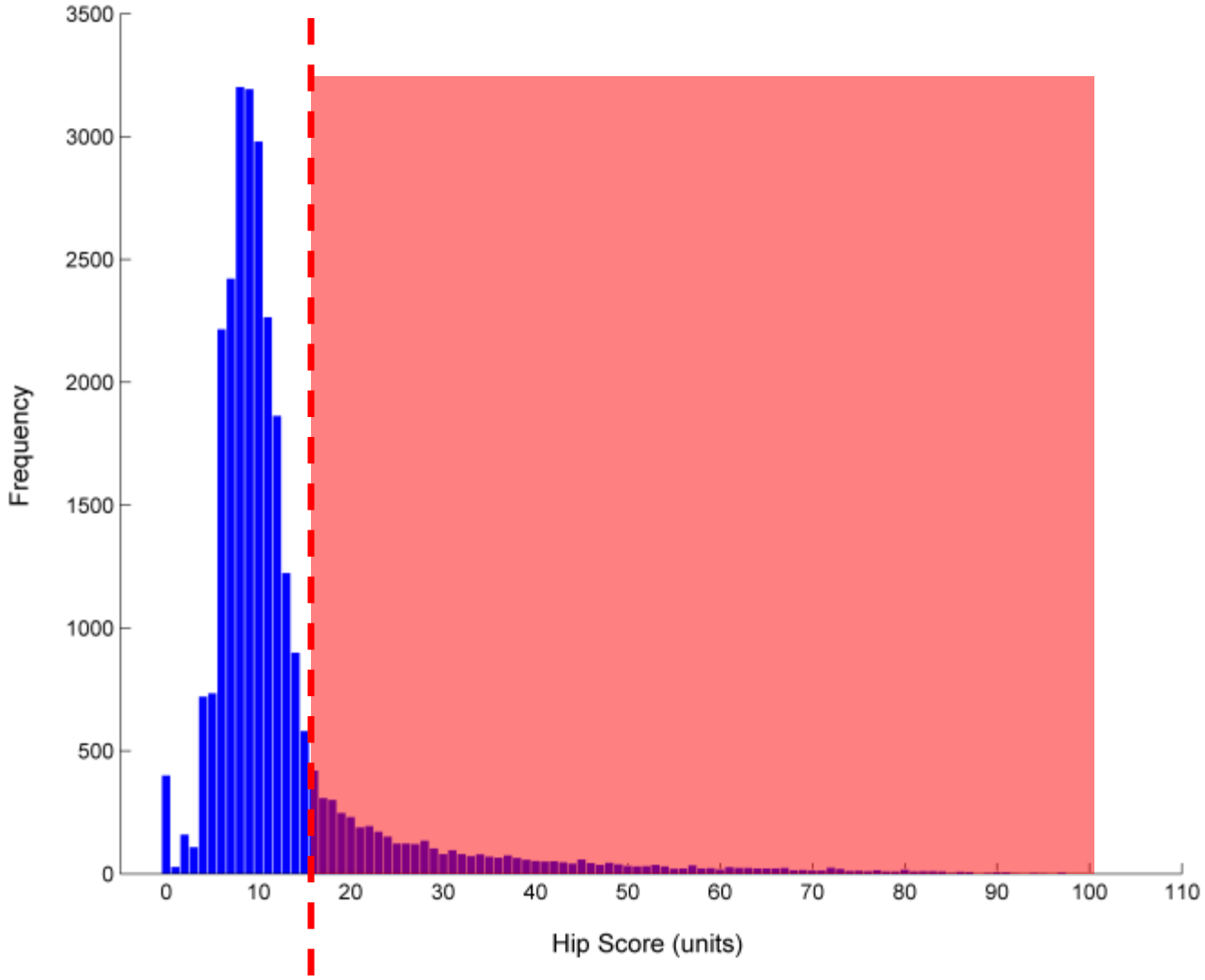
To prioritise health we need to:

1) Foster the MOTIVATION

2) Make better use of the INFORMATION

→ centralised data streaming and co-ordination between authorities

Making better use of INFORMATION



To prioritise health we need to:

1) Foster the MOTIVATION

2) Make better use of the INFORMATION

→ centralised data streaming and co-ordination between authorities

→ EBVs, DNA tests, individual and $\Delta F/\Phi$

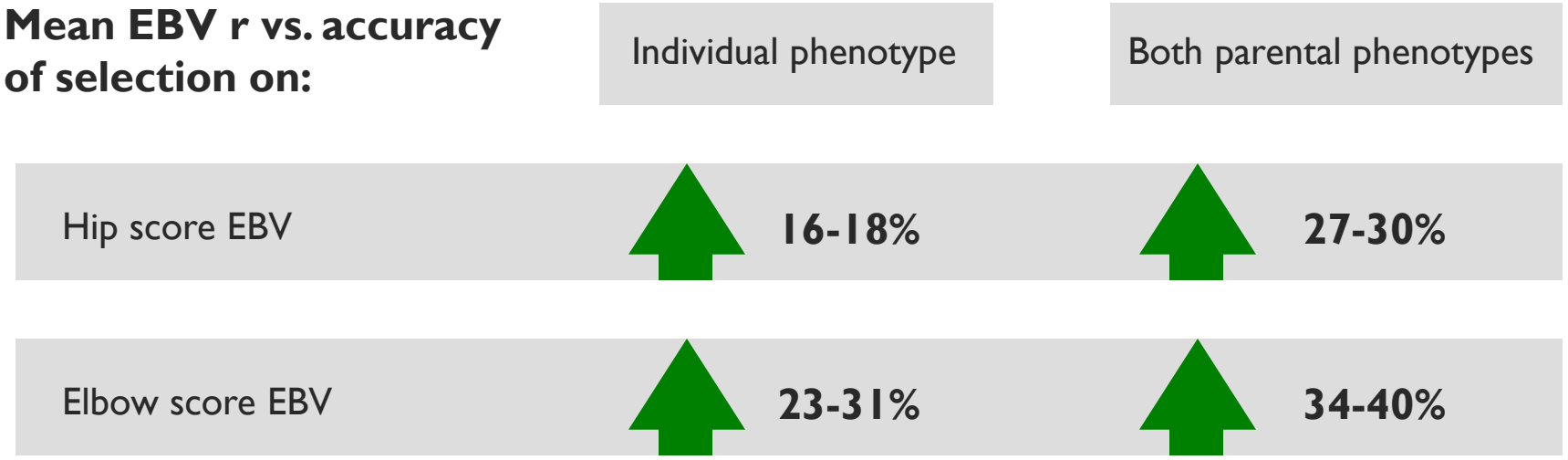
Making better use of INFORMATION

EBVs for HD/ED…

are more accurate

& more abundant

… than phenotype.



Lewis et al (2012) submitted

Making better use of INFORMATION

EBVs for HD/ED…

are more accurate

& more abundant

… than phenotype.

Proportion of 2011 born Labradors:	Both parental phenotypes	Higher EBV accuracy	
Hip score	**0.49**	**0.68**	**1.39**
Elbow score	**0.10**	**0.60**	**5.76**

Lewis et al (2012) submitted

Making better use of INFORMATION

Bivariate analysis of HD and ED:

r_G = 0.4 (Labradors)

Bivariate vs. univariate analysis:

	Elbow & Hip score	Elbow score only	Hip score only
Elbow EBV accuracy	↑ 7-11%	↑ 4-6%	↑ 

	Hip score only	Elbow score only
Accuracy of selection vs. optimum index for improvement in both traits:	↓ 14%	↓ 44%

Lewis et al (2011)

Making better use of INFORMATION

DNA tests … AND breeding strategy advice

The Veterinary Journal xxx (2011) xxx–xxx

Contents lists available at ScienceDirect

The Veterinary Journal

journal homepage: www.elsevier.com/locate/tvjl

Review

Genetic diversity, inbreeding and breeding practices in dogs: Results from pedigree analyses

Grégoire Leroy *

AgroParisTech, UMR 1313, Génétique Animale et Biologie Intégrative, F-75000 Paris, France
INRA, UMR 1313, Génétique Animale et Biologie Intégrative, F-78000 Jouy-en-Josas, France

ARTICLE INFO

Article history:
Available online xxxx

Keywords:
Canine
Inherited disorders
Pedigree analysis
Genetic diversity
Breeding

ABSTRACT

Pedigree analysis constitutes a classical approach for the study of the evolution of genetic diversity, genetic structure, history and breeding practices within a given breed. As a consequence of selection pressure, management in closed populations and historical bottlenecks, many dog breeds have experienced considerable inbreeding and show (on the basis of a pedigree approach) comparable diversity loss compared to other domestic species. This evolution is linked to breeding practices such as the overuse of popular sires or mating between related animals. The popular sire phenomenon is the most problematic breeding practice, since it has also led to the dissemination of a large number of inherited defects. The practice should be limited by taking measures such as restricting the number of litters (or offspring) per breeding animal.

Introduction

Even though the word *pedigree*, which comes from the Old French term '*pié de grue*' (meaning foot of a crane) has been known and employed for centuries, its use on a population scale in dogs began to be developed only at the end of the 19th century with the creation of the first studbooks and kennel clubs. Since then, genealogical registries have proved to be crucial as selection and monitoring tools for breeding. Together with the breed standard, they also represent a key unifying element for breeders of a given breed.

Since a registry is intended to record all the information about known relationships within a given population, it also constitutes a useful source of data for the analysis of genetic diversity and structure of that population. Methods that measure this diversity (and more precisely average inbreeding coefficients) require computing time proportional to population size (Meuwissen and Luo, 1992). As a consequence, the first population studies on dogs were conducted only 20 years ago. Over the same time period, a large set of indicators has been developed for different purposes, such as computation of effective population size, analysis of genetic structure, genetic diversity and increasing the incidence of inherited diseases (Mellersh, 2008). An increasing number of studies has been conducted, either to characterise genetic structure, diversity and inbreeding of canine populations (Karjalainen and Ojala, 1997; Nielen et al., 2001; Cole et al., 2004; Lüpke and Distl, 2005; Leroy et al., 2006, 2009; Calboli et al., 2008; Głażewska, 2008; Oliehoek et al., 2009; Voges and Distl, 2009; Mäki, 2010), or to determine the prevalence of inherited defects (Ubbink et al., 1992, 1998, 1999, 2000; van der Beek et al., 1999; Mäki et al., 2001; Ólafsdóttir and Kristjánsson, 2008; Urfer, 2009; Wellmann and Pfeiffer, 2009; Lewis et al., 2010; Leroy and Baumung, 2011).

The aim of this article is to provide an overview of genealogical studies in dog breeds: (1) to recall the principles, specificities and possible limits of pedigree analyses; (2) on the basis of existing studies, to analyse the situation of dog breeds, with regard to their levels of genetic diversity, their population structure and their breeding practices, especially in relation to dissemination of inherited disorders and inbreeding depression; and (3) to provide recommendations for breeders and kennel clubs for management of diversity and control of inherited disorders.

ANIMAL GENETICS Immunogenetics, Molecular Genetics and Functional Genomics

doi: 10.1111/j.1365-2052.2010.02079.x

Mating practices and the dissemination of genetic disorders in domestic animals, based on the example of dog breeding

G. Leroy*,† and R. Baumung‡

*AgroParisTech, UMR 1313 Génétique Animale et Biologie Intégrative, F-75231 Paris, France. †INRA, UMR 1313 Génétique Animale et Biologie Intégrative, F-78352 Jouy-en-Josas, France. ‡Department of Sustainable Agricultural Systems, University of Natural Resources and Applied Life Sciences, Vienna, Austria

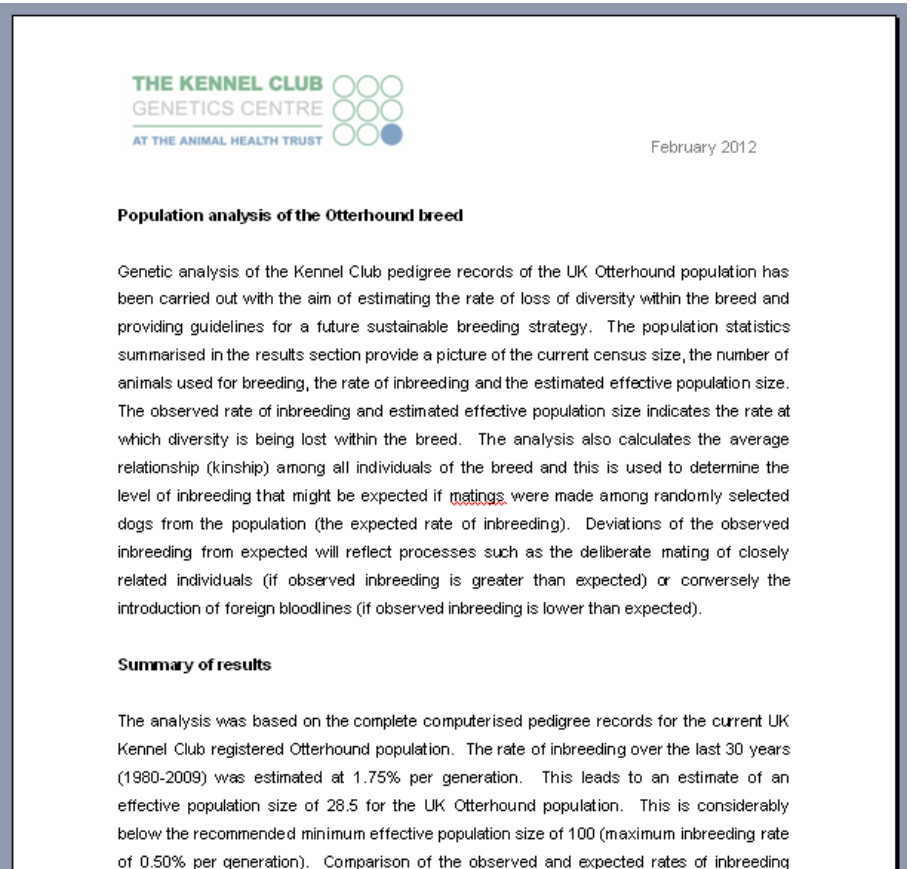
Summary

On the basis of simulations and genealogical data of ten dog breeds, three popular mating practices (popular sire effect, line breeding, close breeding) were investigated along with their effects on the dissemination of genetic disorders. Our results showed that the use of sires in these ten breeds is clearly unbalanced. Depending on the breed, the effective number of sires represented between 33% and 70% of the total number of sires. Mating between close relatives was also found to be quite common, and the percentage of dogs inbred after two generations ranged from 1% to about 8%. A more or less long-term genetic differentiation, linked to line breeding practices, was also emphasized in most breeds. F_{IT} index based on gene dropping proved to be efficient in differentiating the effects of the different mating practices, and it ranged from −1.3% to 3.2% when real founders were used to begin a gene dropping process. Simulation results confirmed that the popular sire practice leads to a dissemination of genetic disorders. Under a realistic scenario, regarding the imbalance in the use of sires, the dissemination risk was indeed 4.4 times higher than under random mating conditions. In contrast, line breeding and close breeding practices tend to decrease the risk of the dissemination of genetic disorders.

Keywords dog, genetic disorders, mating practice, simulations.

Making better use of INFORMATION

Breed reports



THE KENNEL CLUB GENETICS CENTRE
AT THE ANIMAL HEALTH TRUST

February 2012

Population analysis of the Otterhound breed

Genetic analysis of the Kennel Club pedigree records of the UK Otterhound population has been carried out with the aim of estimating the rate of loss of diversity within the breed and providing guidelines for a future sustainable breeding strategy. The population statistics summarised in the results section provide a picture of the current census size, the number of animals used for breeding, the rate of inbreeding and the estimated effective population size. The observed rate of inbreeding and estimated effective population size indicates the rate at which diversity is being lost within the breed. The analysis also calculates the average relationship (kinship) among all individuals of the breed and this is used to determine the level of inbreeding that might be expected if matings were made among randomly selected dogs from the population (the expected rate of inbreeding). Deviations of the observed inbreeding from expected will reflect processes such as the deliberate mating of closely related individuals (if observed inbreeding is greater than expected) or conversely the introduction of foreign bloodlines (if observed inbreeding is lower than expected).

Summary of results

The analysis was based on the complete computerised pedigree records for the current UK Kennel Club registered Otterhound population. The rate of inbreeding over the last 30 years (1980-2009) was estimated at 1.75% per generation. This leads to an estimate of an effective population size of 28.5 for the UK Otterhound population. This is considerably below the recommended minimum effective population size of 100 (maximum inbreeding rate of 0.50% per generation). Comparison of the observed and expected rates of inbreeding

Population Analysis Results

Breed	Otterhound
*Average no. KC registrations/year	44.3
Estimated census size	450
No. sires used/year	7.5
No. dams used/year	8.2
Mean no. dams/sire	1.09
Maximum no. offspring (sire)	43
Maximum no. offspring (dam)	28
Mean no. offspring/sire	6.92
Mean no. offspring/dam	6.11
Generation interval (sire) in years	4.52
Generation interval (dam) in years	4.24
Average inbreeding coefficient	0.114
Average kinship coefficient	0.142
Estimated rate of inbreeding (per year)	0.40%
Estimated rate of inbreeding (per generation)	1.75%
Estimated effective population size (Ne)	28.5

*All statistics are estimated based on dogs born between the years 1980-2009. Inbreeding calculations utilise all recorded pedigree information, including that recorded prior to 1980.

To prioritise health we need to:

1) Foster the MOTIVATION

2) Make better use of the INFORMATION

3) Disseminate information to allow CONTROL

→ make it easy to do via publically available tools

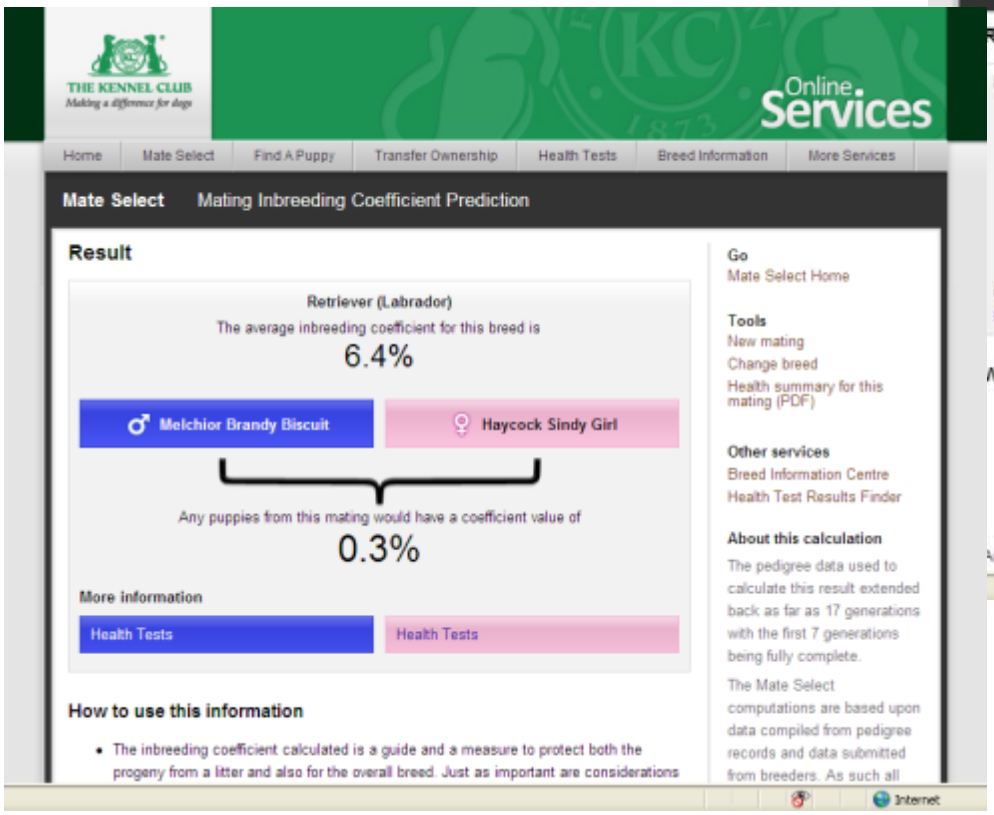
→ breeders can access indicators made using all data (for ΔG and ΔF)

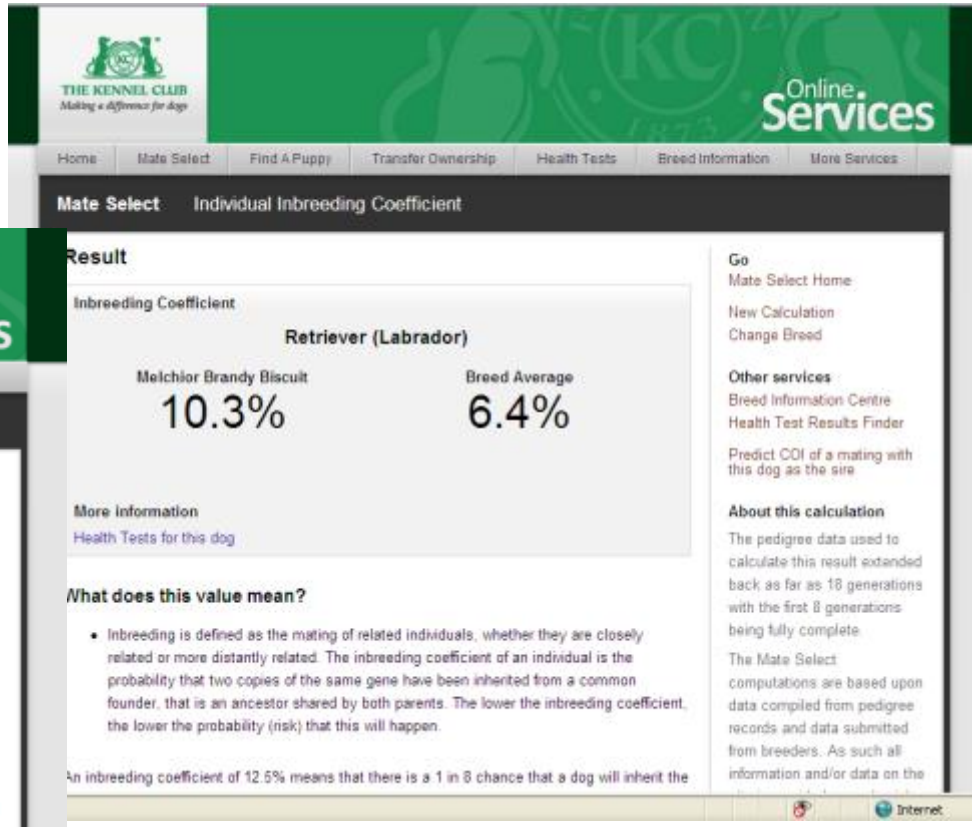
→ pet owners can do the same (influencing demand for puppies)

→ restrictions on registration, or 'nudge' towards doing the right thing

Disseminate information to allow CONTROL

Publication of inbreeding levels





Acknowledgements

Dr Sarah Blott

Prof John Woolliams

The UK Kennel Club (Prof Jeff Samson)

The British Veterinary Association