

## Unnatural Selection: Breeding Practices in Pedigree Dogs

*Discusses mechanisms responsible for disseminating inherited diseases in pedigree dogs and examines the tools available to improve the health and welfare of those breeds most severely affected.*

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### Introduction

Arguably, selecting for aesthetic traits in dogs started with the founding of the UK Kennel Club and implementation of a set of breed standards that acted as guidelines to describe the ideal characteristics, temperament and appearance of each breed. These standards encouraged breeders to move toward particular morphological types and failed to take into account negative health consequences arising from alterations to anatomy that were the result of thousands of years of natural selection. Consequently, breeding practices tend to focus on a few individuals perceived as desirable, which has compromised the genetic status of each breed, with dogs now having more than 1000 known inherited conditions (Mellersh, 2008). This paper examines the effects of breeding practices on the health and welfare of pedigree dogs and suggests strategies to improve life quality for future generations.

### Discussion

What mechanisms are at work and what evidence do we have that contemporary breeding practices are perpetuating inherited disorders? Leroy and Baumung (2011) examined the effect of three popular mating practices on pedigree dog breeds: popular sire, line breeding, and close breeding. First, the study aimed to evaluate the prevalence of these breeding practices in 10 breeds, based on genealogical data from the French Kennel Club (n=80,785). Second, they examined the effects of these breeding practices on the dissemination rate of deleterious alleles, using simulations following Mendelian segregation rules. Simulations were carried out using an autosomal recessive mode of inheritance. Of those diseases with known modes of inheritance, two thirds are passed to offspring by autosomal recessive means (Patterson, 2000).

Use of popular sires in the genealogical data from the French Kennel Club was observed and confirmed. The effective number of breeding sires represented between 33-77% of the total number of sires in the study (Leroy & Baumung, 2011). The use of close breeding was quite common, with 1% to 8% of dogs being inbred after two generations (Leroy & Baumung, 2011). Simulation results confirmed that the popular-sire practice leads to a dissemination of recessive genetic disorders. The dissemination rate was 4.4 times higher than random mating, providing evidence for a single mechanism allowing the continued spread of inherited diseases (Leroy & Baumung, 2011).

Conversely, line breeding and close breeding tended to decrease the risk of dissemination (Leroy & Baumung, 2011), since backcrossing and inbreeding of individuals with lethal recessive alleles results in an increased proportion of homozygous recessive progeny and removal of these alleles from the population (Leroy & Baumung, 2011). The death of such progeny, highlights important animal welfare consequences for individual animals when these practices are employed. Furthermore, line breeding and close breeding reduces the genetic diversity of a population and negatively impacts on its overall fitness.

Leroy & Baumung's (2011) study examined single-gene disorders with a recessive mode of inheritance, but what about more complex multifactorial diseases? These can be examined by investigating syringomyelia (SM) in Cavalier King Charles spaniels (CKCS). Knowler *et al.* (2011) sought to identify the prevalence of SM in CKCS in a known population and evaluate if breeding guidelines set out by Cappello & Rusbridge (2007) are appropriate. These guidelines identify CKCS for breeding suitability based on age, presence of clinical signs associated with SM and presence of SM detected by MRI. Animals were ranked using an alphabetical system based on these parameters and assigned as either A, C, D, E or F.

In this study 550 CKCS were identified as having one (392) or both parents (158) with a confirmed SM status. Offspring classed grade A, that is dogs over 2.5 years with no SM signs, generally occurred only when there was at least one grade A parent (Knowler *et al.*, 2011). Offspring from dogs with at least one parent over 5 years with no MRI-identified SM, had an even greater chance of being SM-free (Knowler *et al.*, 2011). Furthermore, no offspring from two parents over 5 years without SM were found to have SM (Knowler *et al.*, 2011). Conversely, offspring with SM were more likely when both parents had SM (92%), but even one SM-affected parent increased the probability of SM-affected offspring (77%) (Knowler *et al.*, 2011). These findings highlight the heritability of complex debilitating diseases and the importance of screening for these diseases. Great care must be taken when selecting breeding individuals.

An objective measure is required to quantify the impact of pedigree dog diseases and to identify breeds most at risk and diseases with greatest impact on health and welfare. Collins *et al.* (2011) outlined one such method, improving

upon the existing generic illness severity index for dogs (GISID) (Asher *et al.*, 2009). Augmentation of the GISID by Collins *et al.* (2011) resulted in the breed-disorder welfare impact score system (BDWIS). This is calculated taking into consideration the prevalence and severity of a disease, and adjusting for the proportion of the animal's life affected by the disease.

Collins *et al.* (2011) outlined a process that could be implemented once breeds and disorders have been identified, to improve health and welfare. One limitation in applying the BDWIS is the lack of prevalence data to use for calculations. Only 1% of data is available for each of the 396 disorders in the 50 most popular breeds (Collins *et al.*, 2011). Future research should focus on gathering data for these conditions. Once collected and reliable BDWIS scores are obtained, we can focus on those breeds and conditions that have received the highest scores. This will result in the biggest improvement in health and welfare for those dogs most severely afflicted.

## Conclusions

Resolving the issues involved in pedigree-dog breeding is multifaceted and complex. Veterinarians must work with breeding organisations to move away from detrimental breeding practices and toward programs that value health and welfare. Careful consideration must be taken when altering breeding practices in order not to further negatively impact the genetic diversity of each breed. Sound science should be used to convince breeding organisations and the public that we need change to achieve a future of improved health and welfare for dogs.

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