

## Building effective systems to manage inbreeding in pedigree dog breeds

T. W. Lewis<sup>1</sup>, S. C. Blott<sup>1,2</sup>, D. M. Howard<sup>3</sup>, and J. A. Woolliams<sup>3</sup>.

<sup>1</sup>Kennel Club Genetics Centre, Animal Health Trust, Suffolk; <sup>2</sup>School of Veterinary Medicine and Science, University of Nottingham; <sup>3</sup>The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

**ABSTRACT:** A new approach to delivering advice on inbreeding in pedigree dog populations is developed by tracking the relative importance of components of the sum of squared genetic contributions. Using pedigree data from 12 dog breeds, contributions of animals born in 1990 to animals born in subsequent years (1991 to 2012) were calculated. The proportion of variance attributable to the mean, the regression of ‘final’ on ‘current’ contributions and the residuals were plotted using barycentric coordinates showing the relative importance of each. Results showed that variance due to regression, indicating the predictive ability of ‘ultimate’ by ‘early’ contributions, was increasingly predominant over time. Differences in the rate that this occurred were apparent across sexes and breeds. Results indicate that it is feasible to both make reasonable predictions of ultimate contributions and at what ages such predictions become useful, and to develop a dynamic tool for informing breeders using this approach.

**Keywords:** genetic contributions; inbreeding; dogs

### Introduction

Managing the rate of inbreeding ( $\Delta F$ ) in pedigree dog breeds is a major challenge for breeders and population geneticists. Many such breeds have a small census size predisposing them to greater rates of inbreeding and the populations are also subject to strong influences of fashion in breeding for particular types. These influences reduce the effective population size ( $N_e = [2\Delta F]^{-1}$ ) of numerically large breeds and makes numerically small breeds smaller in  $N_e$ . The genetic risks to a population increase as  $\Delta F$  increases; increasing the magnitude of inbreeding depression that might be observed, and increasing the probability that deleterious recessive alleles will appear at a sufficient frequency to create problems for the breed.

When the breeding pyramid is controlled by a single organization, as may happen in livestock with major breeding companies or in zoo populations, the problem of managing  $\Delta F$  has effective solutions that have been well studied. This is often using algorithms akin to optimum contributions (Meuwissen (1997)) which deliver maximum genetic gain within the constraint of a specified  $\Delta F$ , or simply minimize  $\Delta F$  within other constraints. However these solutions rely on an ‘optimum selection’ among candidates being implemented. In populations such as pedigree dogs this cannot be delivered as control is shared amongst many independent, perhaps competitive, decision makers. Therefore it is only possible to provide guidance and promote awareness of the problem. Typically this

advice is concerned with giving inbreeding coefficients of potential offspring, or giving the average relationship of an individual with the population. Whilst both of these will influence the inbreeding coefficient of an offspring, which may help reduce the immediate impact of inbreeding depression, *neither* of these will help to reduce  $\Delta F$  and increase  $N_e$ .

Here we outline a system for guidance on breeding that directly addresses reductions in  $\Delta F$ . This is based upon long term genetic contributions ( $r_i$ , for individual  $i$ ) which have been shown to be related to the rate of inbreeding (Wray and Thompson (1990); Woolliams and Thompson (1994)):  $\Delta F = \frac{1}{4} \sum r_i^2$ . Therefore, monitoring genetic contributions allows prospective identification of breeding decisions that will result in a high  $\Delta F$ , by identifying proposed matings that increase the contributions of individuals that are already considered to be over-represented. However, for this strategy to be successful it is necessary to determine to what extent early genetic contributions predict long term genetic contributions, since identifying popular sires as soon as possible is crucial. The objectives of this study are therefore to use historical pedigree information from UK registered dog breeds to determine how predictable long term genetic contributions are both during and after breeding life.

### Materials and Methods

**Data.** Pedigree data was supplied by the UK Kennel Club for 12 dog breeds varying in absolute and changing census size (Border Terrier [BT], Bulldog [BD], Cairn Terrier [CT], smooth coat Chihuahua [CH], Cavalier King Charles Spaniel [CK], miniature long haired Dachshund [DA], French Bulldog [FB], Irish Setter [IS], Pointer [PT], standard Poodle [PD], Scottish Terrier [ST], Shih Tzu [SH]).

**Calculation of genetic contributions.** Mean genetic contributions of breeding animals born in a single calendar year ( $t_0 = 1990$ ) to cohorts of animals born in subsequent years ( $t = 1991 \dots 2012$ ) were calculated. Mean genetic contributions of individual  $i$  to the cohort at time  $t$ , are denoted  $r_i(t)$  and contributions to the final cohort at  $T = 2012$ , i.e. the ‘final’ genetic contributions after 22 cohorts, are denoted  $r_i(T)$ . This was done for each breed.

**Statistical analyses.** For each breed and each sex, the sum of squared ‘final’ contributions  $\sum r_i(T)^2$  was then decomposed by linear regression of  $r_i(T)$  on  $r_i(t)$ . This

decomposition was repeated progressively for  $t = t_0+1, t_0+2 \dots T$ . The linear regression model was

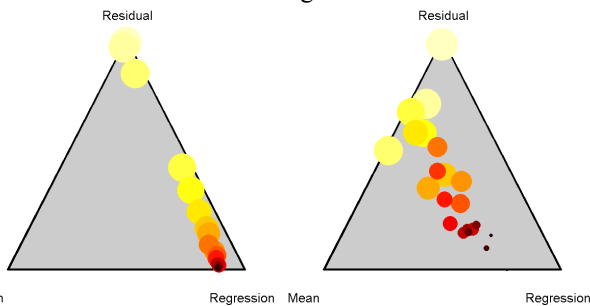
$$r_i(T) = \bar{r} + \beta [r_i(t) - \bar{r}] + \varepsilon \quad (1)$$

where  $\bar{r}$  is the mean contribution of the  $n$  individuals of that breed and sex which became parents of registered offspring,  $\beta$  is the regression coefficient and  $\varepsilon$  the residual. This decomposes  $\Sigma r_i(T)^2$  into components: ‘Mean’,  $n\bar{r}^2$ ; ‘Regression’,  $\beta^2 \Sigma [r_i(t) - \bar{r}]^2$ ; and ‘Residual’,  $\Sigma \varepsilon^2$ .

The components in contributions due to Mean, Regression and Residual were scaled to sum to one by division by  $\Sigma r_i(T)^2$ . The relative importance of each variance component was then plotted using barycentric coordinates (Kearsley et al. (2008)) to show the relative importance of Mean, Residual and Regression components as they develop over time. It should be noted that because genetic contributions converge it would be expected that the Residual component should diminish over time as the correlation of  $r_i(t)$  and  $r_i(T)$  increases and the partition becomes dominated by Mean and Regression.

## Results and Discussion

**Trends in variance components.** For both sexes and in all breeds, the variance in genetic contributions due to Regression became the major component of  $\Sigma r_i(T)^2$ . The minimum final (at  $T$ ) fraction explained was 0.77 in female PT, and the maximum was 0.96 in female CK. In the barycentric plots shown (see Figure 1) the Mean and Regression partition is at the base of the triangle and the progression towards the base over time is clearly observed. In all breeds and in both sexes the trend was for  $\Sigma r_i(T)^2$  to be dominated initially by Residual, and to become dominated by Regression. This is indicative of the widely differential usage of breeding animals, since if all breeding animals were used equally the total variance would be dominated by Mean and the barycentric plots would show a path confined to the left hand side of the triangle.

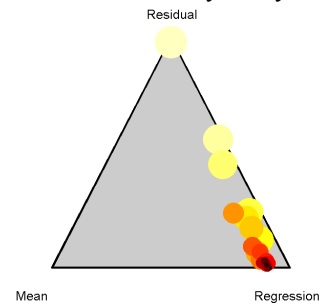


**Figure 1a(left) and 1b (right): Barycentric plots indicating the composition of  $\Sigma r_i(T)^2$  of breeding animals born in 1990 to cohorts of animals born in each of the 22 following years. Circles decrease in size and darken in color with each year since 1990. The development of contributions for BT males (left) shows rapid predominance of variance due to Regression, indicating early contributions are predictive of long term genetic contributions. The development of contributions in Pointer females (right) shows a greater**

## influence of Mean and Residual indicative of more equal usage and random deviation in contributions.

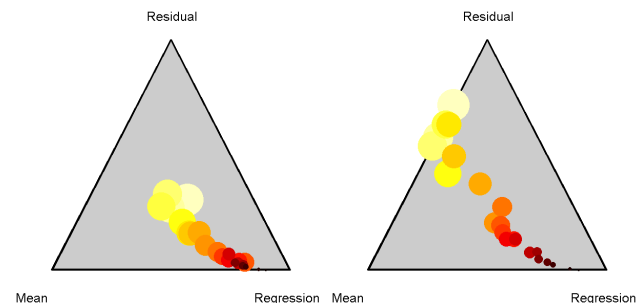
**Rate of development of regression variance.** The rate at which Regression came to dominate  $\Sigma r_i(T)^2$ , was more variable than the directional trend. In male PT the Regression variance component rose quickly, reaching 0.71 of  $\Sigma r_i(T)^2$  four years after birth and 0.81 in the fifth year (Figure 2). In contrast the female PT had the slowest rate of progression with just 0.27 of  $\Sigma r_i(T)^2$  comprised of Regression at 12 years after birth (Figure 1b). This indicates that while early years contributions are a reliable indicator of long term genetic contribution of males in this breed, this is not true of females to the same extent.

The height in the triangle represents what fraction of the  $\Sigma r_i(T)^2$  is predictable, i.e. from the Mean and Regression components. So predicting, say, 50% of  $\Sigma r_i(T)^2$  is signified as the path progresses into the bottom half of the barycentric plot. Thus examination of figures 1 and 2 reveals at what age for each breed and sex depicted a reasonable prediction of ultimate contributions may be made. In males this can be as early as 4 years.



**Figure 2: Barycentric plots for PT males, which displayed the quickest progression in the proportion of  $\Sigma r_i(T)^2$  due to Regression.**

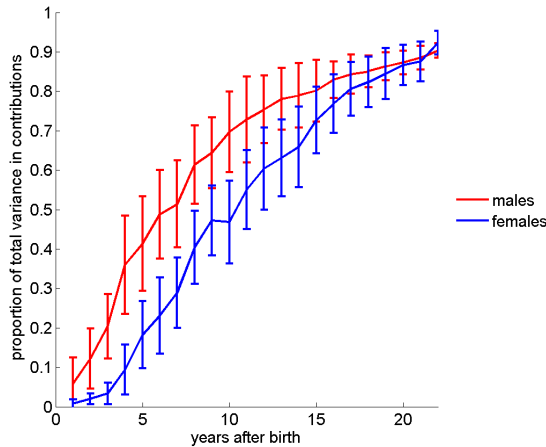
Interestingly the plots for FB show Mean having a greater influence over  $\Sigma r_i(T)^2$  in early years (Figure 3). This breed has undergone a rapid recent expansion in census size - prior to 2006 the mean number of registered animals was 260.25 (+/-63.15), but registrations have risen steadily since to 4931 in 2012. The sudden popularity of the breed may have been accompanied by a change in breeding practice which has resulted in this characteristically different profile.



**Figure 3: Barycentric plots for FB (males left, females right). The plots for this breed were characteristically different from all other breeds in the greater influence**

of Mean in early years, possibly due to changes in breeding practice which accompanied a rapid population expansion since 2005.

**Differences due to sex.** The average proportion of  $\sum r_i(T)^2$  attributable to Regression over years for males and females separately (across all breeds) is shown in Figure 4. The proportion is generally higher in males between 2 and 10 years after birth. Beyond this, the difference between the sexes diminishes, and disappears at approximately 20 years after birth. This result indicates that the ranking of contributions of males to animals born 2-10 years is more consistent than for females.



**Figure 4.** Plot of the mean proportion of  $\sum r_i(T)^2$  comprised of Regression for males (red) and females (blue) across all 12 breeds (error bars = 1.96 x standard deviation).

The component of  $\sum r_i(T)^2$  arising from males is also greater in most breeds. Table 1 shows the proportions of the total sum of squared contributions  $\sum r_i(T)^2$  from males and females in all 12 breeds. For most breeds  $\sum r_i(T)^2$  from males exceeds that of females;  $\sum r_i(T)^2$  are approximately equal across sexes in just three breeds (CT, DA and PD) and are greater from females in only one breed (ST, 0.57 from females vs. 0.43 from males). The imbalance in favor of males is in some cases quite large, for example in PT 0.928 of  $\sum r_i(T)^2$  comes from males and just 0.072 from females. Thus, while the predictability of female contributions in PT appears poor (Figure 1b) relative to males (Figure 2), the influence of PT females in determining  $\Delta F$  is dwarfed by that of PT males. It is the differential usage of males in this breed that drives  $\Delta F$ .

**Table 1.** Proportions of sum of squared contributions ( $\sum r_i(T)^2$ ) from males and females.

Breed	Proportion of sum of squared contributions	
	Males	Females
BT	0.583	0.417
BD	0.793	0.207
CT	0.513	0.487
CH	0.764	0.236
CK	0.782	0.218
DA	0.520	0.480

FB	0.828	0.172
IS	0.899	0.101
PT	0.928	0.072
PD	0.486	0.514
ST	0.431	0.569
SH	0.646	0.354

**Challenges of implementation.** Whilst the results show some variation in the development of contributions across breeds, they imply that it is feasible to make reasonable predictions of contributions and inform at what age such predictions may be made for each breed. However in addition to the examination of a single cohort considered here (1990), there is a need to ensure reasonable consistency in the patterns of contributions across cohorts. Further development will require flagging scenarios where the current profile of contributions is predicting a risk of high  $\Delta F$  in a way that may have an impact on the actions of breeders. Flagging of contributions may take two forms: (i) an indication of whether the number of breeding individuals is adequate to maintain a sustainable  $N_e$  and an encouragement to recruit new breeders; (ii) an indication of over-representation that might be predicted to lead to an unsustainable  $N_e$ . It is not sufficient to indicate concerns over contributions of the current cohort of active breeding individuals, and it will be necessary to flag matings that promote the contributions of older dogs and bitches that are already considered to be over-represented. These steps will require planning of the appropriate thresholds to achieve sustainable  $N_e$ . Whilst this provides relevant information for breeders to decelerate inbreeding, it does not (and cannot) assure that breeders respect recommendations.

## Conclusion

The results presented show the challenges inherent in devising a strategy to manage  $\Delta F$  in pedigree dog breeds. Not only are the breeds under the control of many independent decision makers, but the population parameters vary significantly from breed to breed and over years. Nevertheless, we have shown that monitoring genetic contributions has the potential to offer valuable guidance on the management of  $\Delta F$  and reduce the problems often associated with dwindling  $N_e$  that is observed in some dog breeds. We have demonstrated that such guidance will be most pertinent to managing breeding males, since male long term genetic contributions are more reliably predicted from contributions to animals born 2-8 years later than themselves than for females. Also in most breeds males contribute more to driving  $\Delta F$ .

## Literature Cited

- Kearsley, C. G. S., Woolliams, J. A., Coffey, M. P. et al. (2008). *Livestock Sci.* 118:72-81.  
 Meuwissen, T. H. E. (1997). *J Anim Sci.* 75:934-940.  
 Woolliams, J.A., and Thompson, R. (1994). 5th World Congress on Genetics Applied to Livestock Production. 19: 127-134.  
 Wray, N. R., and Thompson, R. (1990). *Genetical Res.* 55:41-54.