

# Estimation of effective population size using bivariate discrete distributions for modeling family size in beef cattle

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Received 3 January 2007; received in revised form 5 November 2007; accepted 8 November 2007

## Abstract

Pedigree records of 72,808 animals (45,668 females and 27,140 males) from the genetic evaluation program of the Argentine Brangus Association were used to estimate effective number of founders ( $N_f$ ), effective number of ancestors ( $N_a$ ), and effective population size under random mating ( $N_e$ ) or selection ( $N_{eS}$ ), in order to assess genetic variability. The average level of completeness of the pedigree was low (0.17) and the average level of inbreeding ( $F$ ) calculated from the pedigree was equal to 0.24%. Animals in the reference population were 21,662 calves born from 2001 to 2005. The estimated measures of variability were  $N_f=765.7$  and  $N_a=387.5$ . The numbers of ancestors responsible for 100%, 50%, or 20% of the genes in the reference group, were equal to 12,471, 273, and 22, respectively. Direct estimates of  $N_e$  and  $N_{eS}$  were calculated using the variances and covariances of family sizes, i.e. male and female progeny numbers for bulls and cows. Estimates of the dispersion parameters were from the Bivariate Poisson model for the cows, and from the Generalized Bivariate Negative Binomial (GBIVARNB) distribution for the bulls. The latter probability mass function accounted for overdispersion, a characteristic present in the sampling distribution of family size of bulls. The estimated variances of male and female progeny and the covariance between them for the bulls were 5.70, 271.28, and 30.15, respectively, and 1.15, 2.10, and 1.06 for the cows. Generation intervals (in years) were: sires of bulls=5.0, sires of cows=5.7, dams of bulls=4.4, and dams of cows=5.2. The estimated  $N_e$  was 274, which corresponds to a rate of inbreeding ( $F$ ) of 0.18%, whereas  $N_{eS}=125$  and  $F=0.40\%$ . As a check of the proposed methodology, all analyses were also performed using the pedigree records of 10,483 Angus animals from a herd with an average level of completeness of 0.68. Using the GBIVARNB model for both bulls and cows the estimated  $N_e=95.4$ , thus  $F=0.5\%$  in perfect agreement with the calculated average inbreeding from pedigree records. Under selection,  $N_{eS}=79.3$  and  $F=0.6\%$ . The larger difference between estimated  $N_e$  and  $N_{eS}$  in the Brangus was related to the smaller bull to cow ratio in the breed. Therefore, it seems desirable to continue monitoring the effective size of the Argentine Brangus to prevent problems of inbreeding and lack of variability in the future.

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**Keywords:** Brangus; Effective population size; Family size; Bivariate discrete distributions; Overdispersion; selection

## 1. Introduction

In order for a composite breed not to dissipate the initial advantage of increased heterozygosity by becoming inbred, it is essential that heterozygosity (heterosis)

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be retained by maintaining an effective population size ( $N_e$ ) sufficiently large (Gregory et al., 1993). Also, Hill (2000) observed that for a trait with heritability 1/3, (for example weaning weight in beef cattle), a value of  $N_e=250$  is required to maintain the additive variance at its initial value. The Brangus breed is the largest composite population of beef cattle in the subtropics of Argentina. Since its creation in 1978, the Argentinean Brangus Breeders Association (AAB) has kept an open registry policy to maintain high levels of variability and to retain a high level of heterosis. The initial motivation for the research presented here was to quantify what is the current level of genetic variability, and to evaluate the pedigree structure of Brangus in Argentina.

Estimation of the  $N_e$  when pedigree records are available, can be accomplished indirectly by calculating the change in inbreeding ( $\Delta F$ ) since the breed formation, and then solving the expression  $\Delta F=1/(2N_e)$  (Wright, 1931). However, this estimate is affected by the level of completeness in the pedigree, which causes underestimation of inbreeding (Miglior and Burnside, 1995; Lutaaya et al., 1999; Cassell et al., 2003). There is an extensive literature on direct calculation of  $N_e$  (see the review by Caballero, 1994) and several formulae are available depending on the assumptions of the data at hand. Hill (1979) obtained an expression for  $N_e$  that takes into account overlapping generations and the structure of the mating system through the variances and covariances of progeny numbers, or family sizes. In case of selection, the expression by Hill (1979) does not account for inherited selective advantage, i.e. the process by which the progeny from selected parents tend to have larger family size than those offspring from parents with smaller family size. Based on Santiago and Caballero (1995), Nomura (1996) derived an expression for  $N_e$  in selected populations with overlapping generations.

It is frequently assumed that the random variable family size in different animal species follows a Poisson distribution (Harris and Allenford, 1989; Goddard and Smith, 1990; Caballero, 1994; Joshi et al., 1999) in which mean and variance are equal. This assumption is unlikely to be fulfilled for most farm animal species where a small group of sires have a large contribution to the progeny pool. This, in turn, may induce overdispersion from a Poisson probability mass function. In addition, the family sizes of sires and dams in the formulae of Hill (1979) and Nomura (1996) require a bivariate specification, so that the covariance of male and female progeny numbers for both bulls and cows can be calculated. Possible discrete bivariate distributions for family sizes are the Bivariate Poisson (BP) and the Generalized Bivariate Negative Binomial (GBI-

VARNB, Gurmu and Elder, 2000). Both distributions account for correlations between male and female progeny numbers, but only the GBIVARNB takes overdispersion into account. The goals of this research are threefold: 1) to evaluate the pedigree structure through the effective number of founders ( $N_f$ ), and the effective number of ancestors ( $N_a$ ); 2) to estimate the (co) variances of family sizes of bulls and cows using either the BP or the GBIVARNB distribution to account for overdispersion, and 3) to estimate  $N_e$  using the (co) variances from the previous step. In doing so we used the data from purebreds and grades from the genetic evaluation program of the Brangus breed in Argentina. As a control population for the proposed methodology, we analyzed an Angus herd that has a more complete pedigree information than the Brangus breed.

## 2. Methods

### 2.1. Data

Data used for the study consisted of the pedigree records from 72,808 animals (45,668 females and 27,140 males) supplying records to ERBra, the genetic evaluation program of AAB. The animals were born from 1959 to 2005, most of them in Argentina but with some individuals originated in USA, Brazil or Bolivia. A large number of Brangus animals included in the ERBra are grades, which usually lack either sire or dam identification. The number of participating herds in 2005 was 56, from which 17 produce both purebred and grade animals whereas the rest raise grade cattle only. It is estimated that more than 75% of all purebred and grade Brangus animals participate of the ERBra. Most herds register both purebreds and grades, with a ratio of about 1:5. The AAB keeps the registry for the grades, whereas the national association of cattlemen keeps the herdbook for the purebreds of all breeds including the Brangus. Since its beginning in 1978, the AAB has kept an open policy of registering grade animals in order to maintain a high level of variability, and to retain the maximum possible levels of heterosis between Angus and Zebu cattle. Selection policies in the breed have resulted in the most popular bull sires being born in Argentina. Two herds are involved in an active embryo transfer program from a US based cattle company and register animals born locally but out of US parents. The total fraction of calves that are born to US bulls, either by embryo transfer or by artificial insemination, is about 3%.

The control purebred Angus herd consisted on records of 10,483 animals (4700 males and 5783 females) born between 1938 and 2005. The herd is located in Pasteur, western Buenos Aires province. The number of cows at any given year was about 250 up to 1990, moment at which was reduced to its actual size of about 100 females. A large proportion of all matings where to popular US bulls through artificial insemination. Since 1990, embryo transfer has become a common management practice with the 10% superior cows.

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