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Population structure and effects of inbreeding on milk yield and quality of Murrah buffaloes

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ABSTRACT

To provide data for conservation, selection, and expansion programs of buffalo herds, this study evaluated the history of a population of Murrah buffaloes based on population structure and the effect of inbreeding on accumulated 305-d milk yield (MY), fat yield (FY), protein yield (PY), mozzarella production (MProd), and somatic cell score (SCS). The usefulness of including the individual inbreeding coefficient (F) or individual increase in inbreeding coefficient (ΔF) in the model to describe inbreeding depression was evaluated. Pedigree information from 8,054 animals born between 1976 and 2008 and 4,497 lactation records obtained from 12 herds were used. The realized effective population size was 40.10 ± 1.27, and the mean F of the entire population was 2.14%. The ratio between the number of founders and ancestors demonstrated the existence of a bottleneck in the pedigree of this population, which may contribute to a reduction of genetic diversity. The effect of F on MY, FY, PY, MProd, and SCS was −1.005 kg, −0.299 kg, −0.246 kg, −1.201 kg, and −0.002 units, and the effect of ΔF transformed to equivalent F (%) for a mean of 2.57 equivalent generations was −4.287 kg, −0.581 kg, −0.383 kg, −2.001 kg, and −0.007 units, respectively. The inbreeding depression observed may have important economic repercussions for production systems. The ΔF can be considered the better of the two indicators of inbreeding depression due to its properties that prevent underestimation of this effect. A designed mating system to avoid inbreeding may be applied to this population to maintain genetic diversity.

Key words: buffalo, inbreeding depression, milk yield, somatic cell

INTRODUCTION

Buffaloes (*Bubalus bubalis*) account for only about 10% of the effective world cattle population but are of marked socioeconomic importance in view of their strong presence in Asian countries where they have important functions as working animals; for example, in rice production (FAO, 2007). Particularly in India, Pakistan, and Egypt, these animals are responsible for most of the milk produced and consumed by the local populations (Nanda and Nakao, 2003). Buffaloes play an important role in Italy, where their milk is used for the production of the traditional mozzarella cheese. Brazil has the largest buffalo population in America (1.2 million animals). The Brazilian buffalo herd consists of animals of the Jafarabadi and Murrah breeds originating in India and animals of the Mediterranean breed originating in Italy. The main and last entry of Murrah animals in Brazil occurred in 1962, when 5 males and 12 females were imported. Only a few animals gave origin to the animals that today comprise the national herd, suggesting that the effective population size may be small and the level of inbreeding high.

According to Gutiérrez et al. (2008), the evaluation of population structure by pedigree analysis is an important tool to describe genetic variability and its evolution over generations. Falconer and Mackay (1996) suggested that inbreeding should be controlled in a population because of its unfavorable effect on economically important traits (inbreeding depression) and on additive genetic variance.

Various investigators have studied inbreeding depression, with the inbreeding coefficient of the animal (***F***) being included as a covariate in the genetic evaluation model in most cases. However, because F is not linearly dependent on pedigree knowledge of the animal, González-Recio et al. (2007) proposed the use of the individual increase in inbreeding coefficient (**Δ*F***) instead of F in the model to describe the effect of inbreeding depression considering pedigree knowledge over generations. The use of ΔF corrects the cumulative inbreeding coefficient F with regard to the pedigree depth of the animal. In case of equally complete generations of animals under analysis, this correction will have no effect.

Milk production has increased over the last years in southeastern Brazil due to the better prices paid by dairy industries specializing in the production of

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mozzarella. Buffalo milk has excellent physical and chemical qualities because of the high concentration of its components (Tonhati et al., 2000; Rosati and Van Vleck, 2002; Aspilcueta-Borquis et al., 2010). In view of the importance of buffaloes for global agriculture in general, and for the southeast region of Brazil in particular, the objective of the present study was to investigate the population structure and effect of inbreeding on milk production and quality traits of buffaloes.

MATERIALS AND METHODS

Data

Pedigree and production data were obtained from the Buffalo Milk Test Program developed by the Animal Science Department of São Paulo State University (FCAV, Jaboticabal, São Paulo, Brazil). The complete pedigree included 8,054 animals born between 1976 and 2008.

Most herds considered in this study use fixed-time AI in 2 cycles. The cows that remained nonpregnant after 2 cycles were exposed to natural mating at a rate of 1 bull to 30 cows. In general, the bulls used in natural service were unrelated. Animals were raised on pasture with feed supplementation during the dry period from April to September. Machine milking was performed twice daily and milk yield and its components were measured monthly.

Population Structure and Inbreeding

Population structures were analyzed in terms of pedigree completeness level ($\boldsymbol{I}$), individual inbreeding coefficient (F), average relatedness (**AR**), generation interval, individual increase in inbreeding coefficient (ΔF), "realized" effective population size $\left(\overline{Ne}\right)$, and effective number of founders ($\boldsymbol{f_e}$), ancestors ($\boldsymbol{f_a}$), and founder genome equivalents ($\boldsymbol{f_g}$). All parameters were computed for the animals belonging to the reference population, defined as animals born in the last generation interval (n = 6,300). The software programs ENDOG version 4.6 (Gutiérrez and Goyache, 2005) and Poprep (Groeneveld et al., 2009) were used for pedigree analysis.

The following formulas were used to compute pedigree completeness (MacCluer et al., 1983):

$$I_d = \frac{4 I_{d_{pat}} I_{d_{mat}}}{I_{d_{pat}} + I_{d_{mat}}} \text{ and}$$

$$I_{d_k} = \frac{1}{d}\sum_{i=1}^{d} a_i,$$

where k corresponds to the paternal (pat) or maternal (mat) line of an individual, a_i is the proportion of known ancestors in generation i, and d is the number of generations considered in the calculation of pedigree completeness. The level of pedigree completeness ranged from 0 to 100%.

The F was calculated as proposed by Meuwissen and Luo (1992). The AR was calculated for each individual and is defined as the probability that an allele randomly chosen from the whole population in the pedigree belongs to a given animal. The AR was then interpreted as the representation of the animal in the whole pedigree regardless of knowledge of its own pedigree. The generation interval was defined as average age of parents at the birth of their progeny that were subsequently kept for reproduction.

The ΔF was calculated as described by Falconer and Mackay (1996) and modified by González-Recio et al. (2007) and Gutiérrez et al. (2009):

$$\Delta F = 1 - \sqrt[t-1]{1 - F}, \quad [1]$$

where F is the inbreeding coefficient of individual and t is the "equivalent complete generations" for this individual (Maignel et al., 1996; Boichard et al., 1997). A better expression for ΔF would be "F corrected for equivalent complete generations." The expression relating inbreeding in generation t to the inbreeding rate proposed by Gutiérrez et al. (2009) is

$$F_t = 1 - \left(1 - \Delta F\right)^{t-1}. \quad [2]$$

The effective population size $\overline{Ne}$ (Gutiérrez et al., 2008), called realized effective size by Cervantes et al. (2008), was estimated from $\overline{\Delta F}$, which can be computed by averaging the ΔF of n individuals included in a given reference subpopulation, as $\overline{Ne} = 1\big/2\overline{\Delta F}$. The standard error of $\overline{Ne}$ was calculated as described by Gutiérrez et al. (2008).

The parameters f_e and f_a were obtained to evaluate the concentration of the origin of both animals and genes. Parameter f_e is defined as the number of equally contributing founders that would be expected to produce the same genetic diversity as observed in the population under study (Lacy, 1989). When founders contribute to the reference population more equally, the effective number of founders is higher. This parameter was calculated as

$$f_e = 1\bigg/\left(\sum_{k=1}^{f} q_k^2\right),$$