Pedigree Analysis in a Large Brazilian Nellore Herd

*F. Brito*, M. Sargolzaei†, J. Braccini*, J.A. Cobuci* and F. S. Schenkel†

**Introduction**

In recent decades, due to advances in animal breeding methods and in farming technologies, more Nellore cattle herds in Brazil have been under intensive genetic improvement programs. These programs have resulted in higher accuracy of genetic evaluations and decreased generation intervals, which potentially increased inbreeding rates and reduced genetic diversity. One way to monitor the genetic diversity of a population is based on pedigree information. Besides the coefficient of inbreeding and effective population size, statistics based on the probability of gene origin (Boichard, D., Maignel, L. and Verrier, E. (1997)) provide valuable information for studying a population undergoing several years of selection.

Artificial insemination (AI) has been used as a powerful tool for genetic improvement, but large scale use of AI is challenging. Therefore, the use of multiple selected young sires (MS, groups of bulls mated to groups of cows) has been a common practice in Nellore cattle. The use of MS often results in good genetic gain, but it also results in loss of pedigree information. In inbreeding calculation, missing pedigree information can be partly taken into account assuming that relationships between known and unknown parents are on average twice of the inbreeding of progeny of known parents for the same generation (VanRaden (1992)).

The aims of this study were: 1) to estimate the inbreeding coefficients and the effective population size of a commercial Nellore population under an intensive breeding program that uses MS mating; 2) to analyze the genetic variability of this population using the statistics derived from the probability of gene origin.

**Material and methods**

**Data.** A large Nellore cattle herd belonging to Agropecuaria Jacarezinho, consisting of 146,291 animals born from 1984 to 2007, was investigated. In addition the database of the Brazilian Association of Zebu Breeders was used to trace back the pedigree of the herd to a 1938 base, resulting in 162,244 genealogical records. The genetic evaluation in this herd is based on BLUP estimates of breeding values. Every year the best two-year old young bulls (20%) are used for MS mating and the top 1% bulls are used for AI.

**Methodology.** The regular inbreeding coefficients and inbreeding taking into account missing pedigree data (VanRaden (1992)) were calculated. The inbreeding coefficient

*Department of Animal Science, UFRGS, Porto Alegre, RS, Brasil, 91540-000
†Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, N1G2W1
expected under random mating proposed by Wright (1969) was calculated and compared to the realized levels of inbreeding to assess the mating strategies used in the breeding program. **Effective population size** ($N_e$) was calculated as $N_e = 1/2\Delta F_t L$ where $\Delta F_t$ is the annual rate of inbreeding and $L$ is the average generation interval. **Effective number of founders** ($E_f$) was calculated as in Lacy (1989): 
$$E_f = \frac{1}{\sum_{j \in F} \left( \frac{\sum_{i \in G} t_{ij} \cdot \eta_i}{n_G} \right)^2}$$
where $F$ is the set of founders, $G$ is the set of individuals, $n_G$ is the number of individuals, and $t_{ij}$ is an element of matrix $T$ representing the fraction of the genes that individual $i$ inherited from founder $j$. **Effective number of founder genomes** ($E_{fg}$) was calculated as:
$$E_{fg} = \frac{\sum_{i \in F} \eta_i F_{ij}}{\sum_{i \in F} \sum_{j \in F} \eta_i \eta_j}$$
where $F$ is the set of founders, $G$ is the set of individuals, $n_G$ is the number of individuals, and $t_{ij}$ is an element of matrix $T$ representing the fraction of the genes that individual $i$ inherited from founder $j$. **Effective number of non-founders** ($E_{nf}$) accounts for loss of genetic diversity due to drift accumulated over non-founder generations. It was calculated as: 
$$E_{nf} = \frac{1}{\sum_{i=1}^{n_a} p_i^2}$$
where $p_i$ is the marginal genetic contribution of ancestor $i$ to the population, and $n_a$ is the number of ancestors. In this study the 1000 most contributing ancestors were used.

**Software.** The CFC software (Sargolzaei, M., Iwaisaki, H. and Colleau, J.J. (2006)) was used to calculate pedigree statistics, regular inbreeding coefficient, $E_r$, $E_{fg}$, and $E_{nf}$. Inbreeding expected under random mating was calculated using the EVA software (Berg, P., Sorensen, M.K. and Nielsen, J. (2007)). The PEDIG package (Boichard (2002)) was used to calculate generation intervals, $E_a$ and to identify ancestors with the highest genetic contributions.

**Results and discussion**

Out of the total of 162,244 animals, 9.2% were considered founders (both sire and dam were unknown), 34.4% had both parents known, and 56% had only the dam known. The regular average inbreeding for animals born in 2007 was 0.25%, but was 1.73% when calculated by VanRaden’s method, which was nearly 7 times higher (Figure 1a). This sizeable difference can be attributed to the large number of unknown sires and it indicates that VanRaden’s method recovered some of the inbreeding missed by the regular method. Lutaaya, E., Misztal, I., Bertrand, J.K. et al. (1999) tested the efficacy of this method by simulating missing dam information only, ranging from 10% to 50% and concluded that up to 20% of missing information VanRaden’s method could recover most of the inbreeding. However, the deletion of dam’s information was done randomly and the dams could have come from any of the previous generations. Therefore, the authors chose to assign the average inbreeding coefficient of the animals born in the 4 years preceding the birth of their progeny. As in the current data set, the bulls used in MS matings were all selected from the same generation that preceded the birth of their offspring, VanRaden’s method seems to be appropriate, even with higher levels of missing pedigree records. Inbreeding levels in Brazilian Nellore have been reported by Faria, F.J.C., Filho, A.E.V., Madalena, F.E. et al. (2009) and were slightly higher than those found using the VanRaden’s method in the current study.
Despite the fact that the inbreeding coefficients in Figure 1b have been calculated by the regular method, the difference in inbreeding levels between the random mating and actual matings is still relevant. The inbreeding under random mating was on average 1.3 times higher than the inbreeding coefficient calculated using the actual matings, reaching levels 4 times higher in 2005 (Figure 1b). This difference indicates an appropriate control of inbreeding by optimizing matings using a software called PAD, which was adopted in the herd since the late 90s (Roso, V.M. and Fries, L.A. (1998)).

Figure 1a
Figure 1b

Figure 1a. Regular average inbreeding coefficient and average inbreeding coefficient calculated by VanRaden’s method; Figure 1b. Average inbreeding (Avg_F), inbreeding expected under random mating (F.ST) and deviation from random mating (f.is)

The effective population size showed fluctuations since the beginning of the breeding program (Table 1). In the first period, with the extensive use of AI and the use of one important ancestor, \( N_e \) was 114. In the subsequent period \( N_e \) was increased, which could be speculated to be a consequence of the implementation of the PAD mating software. More recently there was a decrease in \( N_e \), which could be explained by an increasing use of descendants from an important ancestor (Table 2) that contributed to 10.6% of gene pool of herd in the 2003-2007 period. For this period 8, 31 and 844 ancestors contributed to 20%, 30% and 50% of the gene pool, respectively. Studies involving other herds of Brazilian Nellore reported similar contributions from the first 30 main ancestors (Faria, F.J.C., Filho, A.E.V., Madalena, F.E. et al. (2009); Vozzi, P.A., Marcondes, C.R., Bezerra, L.A.F. et al. (2007)).

Although rate of inbreeding has probably been controlled by mating strategies, the statistics based on the probability of gene origin showed that loss of genetic diversity has occurred (Table 1). Nevertheless recent values of \( N_I \), \( N_e \) and \( N_{gt} \) are larger than those presented by Faria, F.J.C., Filho, A.E.V., Madalena, F.E. et al. (2009) for the entire registered Nellore population in Brazil.

Conclusions

Even though the pedigree records contained a large number of unknown sires, VanRaden’s method for calculating inbreeding and the statistics based on the probability of gene origin seemed suitable for assessing the genetic diversity in the herd. Although the analyses show
loss of diversity, mating strategies seem to be properly controlling the rate of the loss. However, it is important to continue monitoring the diversity of this population.

Table 1: Generation interval (Gen Int), inbreeding calculated by VanRaden’s method (∆F) and effective numbers in the Nellore herd

<table>
<thead>
<tr>
<th>Period</th>
<th>Gen Int</th>
<th>∆F</th>
<th>N_e</th>
<th>E_f</th>
<th>E_a</th>
<th>E_fg</th>
<th>E_nf</th>
</tr>
</thead>
<tbody>
<tr>
<td>1995-1999</td>
<td>6.85</td>
<td>0.00064</td>
<td>114</td>
<td>607</td>
<td>239</td>
<td>152</td>
<td>204</td>
</tr>
<tr>
<td>1999-2003</td>
<td>6.47</td>
<td>0.00032</td>
<td>245</td>
<td>436</td>
<td>87</td>
<td>74</td>
<td>89</td>
</tr>
<tr>
<td>2003-2007</td>
<td>6.83</td>
<td>0.00073</td>
<td>101</td>
<td>479</td>
<td>77</td>
<td>67</td>
<td>78</td>
</tr>
</tbody>
</table>

N_e = effective population size; E_f, E_a, E_fg, E_nf= effective numbers of founders, ancestors, founder genomes and non-founders.

Table 2: The 8 ancestors with highest genetic contributions to the gene pool of animals born between 2003 and 2007.

<table>
<thead>
<tr>
<th>Ancestor</th>
<th>Sex</th>
<th>Birth Year</th>
<th>Number of progeny</th>
<th>Number of descendants</th>
<th>Genetic contributions (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kulal AJ</td>
<td>M</td>
<td>1993</td>
<td>7,593</td>
<td>20,745</td>
<td>10.6 10.6 10.6</td>
</tr>
<tr>
<td>Gilm de Garça</td>
<td>M</td>
<td>1976</td>
<td>333</td>
<td>29,154</td>
<td>2.1  2.1  12.7</td>
</tr>
<tr>
<td>Tiete</td>
<td>M</td>
<td>1987</td>
<td>1,351</td>
<td>7,409</td>
<td>1.6  1.6  14.3</td>
</tr>
<tr>
<td>Cabral AJ</td>
<td>M</td>
<td>1997</td>
<td>892</td>
<td>1,722</td>
<td>1.5  1.5  15.7</td>
</tr>
<tr>
<td>Solimões AJ</td>
<td>M</td>
<td>1995</td>
<td>777</td>
<td>2,700</td>
<td>1.3  1.3  17.1</td>
</tr>
<tr>
<td>Karvardi</td>
<td>M</td>
<td>1955</td>
<td>89</td>
<td>50,127</td>
<td>1.8  1.2  18.3</td>
</tr>
<tr>
<td>Di Cavalcanti AJ</td>
<td>M</td>
<td>1998</td>
<td>646</td>
<td>1,408</td>
<td>1.2  1.0  19.3</td>
</tr>
<tr>
<td>Rondon AJ</td>
<td>M</td>
<td>1997</td>
<td>533</td>
<td>956</td>
<td>0.9  0.9  20.1</td>
</tr>
</tbody>
</table>

References