Online journal ISSN - 1676-5680
GMR Genetics and Molecular Research
EVOLUTION AND TECHNOLOGY

Pedigree analyses in the Breeding Program for Nellore Cattle

P.A. Vozzi[1], C.R. Marcondes[2], L.A.F. Bezerra[1] and R.B. Lôbo[1,3]

[1]Departamento de Genética, Faculdade de Medicina de Ribeirão Preto, Universidade de São Paulo, Ribeirão Preto, SP, Brasil
[2]EMBRAPA, Amazônia Oriental, Pará, PA, Brasil
[3]UNIDERP, MS, Brasil
Corresponding author: P.A. Vozzi
E-mail: pavozzi@genbov.fmrp.usp.br

Genet. Mol. Res. 6 (4): 1044-1050 (2007)
Received May 10, 2007
Accepted October 6, 2007
Published November 27, 2007

ABSTRACT. Parameters based on the probability of gene origin were used to describe genetic variability in three reproductive groups from the Breeding Program for Nellore Cattle (PMGRN). The three reproductive populations (cows in reproductive age, bulls from artificial insemination centers and young bulls in progeny test) generated medium to low values. The effective number of founders (N_f), the effective number of ancestors (N_a) and the remaining genomes (N_g) suggest low founder representativeness, high genetic contribution by some ancestors, considerable loss of founder alleles and lack of allelic representativeness in bulls kept in artificial insemination centers and young sires in progeny test in relation to the diversity on the farms participating in the PMGRN. The parameters based on the probability of gene origin in the three reproductive groups were: 84.3, 53 and 54.2 (N_f); 71, 36.6 and 30 (N_a) and 51.4, 19.3 and 19 (N_g) for cows, bulls from artificial insemination centers and young sires in progeny test, respectively. Future matings and the introduction of selected progeny reproduction may decrease the parameters based on the probability of gene origin in each reproductive group, thereby increasing considerably the additive relationship in the three reproductive groups and consequently increasing the probabil-

ity of inbreeding in the future. Strategies to maintain genetic variability in bull populations must be implemented.

Key words: Gene flow, Genetic variability, Mating strategies, Nellore, Population structure

INTRODUCTION

As the improvement programs unfold, loss of genetic variability generally occurs, especially due to the increased levels of inbreeding and loss of founder alleles through genetic selection and drift. Even though reproductive biotechnologies and methods to estimate genetic parameters and breeding values allow for important genetic developments in a number of economically important traits, they also contribute to increasing variance in family size, limiting the genetic contribution to fewer bulls.

The pedigree information of several bovine (Maignel et al., 1996; Boichard et al., 1997; Sölkner et al., 1998; Perez Torrecillas et al., 2002; Faria et al., 2002; Gutierrez et al., 2003; Vozzi et al., 2006; Honda et al., 2006) and equine breeds (Glazewska and Jezierski, 2004; Valera et al., 2005) has been recently used to describe and monitor genetic variability in different domestic species. Parameters based on the probability of gene origin represented by the effective number of founders (N_f), ancestors (N_a) and remaining genomes (N_g) allow for the assessment of genetic variability after a small number of generations and is very sensitive to changes in pedigree, whereas the inbreeding coefficient and the effective population size are useful in monitoring the genetic variability over longer periods of time (Lacy, 1989; Boichard et al., 1997).

In Brazil, the genetic makeup of Nellore is mainly the result of animals imported from India since the end of the 19th century up until 1963. The herdbook for the Nellore breed in Brazil has been kept since 1939. In 2006, the number of registered animals exceeded 3,400,000, which represents 80% of zebu registries in Brazil (ABCZ, 2007). It is estimated that the number of bulls imported has not exceeded 7000 animals. The breed showed amazing adaptation to the local environment, which led to a significant population increase since the last importation. The importation of animals, semen and embryos has been banned as of 1963, thus, the breed has been kept impervious to new genetic material since then. Magnabosco et al. (1997) studied the genetic makeup of selection centers for Nellore in Brazil and concluded that approximately 20% of the genes present in the animals that participate in the breeding programs can be accounted for by the genetic contribution of only six founder sires imported from India. Faria et al. (2002) and Vozzi et al. (2006) reported genetic variability indexes for Nellore in Brazil. The parameters based on the probability of gene origin, the kinship level and the percentage of animals with inbreeding born recently within the selection programs reveal that few families have effectively participated in reproduction, that ancestors are progressively more related, and as a result, the number of animals with inbreeding has alarmingly increased in the last decade (Vozzi, 2004).

The present study aimed to evaluate the genetic variability in the several groups of animals participating in the Breeding Program for Nellore Cattle (PMGRN), assessing parameters based on the probability of gene origin, and to identify variability trends within the groups, depending on the gene flow between each reproductive population.

MATERIAL AND METHODS

The three reproductive groups investigated are part of the PMGRN coordinated by the Associação Nacional de Criadores e Pesquisadores (ANCP, 2007; Lôbo et al., 2007). The PMGRN has a database of over 3,385,000 weight measurements and 565,000 scrotal circumference measurements, totaling 955,000 animals in the pedigree. A total of 399 farms all over Brazil and in four other South American countries take part in the breeding program. The inbreeding coefficient of the animals born on the farms of the breeding program between 1998 and 2001 was 2.25% (only animals with inbreeding). In the same period, 54.7% of the animals born in the breeding program were endogamous (Vozzi, 2004).

The number of records and means of the main traits utilized in the breeding program are summarized in Table 1.

Table 1. Number of observations and means by trait.

Trait	Number of observations	Mean
Age at first calving (months)	154,847	37
Gestation length (days)	211,032	296
Body weight at 120 days (g)	388,772	123
Body weight at 365 days (kg)	305,150	233
Body weight at 450 days (kg)	277,820	270
Mature weight (kg)	63,776	452
Scrotal circumference at 365 days (cm)	88,477	20
Scrotal circumference at 450 days (cm)	99,769	23

Pedigrees were analyzed to determine genetic variability in the three reproductive groups.

Cows

A total of 114,544 reproductively active cows participated in the PMGRN (born between 1990 and 1999). The importance of the genetic variability study in the groups lies in the determination of the potential genetic variability on the farms that take part in the PMGRN.

Bulls at artificial insemination centers

A sample of 100 bulls with genetic evaluation take part in the PMGRN and at artificial insemination centers.

Young bulls in progeny tests

The participants of this group were 41 animals with positive expected progeny differences for the growth traits prior to and after weaning, fertility and maternal ability. The 41 young bulls were selected of 25,000 animals born in 2001. Pedigree analysis in both bull populations is absolutely important to allow for the determination of genes that are present or that will enter the semen market for the Nellore breed in Brazil.

Parameters based on the probability of gene origin, represented by the effective number of founders, ancestors and remaining genomes, were used to describe the genetic variability of each reproductive group.

The N_f represents the number of equally contributing founder animals that would produce the same genetic variability found in the investigated population. N_f was calculated as $N_f = 1 / \sum (p^2_i)$, where p_i is the ratio of alleles in the reference population contributed by founder i. When each founder (animal whose pedigree is unknown) has the same expected contribution in the population, the N_f equals the number of founders (N_{fun}). In selection programs, the genetic contribution of founders is generally unbalanced, the N_f being considerably lower than the N_{fun}.

The N_a determines the minimum number of ancestors (founders or not) required to explain the complete genetic diversity in the reference population. The N_a is obtained by computing the marginal contribution of each ancestor (Boichard et al., 1997) as $1 / \sum (p^2_k)$, where p^2_k is the marginal contribution of ancestor k in the population. An ancestor may not be a founder animal; however, it may share genes with other ancestors, and the expected contribution in the population q_k may be redundant and add up to more than one. As a result, only the marginal contribution of the ancestor under investigation can be used to assess the contribution of an ancestor's allele in the reference population.

The N_g represents the number of founders with the same contribution that would lead to the same genetic diversity found in the population and that would not cause loss of alleles due to genetic drift. N_g was computed as $1 / \sum (p^2_i / r_i)$, where r_i is the expected ratio of alleles from founder i that would remain in the reference population, and p_i is the expected ratio of alleles from founder i that contributed to the reference population. A total of 1000 segregations were simulated for the calculation of N_g in each reproductive group.

The marginal contribution of the main founders and ancestors was used to determine the family structure in each reproductive group.

The kinship coefficient (Malécot, 1948) and parameters N_f, N_a and N_g were estimated by the PEDIG® software (Boichard, 2002).

RESULTS AND DISCUSSION

Pedigree analyses

Table 2 shows the genetic variability (represented by N_f, N_a and N_g) for each reproductive group as a result of pedigree analysis.

Table 2. Pedigree analysis in the three reproductive groups studied.

Reproductive group	Pedigree	N_{fun}	N_f	N_a	N_g	R
Cows born between 1990-1999	424,139	45,413	84.3	71.4	51.4	2.2%
Bulls (artificial insemination centers)	1,409	461	53.0	36.6	19.3	4.8%
Young bulls in progeny test	1,052	361	54.2	30.9	13.9	4.6%

Pedigree = number of animals in the pedigree; N_{fun} = number of founders in each reproductive group; N_f = effective number of founders in each reproductive group; N_a = effective number of ancestors; N_g = number of remaining genomes; R = additive relationship coefficient.

In the three groups investigated, the parameters based on the probability of gene origin were of medium or low magnitude when results were compared to those obtained for other

bovine breeds (Sölkner et al., 1998; Perez Torrecillas et al., 2002; Gutierrez et al., 2003). Faria et al. (2002) found lower values in the polled Nellore breed born between 1994 and 1998 than in cows of reproductive age, and similar values for the two populations of bulls. For the variability values recorded in the polled Nellore, the two groups of bulls led to variability levels that were lower than those present in the Nellore polled breed. N_f, N_a and N_g parameters were reduced in the following order: reproductive cows → bulls at artificial insemination centers → young bulls in progeny test. In the bulls from artificial insemination centers and in progeny tests, a considerable reduction of genetic variability was recorded through the N_f, N_a, and N_g parameters. The low N_g pointed to a significant loss of founder genes in the stock of sires and in the progeny tests. The additive relationship coefficient among bulls present at insemination centers and among those participating in the progeny test led to values more than twice as high as those of reproductive females. The genetic variability present in the market of Nellore breed semen is not representative of the diversity on the PMGRN farms. This genetic pool present on the farms needs to be explored in order to increase the variability in the Nellore semen market.

Genetic contribution of the principal ancestries in each reproductive group

Table 3 shows the marginal contributions by the main ancestors in each reproductive group. The animals with the highest marginal contribution within each reproductive population were regarded as the main ancestors (Boichard et al., 1997).

Table 3. Genetic contribution of the principal ancestries in each reproductive group.

Genetic contribution	Cows born between 1990-1999	Bulls (A.I.C.)	Young bulls in progeny test
*Principal ancestry	9.1%	11.4%	10.7%
*Ten principal ancestries	27.8%	37.6%	47.0%
*Twenty principal ancestries	35.4%	50.2%	61.2%
*Thirty principal ancestries	40.0%	57.7%	74.0%

*Marginal contribution. A.I.C. = artificial insemination centers.

The high genetic contribution of few bulls has been recorded within the three reproductive populations analyzed. The marginal contribution by the main ancestor was nearly 10% in each group under consideration. Among the bulls at artificial insemination centers, the 50% genetic variability can be accounted for by genetic contribution by 20 ancestors, whereas among the bulls in progeny tests only 10 ancestors hold 50% of the genes.

The fact that the Nellore breed had been genetically impervious to the importation of genetic material (bulls, semen and embryos), that it has originated from a small number of founder animals (imported from India) and that the use of some bulls has been a preference of some cattle breeders, may explain the variability levels which are lower than those in several other bovine breeds (Boichard et al., 1997; Sölkner et al., 1998; Perez Torrecillas et al., 2002). The genetic representativeness of females participating in the breeding programs was similar to that found in the overall population for the breed (Faria et al., 2002; Vozzi et al., 2006). Even though a larger genetic variability had been recorded (Table 2) in the population of cows, the population size does not match its genetic size. Similarly, few bulls had a high genetic contribution in the other reproductive groups studied (Table 3). The marginal contribution of the main ancestors (Table 2) and the N_g (Table 1) found in both bull populations indicated a significant loss of founder-alleles due to genetic selection and drift. Similar results were obtained by Vozzi et al. (2004), where

93% of the active sires at insemination centers descended from the main ancestor and 20% of their variability can be accounted for the genetic contribution of the six Nellore founding sires. Following progeny tests, Vozzi (2004) reported that 50% of the genes in young animals are accounted for the genetic contribution of only two families of bulls.

Figure 1 illustrates the genetic variability (represented by N_a) and the gene flow among each reproductive group. Note that the genetic variability in the population of reproductive females does not show in sires on the semen market and, even less, in those that are tested for admission into artificial insemination centers. Simulations of future matings among reproductive groups produced smaller progenies with parameters based on the probability of gene origin than those found in this study. The progenies that were later chosen as breeders in the breeding program (progeny test, bulls in artificial insemination centers, cows, and embryo donors) will have lower genetic variability than that found in the present reproductive populations. Should this trend continue, it is expected that higher kinship within each group will occur, as well as a reduction in the parameters based on the probability of gene origin. The increment in kinship level in the reproductive breeding stocks and the small number of animals selected in progeny tests increase the probability of selection of related animals and continuous loss of founder alleles through genetic drift.

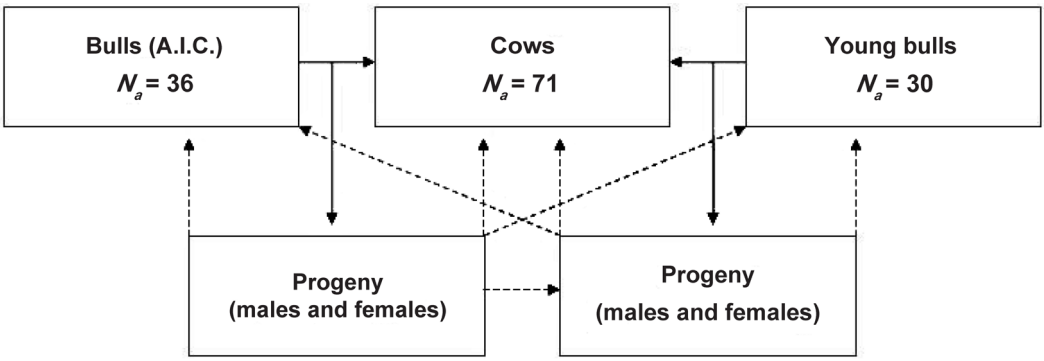

Figure 1. Gene flow and genetic variability in each reproductive group analyzed. The solid line is the actual mating, and the broken line is the simulated future mating. A.I.C. = artificial insemination centers. N_a = effective number of ancestors.

The use of pedigree information as a selection criterion in progeny tests, the control of kinship among sires at artificial insemination centers, the use of computerized mating programs, and better use of genetic variability among reproductive females may control the genetic variability levels within each reproductive group.

CONCLUSIONS

The results indicate that genetic variability within the different Nellore groups studied has to be monitored constantly in order to prevent or minimize loss of founder alleles due to genetic selection or drift. This would also prevent or control kinship in reproductive breeding stocks. The intensive use of few families for reproduction, the biotechnologies employed to speed up genetic progress, and the preference by breeders for the use of certain families of

reproducers have contributed to the reduction of the breed's genetic variability. Variability values and gene flow in each group reveal that considerable loss of diversity will occur in addition to an increase in additive relationship in reproductive herds, which will increase the odds of inbreeding mating in the future, thereby jeopardizing the genetic enhancement of economically important traits for the Nellore breeding program.

ACKNOWLEDGMENTS

Thanks go to the Brazilian agencies CAPES, PRONEX, FAEPA, FAPESP, and ANCP.

REFERENCES

Associação Brasileira dos Criadores de Zebu (ABCZ) (2007). Estatísticas de registro genealógico. http://www.abcz.org.br/site/tecnica/estatistica.xls. Accessed May 8, 2007.

Associação Nacional de Criadores e Pesquisadores (ANCP) (2007). Sumário eletrônico de avaliação genética (Nellore Breed). http://www.ancp.org.br/sumario_2007.pdf. Accessed August 10, 2007.

Boichard D, Maignel L and Verrier E (1997). The value of using probabilities of gene origin to measure genetics variability in a population. *Genet. Sel. Evol*. 29: 5-23.

Faria FJC, Vercesi Filho AE, Madalena FE and Josahkian LA (2002). Estrutura populacional da raça Nellore Mocho. *Arq. Bras. Med. Vet. Zootec*. 54: 501-509.

Glazewska I and Jezierski T (2004). Pedigree analysis of Polish Arabian horses based on founder contributions. *Livest. Prod. Sci*. 90: 293-298.

Gutierrez JP, Altarriba J, Díaz C, Quintanilla R, et al. (2003). Pedigree analysis of eight Spanish beef cattle breeds. *Genet. Sel. Evol*. 35: 43-63.

Honda T, Fujii T, Nomura T and Mukai F (2006). Evaluation of genetic diversity in Japanese Brown cattle population by pedigree analysis. *J. Anim. Breed. Genet*. 123: 172-179.

Lacy RC (1989). Analysis of founder representation in pedigrees: founder equivalents and founder genome equivalents. *Zool. Biol*. 8: 111-123.

Lôbo RB, Bezerra LAF, Barros PS, Magnabosco CU, et al. (2007). Avaliação genética de touros e matrizes da raça Nelore: Sumário 2007, ANCP, Ribeirão Preto.

Magnabosco CU, Cordeiro CMT, Trovo JBF, Mariante AS, et al. (1997). Catálogo de linhagens do germoplasma zebuino: raça Nelore. Embrapa-Cenargen, Documentos, 23, Brasília.

Maignel L, Boichard D and Verrier E (1996). Genetic variability of French dairy breeds estimated from pedigree information. *Interbull Bull*. 14: 49-54.

Malécot G (1948). Les Mathématiques de L´Hérédité. Masson et Cie, Paris. In: Probability models and statistical methods in genetics (Elandt Johnson RC, ed.). John Wiley and Sons Inc., New York, 592.

Boichard (2002). Pedig: a fortran package for pedigree analysis suited to large populations. 7th World Congress on Genetics Applied to Livestock Production, Montpellier, October 19-23, 2002, 28-13.

Perez Torrecillas C, Bozzi R, Negrini R, Filippini F, et al. (2002). Genetic variability of three Italian cattle breeds determined by parameters based on probabilities of gene origin. *J. Anim. Breed. Genet*. 119: 274-279.

Sölkner J, Filipcic L and Hampshire N (1998). Genetic variability of populations and similarity of subpopulations in Austrian cattle breeds determined by analysis of pedigrees. *Anim. Sci*. 67: 249-256.

Valera M, Molina A, Gutierrez JP, Gomez J, et al. (2005). Pedigree analysis in the Andalusian horse: population structure, genetic variability and influence of the Carthusian strain. *Livest. Prod. Sci*. 95: 57-66.

Vozzi PA (2004). Análise da estrutura e variabilidade genética dos rebanhos participantes do programa de melhoramento genético da Raça Nelore. MSc thesis, Universidade de São Paulo, Faculdade de Medicina de Ribeirão Preto, Ribeirão Preto.

Vozzi PA, Marcondes CR, Magnabosco CU, Bezerra LAF, et al. (2006). Structure and genetic variability in Nellore (*Bos indicus*) cattle by pedigree analysis. *Genet. Mol. Biol*. 29: 482-485.