Genealogical information analysis of Gyr and Nelore cattle from Costa Rica

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ABSTRACT: The objectives were to analyze the genealogical information of Gyr (GY) and Nelore (NL) cattle from Costa Rica. Analyzed: pedigree integrity (GY, 13272; NL, 18153); number of complete, maximum traced and equivalent complete generations; inbreeding (FI); generation interval (GI) through four selection routes; average additive genetic ratio (AGR); effective number of founders (*fe*); effective number of ancestors (*fa*); effective population size (Ne). The analysis was performed with the ENDOG software. The maximum proportion of unknown parents, grandparents, and great-grandparents was 18.6%, 39.9%, and 59.3%, respectively. The average FI for NL was 8.87% and 2.85% in GY. The average consanguineous population (%) and FI was 53.9 and 16.5% in NL, 28.9 and 9.9% in GY. The average and maximum values of AGR for NL were 3.5 and 12.8, 1.4 and 5.6 in GY. The fe and fa for NL were 65.0 and 38.0, in GY 145.7 and 59.0. The Ne indicated increases in FI in the range of 1 to 2% in GY, for NL greater than 2%, with a status of care to monitor the evolution of F and AGR and their possible implications in genetic improvement. The GI ranged from 6.3 to 7.9 years with a general average of 6.9 years. These results show a summary of the genetic and reproductive management those breeders have carried out.
Key words: inbreeding, generation interval, effective size, ancestors, zebu cattle.

Análise de informações genealógicas de bovinos Gir e Nelore da Costa Rica

RESUMO: Os objetivos foram analisar as informações genealógicas de bovinos Gir (GY) e Nelore (NL) da Costa Rica. Foram considerados: integridade do pedigree (GY, 13272; NL, 18153); número de gerações completas, máximas traçadas e equivalentes completas; endogamia (FI); intervalo de geração (GI) por meio de quatro rotas de seleção; razão genética aditiva média (AGR); número efetivo de fundadores (*fe*); número efetivo de ancestrais (*fa*); tamanho efetivo da população (Ne). A análise foi realizada com o software ENDOG. A proporção máxima de pais, avós e bisavós desconhecidos foi de 18,6%, 39,9% e 59,3%, respectivamente. O FI médio para NL foi de 8,87% e 2,85% no GY. A média da população consanguínea (%) e FI foi de 53,9 e 16,5% em NL, 28,9 e 9,9% em GY. Os valores médios e máximos de AGR para NL foram 3,5 e 12,8, 1,4 e 5,6 no GY. Os *fe* e *fa* para NL foram 65,0 e 38,0, no GY 145,7 e 59,0. O Ne indicou aumentos de FI na faixa de 1 a 2% no GY, para NL superiores a 2%, com status de cuidado para acompanhar a evolução de F e AGR e suas possíveis implicações no melhoramento genético. O IG variou de 6,3 a 7,9 anos com média geral de 6,9 anos. Esses resultados mostram um resumo do manejo genético e reprodutivo realizado por esses criadores.
Palavras-chave: endogamia, intervalo de gerações, tamanho efetivo, ancestrais, zebuínos.

INTRODUCTION

Genealogical information defines the kinship relationships of the entire population through the pedigree of each animal. Pedigree analysis allows characterizing the demographic structure, analyzing the levels, trends, and possible effects of inbreeding, as well as examining changes in genetic diversity, with the aim of preventing losses, particularly in populations under a selection process (CAÑAS-ÁLVAREZ et al., 2014; SANTANA et al., 2016).

Selection based on predictions of breeding values, through the animal model and product of genetic evaluations, favors the selection of related animals; and therefore, increases in inbreeding; likewise, the levels of inbreeding and kinship are involved in the process of genetic evaluations (MEHRABANI-YEGANEH et al., 2000; RAMÍREZ-VALVERDE et al., 2018).

In Costa Rica, the genealogical registry (RG) of the Zebu cattle populations began in 1946, under the responsibility of the Secretary of Agriculture;

in 1989, the state transfers the RG to the registration and specialized breeders' associations; later, in 1994, the Association of Zebu Cattle Breeders (ASOCEBU) of Costa Rica was formed (QUIRÓS, 2006; VÁSQUEZ-LOAIZA & MOLINA-CASTRO, 2020). The ASOCEBU coordinates and controls the RG and the productive database of the Zebu cattle populations, designs and develops genetic improvement programs based on the selection criteria and objectives of each of the breeds it manages (ASOCEBU, 2007; VÁSQUEZ-LOAIZA et al., 2021).

Livestock in Costa Rica takes place in a tropical environment, with its environmental characteristics and pasture-based feeding, where the Gyr and Nelore bovine populations have developed based on their selection criteria and objectives. The development of populations in diverse production systems, regions o countries can transcend the structure of the pedigree and genetic variability. The objectives were to characterize the structure and integrity of the pedigree, as well as the genetic variability, of the Gyr and Nelore cattle populations based on the analysis of the RG database.

MATERIALS AND METHODS

The information analyzed corresponded to the RG database of Gyr (GY) and Nelore (NL) bovines born after 1965, table 1 describes the genealogical information analyzed. The GY and NL herds are distributed in the six socio-economic regions of Costa Rica, where 82% of milk production and 94% of meat production derives from grazing-based feeding. In the structure of the herds, in dairy cattle, 61% of the population corresponds to females with an age equal to or greater than two years; in beef cattle, 27% of the population is in the range of one to two years and 37% equal to or greater than two years (ENA,

2021). The integrity of the pedigree was considered (CAROLINO et al., 2020; VÁSQUEZ-LOAIZA et al., 2021), as a proportion of known ancestors up to the fourth generation; also, the number of complete generations (NGC), maximum traced (NGT) and complete equivalents (NGE). The average additive genetic relationship (AGR) was estimated from the matrix of additive genetic relationships among all the individuals of the pedigree; the calculation corresponds to the average value of the coefficients of each animal with the rest of the pedigree (GUTIÉRREZ et al., 2003; CHIARA et al., 2019). In addition, the inbreeding (FI) of everyone was obtained (GUTIÉRREZ & GOYACHE, 2005) and with the year of birth the trends were generated over time. Based on NGC, NGT and NGE, the effective population size (Ne) was calculated, which is defined as the number of reproducers that determine the rate of change of inbreeding and genetic variance, under the ideal population scheme (PEIXOTO et al., 2010; REIS et al., 2010; LEROY et al., 2013).

The generation interval (GI) was calculated through the four selection routes: father – son, father – daughter, mother – son and mother – daughter (CAROLINO et al., 2020, HAGAN & CUE, 2019). Animals with founder and ancestor contributions were identified, and the effective number in both contributions was estimated. A founder individual is any animal with unknown parents, the effective number of founders (*fe*) was defined as the number of founders that, contributing equally, would produce the existing genetic diversity in the population. An ancestor animal, founder or not, is one that has contributed to the genetic variability of the population; the effective number of ancestors (*fa*), was defined as the number of ancestors necessary to explain the total genetic variability of the population, considering the genetic variability contributed by an animal, which

Table 1 - Pedigree (Ped) structure, ancestors (Anc) and founders (Fou) in Nelore and Gyr cattle from Costa Rica.

Breed	Ped Hs	sx	Fathers (PS)	Mothers (PM)	Fou	Anc	A50	A95
Nelore	18,153 21	43.1 M 56.9 F	971 (16.8)	5,548 (2.9)	1,898	1,622	18 (10.4)	583
Gyr	13,272 21	38.5 M 61.5 F	825 (13.1)	4,472 (2.4)	2,513	2,257	30 (6.8)	1,212

Hs, number of active herds. sx, percentage of males (M) and females (F) in the pedigree. Fathers, total sires in the pedigree (PS, average offspring per sire). Mothers, total cows in the pedigree (PM; average offspring per cow). A50, number of ancestors that explain 50% of the variability of the pedigree (maximum percentage contribution of an ancestor). A95, number of ancestors that explain 95% of the variability of the pedigree.

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is not explained by the contribution of any of its offspring (VOZZI et al., 2006; PRATES et al., 2012; CAÑAS-ÁLVAREZ et al., 2014). The analyzes were performed with the ENDOG software (GUTIÉRREZ & GOYACHE, 2005).

RESULTS AND DISCUSSION

Figure 1 shows the proportion of known ancestors up to the fourth generation, where it was observed that the maximum percentage of unknown (both breeds) parents, grandparents and great-grandparents was 18.6, 39.9 and 59.3, respectively. The percentage of animals with unknown parents is associated with the founders (Table 1); the RG of the evaluated populations requires at least three generations of known ancestors to issue a certificate of purity breed (ASOCEBU, 2007). The veracity and integrity of the pedigree have effects on the certainty of racial purity, in the definition of founding ancestors and assignment of individuals to generations, as well as in the calculations of inbreeding levels. In genetic evaluations, it has consequences in the estimation of variance components and genetic parameters, as well as in the prediction of breeding values and ranking of sires; consequently, it also affects the response to selection and genetic progress. For Brahman cattle from Costa Rica, VÁSQUEZ-LOAIZA et al., (2021) reported percentages of known ancestors higher than GY, and lower than the results in NL. In NL

populations (FARIA et al., 2009; SANTANA et al., 2010; BORGES et al., 2013; COSTA et al., 2019) reported proportion of known ancestors of equal to lesser magnitude, with values below the 50% from the second generation; for GY and Brahman (FARIA et al., 2009; FARIA et al., 2010; SANTANA et al., 2014), the evaluated populations showed genealogical information contents like those of the present study.

The average FI for NL was 8.87% and 2.85% for GY. The consanguineous population, as a percentage of the total population, was 53.9 in NL and 28.9 in GY; likewise, the average FI in the consanguineous population was 16.5% in NL and 9.9% in GY. Figure 2 describes the proportion of inbred animals and their levels of FI over time; in GY negative tendencies can be considered in the two graphed concepts; for NL, the proportion of inbred animals showed a marked negative trend in the last six years, with average inbreeding levels ranging from 15 to 20%. For AGR, the average and maximum values for NL were 0.64 and 4.1, as well as 1.4 and 5.6 for GY. Figure 3 shows the evolution of AGR levels over time, which is associated with the behavior described in figure 2; where, NL presents a positive trend at the beginning with an evident decrease in the last six years; in GY, a negative trend is observed throughout the period. For Brahman (VÁSQUEZ-LOAIZA et al., 2021) and Sardo Negro (DOMÍNGUEZ-VIVEROS et al., 2022) cattle, positive trends were reported in average AGR and FI levels in the inbred
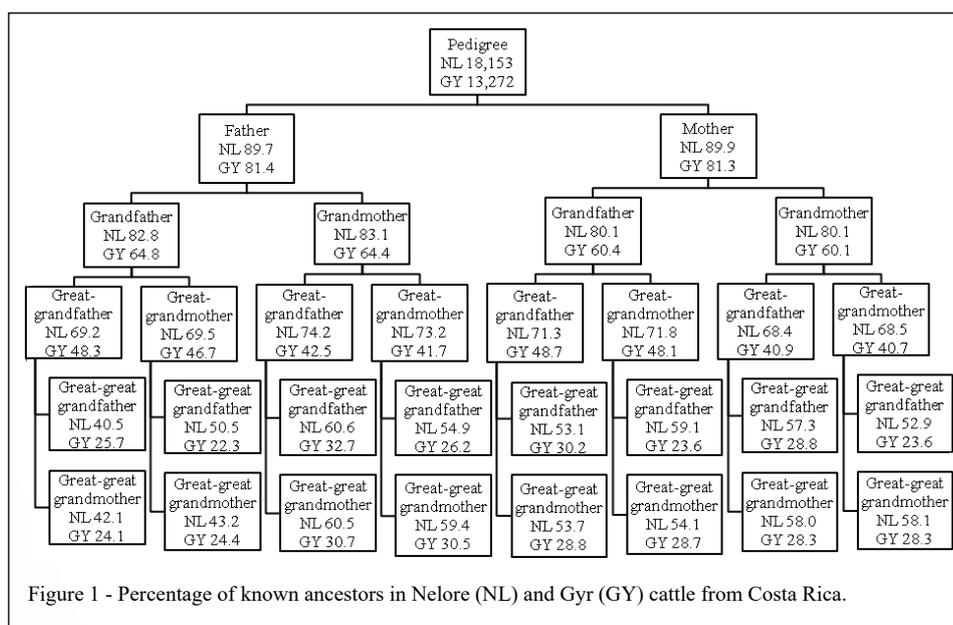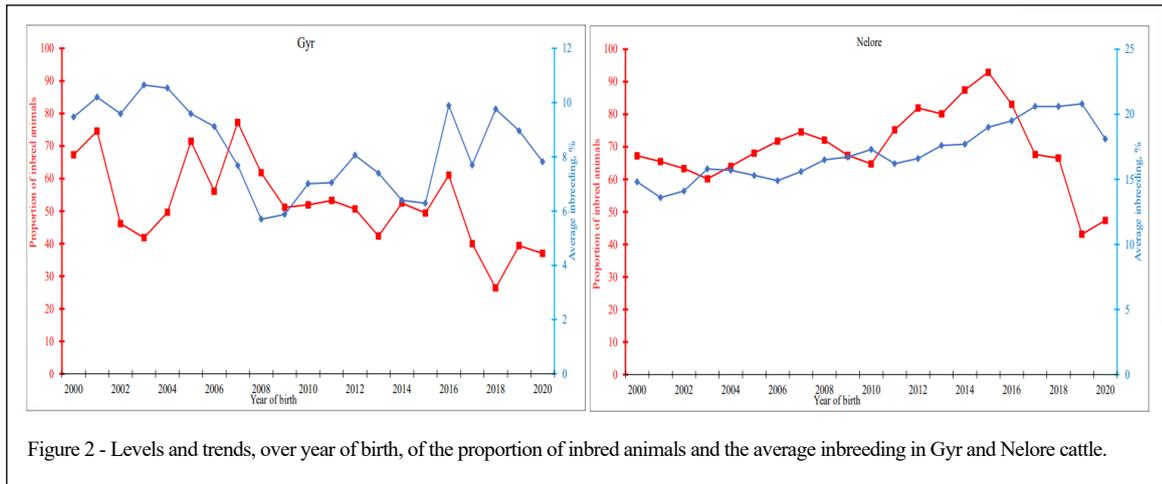

Figure 1 - Percentage of known ancestors in Nelore (NL) and Gyr (GY) cattle from Costa Rica.

Figure 2 - Levels and trends, over year of birth, of the proportion of inbred animals and the average inbreeding in Gyr and Nelore cattle.

population, with negative trends in the proportion of inbred animals. FI levels and trends, as well as its components (AGR, Ne), allow evaluating the evolution of genetic variability over time; inbred animals are directly affected by the effects of inbreeding depression and all the consequences that the increase in FI brings; AGR allows breeding to be designed while maintaining certain FI levels in the progeny (ALFONSO, 2018). The scenario observed in both populations is the product of the selection and reproductive management schemes adopted by the breeders; can be attributed to the introduction of

unrelated sires with low levels of AGR, for the case of NL in the last six years.

The integrity of the pedigree is related to the estimates of NGC, NGT and NGE (Table 2); the genetic relationships between the founders and the *fe* expose the initial genetic variability; the founders' contribution to pedigree variability exhibits the gene pool that has been maintained through generations (BOICHARD et al., 1997); a reduced number of ancestors that explain the variability of the pedigree (Table 1) is associated with increases in the levels of AGR and FI. Table 2 presents the results for *fa* and
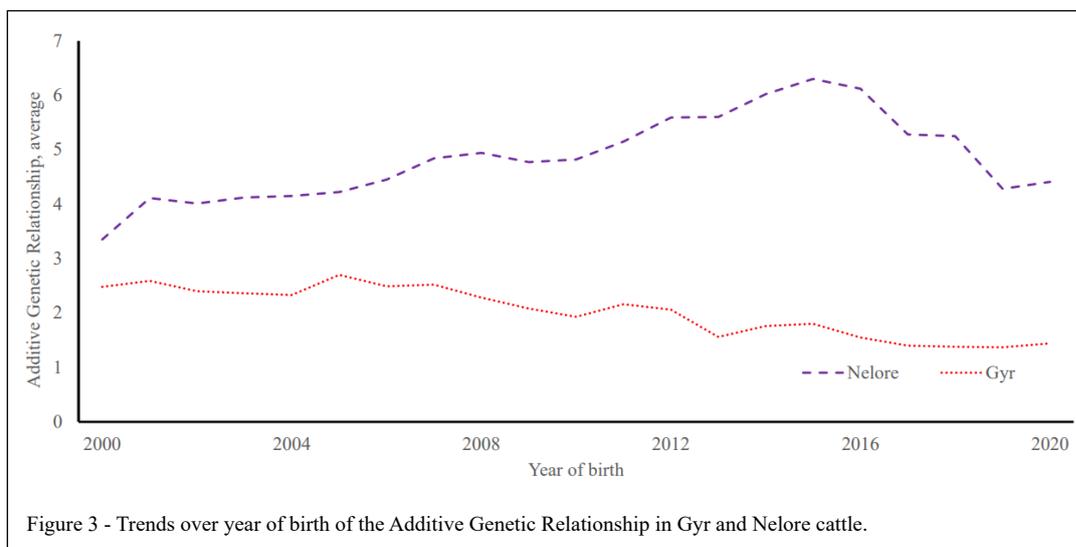

Figure 3 - Trends over year of birth of the Additive Genetic Relationship in Gyr and Nelore cattle.

Table 2 - Results for the number of generations and effective size.

Item	NGC	NGT	NGE	fa	fe
--Nelore--					
Max	6	13	8.2		
Mean	2.54	5.3	3.5	38.0	65.2
ΔF	4.2	1.5	2.9		
Ne	11.9	33.1	17.5		
--Gyr--					
Max	6	11	7.2		
Mean	1.72	3.4	2.3	59.0	145.7
ΔF	2.0	0.75	1.4		
Ne	24.7	66.4	36.2		

NGC, complete generations. NGT, maximum generations traced. NGE, equivalent complete generations. Maximum values (Max) and averages (Mean). ΔF, rate of change (%) in inbreeding levels. Ne, effective size as a function of the number of known generations. Effective number of founders (fe) and ancestors (fa).

fe; generally, fe>fa, as this difference increases it indicates a lower participation of the founders over generations. The fe / fa ratio shows a differential reproductive management and considers the possible bottlenecks that the population has experienced; as this ratio increases, it indicates that most of the ancestors were founders, with no bottlenecks (PRATES et al., 2012; BERNARDES et al., 2016). In NL, the published results for fa and fe are in the range of 30 to 617 and 53 to 639, respectively; the fe / fa ratio ranged from 0.56 to 0.98 (VOZZI et al., 2006; VOZZI et al., 2007; BORGES et al., 2013; COSTA et al., 2019). For GY, the reports of fe and fa are from 143 to 286 and 76 to 260, with estimates of Ne in the range of 35 to 308 (REIS et al., 2010; PRATES et al., 2012; SANTANA et al., 2014).

The estimates of Ne (Table 2) indicated that the increases in FI in GY are in the range of 1 to 2% and for NL greater than 2%; these results indicate the status of care to monitor the evolution of FI and AGR and their possible implications in genetic improvement. In other NL and GY populations, effects of inbreeding depression have been reported for growth and reproductive variables, with FI levels and percentages of inbred individuals of equal or lesser magnitude (AIDAR et al., 2000; SANTANA et al., 2010; PEREIRA et al., 2016). The Ne performed reflects the accumulation of genetic relationships between individuals and allows predicting changes in FI levels; low Ne are related to a decrease in genetic variability, an increase in mating between related individuals, allele fixation and a greater reduction in response to selection (GUTIÉRREZ et al., 2009; LEROY et al., 2013); for populations subject to genetic improvement, they recommend Ne that allow optimizing the response to selection with the minimum increase in FI (MEUWISSEN & SONESSON, 1998). In the relation of fe and FI, the AGR of a founder indicates the percentage of the population originated by him (GUTIÉRREZ & GOYACHE, 2005).

Table 3 presents the estimates of the GI by the four selection pathways, the values ranged from 6.3 to 7.9 years with a general average of 6.91 years. The magnitude of the GI can be associated with the production system, selection route and the market. For GY in milk production systems, the published

Table 3 - Estimates of the generation interval (years ± standard error), through four selection routes.

Breed	Father – son	Father – daughter	Mother – son	Mother – daughter	Average
Nelore	7.8 ± 0.24	7.5 ± 0.21	6.3 ± 0.17	6.4 ± 0.14	7.00
Gyr	7.9 ± 0.29	6.5 ± 0.19	6.7 ± 0.21	6.4 ± 0.19	6.88

GI are greater than 7 years with maximum values of 12 years (REIS et al., 2010; SANTANA et al., 2014; SANTANA et al., 2016). In NL populations, GI estimates have been reported in the interval of 6.5 to 10 years (BORGES et al., 2013; COSTA et al., 2019). In *Bos taurus* breeds specialized in meat production, reported GI estimates have been in the range of 5.4 to 7.7 years (PARLAND et al., 2007) and 4.9 to 8.2 years (RAMÍREZ-VALVERDE et al., 2018), or average values from 6.0 to 6.4 years (PICCOLI et al., 2014). For Brahman cattle, average GI of 4.0 years have been reported (CAVANI et al., 2018) or estimates in the range of 5.0 to 9.8 years (SANTANA et al., 2016; VÁSQUEZ-LOAIZA et al., 2021).

CONCLUSION

These results showed a summary of the genetic and reproductive management those breeders have carried out; they are useful in the design of selection programs, anticipating the relationship between response to selection and increases in inbreeding. In the next generations, the proportion of inbred animals and the average inbreeding should be followed up, and in due course the possible effects of inbreeding depression on variables of economic interest for genetic improvement schemes should be evaluated.

DECLARATION OF CONFLICT OF INTEREST

All authors declare no conflict of interest.

AUTHORS' CONTRIBUTIONS

All authors contributed equally for the conception and writing of the manuscript. All authors critically revised the manuscript and approved of the final version.

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