Interaction of genotype-environment Nellore cattle using models of reaction norms

Interação genótipo-ambiente de bovinos da raça Nelore utilizando modelos de normas de reação

Wéverton José Lima Fonseca ▪ Wéverson Lima Fonseca ▪
Carlos Syllas Monteiro Luz ▪ Gioto Ghiarone Terto e Sousa ▪
Marcelo Richelly Alves de Oliveira ▪ Karen Jamile Viana de Sousa ▪
Mardoqueu Bruno Guimarães Costa ▪ Augusto Matias de Oliveira ▪
Severino Cavalcante de Sousa Júnior

WJL Fonseca (Autor para correspondência) ▪ **WL Fonseca**
▪ **CLM Luz** ▪ **GG Terto e Sousa** ▪ **MRA Oliveira** ▪ **AM
Oliveira** ▪ **SC Sousa Júnior**
Federal University of Piauí (UFPI), Teresina, Piauí, Brazil
email: wevertonsbz@yahoo.com

KJV Sousa ▪ **MBG Costa**
Instituto Higher Education Multi – IESM, Brazil

Abstract The aim with this review was to approach the importance of the genotype-environment interaction of Nelore cattle by using reaction norms models. The beef cattle's ranching has stood out as one of the main activities of the Brazilian agribusiness, inclusive in the international setting. One way to assess the genotype-environment interaction for various traits in beef cattle is the use of reaction norm models. The genotype's reaction norm is the systematic change in average phenotypic expression in response to a change in the environmental variable, and describes the phenotype of an animal as an environmental continuous function and expresses the phenotype as polynomial function of the environmental value, wherein they are assumed to be under genetic influence. Thus, the reaction norm describes characteristics which gradually and continuously change on an environmental gradient, can thus be used to study the genotype-environment interaction.

Palavras-chave: conforto térmico, nutrição, tempo de pastejo

Resumo Com essa revisão de literatura objetivou-se abordar a importância da iteração genótipo-ambiente de bovinos da raça Nelore utilizando modelos de normas de reação. A bovinocultura de corte vem se destacando com uma das principais atividades do agronegócio brasileiro, inclusive no cenário internacional. Uma das formas de se avaliar a interação genótipo-ambiente para várias características em bovinos de corte é a utilização dos modelos de normas de reação. A norma de reação de um genótipo é a mudança sistemática na expressão média fenotípica em resposta a uma mudança na variável ambiental, e descreve o fenótipo de um animal como função contínua do ambiente e expressa o fenótipo como função polinomial do valor ambiental, em que são assumidos estar sob influência genética. Dessa forma, a norma de reação descreve características que mudam gradualmente e continuadamente sobre um gradiente ambiental, assim, pode ser utilizado para o estudo da interação genótipo-ambiente.

Keywords: thermal comfort, nutrition, grazing time

Introduction

In Brazil, beef cattle has emerged as one of the most important production chains in the country, as the production of beef that has been featured in the Brazilian agribusiness sector, making Brazil one of the largest producers in the world, including in the scenario international. In this scenario, Brazil stands out for its ability to increase its agricultural production, especially of animal protein, which always excelled internationally (Carvalho et al 2013).

The genotype-environment interaction (IGA) has been disregarded in the assessment of individual breeding values in most genetic evaluation programs. May damage the genetic progress of the populations of beef cattle due to inappropriate use of players that were extremely important consideration in the genetic evaluations when there is a

genotype is more efficient in an environment that in another. The relative merit exists when two or more genotypes is dependent on the environment in which they are compared (Mascioli et al 2006).

The model reaction norms (MNR) have been used to analyze the importance of genotype by environment interaction of different characteristics, so that the expression of a genotype in different environments is described as standard reaction environmental value or gradient. One way to assess the genotype-environment interaction and that has been widely used for various traits in beef cattle is the use of models of reaction norms (Espasandin et al 2011).

Thus, in this literature review we aimed to approach the importance of the genotype-environment interaction for growing traits of Nelore cattle by using reaction norm models.

Genotype environment interaction

The genotype environment interaction (IGA) is basically in the description of the phenomenon occurring in changing the performance of different genotypes, when they are subject to change and when subjected to different environments. This interaction can be expressed in different ways and with different intensities, and the most extreme expression can be represented by the reversal of classification of different genotypes depending on the environment were evaluated (Pegolo et al 2009).

However, the genotype-environment interaction can cause changes in the magnitude of genetic, environmental and phenotypic variances allowing changes and selection strategies, so the environment can narrate as one of the factors that affect the individual's performance. A (IGA) causes changes in performance rating of animals in different environments, cause changes in the absolute or relative magnitude of genetic variance, environmental and phenotypic (Correa et al 2009).

Eventually, the IGA is evaluated by means of genetic correlations obtained by estimation models that consider a particular character in different environments as distinct features. However, the genetics and the environment is of paramount importance for breeding, as well as its IGA in the study of characteristics of economic interest. Are disregarded as well, the differences in the behavior of the same genotype at different levels of production and the particular variances of different locations evaluated (Diaz et al 2011).

The genotype-environment interaction is of great importance for breeding, since its existence is possible that the best genotype in an environment will not be more favorable in another. Several surveys were conducted in order to verify the existence of (IGA) for growth traits through the estimation of genetic correlations of the same trait in different environments or the value of the Spearman correlation between breeding values of bulls in the environments (Nepomuceno et al 2013).

Methodology for the study of the interaction genotype environment

The methodology that estimates the values of Pearson and Spearman correlation coefficients, in genotype environment interaction studies, as the authors Alencar et al (2005) and Toral et al (2004), indicating, respectively, the influence of the environment on estimates of breeding values and changes in ranking of animals based on these estimates in different environments. These estimators are widely used in studies of IGA, as is presented by Carvalho (2007) found a high correlation coefficient of Spearman's rank for weaning weight of Canchim cattle between the Southeast and Midwest of Brazil, indicating that best bulls ranked in a region also had similar position in another region.

Another methodology for the assessment of genotype environment that has been highlighted in the scientific community is the one that uses Bayesian inference (Simonelli 2004; Falcon et al 2006), and others make use of both models and reaction norms to the environment (Calus and Veerkamp 2003; Kolmodin Bijma 2004). Currently, research in interaction with genotype-environment-reaction using standard models is gaining prominence. The method described allows the phenotype expressed by a genotype in an environmental gradient, which is useful when the phenotypes vary gradually and continuously under different environments (De Jong 1995).

In studies conducted by Espasandin et al (2011) evaluated the importance of genotype-country interaction in the genetic evaluation of Angus cattle in Brazil and Uruguay. Bi-character analyzes were performed considering the characteristic weaning weight in each country as different characteristics. In addition, the authors compared two statistical models, with the results obtained, the authors reported the existence of genotype-environment interaction and the need to consider it in the joint genetic evaluations of Angus cattle in Brazil and Uruguay.

According to Ambrosini et al (2012) evaluated the genotype-environment interaction for P365 in cattle Nelore Mocha Northeast Brazil, through reaction of standard models (MNR), via random regression with Bayesian approach. Based on this research the Spearman correlation estimates ranged from 0.69 to 0.99, in different environments, which suggests a change in the classification. The authors concluded in this study that the identification of genotype-environment interaction level necessitates specific assessments of individuals and herds for low environments, medium and high level of production.

Recently, Nepomuceno et al (2013) working with Nellore cattle raised on pasture, analyzed the effect of

genotype-environment interaction on the weights at 120 and 210 days of age. In the study by these authors, estimates of genetic correlations between the performances of the progeny of the same player in different states ranged from 0.13 to 0.70; It concluded that there are important genotype-environment interaction, both in weight at 120 days of age and weight at 210 days of age, which directly influenced the prediction of genetic value of breeding, resulting in different classification of the same bull in each state.

Random regression models

In Brazil, the random regression models (MRA) allows to estimate genetic parameters for coefficients in growing animals weights by the method of restricted maximum likelihood. The use of such random regression models weight characteristics obtained at different ages enables the achievement of ESD (expected progeny differences) for every age of the animal, in addition, allows the accuracy of the assessment is increased due primarily to elimination of the pre-ajustes the data and the possibility of working with all available and appropriate covariance weighing (Sousa Júnior et al 2010).

Several studies using random regression models have been undertaken to estimate genetic parameters for growth traits in beef cattle (Palharim et al 2013). Other researchers to use the (MRA) to evaluate growth characteristics in beef cattle, reported difficulties in the use of high degree polynomials and lack of uniformity adjustment along the curve (Meyer 2005). With the use of weights obtained from birth to adulthood, requiring polynomials higher grades, the use of these models can result in unrealistic estimates and convergence problems (Boligon et al 2010).

Random regression models are more suitable for modeling weights, because they consider the continuous modification of the phenotype and all fixed and random effects that compose it and its parameters in the individual's age (Valente et al 2008). The random regression models (ARM) do not require adjustments, which preserves the quality of information and prevents the elimination of data to be collected in distant ages set as default (Robbins et al 2005). The best qualitative and quantitative use of information has a positive impact on the accuracy of ratings (Bertrand et al 2006).

According to Albuquerque and Meyer (2001) working with Nellore herds of animals, estimated covariance functions using these random regression models (MRA) for records of birth weights at 630 days of age, and concluded that random regression adequately described changes of covariance with age. However, analyzed the growth curve of birth Nellore to 683 days of age using multi features models and random regression and observed that the random

regression models were more sensitive to sampling problems that multi features (Noble et al 2003).

Reaction norms models

The reaction of standard models are being used to assess the effects of genotype environment interaction (IGA) on different traits of economic importance. The expression of a genotype in different environments is described as a linear function of a value or environmental gradient. As the ways of evaluating the (IGA), the application of the standard reaction models (MNR) have stood out throughout the country, with research on the various livestock species as Pegolo et al (2009), for cattle cutting; Fikse et al (2003); Bohmanova et al (2008), for dairy cows; Pollott and Greeff (2004) for sheep; and Knap and Su (2008) for pigs.

In the standard reaction model, the expression of genotypes in different environments is described as a linear function (standard reaction) or an environmental gradient value, or the standard reaction describes the phenotype expressed by a function of genotype and environment (Kirkpatrick et al 1990). However, the genotype does not determine only one phenotype, but rather a range of possible phenotypes, a standard reaction. Although this method include information of a dependent variable in the explanatory model has the advantage of objectively discriminate environments as more or less favorable (Kolmodin et al 2002).

According to De Jong (1990), the reaction norm of a genotype is the systematic change in average phenotypic expression that occurs in response to a systematic change in the environmental variable. The reaction norm model (RNM) characterizes the phenotype of an animal as a continuous function of the environment and expresses the phenotype as a polynomial function of the environmental value, wherein the polynomial coefficients are assumed to be under genetic influence (De Jong 1995). However, the food norms describe traits gradually in an environmental gradient which may be used to study genotype-environment interaction.

Through the reaction of standard models, an extremely useful methodology called "random regression", which allows drawing a line from the animal's genotype in each environment in relation to the environmental gradient. In environmental sensitivity analysis, the genotype performance is regressed from the average population performance in each environment (Falconer and Mackay 1996). This method includes information of a dependent variable in the explanatory model has the advantage of objectively discriminate environments as more or less favorable and was successfully used to identify the genotype environment interaction in dairy cattle (Kolmodin et al 2002).

The NR reaction norms have been widely applied to detect the presence of the interaction-genotype-environment for multiple traits of economic importance in cattle milk (Calus et al 2005; Calus et al 2006; Windig et al 2006; Strandberg et al 2009). Most research has analyzed milk production and its components, however, are few studies addressing indicator characteristics of sexual precocity. In this sense, in Holstein cattle, genetic parameters estimated using reaction norms for the characteristic birth-conception interval in various environments, defined by an environmental stress index (Oseni et al 2004).

In Brazil, Pegolo et al (2009) using information from 366 herds Nellore, studied the presence of genotype-environment interaction for weight adjusted to 450 days of age using reaction norms.

The authors evaluated various models in which the definition of the environmental gradient ranged, according to six different environments. For all the evaluated models, estimates of components of (co) variance and heritability had a similar behavior. The heritability estimates for weight adjusted to 450 days of age were higher in extreme environments (favorable or unfavorable), ranging from 0.35 to 0.40, and lower in intermediate environments, 0.20 to 0.25. The genetic correlations between weights of groups from opposite environments were low, less than 0.80, indicating the presence of genotype environment interaction for this trait.

Have Corrêa et al (2009) studied the presence of IGA to the standard post-weaning gain to 345 days in Devon cattle breed in Rio Grande do Sul. The authors compare several models for the estimation of genetic parameters for this feature via reaction norms obtained by random regression. Estimates of the environmental gradient were obtained based on the solution of the deviations of contemporary groups. Hierarchical models of reaction norms with homogeneous and heterogeneous residual variances and random linear regression coefficients corresponding to the animal's reaction standard were applied to estimate the covariance components. According to the authors, the model that best fit to the data was the reaction norms with homogeneous residual variance.

Covariance functions

The estimated covariance functions (FC) are considered, to date, interesting alternatives to work with data that enables longitudinal description of changes in the covariance function of the prediction time and the variances and covariances for points along the growth curve animals. The (FC) are equivalent of "finite-dimensional" the covariance matrix in a multivariate analysis of "finite-dimensional", can be obtained by the matrices of variance and covariance of these models, or from the covariance

matrices of the estimated regression coefficients by random regression models (Meyer, 1998).

According om Kirkpatrick and Heckman (1989) present three advantages of the model covariance functions over traditional models multi-features. The first is that the covariance functions produce a description for any point along a continuous scale measures, allowing the covariance measured between ages not be easily obtained by interpolation. Another advantage is that each covariance function has a set of eigenvalues and eigenfunctions that provide information about the direction in which the mean curve (growth, lactation, etc.) are more likely to be modified by selection, since they have greater genetic variance.

A covariance function can be defined as a continuous function that provides the features of covariance measurements at different points of a trajectory, describing the covariance between the measures taken at certain ages, as a function of these ages (Van Der Werf and Schaeffer, 1997). Thus, when setting a random regression model, we assume a certain covariance structure between random regression coefficients, which is imposed by the fitted function, and can be characterized by a continuous function and a covariance function (Person, 2011).

According to Meyer (1998), the random regression models are a special case of covariance functions, and allow to estimate the coefficients of the covariance functions by the restricted maximum likelihood (REML). In growth for selection experiment, using random regression model to estimate genetic parameters for days to calving in Nelore females, indicating that its application to records of days for delivery provided detailed analysis of the behavior of genetic covariance and the genetic value the female reproductive performance over the course of your life, it may be appropriate in many studies (Mercadante et al 2002).

Conclusions

Brazil has the second biggest cattle population basically composed of zebu in the world, making it one of the most important supply chains in the country. Thus, the beef cattle herds present great variability in production between and within the different regions of Brazil.

The reaction norm models (RNM) are being used to assess the effects of the genotype environment interaction on different traits of economic importance. In the RNM, the expression of genotypes in different environments is described as a linear function of an environmental gradient, ie the reaction norm describes the phenotype expressed by a genotype as function of the environment.

The breeding programs of beef cattle aim to change the averages of the traits of economic interest and increase the profit on production systems. However, the reaction norms allow determining alternative routes of development

and metabolism of a genotype in various possible environments.

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