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# Multi-trait selection index and cluster analyses in Angus cattle

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## Abstract

In breeding programmes, the genetic selection process is based on the prediction of animal breeding values, and its results may vary according to the employed selection method. The current study developed an economic selection index for animals of the Angus breed; performed cluster analyses using the breeding values in order to evaluate the genetic profile of the animals candidates to selection, and compared the obtained results between the economic selection index and the cluster analyses. The evaluated traits included weaning weight, 18-month weight, scrotal circumference, fat thickness and ribeye area. Economic values were obtained using bioeconomic modelling, simulating a complete cycle production system of beef cattle breeds in Brazil, and the selection objective were the weaning rate and slaughter weight. The chosen selection index was composed of all of the traits used as selection criteria for the simulated production system. During the cluster analyses, the population was divided into two to four groups, in which the groupings containing potential animals were assessed. The animals of the grouping which was used for comparison with the selection index were identified, and most of the bulls that were included in the index were among the best in the analysed group. These results suggest that the cluster analyses can be used as a tool for the selection of animals to be used as parents for future generations.

## Introduction

Several traits are considered to be economically important in beef cattle production. The impact of these traits on the production system has been employed in economic selection indices. In recent decades, these indices have been used more frequently in beef cattle production, enabling the combination of economic (economic values) and genetic (genetic and phenotypic variances and covariances) information. These data can be applied to several traits simultaneously, with the purpose of obtaining maximum genetic progress to quickly achieve the breeding objectives of a breeding programme (Hazel, 1943). Also, the economic index is more efficient when it considers several traits that differ in variability, economic importance, heritability and degree of genetic and environmental correlation (Hazel, 1943; Hazel *et al.*, 1994).

The first step required to generate an economic selection index is to define the breeding objectives (Ponzoni and Newman, 1989; Groen *et al.*, 1997), given they exert considerable influence on the development of genetic improvement strategies and the identification of traits that constitute the selection criteria (Amer *et al.*, 1994). Traits that can be measured easily, with low cost, with medium to high heritability and that are related to the targeted trait should be employed as selection criteria to predict the breeding values of the animals (Euclides Filho, 1999; Queiroz *et al.*, 2005).

Genetic parameter estimates and predictions of breeding constitute the necessary information for the development of selection indices. The genetic selection process is based on the prediction of breeding values of animals, intensity of selection, generation interval and magnitude of genetic variance. The selection efficiency and the expected genetic progress are determined by the predictive accuracy of the breeding values (van der Werf, 2006), which takes into account the quality and quantity of pedigree information and the phenotypes of the animals designated for selection.

Cluster analysis can be applied to examine information using significant amounts of data when multiple variables are assessed simultaneously. There are basically two types of cluster analyses: hierarchical and non-hierarchical. Hierarchical cluster analysis aggregates rows of databases (animals, individuals, objects, etc.) based on grouping characteristics. The result of this analysis is expressed by a graph (dendrogram), in which individuals are ordered by proximity and grouped according to the chosen variables. There are several methods of

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grouping. One that is widely used is Ward' method (Ward, 1963). According to Hair *et al.* (2009), the use of this technique results in groupings of approximately equal sizes due to the internal variation minimization of the groups. The non-hierarchical cluster analysis employs the K-means method (Hartigan, 1975; Hartigan and Wong, 1979), and its objective is to agglomerate individuals in previously established groups, based on Euclidean distance, which is used to measure the distance between individuals and the centre of the group, known as centroid. The centroid consists of a vector of means of the variables used in the cluster analysis. In general, the number of groups is pre-established in hierarchical cluster analyses, in which there is no defined criterion for group creation (Hair *et al.*, 2009).

Cluster analysis can be used to group animals based on the breeding values of traits that are evaluated in breeding programmes to detect the genetic profile of the groups of animals that meet the programme selection objectives. This analysis has been used to explore the genetic curve pattern to identify the genetic profile of the genetic curve for milk production in Holstein cows, based on the breeding values regarding milk production (Cruz *et al.*, 2016; Savegnago *et al.*, 2016).

The objectives of the current study were (1) to develop an economic selection index using economic values for Angus cattle; (2) to perform cluster analyses using the breeding values in order to evaluate the genetic profile of the animals candidates to selection, and (3) to compare the obtained results between the economic selection index and the cluster analyses to verify if the same bulls were identified as the best sires in both methods of analysis.

## Materials and methods

### Economic values

The economic values were obtained by bioeconomic modelling using the Microsoft Excel 2010 computer programme to simulate a complete cycle in Angus–Nellore crossbred production system. In order to obtain the economic selection index for Angus bulls, the used breeding objective was chosen according to economically significant traits and determined according to the methodology described by Ponzoni and Newman (1989). The adopted breeding objective consisted of the weaning rate and slaughter weight according to the aim of the simulated production system, which was the production of crossbred animals for commercialization at the moment of slaughter.

Information on biological parameters (mortality rate, pre-slaughter mortality, disposal rate, weaning rate, conception rate and weights from birth to slaughter), gathered from technical and scientific literature (Kaps *et al.*, 2000; Martha *et al.*, 2003; Weber *et al.*, 2009; Valadares Filho *et al.*, 2010) and information from real herds, were used in the simulation of a stabilized herd, obtaining the number of animals per category, which was used to calculate the sources of income and expenses (Anualpec, 2017; Cepea, 2018) in the evaluated system. The model comprised an intensive production system, distributed in pasture areas containing *Brachiaria brizantha* cv. Marandu, and the herd consisted of 1000 Nellore cows, including 24-month-old heifers, and seven Aberdeen Angus bulls. Calves were weaned on average at 7 months of age and maintained in the pasture with their mothers. After weaning, they were separated into batches by sex, and remained in the pasture until 18 months of age, after which they were transferred to a feedlot until 21 months of age. At the end of the cycle, all of the animals (males and females) were sold for slaughter; disposal cows and bulls had the same destination. The average prices of the expenses and revenue components for the production system are shown in Tables 1 and 2, respectively.

**Table 1.** Annual expenses of the complete-cycle production system

| | Values (US$) | Costs (proportion) |
|---|---|---|
| Pasture (planting and maintenance) | 192 342.50 | 0.35 |
| Food (supplementation) | 264 497.84 | 0.48 |
| Mineral salt | 10 485.38 | 0.02 |
| Veterinary costs (vaccination, labour, insemination) | 16 598.34 | 0.03 |
| Purchase of animals (replacement) | 65 887.88 | 0.12 |
| Total | 549 811.94 | 1.00 |

**Table 2.** Annual revenues of the complete-cycle production system

| | Values (US$) | Revenues (proportion) |
|---|---|---|
| Male calves at weaning | 376 907.36 | 0.43 |
| Female calves at weaning | 361 215.46 | 0.45 |
| Disposal cows | 87 700.50 | 0.10 |
| Disposal bulls | 1409.33 | 0.02 |
| Total | 827 232.65 | 1.00 |

The economic values were based on economic and productive assessments, relating the expenses, revenues, biological information and management of the production system, which were calculated for each evaluated trait. The influence on the annual profitability of the production system was verified by simulating 1.0% increase in the performance of a particular trait, maintaining the others traits constant, according to the following equation:

$$EV = \left(\frac{1}{n}\right) \times \left(\frac{MP}{GG}\right)$$

where: $EV$ economic value; $n$ corresponds to the number of animals in each category; $MP$ represents the marginal profit obtained by the difference between the profit before and after trait improvement, and $GG$ was calculated by the difference between the performance of the trait before and after the improvement (Groen *et al.*, 1997). The calculations were based on Brazilian currency (R$) and converted to North American currency (US$) using the average price in 2017 (US$1.00 = R$3.19). The economic value was expressed in American currency (US$) per change in trait unit, based on cow/year. The profit equations can be represented by the following equations:

$$P = (P_M + P_F + P_{DC} + P_{DB}) - TE$$

$$P_M = Nx0.5x(1 - R_{MW})x(1 - R_{M12})x(1 - R_{M18})x(1 - R_{MS}) \\ x(FW_M xUS/@)$$

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$$P_F = Nx0.5x(1 - R_{MW})x(1 - R_{M12})x(1 - R_{M18})x(1 - R_{MS}) x(FW_F xUS/@)$$

$$P_{DC} = (N_C + N_H)x(1 - R_M) + (1 - R_{DC})x(FW_{DC} xUS/@)$$

$$P_{DB} = N_B x(1 - R_{DB})x(FW_{DB} xUS/@)$$

where $P$, marginal profit; $P_M$ and $P_F$, profit from sale of male and female, respectively; $P_{DC}$, profit from sale of disposal cows; $P_{DB}$, profit from sale of disposal bulls; $TE$, total expenses; $N$, number of animals born; $R_{MW}$, mortality rate from birth to weaning; $R_{M12}$, mortality rate at 12 months; $R_{M18}$, mortality rate at 18 months; $R_{MS}$, mortality rate at slaughter age; $FW_M$ and $FW_F$, final weight of male and female, respectively; $N_C$, number of mature cows; $N_H$, number of heifers 2 years; $R_M$, mortality rate of cows; $R_{DC}$, discard rate of cows; $N_B$, number of bulls; $R_{DB}$, discard rate of bulls; $FW_{DC}$ and $FW_{DB}$, final weight of disposal cows and bulls, respectively.

### Estimation of variance components and genetic parameters

The data regarding performance and pedigree of the animals of the Angus breed were provided by *Gensys Consultores Associados* S/S Ltda. and PROMEBO (*Programa de Melhoramento de Bovinos de Carne* - Beef Cattle Breeding Programme) of the National Breeders Association (ANC) 'Herd-Book Collares'. The employed traits consisted of weaning weight, 18-month weight, scrotal circumference, fat thickness and ribeye area. The 18-month weight was adjusted to 550 days as recommended by BIF (1996), and calculated by applying the following equation:

$$W18_{aj} = \frac{W18 - WW}{N_1} \times 345 + W_{205}$$

where: $W18$ and $WW$ represent 18-month weight and weaning weight, respectively, expressed in kilograms, and $N_1$ corresponds to the number of days from weaning until 18 months of age, and $W_{205}$ correspond to adjusted 205-day weight calculated as recommended by BIF (1996).

The assembly of the files for analyses was performed using the SAS software (2003) computer programme for data file editing. Four seasons were created with the month of the year (1 = October, November and December; 2 = January, February and March; 3 = April, May and June; 4 = July, August and September) for dates of birth, weighing at weaning and yearling, date of scrotal circumference measurement and date of ultrasound for subcutaneous fat thickness and ribeye area. The contemporary groups were formed for birth weight with animals from the same farm, year, sex and season of birth. For the weaning weight and yearling weight, the contemporary groups contained animals of the same farm, sex, year of birth, year and season at the time of measurement and management group. For scrotal circumference, the contemporary groups were composed of animals from the same year and season of birth, management group and year and season at the time of measurement. For the ribeye area and the subcutaneous fat thickness the contemporary groups included animals of the same sex, year of birth, management group, year and season at the time of ultrasound.

Were deleted records of animals with incomplete information, bulls with less than five offspring, cows with reproductive ages of less than three and greater than 13 years, contemporary groups with less than five animals and observations displaying plus or minus 3.5 standard deviations from the mean of the traits within the contemporary group.

After data editing, a total of 1242 animals remained with information regarding all of the traits considered for analyses. The animal model for all of the traits included the fixed effect of the contemporary group, the random effects of the animals (direct) and the random residual effects. For weaning weight, the age of cow at calving was used as a covariate (linear and quadratic). For scrotal circumference, fat thickness and ribeye area, the age of the animals on the date in which the measurement was taken was considered as a covariate (linear and quadratic). The pedigree file contained 220 045 animals, which were used in the relationship matrix. The genetic parameters were estimated in bivariate analyses, employing the restricted maximum likelihood method using the WOMBAT software (Meyer, 2007). The animal model applied can be written as:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} * \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} * \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} M_1 & 0 \\ 0 & M_2 \end{bmatrix} * \begin{bmatrix} m_1 \\ m_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

where: $y_1$ and $y_2$ are the vectors of observation for traits 1 and 2; $X_1$ and $X_2$ represent the incidence matrices relating the elements of trait 1 and 2 to the fixed effects; $\beta_1$ and $\beta_2$ correspond to the vectors of the fixed effects for traits 1 and 2; $Z_1$ and $Z_2$ are incidence matrices which relate the elements of trait 1 and 2 to the direct effects; $a_1$ and $a_2$ represent the vectors of the random effects of the animal (direct) for traits 1 and 2; $M_1$ and $M_1$ are incidence matrices which relate the elements of traits 1 and 2 to the maternal additive genetic; $m_1$ and $m_2$ represent the vectors of the random maternal genetic effects; and $e_1$ and $e_2$ are the vectors of the random residual effects for traits 1 and 2.

### Development of the economic selection index

The selection index was defined for animals of the Angus breed in order to select potential bulls for the production of crossbred animals (Angus × Nellore). Weaning rate and final weight at slaughter were adopted as the breeding objective for the selection index. In order to achieve the objective, weaning weight, 18-month weight (adjusted to 550 days of age), scrotal circumference, subcutaneous fat thickness and ribeye area were used as selection criteria.

The Angus breed data file did not contain the measurements of the final weight at slaughter. Therefore, in order to construct the index, the final weights were estimated using the 18-month weights and the weight gain from weaning to 18-month. The economic selection index (I) was generated by combining the expected progeny difference (EPD) of the animals for each trait with their respective index coefficients ($b$) of the selection criteria, according to the following equation:

$$I = (b_1 \times EPD_1) + (b_2 \times EPD_2) + \cdots + (b_n \times EPD_n)$$

The methodology used for the calculation of regression coefficients of the indices was proposed by Schneerberger *et al.* (1992),

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where the coefficients are calculated as

$$b = G_{11}^{-1} \times G_{12} \times v$$

where $b$ is the vector of selection index coefficients; $G_{11}$ represents genetic (co-) variances matrix among the selection criteria in the index; $G_{12}$ corresponds to the genetic covariance matrix between the breeding objective and the selection criteria, and $v$ is the vector of the economic values of the breeding objective. The regression coefficients were calculated using the R software (R Core Team, 2016).

Some (co) variance components between the objectives and selection criteria for Aberdeen Angus used in the current study had been estimated previously by Fernandes *et al.* (2018). The covariance components not found were assumed as zero in the simulation of the current study.

### Cluster analyses

Hierarchical and non-hierarchical cluster analyses were performed using predicted breeding values of the traits used as selection criteria (weaning weight, 18-month weight, scrotal circumference, subcutaneous fat thickness and ribeye area) to group animals based on similarities of the genetic values in order to evaluate the genetic profile of the groups within the population. The breeding values were standardized using the normal standard distribution ($z$ scores) before carry out cluster analyses. The hierarchical cluster analysis was used to choose the number of clusters into which the population could be initially divided. The Euclidean distance was applied as a measurement of dissimilarity between the animals, and the employed clustering algorithm for group formation was Ward' method (Ward, 1963). After defining the number of clusters, the non-hierarchical analysis using the K-means method was conducted to explore the genetic profile of the groups, based on the breeding values of the evaluated traits. In both analyses, the genetic values of the animals were considered for all the traits used as selection criteria. The PROC CLUSTER procedure of the SAS software (2003) was used for cluster analysis.

## Results

### Economic values and selection index

The weaning rate and slaughter weight, considered as the breeding objectives for the complete cycle production system, displayed a positive changes in profit after the simulation of the selection process (Table 3).

The estimated genetic correlations and heritabilities of the traits used in the analysis of the selection index are shown in Table 4. Weaning weight exhibited a high genetic correlation with 18-month weight and slaughter weight, and showed a median correlation with scrotal circumference, fat thickness and ribeye area. In other words, the selection of one of these traits increases the other. A positive and median magnitude genetic correlation was observed between the scrotal circumference and the other traits, ranging from 0.41 to 0.57, indicating that the use of this attribute as a selection criterion contributes to the identification of animals with greater growth potential, and is also associated with animals displaying improved carcass quality. The fat thickness trait exhibited moderate correlations with the growth traits and the scrotal circumference, ranging from 0.24 to 0.45.

**Table 3.** Marginal profit (MP), genetic gain (GG) and economic value (EV) of the breeding objective after the 1.0% increase in performance of the trait

| Trait | MP[a] (US$) | GG | EV[b] (US$) |
|---|---|---|---|
| WR[c] (kg) | 4133.32 | 0.89 | 4.66 |
| SW[d] (kg) | 6234.69 | 5.38 | 1.16 |

[a]Based on 1000 cows/year.
[b]Based on cow/year.
[c]WR = weaning rate.
[d]SW = slaughter weight.

The ribeye area showed medium to high correlations with all of the traits, indicating that some of the genes that control the ribeye area also regulate the other traits. Thus, the improvement of one trait will possibly cause an increase in another.

Genetic correlations of slaughter weight with the other analysed traits were medium to high. Moderate correlations were observed with the carcass traits, fat thickness and ribeye area, and the high ones with the growth traits and scrotal circumference. Heritability estimates of the traits ranged from 0.12 to 0.62. These correlations and heritabilities show the significance of the weaning rate and slaughter weight as breeding objectives within the production system. The obtained values demonstrate the efficiency of the use of growth traits to achieve carcass with minimum fat thickness demand by cold stores, taking into account that the farmer aims at producing early animals without losses in carcass quality.

The economic values (EV) and genetic (co-) variance matrices of the breeding objective (weaning rate – WR and slaughter weight – SW) and the selection criteria (weaning weight – WW; 18-month weight – W18; scrotal circumference – SC; subcutaneous fat thickness – FT; and ribeye area – RA) employed in the development of the economic selection index for the simulated complete cycle production system are shown below:

$$EV = \begin{bmatrix} 1.16 \\ 4.66 \end{bmatrix}$$

$$G_{12y} = \begin{bmatrix} \sigma_{SW\ WW} & \sigma_{WR\ WW} \\ \sigma_{SW\ W18} & \sigma_{WR\ W18} \\ \sigma_{SW\ SC} & \sigma_{WR\ SC} \\ \sigma_{SW\ FT} & \sigma_{WR\ FT} \\ \sigma_{SW\ RA} & \sigma_{WR\ RA} \end{bmatrix} G_{12y} = \begin{bmatrix} 121.59 & 0 \\ 112.50 & -0.35 \\ 11.75 & 0.68 \\ 3.63 & 0 \\ 34.68 & 0 \end{bmatrix}$$

$$G_{11y} = \begin{bmatrix} 120.31 & 186.51 & 8.4584 & 0.5906 & 13.745 \\ 186.51 & 326.75 & 15.405 & 2.6725 & 35.325 \\ 8.4584 & 15.405 & 1.386 & -0.0377 & 2.739 \\ 0.5906 & 2.6725 & -0.0377 & 0.2778 & 1.693 \\ 13.745 & 35.325 & 2.739 & 1.693 & 60.36 \end{bmatrix}$$

With the economic value and regression coefficients ($b$) obtained, the economic selection index for the complete cycle system was constructed as

$$I_{=} 11.651 \times EPD_{WW} - 9.108 \times EPD_{W18} + 47.614 \times EPD_{SC} + 93.173 \times EPD_{FT} - 1.430 \times EPD_{RA}$$

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**Table 4.** Estimated genetic correlations (above diagonal) and heritabilities (diagonal) of the traits used in the selection index

| Traits[a] | WW | W18 | SC | FT | RA | SW |
|---|---|---|---|---|---|---|
| WW | 0.12 (±0.010) | 0.91 (±0.020) | 0.48 (±0.060) | 0.24 (±0.090) | 0.31 (±0.090) | 0.88 (±0.030) |
| W18 | | 0.22 (±0.020) | 0.41 (±0.060) | 0.32 (±0.080) | 0.39 (±0.070) | 0.94 (±0.020) |
| SC | | | 0.61 (±0.040) | 0.45 (±0.100) | 0.42 (±0.080) | 0.57 (±0.060) |
| FT | | | | 0.20 (±0.040) | 0.62 (±0.070) | 0.29 (±0.020) |
| RA | | | | | 0.51 (±0.050) | 0.42 (±0.090) |
| SW | | | | | | 0.16 (±0.020) |

[a]WW = weaning weight; W18 = 18-month weight; SC = scrotal circumference; FT = fat thickness; RA = ribeye area; SW = slaughter weight.

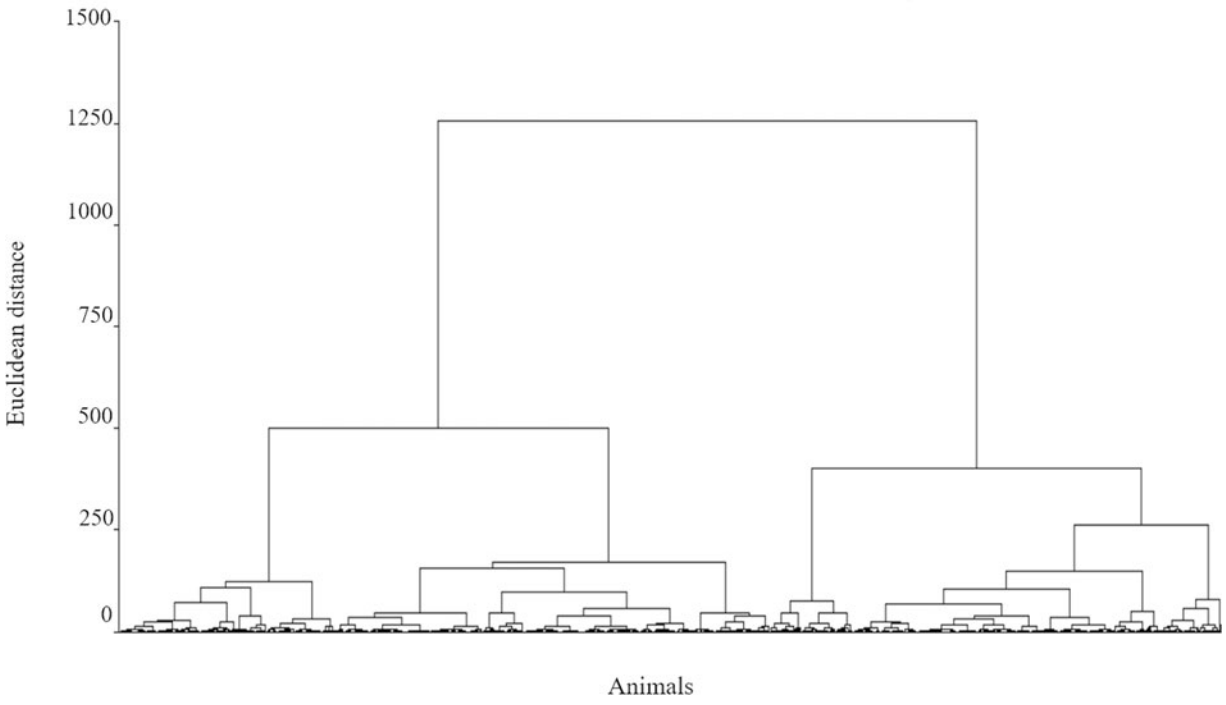



**Fig. 1.** Dendrogram based on EBVs for the traits of the weaning weight, 18-month weight, scrotal circumference, subcutaneous fat thickness and ribeye area of Angus bulls.

where: *EPD* is the expected progeny difference, *WW* is the weaning weight, *W*18 is the 18-month weight, *SC* is the scrotal circumference, *FT* is the fat thickness, *RA* is the ribeye area.

### *Cluster analyses*

The traits used in the cluster analysis were the same as those used in the calculation of the selection index: weaning weight, 18-month weight, scrotal circumference, subcutaneous fat thickness and ribeye area. According to the dendrogram of the hierarchical cluster analysis, the population could be separated into two to four groups (Fig. 1). The means of the breeding values for the traits in each grouping revealed that the population contained groups of animals with different genetic profiles (Fig. 2).

The non-hierarchical analysis with the grouping of the animals into two clusters (Fig. 2*a*) exhibited bulls with EBVs that were positive and above average regarding all of the traits in group 1, containing 190 of the 1242 analysed animals. The other bulls were clustered into group 2, with EBVs that were negative and below average. In Fig. 2*b*, divided into three groups, group 2 displayed EBVs that were closer to the mean. Consequently, this grouping will not contribute to the genetic improvement of the population regarding this set of traits. Group 3 showed EBVs that were below the mean and with negative values. Therefore, the disposal of these animals should be considered. The animals in group 1 retained the highest EBVs in the population, rendering them the optimal sires to be used for selection, given the objective is beef cattle production considering the evaluated traits. In this analysis, group 1 exhibited the highest number of grouped animals (976), followed by group 2 (264) and group 3 (02).

When the non-hierarchical analysis was conducted considering the four groups (Fig. 2*c*), the estimated breeding values of group 3 (485 animals) grouped the bulls with the best EBVs, with all values above average. Group 1 (353 animals), group 2 (402 animals)and group 4 (2 animals) concentrated its animals close to average and with some negative values. After obtaining the economic selection index and the clusters formed by the cluster analyses, it was possible to identify the best bulls considering

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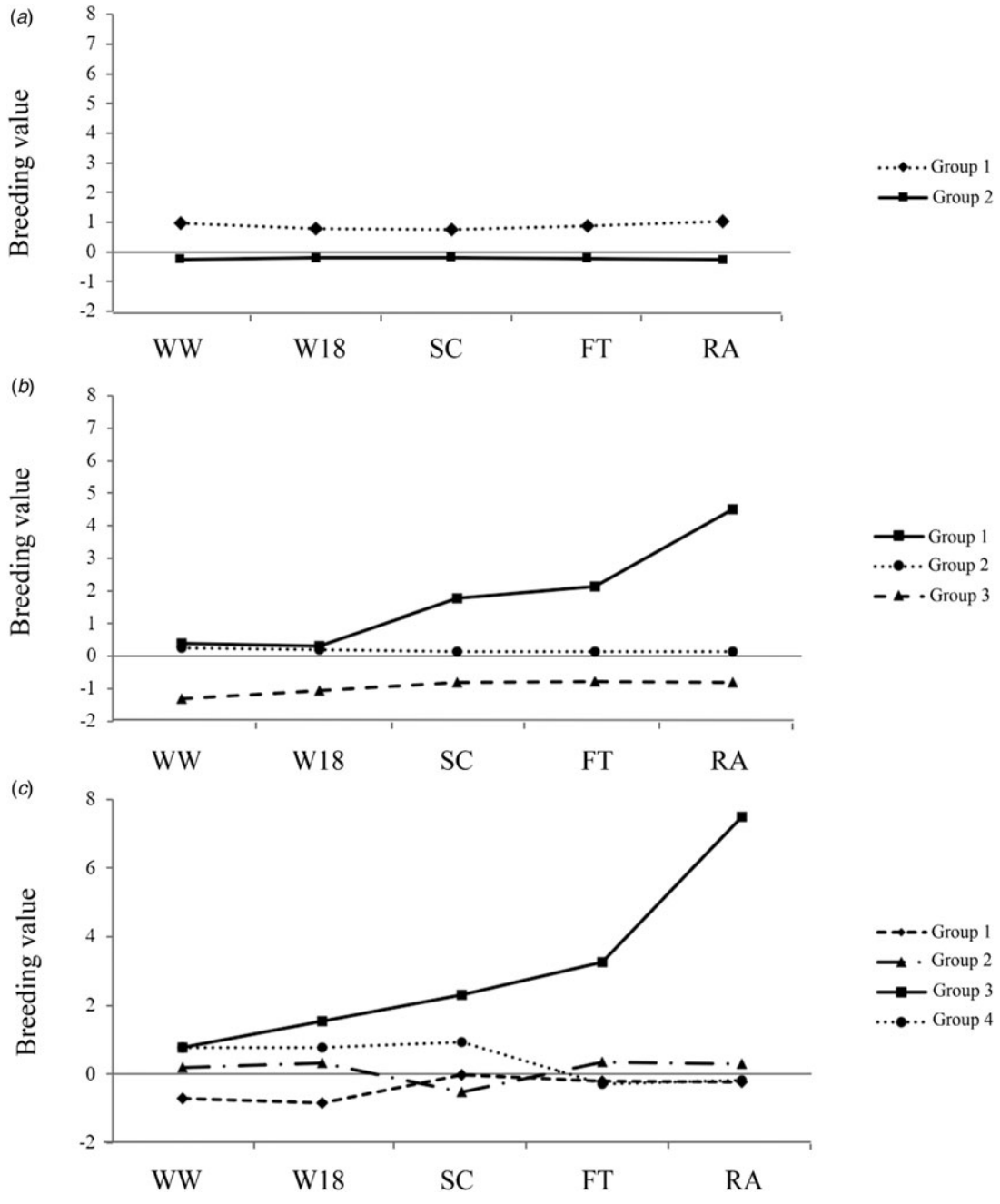



**Fig. 2.** Non-hierarchical cluster analyses with *K*-means method with two (*a*), three (*b*) and four (*c*) groups, using EBVs of weaning weight (WW), 18-month weight (W18), scrotal circumference (SC), subcutaneous fat thickness (FT) and ribeye area (RA).

the composition of each of the formed clusters and verify in which position they were in the proposed index (Supplementary material).

## Discussion

The 1.0% increase in performance resulted in the economic values of US$ 1.16/cow/year and US$ 4.66/cow/year gain in profit for the slaughter weight and weaning rate, respectively. A bioeconomic model for a complete-cycle production system was also developed for the Aberdeen Angus breed (Campos *et al.*, 2014), and the authors obtained lower economic values regarding the slaughter weight (US$ 0.43). Nevertheless, according to Urioste *et al.* (1998), the comparison of results from different studies is not recommended due to the distinct production conditions, costs and expenses, breeds and employed methodologies. Moreover, each production system will retain different economic values and, therefore, should not be used as a basis for any company or farm. The weaning weight and slaughter weight trait had a positive effect on the simulated production system, given it is directly related to the other growth traits throughout the animal' life. These traits are traditionally considered important in any production system or breeding programme.

The use of the weaning weight and slaughter weight as a selection objectives are essential. The current breeding objective of beef cattle production systems is to produce more animals and early

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animals that reach the slaughter weight sooner, with carcass qualities according to the cold stores and the final customer requirement. In turn, growth traits are related to age at slaughter and carcass quality (Araujo Neto *et al*., 2012), and there is a linear relationship between live weight and the development of the ribeye area and fat deposition (Devincenzi *et al*., 2012).

Considering the conditions of the simulated production system in the current study, the proposed selection index was composed of all of the traits that were used as selection criteria. Breeders should be attentive to the choice the traits, because the accuracy may be lower, and the sires may not be ranked according to the proposed breeding objectives. In addition, even if the expected response is greater in the next generation, it may change over the generations and undermine the selection process. The relationship between genetic correlation, heritability and economic values can significantly affect the accuracy value, becoming essential for the optimization of response to selection (Haberland *et al*., 2013).

In the proposed index, the fat thickness exhibited the highest value (+93.173), representing considerable significance in the simulated production system, followed by scrotal circumference (+47.614), weaning weight (+11.651), ribeye area (−1.430) and 18-month weight (−9.108). The index displayed negative values for the 18-month weight and ribeye area traits, which does not imply in trait loss but a reduction in importance in the index composed of several simultaneously analysed traits. Despite the negative values, 18-month weight and ribeye area showed positive genetic correlations (median to high) with all of the traits that constituted the index. In other words, the selection to increment the performance of one of these traits can increase the performance of the others, and their simultaneous use may improve response to selection.

Defining the optimal index and determining the significance of each trait, the expected response, and the accuracy depends on the correct breeding objective and the choice of the traits that will be used as selection criteria, the correct estimation of the genetic and phenotypic (co-) variances, the genetic parameters of the traits included in the index, and the calculation of the economic values for the traits considered as breeding objectives. The farm expenses and revenues used to obtain the economic values should realistically reflect the employed production system, and the database of the animals considered for selection should contain sufficient and reliable information for genetic evaluation. The comparison between studies conducted with selection indices can complicate comprehension since the economic values and accuracies can vary significantly, given they are dependent on a set of information that differs by region, state, or country, such as the utilized production system, the variation in costs, the data set and the breed that is being analysed to obtain estimates of the genetic parameters. In addition to the difficulty in comparing data, few studies on selection indices have been carried out in Brazil.

Regarding the cluster analyses, the population was divided into two groups. According to Hair *et al*. (2009), the choice of the number of clusters is empirical and depends on the results that best explain a particular data division problem. In the current work, the division into two groups was carried out since one of the groups met the breeding objectives, and the division results in a larger number of animals per group, reducing the intensity of selection and increasing the choice of the next generation of breeding bulls. Group 1, which was composed of 190 animals, obtained by dividing the animals into two groups, retained the optimal EBVs for the studied set of traits, and their genetic curve was above average.

Following cluster analyses and the attainment of the groups of bulls with the best EBVs, it was possible to verify if the economic selection index proposed in current study exhibited the same candidates for selection. After analysing the animals grouped by the EBVs in group 1 of the cluster with two divisions, 100 were positioned among the 100 best animals ranked in the economic selection index, showing that the cluster analyses may be used as a tool in genetic breeding. Cluster analyses determine the relationships between the evaluated traits (Karacaoren and Kadarmideen, 2008) by gathering the information according to similarities within each group and differences between them. In turn, the calculations performed in the development of selection indices involve the use of genetic and phenotypic variances of the animals and the zootechnical and economic information of the employed production system. Also, they take into account the heritability of the analysed traits and the correlations between them. The means by which the results were obtained were different. However, while comparing the results of the two types of analyses, it was observed that both could be used complementarily or individually when involving selection with the use of several traits simultaneously.

In conclusion, the economic selection index and cluster analyses composed of all of the traits that were used as selection criteria would result in a considerable response to selection since the employed breeding objectives (weaning rate and slaughter weight) displayed a positive economic return regarding the simulated production system. All bulls that ranked among the top 100 in the selection index were also present in the group with the best EBVs, which was formed during the cluster analyses. This result confirms that the cluster analyses can be used as a tool for the selection of animals to be used as parents for further generations.

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**Ethical standards.** Not applicable.

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