






Optimum contribution for mate selection in Santa Inês sheep

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ABSTRACT - The objective of this research was to simulate the genetic gains expected comparing random mating strategies and mate selection by optimum contribution with different penalty levels in the inbreeding rate of Santa Inês sheep. The optimum contribution theory was thus applied to optimize genetic gain in the long term in twelve selection groups by selectively mating 500 females with the respective males, increasingly penalizing the increase in inbreeding in the objective function. Genetic algorithms were used to find the optimum contribution. Optimization was achieved via EVA software. Selection candidates had their contribution defined into four treatments, using different values to weigh the genetic merit and penalize increases in inbreeding. This made it possible to measure the degree of control over those parameters that can be obtained with this methodology. This selection offers different levels of genetic gain, which are achievable from restrictions on the coancestry. The number of males selected and their distribution into selection groups varied according to the penalty attributed to inbreeding in the objective function. Mate selection using optimum contribution should be adopted when aiming to limit the increase in inbreeding. Increasing the exchange of genetic material between groups is recommended to elevate genetic gain and maintain control over inbreeding.

Keywords: EVA, genetic algorithms, genetic contribution theory, mathematical optimization, selective mating

1. Introduction

In the last two decades, sheep farming in the tropical part of Brazil has gained prominence. Today, this region represents over 60% of the total national herd and consists mainly of the Santa Inês breed (Paiva et al., 2005). The reproductive performance and growth rate of animals are among the main components responsible for the success of the production, and this is one of the most important characteristics of Santa Inês breed, which for being polyestrous annually, can be mated in any season of the year, provided that ewes are in adequate nutritional status (Mexia et al., 2004).

The animal breeding process consists of three stages: determination of genetic value of individuals, selection of those considered of greatest value for the desired goals, and mating between selected individuals to produce a new generation. The last stage — mating — has been practiced in an empirical

and non-systematized manner, which leads to reduced yearly genetic gains and no effective control over increases in inbreeding (Kingham, 2011).

When associated with mathematical optimization techniques, the “optimum genetic contribution” theory is the ideal tool to address this problem, unifying the selection and mating stages in one single process called mating selection. Villanueva et al. (2006) observed increases of up to 45% in genetic gains with the same increase in inbreeding when compared with truncation selection.

Optimization via evolutionary algorithms can also deal with restrictions of tactical nature such as the geographic location of individuals and cost of semen, among other factors. The evolution of computer resources has made this technique accessible to users of personal computers. In Brazil, this methodology was used in cattle by Carvalheiro et al. (2010), in sheep by Santos et al. (2016), and in fish by Yoshida et al. (2017), who concluded that selection based on optimum genetic contribution allows for the maximization of different levels of genetic gain, which are achievable through restrictions on coancestry (inbreeding) simultaneously.

The objective of this research was to simulate genetic gains expected comparing random mating strategies and mate selection by optimum contribution with different penalty levels in inbreeding rate of Santa Inês sheep.

2. Material and Methods

The optimum genetic contribution for the next generation was determined by maximizing the objective function (OF):

$$OF = w_{dep} \cdot cg - w_{cr} \cdot cAc,$$

in which W_{dep} is the scalar factor that assigns a weight to genetic gain, c is the vector of the individual optimum contribution to the next generation (c_i) to be calculated, g is the vector with the expected progeny differences (EPD), W_{cr} is the scalar factor that penalizes increases in inbreeding, and A is the numerator matrix of Wright’s relatedness coefficient (Wright, 1922).

For selection candidates, restrictions were defined in terms of the maximum number of matings allowed, i.e., maximum values c_i could assume (c_i max), in which c_i max = 1 for females and c_i max = 40 for males, observing the biological capacity of the species for natural mating. Live males between one and four years of age and live females between one and five years of age that had not given birth within the past three months were considered to be able to reproduce. The individuals previously excluded from the selection process had c_i max = 0.

The g values used were the EPD of Santa Inês sheep for weight at 60 days (EPD W60), obtained from commercial herd database with 27,546 animals born since 2000. Of these, 19,402 belong to the 51 selection centers (farms) registered in the Associação Sergipana dos Criadores de Caprinos e Ovinos (ASCCO) and the others are ancestors of these animals. These animals were dispersed across 13 Brazilian states in the Caatinga, Atlantic Forest, Cerrado, and Amazonian biomes. The A values were calculated from pedigree information from the same database.

The animal model of genetic evaluation was thus defined: fixed effects – contemporary group (herd year and season), sex, type of birth, age of mother at birth (covariate with linear and quadratic effect), and age of animal at the time of weighing (covariable with linear and quadratic effect); random effects – direct additive genetic, genetic maternal, maternal environment, and residual.

The EVA (Berg et al., 2006) software, version 2.0, calculates the c vector of individual contributions to the next generation, using the selective-mating principle according to the optimization of genetic contribution (Meuwissen, 1997; Meuwissen and Sonesson 1998; Grundy et al., 2000). The parameterization of the optimization algorithm was maintained in default mode as given in the software manual.

In addition to being individually identified, the animals were allocated according to a specific selection center. The 51 selection centers (farms) were classified as to the mean EPD W60 values and inbreeding coefficient (F) of their components (animals). Each center could assume a high (A) or low (B) value depending on whether it was in the upper or lower quadrant of the scatter plot (Figure 1). After this stage, groups were created for selection that were categorized into four possibilities: high EPD W60 and high inbreeding (AA), high EPD W60 and low inbreeding (AB), low EPD W60 and high inbreeding (BA), and low EPD W60 and low inbreeding (BB).

The choice of selection candidates followed the restriction of choosing individuals from three selection centers randomly in each of the categories (AA), (AB), (BA), and (BB), totaling 2,071 males and 3,047 female selection candidates, belonging to seven different generations and twelve selection centers. Free mating between females from one group and males from another group was allowed.

Seven strategies (treatments) for selection for optimum contribution were considered to evaluate the impact of controlling the evolution of inbreeding in the subsequent generation on the average genetic merit of the next generation as well as to compare values obtained from optimum genetic contribution with those obtained randomly (considered the control method). In all seven treatments, the total number of matings was limited to 500. The values used for the W_{dep} scalars, which assign a weight to genetic merit, and W_{cr} , which penalizes increases in inbreeding, are shown in Table 1.

The following parameters were analyzed: number of cycles used by the program to find optimum solution (NC) (maximum 10,000 cycles), mean EPD W60 of generation produced from the matings (EPD W60), mean relatedness coefficient in the subsequent generation (CR), mean F of subsequent generation, number of males used in matings (Mut), and expected rate of increase in the degree of inbreeding in the long term (EvF).

For comparison purposes, the same parameters were calculated using truncation selection (TS) of the best males and the 500 best females. Subsequently, they were mated randomly using EVA software, adopting W_{dep} and W_{cr} equal to 0, termed treatments TS_1 to TS_5, which differed from each other based exclusively on the truncation point chosen for the males. This truncation point was defined to produce the subsequent generation, with an EPD W60 similar to those obtained with optimum contribution selection (OC), in treatments OC_1 to OC_5, respectively.

The distribution of males selected for mating into treatments OC_1 to OC_6 in relation to the categories of the groups where they belonged (AA, AB, BA, and BB) was also analyzed. Genetic values of selected males were plotted in relation to the contribution to the next generation for each treatment from OC_1 to OC_6.

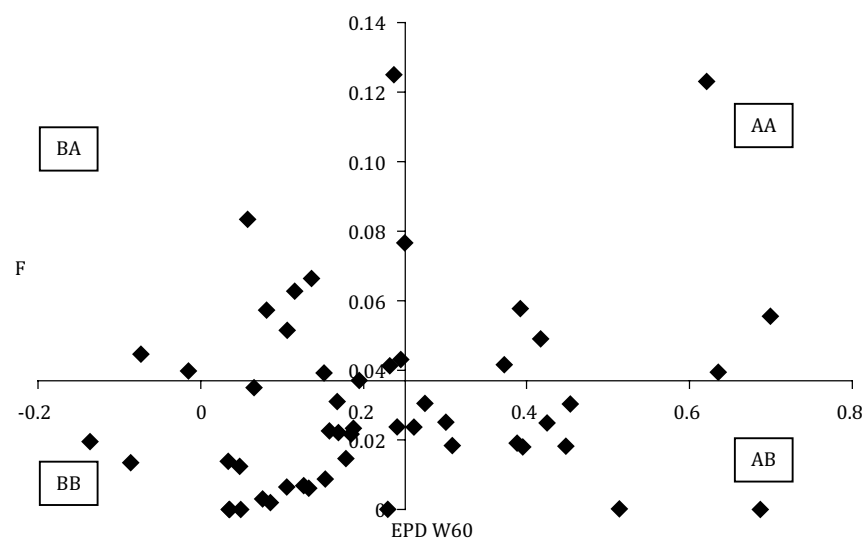


Figure 1 - Quadrant clusters (AA, AB, BA, BB) depending on relationship between the means of genetic values (EPD W60) and inbreeding coefficient (F) values in each of the 51 selection centers.

Table 1 - Weighed values and parameters evaluated for each treatment employing selection via optimum genetic contribution in Santa Inês sheep

Treatment	Weighing		Parameter					
	W_{dep}	W_{cr}	NC	EPD W60	CR	F	Mut	EvF
OC_1	1.0	0.0	1	151.777	0.03881	0.03173	13	-0.01644
OC_2	1.0	-25.0	9,713	148.358	0.03513	0.02534	22	-0.01834
OC_3	1.0	-50.0	9,331	142.673	0.03273	0.01628	30	-0.01959
OC_4	1.0	-75.0	9,744	135.255	0.03076	0.01301	39	-0.02061
OC_5	1.0	-100.0	9,973	127.467	0.02928	0.01161	49	-0.02137
OC_6	0	-100.0	501	0.09469	0.02141	0.00539	77	-0.02545
AC	0	0.0	1	0.22993	0.03205	0.01868	436	-0.01994

OC - optimum genetic contribution; AC - random mating; W_{dep} - scalar weighting factor for weight gain; W_{cr} - scalar factor that penalizes increases in inbreeding; NC - mean number of cycles used to reach the optimum point; EPD W60 - mean value of the expected progeny difference for weight at 60 days in the subsequent generation; CR - mean correlation coefficient of the subsequent generation; F - mean inbreeding coefficient of the subsequent generation; Mut - number of males used in matings; EvF - expected rate of alteration in the degree of inbreeding in the next generation.

3. Results

The number of cycles (NC) used by the software to converge to the optimum point of the objective function was within parameterized limits, a maximum of 10,000 cycles (Table 1). The higher number of cycles used to reach optimum solution in treatments OC_2 to OC_5 is because penalties in these treatments for genetic merit and inbreeding were different from 0, whereas in the other treatments (OC_1, OC_6, and random mating), at least one of those was equal to 0, facilitating convergence.

The highest average EPD W60 of the generation obtained from the matings was achieved with treatment OC_1, in which the penalty for increases in inbreeding was 0, maintaining a positive value, equal to 1, to weight g . The EPD W60 values were successively lower from OC_2 to OC_5 as the penalty for increases in inbreeding were elevated, maintaining the factor 1 for genetic merit. In OC_6, EPD W60 reached its lowest value, because the objective was solely to minimize increases in inbreeding ($W_{dep} = 0$ and $W_{cr} = -100$).

The CR and F values responded in a downward trend to treatments OC_1 to OC_6, with W_{cr} assuming the respective values of 0, -25, -50, -75, -100, -100. In treatment AC, however, CR and F were higher than those found in OC_4 and OC_6, though with a substantially lower EPD W60 value, indicating the superiority of the method for attaining progress in both parameters.

The values observed in each treatment for EPD W60 and for F were plotted onto orthogonal axes, generating a relative response curve (Figure 2). Thus, the optimum response in EPD W60 could be observed for each coancestrality value allowed for the parents, i.e., the F of next generation in the studied population. This plot can be used for parameterization of penalty for inbreeding (W_{cr}), when a maximum value allowed for F is set. The comparison between matings occurring after truncation selection and those carried out using optimum genetic contribution showed that for similar EPD W60 values, F values obtained from optimum contribution were invariably lower than those produced by truncation. As the penalty for increases in F is elevated, the superiority of optimum contribution also increases. In treatments OC_5 and TS_5, the difference in inbreeding was almost three times higher (Figure 2).

The Mut required for 500 matings rose from treatments OC_1 to OC_6, demonstrating that individual contributions must be reduced to maintain inbreeding under control. Compared with truncation selection followed by random mating between the pre-selected individuals, the Mut of matings through OC were lower than those obtained through TS to produce similar EPD W60 results when the F control requirements were increased (Figure 3). Given the cost of maintenance of males, this is a desirable advantage.

The evolution of inbreeding degree in the next generation relative to the previous one also declined from OC_1 to OC_6. All obtained values were negative, indicating the possibility of still obtaining genetic gains without increases in inbreeding.

As for the percentage distribution of selected males, in the many treatments using OC, in relation to the group category to which they belong, the groups of category AB (high EPD W60 and low F) had their participation markedly reduced in the selected total, while W_{cr} assumed more penalized values for inbreeding. The opposite situation was observed for the groups of category BB (Figure 4). Even when the penalty for inbreeding was low, the participation of groups AA and BA was reduced, suggesting a need for controlling this parameter by the groups.

Figure 5 describes the relationship between the individual contribution (N_mating) of the males chosen using the different evaluated treatments to the next generation. Each point relates the number

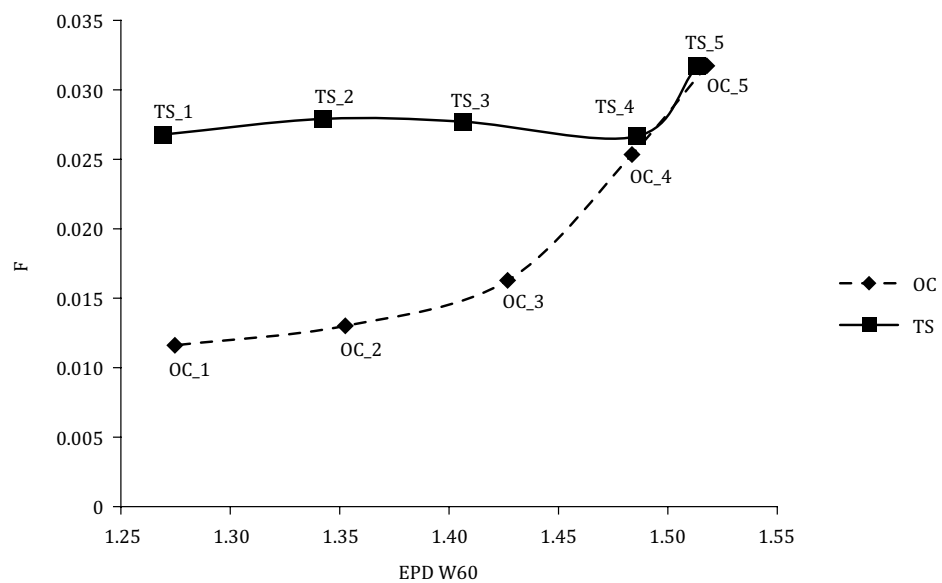


Figure 2 - Genetic values (EPD W60) and inbreeding coefficients (F) in different mating strategies carried out using optimum contribution (OC) and truncation selection (TS).

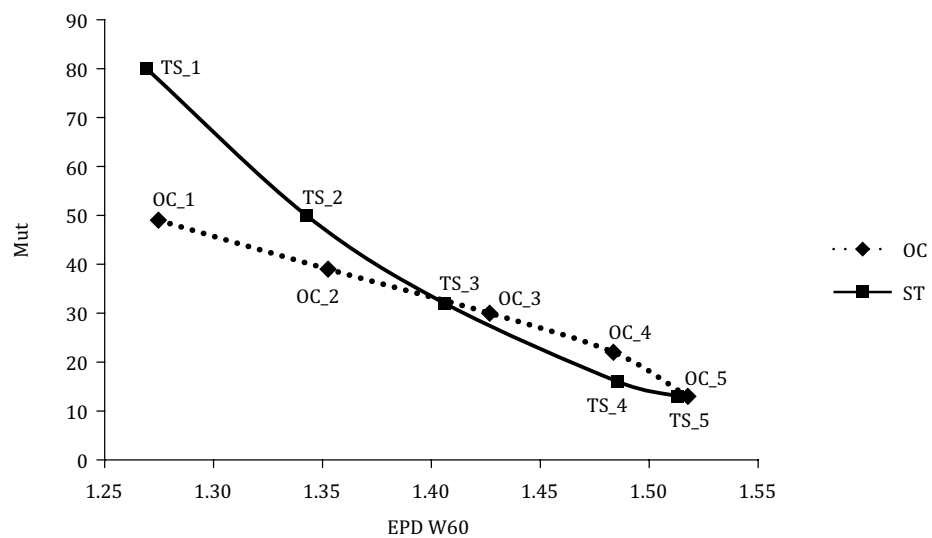


Figure 3 - Number of males used (Mut) as a function of the genetic value (EPD W60) for different strategies carried by optimum contribution (OC) and truncation selection (TS).

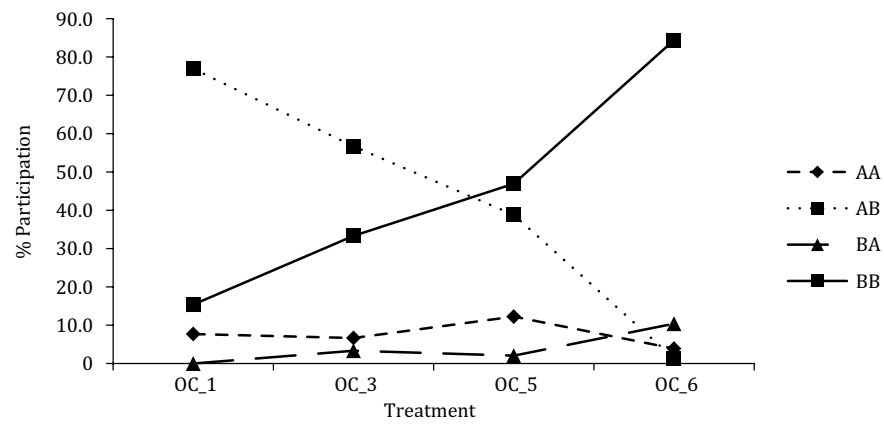


Figure 4 - Percentage participation of each categorical group (high EPD W60 and high inbreeding - AA; high EPD W60 and low inbreeding - AB; low EPD W60 and high inbreeding - BA; and low EPD W60 and low inbreeding - BB) in the total males selected per different selection strategies by optimum contribution (OC).

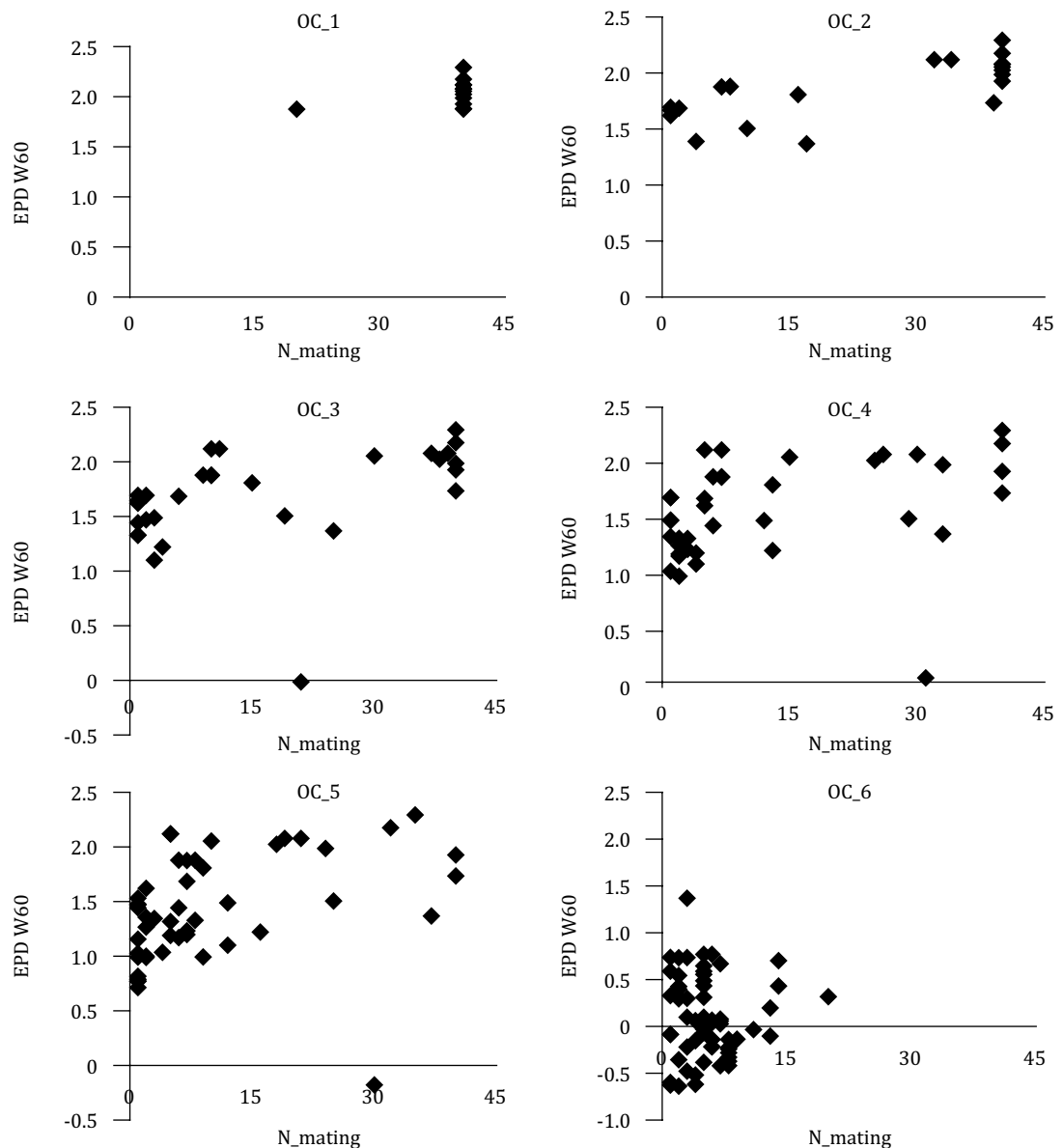


Figure 5 - Association between number of matings (N_mating) and genetic value (EPD W60) in different selection strategies by optimum contribution (OC).

of matings allocated to one selected male with its genetic value (EPD W60). While W_{cr} penalizes inbreeding, assuming OC_1, OC_2, OC_3, OC_4, OC_5, and OC_6 values of 0, -25, -50, -75, -100, and -100, respectively, the number of selected males increases and so do the differences in contribution across selected individuals.

It is noteworthy that when the penalty for inbreeding is low, individuals with higher EPD W60 have a greater contribution. However, when the penalty for inbreeding is elevated, males with greater genetic merit do not necessarily contribute more.

The map of matings for treatment OC_4, $W_{cr} = -0.75$, representing a situation with strong penalty for inbreeding, is summarized in Table 2, where rows contain the groups of selected females and columns represent the groups of males selected for the matings. In all cases, males were chosen from other groups, usually more than one.

Table 2 - Groups of selected males in relation to the female chosen for treatment OC_4

Female chosen	Selected males/No. of males							Total
	A	B	F	G	I	K	L	
	5	5	4	11	1	1	12	39
A	1	5	23	13	-	-	-	42
B	-	-	6	35	-	-	1	42
C	-	-	1	-	-	-	6	7
D	23	20	14	4	2	-	34	97
E	-	-	-	11	-	-	1	12
F	6	8	-	2	1	1	29	47
G	3	29	11	7	1	2	66	119
H	-	-	-	1	-	-	1	2
I	2	1	-	13	-	-	-	16
J	-	1	8	15	-	-	-	24
K	-	1	1	5	1	-	5	13
L	5	8	24	38	-	-	4	79
Total	40	73	88	144	5	3	147	500

OC - optimum genetic contribution.

4. Discussion

The results of this research can be explained by the fact that BLUP uses information on all relatives to predict the EPD of animals. Thus, when data of the entire family are used, those with individuals with better performance have a greater chance of being selected together. Consequently, future matings between those animals can elevate the inbreeding rate of the population (Santos et al., 2016). In this way, a direct consequence of elevated consanguinity between breeding animals is an increased inbreeding rate, which in turn may compromise the variability and genetic progress in the medium and long terms.

The superiority of OC over truncation rose as the control of inbreeding became more restrictive. Colleau et al. (2009) concluded that OC was superior in controlling inbreeding and in the evolution of genetic merit in two French dairy cattle herds of Holstein and Normande breeds. Gizaw et al. (2013) conducted a simulation to reconstitute the body weight data observed in Menz sheep and found that, in a 10-year interval, OC produced higher genetic gains than selection via EPD-BLUP (7.58 and 7.16, respectively), in addition to being highly effective in the control of inbreeding (OC: 0.32 vs. EPD-BLUP: 1.67).

Results obtained in this study agree with the findings of König et al. (2010), who described, for egg production, an inverse relationship between the genetic values of the products from matings and the number of breeding candidates used, the latter of which increased as restrictions to inbreeding were applied.

The number of males used decreased as higher increases were allowed in F in selective mating using optimum genetic contribution. Similar results were reported by Avendaño et al. (2003) in MeatLinc sheep and Aberdeen Angus cattle.

Structuring herds with less extreme relationships can increase the selection of sire and dam candidates in the next generation via optimum genetic contribution. This finding also makes clear the difference between truncation selection and selection via optimum genetic contribution in regard to the use and number of selected sires and dams. Considering that the same proportions of matings are assigned to all individuals with genetic value above the cutoff point in truncation selection, optimum selection contribution made it possible to vary the use across selected candidates (Santos et al., 2016). The same trend was observed by Kearney et al. (2004) regarding the number of selected males. However, the dispersion of individual contribution increases in the opposite direction of restrictions to inbreeding.

These results clearly demonstrate the benefit of increasing the exchange of genetic material between groups and evidence the utility of using artificial insemination with this purpose. As with these evaluated herds, the use of artificial insemination is still limited in many sheep breeding programs.

5. Conclusions

Mate selection using optimum contribution should be adopted when aiming to limit increases in inbreeding. Increasing the exchange of genetic material between groups is recommended to maximize genetic gains while maintaining control over inbreeding.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Conceptualization: J.L.R. Sarmiento, L.T. Barbosa, A.D. Barreto Neto, A.B. Celeste and N.P.S. Santos. Investigation: L.T. Barbosa and A.D. Barreto Neto. Methodology: J.L.R. Sarmiento, L.T. Barbosa, A.D. Barreto Neto, A.B. Celeste and N.P.S. Santos. Project administration: L.T. Barbosa and A.D. Barreto Neto. Writing-review & editing: J.L.R. Sarmiento, L.T. Barbosa and N.P.S. Santos.

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