





Impact of reproductive and productive rates on levels of inbreeding and genetic gain of pigs through data simulation

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Received: April 26, 2018

Accepted: April 25, 2019

How to cite: Lopes, J. S.; Rorato, P. R. N.; Breda, F. C.; Freitas, M. S.; Farah, M. M.; Duitama Carreño, L. O. and Oliveira, M. M. 2019. Impact of reproductive and productive rates on levels of inbreeding and genetic gain of pigs through data simulation. *Revista Brasileira de Zootecnia* 48:e20180067.
<https://doi.org/10.1590/rbz4820180067>

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ABSTRACT - The objective of this study was to evaluate the impact of farrowing and mortality rates on inbreeding levels and genetic gain through data simulation. Data came from two real populations A and B, composed of Pietrain and Landrace breed pigs, respectively. To generate the simulated populations, a Fortran-language simulator was developed using the (co)variances of the breeding values and productive and reproductive information obtained from populations A and B, as well as restrictions on mating and animals selected per generation. Two data files were created. The first contained the pedigree of the previous 10 years, with 21,906 and 251,343 animals in populations A and B, respectively. The second included the breeding values for age, backfat thickness, and feed conversion, all of which were adjusted for 110 kg live weight, for both populations; *longissimus dorsi* muscle depth adjusted for 110 kg live weight, for population A only; and number of live piglets at the fifth day of life per farrowing, for population B only. Three scenarios were simulated by varying the farrowing and mortality rates during the lactation period. Ten generations were simulated, with 30 replicates for each generation and scenario. Inbreeding levels in closed production units increase with productive and reproductive losses, and these reduce the variances of breeding values, selection intensity, and genetic gains by reducing the number of animals available for selection. Actions that maximize farrowing rates are more important than those that minimize mortality rates during the lactation period, since a reduction in simulated farrowing resulted in greater losses of genetic gains.

Keywords: farrowing rate, mortality rate, viability of piglets

Introduction

Selection differential is a measurement of the difference between the average of individuals selected to be parents in the next generation and the average of the entire population available for selection, which has a great impact on genetic gain. Assuming that the population follows a normal distribution, it is understood that the selection differential value depends on the relationship between the proportion selected and the existing variation in the population. In this context, the relationship between the selection differential and the phenotypic standard deviation is termed “selection intensity” (Bourdon, 2013; Willoughby et al., 2015).

Selection intensity is one of the main factors influencing genetic gain and is affected by all the causes that lead to decreasing production rates, such as mortality, and reproductive rates, such as conception problems, in a herd.

With respect to reproductive rates, according to several researchers (Dobao et al., 1983; Fuentes et al., 2000; Peltoniemi et al., 2000; Lipenský et al., 2010; Bell et al., 2015; Peltoniemi and Oliviero, 2015), many factors influence the performance of a female pig, e.g., genotype effects, sow and boar age, number of farrowings, feeding level, season of the year when mating occurs, among others.

Addressing mortality losses, which can reach high rates in the swine species, Abrahão et al. (2004) stated that, in the entire world scenario, 4 to 10% of live-born pigs die during birth. A study conducted by Lisboa (1996) concluded that mortality in the swine species can reach high rates (15 to 18%) from birth to weaning, 2.4 to 10% of which occur during farrowing, with high mortality rates in the first week of life of piglets.

Mortality occurring during the growth and finishing stages also has a great impact on the profitability of pig farming, especially because these animals accumulate the entire cost of previous phases. In these phases, mortality may have infectious and non-infectious origins such as gastric ulcer and mesenteric torsion (Christianson, 2006).

Considering that, in addition to the above-stated factors, productive and reproductive rates are also impacted by the quality of labor of animal handlers and by the structure of facilities; information about the magnitude of such impacts is essential for resource allocation.

The objective of this study was to evaluate the impact of farrowing and mortality rates on inbreeding levels and genetic gains in a pig genetic breeding program, through data simulation.

Material and Methods

The data used in this study came from two lineages raised on farms located in western Santa Catarina State, Brazil. Real populations A and B were composed of Pietrain and Landrace pigs, respectively. Population A had 125 females and 25 males, while population B had 400 females and 45 males.

Piglets were identified at birth, weighed, and injected with iron dextran. Litters were equalized among the females that gave birth in the same week, considering the weight and number of piglets.

The animals were kept in the nursery phase until the 10th week of age, when males were separated and raised in individual pens and females were raised in collective pens that housed 12 animals. Live weight, backfat thickness, and *longissimus dorsi* muscle depth were measured when the animals finished the performance test (at approximately 20 weeks of age). Feed conversion was measured only in males in this period.

To generate simulated populations, a Fortran-language simulator was developed using the (co) variances of the breeding values and the productive and reproductive rates and means obtained from the real populations, composed of the animals selected in 2014 [Generation (G) 0 – G₀]. These simulated populations also used information on restrictions regarding mating rate and number of animals selected in each generation. Two data files were created. The first contained the pedigree of the animals in the previous ten years, with 21,906 animals in population A and 251,343 animals in population B. The second contained the estimated breeding values for age (AGE110), backfat thickness (BFT110), and feed conversion (FC110), all of which were adjusted for 110 kg live weight, for both populations; *longissimus dorsi* muscle depth adjusted for 110 kg live weight (D110), for population A only; and number of live piglets at the fifth day of life per farrowing (LP5), for population B only, with 263 animals in population A and 747 animals in population B.

Estimates of (co)variance components of real populations were obtained using REMLF90 (Misztal, 2002) software, which adopts the maximum expectation of the restricted maximum likelihood function (EMREML). The convergence criterion used, defined by the mean square of the differences between consecutive solutions, was 1×10^{-11} . Estimated heritabilities and predicted breeding values were obtained from these variance components using a multi-trait animal model for AGE110, BFT110, FC110, and D110 for population A, and a multi-trait animal model for AGE110, BFT110, FC110, and the single-trait model for LP5 for population B.

The model below was used for the multi-trait analyses involving the real populations:

$$y = X\beta + Z\mu + e,$$

in which y = vector of observations; β = vector of fixed effects of contemporary group (GC) (animals born in the same conditions of lineage, sex, production unit, and year and week of the end of performance test); μ = vector of direct additive random genetic effects; e = vector of residual random effects; and X and Z = incidence matrices for fixed direct additive and genetic effects, respectively.

For the single-trait analysis, the model used is given below:

$$y = X\beta + Z_1\mu + Z_2pe + e,$$

in which y = vector of observations; β = vector of fixed effects of GC (animals born in the same conditions of lineage, sex, production unit, and year and week of farrowing) and order of farrowing (from one to five farrowings); μ = vector of random direct additive genetic effects; pe = vector of random genetic effects of permanent environment; e = vector of random residual effects; and X , Z_1 , and Z_2 = incidence matrices of fixed, direct additive genetic, and permanent environmental effects, respectively.

From the animals of G_0 , the simulator applied post-selection losses and performed random matings by means of a uniform distribution $U \sim (0,1)$, considering the following imposed restrictions: number of matings per animal (up to 15 matings per male and five per female, in population A, and up to 25 matings per male and five per female, in population B), relatedness between couples (up to 0.107, plus 0.01 per generation, in population A and 0.055, plus 0.01 per generation, in population B), number of farrowings per female (considering 49% of females with only one farrowing in population A and 54% of females with only one farrowing in population B), and farrowing rate (88% in population A and 91% in population B). Coefficients of relationship between the animals used in mating restrictions were calculated using par3.f software (Boichard, 2002). From each successful mating, the number of piglets at the end of the performance test per farrowing (NFT) in G_1 was calculated, considering data such as number of piglets born, mortality rates in farrowing, maternity, nursery phases, and performance test, in addition to other losses. Based on the real populations, the mean (MEANNFT) and the standard deviation (SDFT) of the NFT were calculated and used to calculate the NFT of each successful mating, as follows:

$$\text{NFT} = \text{MEANNFT} + z \times \text{SDFT},$$

in which z = random value obtained from a standardized normal distribution - $N \sim (0,1)$.

According to van der Werf and de Boer (1990), the breeding value of each animal is calculated by the following equation:

$$a_i = \frac{1}{2} a_{s_i} + \frac{1}{2} a_{d_i} + \phi_i,$$

in which a_{s_i} and a_{d_i} correspond to the breeding values of boar and sow, respectively, for trait i ; and ϕ_i results from Mendelian segregation, which is independent of a_{s_i} and a_{d_i} (Bulmer, 1971). The variance of ϕ_i can be described as follows:

$$\phi_i = \frac{1}{2} \left[1 - \frac{1}{2} (F_s + F_d) \right] \sigma_a^2,$$

in which F_s and F_d correspond to the inbreeding coefficients of boar and sow, respectively.

The variance components used were the (co)variance matrix of the breeding values of the four traits (A) obtained from each real population (Table 1), so that the additive breeding value (α_i) of each animal of the next generation was obtained as follows:

$$a_i = \frac{1}{2} a_{s_i} + \frac{1}{2} a_{d_i} + z \sqrt{\frac{1}{2} \left[1 - \frac{1}{2} (F_s + F_d) \right] A},$$

in which z = random value obtained from a standardized normal distribution - $N \sim (0,1)$.

After the α_i values of the animals at the end of G_1 performance test were generated, the animals were classified according to a selection index that grouped the four traits (AGE₁₁₀, BFT₁₁₀, FC₁₁₀, and D110, or LP5) (Table 2), and a random loss rate was applied in the selection. Subsequently, a fixed number of animals was selected (equivalent to an approximate 140% annual turnover for females and 200% for males), considering restrictions of full- and half-sibs, for males and females. With the information of the animals selected in G_1 , the entire process was repeated up to ten generations, as defined in the parameters card.

Three scenarios were simulated: scenario 1 was simulated from the averages of the real populations; scenario 2 simulated the impact of a 5% increase in mortality rate in the weaning period; and scenario 3 simulated the impact of a 5% decrease in farrowing rate (Table 3).

According to Carneiro et al. (2008), in simulation processes with only one replicate, genetic oscillation influences the genetic gain, mainly in populations of small effective size, compromising the comparison

Table 1 - Estimated variance (on diagonal) and covariance (out of diagonal) components of the breeding values for the studied traits obtained from each real population

Trait	Population A			
	BV AGE ₁₁₀	BV BFT ₁₁₀	BV FC ₁₁₀	BV D ₁₁₀
BV AGE ₁₁₀	33.2300	0.2600	0.3106	1.9000
BV BFT ₁₁₀	0.2600	0.1892	0.0250	-0.3500
BV FC ₁₁₀	0.3106	0.0250	0.0134	-0.0834
BV D ₁₁₀	1.9000	-0.3500	-0.0834	10.2000
Trait	Population B			
	BV AGE ₁₁₀	BV BFT ₁₁₀	BV FC ₁₁₀	BV LP5
BV AGE ₁₁₀	43.5700	0.0200	0.2874	-
BV BFT ₁₁₀	0.0200	0.3845	0.0264	-
BV FC ₁₁₀	0.2874	0.0264	0.0098	-
BV LP5	-	-	-	1.0360

Breeding values (BV) for age (AGE₁₁₀), backfat thickness (BFT₁₁₀), feed conversion (FC₁₁₀), and *longissimus dorsi* muscle depth (D110), all of which adjusted for 110 kg live weight, and number of live piglets at the fifth day of life per farrowing (LP5).

Table 2 - Weights for each trait in the selection index composition for populations A and B, by sex

Trait	Population A		Population B	
	Male	Female	Male	Female
BV AGE ₁₁₀	-0.7837	-0.8207	-0.6212	-0.7472
BV BFT ₁₁₀	0.0000	0.0000	0.0000	0.0000
BV FC ₁₁₀	-169.3968	-155.9077	-81.1083	-68.8255
BV D ₁₁₀	0.7462	0.7982	-	-
BV LP5	-	-	14.7563	14.6681

Breeding values (BV) for age (AGE₁₁₀), backfat thickness (BFT₁₁₀), feed conversion (FC₁₁₀), and *longissimus dorsi* muscle depth (D110), all of which adjusted for 110 kg live weight, and number of live piglets at the fifth day of life per farrowing (LP5).

Table 3 - Farrowing and mortality in weaning period rates, by percentage, according to population for each simulated scenario

Scenario	Population A		Population B	
	Farrowing rate	Lactation mortality rate	Farrowing rate	Lactation mortality rate
Scenario 1	88	5.8	91	6.9
Scenario 2	88	10.8	91	11.9
Scenario 3	83	5.8	86	6.9

of genetic evaluation methodologies. The use of 30 replicates in the simulation process provides consistent results in comparative studies of genetic evaluation methodologies using simulation. Thus, for each simulated scenario, 30 replicates were used per generation.

The efficiency of each scenario was estimated considering the control of the increases in the average inbreeding of the population, which is calculated as follows:

$$\Delta F_t = (F_t - F_{t-1}) / (1 - F_{t-1}),$$

in which t = generation number and F_t = mean inbreeding coefficient of generation t (Wright, 1922). Genetic gains were also calculated per generation, for each trait, as shown below:

$$GG_t = VGFT_t - VGFT_{t-1},$$

in which t = generation number, GG_t = genetic gain in generation t , and $VGFT_t$ = average of genetic values of the animals at the end of the test in generation t .

Results

Farrowing rates for populations A and B were 88 and 91%, respectively, which are within acceptable limits for intervention. The same was true for mortality rates during the lactation period, which were 5.8% for population A and 6.9% for population B. These farrowing and mortality rates were used to simulate scenario 1.

The larger simulated losses in scenarios 2 and 3 had an impact on inbreeding levels up to G_{10} in both populations (Table 4). In comparison with scenario 1, in population A, the increases in inbreeding coefficient in the last generation were 1.8 and 3.6% for scenarios 2 and 3, respectively. For population B, in turn, the increases were 2.2 and 4.3% for the respective scenarios. Inbreeding increases (ΔF_a) were also higher numerically for scenarios 2 and 3, compared with scenario 1, in both populations (Table 5). On the average of generations, for population A, scenario 1 produced a ΔF_a of 0.0054 ± 0.00014 ; scenario two, 0.0056 ± 0.00014 ; and scenario three, 0.0058 ± 0.00015 . For population B, ΔF_a values were 0.0051 ± 0.00009 , 0.0053 ± 0.00010 , and 0.0054 ± 0.00010 for scenarios 1, 2, and 3, respectively.

The variance of breeding values for feed conversion adjusted for 110 kg ($\sigma^2_{GV_{FC110}}$) decreased by 2.89%, on average, up to G_{10} for population A, which has FC110 as the main feature of the selection index. For

Table 4 - Inbreeding coefficient for populations A and B by generation, according to the different simulated scenarios

Generation	Population A			Population B		
	Scenario 1	Scenario 2	Scenario 3	Scenario 1	Scenario 2	Scenario 3
0	0.0399	0.0399	0.0399	0.0235	0.0235	0.0235
1	0.0434	0.0456	0.0482	0.0280	0.0302	0.0318
2	0.0509	0.0534	0.0545	0.0325	0.0370	0.0374
3	0.0566	0.0573	0.0606	0.0402	0.0409	0.0432
4	0.0610	0.0624	0.0641	0.0446	0.0460	0.0477
5	0.0673	0.0662	0.0673	0.0499	0.0498	0.0509
6	0.0701	0.0725	0.0723	0.0537	0.0561	0.0569
7	0.0744	0.0781	0.0773	0.0580	0.0607	0.0609
8	0.0804	0.0818	0.0829	0.0630	0.0654	0.0665
9	0.0854	0.0854	0.0878	0.0680	0.0690	0.0714
10	0.0906	0.0922	0.0939	0.0722	0.0738	0.0753
Average	0.0655	0.0668	0.0681	0.0485	0.0502	0.0514

Scenario 1 – 88% of farrowing rate and 5.8% of lactation mortality rate in population A, and 91% of farrowing rate and 6.9% of lactation mortality rate in population B; scenario 2 – 88% of farrowing rate and 10.8% of lactation mortality rate in population A, and 91% of farrowing rate and 11.9% of lactation mortality rate in population B; scenario 3 – 83% of farrowing rate and 5.8% of lactation mortality rate in population A, and 86% of farrowing rate and 6.9% of lactation mortality rate in population B.

population B, which has LP5 as the main trait in the selection index, the variance of breeding values for LP5 ($\sigma^2_{GV_{PA5}}$) decreased, on average, by 2.79% up to G_{10} .

The variance of traits is one of the elements that affect genetic gain, the main indicator of success in a breeding program. Genetic gains for FC110 were, on the average of the scenarios, -0.074 and -0.035 kg/kg for populations A and B, respectively (Table 6).

In comparison with scenario 1, the average genetic gain obtained in 10 years for the trait FC110 by populations A and B was 1.1 and 1.5% lower in scenario 2 and 1.6 and 2.4% lower in scenario 3, respectively. Similarly, the average genetic gain obtained in 10 years for the trait LP5 by population B was 0.4% lower in scenario 2 and 0.6% lower in scenario 3, in comparison with scenario 1.

Table 5 - Increase in inbreeding coefficients in populations A and B by generation according to the different simulated scenarios

Generation	Population A			Population B		
	Scenario 1	Scenario 2	Scenario 3	Scenario 1	Scenario 2	Scenario 3
1	0.0036	0.0059	0.0086	0.0046	0.0068	0.0084
2	0.0078	0.0082	0.0066	0.0046	0.0071	0.0058
3	0.0060	0.0040	0.0064	0.0080	0.0040	0.0060
4	0.0047	0.0054	0.0037	0.0046	0.0053	0.0047
5	0.0067	0.0041	0.0034	0.0055	0.0040	0.0033
6	0.0030	0.0068	0.0054	0.0040	0.0067	0.0064
7	0.0046	0.0060	0.0053	0.0045	0.0049	0.0042
8	0.0065	0.0040	0.0061	0.0053	0.0050	0.0060
9	0.0054	0.0039	0.0053	0.0053	0.0039	0.0052
10	0.0058	0.0074	0.0067	0.0046	0.0051	0.0042
Average	0.0054	0.0056	0.0058	0.0051	0.0053	0.0054

Scenario 1 - 88% of farrowing rate and 5.8% of lactation mortality rate in population A, and 91% of farrowing rate and 6.9% of lactation mortality rate in population B; scenario 2 - 88% of farrowing rate and 10.8% of lactation mortality rate in population A, and 91% of farrowing rate and 11.9% of lactation mortality rate in population B; scenario 3 - 83% of farrowing rate and 5.8% of lactation mortality rate in population A, and 86% of farrowing rate and 6.9% of lactation mortality rate in population B.

Table 6 - Genetic gain for feed conversion adjusted to 110 kg live weight for populations A and B by generation, according to the different simulated scenarios, in kg

Generation	Population A			Population B		
	Scenario 1	Scenario 2	Scenario 3	Scenario 1	Scenario 2	Scenario 3
1	-0.0765	-0.0776	-0.0779	-0.0351	-0.0346	-0.0335
2	-0.0742	-0.0726	-0.0727	-0.0367	-0.0354	-0.0354
3	-0.0736	-0.0714	-0.0708	-0.0357	-0.0348	-0.0354
4	-0.0752	-0.0740	-0.0729	-0.0345	-0.0346	-0.0339
5	-0.0742	-0.0742	-0.0724	-0.0355	-0.0347	-0.0345
6	-0.0727	-0.0737	-0.0734	-0.0350	-0.0345	-0.0350
7	-0.0759	-0.0737	-0.0739	-0.0356	-0.0350	-0.0340
8	-0.0752	-0.0738	-0.0731	-0.0357	-0.0347	-0.0343
9	-0.0746	-0.0740	-0.0744	-0.0353	-0.0349	-0.0347
10	-0.0757	-0.0747	-0.0747	-0.0354	-0.0357	-0.0343
Average	-0.0748	-0.0740	-0.0736	-0.0354	-0.0349	-0.0345

Scenario 1 - 88% of farrowing rate and 5.8% of lactation mortality rate in population A, and 91% of farrowing rate and 6.9% of lactation mortality rate in population B; scenario 2 - 88% of farrowing rate and 10.8% of lactation mortality rate in population A, and 91% of farrowing rate and 11.9% of lactation mortality rate in population B; scenario 3 - 83% of farrowing rate and 5.8% of lactation mortality rate in population A, and 86% of farrowing rate and 6.9% of lactation mortality rate in population B.

Considering the larger simulated losses in scenarios 2 and 3 compared with scenario 1, the mean selection intensities applied to boars over the ten generations were 1.1 and 1.3% lower, respectively, for population A, and 1.0% lower in both scenarios for population B. Similarly, for sows, the mean selection intensities applied in scenarios 2 and 3, compared with scenario 1, were 1.9 and 2.3% lower, respectively, for population A, and 1.7 and 1.8% lower, respectively, for population B.

Estimated heritability for number of live piglets at the fifth day of life was 0.11, simulated in population B only. For age at 110 kg live weight, heritability estimates were 0.47 and 0.49 for populations A and B, respectively.

Additionally, scenario 3 presented greater losses of genetic gains for feed conversion adjusted for 110 kg live weight. The 5% reduction of farrowing rate in this scenario is equivalent to a 0.4 standard deviation from the weekly variation during the year 2014. Mortality rate during the lactation period was reduced by 5% in scenario 2, which is equivalent to a 1.1 standard deviation from the weekly variation during the year 2014.

Discussion

Similar farrowing rates were observed by van Rensburg and Spencer (2014) in commercial herds in South Africa, ranging from 88.3 to 91.1%. Slightly lower farrowing rates were reported by Sevillano et al. (2016) for the Large White breed in 14 countries of the Northern Hemisphere (average 87%). In Japan, Kaneko et al. (2013) found an average farrowing rate of 85.5% in an evaluation of 115 commercial herds.

Caramori Júnior et al. (2010) reported mortality rate during lactation of 7.4% on a farm in the western region of Brazil, which is slightly higher than the values found in this study. Sesti and Sobestiansky (1998) suggested as a productivity parameter for modern, high-technology pig production systems, a maximum pre-weaning mortality rate of 6%, which is close to the present values. Bell et al. (2015) reported a mortality rate of 12% between birth and weaning in an extensive production system in Uruguay.

According to FAO (2000), ΔF_a should not exceed 0.01. Therefore, the ΔF_a values found in the current study agree with the recommended parameters.

In this regard, Meuwissen and Woolliams (1994) recommended a $\Delta F_a < 1\%$ to maintain deleterious mutations under control. These authors described effective population size (N_e) as one of the main factors influencing ΔF_a and suggested an N_e equal to or higher than 50 for maintaining $\Delta F_a < 1\%$. Thus, the slightly larger increments observed in population A compared with population B may be related to their smaller effective size, since the N_e of population A was 83 and that of population B was 162. Other authors have also suggested that N_e equal to or greater than 50 are sufficient to control inbreeding depression in the short term (Kristensen and Sørensen, 2005). Franklin and Frankham (1998), on the other hand, reported that maintenance of genetic variance in the long term requires $N_e > 500$.

Inbreeding increases smaller than those observed in this study were reported by Krupa et al. (2015), who evaluated swine populations in Czech Republic, where N_e ranged from 29 to 225, with ΔF_a values varying from 0.0017 to 0.0056; as well as by Gandini et al. (2014), who found a ΔF_a equal to 0.003 in a simulated population with N_e equal to 120. By contrast, Pereira Filho (2005) simulated some scenarios that encompassed different mating types and found an inbreeding increase of 0.005 for a population with $N_e = 120$, which is similar to the values found in the present study. Although the N_e of the population is one of the aspects that most influence inbreeding, in larger populations, inbreeding increases are smaller. The main restriction for the use of larger populations is their high maintenance cost.

Smaller N_e may be acceptable with the inclusion of adaptation traits in the selection criteria; thus, selection against deleterious alleles will be more effective (Kristensen and Sørensen, 2005). In addition, higher F_a rates are related to reduced adaptive capacity of populations, and this work has shown that this becomes a vicious cycle, as adaptive losses (increased mortalities and decreased farrowings) ultimately result in higher F_a rates.

One of the main disadvantages of increased inbreeding is the reduction of genetic variance, which reduces the potential genetic gains of populations (Kristensen and Sørensen, 2005; Willoughby et al., 2015).

Genetic variability losses can be slowed by stabilizing the population size (Willoughby et al., 2015) and the reproductive efficiency (Frankham et al., 2001; Willoughby et al., 2015).

The genetic gains obtained in this study are superior to those described by Tribout et al. (2010) for a population of Large White pigs in France (-0.300 kg/kg from 1977 to 1998); by Do et al. (2013) for pig populations of the Landrace (around -0.027 kg/kg each year) and Large White (around -0.030 kg/kg each year) breeds in Denmark; and by Orlando et al. (2016) for pigs of PIC genetics in the commercial sector (-0.020 kg/kg on the average of the previous three years).

The lower genetic gains in scenarios 2 and 3 were mainly due to the reduction in the intensities of selection practiced in these scenarios when compared with scenario 1. Initially, selection intensities were set to be close to 1.97 and 2.20 for boars and 1.40 and 1.55 for sows for populations A and B, respectively.

The lower selection intensities applied to scenarios 2 and 3 were a consequence of higher simulated losses in these scenarios, which reduced the number of animals available for selection. Furthermore, the number of selected animals was kept fixed (equivalent to an approximate 140% annual turnover for boars and 200% for sows).

Bourdon (2013) reported that selection intensity is determined by the number of animals selected for replacement in relation to the number of animals available for selection. High selection intensity is obtained when a small group of animals is selected for replacement within a large available group, which can be achieved by reducing the number of selected animals while maintaining the same number of available animals or by increasing the number of animals available and maintaining the number of selected animals. High selection intensities allow for the selection of animals above average, while low intensities lead to the selection of animals below or near average.

Conclusions

In this situation of selection indexes and genetic composition, inbreeding levels in closed production units increase with productive and reproductive losses. Inbreeding increases are higher in populations of smaller effective size. Productive and reproductive losses reduce the variances of breeding values and, especially, selection intensities, by reducing the number of animals available for selection, thereby reducing genetic gains. Actions that maximize farrowing rates are more important than those that minimize mortality rates during the lactation period, considering that the reduction of farrowing rate simulated in scenario 3 resulted in greater losses in genetic gains and slightly higher inbreeding increments when compared with the other scenarios.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Conceptualization: J.S. Lopes and M.S. Freitas. Data curation: M.S. Freitas. Software: M.S. Freitas. Supervision: P.R.N. Rorato and F.C. Breda. Visualization: M.M. Farah, L.O. Duitama Carreño and M.M. Oliveira. Writing-original draft: J.S. Lopes. Writing-review & editing: J.S. Lopes.

Acknowledgments

We are grateful to Company BRF S/A and its Genetic Breeding Program for Pigs, for providing the data and for enabling the execution of the present study; to the Laboratório de Melhoramento Animal and

the Programa de Pós-Graduação em Zootecnia of the Universidade Federal de Santa Maria, for the opportunity; and, especially, to Marcelo Silva de Freitas, for the development of the simulator employed in this work.

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