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1 Estimation of genetic parameters and inbreeding depression in Piau breed pigs

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7 Abstract

8 This study aimed to estimate genetic parameters, effective population size, inbreeding, and
9 inbreeding depression for birth weight, weaning weight, and average pre-weaning daily weight gain (ADG)
10 in Piau breed pigs. We used information from 3841 Piau pigs, and four linear models were fitted in single
11 trait analyzes including or excluding maternal genetic effect, common litter effect, or a combination of
12 these. The models' adjustments were compared by likelihood ratio test, in which the model that presented
13 the best fit for each trait was used to estimate (co)variance components. The inbreeding depression effect
14 was evaluated using a linear model that included the fixed effects of sex, parity order, contemporary group,
15 and inbreeding coefficient as a fixed covariate. Weight at birth and weaning showed low direct heritabilities
16 (0.08 and 0.05, respectively), while ADG showed moderate heritability (0.20). Weight at birth showed high
17 genetic correlations with weight at weaning (0.90) and with ADG (0.82). Weight at weaning and ADG also
18 showed a high genetic correlation (0.99). There was an inbreeding increase over the generations and a
19 reduction of the effective population size. In the last generation evaluated all animals were inbred, the
20 average inbreeding coefficient was 0.07 and the effective population size was 20.8. It was observed a
21 significant inbreeding effect on ADG, wherein an increase of 1% on the inbreeding coefficient resulted in
22 a decrease of 0.005 grams on ADG. Thus, increase effective population size is mandatory for the inbreeding
23 control and to reduce the loss of variability in this Piau population.

24
25 Keywords: Conservation. Local breeds. Inbreeding. Heritability.

27 Introduction

28 The local Brazilian pig breeds are descents of those animals introduced in Brazil by Portuguese
29 settlers in the 16th century (colonial period), therefore, they have influences of Portuguese (Alentejana and
30 Bísara), Spanish (Galega and Perijordina), Italian (Neapolitan), and Asia (Macau) breeds (Castro et al.,

31 2002). During the following centuries, these different breeds were crossed and naturally selected under
32 Brazilian environmental conditions, which resulted in gradual changes in their reproductive, performance
33 and racial traits and in the emergence of several local breeds, such as Piau, Canastra, Moura, Caruncho,
34 Pereira, and Nilo (Souza et al., 2009). In general, the local Brazilian pig breeds are characterized by high
35 fat deposition, rusticity, disease resistance, lower handling and feeding requirements, and present higher
36 adaptability to tropical climate environments (Mariane et al. 2003; Sollero et al. 2009; Silva et al., 2019;
37 Sprícigo et al., 2019).

38 In the past, some local Brazilian pig breeds (e.g. Piau) were extensively raised to attend the lard
39 industry. However, due to changes in consumer preferences, around the 1960s, the producers started to
40 import foreign breeds with greater aptitude for meat deposition (Fávero and de Figueiredo, 2009). The high
41 productivity of foreign breeds and the crossings with local breeds caused a rapid replacement and erosion
42 of local breeds. Currently, local breeds have practically disappeared in the Brazilian productive system
43 (Araújo et al., 2020). Piau and Moura breeds still raised by small producers or in conservation centers,
44 however, they are also on the list of endangered breeds (Mariane et al., 2005; Albuquerque et al., 2016;
45 Araújo et al., 2020). This scenario highlights the need for genetic conservation of local breeds since the
46 loss compromises access to their genes and consequently to their unique traits that could be useful in the
47 future (Bermejo et al., 2019; Bennewitz et al. 2008).

48 The genetic characterization of local breeds become crucial for the establishment of conservation
49 programs (Jordana et al., 2010). The analysis of inbreeding, effective number of founders, and effective
50 population size provides information about the status of the breed, which is essential for planning strategies
51 to be implemented in the conservation program and avoid the loss of genetic variability (Veroneze et al.,
52 2014). Moreover, monitoring the additive genetic variance may reveal the variations related to fitness and
53 produce interesting insight about genetic and environmental effects in the genetic diversity changes (Toro
54 and Caballero, 2005).

55 Given the endangered status of the Piau breed population and the existence of few conservation
56 centers, the knowledge about genetic parameters, population structure, and inbreeding is fundamental for
57 the development of strategies for the breed genetic conservation. Then, this study aimed to estimate genetic
58 parameters, effective population size, inbreeding, and inbreeding depression for birth weight, weaning
59 weight, and average pre-weaning daily weight gain in Piau breed pigs.

60 MATERIAL AND METHODS

61 Data description

62 Data used in this study were obtained from a conservation herd of Piau breed located at the Unit
63 for Teaching, Research and Extension in Pig Breeding at the Federal University of Viçosa, Viçosa, Minas
64 Gerais, Brazil. The pedigree included data from 3841 animals. The traits analyzed were birth weight,
65 weaning weight, and average pre-weaning daily gain (ADG) from animals born between 2002 and 2018.

66 The data were edited using the R software (R Core Team, 2019) where observations with more
67 than two standard deviations above or below the mean were removed. The contemporary groups were
68 established according to the year and birth period (warm season = October to March, cold season = April to
69 September). The contemporary group containing at least 12 animals with observations for each trait. The
70 descriptive statistics of data used after the edition are shown in Table 1.

71

72 Table 1. Descriptive statistics of data

Trait	Number of observations	Mean	Minimum	Maximum	Standard deviation	CV* (%)
Birth weight	3548	0.997	0.300	1.766	0.271	27.12
Weaning weight	1644	6.600	2.500	10.900	1.841	27.89
ADG**	1362	0.154	0.058	0.257	0.042	27.12

*CV: coefficient of variation; **ADG: average pre-weaning daily gain.

73

74 Statistic models

75 Four linear models, including or excluding maternal genetic effect, common-litter effect, or the
76 combination of them were used in the single-trait analysis for each trait to identify the best model for
77 evaluation of each trait. The same fixed effects were used in all models in which sex, parity order, and
78 contemporary group were included. For weaning weight, the age at weaning was included as a covariate.

79 The models were described as follow:

80 M1: Animal model with a direct additive genetic effect:

$$81 \quad \mathbf{y} = \mathbf{Xb} + \mathbf{Z}_a \mathbf{a} + \mathbf{e}$$

82 M2: Animal model with a direct additive genetic effect and maternal additive genetic effect:

$$83 \quad \mathbf{y} = \mathbf{Xb} + \mathbf{Z}_a \mathbf{a} + \mathbf{Z}_m \mathbf{m} + \mathbf{e}$$

84 M3: Animal model with a direct additive genetic effect and common-litter effect:

$$85 \quad \mathbf{y} = \mathbf{Xb} + \mathbf{Z}_a \mathbf{a} + \mathbf{Wc} + \mathbf{e}$$

86 M4: Animal model with a direct additive genetic effect, maternal additive genetic effect, and
 87 common-litter effect:

$$88 \quad \mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_a\mathbf{a} + \mathbf{Z}_m\mathbf{m} + \mathbf{W}\mathbf{c} + \mathbf{e},$$

89 where \mathbf{y} is the vector of observations, \mathbf{b} is the vector of fixed effects, \mathbf{a} is the vector of random direct
 90 additive genetic effect; \mathbf{m} is the vector of random maternal additive genetic effect; \mathbf{c} is the vector of random
 91 common-litter effect; \mathbf{e} is the vector of residuals, \mathbf{X} is the incidence matrix of fixed effects, and \mathbf{Z}_a , \mathbf{Z}_m
 92 and \mathbf{W} are incidence matrices of random direct additive genetic, maternal additive genetic, common-litter
 93 effects, respectively. The random effects distribution was as follow:

$$94 \quad \text{Var} \begin{bmatrix} a \\ m \\ c \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & 0 & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I\sigma_c^2 & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix},$$

95 where σ_a^2 is the direct additive genetic variance, σ_m^2 is the maternal additive genetic variance, σ_{am} is the
 96 covariance between direct and maternal genetic effects, σ_c^2 is the common-litter variance and σ_e^2 is the
 97 residual variance.

98 The analyses were performed using the AIREMLF90 software (Misztal, 2002). The likelihood
 99 ratio test (LRT) was used to compare the fit of the different evaluated models, such that

$$100 \quad \text{LRT} = -2(\text{LogL}_{\text{reduced model}} - \text{LogL}_{\text{complete model}}),$$

101 where $\text{LogL}_{\text{reduced model}}$ and $\text{LogL}_{\text{complete model}}$ are the likelihood logarithm for reduced and complete models,
 102 respectively. The level of significance of 0.05 were used for the comparison.

103 The best model defined from the LRT was used to estimate (co)variance components under
 104 bivariate analyses combining all evaluated traits.

105 Estimates of direct heritability (h_a^2) and maternal heritability (h_m^2) were respectively calculated as
 106 the ratio of estimates of direct additive genetic variance (σ_a^2) and maternal additive genetic variance to the
 107 total phenotypic variance (σ_p^2).

108

109 **Effective population size and inbreeding**

110 The effective population size (N_e) and inbreeding coefficients (F) are important parameters for
 111 monitoring the genetic diversity in a population. The software ENDOG v. 4.8 (Gutiérrez and Goyache,
 112 2005) was used to calculate the N_e , which is obtained from the regression coefficient (b) of the individual
 113 inbreeding coefficient over the equivalent complete generations:

114
$$Ne = \frac{1}{2b},$$

115 where $b = F_t - F_{t-1}$; F_t and F_{t-1} are the average inbreeding coefficients at the t e $t - 1$ generations,
 116 respectively.

117 The average relatedness coefficient, which is a complementary measure to the inbreeding
 118 coefficient (Gutiérrez et al. 2005), was also calculated. This parameter represents the probability of one
 119 allele randomly chosen from the whole population in the pedigree belongs to a given animal.

120 The inbreeding coefficients (F) to each animal on pedigree were calculated according to
 121 Meuwissen and Luo (1992) and used to estimate the inbreeding depression effect according to the following
 122 linear model:

123
$$y_{ijkl} = \mu + sex_j + cg_k + po_l + b(F_{ijkl} - \bar{F}) + e_{ijkl}$$

124 where y_{ijkl} is the phenotypic observation of animal i , μ is the general mean; sex_j is the effect of j^{th} sex;
 125 cg_k is the effect of k^{th} contemporary group; po_l is the effect of l mother parity order; F_{ijkl} is the individual
 126 inbreeding coefficient; b is the linear regression coefficient and \bar{F} is the average inbreeding; and e_{ijkl} is the
 127 random residual. The analysis was performed using the *lm* function from R software (R Core Team, 2019).

128

129 **RESULTS**

130 **Genetic parameters**

131 According to the likelihood ratio test (LRT) the complete model (M4), including direct additive
 132 genetic, maternal additive genetic, and common-litter random effects was superior to all other evaluated
 133 models (M1, M2, and M3) for all analyzed traits (Table 2).

134

Table 2. Likelihood ratio test (LRT) of comparable models

Trait	Comparison	LRT	df*	p-value
Birth weight	M1 vs M4	7608.4673	2	<0.0001
	M2 vs M4	356.4222	1	<0.0001
	M3 vs M4	7158.6400	1	<0.0001
Weaning weight	M1 vs M4	7422.4858	2	<0.0001
	M2 vs M4	276.9984	1	<0.0001
	M3 vs M4	7126.7848	1	<0.0001

	M1 vs M4	7240.4327	2	<0.0001
ADG**	M2 vs M4	90.1745	1	<0.0001
	M3 vs M4	7128.0156	1	<0.0001

*df: degrees of freedom for the LRT; **ADG: average pre-weaning daily weight gain.

135 The variance components and genetic parameters were estimated using the model M4 that showed
136 a better fit on the single-trait analysis and it is presented in Table 3. Weight at birth and weight at weaning
137 showed low direct heritabilities (0.08 and 0.05, respectively), while ADG showed moderate direct
138 heritability (0.20).
139

Table 3. Variance components, direct and maternal heritability (standard error within parentheses) for birth weight, weaning weight, and average pre-weaning daily weight gain (ADG) in Piau breed

Trait	σ_a^2	σ_m^2	σ_{am}	σ_c^2	σ_e^2	σ_p^2	h_d^2	h_m^2
Birth Weight	0.0071	0.0177	- 0.0008	0.0187	0.0436	0.0863	0.08	0.20
	(0.0050)	(0.0061)	(0.0052)	(0.0020)	(0.0029)	(0.0048)	(0.06)	(0.07)
Weaning Weight	0.1947	0.5070	- 0.3137	1.3670	1.9076	3.6626	0.05	0.14
	(0.1300)	(0.2732)	(0.1829)	(0.1784)	(0.1028)	(0.2075)	(0.05)	(0.07)
ADG	0.0005	0.0002	0.0001	0.0005	0.0011	0.0025	0.20	0.10
	(0.0003)	(0.0002)	(0.0002)	(0.0001)	(0.0002)	(0.0002)	(0.12)	(0.08)

σ_a^2 : direct additive genetic variance; σ_m^2 : maternal additive genetic variance; σ_{am} : covariance between maternal and direct additive genetic effects; σ_c^2 : common-litter variance; σ_e^2 : residual variance; σ_p^2 : phenotypic variance; h_d^2 : direct heritability; h_m^2 : maternal heritability.

140
141 The covariances and correlations were estimated under a bivariate analysis and are presented in
142 Table 4. Birth weight presented high correlation with weaning weight (0.90) and with ADG (0.82).
143

Table 4. Covariance ($\sigma_{a1,2}$) and genetic correlations (r_g) (standard error within parentheses) between the traits birth weight, weaning weight, and average pre-weaning daily weight gain (ADG) in Piau breed

Traits	$\sigma_{a1,2}$	$r_{g1,2}$
Birth Weight	Weaning weight	0.25119 (0.0163)
	ADG	0.00465 (0.0004)

Weaning Weight ADG 0.10858 (0.0042) 0.99 (0.0043)

144

Effective population size

145

146 The effective population size and inbreeding over the generations are relevant to monitoring the
 147 changes in genetic diversity in the population. The inbreeding increased over the generations, which
 148 promoted the effective population size decrease (table 5). Moreover, it is noteworthy that in generation 4
 149 all animals from the population became inbred and the average relatedness increased.

150

Table 5. Number of individuals (N), average inbreeding coefficient (F), percentage of inbred individuals (% inbred), average inbreeding coefficient for inbred (F_{inbred}), average relatedness coefficient (AR), and effective population size (N_e) in the equivalent complete generations

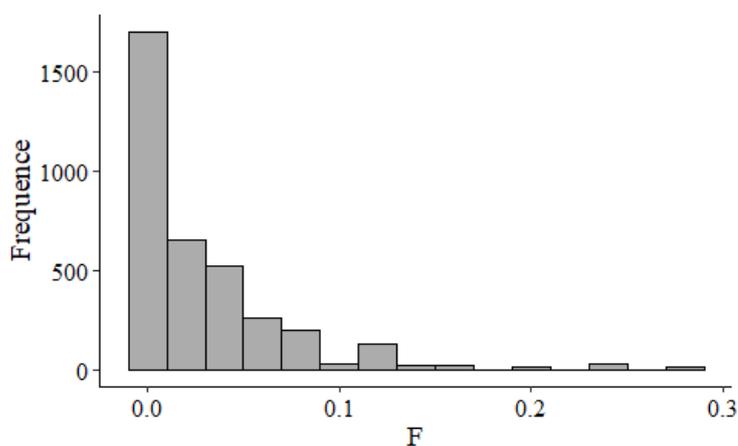
Generation	N	F	% inbred	F_{inbred}	AR	N_e
0	596	0.0000	0.00	0.0000	0.0538	-
1	630	0.0088	32.86	0.0269	0.0782	56.5
2	1170	0.0291	43.08	0.0675	0.1158	24.4
3	1211	0.0487	98.02	0.0497	0.1430	24.7
4	235	0.0715	100.00	0.0715	0.1509	20.8

151

Inbreeding depression adjustment

152

153 The inbreeding coefficient (F) distribution for all animals in the pedigree is presented in Figure 1.
 154 It is possible to observe that most of the animals have low inbreeding levels with the maximum inbreeding
 155 coefficient equal to 0.28.



156

157 **Fig. 1** Inbreeding coefficient (F) distribution from Piau breed animals.

158

159 The inbreeding effects on the traits evaluated are presented in table 6. The regression coefficient
160 was significant only for ADG ($p < 0.10$), for this trait the regression shows that for each 1% increase in the
161 inbreeding coefficient there is a decrease of 0.0005 grams in ADG (Table 6).

162

Table 6. Linear regression coefficient estimates (standard error within parentheses) of inbreeding for weight at birth, weight at weaning, and average pre-weaning daily weight gain (ADG)

Traits	Coefficient	p-value*
Birth weight	0.0005 (0.0011)	0.640
Weaning weight	-0.0073 (0.0106)	0.494
ADG	-0.0005 (0.0003)	0.054

* $\alpha = 0.10$

163

164 **DISCUSSION**

165 **Genetic parameters**

166 The best fitting model included the maternal additive genetic and common-litter effects in addition
167 to the direct additive effect. The evaluated traits are influenced by factors like uterine nutrient supply,
168 uterine capacity, and milk production (Kaufmann et al., 2000), which are controlled by the mother's genes.
169 Thus, it was expected that a model including the maternal additive genetic would present a better fit.
170 Besides, the common-litter effect is important for the evaluation of traits measured from animals that share
171 a common environment because it contributes to the resemblance between the individuals (Cavalcante Neto
172 et al., 2009; Falconer and Mackay, 1996).

173 Although small breeds are subjective to genetic drift (Alderson, 2018), the existence of additive
174 genetic variance for the traits evaluated indicates that Piau breed still presents genetic variability. The
175 presence of genetic variability is essential to establish a conservation program for a local breed.
176 Conservation of genetic diversity is important to overcome future challenges and meet consumer needs,
177 encompassing social, cultural and heritage components of a particular region (Alderson, 2018).

178 Piau birth weight showed a low direct heritability estimate (0.08), which is in line with the
179 literature (Akanno et al., 2013; Alves et al., 2018a; Tomiyama et al., 2010). Alves et al. (2018a, b) reported

180 direct heritabilities estimates ranging from 0.05 to 0.08 and from 0.07 to 0.15 to birth weight in Yorkshire
181 and Landrace breeds, respectively. In a meta-analysis using studies evaluating tropical local pig breeds,
182 Akanno et al. (2013) reported the heritability of 0.10 for birth weight. Studying Berkshire pigs, Tomiyama
183 et al. (2010) reported a heritability of 0.07 for birth weight. Although, low genetic gain per generation is
184 expected through selection for birth weight, this trait is directly associated with piglet's survival, behavior,
185 and weight gain pre- and post-weaning (Fix et al. 2010; Muns et al. 2013; Alves et al. 2018a).

186 The maternal heritability for birth weight was much higher than the direct heritability showing a
187 strong contribution of the maternal genetics in the phenotypic variance in Piau breed. Other studies showed
188 the importance of maternal variance for birth weight. Alves et al. (2018ab) estimated maternal heritabilities
189 from 0.18 to 0.22 in Yorkshire breed. Evaluating Berkshire breed, Tomiyama et al. (2010) reported maternal
190 heritability of 0.19 for birth weight.

191 The low direct heritability estimate for weaning weight (0.05) is close to those reported by Alves
192 et al. (2018a), which ranged from 0.03 to 0.04 in Yorkshire breed, and 0.01 in Landrace breed. However,
193 studying Ashanti Black Pigs, a Ghanaian local breed, Darfour Oduro et al. (2009) reported heritabilities
194 from 0.14 to 0.16 for weaning weight. In a meta-analysis study, Akanno et al. (2013) reported a heritability
195 of 0.17 for weaning weight in local breeds.

196 The maternal heritability estimate for weaning weight corroborates to estimates from 0.11 to 0.13
197 reported by Zhang et al. (2000) and Alves et al. (2018a), but was lower than estimates from 0.24 to 0.25
198 reported by Ilatsia et al. (2008) and Darfour-Oduro et al. (2009). The divergences on the genetic parameter
199 estimates among the different studies may be attributed to the differences between the evaluated
200 populations, which come from different breeds, lines, and crossings. As observed for birth weight, the
201 maternal genetic variance in Piau breed had greater contribution for phenotypic variance of weaning weight
202 than direct additive genetic. Thus, selection on maternal genetic effects may be an interesting strategy for
203 the improvement of Piau birth and weaning weight.

204 The direct heritability estimate for ADG (0.20) was in line with the estimate of 0.21 reported by
205 Darfour-Oduro et al. (2009) in Ashanti Black Pigs. However, studies evaluating commercial breeds
206 reported higher direct heritabilities for ADG, with values equal to 0.32 in Yorkshire breed (Wurtz et al.
207 2017), and 0.46 in Large White breed (Ilatsia et al. 2008). The maternal heritability estimate for ADG
208 (0.10) was lower than 0.24 reported for Ashanti Black Pigs (Darfour-Oduro et al. 2009) and 0.18 reported
209 for Large White breed (Ilatsia et al. 2008).

210 The genetic correlation between birth weight and weaning weight, and between birth weight and
211 ADG were strong and positive (0.90 and 0.82, respectively), corroborating to Darfour-Oduro et al. (2009)
212 who estimated genetic correlations equal to 1.00 between weight at birth and weaning weight and equal to
213 0.87 between birth weight and ADG. The high correlations suggest that a similar group of genes control
214 weight at birth, ADG, and weight at weaning.

215 The genetic correlation between weaning weight and ADG was high and positive (0.99)
216 corroborating to estimates reported in other studies (Darfour-Oduro et al. 2009; Akanno et al. 2013). A high
217 correlation between these traits was expected, since weaning weight is used to calculate the ADG. Thus,
218 the selection based on one of those traits may provide correlated gains in other traits in the same direction.
219 As ADG presented higher heritability than the other traits and high genetic correlation with then, this trait
220 may be a relevant selection criterion for Piau pigs.

221

222 **Effective population size and inbreeding**

223 In conservation programs for local animal genetic resources, control the increasing in inbreeding
224 and maintaining genetic variability are crucial (Saura et al. 2013). The evaluated Piau pig population
225 presented low effective population size (since the first generations) and increasing in average inbreeding
226 across generations. The effective population size from generation 2 onwards is lower than 50, which is
227 recommended by Food and Agriculture Organization (FAO) (1998) for the maintenance of genetic
228 resources. Thus, it is crucial for Piau breed conservation to increase the effective population size to reduce
229 the rate of inbreeding.

230 The AR increased across generation and a high value (0.15) is observed in the last generation.
231 Evaluating the same population of this study, Veroneze et al. (2014) also reported a growing average
232 relatedness coefficient over the generations, which was attributed to the population expansion from a small
233 initial herd. The average relatedness, proportion of inbred individuals, and effective population size of the
234 last generation indicated that the population is already in a critical situation and further increase in
235 inbreeding will occur in future generations. If inbreeding continues to increase, many genetic phenomena
236 such as reduction in genetic diversity and genetic drift will occur, leading to changes in population structure
237 decreasing population means (Curik et al., 2014). Thus, the expansion of effective population size and the
238 introduction of unrelated individuals in the population is paramount to control inbreeding rate and breed
239 conservation.

240 The number of known purebred Piau herds is very limited and there is no recent census of
241 endangered breeds in Brazil. This lack of information poses a great challenge for the breed conservation,
242 since it does not allow us to truly understand the actual breed endangerment situation and it limits animal
243 and information exchange across herds. In a census conducted 20 years ago in Paraiba state, only 56 animals
244 were classified as local breed, among these pigs 16 were classified as Piau (Cavalcante Neto et al., 2007).
245 Despite that, Piau breed is not included in Conservation Program from Brazilian Agricultural Research
246 Corporation (EMBRAPA), in which the unique pig bred included is Moura (Albuquerque et al., 2016).

247 The number of animals that can be kept by conservation centers is limited, thus policies to
248 encourage pig producers to rear local breeds would be essential for the expansion of Piau pig population
249 in Brazil.

250

251 **Inbreeding depression adjustment**

252 A consequence due to increase in inbreeding is the reduction of the mean phenotypic value of traits
253 mainly connected with reproductive capacity or physiological efficiency, what is known as inbreeding
254 depression (Falconer and Mackay, 1996). In this study, a significant inbreeding effect on ADG was found,
255 such that an increase of 1% on inbreeding corresponded to a decrease of 0.005 grams on ADG.

256 The regression coefficient was not significant for the other evaluated traits, which suggest that
257 inbreeding depression is not occurring for birth weight and weaning weight in the studied population. These
258 results can be attributed to the fact that most animals in the dataset have inbreeding equal to zero (Figure
259 1) and a reduced number of animals showed a high inbreeding coefficient. The negative effect of inbreeding
260 on ADG, although small, is worrisome seeing that inbreeding increase is expected in the next generations
261 according to the population structure (N_e and AR).

262 Devi and Jayashankar (2014) found a considerable, but not significant, difference between average
263 litter weight at birth from inbred and non-inbred Large White sows. The same authors found significant
264 reductions in litter weight at weaning due to the inbreeding effect. However, Gowrimanokari et al., (2019)
265 observed a positive inbreeding effect in weaning weight, pre-weaning average daily gain and in litter weight
266 at weaning in Large White breed. Gowrimanokari et al. (2019) also explained that the low level of
267 inbreeding could be the reason for absence of significant inbreeding depression in their study.

268

269 **CONCLUSION**

270 Although the whole current population is inbred and shows reduced effective population size, all
271 traits evaluated exhibited additive genetic variance showing the existence of genetic variability in the
272 population.

273 The small effective population size in the last generation indicated that the inbreeding will increase
274 considerably in the next generations. Thus, increase effective population size is mandatory for the
275 inbreeding control and to reduce the loss of variability in this Piau population.

276

277 **DECLARATIONS**

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283 the Federal University of Viçosa.

284

285 **Conflicts of interest**

286 The authors declare that they have no conflicts of interest.

287

288 **Ethics approval**

289 The approval of the animal care and use committee was not needed because this research used
290 existing datasets.

291

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