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Heritability and genetics correlations for body weight in *escargots*

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ABSTRACT. The objective of this study was to estimate genetic parameters for body weight at 60 (P60), 90 (P90), and 120 (P120) days of age in *escargots* of the subspecies *Cornu aspersum maximum*, evaluating the influence of fixed and covariable effects on these traits. The data used were collected from *escargots* kept in a total confinement system. The significant fixed effects and covariates for these traits were tested in a general linear model by the F-test, considering a level of significance of 5%. Both the fixed effects of box and birth year and the quadratic effect of age of weighing as a covariate were significant ($p < 0.05$) for P60, P90, and P120. The Restricted Maximum Likelihood (REML) methodology was used to estimate (co)variance components and genetic parameters. High heritability for P60, P90, and P120 (0.38, 0.55 and 0.78, respectively) and high genetic correlations (0.58 to 0.77) among the traits were observed. The genetic parameters can be used as a basis for studies and practical applications to increase zootechnical indexes in this population.

Keywords: animal model; *Cornu aspersum*; genetic parameters; heliciculture, snails.

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Introduction

Heliciculture is an expanding activity in Brazil and countries where the consumption of *escargots* meat is traditional (Pissia, Matsakidou, & Kiosseoglou, 2021). In this sense, an opportunity is identified for animal scientists to work on technologies and improvements to the raising systems of these animals.

Compared to other species of edible snails, the subspecies *Cornu aspersum maximum* (*Gros Gris*) stands out for presenting high prolificacy, fast growth (Nicolai & Ansart, 2017), greater rusticity, low generation interval and high market value when compared to other sources of animal protein. The use of technological tools can make it possible to increase the zootechnical indexes in these animals, improving performance and making breeding more profitable. Among these, the use of animal breeding stands out for promoting permanent advances, even in the long term. In the subspecies *Cornu aspersum maximum* there are few studies in this context.

Body weight is a trait of economic interest, especially if we considered that the main product of snails, meat, is based on the final weight of the animal and how long it takes to reach it (Sherpa et al., 2018). Thus, studies involving the evaluation of weight traits during the initial growth phase in the species are recommended. Obtaining genetic parameters (heritability and genetic correlations) for growth traits can help the decision about the selection criteria to be applied in the population as well as providing management and breeding adjustments (Eler et al., 2004).

For genetic parameters to be correctly estimated, it is necessary to define a statistical model that explains the behavior of the traits, established from a study of possible fixed and covariate effects. These studies have a fundamental character in the results of the evaluations because it makes it possible to isolate most of the environmental effects, bringing greater accuracy to the estimates of genetics parameters (Eler, Santana Júnior, & Ferraz, 2012).

The objectives of this study were: i) to investigate the influence of covariates and fixed effects on traits and to structure a model of genetic evaluation for body weight at 60 (P60), 90 (P90) and 120 (P120) days of age in *escargots* of the subspecies *Cornu aspersum maximum*. ii) to estimate genetic parameters (heritability

and genetic correlations) for P60, P90 and P120, for an initial understanding of the quantitative genetic architecture for traits of body weight in *escargots*.

Material and methods

Data were collected at the Heliciculture Sector of the Department of Animal Science of the Federal University of São João del-Rei, between 2018 and 2019, where matrices of the subspecies *Cornu aspersum maximum* were kept. The raising system adopted was that of total confinement, with a cycle of natural light with a shade screen to mitigate the solar incidence in the critical periods of the day. Humidity and temperature were controlled by daily recording, where it was used a humidification system, as well as manual spraying, if necessary, in addition to restricted access. The experimental period was of 499 days, with an average temperature of 21.3°C and average relative humidity of 87.7%.

The founding dams were identified individually for the genealogical control. As the species is hermaphrodite, it was not possible to control the paternity of the animals. The dams are identifiable because they lay the eggs. All other individuals in the same box are possible sires. The laying was carried out on non-clay soil, with a pH between 6.5 and 7.5. At each laying, the nests containing the eggs were removed from the matrix box and packed in an individual box until hatching. After hatching, the chicks were counted and transferred to a plastic box with a polypropylene mosquito net in nylon and kept shelf.

For animals younger than 30 days, it was offered roughage with speckled concentrate and later, concentrated in plastic containers. The feed was standardized and composed of balanced mash feed, following the nutritional composition recommended for the species under commercial breeding conditions. The cleaning of the boxes was carried out daily, with the change of feed and roughage, and avoiding the manipulation of animals so that there was no possible rupture of the epiphragm, reducing the occurrence of stress due to handling. Water was offered *ad libitum* in troughs, and when necessary, the animals were sprayed manually to maintain moisture in the box's microenvironment.

The *escargots* in the initial period of growing up to 60 days old were placed in boxes called 'juvenile'. When reached 60 days of age, all animals received an individual marking with a combination of two enamel colors in the shell and their body weights were collected. Then, the groups of progenies from at least 3 different dams were placed in boxes called 'adults'. They were grouped by weight (50% heavier, 50% lighter), with between 22 and 55 animals in each box and remained until slaughter or death. Body weights were also measured at 90 and 120 days of age. Due to the differences between the breeding protocols and environmental conditions of the years 2018 and 2019, all snails were included in the analyses with the year of birth duly identified.

The pedigree file was formed by 3,158 animals, including 67 dams, and presented 4 generations. The number of animals in generations 1 to 4, was 616, 1,534, 886 and 122, respectively. The families per dam consisted of 3 to 140 animals. There were 2,542 animals with dam information and 634 animals had a degree of kinship (0.015625 to 0.50) with some other individuals.

The database consisted of animal identification, year and season of birth, box identification (juvenile and adult) to which the animal belonged, class of capacity of the adult box (number of individuals in the adult box), age at weighing, and traits of interest P60, P90 and P120.

The data were submitted to consistency analyses, excluding individuals without phenotypes, with duplicate data, in addition to considering an amplitude of three standard deviations the population average ($\bar{x} \pm 3\sigma$) for the traits, with the consequent removal of weight data beyond this range.

To determine the fixed effects and the significant covariates for each trait, a general linear model was used, by using F-test in PROC GLM of SAS software (Statistical Analysis System [SAS], 2008), and considering a significance level of 5%. For P60, the fixed effects tested were year and season of birth, and juveniles' box, and as a covariate, the age at weighing (linear and quadratic). For P90 and P120, the fixed effects of year and season of birth and adult box were tested, and as covariates, age at weighing and the number of individuals in boxes.

The (co)variance components were estimated by Maximum Restricted Likelihood (REML) methodology, using the AIREMLF90 software (Misztal et al., 2002). The animal model used was:

$$y = Xb + Za + e$$

where: y is the vector of observations (weight); b is the vector of fixed effects; a is the vector of additive genetic effects; e is the vector of residual effects; X and Z are incidence matrices, which associate b and a to y, respectively.

Results and discussion

Descriptive statistics

The descriptive statistics of the traits evaluated are presented in Table 1.

Table 1. Number of observations (N), mean ($\bar{X}$), standard deviation (SD), coefficient of variation (CV, %), minimum (MIN) and maximum (MAX) of the traits analyzed.

Traits ¹ (g)	N	M	SD	CV	MIN	MAX
P60	2,787	1.55	0.93	60.26	0.12	4.69
P90	2,333	4.31	2.13	49.52	0.28	16.29
P120	1,733	7.73	3.65	47.16	0.81	21.38

¹P60, P90 and P120 = body weight at 60, 90 and 120 days of age, respectively.

High coefficients of variation are noted for body weight at all ages evaluated, which can be explained by the absence of selection in this species, leading to a high variation for these traits (Bleakney, Fleming, & Marks, 2015). Besides, the environmental component can interfere with the growth of these animals, such as the number of animals per area for each growth phase (newborns, youngsters, and adults), which in turn interferes in the dispute for food (Chapuis & Ferdy, 2012; Nicolai & Ansart, 2017).

Thermal oscillations can also affect the development of animals more susceptible to environmental conditions, and at temperatures above 25°C, the snails tend to be stagnant (Porcel, Bueno, & Almendros, 1996). Also, these animals are sensitive to handling (Février, Russo, & Madec, 2009), which may cause a restriction in consumption, causing differences in size among snails. Additionally, this variation may also be due to differences in the hydration status of snails, since the species is extremely dependent on the relative humidity of the air, directly affecting the weight of *escargots*.

Fixed and covariate effects

For P60, the fixed effects of juvenile box and year of birth were significant ($p < 0.05$). For P90 and P120, the adult box and year of birth were significant. It was also possible to observe a significant linear and quadratic effect ($p < 0.05$) from age at weighing for the three traits. The linear effect of the number of individuals in the boxes on the day of animal selection was significant for P90 and P120 ($p < 0.05$). Significant effects with biological interpretation were included in the models for each of the characteristics evaluated.

Despite the existence of a protocol to standardize conditions, they can vary according to the snail's allocation box (number of different individuals), management, year of birth (thermo-hygrometric variations and light intensity) (Sherpa et al., 2018). For example, the number of animals present in the box, as well as the size of them can directly influence the competition for food, causing variations in weight. Another important factor is age, as snails show a sigmoid growth curve of weight gain, and since these animals were in the growth phase during the experimental period, a small difference in days could represent a great difference in size.

Genetic analysis

Heritability and genetic correlations

The variance component estimates for traits P60, P90 and P120 are presented in the Table 2 and the heritability and genetic correlations are presented in Table 3.

The standard deviations obtained for the estimates of genetic parameters were low, suggesting low dispersion of the estimates and high reliability of such results. The estimates of heritability coefficients showed higher values at P90 and P120 (0.55 and 0.78, respectively), and lower at P60 (0.38). Even so, all heritability was high, that is, a large part of the expression of the phenotype is due to the action of additive genetics, in addition of indicating a high capacity for transmitting alleles to the following generations (Eler et al., 2012).

Table 2. Estimates of variance components and their respective standard deviation for body weight at 60 (P60), 90 (P90) and 120 (P120) days of age for the *escargot* population.

Traits (g)	σ_a^2	σ_r^2
P60	0.15 (± 0.06)	0.25 (± 0.05)
P90	1.64 (± 0.29)	1.19 (± 0.23)
P120	7.58 (± 1.43)	2.12 (± 1.10)

σ_a^2 = additive genetic variance; σ_r^2 = residual variance.

Table 3. Estimates of heritability (diagonal) and genetic correlation (above diagonal), with their respective standard deviation, for body weight at 60 (P60), 90 (P90) and 120 (P120) days of age for the *escargot* population.

Traits (g)	P60	P90	P120
P60	0.38 ($\pm$ 0.13)	0.91 ($\pm$ 0.07)	0.58 ($\pm$ 0.30)
P90	-	0.55 ($\pm$ 0.09)	0.77 ($\pm$ 0.08)
P120	-	-	0.78 ($\pm$ 0.01)

If the selected fraction is different from zero, high heritability values can contribute to a faster genetic gain (Eler et al., 2004), since they are directly related to the genetic progress of the variables (Li, Wang, Liu & Kong, 2011), which may be favorable for the characteristics evaluated in this population. In this sense, a low selection pressure can be applied and still present genetic gain in this population. Besides, it is possible to obtain genetic gains via phenotypic (or mass) selection, such as that conducted in the study population.

So far, reports of heritability estimates for the subspecies *Cornu aspersum maximum* are scarce. However, for comparison, Dupont-Nivet, Guiller, & Bonnet, (1997) reported lower heritability values for adult body weight in snails of the subspecies *Helix aspersa* of 0.45 ± 0.16 (through regression of offspring on mid-parent), 0.68 ± 0.11 (through variance components of offspring).

In general, the values reported in the present study were higher than the values found in literature for other species. These high estimates may have been the result of an overestimation of the genetic variances of P90 and P120, due to the possibility of not including unknown environmental effects because this is a preliminary study in our population.

The traits showed high genetic correlations among them, which suggests, therefore, a high degree of occurrence of pleiotropy, and/or gene linkage (Knott & Haley, 2000), especially between those that had a shorter interval of days, as it is the case of P60 and P90 (0.91), and P90 and P120 (0.77). When the measurement range is longer, the genetic correlation remained high, as in the case of P60 and P120 (0.58). Analogously to the heritability estimates, until now, few genetic correlations have been reported among weight traits for *Cornu aspersum maximum* snails. This points out to the importance of an earlier selection in populations of snails, due to the high correlation values obtained for the evaluated body weight traits.

The genetic correlation values reported in the present study are indicative that heavier individuals at 60 days will be heavier at 120 days. A precocious slaughter of snails it is desired, that is, animals that would show greater weight development at 120 days of age. Thus, an earlier selection at 60 days can have a favorable impact on weight at 120 days in this population. The selection at 60 days for body weight, in turn, can directly influence an earlier reproductive contribution, since these animals have their maturity linked to their growth. Selection could also affect the generation interval, making it smaller over time, favoring genetic gain and bringing benefits for increasing the efficiency of the activity (Milinsk et al., 2004).

The authors understand the limitation of the use of an animal model only with the information of maternal relationship. However, the animal model is still more suitable than a sire model, for example. In the sire model, there are no phenotypes for sires and there is a pedigree with both parents, linking the sires, which does not occur in the present study. The database used in this study had phenotypes for dams (the 'sires') and there is no parent's information for dams, that is, sires are unknown in all pedigree.

It is emphasized that it is the first study carried out in this *escargot* population and therefore has limited number of observations. This was a preliminary study that sought to understand the impact of possible fixed and covariable effects on specific measures of body weight of animals, and for this reason, single and two-trait models were used. In addition to being the first study involving genetic parameters in this population, there are few studies that address this aim in other populations, being an important contribution to future studies involving animals of subspecies *Cornu aspersum maximum*.

It is suggested, in the future, the test of other fixed and covariable effects for these and other traits in this population of snails, as well as the application of other types of analysis as multiple sires, random regression models, and the application of techniques of molecular markers (SNPs) to improve the relationship matrix, aiming at improving the model and the strategies used.

Conclusion

This study is an initial approach for understanding the quantitative genetic architecture for traits of body weight in escargots. The structure of the genetic evaluation model proposed for the snail body weight variables, at the ages of 60, 90 and 120 days, proved to be adequate to estimate the components of variance. The genetic parameters can be used as a basis for studies and practical applications to increase zootechnical indexes in this population.

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