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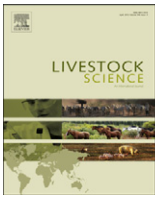

Short communication

Correlated genetic trend in the environmental variability of weight traits in mice

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ABSTRACT

Genetic trends for weight traits and their environmental variability were analysed in an experimental mice population selected during 17 generations to increase weight gain by comparing three selection methods: classic selection with random mating (Method A), classic weighted selection with random mating (Method B) and classic selection with minimum coancestry mating (Method C). Males were selected based on their own phenotypic records for WG. The analysis involved three traits: weight at 21 days (W21), weight at 42 days (W42) and weight gain between 21 and 42 days (WG). Genetic trends were obtained by averaging, within generations, the breeding values obtained for the traits and their environmental variability under a classical animal model assuming that the environmental variance is homogeneous and an alternative model assuming the heterogeneous environmental variance is partly under genetic control. All the genetic trends were positive for the traits and negative for their environmental variability but the trend in phenotypic variances was steady showing that the model analysing the environmental variability failed to separate correctly the genetic from the systematic effects under an artificial selection scenario. The higher additive genetic variance estimated under the heterogeneity model led to higher genetic trends when this model was used, thus changing the order of the preferred methods of selection moving Method B form intermediate to be the worst. The results also showed that correlated changes in the variability of weight gain and related traits originated as a consequence of selection process in the trait, but these changes do not seem to be unfavourable for the animals since the scale effect tends to compensate the correlated reduction in variability of these traits.

1. Introduction

Growth has been shown to be an economically important trait in livestock species. Nevertheless, in recent years the homogeneity of the body weight is also becoming important. The hypothesis of the existence of a pool of genes controlling the mean of the performance and another pool of genes controlling the homogeneity of the performance (Schneiner and Lyman, 1991) makes it possible to change traits, growth rate and its homogeneity. Additionally, this hypothesis would enable studying the genetic correlation between mean and variability.

Several studies have shown evidence of heterogeneity in the residual variance in different livestock species (Högberg and Rydhmer, 2000; Jaffrezic et al., 2000; See, 1998). There are now also studies fitting a model that assumed additive genes controlling both the mean and variance of a trait (SanCristobal-Gaudy et al., 1998) that

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have shown statistical evidence of genetic control of the trait homogeneity for farm animals (Hill and Mulder, 2010, for a review).

The mouse is the experimental mammal of choice because conclusions based on these populations can be easily extrapolated to sheep, pigs and rabbits (Hill and Caballero, 2000). Therefore, selection experiments have been conducted in mice (Fernández et al., 1998; Moreno et al., 2011) to quantify the expected success before implementing them in other mammals. Populations under selection, such as the presently analysed, are expected to theoretically reduce their genetic variability (Falconer and Mackay, 1996). Thus, models analysing parameters concerning environmental variability could present difficulties in disentangling the total phenotypic variability and should be carefully checked in these scenarios. Moreno et al. (2011) have shown an important success of artificial selection after 17 generations for weight gain in mice, comparing three different selection methods and concluding that all gave similar responses.

Ibáñez-Escriche et al. (2008a) estimated the genetic parameters for weight at 21 days (W21), weight at 42 days (W42) and weight gain between 21 and 42 days (WG) with this data by fitting a model which assumed the residual variance to be heterogeneous. Results showed a decrease in the heritability of the traits when considering such a model jointly with a negative genetic correlation between the mean and environmental variance. They also found signs of a correlated response in the environmental variability by a reduction of the coefficient of variation across generations. Furthermore, genetic trends have not been assessed under this model with this data. The presence of genetic variation at the level of the residual variance suggests the possibility of being indirectly modified when selecting the trait if there is a genetic correlation between the trait and its environmental variability. Also, the mean and environmental variability of other traits could be affected and, in turn, the profits from livestock production.

The aim of the present study was to analyse and discuss the implications of the correlated genetic trends on W21 and W42 and the environmental variability of the three traits when selecting to increase WG during this period, as well as to study the performance of the SanCristobal-Gaudy et al. (1998) model under a scenario of artificial selection.

2. Material and methods

A highly variable population of mice was split randomly into nine lines, three replicates of each of the three essayed selection methodology: classic selection with random mating (A), choosing animals according to their performance and randomly mating selected individuals, classic weighted selection unbalancing the offspring of each animal according to its genetic superiority (B), and classic selection with minimum coancestry (C), same as (A) but designing mating according to minimum coancestry criterion. The design was conducted in such a way that selection intensities were equivalent across models. The selection was carried out during 17 generations, where 32 males within replicate were evaluated for WG and those eight with the largest phenotypic record for WG were selected. The females were not evaluated nor selected. Other details of the design can be found in Ibáñez-Escriche et al. (2008a) and Moreno et al. (2011).

Genetic parameters were estimated by Ibáñez-Escriche et al. (2008a) using a Bayesian approach (Sorensen and Waagepetersen, 2003) to solve both a classical additive genetic model and the model developed by SanCristobal-Gaudy et al. (1998) to study the genetics of environmental variability. The results of their analysis have been used here to study direct and correlated genetic trends.

Independent univariate analyses were carried out for the three measured traits. The same models were fitted to each of the traits:

- Homogeneity Model (HO), the classical model assuming the environmental variance being homogeneous by fitting the animal effect and litter effect as random effects with the selection-replicate-generation the only systematic effect with 163 levels (18 generations, three selection methods and three replicates by method of selection $=18\cdot 3\cdot 3$) and one level for founder population. This analysis has already been performed to analyse the genetic trend of WG by Moreno et al. (2011) and as they argued, the maternal genetic effect was not explicitly fitted in the model because previous analysis on performances, fitting together both litter and maternal genetic effects, showed that the litter was carrying all the variability explained by the maternal genetic effects.
- The Heterogeneity Model (HE) by SanCristobal-Gaudy et al. (1998), in which it is assumed that the environmental variance was heterogeneous and partly under genetic control, fitted the same effects as in Model HO both for the mean of the trait and for its environmental variability.

Breeding values for each trait and its variability were averaged and plotted within generation and selection method to study the genetic trend of the selected (WG) and the other (W21 and W42) correlated traits, as well as their environmental variability.

The expected phenotypic variances were obtained within the level of systematic effect as: $E(\sigma_i^2)=\sigma_u^2+\sigma_c^2+e^{b_i^*+u_i^*+c_i^*}$, where σ_u^2 and σ_c^2 are the additive genetic and litter variances, b_i^* is the estimation of the i level of the systematic effect, and u_i^* and c_i^* are the average of the additive genetic values and litter effects affecting the corresponding level i of the systematic effect.

In order to discuss the magnitude of the correlated genetic response, a multitrait animal model, as the one described in model HO, was also used to estimate the heritability of the traits as well as their genetic correlations via REML. The VCE v.6.0 program (Neumaier and Groeneveld, 1998) was used for this purpose.

3. Results and discussion

In the present study genetic trends of the selected WG trait as well as the correlated response on W21 and W42