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No G×E on egg qualities and body weight between cage and floor systems, implications for breeding programmes in laying hens.

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Abstract

The main objective of this study was to quantify genotype-by-environment interactions for egg quality traits and body weight in laying hens between cage and cage-free systems. Records of 18,524 eggs for quality traits and 10,266 hens for body weight from a pedigreed Rhode Island Red line were used. Hens were hatched across 5 batches from 2018 to 2020, siblings are housed in two systems: a cage and a floor system. Random regressions were modelled to estimate variance components. Heritability estimates were moderate to high in both systems (0.29-0.77). Genetic correlations between the cage and the floor system were high (≥ 0.79), and genetic correlations between the intercept and the slope of the reaction norm ranged from -0.69 to 0.27. The results indicate that there is no need to maintain a dedicated breeding programme per system, if the breeding goals are identical, which is unlikely.

Introduction

A few breeding companies are supplying farmers with laying hens all over the world. Purebred birds of the *nuclei* of these breeding companies are housed in cages to ensure pedigree and performance monitoring. Although most of the egg production is produced in cage systems, there is a large diversity in farming systems. Some alternative systems to cage are expanding, for instance in 2020, 52% of laying hens are raised in cage-free systems in E.U. (barn, free-range, and organic; European Commission, 2021). In all these systems, breeding goals include the number of eggs produced, egg qualities (regarding the albumen, yolk, and shell), feed efficiency, behaviour, fertility and disease resistance. In the current situation, birds are selected in the *nuclei* based on performance in cage system. Some studies indicate that some major traits such as egg production traits may be under the influence of genotype-by-environment interactions (G×E), which can affect the ranking of selection candidates (Icken et al., 2008; Mulder, 2017). However, it is still unclear whether there is a need to develop a breeding programme dedicated to cage-free systems because the selection candidate would be different from those in the cage system. Our objective is to quantify G×E for egg quality traits and body weight in laying hens between cage and cage-free systems.

Materials & Methods

Birds and Farming system. Records from the *nucleus* of a Rhode Island Red line of the breeding company Novogen were used in this study. Hens were hatched across 5 batches from 2018 to 2020. They were raised on a floor in a barn until 17 weeks of age. Then, they were either bred in collective cages or a floor system until 64 weeks of age. On average, data from 1,633 cages for the cage system and 365 hens for the floor system was retrieved per batch. The cages included a living area (with free access to food and water). The floor system included individual nests overlaid on two rows (about 1 nest for 5 hens), and a living area on floor pens (with free access to food and water). Hens were housed in cages of 5 full sisters in the cage system and raised with the entire cohort in the floor system, including the cocks (about 1 cock for 10 hens).

The pedigree for each recorded individual was traced back over at least 5 generations.

Traits. At 50 weeks of age, egg quality was recorded twice for each cage in the cage system or each hen in the floor system, and body weight once. A total of 18,524 eggs were collected: 16,331 from the cage system and 2,193 from the floor system. A total of 10,266 hens were weighed: 9,025 from the cage system and 1,412 from the floor system. All traits were named according to the Animal Trait Ontology for Livestock (ATOL). Five egg quality traits were studied: eggshell colour (ESC), eggshell strength (ESS), eggshell shape index (ESshape), Haugh value (HV), and egg weight (EW). The body weight was recorded at 50 weeks of age (BW). ESC was determined by a chromameter, ESS was determined by a compression instrument, EW was determined by a weighing scale, ESshape is calculated from egg diameter and EW, HV was determined by a tripod methodology, and BW was determined by a weighing scale. Further details on the measurements are available on the ontology website (Picard Druet *et al.*, 2020).

Models. Because the hens in a cage are full sibs, the sire and dam of the cage were known: animal models were used for both cage and floor environments, considering each egg as an individual. Body weight was recorded at the individual level in both systems. Variance components were estimated using an average information restricted maximum likelihood method applied to univariate reaction norm models:

$$y_{ij} = \mu + CG_{ij} + \beta_1 age_{ij} + \beta_2 x_{ij} + a_{int_i} + a_{stp_i} x_{ij} + e_{ij}$$

Where y_{ij} was the observed phenotype on the j^{th} egg of the i^{th} “animal” (either egg or hen, depending on the system), μ the overall mean, CG_{ij} was the fixed effect for the contemporary group (hatching date, location of the cage in the barn), β_1 was the regression coefficient on the age in weeks, β_2 was the regression coefficient on the environmental gradient x ($x = 0$ for the cage system and $x = 1$ for the floor system), a_{int_i} was the random additive genetic effect for the intercept of the reaction norm of the i^{th} “animal”, a_{stp_i} was the random additive genetic effect for the slope of the reaction norm of the i^{th} “animal”, and e was the random residual effect. For BW, the same model was used except that there is a single record per animal. The additive genetic effects were assumed to be normally distributed. Heterogeneity in residual variance was modelled with a residual variance for the cage system and a residual variance for the floor system. The residual effects were assumed to be normally distributed.

Genetic parameters were calculated from the estimated variance components (additive genetic variance for the intercept, additive genetic variance for the slope, additive genetic covariance of the intercept and the slope, and the residual variance) according to the theory (Falconer and Mackay, 1996; de Jong and Bijma, 2002).

Log-likelihood ratio test (LRT) with a reduced model without the random regression term were performed to test the significant level of the random additive genetic effect for the slope of the reaction norm.

Software. Data handling was performed with base-R (R Core Team, 2020). The variance components estimation and the calculations of genetic parameters were performed with the statistical software ASReml 4.2 (Gilmour *et al.*, 2021).

Results and discussion

We found that egg quality traits and BW were moderately to highly heritable in both environments (with heritability estimates ranging from 0.29 to 0.77; **Table 1**). This is consistent with other studies where heritability for these traits ranged from 0.24 to 0.60 (Beaumont et al., 2010; Mulder et al., 2016; Picard Druet et al., 2020). Our results indicated that heritability estimates in the floor system were often higher than in the cage system. Both the additive genetic variance tended to be higher and the residual variance tended to be lower in the floor system compared to the cage system (data not shown). It is possible that the additive genetic variance was underestimated because of the loss of information about the individual that laid the egg and that estimation of a permanent environment variance was needed (repeated measures with 2 eggs per hen), or that the unbalanced design biased the estimation of variance components (88% of the observation came from the cage system and 12% from the floor system). We tried to fit a permanent environment random effect of the cage in the cage system and of the hen in the floor system but the model did not converge.

Table 1: Genetic parameters¹ for egg production traits and mature body weight.

Traits	h_{cage}^2	h_{floor}^2	$r_{(cage,floor)}$	$r_{(int,slp)}$
ESC	0.55 (0.03)	0.74 (0.02)	0.79 (0.05)	-0.03 (0.09) ²
ESS	0.33 (0.02)	0.31 (0.04)	0.93 (0.05)	0.15 (0.23) ²
ESshape	0.47 (0.03)	0.58 (0.03)	0.92 (0.04)	0.19 (0.18) ²
HV	0.29 (0.02)	0.45 (0.03)	0.96 (0.04)	0.04 (0.26) ²
EW	0.62 (0.03)	0.77 (0.01)	0.93 (0.03)	0.27 (0.13)
BW	0.61 (0.02)	0.50 (0.01)	0.87 (0.04)	-0.69 (0.08)

¹Estimates, with standard errors in brackets, of heritability of the traits in cage (h_{cage}^2) or floor system (h_{floor}^2), and genetic correlation between the two systems ($r_{(cage,floor)}$) and between the intercept and the slope of the reaction norm ($r_{(int,slp)}$).

²Not significantly different from zero (LRT)

We found that the genetic correlations between the cage and the floor system were very high ($r_{(cage,floor)} \geq 0.79$). To our knowledge, this is the first study about the same traits with the same purebred population in two environments. It is often admitted that when a genetic correlation between two traits is higher than 0.80, then these two traits are genetically similar enough to consider only one of them in the breeding programme. This genetic correlation is also used as an indicator of the importance of G×E when using a character-state model (same trait in different environments like in our study; Falconer and Mackay, 1996). Although a genetic correlation of 0.80 is high, it is not one (unity). Therefore, re-ranking of selection candidates may occur due to G×E. We used univariate random regression models to assess the stability of the genotype thanks to another genetic parameter: the genetic correlation between the intercept and the slope of the reaction norm models (de Jong and Bijma, 2002). We assumed the systems to be on a continuous scale from the reference environment (cage system) to another graduation of the environment (floor system). We found that the genetic correlations between the intercept and the slope of the reaction norms varied from -0.69 to 0.27 and that most of them were not significantly different from zero. The estimated $r_{(int,slp)}$ for EW was 0.27, meaning that the higher the breeding value for EW in the cage system (reference environment), the higher the genetic sensitivity to changing to floor system. However, this trait is particular because the breeding goal is not to increase EW but to keep it within a defined range. Giving the high $r_{(cage,floor)}$, it is possible that re-ranking only occur for extreme breeding values, which would not be a problem. The estimated $r_{(int,slp)}$ for BW is -0.69, meaning that the higher the breeding

value for BW in the cage system (reference environment), the lower the genetic sensitivity to changing to floor system. The estimated $r_{(int,slp)}$ for the other traits were not significantly different from zero, indicating that selecting on the level would not change the sensitivity to environmental change.

Conclusion

In the present study, all egg quality traits and adult body weight displayed high heritability estimates, high genetic correlations between the cage and the floor systems, yet different genetic correlations between the intercept and the slope of the reaction norm models. Considering the breeding goals for all these traits, our results indicate that there is no need to maintain a breeding programme per system. However, other major traits need to be studied (egg number or disease resistance). These conclusions hold only if the breeding goals are the same between the two systems, which is unlikely (see Phocas et al., 2016).

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