86. Heritability of daily activity over time in broilers

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Abstract

Individual activity is related to the health, welfare and performance of broilers. In previous work using a radio frequency identification system, we were able to collect individual activity data over time, and activity was found to be heritable. The aim of the current study was to estimate genetic parameters for activity while taking into account the effect of age. Therefore, two repeated measurement models were fitted. The model with an intercept and slope for genetic and permanent environmental effect, and a heterogeneous residual variance, yielded the best goodness-of-fit. First results showed that daily heritability varied between 7 and 30%. The heritability was lowest at the start and at the end of the production life. This study shows potential for selection on activity in broilers. Furthermore, this study shows that activity patterns (in time) can be changed, as both the intercept and slope of activity are heritable.

Introduction

Activity levels of broilers are related to their health, welfare and performance (Bokkers *et al.*, 2007; Van Hertem *et al.*, 2018; van der Sluis *et al.*, 2019, 2021). Therefore, individual activity levels appear to have potential to serve as a proxy for other traits in broiler breeding programmes. However, before implementation of activity as a proxy in breeding programmes, it is important to gain insight into the heritability of activity. Several studies have examined this topic. For example, it has been reported that the heritability of activity (recorded as the number of observations during which an animal was moving) at 16 days old, in a cross between two broiler lines that were divergently selected on digestive efficiency, was low (0.09±0.07) and not significantly different from zero (Mignon-Grasteau *et al.*, 2017). In another study, the average activity from hatching until approximately 35 days old was found to be heritable (0.31±0.11; Ellen *et al.*, submitted).

Studies on the heritability of activity have, however, been limited due to the labour required for personal observations, complicating for example the study of changes in heritability with age. To genetically improve activity in broilers, it is, however, important to take into account changing activity levels and variation due to age. In addition, previous research showed that activity decreases with age, suggesting that heritability might change over time. Therefore, research is needed to investigate the heritability pattern of activity. In this study, we examine the heritability of activity in broilers based on individual records of daily activity levels, recorded using a radio frequency identification (RFID) tracking system, over time. We compare two repeated measurements models that take into account heterogeneous variance and an effect of time to estimate genetic parameters for activity. The results of this study contribute to an improved understanding of the genetic variation of daily activity in broilers.

Materials & methods

Animals, housing and pedigree. Data on a total of 387 purebred male broilers were used for the analysis, collected across five consecutive production batches. The broilers were housed on a farm in the Netherlands, in a pen with a size of 4.7 m². Food and water were provided *ad libitum*, and wood shavings were provided as bedding.

Nearly the same sires (31 in total) and dams (96 in total) were used in each batch, but with different numbers of offspring. Each sire was mated with approximately 3 dams, and each dam contributed on average 3.7 male offspring. Approximately six generations of pedigree were included in the calculation of the relationship matrix.

Activity recording. All broilers were tracked continuously with an RFID tracking system, using leg tags on the broilers and an RFID antenna grid underneath the pen floor (see van der Sluis *et al.* (2020) for details on the activity tracking). Approximate distances moved during the main light period from 07.00-23.00 were calculated for each day and bird, using the recorded tag positions during this period. The recorded distance was then divided by the recording duration between 07.00 and 23.00 for that specific day, to obtain an average distance moved per hour for each day. This allowed for comparisons between days and batches, even when data were missing for part of a day due to for example weighing of the birds.

Data analysis. For each day and bird, activity was recorded, resulting in 12,232 activity records. R software version 4.1.0 (R Core Team, 2021) was used for an initial analysis and to decide which fixed effects to include in the full model to estimate genetic parameters. The initial model included a fixed effect for batch, day, and the interaction between batch and day. The ASReml software package (Gilmour *et al.*, 2015) was used to estimate genetic parameters for daily activity. Two models were compared using the Likelihood-ratio test (Wald, 1943):

$$y = Xb + Za + Ze_p + e \tag{1}$$

$$y = Xb + Za_0 + Za1.xt + Ze_{p0} + Zep1.xt + e \tag{2}$$

where y is a vector of daily activities, b is a vector of fixed effects, with incidence matrix X linking observations to the fixed effects, a is a vector of breeding values, with incidence matrix Z linking records to individuals, e_p is a vector of permanent environmental effects of individuals to account for repeated measurements, and e is a vector of random residuals, allowing for a different variance for each day. For Model 2, both a genetic and a permanent environmental effect are fitted as an intercept, and as a function of time, where $x_t = 36 - Day$ (Day ranging from 1 to 35). We used $x_t = 36 - Day$, rather than $x_t = Day$, because an initial analysis showed that the variance decreased over the growing period.

The genetic variance as a function of time is, $\sigma_{A_t}^2 = \sigma_{A_0}^2 + x_t^2 \sigma_{A_1}^2$, where t is Day (1-35), $\sigma_{A_0}^2$ is the genetic variance in the intercept, and $\sigma_{A_1}^2$ is the genetic variance in the slope. The variance due to the permanent environmental effect, as a function of time, is $\sigma_{Pe_t}^2 = \sigma_{Pe_0}^2 + x_t^2 \sigma_{Pe_1}^2$. We assumed that effects on intercept and slope were independent, to avoid overfitting the data, which contained only 387 individuals. The phenotypic variance as a function of time is $\sigma_{P_t}^2 = \sigma_{A_t}^2 + \sigma_{Pe_t}^2 + \sigma_{e_t}^2$, where $\sigma_{e_t}^2$ is the residual variance for a specific day. The heritability for each day is $h_t^2 = \sigma_{A_t}^2 / \sigma_{P_t}^2$.

Results

Figure 1 shows the average daily activity per batch. As expected, activity decreased with age. Furthermore, differences in activity levels were found between the different batches. Table 1 shows the comparison of the different genetic models. Statistical comparison showed that the model with an intercept and slope for both the genetic and permanent environmental effect yielded the best goodness-of-fit. Figure 2 shows the heritability for each day, which ranged from 0.07 to 0.30.
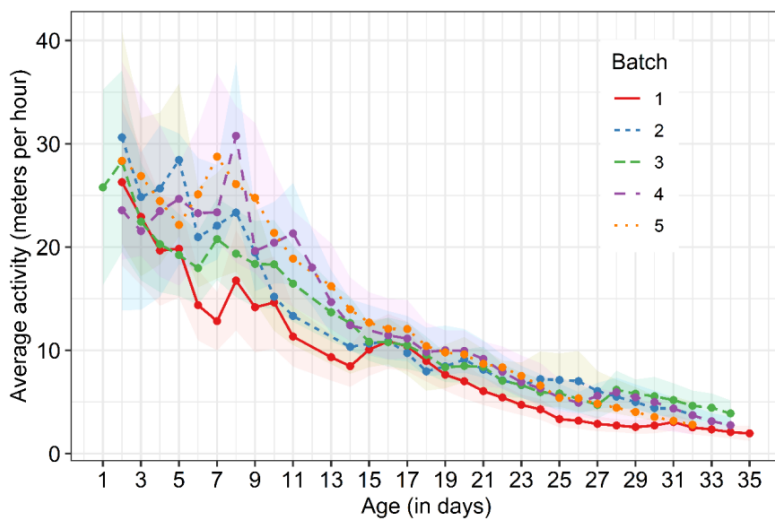
Figure 1. Average daily activity per production batch.

Table 1. Model comparison using the Likelihood ratio-test.

Model	Log Likelihood	LR[1]	P	σ^2_{A0}	σ^2_{A1}
1	-14514.35				
2	-13520.87	1333.34	<0.001	0.25±0.16	0.005±0.002

[1] LR is two times the difference in log likelihood between the complex and less-complex model.
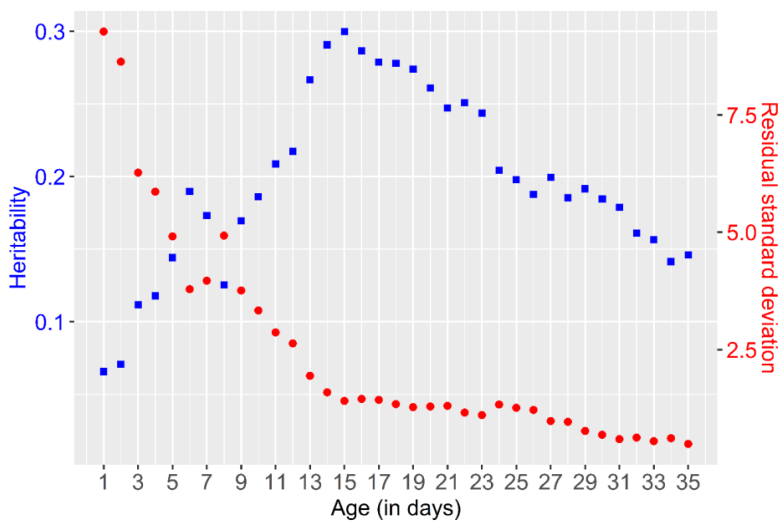

Figure 2. Heritability and residual standard deviation (2nd y-axis) over time.

Discussion

In this study, we found that a repeated measurements model with an intercept and slope for both the genetic and permanent environmental effects, and a heterogeneous residual variance, yielded the best fit. Daily activity is heritable, and heritability changes over time. Despite the limited number of individuals in our data and the presence of up to four random effects in the model, all analyses showed good convergence, and all estimated genetic parameters were significantly different from zero. This is, at least in part, due to the large number of records per individual (35 here), illustrating the power of longitudinal sensor data for genetic analysis.

In our previous study (Ellen *et al.*, *submitted*), we estimated genetic parameters for overall broiler activity and showed that this trait is heritable. However, the activity level changes considerably over time, and so does the variation in activity per day (Figure 1). Furthermore, when repeated observations are available (such as daily activity records), it could be of added value to consider a model that can handle these kind of longitudinal data, to better pick up on changes over time, instead of summarizing across periods and running separate analyses. In this study, a repeated measurements model with a genetic and a permanent environmental effect as a linear function of time was therefore implemented. However, activity is not necessarily fully linear (see Figure 1). In other studies dealing with longitudinal data, random regression models with non-linear terms have also been implemented. Future research could focus on finding the most appropriate model to take into account the effect of time, potentially also as a non-linear function, for daily activity levels in broilers.

In this study, the heritability of daily activity varied between 0.07 and 0.30. Overall, the estimated heritability was lowest at the start and at the end of the production life. At 15 days of age the highest heritability was found. Moreover, differences between animals in their activity patterns over time were observed. This highlights the value of repeated activity recordings, as single-age records might miss important nuances to the (heritability of) activity in broilers. Therefore, future research could focus on investigating the relation between the intercept and slope and the possibilities of changing the activity pattern of a broiler in relation to their health and performance. Furthermore, detailed interpretation of the results and how to implement these results in a broiler breeding program is needed.

Funding

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