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Genetic analysis and a simulation tool of locomotion and social traits in turkeys

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Introduction

Behavioral traits like locomotion and social interactions are important components of animal behavior and welfare in group-housed turkeys. In commercial and breeding populations of turkeys, behavioral issues related to reduced walking ability, leg disorders, and injurious feather pecking occur (Shehata et al., 2024). While numerous studies have investigated individual locomotion traits in turkeys, such as running abilities (Hahn *et al*., 2020), physical activity (Stevenson, 2018), and walking speed (Stover *et al*., 2018), little is known about the movement dynamics of turkeys in large groups. Specifically, it is unknown how a turkey's movement is influenced by interactions with pen mates.

Recent developments in automated tracking systems enable continuous monitoring of individual animals in commercial scale farms (Li *et al*., 2021). Marker-based tracking using ArUco tags can provide accurate long-term trajectories for large groups of animals, creating opportunities to derive quantitative behavioral traits related to movement and social positioning (Crall *et al*., 2015). Such data allow estimation of genetic parameters and breeding values for behaviors and open possibilities for integrating behavioral traits into selection programs.

In addition to genetic analysis, simulation models can help to understand how individual-level behavioral tendencies generate group-level patterns. Agent-based models are widely used for this purpose, as they allow explicit modelling of individual movement decisions and social responses. When parameterized using empirically derived traits, these models can serve as tools for hypothesis testing and for exploring the genetic consequences of behavioral variation.

The objectives of this study were therefore (1) to quantify the genetic basis of locomotion and social tendency traits in turkeys using long-term automated tracking data, and (2) to develop an agent-based simulation model capable of reproducing observed variation in these traits.

Materials & Methods

Animals, housing, and tracking system. A total of 296 genotyped turkeys were housed in a single pen of approximately 86 m². Birds were fitted with lightweight backpacks carrying ArUco markers, enabling individual identification (Fig. 1a). The pen was monitored by 31 overhead cameras, providing full spatial coverage (Fig. 1b). Tracking was conducted continuously from 05:00 to 17:00 over a period of seven days. Camera data were processed to extract two-dimensional trajectories for each bird (Fig. 1c shows an example field of view). Quality-control procedures were applied to remove false ArUco detections.

All procedures involving animals were conducted in accordance with the Dutch Experiments on Animals Act and relevant European legislation, and complied with institutional guidelines for animal care and welfare.

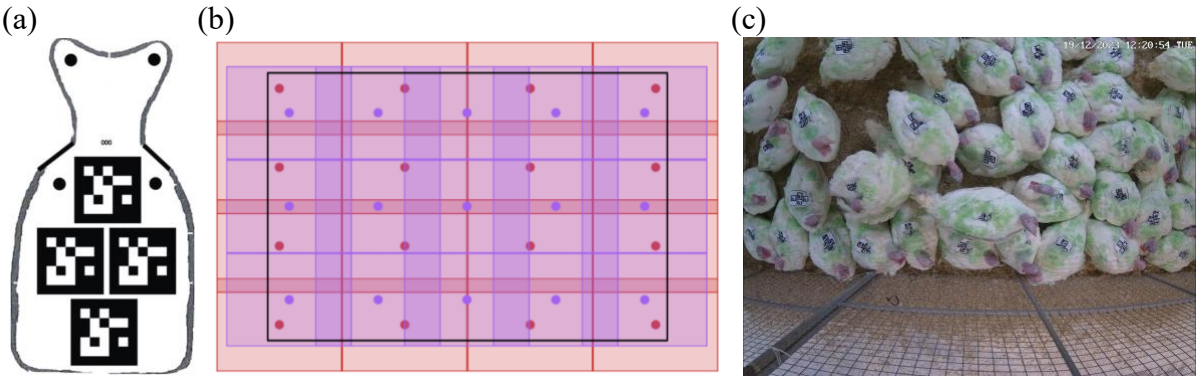

Figure 1. Backpacks with ArUco markers for tracking. (a) Design of the backpack, with the ArUco marker replicated four times. (b) Position and field of view (FOV) of the cameras. The points in the figure represent the centers of the FOV. The rectangles represent the boundaries of each FOV. The purple and red areas correspond to two separate camera setups, which together provide double coverage of the pen area. (c) Example of a FOV capturing turkeys with backpacks.

Genetic analysis. From individual trajectories, four behavioral traits were derived. The traits were: (1). Proportion of time spent in locomotion, calculated as the fraction of observation time during which the bird was moving; (2). Speed during locomotion (m/s), defined as the mean speed when the bird was classified as moving; (3). Number of pen mates within 1 m, averaged over all time points; (4). Density of pen mates ahead within 5 m during locomotion, defined as the number of birds located within a 5 m sector in the direction of movement. Traits (3) and (4) were intended to capture individual social tendencies related to position and movement relative to conspecifics.

Genetic parameters were estimated using univariate animal models with repeated records.

The model for each trait was: $y_{ij}=\mu+DAY_i+a_j+e_{p,i}+e_{ij}$

where y_{ij} represents the daily record of individual j on day i; μ is the overall mean; the fixed effect DAY_i accounts for the day effect; a_j reflects the random genomic breeding value of individual j; $e_{p,i}$ reflects the random permanent environmental effect of individual j; and e_{ij} indicates the residual term. Heritabilities and repeatabilities were calculated from estimated variance components.

Simulation tool. An agent-based simulation tool was developed to reproduce the observed locomotion and social traits. The model was based on Wang *et al*. (2021), with the main modification concerning the movement direction. In Wang *et al*. (2021), movement direction was continuous, with angles sampled uniformly from 0° to 360°. In the present study, we simplified the sampling space by restricting movement directions to eight discrete angles (0°, 45°, 90°, 135°, 180°, 225°, 270°, and 315°), facilitating subsequent simulations.

Next, these movement directions were not equally probable; instead, they depended on an individual-specific social tendency value and the density of nearby pen mates. At each time step, the spatial distribution of pen mates around an individual was summarized using a Gaussian-blurred density map. For each orientation, local density was computed, and the probability of selecting a movement direction was defined as the sum of a baseline random probability (1/8) and a deviation term. This deviation term is the product of the individual's social tendency and the relative density of pen mates in that direction. Positive social tendency values increased the probability of moving toward denser areas, whereas negative values favored movement toward less dense regions.

Results & Discussion

After filtering out ArUco detections that were excessively large or small, located outside the pen area, exhibited extreme aspect ratios, or showed no movement, a total of 4,139,735,040 ArUco detections from 278 animals remained over the observation period; 18 animals lost their backpacks during recording. This number was compared with the theoretical maximum number of detections for 296 animals, calculated as 296 animals × 7 days × 12 hours per day × 3,600 seconds per hour × 30 frames per second, accounting for double camera coverage, yielding 5,370,624,000 expected detections. Overall, approximately 77% of the maximum possible detections were obtained, demonstrating robust performance of the multi-camera tracking system under group-housing conditions.

The tracking system enabled continuous monitoring of individual turkeys over multiple days. Most uninterrupted tracks lasted longer than three hours, with some extending up to nine hours (Fig. 2a). A substantial number of tracks were short, with over 90% lasting less than one minute. Because detection reliability is limited for such brief tracks, all tracks shorter than five minutes were excluded from subsequent analyses. At the daily level, the majority of animals were tracked for more than eight hours per day (Fig. 2b). A small number of outliers were observed, corresponding to individuals whose backpacks detached or whose markers were frequently occluded by feathers.

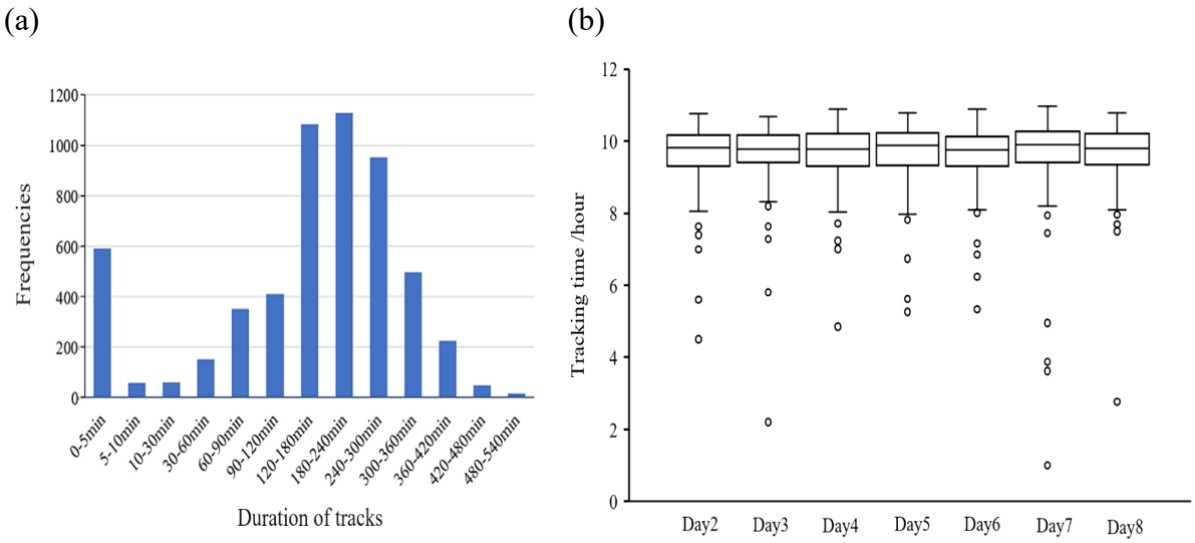

Figure 2. Distribution of tracking time. (a) Distribution of the duration of uninterrupted tracks. (b) Distribution of total tracking time per day across turkeys.

Using the filtered trajectories, four locomotion and social movement traits were quantified: proportion of time spent moving, average moving speed, number of pen mates nearby, and number of pen mates ahead. Repeatability estimates were high for all traits, ranging from 0.65 for average moving speed to 0.96 for the number of pen mates nearby (Table 1), indicating strong consistency of individual behavior across days. This high repeatability suggests that permanent environmental effects, such as early-life experiences or established social positions, play a major role in shaping these traits.

Heritability estimates ranged from 0.08 for average moving speed to 0.23 and 0.23 for the number of pen mates nearby and ahead, respectively. All traits except average moving speed showed heritabilities significantly different from zero, indicating genetic variation and potential for selection.

Table 1. Heritability and repeatability estimates for the locomotion traits.

Trait	Heritability (h^2)	Repeatability (r)
Proportion of time moving	0.15±0.04*[1]	0.87±0.01*
Average moving speed	0.08±0.15	0.65±0.03*
Number of pen mates nearby	0.23±0.12*	0.96±0.01*
Number of pen mates ahead	0.23±0.09*	0.93±0.01*

[1]Values are presented as estimates ± SE. * indicates statistical significance.

The combination of high repeatability and moderate heritability implies that both genetic and permanent environmental effects contribute substantially to these behaviors. For the number of pen mates nearby and the number of pen mates ahead, genetic and permanent environmental effects together accounted for 96% and 93% of the total variance, respectively. This indicates that once social substructure and dominance relationships within the group are established, individual behavior becomes highly stable, with limited day-to-day stochastic variation.
Based on the observed individual differences in social tendency, we developed an agent-based simulation model to reproduce livestock movement and interactions. The model allows users to specify an overall social tendency through input parameters, which influence movement decisions by modulating the probability of moving toward or away from regions with higher pen-mate density. Individuals with higher trait values are more likely to move toward denser areas, whereas individuals with lower trait values show the opposite tendency. This simulation framework provides a tool for exploring how individual-level social tendencies can scale up to group-level movement patterns and is publicly available at: https://github.com/CiaranWang/LIS.

Conclusions

Daily records of locomotion and social tendency traits in turkeys show significant genetic variation and very high repeatability. We provide a tool to simulate these traits using an agent-based model parameterized with individual social tendencies. Together, these results indicate that behavioral traits derived from automated tracking can be integrated into breeding programs and that simulation models can support further genetic and behavioral research.

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