Strain by strain: comparative growth performance of seven production-adapted yellow mealworm lines

Emmanuel Osei [1], Jens Tetens [1], Elena Werner [2], Rafael H. Mateus-Vargas [1]
[1]University of Göttingen, Department of Animal Sciences, Göttingen, Germany
[2]Alpha-Protein GmbH, Bruchsal, Germany

1. Introduction and background

In the edible insect farming industry, the Tenebrio molitor or the yellow mealworm, is among the top-produced insects (Kuff et al., 2023; Rowe, 2020; Tavares et al., 2022). Despite its prominence, reliance on a few genetic strains raises sustainability concerns. Intensive selection can lead to inbreeding, loss of genetic diversity, and reduced adaptability (Weigel, 2001). While these issues may occur unintentionally in insect farming, they pose potential long-term risks for the industry. For instance, traditional livestock farming is encountering similar challenges, where genetic erosion in dairy cattle and pigs is expected to increase disease risk, diminish resilience to climate change, and economic setbacks (Carolino & Gama, 2008; Kasprzyk & Walenia, 2023). Experiences from these sectors demonstrate that prioritising short-term gains over genetic diversity can lead to significant long-term issues, a potential emerging concern in insect farming. Although there has been extensive research on environmental and nutritional optimisation in insect rearing systems (Bordiean et al., 2020, 2022; Johnsen et al., 2021; Kopecká et al., 2024), the impact of selecting specific genetic strains on production efficiency remains understudied. Factors such as regional adaptations, selective breeding, and founder effects can result in significant performance variations among different lines. However, studies comparing genetically distinct populations are limited. The current study evaluates key performance metrics: average daily gain, survival rate, and feed conversion efficiency of seven yellow mealworm lines from Africa, the United States of America (USA), Scandinavia, Central Europe, and Southern Europe. By analysing their growth patterns under standardised conditions, we aim to identify top-performing lines for industrial production and to establish a foundation for future genetic improvement efforts, including breeding programmes.

2. Materials and methods

Experimental design

We used seven strains that were raised in a controlled environment set at 25°C with 65% relative humidity and a 0:24 light-dark cycle. They were fed an autoclaved wheat bran-based diet and had unlimited access to autoclaved water. Before the experiment, individual yellow mealworms were carefully selected based on strict criteria: they had to display uniform, healthy colouration without any deformities, dark spots, or abnormal signs, ensuring they were healthy through visual inspection. Each genetic strain had four replicates, and each replicate consisted of 50 individuals.

Strain and origin: The lines included in this study are all production-adapted and are currently being reared on a commercial scale in Europe. Regarding distribution, the lines consist of one African, one USA, and five European lines spread across Scandinavia, Central, and Southern Europe.

Figure 1. Distribution of yellow mealworm lines from across the world. The red stars show an approximate origin of the lines.

Measured traits

Regarding the traits measured, the average daily gain was calculated by dividing the difference between final and initial mass by the number of days. The survival rate was expressed as the percentage of larvae alive at the end of the trial. Feed conversion efficiency (FCE) was defined as the biomass gain per unit of feed consumed, based on dry matter. While these experiments are ongoing, statistical analysis will be conducted using ANOVA followed by post-hoc Tukey tests ($p<0.05$) to compare the performance of different strains.

3. Preliminary findings and potential impact

While these experiments are ongoing, preliminary results from a test trial indicate variability in survival and growth among the different lines, suggesting underlying genetic variations. As such, the results of the current experiment could indicate notable phenotypic variations among the lines that could be utilised to enhance certain strains. While no specific genetic parameters will be calculated, the results may offer a helpful baseline for selecting top-performing lines and planning future breeding programmes. What is more? It could also help suggest which genetic lines could be used to boost specific traits and in which direction.

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