

# The environmental variance on daily feed intake as indicator of resilience in pigs

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## Resumen

Understanding how animals adapt to environmental factors is crucial for promoting a more sustainable livestock system. However, identifying a suitable resilience indicator remains a significant challenge. Ideally, such indicators should be rooted in repeated records, encompassing metrics like root mean square error (RMSE), log-deviations from expected patterns (LnVar), or residual variance (VE). The VE of traits is under genetic control and has been proposed as a promising indicator of overall resilience. However, its biological impact on the health status and welfare of the animals is still unclear. This study aimed to disclose the biological mechanisms of resilience in Pietrain pigs. For this purpose, we used the VE of the daily feed intake (DFI) as a novel indicator of resilience in pigs. A dataset comprising 780,112 feed intake (FI) records from 1628 Pietrain pigs aged between 80 and 180 days was collected from automated feeders. Following rigorous data preprocessing, a total of 109,680 DFI records from 1605 animals, each with a minimum of 50 DFI records, were utilised to compute the VE, after pre-correction of DFI by pen, feeder, and body weight. RMSE and LnVar were also calculated for comparison with VE. A high correlation exceeding 0.8 was found among all of them. Genetic parameters for these traits were calculated using the blupf90+ software, revealing substantial genetic correlations between VE and efficiency traits. Specifically, values of  $0.71 \pm 0.09$  for feed conversion rate (FCR),  $0.63 \pm 0.1$  for residual feed intake (RFI), and  $-0.41 \pm 0.14$  for residual gain (RG) suggested a potential link between resilience and efficiency in animals. Genetic parameters of VE were also estimated using a novel software from the blupf90 family, named dhglm, which allowed computing a double hierarchical generalised linear model (DHGLM) with all facilities of blupf90+ software. VE must undergo prior correction for confounding factors to enhance accuracy, obviating the need for intricate and costly timing models. We suggested dhglm software as a user-friendly and fast alternative to estimate genetic parameters from VE properly. Furthermore, Genome-Wide Association Studies (GWAS) for each resilience indicator were conducted using GCTA software, identifying consistent regions on the Sus Scrofa chromosome (SSC) 1 and SSC14. Key candidate genes, including SIN1, PTPRE, DOCK1, INSYN2A, and FOXI2, were identified. Genes from the same family of DOCK1, INSYN2A, and FOXI2 were identified in previous studies for rabbit populations with differences in VE and resilience. Our study suggested that the VE may be a robust indicator of resilience and proposed a family of candidate genes that may have a strong association with the VE and resilience.

*Keywords: Environmental variance, Daily feed intake, resilience, pig, dhglm, genome-wide association*