Genetics of increased importance of health traits

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Abstract

The purpose of this study is to present mechanisms of possible negative effects of genomic selection in secondary traits, especially in health traits, and present steps to mitigate those effects. Selection on production traits causes corresponding declines in antagonistic fitness traits. Under traditional selection, declines were initially compensated or slowed down by continuously improving management. When the deterioration was too strong to ignore, the fitness traits were added to a selection index. Under genomic selection the genetic progress for production traits accelerates causing accelerated declines in fitness traits, and management modifications are not fast enough to compensate. Including the fitness traits in the selection index is only partially effective because of lower accuracy of evaluation due to lower heritability and fewer phenotypes. In particular, genomic selection can give rise to a sudden onset of categorical traits such as diseases. If deteriorating traits are underlying values for categorical traits such as a disease status, such traits are not expressed until a threshold is crossed. Then the incidence can increase rapidly. Mitigating the negative effects of genomic selection for health traits will require several steps. First, the selection pressure on major traits that are antagonistic to the deteriorating health traits needs to be reduced, allowing for management modifications to catch up. Second, selection for health traits needs to intensify, with weight on each trait calculated from recent genetic parameters. As genetic parameters can change rapidly under genomic selection, a challenge is to estimate these parameters for the last generation using complete data, as required for unbiased estimates. Third, methods for evaluating categorical traits can be improved. If the evaluation for health traits is not true multitrait with the production traits, the index weights need to be modified to account for ignored genetic correlations.

Key words: genomic selection, health traits, negative effects

Introduction

Genomic selection was originally perceived as an all-positive technology that facilitates fast genetic improvement at a low cost (Meuwissen et al., 2013). Recent reports indicate declines in secondary traits across species (Misztal and Lourenco, 2024). One of the most visible declines is the deterioration of hatchability in broiler chickens (Cash et al., 2025). While hatchability before genomic selection increased from 81% in 1998 to 85% in 2012, it dropped to 79% by 2024 under genomic selection (*https://innovateanimalag.org/the-hatchability-crisis*). The purpose of this study is to present mechanisms of possible negative effects of genomic selection in secondary traits, especially for categorical health traits, and suggest steps to slow or reverse the decline.

Materials and Methods

Misztal and Lourenco (2024) presented a theory on potential negative effects in genomic selection, as illustrated in Figure 1. Selection on production traits causes negative responses on antagonistic fitness traits. While fitness traits deteriorated under a single-trait selection, the decline was smaller than predicted because it was partly compensated by constantly improving management. When the deterioration could no longer be ignored, fitness traits were added to a selection index, slowing or even reversing the decline. Under

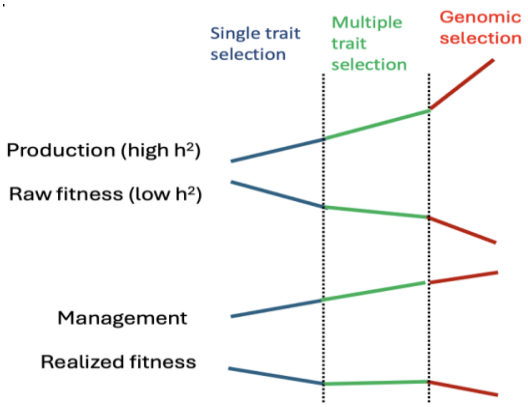


Figure 1. Trend in production and fitness under three types of selection; single trait selection is for the production trait and management applied to the fitness trait.

genomic selection, selection outcomes accelerate and the negative outcomes intensify.

Response to selection for unrecorded trait

Some theory on why we experience increased incidence of problems under selection for new traits can be derived from the theory of the selection index. Assume that selection is for an index of trait $I = \mathbf{a}'\hat{\mathbf{u}}$, where $\mathbf{a}$ is vector of economic weights and $'\hat{\mathbf{u}}$ is vector of EBV. Assume that fitness traits exist that are not yet problematic but may become problematic later. The response to selection for an unrecorded trait u_n is (Van Der Werf, 2025):

$$\begin{bmatrix} R_I \\ R_n \end{bmatrix} = i_I \, acc_I \begin{bmatrix} 1 & \\ & corr_{In} \end{bmatrix} \begin{bmatrix} \sigma_I \\ \sigma_n \end{bmatrix},$$

where R_I is a response to selection for the index, R_n is a response to selection for the unselected trait, i_I is selection intensity for the index, acc_I is accuracy of the index, $corr_{In}$ is correlation between the index and the unrecorded trait, and σ_I and σ_n are standard deviations for the index and the unrecorded trait, respectively. The equation can be generalized to many unrecorded traits.

When the correlation between the index and unrecorded traits is negative, selection on the index elicits a negative response on unrecorded traits. Although the change can be small in a single generation, it accumulates over time. The value of the correlation depends on composition of the index. When the index is composed mainly of production traits, the correlation with fitness traits is likely to be negative, as shown in Figure 2.

When the index I contains many fitness traits ("balanced"), the correlations of the index with fitness traits may be small and even positive, although the genetic progress for the production traits would be lower. In such a case, the unrecorded trait would not deteriorate.

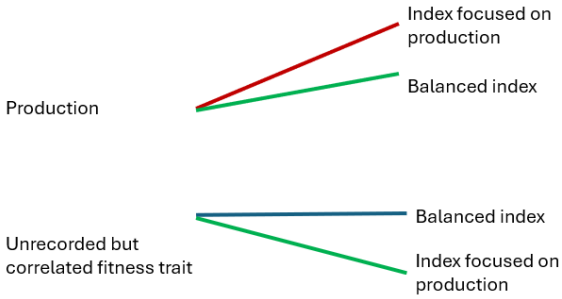


Figure 2. Impact of selection on an unrecorded correlated fitness trait with different indices.

Nonlinearity because of resource allocation issues

Usually, genetic analyses assume that the genetic parameters are static. However, under selection for production, resources allocation issues (van der Waaij, 2004) can cause negative genetic correlations to intensify, with changes accelerating under genomic selection (Hidalgo et al., 2020). If antagonistic traits are included in the selection index that were derived with old parameters, the response to selection for these traits will be progressively lower than expected, as illustrated in Figure 3.

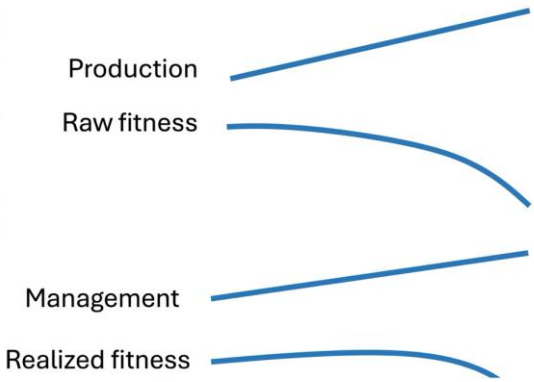


Figure 3. Relationship between production and fitness traits under changing genetic correlation.

Underlying values

A special case in animal breeding is a disease where the incidence increases rapidly, e.g., prolapse in pigs (Supakorn et al., 2017). Assume that the disease status is an effect of a threshold response to an underlying value, like in the threshold model (Gianola, 1982). Assume that the underlying variable is unselected and is antagonistic to the index. Subsequently, changes in the underlying variable will not be visible until that variable approaches the threshold. As is illustrated in Figure 4, then the incidence increases rapidly.

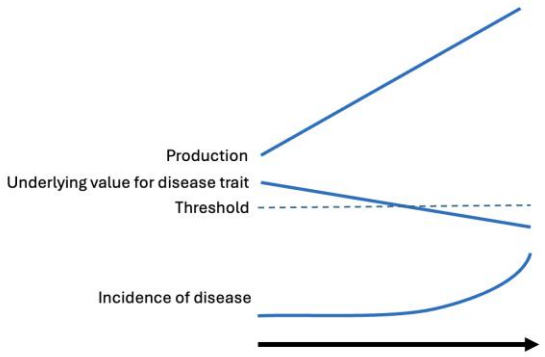


Figure 4. Incidence of a disease when its underlying variable is antagonistic with Production.

Use of incomplete multiple-trait model in the selection index

A selection index using EBV from a multiple-trait BLUP index is composed of only the economic values and EBVs (Van der Werf, 2025). Due to computational efficiency, usually production and fitness traits are evaluated separately. If a trait has little information and its genetic correlation with other traits is ignored in computing EBVs, the index based on such EBVs generates less response for that trait (Van der Werf, 2014). Corrections in such a case result in a custom index with weights adjusted for accuracies and genetic correlations.

Discussion

Mitigating negative effects

Mitigating the negative effects of genomic selection will require several steps, although, due to low heritability of fitness traits, a noticeable improvement can take several cycles of selection. First, the selection pressure on production traits that are antagonistic to the deteriorating traits may have to be reduced, allowing for management modifications to catch up. Second, selection for recorded fitness traits needs to intensify, with weight on each trait calculated from recent genetic parameters preferably by a multiple-trait model. Third, as genetic parameters can change rapidly under genomic selection, these need to be re-estimated for the last generation using the complete data. While traditional methods for parameter estimation are unfeasible with large data, new methods are emerging that are unrestricted by data size, such as genetic estimation by predictivity (GPP) (Misztal and Gopal, 2025) or REML with traces calculated by Monte Carlo methods (Bermann et al., 2025). Fourth, methods for evaluating fitness traits can be improved. While many fitness traits are categorical, current methods allow for the evaluation of a single categorical trait and multiple linear traits, and corresponding computations are expensive. New methods under development will potentially analyze any number of categorical and linear traits simultaneously by a threshold-linear model at a reasonable computing cost (Bermann et al, 2026). Similar advancements would also be helpful for censored traits such as survival.

Conclusions

Genomic selection can cause deterioration of secondary traits as an accelerated selection on production traits causes a correlated decline on antagonistic traits; improving management is too slow to mitigate the decline. Additional factors intensifying the decline is lack of the deteriorating trait in the selection index, genetic correlations become more antagonistic, and possibly a suboptimal index if EBV are not calculated by a complete multiple-trait model. The decline can occur rapidly for categorical traits. Sustaining the long-term progress of genomic selection while managing and

preventing potential negative effects requires including the problematic traits in the selection index at an appropriate weight, possibly with higher weights if the model ignores the genetic correlations, improving the accuracy of fitness traits, and adopting cutting-edge models and computational methods.

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