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Genetics of resilience and feed efficiency in livestock: their genetic relationship and potential trade-offs

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Introduction

Feed is the largest variable cost in livestock production, making genetic improvement of feed efficiency a key priority in animal breeding programs. In parallel, animals are increasingly exposed to various environmental, social, and health-related stressors that can affect their productivity and welfare throughout the production cycle. For decades, breeding programs have focused on genetically improving production traits (e.g., milk yield, carcass weight) with little to no direct selection for other relevant traits such as health, reproductive performance, and functional longevity (Rauw *et al.,* 1998; Brito *et al.,* 2021). Undoubtedly, intensive selection for increased productivity has improved production efficiency but has also led to increased environmental sensitivity (Rauw *et al.,* 1998; Misztal *et al.,* 2025). Efficiency can be defined as the ability of an animal to convert inputs (e.g., feed, energy) into outputs (e.g., milk, eggs, meat). However, this allocation of resources to production traits necessarily reduces the resources available for other essential life functions, potentially giving rise to biological trade-offs (Rauw, 2009). Trade-offs between productive functions and biological processes involved in the maintenance of homeostasis may compromise animal resilience, defined here as the capacity of an animal to be minimally affected by short-term environmental perturbations or to rapidly return to its expected level of performance (Colditz and Hine, 2016). In this context, there is a need to better understand the biological and genetic relationships between feed efficiency (FE) and general resilience (RE) to design balanced and sustainable breeding programs. This presentation will draw on a systematic review of trait derivation and the genetic basis of FE and RE indicators, including their genetic relationships and potential antagonisms. Findings from my research group and the broader literature will be summarized, with a focus on livestock mammals.

Genetics of Feed Efficiency. FE, broadly defined as the amount of product produced per unit of feed intake (FI), influences not only outputs but also vital maintenance-related functions associated with environmental sensitivity (Rauw *et al.,* 2025). FE is a complex trait, influenced by various biological mechanisms (e.g., digestive and metabolic efficiencies), diet, nutritional management, and environmental conditions. Several FE indicators have been proposed and are now used in breeding programs, including residual FI (RFI), dry matter intake (DMI), feed conversion ratio, and different measures of energy intake (Brito *et al.,* 2020a; Patience *et al.,* 2015). FE indicators are moderately heritable, with estimates from different species ranging from 0.02 to 0.67 (Brito *et al.,* 2020, 2025; Davoudi *et al.,* 2022; Maskal *et al.,* 2024), and their genetic correlations are mostly favorable, although their magnitude varies across indicator traits, populations, and management systems. Recording FI can be expensive depending on the production system. Therefore, most FE data collection schemes have focused on specific life stages (e.g., growing phase in pigs; specific parity or lactation stage), generally recorded for reasonably short periods (e.g., 90–150 days), and often measured in farms with better environmental conditions (e.g., pig nucleus herds) than commercial operations. Therefore, the traits evaluated may not fully represent FE across the animal production cycle, environments, or production systems. Given the challenges of recording FI at scale, genomic selection has become essential for genetically improving FE.

Genetics of Animal Resilience. RE describes the capacity of an animal to be minimally affected by or to rapidly bounce back from environmental disturbances of relatively short duration (Colditz and Hine, 2016; Friggens *et al.,* 2023). RE can be divided into specific component traits such as disease or climatic resilience when refering to an animal's response against a specific perturbation. RE indicators can be derived from deviations between expected (in the absence of perturbations) and observed performance trajectories or from variability in high-frequency longitudinal phenotypes collected across different physiological stages and production traits. A variety of RE indicators have been developed by our group and others based on variability in feed intake (including calf RE based on variability in milk intake; Graham *et al.,* 2024a), feeding behavior, body weight, activity level, milk yield, vaginal temperature, and fiber diameter. In contrast to FE traits, RE indicators show greater heterogeneity in both heritability and genetic correlation estimates, with heritability estimates ranging from 0.01 to 0.40 (e.g., Brito *et al.,* 2020b; Laghouaouta *et al.,* 2024). For instance, we derived heritable RE indicators based on variability in milk yield (Chen *et al.,* 2023) and milk electrical conductivity, calf RE based on calf milk intake recorded by automated feeders (Graham *et al.,* 2024a), and climatic resilience based on vaginal temperature (Wen *et al.,* 2024). The statistical properties and biological interpretation of RE indicators depend on the data sources used for their derivation, trait definitions, the animals' life stage, and the nature of the stressors driving the observed fluctuations. This heterogeneity is reflected in the highly variable genetic correlations reported among RE indicators, which underscores the diversity of underlying biological processes. Consequently, genetic improvement of RE will likely require selection based on a sub-index that integrates multiple RE indicators capturing animals' ability to respond to a broad range of perturbations throughout their lifetime. In addition, there is a need to harmonize RE definitions and phenotyping schemes, perform biological validation through experiments with known perturbations, and validate RE indicators across diverse environments while explicitly accounting for genotype-by-environment (GxE) interactions.

Genetic Relationship and Potential Trade-offs Between RE and FE Indicators. The genetic relationship between FE and RE is complex and can be interpreted through the lens of resource allocation theory, which states that animals have a finite pool of resources (e.g., energy) that must be partitioned among competing biological functions (e.g., maintenance, growth, reproduction) (Rauw, 2009). Consequently, selection favoring increased investment in a given function (e.g., milk production) may reduce resources available for other functions, potentially compromising the animal's ability to cope with environmental disturbances (Rauw, 2009; 2025). Studies across species have reported favorable, unfavorable, and near-zero genetic correlations between FE and RE (including those based on variability in feed intake) indicators (Maskal *et al.,* 2024; Mucha *et al.,* 2022). When unfavorable genetic correlations are observed, they are typically of low to moderate magnitude, suggesting that strong trade-offs are not inevitable. This interpretation is consistent with the recent review by Rauw *et al.* (2025), which discusses the concept of metabolic flexibility. Metabolic flexibility refers to the capacity of animals to support the energetic demands of different metabolic processes through the storage and utilization of multiple energy substrates (carbohydrates, lipids, proteins) with varying efficiencies, allowing animals to switch among substrates as needed. Consequently, selection for improved FE does not necessarily constrain metabolic capacity or lead to trade-offs, as energy-sparing mechanisms may compensate for increased FE (Rauw *et al.,* 2025).

Overall, results suggest that the association between FE and RE indicators is context dependent and often weak, with limited evidence for strong antagonistic trade-offs. Experimental studies indicate that the relationship between FE and RE depends on environmental conditions, production system, and the stage of life in which FE is measured.

Martin *et al.* (2024) combined RFI evaluation in beef heifers with subsequent dietary challenges during adulthood and showed that associations between FE at young ages and both short- and long-term RE varied across environments. Feed-efficient heifers tended to produce less milk and lighter calves later in life. In contrast, Barrio *et al.* (2025) reported that although more feed-efficient ewes consumed less feed for a given level of production, no differences were observed in RE indicators during a nutritional challenge. Graham *et al.* (2024b) evaluated the relationship between milk intake traits in dairy calves and found moderate and favorable genetic correlations with the number of times they were treated for bovine respiratory diseases. Similarly, calf RE based on variability in cumulative milk intake was also genetically correlated with calf health traits (Graham *et al.,* 2024a).

In pigs, several studies have examined genetic relationships between FE and RE indicators derived from FI variability and disease challenge data. Cheng *et al.* (2020) reported moderate genetic correlations between average daily FI or feed conversion ratio and health treatment rate and mortality under disease conditions, whereas RFI showed weak correlations with most RE indicators. However, day-to-day variation in FI duration exhibited favorable genetic correlations with mortality (0.79) and treatment rate (0.20). Similarly, Putz *et al.* (2019) found that RE traits derived from daily FI data were moderately to strongly genetically correlated with mortality and treatment rate. Other studies have reported weak or near-zero associations between FE and RE indicators. Madad *et al.* (2026) evaluated genetic correlations between RE indicators derived from FI variability in purebred boars and disease resilience traits in crossbred barrows under a natural polymicrobial challenge. Although estimates were highly variable, average correlations were close to zero, leading the authors to recommend further investigation. Homma *et al.* (2021) likewise reported low or null genetic correlations between FE and RE traits, and Kavlak and Uimari (2024) observed favorable but small genetic correlations between some FI-variability-based RE indicators and FE.

Evidence from long-term selection experiments further suggests that improving FE does not necessarily compromise RE. Dunkelberger *et al.* (2015) showed that pigs selected for improved RFI displayed higher antibody responses and smaller reductions in growth rate following a PRRS virus challenge than pigs selected for lower FE. Consistently, Gilbert *et al.* (2017) reported that 15 years of divergent selection for low RFI in growing pigs did not impair the animals' ability to cope with challenges. Another approach to identifying animals with greater capacity to cope with environmental challenges is to model genotype-by-environment interactions using reaction norms, thereby capturing genetic plasticity (Silva Neto *et al.,* 2024; Misztal *et al.,* 2025). Various studies have demonstrated meaningful genetic variation in environmental sensitivity, particularly under heat stress and other challenging conditions (Misztal *et al.,* 2025; Silva Neto *et al.,* 2024). We evaluated GxE interactions for DMI and RFI in Nellore cattle, with the temperature–humidity index (THI) serving as the environmental descriptor (Silva Neto *et al.,* 2025). The genetic expression of FE traits was influenced by climatic conditions, as heritability estimates varied along the THI gradient for both DMI (0.22 to 0.39) and RFI (0.08 to 0.28). In addition, the genetic relationship between DMI and RFI changed across THI levels, with genetic correlations ranging from 0.64 to 0.72, indicating shifts in the genetic architecture of FE under differing degrees of heat stress (Silva Neto *et al.,* 2025). Together, these results highlight the importance of accounting for genetic plasticity when selecting animals for improved FE.

Another important area of research is understanding the genetic variability of resource allocation coefficients across different life functions, as well as their potential GxE interactions as indication of allocation plasticity (Ithurbide *et al.,* 2025). In this context, simulation studies based on mechanistic models explicitly incorporating physiological processes are particularly informative and have been used to demonstrate that the correlation between FE and RE depends on the duration of the measurement period (Puillet *et al.,* 2016, 2021). These findings underscore the importance of defining appropriate time windows for

measuring FE to develop phenotypes that support selection for sustainable FE. In American Angus cattle, we recently showed that the energy allocation coefficient to growth is moderately heritable, favorably correlated with growth and FE, and minimally antagonistic to RE traits. We also found that there is GxE for the allocation coefficient to growth, indicating that the ability of animals to allocate resources to different biological functions depends on both genetics and environment.

The concept of metabolic flexibility (Rauw *et al.*, 2025) can help reconcile apparent contradictions between FE and RE, as animals may develop energy-sparing mechanisms that enable improved FE without compromising their ability to cope with short-term perturbations. Genetic selection for improved FE may also modify metabolic pathways in ways that maintain or even enhance adaptability to diverse stressors, suggesting that trade-offs are not inevitable when metabolic flexibility is considered (Ithurbide *et al.,* 2025).

Conclusions

In conclusion, strong statements about the genetic relationship between FE and RE are not yet possible, as favorable, null, and unfavorable associations have been reported depending on trait definition, time of measurement, environmental conditions, and modeling strategy. Importantly, the lack of consistently strong antagonisms suggests that FE and RE can be improved simultaneously. Advances in sensor-based phenotyping and quantitative genomics provide new opportunities to achieve this goal while minimizing unintended selection responses across production systems. Given the genetic complexity and context dependency of FE and RE, integrating longitudinal phenotyping, GxE modeling, biologically informed traits, and experimental challenges will be essential to support sustainable genetic improvement for both RE and FE indicators in livestock breeding programs.

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