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Feed efficiency in Fleckvieh dairy cows: First insights into genetic relationships

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Introduction

Feed costs account for up to 60% of the total production costs (Connor, 2015). Including feed efficiency into existing breeding schemes has therefore been of interest for the past decade. Different countries have already incorporated efficiency-related traits into their breeding goals to address the importance of feed efficiency (Gaddis *et al.*, 2021; Jamrozik *et al.*, 2021; Bolormaa *et al.*, 2022). The focus so far has been mainly on Holstein cattle, while for other breeds such as Fleckvieh, the dominant breed in Austria and Southern Germany, the process of developing suitable traits is still ongoing. To date, low to moderate heritabilities have been reported for dry matter intake (DMI) and for efficiency traits such as residual feed intake (RFI) in Fleckvieh cows (Becker *et al.*, 2022). This is comparable to heritabilities reported for Holstein cattle (Vallimont *et al.*, 2010; Becker *et al.*, 2022). Thus, breeding for improved efficiency in Fleckvieh cows also appears promising. Routine feed intake recording, however, is currently unavailable for Fleckvieh and the limited existing data have mainly been collected on research farms. For this reason, the use of routinely available indirect traits for feed intake or efficiency-related traits could provide a valuable alternative. A potential approach is to use prediction equations for DMI based on available production data, such as milk yield (MY) or body weight (BW). Gruber *et al.* (2004) developed several prediction equations for DMI for different breeds, including Fleckvieh. In comparison with other prediction models, this model was the most accurate in a validation study by Jensen *et al.* (2015). The predicted dry matter intake (pDMI) showed a similar heritability to that of actual feed intake in Fleckvieh cows (Köck *et al.*, 2018; Becker *et al.*, 2022). The genetic relationship between DMI and pDMI for Fleckvieh, however, has not yet been reported. Furthermore, little is known about genetic parameters of RFI in Fleckvieh cows. In this study, our aim was to: (1) estimate heritabilities for DMI, pDMI, and RFI, and (2) compare these traits with respect to their genetic correlations, and relate them to MY and BW.

Materials & Methods

Data and data processing. Data from 272 Fleckvieh cows were collected in multiple trials (July 2013 – April 2024) on one Austrian and two German research farms. The dataset included 85,010 daily DMI records and 84,314 daily MY records. Milk samples were either collected daily or weekly, which resulted in a total of 24,240 records. BW was recorded in different frequencies (i.e., daily, weekly, three times per trial), yielding 33,515 body weight records. Feed analyses at varying frequencies quantified dry matter and energy concentration for individual feed components and the total ration. Cows covered different parities and lactation stages. Records were restricted to 6 to 305 days in milk. Data for fat, protein, lactose, and BW

were checked for plausibility and unplausible values were set to missing. Outlier detection for MY and DMI was performed jointly. Records were removed only when one trait exceeded the farm-specific mean ± 3 standard deviations while the others remained within range. Following quality control and outlier detection, the final dataset consisted of 82,426 DMI records, 82,048 MY records, 32,993 BW records, and milk component records comprising 24,191 fat, 24,217 protein, and 24,088 lactose records. Missing values for milk components and BW were imputed using a linear regression. After outlier correction weekly averages were calculated for weeks with at least 4 records. Finally, 11,675 weekly records of 268 cows were used for the analyses. The five-generation pedigree included all animals with phenotypic records and their ancestors, which resulted in 4,781 animals in total.

Dry matter intake prediction. DMI was predicted as described by Gruber *et al.* (2004). This prediction equation is based on breed, parity, days in milk, MY, BW, amount of concentrate, and the average energy density of the forage. DMI was predicted for the daily observations and then also averaged to a weekly predicted DMI (pDMI). The R^2 of the model was 0.69.

Residual feed intake. Two different approaches were used to estimate weekly residual feed intake (RFI): fitting a linear regression model (RFI1) or using the difference between DMI and pDMI (RFI2). For RFI1, DMI was regressed on energy-corrected milk (ECM) and metabolic BW with the test-week as random effect in the model. The resulting residual was then used as RFI1. BW change was not included in the model, for better comparability, as it is also not included in the DMI prediction equation of Gruber *et al.* (2004). ECM was calculated according to GfE (2023) and metabolic BW was defined as $BW^{0.75}$. The regression model was fitted within research farm and the R^2 of the model ranged from 0.49 to 0.62.

Statistical analysis. Genetic analysis was performed with VCE6 (Groeneveld *et al.*, 2010) using a multitrait repeatability animal model. Variance components were estimated for both DMI traits, both RFI traits, and additionally also for MY and BW. For all traits the following model was used:

$$\mathbf{y = X\beta + Z_1h + Z_2pe + Z_3a + e} \quad (1)$$

where y is a vector of observations; β is a vector of systematic effects, including the fixed effects of herd (1, 2, 3), parity (1, 2, 3+), and days in milk (6-305) fitted as linear and quadratic covariates; h is a vector of random herd-trial-test-week effects; pe is a vector of random permanent environmental effects; a is vector of random animal additive genetic effects; e is a vector of random residuals; X and $Z_{1\text{-}3}$ are the corresponding incidence matrices. The significance of the estimates was determined using a t-test.

Table 1. Mean ± standard deviation of weekly averaged dry matter intake (DMI), predicted dry matter intake (pDMI), residual feed intake (RFI1 and RFI2), milk yield (MY), and body weight (BW), overall and for each of the research farms.

Trait	Unit	Farm 1	Farm 2	Farm 3	Overall
Country		Austria	Germany	Germany	
N (Animals)		30	76	162	268
n (records)		2,586	902	8,187	11,675
DMI	kg/d	17.1 ± 3.0	24.4 ± 3.1	22.8 ± 2.9	21.7 ± 3.8
pDMI	kg/d	16.5 ± 2.0	23.6 ± 2.1	21.2 ± 2.2	20.3 ± 3.0
RFI1	kg/d	0.00 ± 1.94	0.00 ± 2.02	0.00 ± 1.74	0.00 ± 1.81
RFI2	kg/d	0.59 ± 2.02	0.80 ± 2.00	1.68 ± 1.71	1.37 ± 1.87
MY	kg/d	21.0 ± 6.4	38.0 ± 5.6	31.7 ± 8.1	29.9 ± 9.1
BW	kg	685 ± 83	784 ± 92	767 ± 77	751 ± 87

Results & Discussion

Table 1 summarises the overall statistics and those for each of the three individual research farms across all traits. The heritability and genetic correlation estimates for all traits are presented in Table 2. The heritabilities for DMI (0.18±0.01) and pDMI (0.19±0.02) were found to be similar. Becker *et al.* (2022) reported a slightly lower mean heritability for DMI in Fleckvieh cows (0.14). The heritability estimated for pDMI in Fleckvieh cows aligns with our previous estimate from a larger on-farm sample of 0.18±0.03 (Köck *et al.*, 2018), which also used the Gruber *et al.* (2004) prediction equation. RFI1, which was the residual of a linear regression, exhibited a lower heritability (0.06±0.01) compared to RFI2 (0.14±0.02), which was calculated as the difference between DMI and pDMI. These estimates are consistent with the values described by Becker *et al.* (2022) for residual energy intake in Fleckvieh cows, which varied between 0.06 and 0.25. The genetic correlation between DMI and pDMI was high and positive (0.80±0.04). A similar relationship was observed in Holstein cattle, where pDMI was predicted through an alternative approach and compared with DMI, resulting in a genetic correlation of 0.84±0.14 (Vallimont *et al.*, 2010). The correlation with MY and BW was moderately positive for both DMI and pDMI, with a slight tendency to be higher for pDMI. This can be explained by the fact that the pDMI prediction equation also includes MY and BW, which may influence this correlation. Vallimont *et al.* (2010) reported a similar trend for the genetic correlation with fat-corrected MY, which was lower with DMI (0.52±0.17) compared to pDMI (0.81±0.05). For BW, the trend was reversed, with DMI exhibiting a higher genetic correlation with BW (0.54±0.16) than pDMI (0.32±0.12). For Fleckvieh cows, Köck *et al.* (2018) reported a similar genetic correlation between pDMI and ECM (0.65±0.07) and a slightly lower correlation between pDMI and BW (0.50±0.07).

Table 2. Heritability (diagonal) and genetic correlation (below diagonal) estimates and their standard errors[1] for dry matter intake (DMI), predicted dry matter intake (pDMI), residual feed intake (RFI1, RFI2), milk yield (MY), and body weight (BW).

	DMI	pDMI	RFI1	RFI2	MY	BW
DMI	**0.182 ± 0.010**					
pDMI	0.803 ± 0.035	**0.190 ± 0.016**				
RFI1	0.513 ± 0.100	0.078 ± 0.068^{ns}	**0.059 ± 0.013**			
RFI2	0.787 ± 0.031	0.265 ± 0.072	0.750 ± 0.088	**0.140 ± 0.023**		
MY	0.484 ± 0.051	0.596 ± 0.048	0.521 ± 0.109	0.168 ± 0.110^{ns}	**0.193 ± 0.018**	
BW	0.507 ± 0.022	0.626 ± 0.039	-0.338 ± 0.106	0.172 ± 0.035	-0.237 ± 0.027	**0.531 ± 0.054**

[1] Estimates that are not statistically significant (P>0.05) are indicated by ns.

A high positive correlation was observed between the two RFI traits (0.75±0.09). Both correlated positively with DMI, with RFI1 weaker than RFI2. Similar correlations have been reported for Holstein (Manafiazar *et al.*, 2016) and Nordic Red (Liinamo *et al.*, 2015). The genetic correlation with pDMI was significant only for RFI2, likely due to the calculation of RFI2, which includes both DMI and pDMI. However, the correlation between RFI2 and pDMI was weaker than with DMI. MY was moderately and positively correlated with RFI1, whereas its correlation with RFI2 was not significant. Liinamo *et al.* (2015) described a strong positive

correlation between residual energy intake and ECM (0.86±0.06) for Nordic Red, while Manafiazar *et al.* (2016) did not find a significant correlation between RFI and ECM (-0.08±0.13) for Holstein cattle. The genetic correlation with BW was slightly negative for RFI1 and slightly positive for RFI2. Non-significant and opposite correlations between BW and RFI have been reported, with a negative tendency in Holstein cows (Manafiazar *et al.*, 2016) and a positive tendency in Nordic Red cows (Liinamo *et al.*, 2015). Differences in correlations between RFI and other traits may reflect differences in how RFI is calculated and whether it is based on daily records or aggregated averages, such as weekly or lactation means.

Conclusions

In conclusion, DMI and pDMI of Fleckvieh cows exhibit low to moderate heritability, are strongly genetically correlated, and show similar correlations with MY and BW. This suggests that the prediction equation for pDMI could serve as an indirect trait when DMI is unavailable. The RFI traits showed heritabilities and genetic correlations comparable to those previously reported for Fleckvieh and other breeds. However, these findings are based on a relatively small number of cows, and further studies are required to confirm these results.

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