

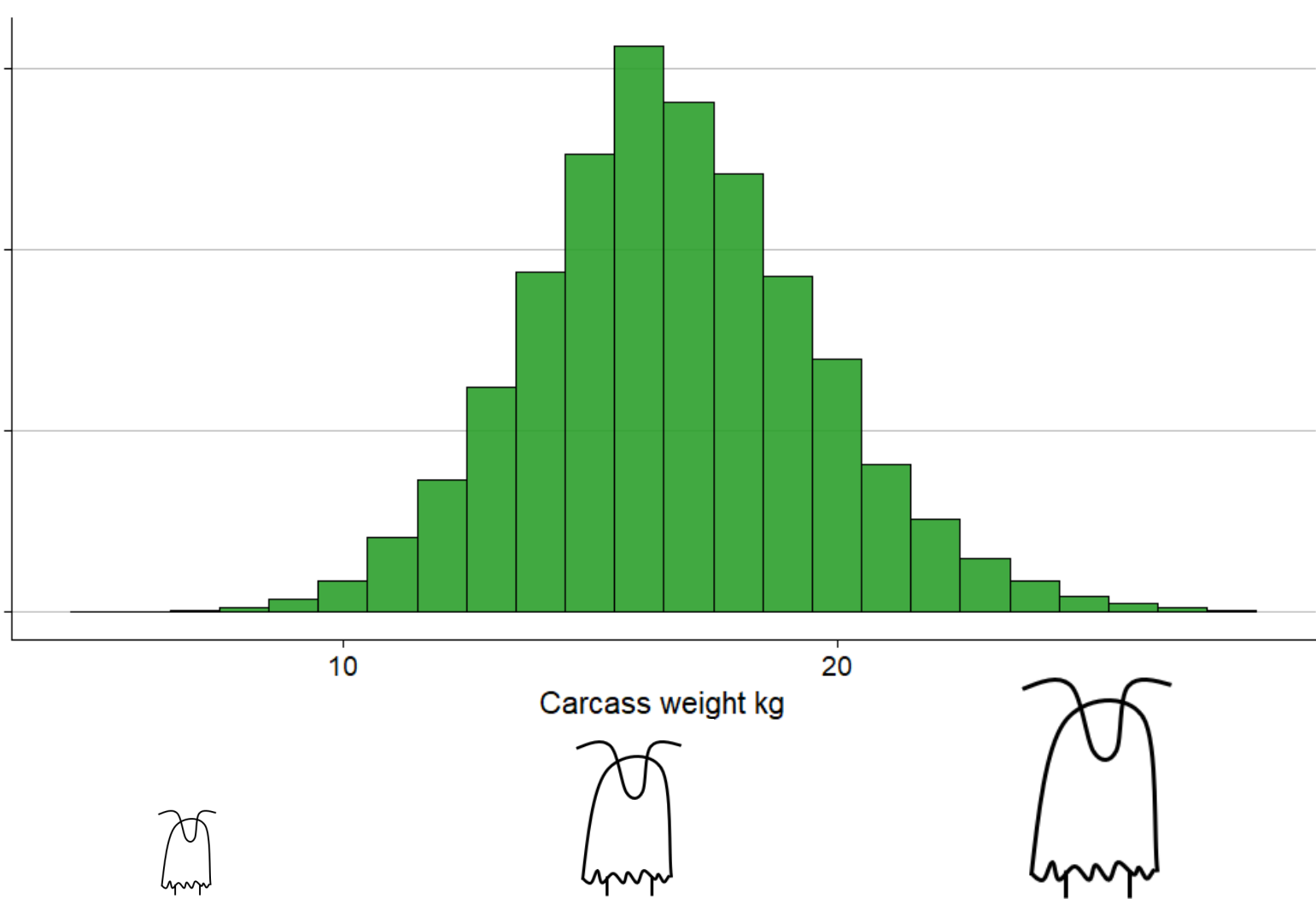
Are carcass traits genetically the same traits in heavy and light lambs?



Jón H. Eiríksson
Agricultural University of Iceland
jonhjalti@lbhi.is

Introduction

In Icelandic lamb production, slaughter age and carcass weight varies greatly between flocks and individuals within flocks. The breeding goals for the population emphasize carcass traits, i.e. carcass weight (CW), carcass fat score (CF) and EUROP carcass conformation score(CC) . The aim of this study was to find out if CW, CC, and CF are the same traits across flocks with different CW and if genetic component related to sensitivity to environmental factors affecting CW is present.



Models

BM – fixed age: $y = X_1 b_1 + Z_d a + Z_m a_m + Z_m e_{pe} + e$

– fixed weight: $y = X_2 b_2 + Z_d a + e$

RRM – fixed age: $y = X_1 b_1 + Z_d a_0 + Z_{sl} a_1 + Z_m a_m + Z_m e_{pe} + e^*$

– fixed weight: $y = X_2 b_2 + Z_d a_0 + Z_{sl} a_1 + e^*$

y is the phenotype (CW, CC or CF)

X_1 and X_2 are incidence matrices for the fixed effects.

b_1 is a vector with the fixed effects of sex, contemporary group, and age at slaughter nested within sex.

b_2 is a vector with the fixed effects of sex, contemporary group, age of dam, type of rearing, carcass weight nested within sex, and weight squared.

Z_d and Z_m are incidence matrices for direct and maternal effects, respectively

a and a_m are vectors of direct and maternal genetic effects, respectively

Z_{sl} is like Z_d , but with normalised CW (for RRMi) or contemporary group solutions for CW (for RRMg) instead of 1's.

a_0 and a_1 are genetic effects of the intercept and slope for RRM

e_{pe} is vector of permanent environmental effect of the dam

e and e^* are vectors of random residuals, without and with 5 heterogeneous residual variance (5 groups), respectively.

The following assumptions were made:

$$\begin{pmatrix} a \\ a_m \end{pmatrix} \sim N(0, A \otimes \begin{bmatrix} \sigma_a^2 & 0 \\ 0 & \sigma_m^2 \end{bmatrix}), \begin{pmatrix} a_0 \\ a_1 \end{pmatrix} \sim N(0, A \otimes \begin{bmatrix} \sigma_{a1}^2 & \sigma_{a1,a2} \\ \sigma_{a1,a2} & \sigma_{a2}^2 \end{bmatrix}),$$

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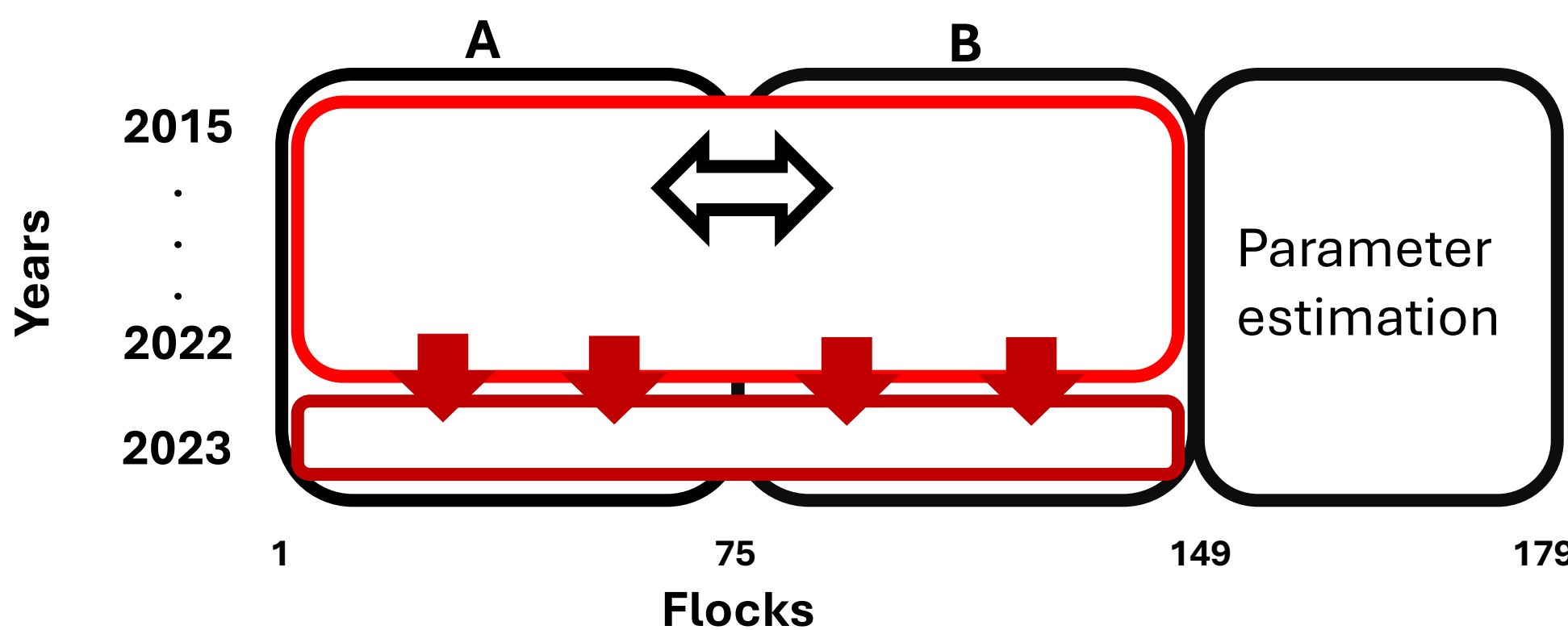
$$e_{pe} \sim N(0, I\sigma_{pe}^2), e \sim N(0, I\sigma_e^2), e^* = \begin{pmatrix} e_1 \\ \vdots \\ e_5 \end{pmatrix} \sim N(0, \begin{bmatrix} I\sigma_{e1}^2 & \dots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \dots & I\sigma_{e5}^2 \end{bmatrix})$$



Methods

The study included 984,412 slaughter records from 179 commercial flocks in Iceland. The tested models were base model (BM), assuming carcass traits are the same for heavy and lighter lambs, and random regression models (RRM), with random regression on contemporary group CW (RRMg) as indication of environment, or individual carcass weight (RRMi). For CC and CF, I either corrected the records for age at slaughter or CW.

I estimated the genetic parameters with data from 30 flocks using AI-REML in the DMU package (Madsen & Jensen, 2023). Available pedigree information traced back for five generations was included to form the genetic relationship matrix A . Using the remaining data, I calculated the correlation of predicted breeding value (PBV) for lambs born in 2023 with records from 2015 to 2022 in the training set. For validating the PBV for the slope in the RRM, I split the validation data into parts (A and B) by flocks and calculated the correlation of the PBVs between the two parts for rams (n=147) with offspring in multiple flocks.



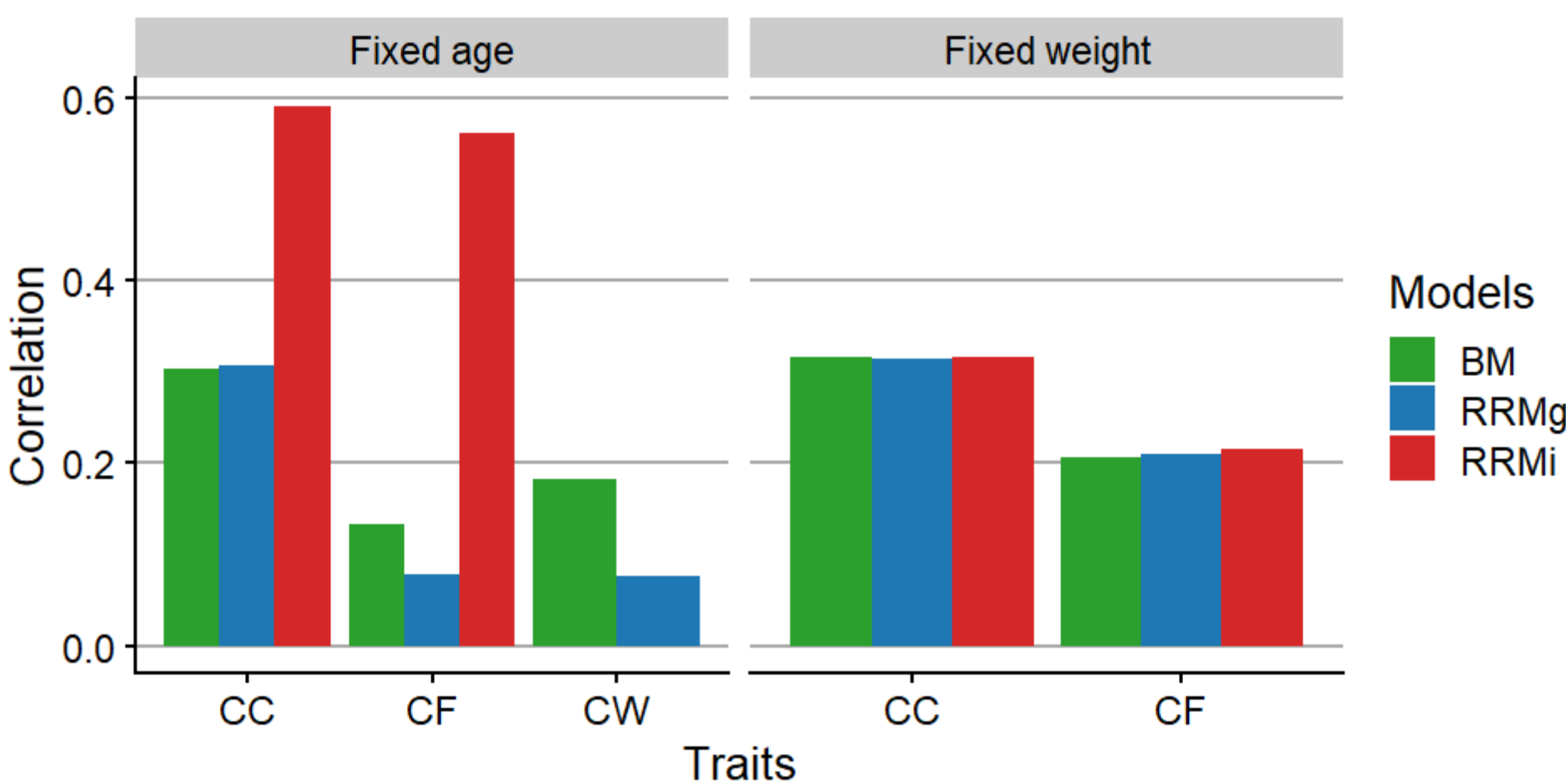
Schematic overview of the validation strategy. indicates the forward validation, while represents the AB validation.

Results and discussions

The RRM showed better fit than BM for all traits and models. For CF and CC at fixed weight, forward validation showed very similar correlation between PBV for lambs born in 2023 and their corrected phenotypes from the three models. For fixed age at slaughter, RRMi gave the highest correlation for CC and CF. However, this result has limited practical relevance because it assumes the slaughter weight already known.

The PBV for slopes were correlated between the A and B data sets for fixed weight and for RRMi for fixed age, with the highest correlation coefficients above 0.6. The PBV for the slope from RRMg indicates environmental sensitivity, like the reaction norm slope in Waters et al. (2024). The correlation of this effect across independent data sets shows that these effects exist in the Icelandic population, at least when working at a fixed weight basis.

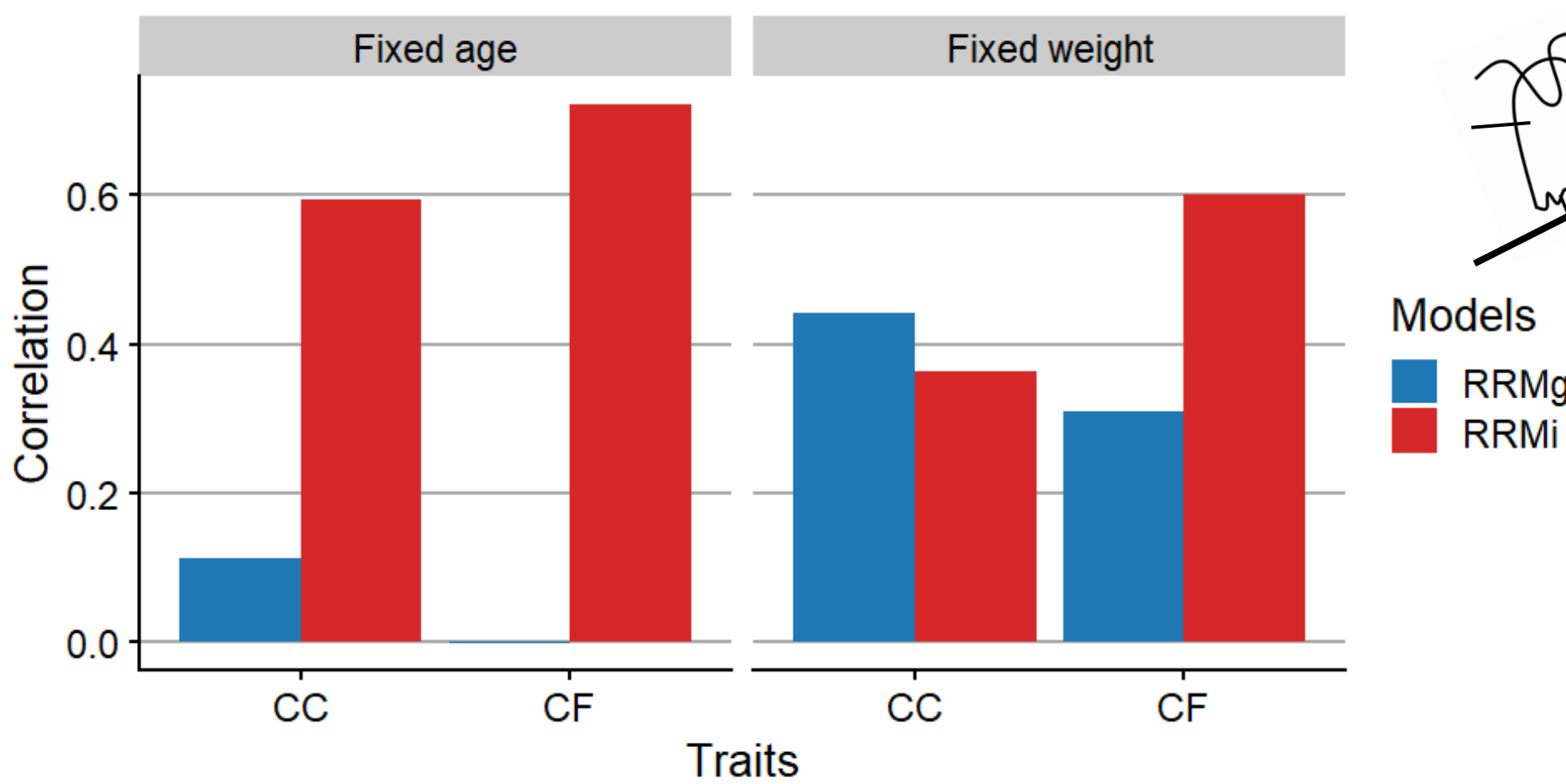
Consistent slope?



Correlation between estimated breeding values for carcass conformation (CC), carcass fat (CF) and carcass weight (CW) and the corrected phenotypes of lambs born in 2023. BM: base model, RRMg: random regression on contemporary group CW, RRMi: random regression on individual CW.

Conclusions

Genetic effects for the random regression slope indicate that genetic effects on carcass traits depend on the weight of the lamb at slaughter to some degree. However, for carcass fat and conformation, genetic evaluations at fixed weight bases did not benefit from accounting for difference in genetic effects in heavy versus lighter lambs.



Correlation of predicted slope of the breeding value for carcass conformation (CC) and carcass fat (CF) between data sets A and B for 147 breeding rams. BM: base model, RRMg: random regression on contemporary group CW, RRMi: random regression on individual CW.



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