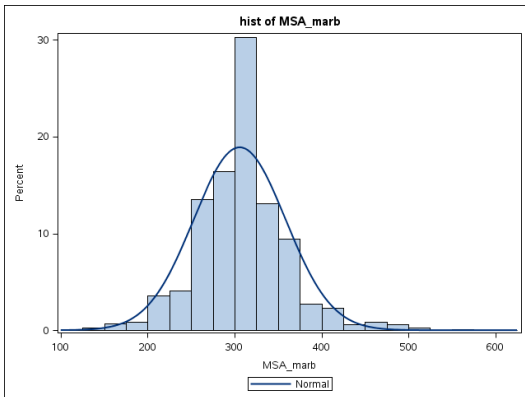# FBC project report
# Author: Mahmoud Shirali

Marbling score
Phenotypic data
In this project, 1930 crossbred animals from BBL sires and HOL dam are used.

Marbling score shows to be normally distributed with range from 100 to 600 which we do not know what it means.

Marbling score shown to be slightly different between crosses from different sire breeds with BBL sired animals have lower and ANN sired animals have higher MS. Female crosses has shown to have slightly higher marbling score than Male crosses.
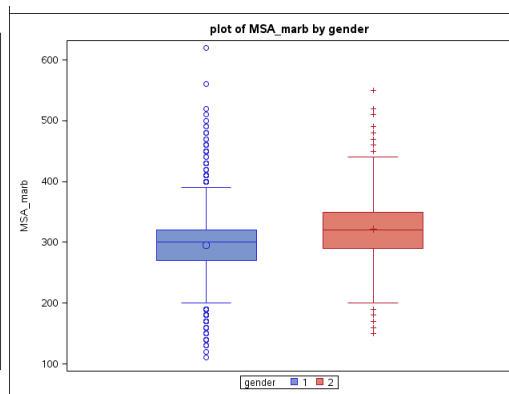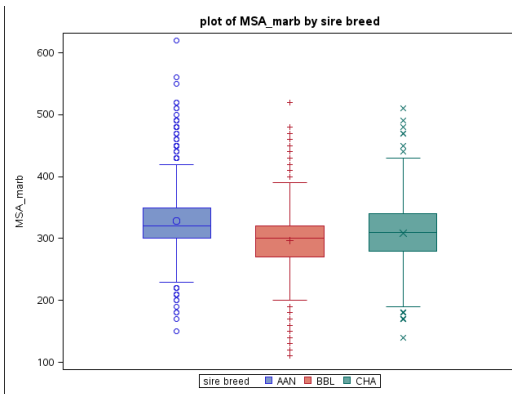
The intramuscular fat shows to have positive relationship with Marbling score; however, discrepancies exist.
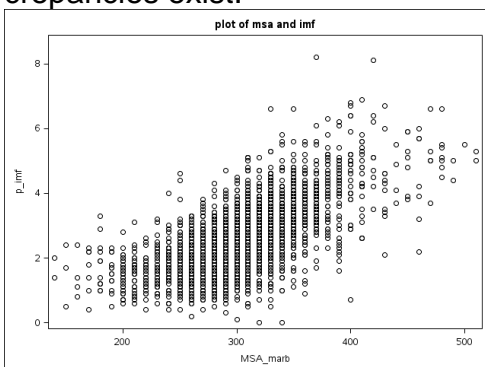
Statistical model

Univariate analysis was performed using the DMUAI to obtain the genetic parameters for traits of Marbling score (MS) using pedigree BLUP. The model was as follow:

$$Y = Xb + Za + e$$

where Y is the matrix for phenotypes of MS; X is the design matrix for fixed effects of slaughter year and month with herd interaction, sex of male and female, and fixed regression of slaughter age; Z is the design matrix for random additive genetics matrix, b is the regression coefficients for the fixed effects, a contains the breeding values for each animal in pedigree, and e is the residual of the model.

	Pedigree BLUP	
	Genetic variance	Heritability
Marbling score	243 (96)	0.15
IMF	0.097 (0.038)	0.15

The genetic correlation between Marbling score and Intermuscular fat is 0.93 (0.09).

Cross validation

From 1300 crossbred animals with phenotype that originated from BBL sires and HOL dam animals, from which 876 of them had genotype data. The entire number of genotyped animals were 2000 which consisted off BBL sires, HOL dams and crossbred animals. Genotyped crossbred animals were divided in 5 categories based on their sires. Each time, one sire category had their phenotypes dropped from prediction analysis. Then the regression between the crossbred breeding values from full (EBV from pedigree BLUP with all phenotypes) and reduced model (SSGBLUP with phenotype of crossbred animals in cross validation dropped) was used for validation. Full model is the EBV that is predicted from pedigree BLUP that contains all the phenotypes. The reduced model is the SSGBLUP model that has the phenotype of the group of genotyped crossbred animals is dropped. The corrected phenotype for marbling score was obtained from pedigree BLUP model as EBV plus the residual.

The corrected phenotype was estimated as the GEBV from full model SSGBLUP. The correlation between corrected phenotype and predicted GEBV is 0.39 and predicted EBV is 0.31 of reduced model for crossbred animals. This indicates that genomic BLUP performs better than the pedigree approach.

$y = 290 + 1.9\,x$
$R^2 = 0.098$
$R = 0.31, p < 2.2e{-}16$

$y = 290 + 2.2\,x$
$R^2 = 0.15$
$R = 0.39, p < 2.2e{-}16$
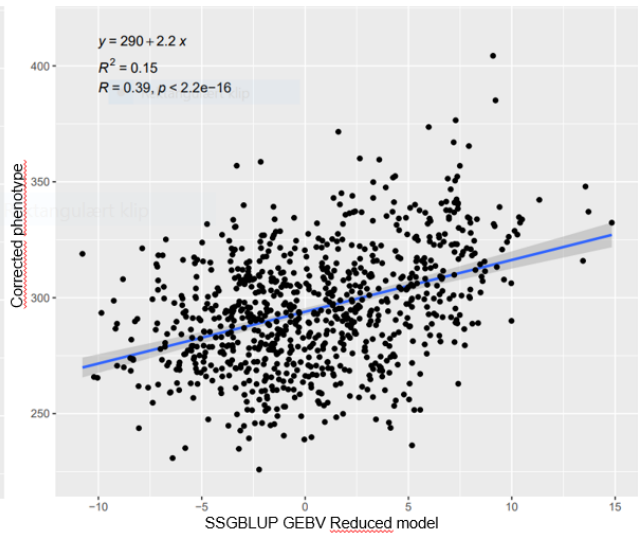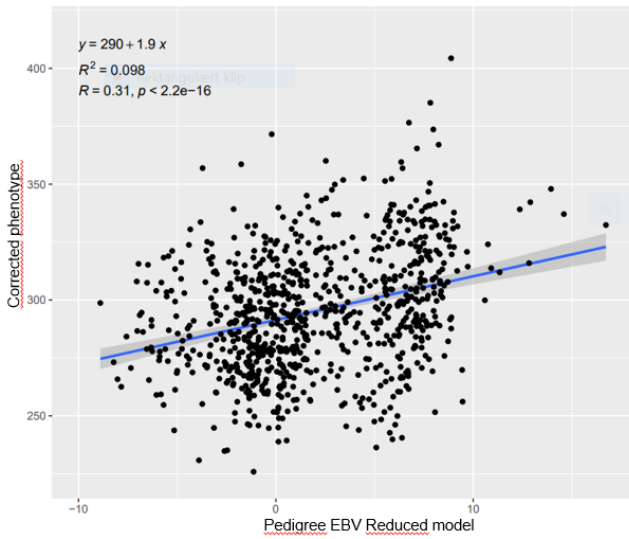
The correlation between EBV from full model and reduced model is 0.32 and regression line of 0.82 for the bulls having their progeny phenotypes removed in the cross validation. This is in comparison to GEBV from full and reduced models of 0.38 correlation and 0.92 regression slope. This indicates that genomic works slightly better than pedigree evaluation.

$y = -1.1 + 0.82\,x$
$R^2 = 0.32$
$R = 0.56, p = 1.7e{-}05$

$y = -1.7 + 0.92\,x$
$R^2 = 0.38$
$R = 0.62, p = 1.4e{-}06$
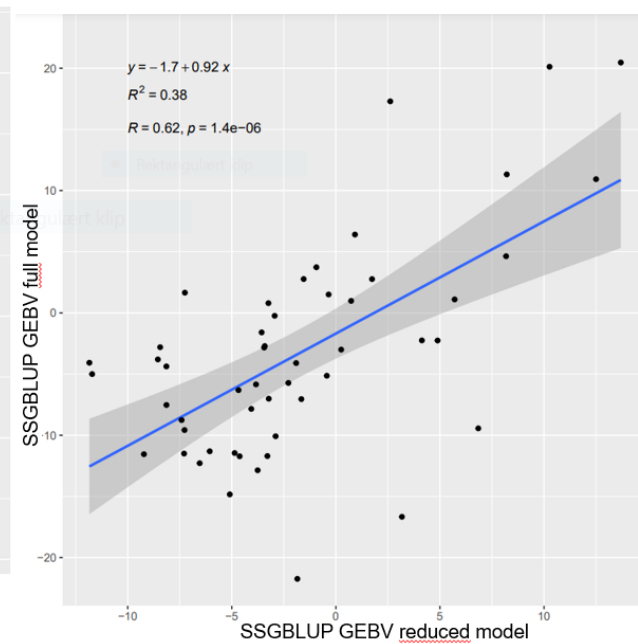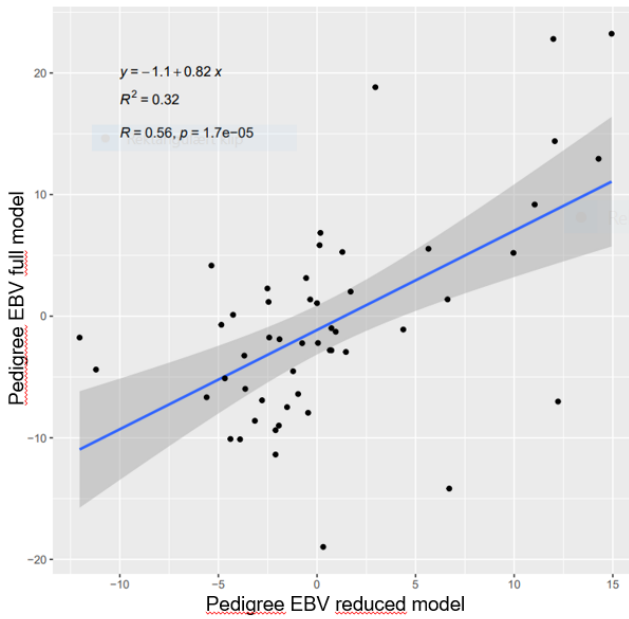
Genetic RFI from longitudinal dry matter intake and weight data

Phenotype files

Feed and weight data across for 7402 crossbred animals was available from which 4863 were from BBL sires and HOL dams.
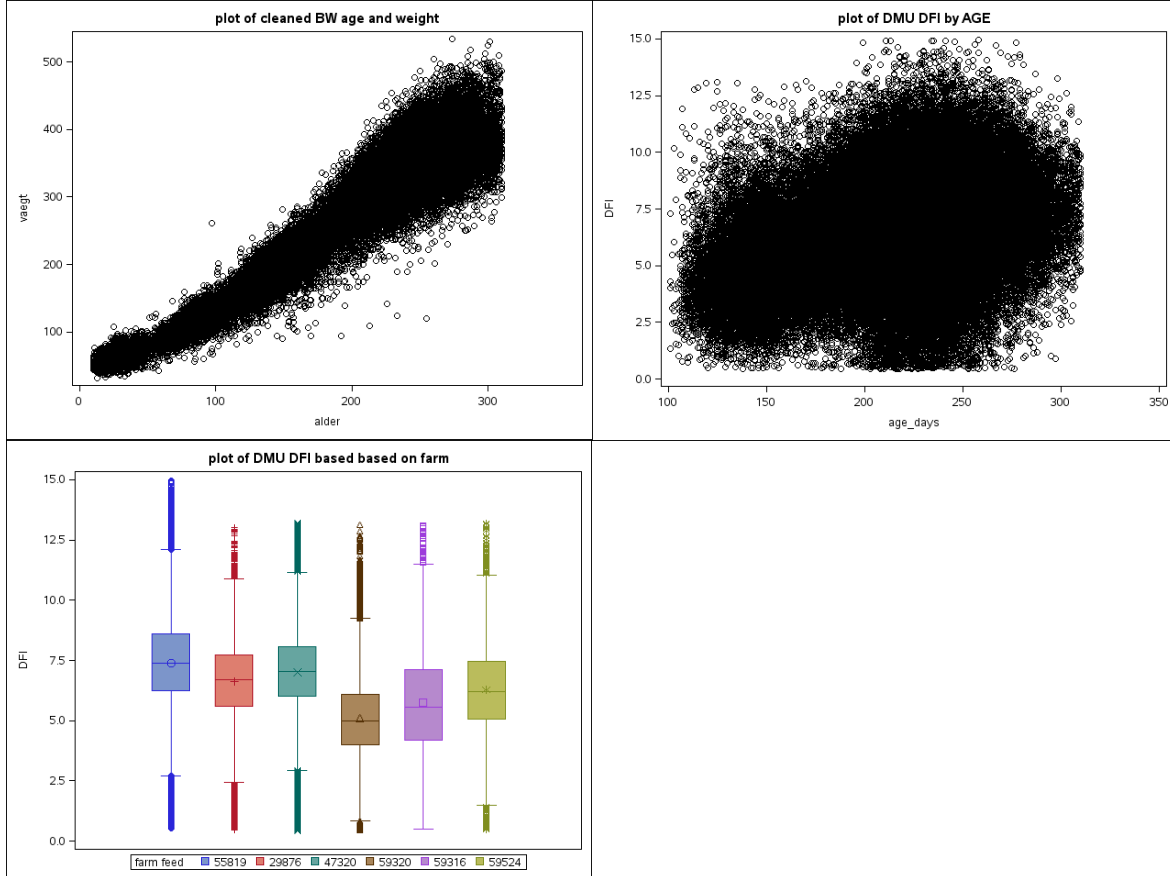
Sire breeds	N of crossbred animals
BBL	4266
ANN	1124
CHA	898

From which 3899 is male and 2389 is female from 6 farms.

Year	N of crossbred animals
2020	1321
2021	1933
2022	2227
2023	807

Statistical model

Bivariate random regression with pedigree structure

Longitudinal Daily dry matter intake (DDMI) and daily body weight (BW) were used in a bivariate random regression analysis with legender polynomial of age at the time of test.

DDMI = HerdYearMonthGender + Sirebreed + Startage+ Startagequadratic + lg1(Sirebreed + Gender + HerdYear) + lg1(genetics) + lg1(permanent environment) + e

BW = HerdYear + Gender + Sirebreed + lg1(Sirebreed + Gender + HerdYear) + lg2(Sirebreed + Gender + HerdYear) + lg1(genetics) + lg1(permanent environment) + e

Table 1. Genetic variance (diagonal) and correlations (off diagonal) from bivariate model

GENETICS	DDMI Int	DDMI slope	BW Int	BW Slope
DDMI Int	0.18 (0.07)			
DDMI slope	-0.14 (0.15)	1.24 (0.44)		
BW Int	0.45 (0.12)	0.19 (0.16)	221 (30)	
BW Slope	0.62 (0.11)	0.11 (0.16)	0.87 (0.02)	123 (20)

Table 2. permanent environment variance (diagonal) and correlations (off diagonal) from bivariate model

GENETICS	DDMI Int	DDMI slope	BW Int	BW Slope
DDMI Int	1.2 (0.08)			
DDMI slope	-0.65 (0.03)	11.11 (0.58)		
BW Int	0.46 (0.04)	-0.01 (0.05)	344 (24)	
BW Slope	0.33 (0.03)	0.09 (0.04)	0.87 (0.02)	345 (17)

	Residual
DDMI	1.90 (0.007)
BW	22 (0.07)

Heritability of DDMI ranged from 0.03 to 0.09 and for BW ranged from 0.30 to 0.35 during 100 to 300 days of age.

heritability of DFI

heritability of BW
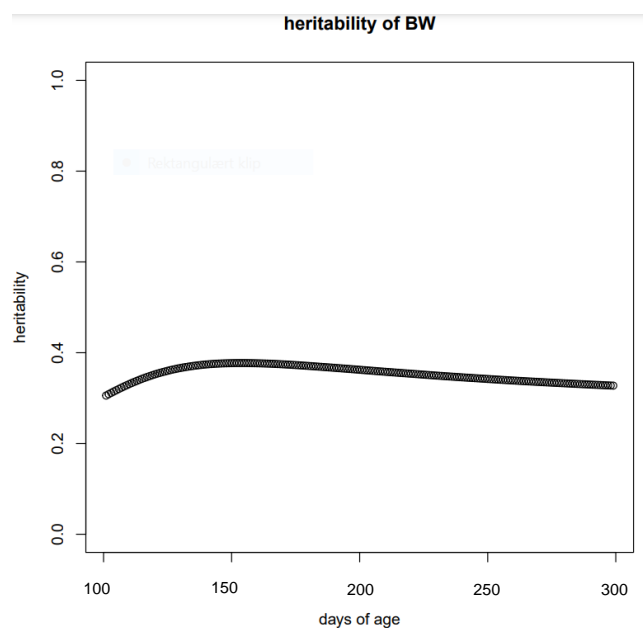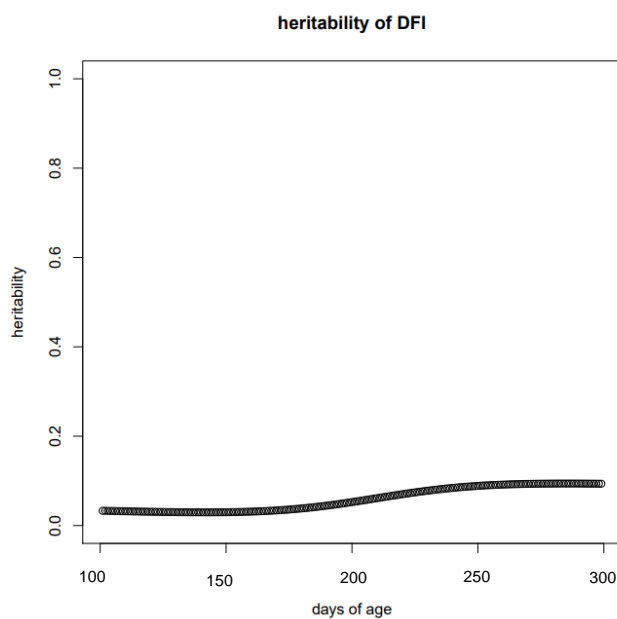
Genetic Residual dry matter intake (RFI)

Genetic RFI was calculated following Esfandiari and Jensen (2022) and Shirali et al. (2018).

$$RFI = TDMI - b_{gain}GAIN - b_{mbw}MBW$$

TDMI was the sum of DDMI from 200 to 280 days of age. $a_{TDMI} = \sum_{t1}^{tn} l_{q1}(t)a_{DDMI}$

GAIN was the total body weight gain during 200 to 280 days of age. $a_{GAIN} = (l_{q1}(t_n) - l_{q1}(t_1))'a_{BW}$

MBW was the average body weight during 200 to 280 days of age. $a_{MBW} = \frac{1}{2}(l_{q1}(t_n) + l_{q1}(t_1))'a_{BW}$

b_{gain} and b_{mbw} are the regression coefficients obtained from Genetic variance covariance matrix.

with b_{gain} and b_{mbw} being the multivariate partial genetic regression coefficients for TDMI on 2 weight traits of GAIN and MBW for the test period. Partial genetic regression coefficients were computed based on the estimated variance and covariance components as follows: $b_{TDMI|GAIN,MBW} = G_{TDMI|GAIN,MBW}G_{GAIN,MBW}^{-1}$ where $G_{GAIN,MBW}$ is the genetic variances and covariances for GAIN and MBW and , $G_{TDMI|GAIN,MBW}$ is the covariances between TDMI and GAIN and MBW from the G matrix.

The heritabilities (diagonal) and genetic correlations (off diagonal) are as follow:

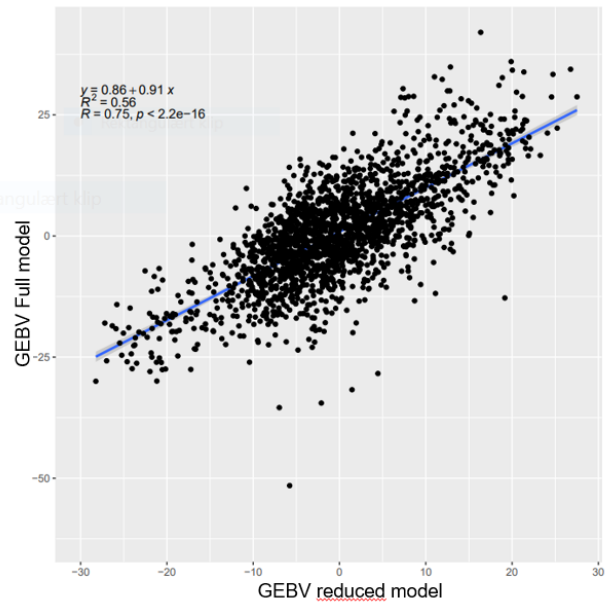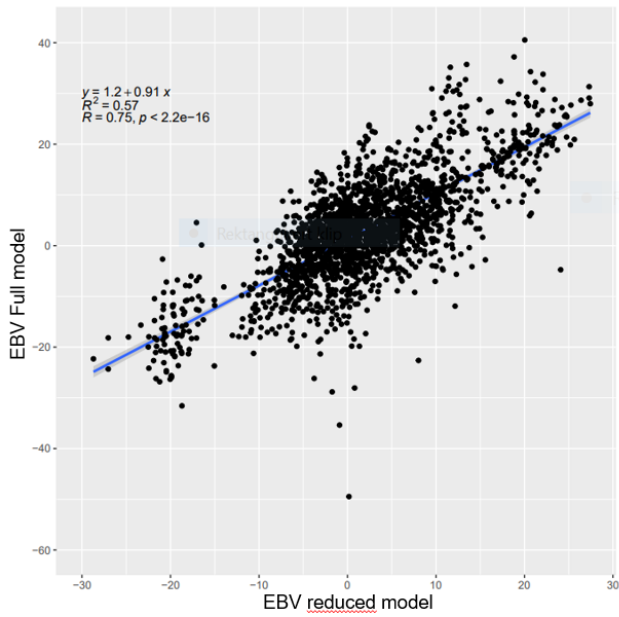|	TDMI	RFI	GAIN	MBW
TDMI	0.24			
RFI	0.84	0.21		
GAIN	0.43	-0.12	0.21	
MBW	0.46	0.00	0.80	0.35

$\frac{a_{RFI}^2}{a_{TDMI}^2} = \frac{484}{675}$ 72% of genetic variance in total dry matter intake is explained by RFI.

Cross Validation
5-fold cross validation analysis was performed by dividing the genotyped and phenotyped crossbred animals from BBL sires in 5 group based on their BBL sires. In each scenario, the phenotype of that group of crossbred animals were dropped out of the analysis and prediction model was run to produce predicted breeding value from reduced model. Full model is the EBV that is predicted from pedigree BLUP that contains all the phenotypes. The reduced model is the SSGBLUP model that has the phenotype of the group of genotyped animals is missing. The breeding values from pedigree BLUP model with full dataset was used as reference breeding values.

The correlation between pedigree BLUP EBV from full model and reduced model is 0.57 and regression slope of 0.91 for crossbred animals and 0.7 correlation and 0.91 regression slop for the bulls having their progeny phenotypes removed in the cross validation. This is in comparison to SSGBLUP GEBV from full and reduced models of 0.56 correlation and 0.91 regression slope for crossbred animals and 0.68 correlation and 0.9 regression slop for the bulls having their progeny phenotypes removed in the cross validation. This indicates that genomic and pedigree BLUP approach work similarly.

Crossbred animals in cross validation

$y = 1.2 + 0.91\,x$
$R^2 = 0.57$
$R = 0.75, p < 2.2e{-}16$

$y = 0.86 + 0.91\,x$
$R^2 = 0.56$
$R = 0.75, p < 2.2e{-}16$

Bulls with progenies in cross validation

$y = -0.29 + 0.91\,x$
$R^2 = 0.7$
$R = 0.83, p = 1.1e{-}12$

$y = -0.29 + 0.9\,x$
$R^2 = 0.68$
$R = 0.83, p = 2.7e{-}12$