

Genotype by environment interaction in beef cattle

El Hamidi A. Hay

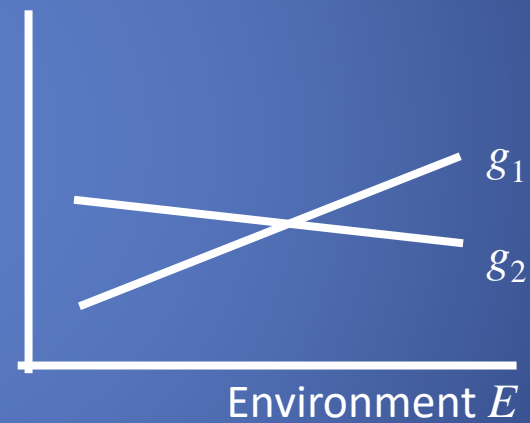
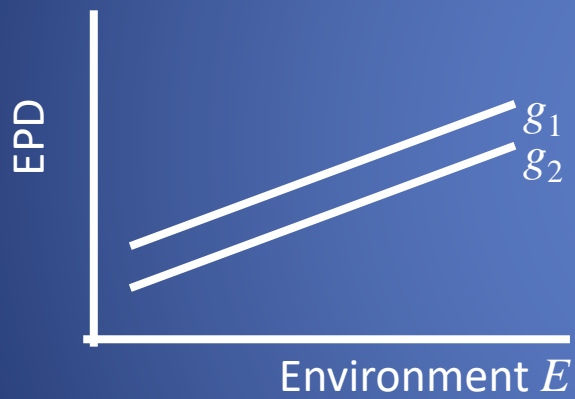
USDA- ARS, Livestock and Range Research Laboratory, Miles City, MT

Genetic by environment interaction

Phenotype= Genetic+ Environment

- Genes control sensitivity to the environment
- Environment controls gene expression

- How does G x E impact beef cattle?



- Implementation:

- Multi-trait model

- Different traits are observations in different environments
 - Potential genetic correlations
 - Examples : different countries, management systems

- Reaction norm model

- Environment descriptor is continuous (THI, disease levels..)
 - Genotype response as a curve

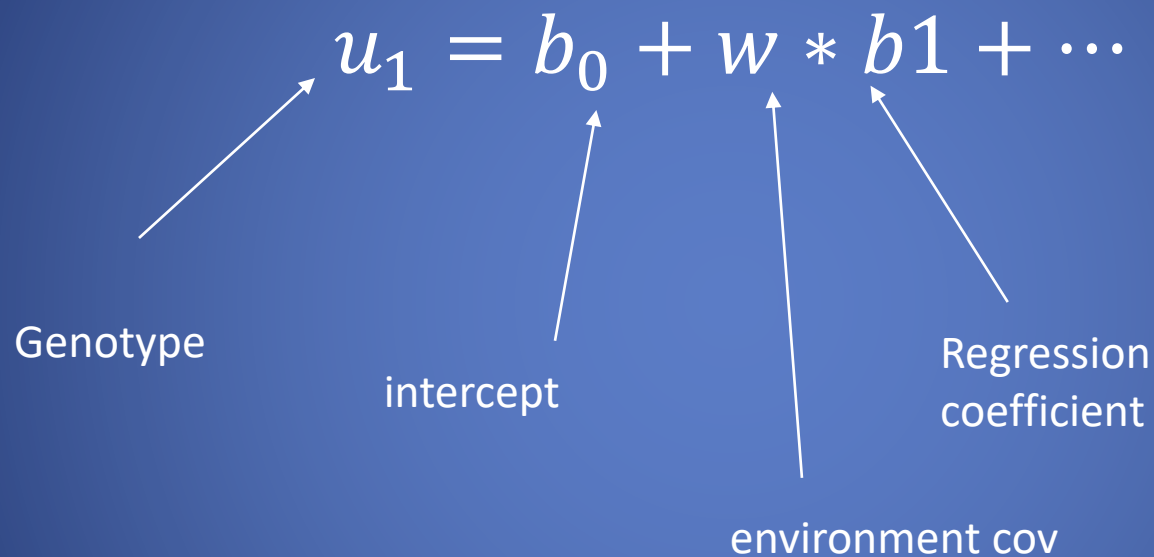
- Multi-trait model:
 - Example: two environments

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & 0 \\ 0 & \mathbf{X}_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_1 & 0 \\ 0 & \mathbf{Z}_2 \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

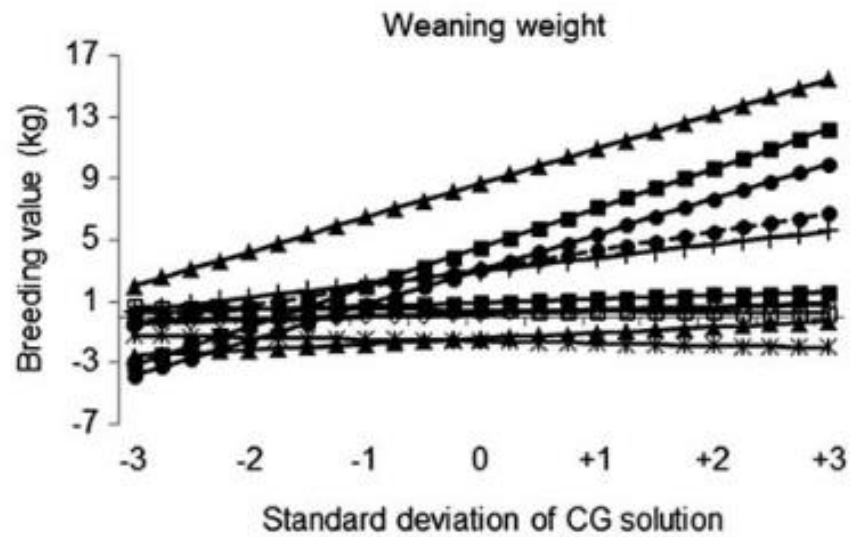
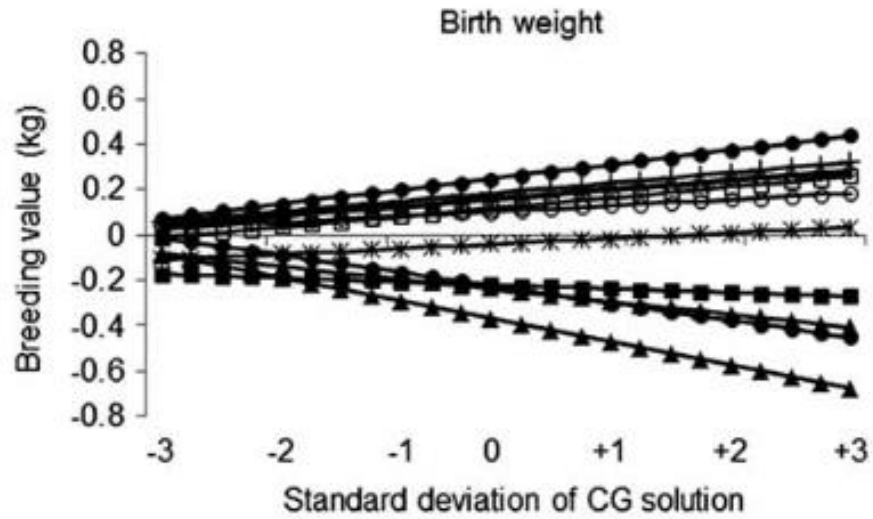
$$\begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \sim N(0, \mathbf{I} \otimes \mathbf{R}); \mathbf{R} = \begin{bmatrix} \sigma_{11}^2 & \sigma_{12} \\ \sigma_{12} & \sigma_{22}^2 \end{bmatrix}$$

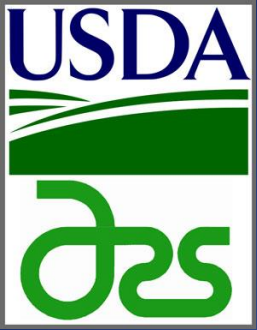
$$\begin{bmatrix} u_1 \\ u_2 \end{bmatrix} \sim N(0, \mathbf{A} \otimes \mathbf{T}); \mathbf{T} = \begin{bmatrix} g_{11}^2 & g_{12} \\ g_{12} & g_{22}^2 \end{bmatrix}$$

- Reaction norm model



$$\text{var}(b) = (\mathbf{A} \otimes \mathbf{W}); \mathbf{W} = \begin{bmatrix} \sigma_{b_0}^2 & \sigma_{b_0 b_1} \\ \sigma_{b_1 b_0} & \sigma_{b_1}^2 \end{bmatrix}$$





Genomic analysis of genotype by prenatal nutritional environment interaction in a crossbred beef cattle herd

El Hamidi A. Hay, Andy Roberts

USDA- ARS, Livestock and Range Research Laboratory, Miles City, MT

Introduction

Table 1. Effect of maternal protein supplementation on heifer progeny performance

Item	Dietary treatment			
	Martin et al. (2007) ¹		Funston et al. (2008) ²	
	NS	SUP	NS	SUP
Weaning BW, kg	207	212	223 ^a	232 ^b
DMI, kg/d	6.50	6.75	7.29	7.30
ADG, kg/d	0.41	0.40	0.81	0.77
Residual feed intake, kg/d	-0.12	0.07	-0.50 ^a	0.01 ^b
Age at puberty, d	334	339	365 ^x	352 ^y
Pregnant, %	80 ^a	93 ^b	83	90

^{a,b}Means within a study with different superscripts differ ($P \leq 0.05$).

^{x,y}Means within a study with different superscripts differ ($P \leq 0.10$).

¹NS = dams did not receive protein supplement while grazing dormant Sandhills range during the last third of gestation; SUP = dams were supplemented 3 times per week with the equivalent of 0.45 kg/d of a 42% CP cake (DM basis) while grazing dormant Sandhills range during the last third of gestation.

²NS = dams did not receive protein supplement while grazing dormant Sandhills range or corn residue during the last third of gestation; SUP = dams were supplemented 3 times per week with the equivalent of 0.45 kg/d of a 28% CP cake (DM basis) while grazing dormant Sandhills range or corn residue during the last third of gestation.

Adapted from Funston et al. 2010

Objective

- To evaluate the existence and the extent of genotype by prenatal nutritional environment on maternal traits

Methods

Data:

- 3020 animals (50% Red Angus, 25% Tarentaise, 25% Charolais)
- Phenotypes of animals born from 2002-2011
- Pedigree consisted of 5371
- All animals genotyped with 50k SNP panel
- Two environments:
 - ADEQ: Adequate levels of winter supplemental feed according to industry guidelines (alfalfa cubes or hay)
 - MARG: ~60% of the supplemental feed provided to ADEQ group
- Phenotypes: Birth weight (BW,) weaning weight (WW), yearling weight (YW)

Methods

- Statistical Model:

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & 0 \\ 0 & \mathbf{X}_2 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_1 & 0 \\ 0 & \mathbf{Z}_2 \end{bmatrix} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{W}_1 & 0 \\ 0 & \mathbf{W}_2 \end{bmatrix} \begin{bmatrix} \mathbf{m}_1 \\ \mathbf{m}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Q}_1 & 0 \\ 0 & \mathbf{Q}_2 \end{bmatrix} \begin{bmatrix} \mathbf{p}_1 \\ \mathbf{p}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix},$$

Where \mathbf{y}_1 and \mathbf{y}_2 are the phenotypes in ADEQ and MARG, respectively, \mathbf{X}_1 and \mathbf{X}_2 are incidence matrices of fixed effects, \mathbf{b}_1 and \mathbf{b}_2 are the solutions of fixed effects in environments ADEQ and MARG, \mathbf{Z}_1 and \mathbf{Z}_2 are the incidence matrices that relate genomic breeding values with the phenotypes, \mathbf{a}_1 and \mathbf{a}_2 are vectors of genomic breeding values in environments ADEQ and MARG, \mathbf{W}_1 and \mathbf{W}_2 are the incidence matrices of maternal genomic breeding values, \mathbf{m}_1 and \mathbf{m}_2 are the vectors of maternal genomic breeding values, \mathbf{Q}_1 and \mathbf{Q}_2 are incidence matrices of maternal permanent environmental effect, \mathbf{p}_1 and \mathbf{p}_2 are vectors of random maternal permanent environmental effects and \mathbf{e}_1 and \mathbf{e}_2 are vectors of random residuals.

Results

Summary statistics for birth weight (BW), weaning weight (WW) and yearling weight (YW)

Trait	Environment	n	mean	SD
BW	MARG	1481	34.31	5.64
	ADEQ	1531	35.34	5.63
WW	MARG	1483	207.19	30.64
	ADEQ	1530	208.53	30.29
YW	MARG	1474	342.46	76.18
	ADEQ	1529	336.27	72.92

Results

Genetic parameters for BW, WW and YW in different environments using a multi-trait model

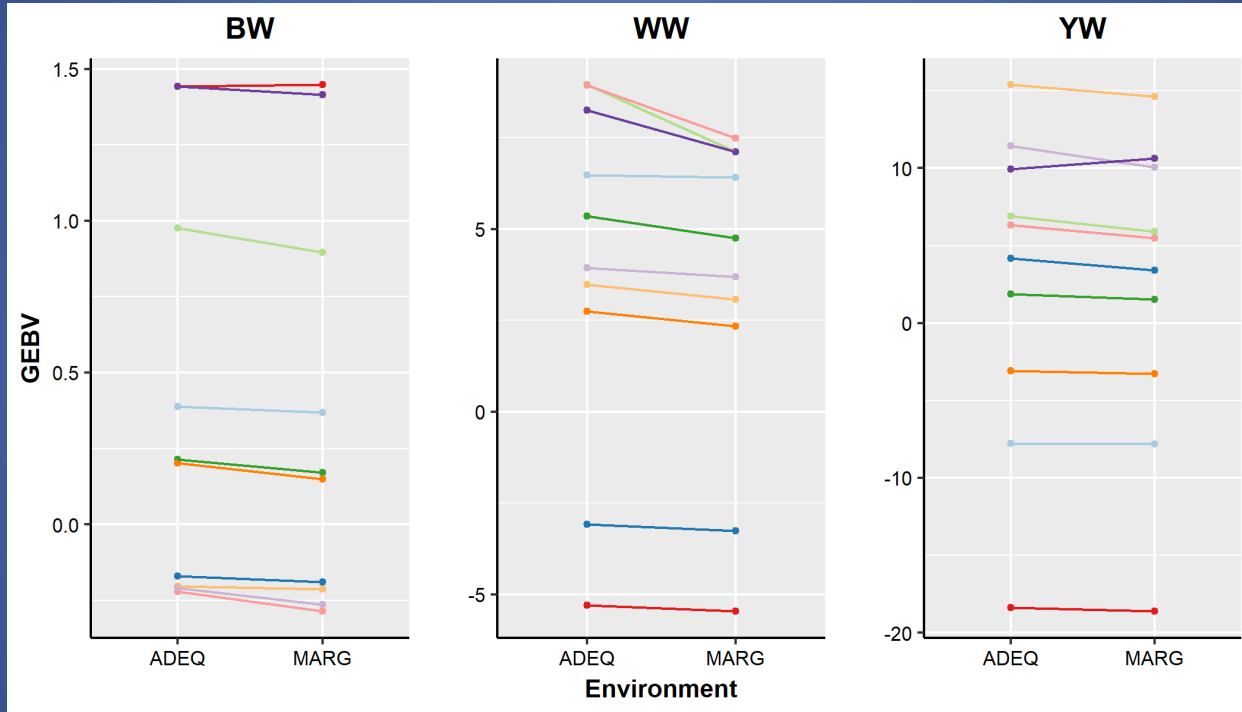
	BW		WW		YW	
	MARG	ADEQ	MARG	ADEQ	MARG	ADEQ
σ_a^2	14.12	11.09	158.81	132.63	282.14	271.60
σ_m^2	5.13	3.53	59.71	50.14	79.37	76.05
σ_e^2	2.87	4.19	157.16	158.33	745.23	743.81
σ_p^2	8.31	7.21	47.15	46.36	58.72	56.91
σ_{am}	-0.47	-0.51	-40.34	-30.15	-10.61	-9.03

Results

Heritabilities and genetic correlations of BW, WW and YW in different environments using a multi-trait model

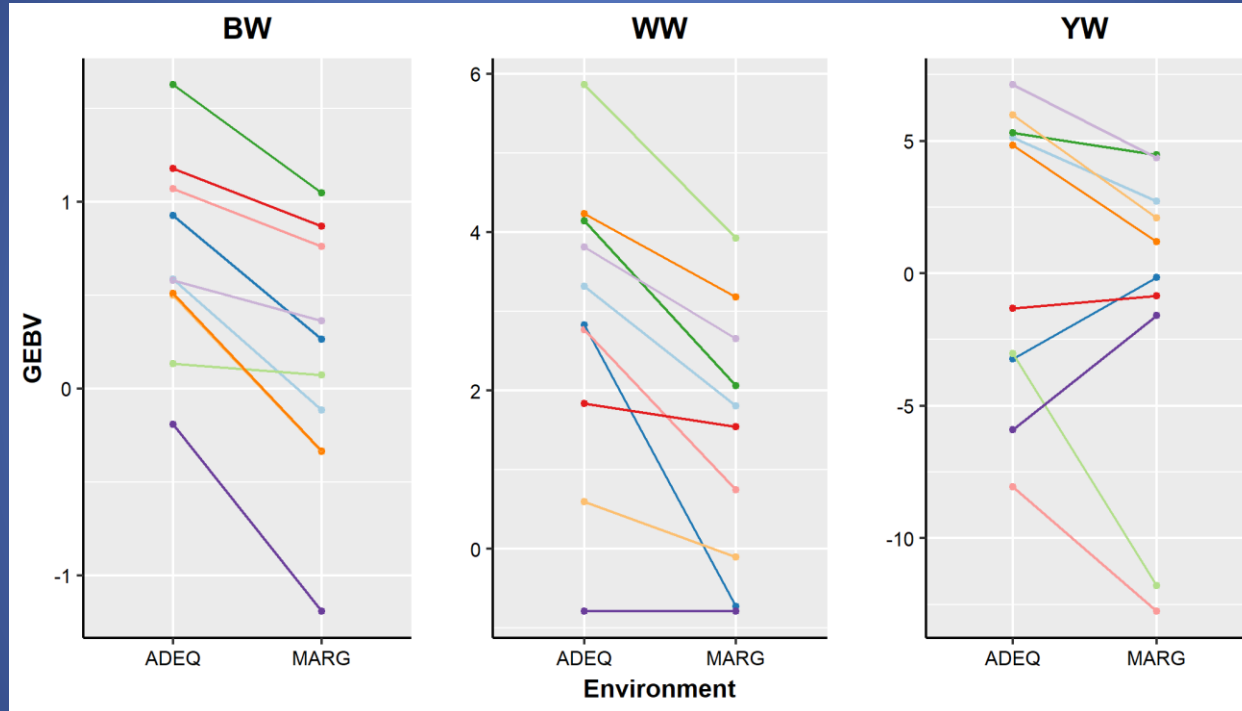
	BW		WW		YW	
	MARG	ADEQ	MARG	ADEQ	MARG	ADEQ
h_a^2	0.46	0.42	0.37	0.34	0.24	0.23
h_m^2	0.16	0.13	0.14	0.12	0.07	0.06
r_a	0.97		0.97		0.99	
r_m	0.62		0.41		0.73	

Results



Estimated direct genomic breeding values for 10 random animals for birthweight (BW), weaning weight (WW) and yearling weight (YW) in different environments using a multi-trait model.

Results



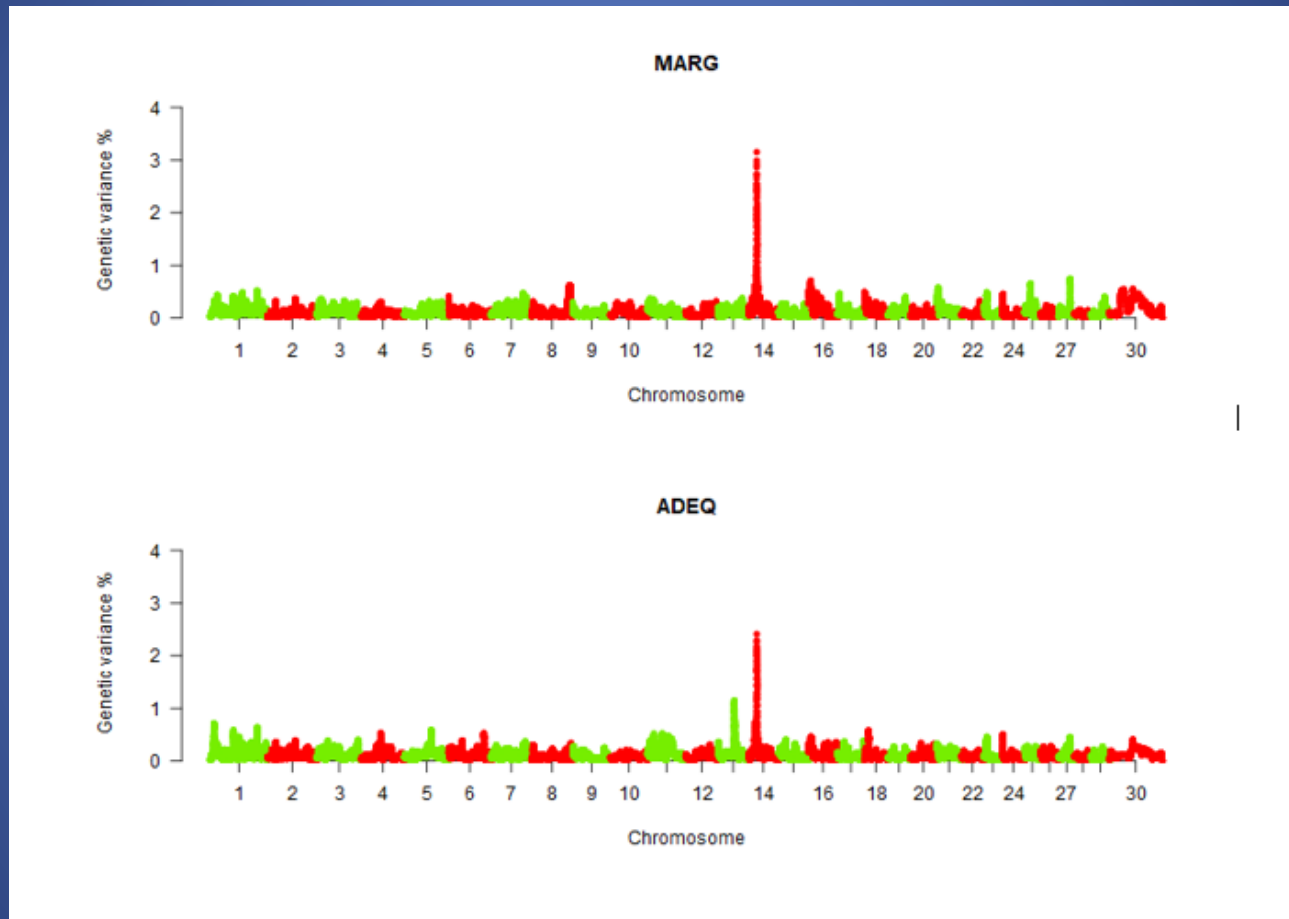
Estimated maternal genomic breeding values for 10 random animals for birthweight (BW), weaning weight (WW) and yearling weight (YW) in different environments using a multi-trait model.

Results

Correlation of SNP effects of maternal genetic effect between environments MARG and ADEQ

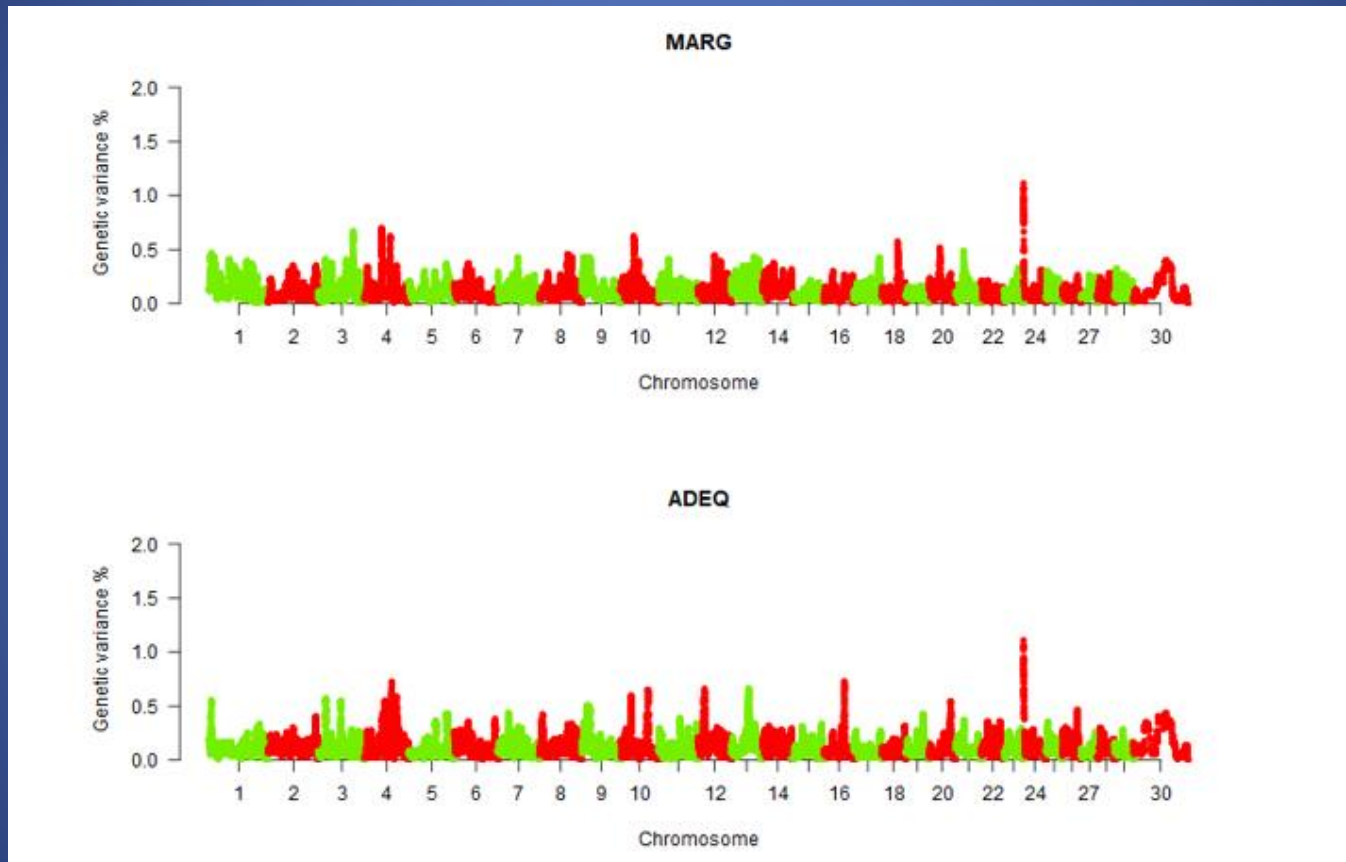
Number of SNP	BW	WW	YW
Top 10	0.84	0.82	0.93
Top 100	0.87	0.84	0.94
Top 1000	0.92	0.90	0.97
All SNP	0.98	0.97	0.98

Results



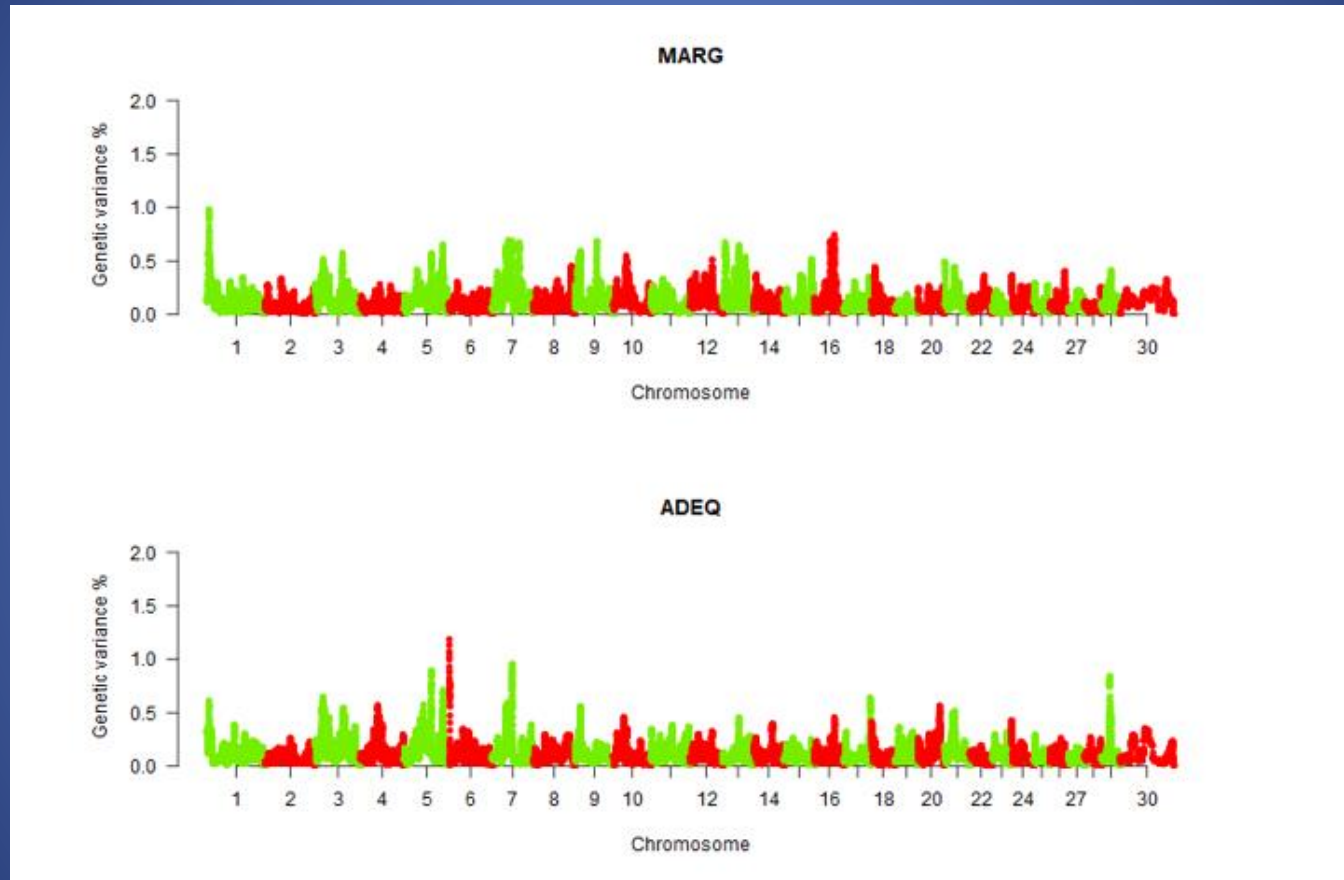
Manhattan plot for maternal effect for birth weight (BW) in ADEQ and MARG environments

Results



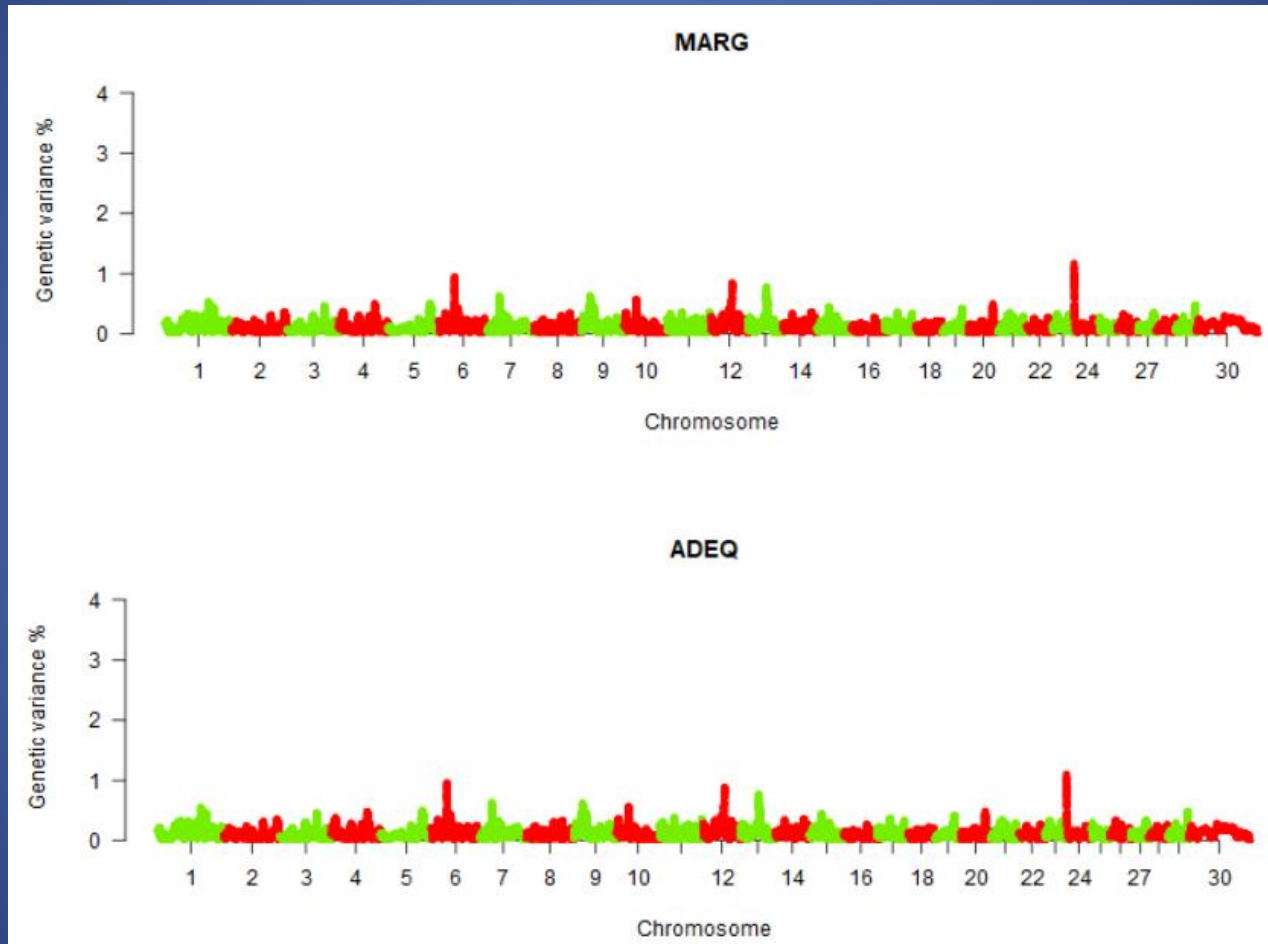
Manhattan plot for maternal effect for weaning weight (WW) in ADEQ and MARG environments

Results



Manhattan plot for maternal effect for yearling weight (YW) in ADEQ and MARG environments

Results



Manhattan plot for direct genetic effect for weaning weight (WW) in ADEQ and MARG environments

Conclusions

- Maternal genetic correlations between the two prenatal environments were lower than 0.8 especially for BW and WW indicating G x E interaction effect
- SNP marker effects are not consistent across environments
- G x E should be taken into consideration when selecting animals raised in different environments

THANK YOU