Genomic prediction and genome-wide association study (GWAS) for fat depth and muscle depth in commercial crossbred Piétrain pigs

Marzieh Heidaritabar, Marco Bink, Abe Huisman, Patrick Charagu, Marcos Lopes, Graham Plastow

University of Alberta

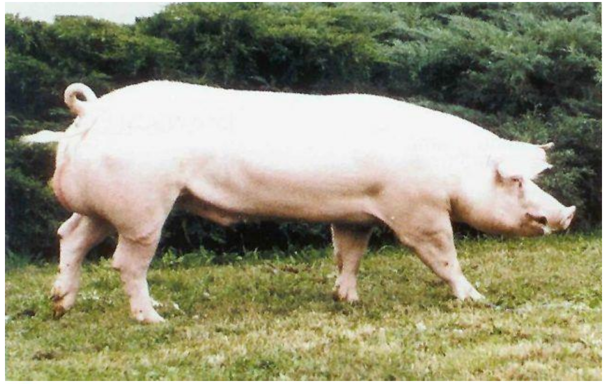
EAAP August 2019

Introduction

- Piétrain pigs originate from Belgium

- Exceptional for muscularity and leanness
- Usable lean:

    - ~ 67% in Piétrain compared to ~ 63% in Belgian Landrace



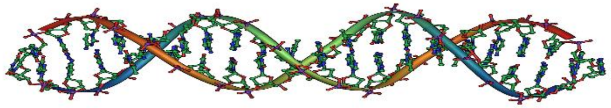
- Fresh meat sold in Belgium

Introduction

- Fat depth (**FD**) and muscle depth (**MD**):

  - Economically important traits

  - Good indicators of carcass lean content, one of the main breeding objectives in pig breeding programs

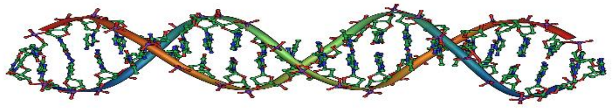


Objectives

- Estimate additive and dominance genetic variance components for **FD** and **MD**

- Quantify gains in accuracy of genomic prediction models:
  - Additive and dominance effects (**MAD**)
  - Only additive effects (**MA**)

- Detect genomic regions associated with **FD** and **MD**
  - Investigate importance of additive and dominance effects



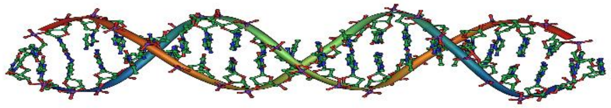
Data

- **Genotypic (50K) and phenotypic data**: 1849 commercial crossbred Piétrain pigs (**Hendrix Genetics**)

- **44025 SNPs** after Quality control
- **Genotype imputation**: FImpute

- **Adjusted FD**: sex (fixed, 2 levels), litter (random)

- **Adjusted MD**: birthyear-month (fixed, 28 levels), sex (fixed, 2 levels), litter (random)



Statistical methods - prediction

- GBLUP (ASReml V4)

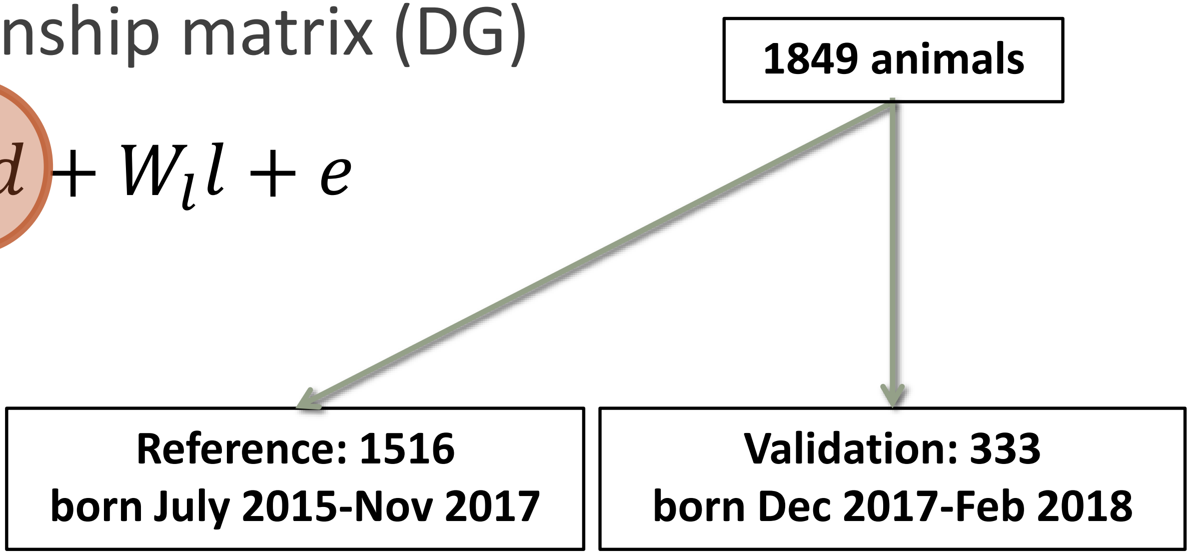
  - MA: additive genomic relationship matrix (G)

$$y = 1\mu + Xb + Z_g g + W_l l + e$$

  - MAD: dominance genomic relationship matrix (DG)

$$y = 1\mu + Xb + Z_g g + Z_d d + W_l l + e$$

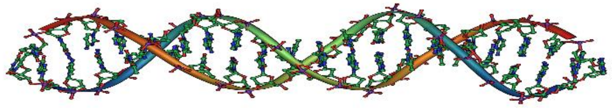
$$\boldsymbol{Accuracy} = r_{BV,Phen}$$



1849 animals

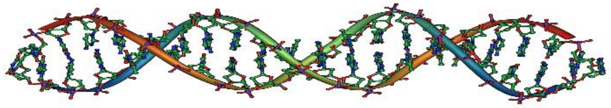
Reference: 1516
born July 2015-Nov 2017

Validation: 333
born Dec 2017-Feb 2018



Variance component estimation

Trait	Model	Method					
		GBLUP					
		σ_a^2 (SE)	σ_d^2 (SE)	σ_l^2 (SE)	σ_e^2 (SE)	h_a^2 (SE)	h_d^2 (SE)
FD	MA	1.51 (0.19)	-	0.36 (0.09)	1.34 (0.10)	0.47 (0.05)	-
	MAD	1.52 (0.19)	0.00 (0.17)	0.38 (0.09)	1.42 (0.15)	0.48 (0.05)	0.00 (0.05)
MD	MA	10.64 (1.21)	-	0.91 (0.43)	6.89 (0.56)	0.58 (0.04)	-
	MAD	10.54 (1.23)	0.49 (0.99)	0.84 (0.46)	6.60 (0.81)	0.57 (0.05)	0.03 (0.05)



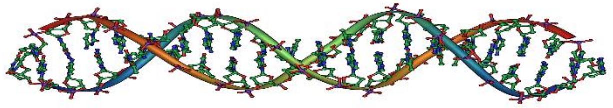
UNIVERSITY OF ALBERTA

Prediction accuracy and bias of predicted breeding values and total genetic values

Total genetic values (TGV) = Breeding value (a) + dominance deviation (d)

Trait	Model	Accuracy of BVs (SE)	Accuracy of TGVs (SE)	Regression BVs (SE)	Regression TGVs (SE)
		Method			
		GBLUP			
FD	MA	0.32 (0.05)	-	0.83 (0.14)	-
	MAD	0.32 (0.05)	0.32 (0.05)	0.82 (0.14)	0.83 (0.14)
MD	MA	0.32 (0.05)	-	0.83 (0.14)	-
	MAD	0.32 (0.05)	0.32 (0.05)	0.82 (0.14)	0.83 (0.14)

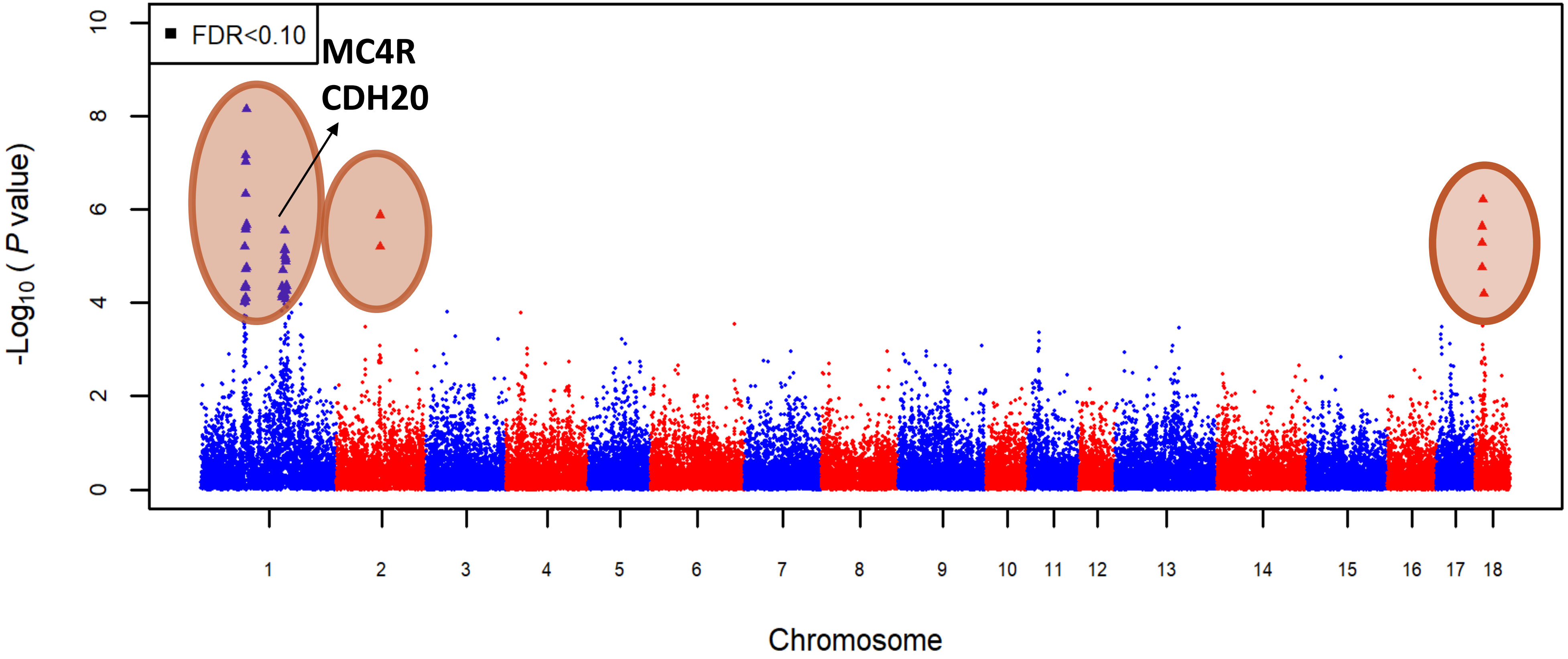
No improvement in prediction accuracy with dominance model

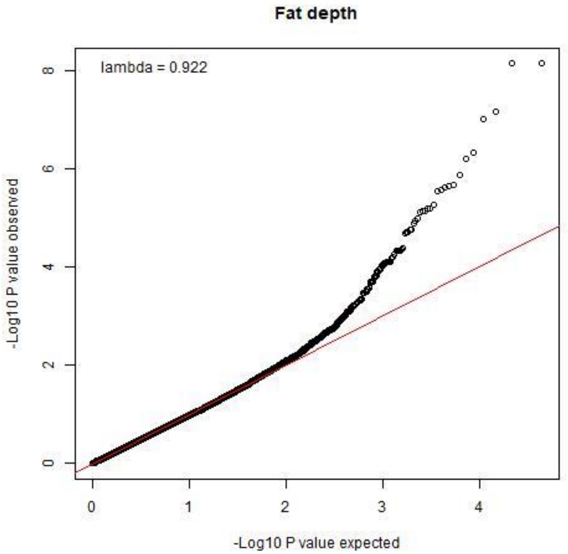


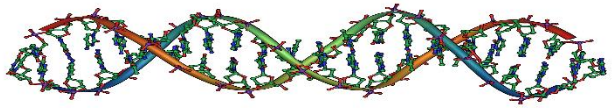
GWAS for additive and dominance effects – FD

single marker association analysis

Phenotype = Mean + Sex + Litter + SNP + Animal + e

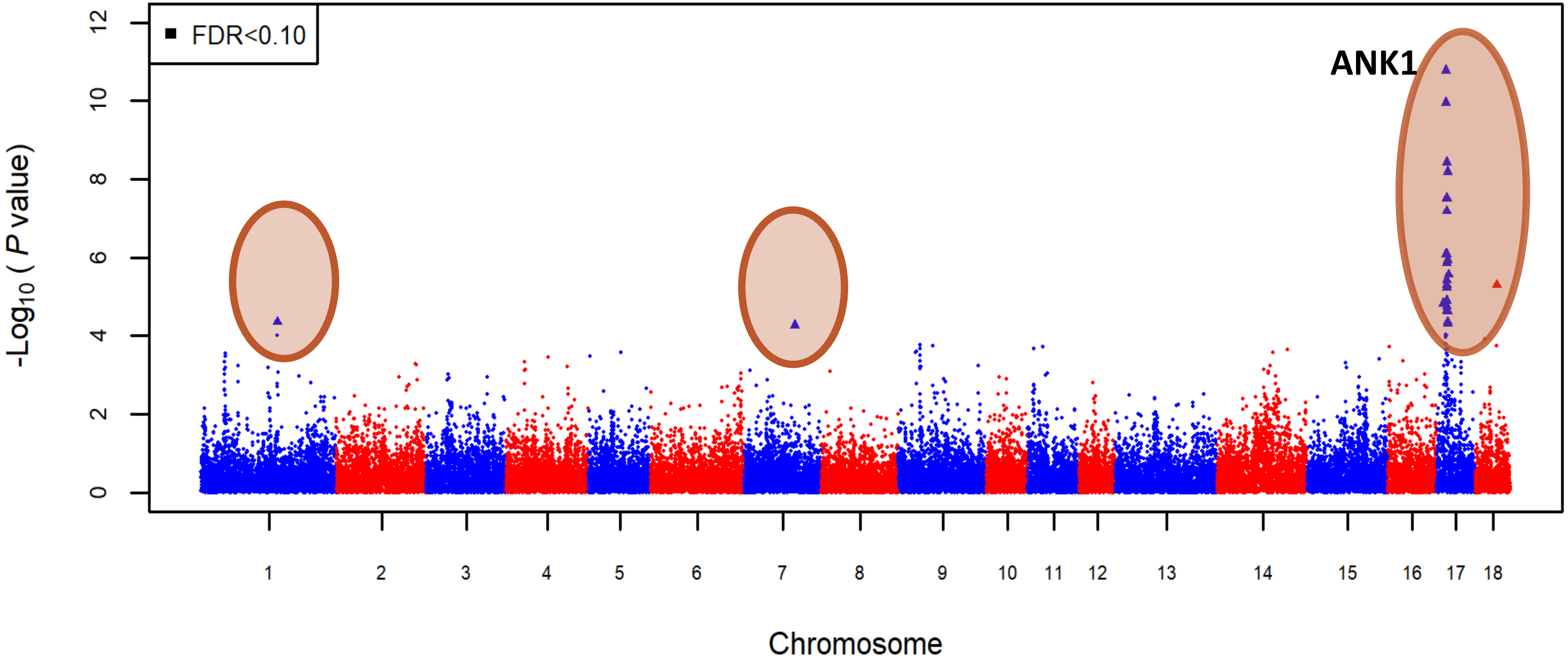


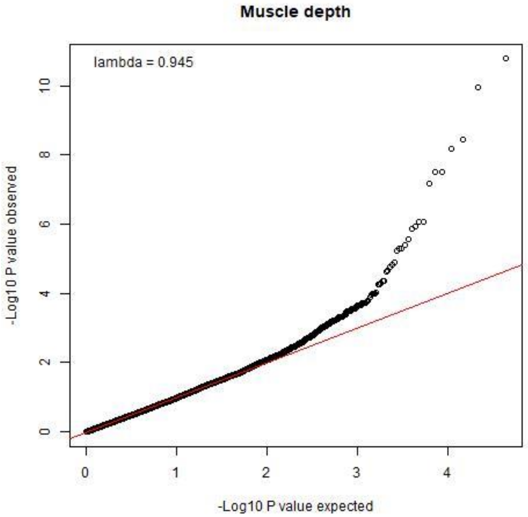




GWAS for additive and dominance effects – MD

single marker association analysis

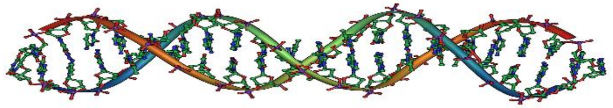




Additive and dominance effects at QTL regions - FD

Fat depth

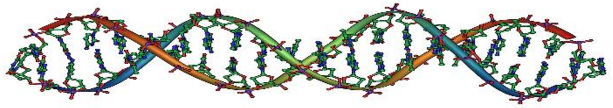
Chr	Position (Mbp)	Minor genotype frequency	Minor allele frequency	-Log10-Pvalue	a	d	SNP variance (a)	SNP variance (d)
1	57.24	0.16	0.41	8.15	0.16	0.02*	0.43	0.002
1	154.79	0.11	0.40	5.55	0.15	-0.06*	0.39	0.02
2	88	0.06	0.32	5.87	0.23*	-0.16*	0.40	0.17
18	10.76	0.29	0.46	6.21	0.13*	0.08*	0.28	0.06
Total							**1.50**	**0.25**



Additive and dominance effects at QTL regions - MD

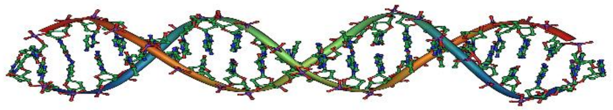
Muscle depth

Chr	Position (Mbp)	Minor genotype frequency	Minor allele frequency	-Log10-Pvalue	a	d	SNP variance (a)	SNP variance (d)
1	134.59	0.08	0.47	4.36	0.24*	0.51*	0.19	0.34
17	14.73	0.03	0.41	10.78	0.76	0.21*	1.31	0.05
Total							**1.50**	**0.39**



Conclusions

- Fitting dominance effects did not impact accuracy of genomic prediction
- Several associated regions are located in or near relevant candidate genes
- Dominance effects may play a role in genetic architecture of **FD** and **MD**



UNIVERSITY OF ALBERTA

Acknowledgment

livestock gentec

HENDRIX GENETICS

Hypor
A Hendrix Genetics Company