ECO-FCE: Integrative genomic models for FCE in monogastrics

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outline

From sequence … *…to consequence*

- **Selective Breeding**
- Models
- Simulation study
- Real data

The ECO-FCE project is funded by the European Union Seventh Frame Programme (FP7 2007/2013) under grant agreement No. 311794.

Selective breeding

Fro… …equence

Phenotypic variation in the population

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Selective breeding

...to consequence

Heritability

Some of this variation is heritable:
Related individuals have more similar phenotypes than unrelated individuals

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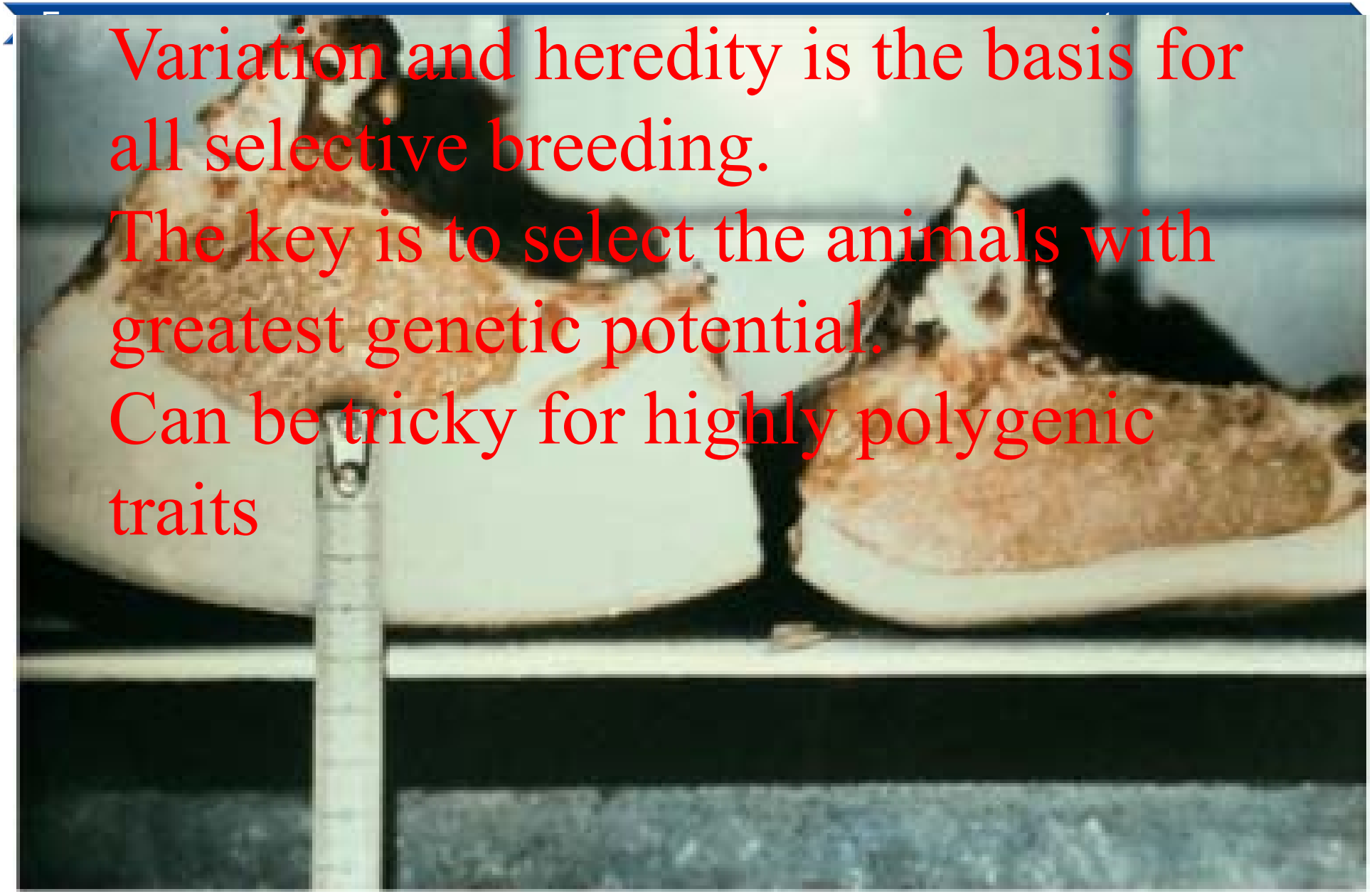

Variation and heredity is the basis for all selective breeding.

The key is to select the animals with greatest genetic potential.

Can be tricky for highly polygenic traits

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BLUP model

From sequence ... ...to consequence

$$\mathbf{y} = \mu + \mathbf{Z}_a\mathbf{a} + \mathbf{e}$$

Breeding values

Genetic relationship

$$\mathbf{a} \sim N(0, \mathbf{A}\sigma_a^2)$$

$$\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$$

Additive genetic variance

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BLUP model

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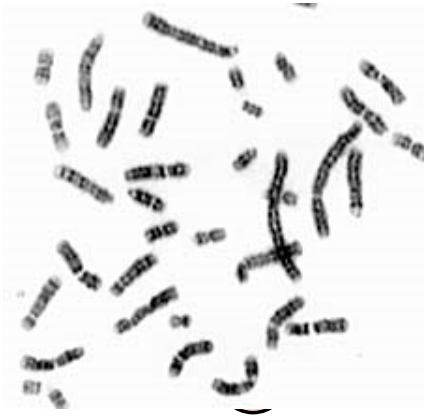

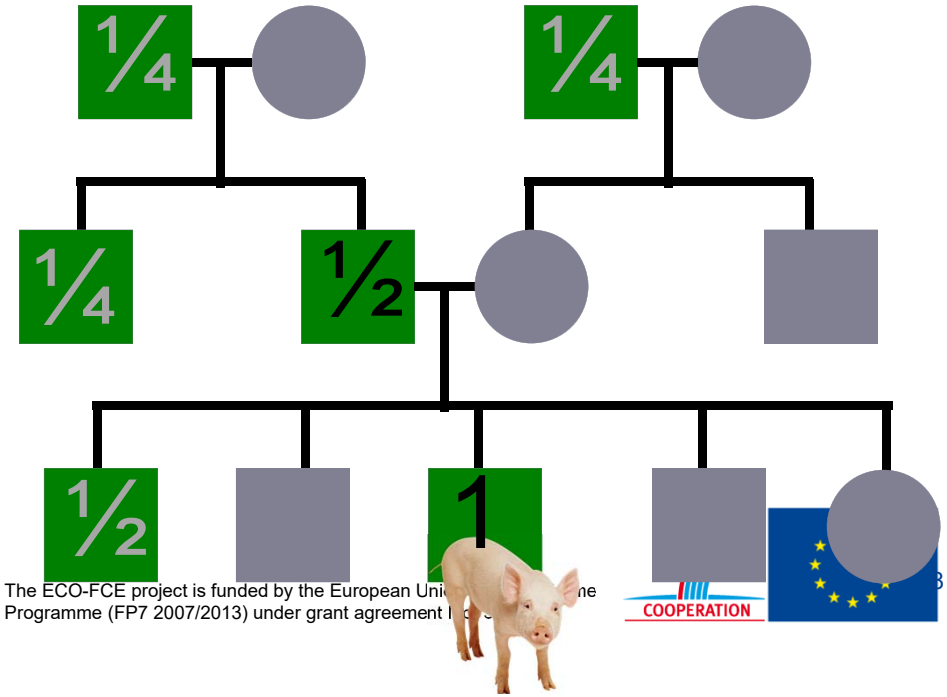

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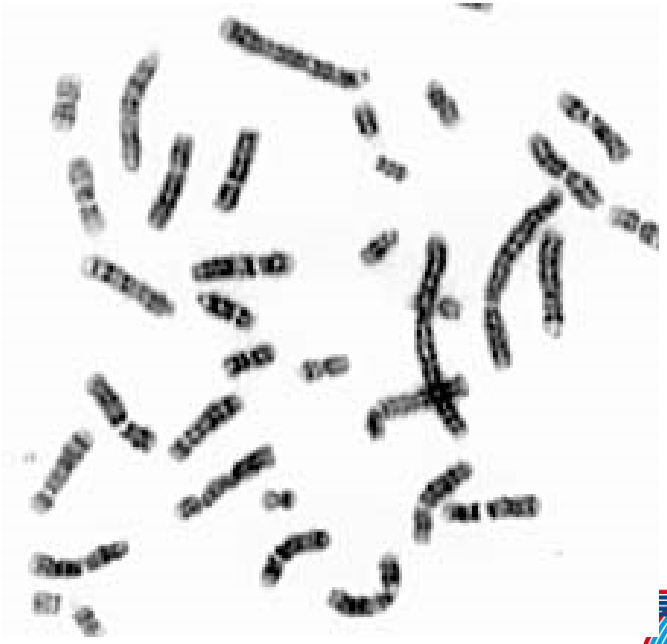
GBLUP model

From sequence ... ...to consequence

$$\mathbf{y} = \mu + \mathbf{Z}_g\mathbf{g} + \mathbf{e}$$

Genomic breeding value Genomic relationship

$$\mathbf{g} \sim N\left(0, \mathbf{G}\sigma_g^2\right)$$
$$\mathbf{e} \sim N\left(0, \mathbf{I}\sigma_e^2\right)$$



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GBLUP model

From sequence ... ...to consequence

$$\mathbf{y} = \mu + \mathbf{Z}_g\mathbf{g} + \mathbf{e}$$

$$\mathbf{g} \sim N\left(0, \mathbf{G}\sigma_g^2\right)$$
$$\mathbf{e} \sim N\left(0, \mathbf{I}\sigma_e^2\right)$$

All markers are from the same distribution - have same chance of being informative

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GBLUP model

From sequence ... ...to consequence

$$\mathbf{y} = \mu + \mathbf{Z}_g\mathbf{g} + \mathbf{e}$$

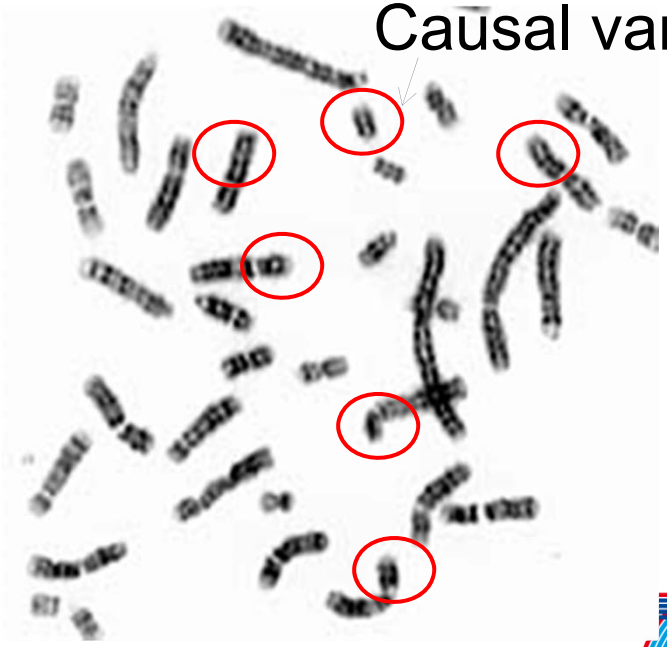
Genomic BV

Genomic relationship

$$\mathbf{g} \sim N(0, \mathbf{G}\sigma_g^2)$$

$$\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$$

Causal variation



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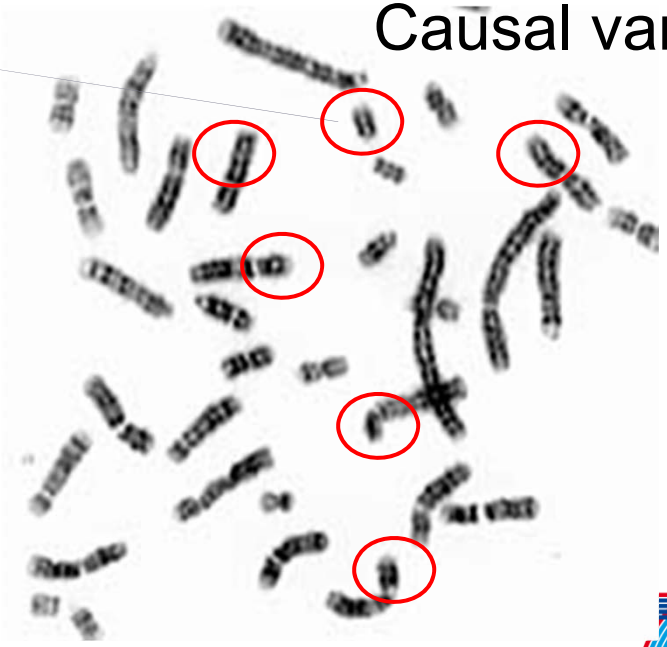
GFBLUP model

From sequence ... ...to consequence

$$\mathbf{y} = \mu + \mathbf{Z}_f\mathbf{f} + \mathbf{Z}_r\mathbf{r} + \mathbf{e}$$

$$\mathbf{f} \sim N\left(0, \mathbf{G}_f\sigma_f^2\right)$$
$$\mathbf{r} \sim N\left(0, \mathbf{G}_r\sigma_r^2\right)$$
$$\mathbf{e} \sim N\left(0, \mathbf{I}\sigma_e^2\right)$$

Causal variation



Some markers are more equal than others

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Simulation study

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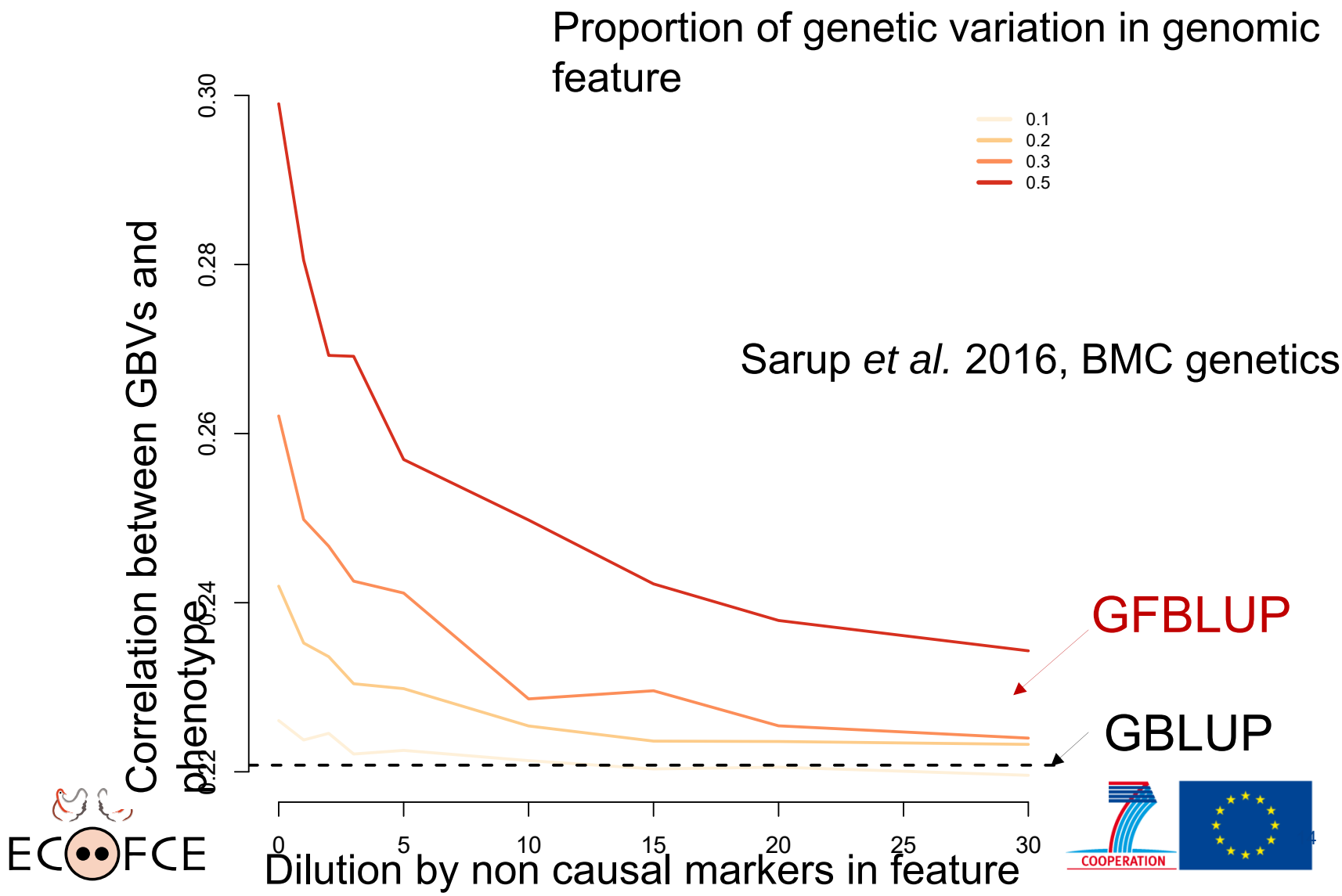

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Real data

From sequence ... ...to consequence

Genotypes for 2213 Hermitage MaxGro pigs from

~55K SNPs.

Corrected phenotypes for genotyped individuals

EBVs + residuals from BLUP on ~14K individuals

Total Feed Intake **TFI**

Residual Feed Intake **RFI**

50 random 10 fold validation sets.

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Defining genomic features

From sequence ... ...to consequence

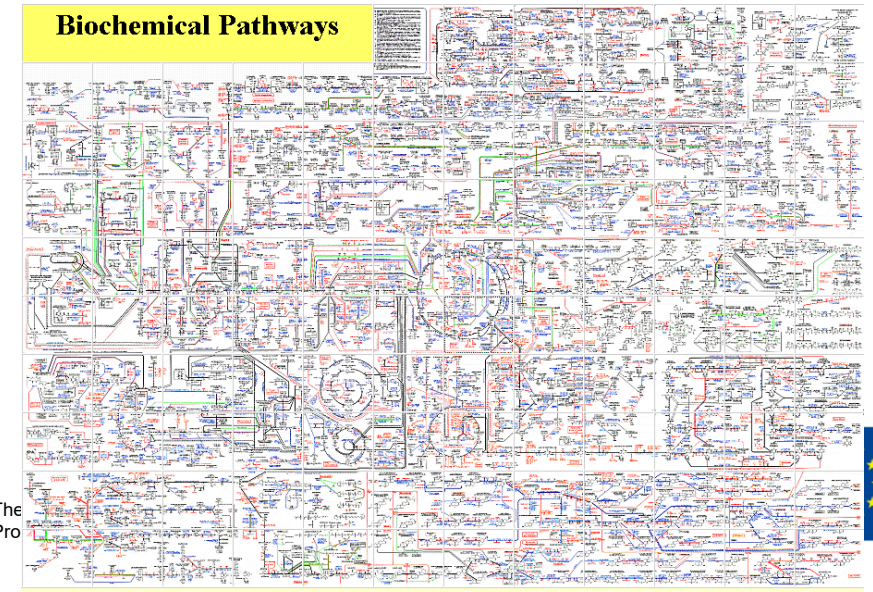
Get information from

The study population

- GWAS, **Gene expression**, proteomic, or metabolomic experiments

Literature/databases

- QTL database
- Gene Ontology
- Kegg pathways



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Defining genomic features

From sequence ... ...to consequence

Some of the SNPs was linked to genes that differ in gene expression between high RFI and low RFI pigs

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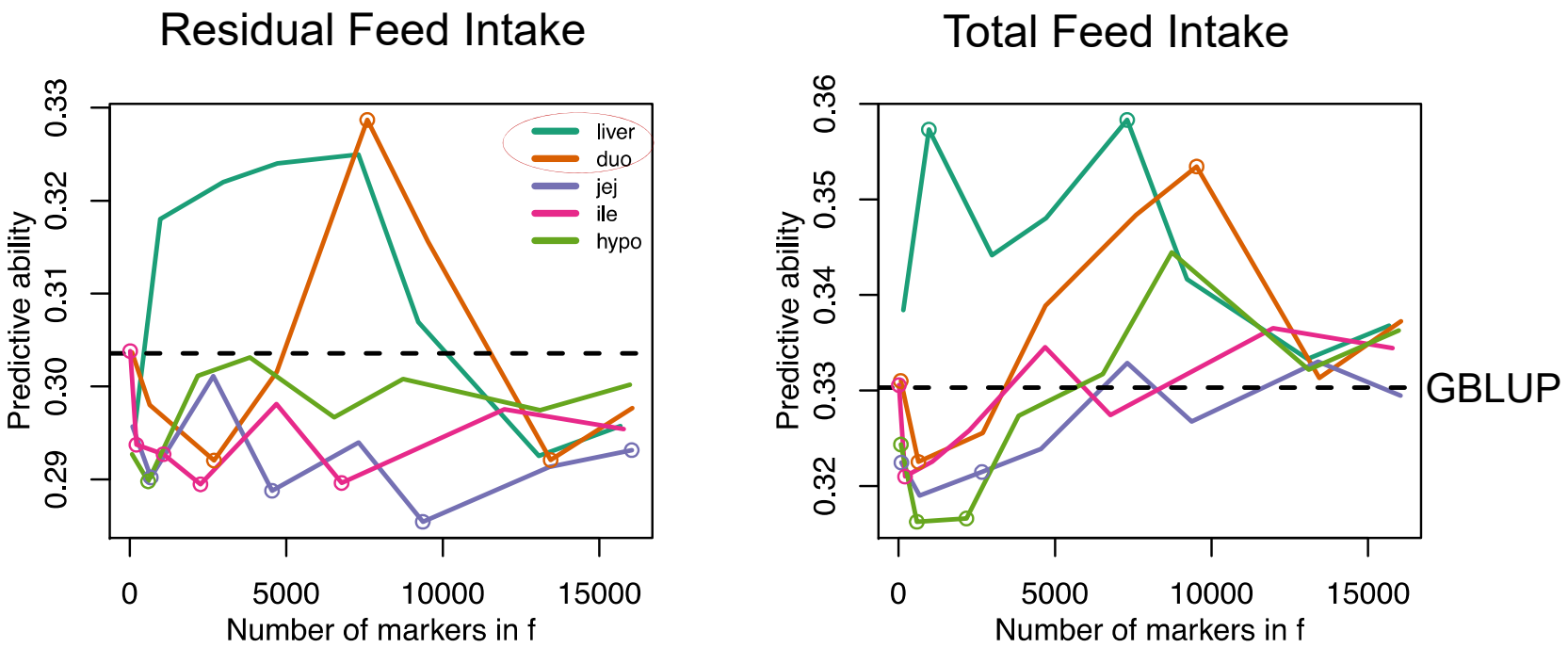
results

From sequence ... ...to consequence



p< 0.001

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Conclusions

From sequence ... ...to consequence

Prediction accuracies improved by ~10%.

Genes that are differential expressed in liver and duodenum most informative.

GFBLUP models can increase prediction ability and contribute knowledge on the biological background of complex traits

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Thank you for your attention

From sequence ... ...to consequence

Genotype and phenotype data provided by:

The Pig Breeding Company Hermitage Genetics

P. Varley

Danish Pig Research Centre

T. Ostersen

Gene expression experiments

K. Wimmers, H. Reyer

FBN

Model development and genomic prediction:

P. Sarup, J. Jensen, M. Shirali, P. Sørense

CENTER FOR QUANTITATIVE GENETICS AND GENOMICS QGG

More on models and analysis in session 55 Thursday 11.15 in Auditorium

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COOPERATION

Real data

From sequence ... ...to consequence

Modeling of the phenotype

EBVs + residuals for genotyped individuals from BLUP on 13572 Hermitage tested animals

$$TFI = CPG + SEX + LITTER + A + SBW + EBW + e$$

$$D110 = CPG + SEX + LITTER + A + e$$

$$LMP = CPG + SEX + LITTER + A + e$$

$$RFI = A_{TFI} - b_{D110} A_{D110} - b_{LMP} A_{LMP} + e_{TFI} - b_{D110} e_{D110} - b_{LMP} e_{LMP}$$

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