EFFICIENT & ECOLOGICALLY-FRIENDLY PIG AND POULTRY PRODUCTION.

ECOFCE

A WHOLE-SYSTEMS APPROACH TO OPTIMISING FEED EFFICIENCY AND REDUCING THE ECOLOGICAL FOOTPRINT OF MONOGASTRICS.

BASIC DATA

Funding:
EU-FP7
(€ 6 million)

Start date:
1 February 2013

Duration:
48 months
(2013 to 2017)

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement No. 311794.

Understanding the genetic architecture of feed efficiency traits in monogastrics

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement No. 311794.

Background – Feed efficiency (FE)

Contributions of ECO-FCE to breeding and producing pig and poultry

- improve energy use efficiency and reduce environmental footprint
- provide strategies to save resources and costs

Common measurement of FCE = feed conversion ratio (FCR)

- $\text{FCR} = \frac{\text{feed intake}}{\text{weight gain}}$
- breeding goal = low FCR (high efficiency)
- recording and measurement in routine is difficult and costly
- clarification of genetic background and development of molecular markers necessary

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Factors influencing feed efficiency

Extrinsic and intrinsic factors affecting FE

- Diet
- Management
- Climate
- Feeding behavior
- Digestion and absorption
- Energy expenditure
- Microbiota

→ genetic factors of diverse biological processes contribute to FE

Heritability of FCE related traits

- moderate heritability of FCR in poultry (0.41)[1] and pigs (≈0.3)[2]
- low to moderate heritability of weight gain, feed intake and feeding behaviour traits [3]

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[1] Aggrey et al. GSE (2010); [2] Gjerlaug-Enger et al. Animal (2011); [3]Chen et al. J Anim Breed Genet (2009)

Objectives

Characterisation of differences in the genetic profile of animals with good and poor FE

→ identify the genetic architecture of feed efficiency traits in pig and chicken

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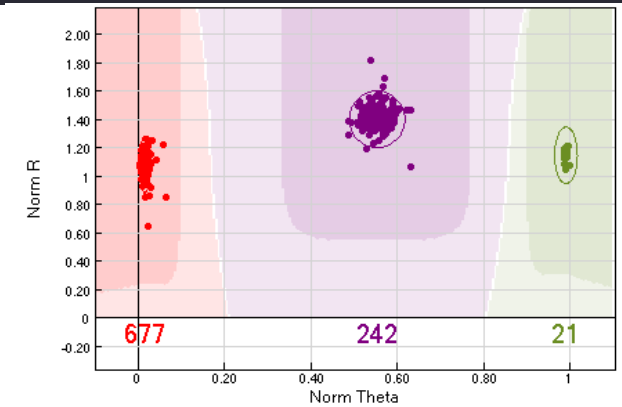
Genetics - Pipeline



- DNA extraction from blood samples
- Genotyping using Illumina SNP Beadchips
- Genotype calling using Genomestudio (call frequency ≥ 0.95)
- Imputation of missing genotypes using fastPHASE[1]
- Single-marker GWAS using JMP Genomics
- Multi-marker GWAS using GenSel (Bayes B)[2]
  - + contribution of 1Mb consecutive windows to genetic variance
- Integration of single- and multi-marker analyses to identify QTL regions and select candidate genes

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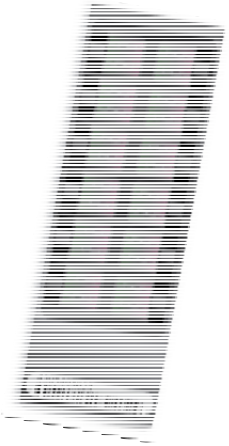
[1] Scheet and Stephens Am J Hum Genet (2006) [2] Fernando and Garrick GenSel (2009)

Genetics of FE traits in broiler

Material – Birds (Cobb-Vantress)

- 5000 birds of the commercial Cobb broiler line A
  → heaviest 1000 birds FE tested between days 39-46
- 859 genotyped broilers (60K SNP chip[1])
- Traits: body weight, feed intake, weight gain, FCR



Heritability

- Broiler line already under selection for ADG and FCR for generations
- Above mentioned preselection based on weight

→ Low heritability of FE and body weight traits (~0.03-0.1)

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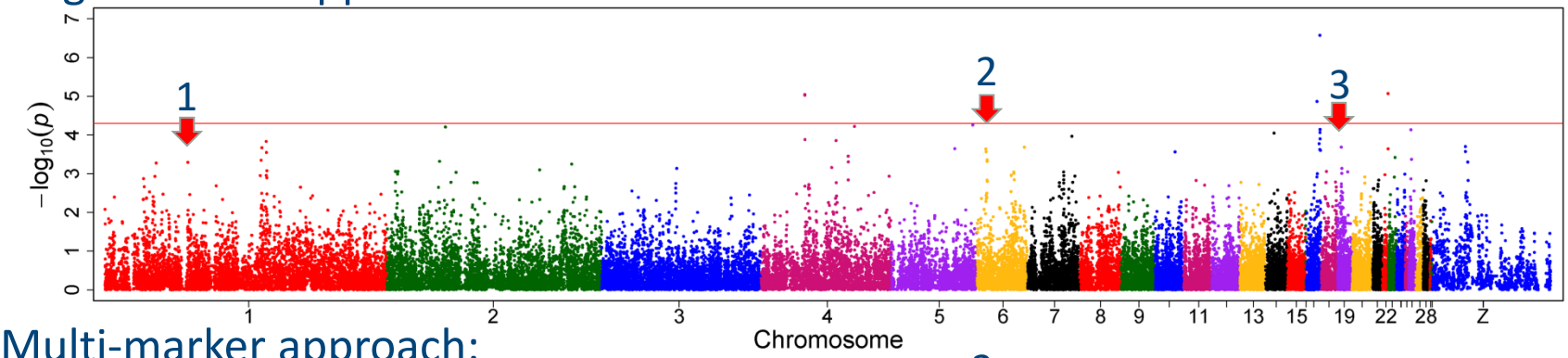
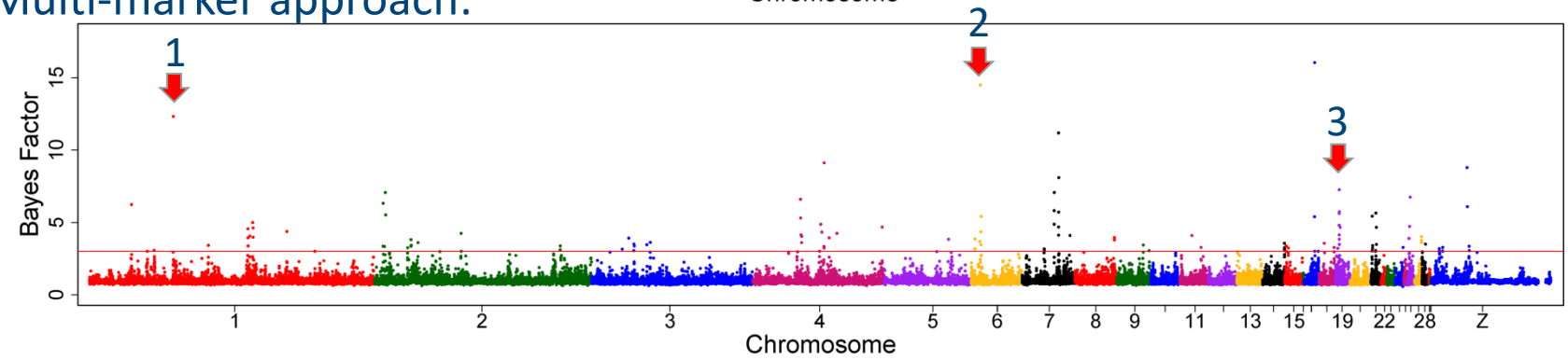
[1] *Groenen et al. BMC GENOMICS (2011)*

Chicken – feed conversion ratio

Single-marker approach:



Multi-marker approach:



	1Mb genetic window				Top SNP in Bayesian GWAS				
	Chr	Start (Mb)	End (Mb)	explained $V_{genetic}$ (%)	SNP	Gga4 position	Bayes factor	p-value	Candidate genes
1	1	57.0	58.0	0.54	GGaluGA019865	57431192	12.32	3.29	***AGK***
2	6	6.0	7.0	0.95	rs14568465	6164912	14.50	3.57	*Sirt1*
3	19	2.0	3.0	0.87	rs14117856	2657299	7.26	2.66	***GTF2I***

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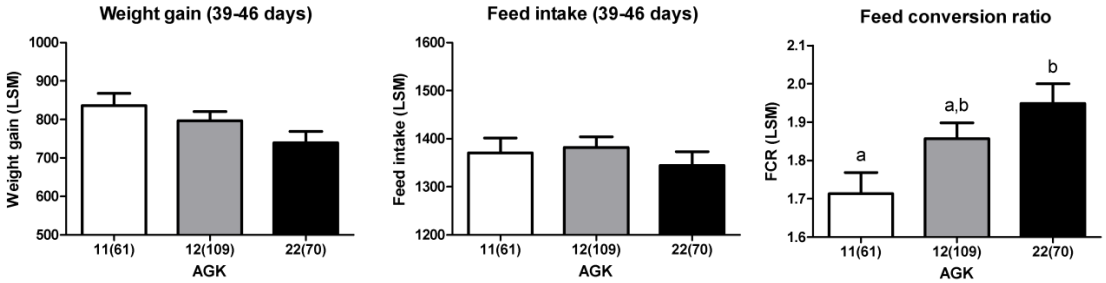
Validation of candidates

➢ Acylglycerol Kinase (*AGK*)

- Involved in biosynthesis of signaling lipids
- Associated with mitochondrial disorders in humans

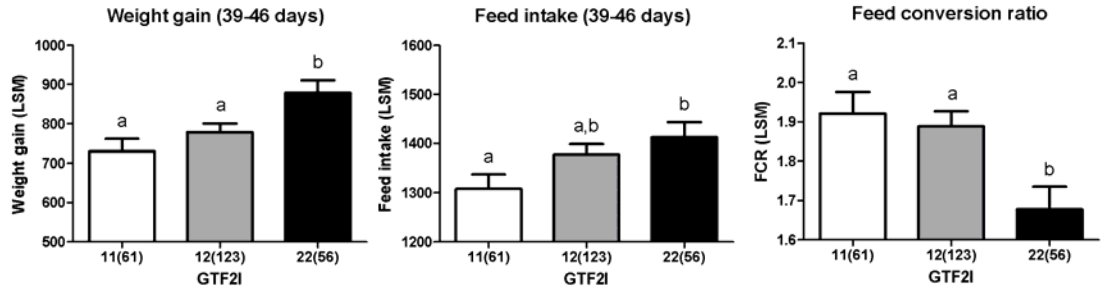
Tagging SNP
AGK c.1166G>A (p.R389H):



➢ General Transcription Factor IIi (*GTF2I*)

- Involved in regulation of growth factor signaling
- Genomic region affected by chromosomal rearrangements in humans

Tagging SNP
GTF2I c.2011A>C (p.K671Q):



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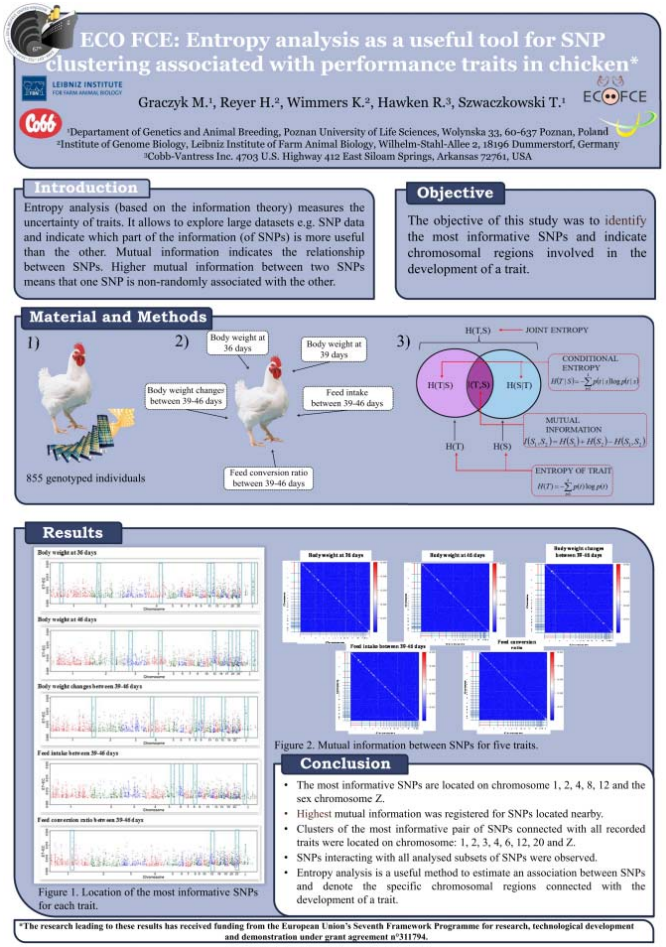
Entropy analysis – Location of the most informative SNPs

Overview of entropy analysis in chickens presented by M. Graczyk (Poster session):



ECO FCE: Entropy analysis as a useful tool for SNP clustering associated with performance traits in chicken*

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[2]Institute of Genome Biology, Leibniz Institute of Farm Animal Biology, Wilhelm-Stahl-Allee 2, 18196 Dummerstorf, Germany
[3]Cobb-Vantress Inc. 4703 U.S. Highway 412 East Siloam Springs, Arkansas 72761, USA

Introduction

Entropy analysis (based on the information theory) measures the uncertainty of traits. It allows to explore large datasets e.g. SNP data and indicate which part of the information (of SNPs) is more useful than the other. Mutual information indicates the relationship between SNPs. Higher mutual information between two SNPs means that one SNP is non-randomly associated with the other.

Objective

The objective of this study was to identify the most informative SNPs and indicate chromosomal regions involved in the development of a trait.

Material and Methods

1) 855 genotyped individuals

2) Body weight at 36 days; Body weight at 39 days; Body weight changes between 39-46 days; Feed intake between 39-46 days; Feed conversion ratio between 39-46 days

3) H(T,S) JOINT ENTROPY; CONDITIONAL ENTROPY; MUTUAL INFORMATION; ENTROPY OF TRAIT; H(T); H(S); H(T|S); H(S|T)

Results

Figure 1. Location of the most informative SNPs for each trait.

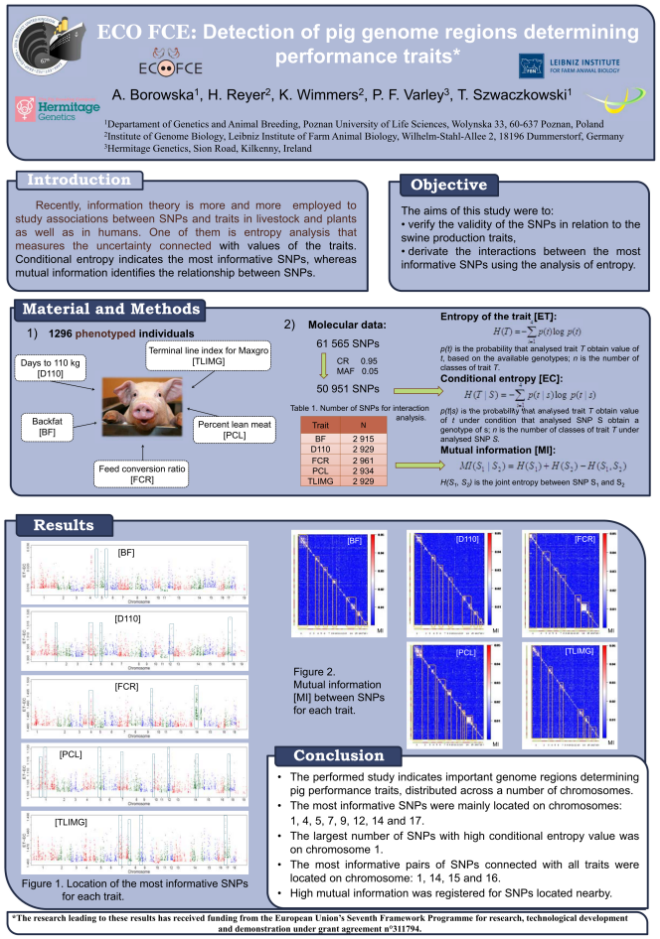
Figure 2. Mutual information between SNPs for five traits.

Conclusion

- The most informative SNPs are located on chromosome 1, 2, 4, 8, 12 and the sex chromosome Z.
- Highest mutual information was registered for SNPs located nearby.
- Clusters of the most informative pair of SNPs connected with all recorded traits were located on chromosome: 1, 2, 3, 4, 6, 12, 20 and Z.
- SNPs interacting with all analysed subsets of SNPs were observed.
- Entropy analysis is a useful method to estimate an association between SNPs and denote the specific chromosomal regions connected with the development of a trait.

*The research leading to these results has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement n°311794.

Overview of entropy analysis in pigs presented by A. Borowska (Poster session):



ECO FCE: Detection of pig genome regions determining performance traits*

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[1]Departament of Genetics and Animal Breeding, Poznan University of Life Sciences, Wolynska 33, 60-637 Poznan, Poland
[2]Institute of Genome Biology, Leibniz Institute of Farm Animal Biology, Wilhelm-Stahl-Allee 2, 18196 Dummerstorf, Germany
[3]Hermitage Genetics, Sion Road, Kilkenny, Ireland

Introduction

Recently, information theory is more and more employed to study associations between SNPs and traits in livestock and plants as well as in humans. One of them is entropy analysis that measures the uncertainty connected with values of the traits. Conditional entropy indicates the most informative SNPs, whereas mutual information identifies the relationship between SNPs.

Objective

The aims of this study were to:
- verify the validity of the SNPs in relation to the swine production traits,
- derivate the interactions between the most informative SNPs using the analysis of entropy.

Material and Methods

1) 1296 phenotyped individuals

Days to 110 kg [D110]; Terminal line index for Maxgro [TLIMG]; Backfat [BF]; Percent lean meat [PCL]; Feed conversion ratio [FCR]

2) Molecular data:

61 565 SNPs → CR 0.95, MAF 0.05 → 50 951 SNPs

Table 1. Number of SNPs for interaction analysis.

Trait	N
BF	2 915
D110	2 929
FCR	2 961
PCL	2 934
TLIMG	2 929

Entropy of the trait [ET]: $H(T) = -\sum_{t} p(t) \log p(t)$

$p(t)$ is the probability that analysed trait T obtain value of t, based on the available genotypes; n is the number of classes of trait T.

Conditional entropy [EC]: $H(T \mid S) = -\sum_{t} \sum_{s} p(t \mid s) \log p(t \mid s)$

$p(t|s)$ is the probability that analysed trait T obtain value of t under condition that analysed SNP S obtain a genotype of s; n is the number of classes of trait T under analysed SNP S.

Mutual information [MI]: $MI(S_1 \mid S_2) = H(S_1) + H(S_2) - H(S_1, S_2)$

$H(S_1, S_2)$ is the joint entropy between SNP S_1 and S_2

Results

Figure 1. Location of the most informative SNPs for each trait.

Figure 2. Mutual information [MI] between SNPs for each trait.

Conclusion

- The performed study indicates important genome regions determining pig performance traits, distributed across a number of chromosomes.
- The most informative SNPs were mainly located on chromosomes: 1, 4, 5, 7, 9, 12, 14 and 17.
- The largest number of SNPs with high conditional entropy value was on chromosome 1.
- The most informative pairs of SNPs connected with all traits were located on chromosome: 1, 14, 15 and 16.
- High mutual information was registered for SNPs located nearby.

*The research leading to these results has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement n°311794.

Genetics of FE traits in pigs

Material – Pigs (Hermitage Genetics)

- Hylean Maxgro terminal sire line
- Sampled between 2006-2015
- FE tested during grower-finisher phase
- 1296 genotyped boars (60K SNP chip)
- Traits: Breeding values, FCR, carcass composition, feeding behaviour

Heritability

- Moderate heritability of carcass composition traits (0.39-0.42) and FE/feeding behaviour traits (0.30-0.40)

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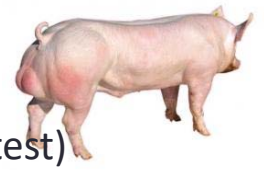
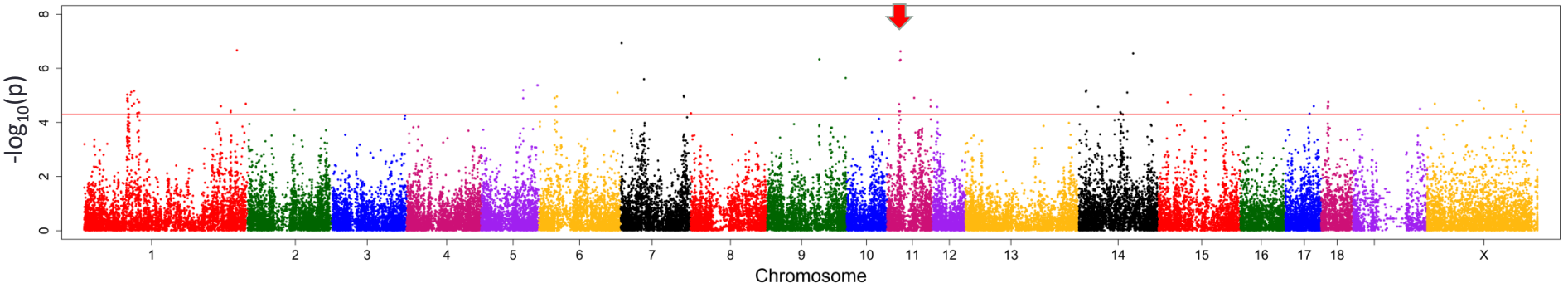
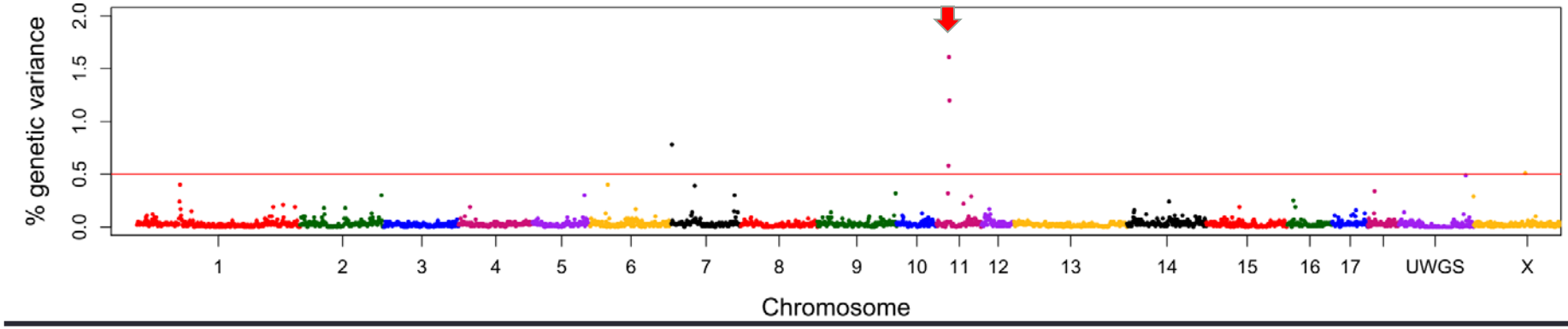
Pig – feed conversion ratio



Single-marker regression model (random effects: pedigree, covariate: average age on test)



Bayesian multi-marker model – contribution of 1Mb windows to the genetic variance



Chromosome	Range (Mb)	% Var	Top SNP (Bayesian)	Position	Bayes Factor	-log$_{10}$ (p-value)	candidate gene
11	24-25	1.61	ASGA0050399	24616066	22.73	4.43	*ENOX1*, ***DnaJC15***
11	25-26	1.2	H3GA0031666	25685231	13.90	3.76	

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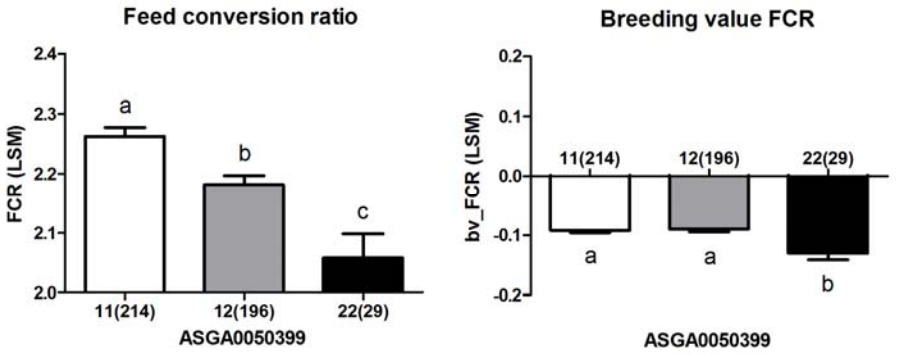
Porcine candidate genes for feed efficiency

➢ *DnaJC15*

- Negative regulator of mitochondrial respiratory chain
- Restricts ATP-generation

Association of *DnaJC15* SNP:



➢ other candidate genes for FE:

- *AQP4* - regulates body water balance and mediates water flow (for FCR)
- *PFKFB4* - involved in synthesis and degradation of fructose 2,6-bisphosphate (regulation of glycolysis) (for daily feed intake)
- *PPP3CA* - regulates bone formation and osteoblast differentiation (for daily feeding rate)

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Overview of QTL regions

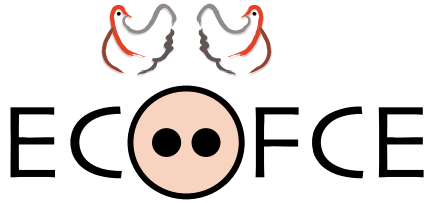
Chicken

Trait	Identified QTL regions
FCR	10
Feed intake	6
Weight gain	2
Body weight (36days)	5
Body weight (46days)	4

Pigs

Trait	Identified QTL regions
FCR	12
Back fat	12
Percent lean	8
Days to 110 kg	11
Daily feed intake	10
Daily occupation time	9
Consumption rate	8
Daily feeder visits	5
Bv days to 110 kg	7
Bv FCR	16

→ resource for the development of informative biomarkers for FE traits



Thank you for your attention!

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