New genomic regions for litter size and its variation in pigs

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EAAP, Warsaw 2015

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Genetic architecture of variation

Quantitative trait loci (QTL) ➔ control level of traits

Variation of traits has also genetic component
➔ heterogeneity of residual variance
➔ vQTL detected in plants, animals and human

Yet no genomic regions for variation of traits in pigs
➔ no success in study on backfat (Yang *et al.* 2011)

Litter size in pigs

Economically important trait

- High number of slaughter pigs per sow per year
  - Closely linked to birth weight

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Optimum litter size

- Lower mortality of piglets
- Easier management

Genetics of litter size variation

Studied by residual variance

- Applying double hierarchical GLM (DHGLM)

Residual variance has genetic component

- Rönnegård *et al.* 2010 and Felleki *et al.* 2012

No genomic regions reported for variation of litter size

Objective

To detect regions associated with
litter size (TNB) and its variation (varTNB)

Data overview

Phenotypes

- 69,549 Large White sows
- 264,419 TNB records
- At least 4 piglets in litter
- Average TNB 12.5 ± 3.2

Genotypes

- 2,389 sows and boars
- Genotyped with 60k SNP Beadchip

Data for genome-wide association (GWAS)

After all quality controls

- 40,969 SNPs
- 2,351 genotyped sows and boars used in GWAS for TNB
- 2,067 genotyped sows and boars used in GWAS for varTNB

Methods

DHGLM (following Felleki *et al.* 2012)

- Estimating breeding values (EBV) for TNB and varTNB

$$\begin{cases} \mathbf{TNB} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Upe} + \mathbf{e} \\ \mathbf{log(var(e))} = \mathbf{Xb_v} + \mathbf{Za_v} + \mathbf{Upe_v} + \mathbf{e_v} \end{cases}$$

Methods

DHGLM ➔ EBV for TNB and varTNB

Deregressed EBV (following Garrick *et al.* 2009)

- Optimising use of data

Methods

DHGLM ➔ EBV for TNB and varTNB

Deregressed EBV ➔ optimal use of data

Multi-SNP GWAS ➔ Detecting associations

Bayesian Variable Selection Method

$y = \mu + X\beta + e \quad \beta \sim \begin{cases} N(0, \sigma^2_{g_0}) & \text{with probability: } \pi_0 \\ N(0, \sigma^2_{g_1}) & \text{with probability: } \pi_1 \end{cases}$

1 in 1,000 SNPs in distribution with large effect

Variance components

Estimate	TNB	varTNB
Additive genetic	1.18 (0.04)	0.030 (0.003)
Permanent sow	0.69 (0.02)	0.15 (0.004)
Heritability	0.14	
GCV_{SD}		0.087

Genetic correlations between random effects on TNB and varTNB

Correlation	DHGLM
Additive genetic	0.49 (0.04)
Permanent sow	-0.83 (0.02)

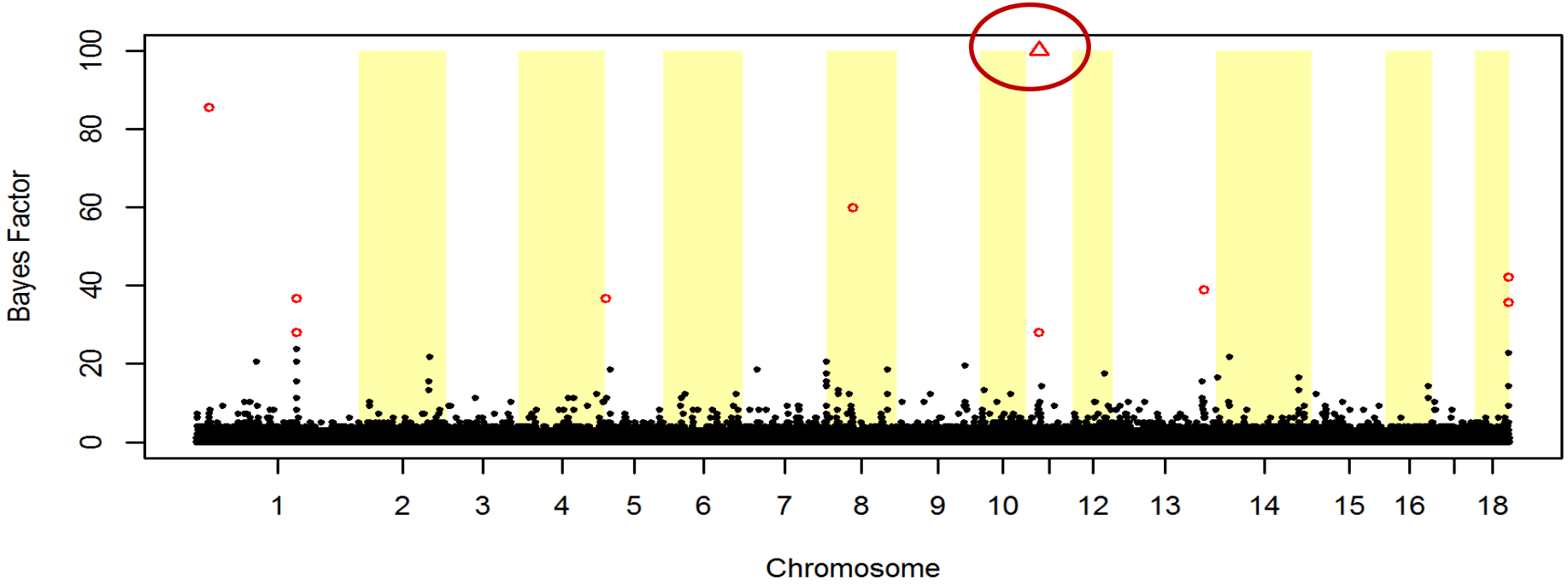
Genetically if TNB ↑ varTNB ↑

Non-genetic disturbances ↓ TNB and ↑ varTNB

Significant SNP for TNB

10 sig. SNPs

New regions on chromosome 11 (SSC11)



Candidate gene for TNB on SSC11

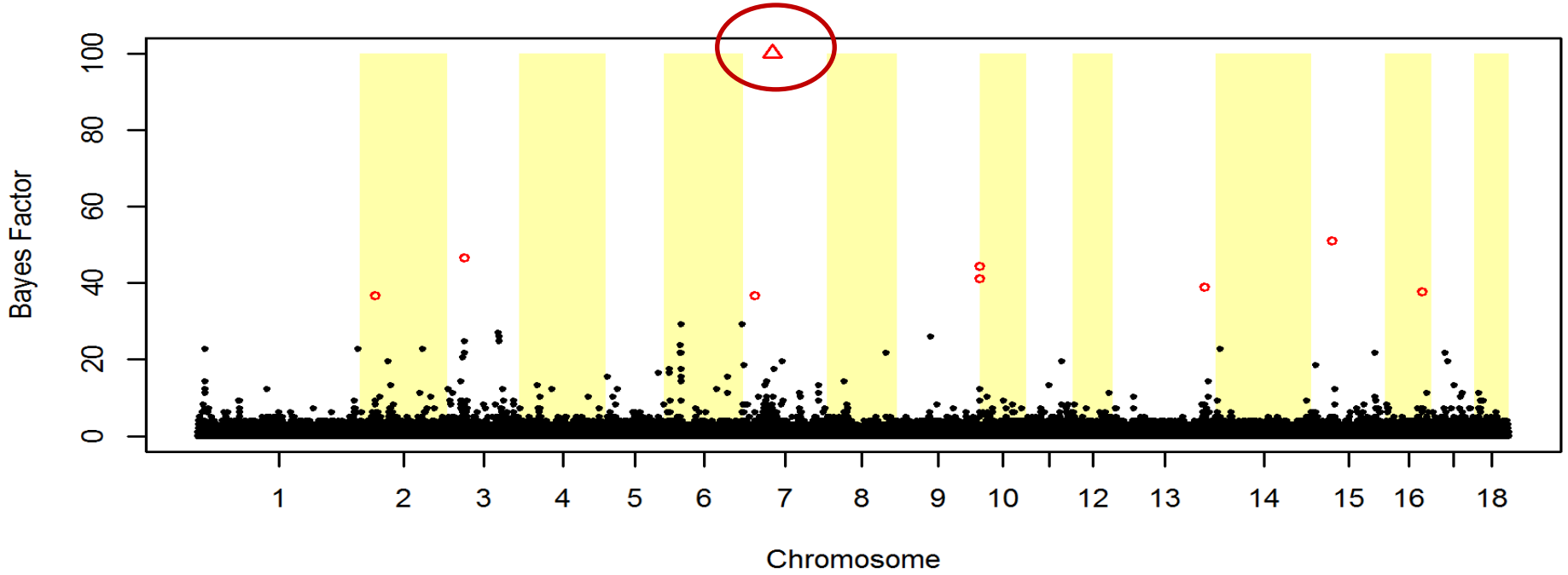
ENOX1 – protein coding gene from ecto-CNOX family

- part of electron transport pathways
- associated with mitochondrial membranes
- functions: cellular defense, growth, cell survival

Significant SNPs for varTNB

9 sig. SNPs

Most sig. SNP on chromosome 7 (SSC7)



Candidate genes for varTNB on SSC7

VEGFA – vascular endothelial growth factor

- activated in angiogenesis and vasculogenesis in fetus (and adult)

HSPCB (= *HSP90)* – from *Sus scrofa* heat shock family

- activated under stress condition (e.g. heat, hyperthermia, or inflammation)
- maintains proper folding of proteins

Conclusions

varTNB has a genetic component

Selection for ↑ TNB also ↑ varTNB

New SNPs for TNB detected on SSC11

- candidate gene ➔ *ENOX1*

First loci for varTNB in pigs, most significant on SSC7

- candidate genes ➔ *VEGFA* and *HSPCB*

Thank you for your attention!

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varTNB has genetic component

↑ TNB also ↑ varTNB

SSC7 most important for varTNB

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