New genomic regions for litter size and its variation in pigs

Ewa Sell-Kubiak

M. Lopes, N. Duijvesteijn, E.F. Knol, L. Janss, P. Bijma, H.A. Mulder
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Acknowledgments

www.nwo.nl

www.stw.nl

www.topigsnorsvin.com

www.breed4food.com
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
Litter size in pigs

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Variation

- Between sows and parities
- Problems with extremely large litters
Litter size in pigs

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Variation
- Between sows and parities
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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 $12.5 \pm 3.2$

### 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 \( \text{varTNB} \)

\[
\begin{align*}
\text{TNB} &= X_b + Z_a + U_p + e \\
\log(\text{var}(e)) &= X_{b_v} + Z_{a_v} + U_{p_v} + e_v
\end{align*}
\]
Methods

DHGLM $\rightarrow$ EBV for TNB and varTNB

Deregressed EBV (following Garrick et al. 2009)
  - Optimising use of data
Methods

DHGLM $\rightarrow$ EBV for TNB and varTNB
Deregressed EBV $\rightarrow$ optimal use of data

Multi-SNP GWAS $\rightarrow$ Detecting associations
Bayesian Variable Selection Method

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

1 in 1,000 SNPs in distribution with large effect
## Variance components

<table>
<thead>
<tr>
<th>Estimate</th>
<th>TNB</th>
<th>varTNB</th>
</tr>
</thead>
<tbody>
<tr>
<td>Additive genetic</td>
<td>1.18 (0.04)</td>
<td>0.030 (0.003)</td>
</tr>
<tr>
<td>Permanent sow</td>
<td>0.69 (0.02)</td>
<td>0.15 (0.004)</td>
</tr>
<tr>
<td>Heritability</td>
<td>0.14</td>
<td></td>
</tr>
<tr>
<td>$GCV_{SD}$</td>
<td></td>
<td>0.087</td>
</tr>
</tbody>
</table>
Genetic correlations between random effects on TNB and varTNB

<table>
<thead>
<tr>
<th>Correlation</th>
<th>DHGLM</th>
</tr>
</thead>
<tbody>
<tr>
<td>Additive genetic</td>
<td>0.49 (0.04)</td>
</tr>
<tr>
<td>Permanent sow</td>
<td>-0.83 (0.02)</td>
</tr>
</tbody>
</table>

Genetically if TNB \( \uparrow \) varTNB. Non-genetic disturbances \( \downarrow \) TNB and \( \uparrow \) 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!

ewa.sell.kubiak@gmail.com

varTNB has genetic component

↑ TNB also ↑ varTNB

SSC7 most important for varTNB