Genetic and genomic selection to reduce boar taint in Danish pigs

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Faculty of Health and Medical Sciences

Pig Research Centre

Dan Avi

Landdistriktører.dk

The Danish National Advanced Technology Foundation
Outline

- Introduction
- Performance testing in Denmark
- Genetic associations to production and reproductive traits in Landrace and Duroc
- Results from genome wide associations
- Summary
Introduction

- Stop surgical castration by 2018???

- animal welfare
- labour intensive, especially with the use of anesthesia
- consumer acceptance
**Skatole and indole:**
- Hindgut microbial metabolism
- Tryptophan is the substrate
- Fecal like odor

**Androstenone:**
- Produced in testis
- Concentrated and secreted in saliva
- Urine like odor

**Deposition in back fat**
Odours perceived by humans

Danish Meat Research Institute (2013)
So why has nothing happened?

😊 Boar taint is heritable
😊 Definition of “boar taint” is inconsistent
😊 No common reference method
😊 Breeding takes time
😊 Unfavourable correlations to other important traits...?
Objective

➢ To develop a feasible selection strategy against boar taint in Danish pig breeds
Outline

- Introduction

- **Performance testing in Denmark**

- Genetic associations to production and reproductive traits in Landrace and Duroc

- Results from genome wide associations

- Summary
Performance testing

- Boar taint trait is recorded at test-station
  - All boars, i.e. AI- and slaughter boars

- Human-nose-score
  - Slaughter boars only – trained panel at DC-Ringsted
  - Photometric determination of skatole Eq

- Boar taint on live AI-boars via biopsi
  - Androstenone, skatole and indole
Human nose score

- Procedure:
  - 100 mL sample bottle
  - 5 g lard (medium size)
  - 75 mL boiling hot water
  - Stand for 2 min

- Scale:
  - 0 = no boar taint,
  - 1 = week boar taint
  - 2 = strong boar taint

- Cat. 2 = Threshold
Human-nose score

Prevalence:
Duroc: 5.3%
Landrace: 21.7%
Yorkshire: 6.2%
Heritability of HNS

**Unitrait model:**

\[
\text{HNS} = \text{Sektion*Panel} + \text{Lwgt} + \text{Age} + \text{Slweek} + \text{Animal} + e
\]

(Fixed effects)

<table>
<thead>
<tr>
<th>Breed</th>
<th>Estimate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Duroc</td>
<td>0.08 (0.05)</td>
</tr>
<tr>
<td>Landrace</td>
<td>0.16 (0.07)</td>
</tr>
<tr>
<td>Yorkshire</td>
<td>0.09 (0.05)</td>
</tr>
</tbody>
</table>
Biopsy procedure

- Biopsy-device from SUISAG
  - Baes et al. Animal. 2013. 7:714-20
- \(~2700\) AI-boars without complications
  - Animal care protocol is needed
Heritabilities of BT-compounds

Multitrait model, \( i = \{\text{Log(Ska)}, \text{Log(Ind)}, \text{Log(And)}\} \):
\[
\text{Log}(\text{BT}_i) = \text{Sektion} + \text{Lwgt} + \text{Age} + \text{Animal} + e
\]
(Fixed effects) (Random effects)

### Duroc:

<table>
<thead>
<tr>
<th></th>
<th>Log(Ska)</th>
<th>Log(Ind)</th>
<th>Log(And)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Log(Ska)</td>
<td>0.22 (0.07)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Log(Ind)</td>
<td>0.78 (0.20)</td>
<td>0.23 (0.07)</td>
<td></td>
</tr>
<tr>
<td>Log(And)</td>
<td>0.28 (0.25)</td>
<td>0.21 (0.24)</td>
<td>0.48 (0.09)</td>
</tr>
</tbody>
</table>

### Yorkshire:

<table>
<thead>
<tr>
<th></th>
<th>Log(Ska)</th>
<th>Log(Ind)</th>
<th>Log(And)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Log(Ska)</td>
<td>0.37 (0.14)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Log(Ind)</td>
<td>0.85 (0.33)</td>
<td>0.19 (0.11)</td>
<td></td>
</tr>
<tr>
<td>Log(And)</td>
<td>0.18 (0.26)</td>
<td>0.58 (0.38)</td>
<td>0.53 (0.14)</td>
</tr>
</tbody>
</table>
Outline

- Introduction
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Danish Landrace

- Boar taint data (SABRE)
  - Skatole(equivalents) – 6000 boars
  - Androstenone – 500 pairs of full sibs
Genetic parameters for Landrace

Bivariate model:
\[
\text{Log(Skatole)} = \text{HYS} + \text{SLwgt} + \text{SLage} + \text{Litter} + \text{Animal} + e
\]
\[
\text{Log(Andro)} = \text{Herd} + \text{SLwgt} + \text{SLage} + \text{Litter} + \text{Animal} + e
\]

<table>
<thead>
<tr>
<th>Trait</th>
<th>( h^2 )</th>
<th>( r_g )</th>
<th>( r_p )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Log(skatole)</td>
<td>0.33 (0.05)</td>
<td>0.37 (0.12)</td>
<td>0.26 (0.03)</td>
</tr>
<tr>
<td>Log(Androstenone)</td>
<td>0.59 (0.14)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Production traits: Landrace

- Multi-trait model for performance traits and boar taint compounds

<table>
<thead>
<tr>
<th>Trait</th>
<th>$r_g(x, \text{Log(skatole)})$</th>
<th>$r_g(x, \text{Log(androstenone)})$</th>
</tr>
</thead>
<tbody>
<tr>
<td>ADG100</td>
<td>-0.04 (0.08)</td>
<td>0.10 (0.11)</td>
</tr>
<tr>
<td>Feed conversion</td>
<td>0.18 (0.19)</td>
<td>-0.04 (0.26)</td>
</tr>
<tr>
<td>Meat percentage</td>
<td>-0.20 (0.07)</td>
<td>-0.18 (0.10)</td>
</tr>
</tbody>
</table>

- Low genetic correlations and largely favorable!

Production traits: Duroc

- Results from fitting bivariate models

<table>
<thead>
<tr>
<th>Trait</th>
<th>$r_g(x, \text{ADG})$</th>
<th>$r_g(x, \text{Meat percentage})$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Log(skatole)</td>
<td>-0.28 (0.22)</td>
<td>-0.01 (0.18)</td>
</tr>
<tr>
<td>Log(Indole)</td>
<td>-0.24 (0.20)</td>
<td>-0.29 (0.18)</td>
</tr>
<tr>
<td>Log(Androstenone)</td>
<td>-0.17 (0.11)</td>
<td>-0.25 (0.10)</td>
</tr>
<tr>
<td>HNS</td>
<td>0.28 (0.33)</td>
<td>-0.33 (0.28)</td>
</tr>
</tbody>
</table>

- In both breeds low genetic correlations
- Consistent with Dutch results
  - Windig et al. (J. Anim. Sci. 2012.90:2120–2129)
Litter size data: Landrace

- Litter size traits: TBN and LP5
  - Full and half sib females to the BT boars
  - 1. parity sows and pure bred litters

<table>
<thead>
<tr>
<th>Trait</th>
<th>No</th>
<th>Mean</th>
<th>SD</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>TBN</td>
<td>35715</td>
<td>13.6</td>
<td>3.80</td>
<td>1.0</td>
<td>28.0</td>
</tr>
<tr>
<td>LP5</td>
<td>34991</td>
<td>10.5</td>
<td>3.45</td>
<td>0.00</td>
<td>22.0</td>
</tr>
</tbody>
</table>
**Model Litter size and BT**

Let \( \mathbf{y}_1, \mathbf{y}_2, \mathbf{y}_3 \) and \( \mathbf{y}_4 \) denote vectors of TNB, LP5, Log(skatole) and Log(androstenone) records with assumptions:

\[
\begin{bmatrix}
\mathbf{y}_1 \\
\mathbf{y}_2 \\
\mathbf{y}_3 \\
\mathbf{y}_4
\end{bmatrix} =
\begin{bmatrix}
\mathbf{X}_1 & 0 & 0 & 0 \\
0 & \mathbf{X}_2 & 0 & 0 \\
0 & 0 & \mathbf{X}_3 & 0 \\
0 & 0 & 0 & \mathbf{X}_4
\end{bmatrix}
\begin{bmatrix}
b_1 \\
b_2 \\
b_3 \\
b_4
\end{bmatrix} +
\begin{bmatrix}
\mathbf{Z}_{ps_1} & 0 & 0 & 0 \\
0 & \mathbf{Z}_{ps_2} & 0 & 0 \\
0 & 0 & \mathbf{Z}_{d_3} & 0 \\
0 & 0 & 0 & \mathbf{Z}_{a_4}
\end{bmatrix}
\begin{bmatrix}
p_s \\
p_s \\
a_3 \\
a_4
\end{bmatrix} +
\begin{bmatrix}
\mathbf{s} \\
\mathbf{d} \\
\mathbf{a}
\end{bmatrix}
\]

- **with assumptions**
  
  \( p_s \sim N(0, I \otimes S_0), c \sim N(0, I \otimes C_0), a \sim N(0, I \otimes R_0) \)

## Litter size and BT: Landrace

- Heritability on the diag. with genetic correlations on the off diag.

<table>
<thead>
<tr>
<th>Trait</th>
<th>TNB</th>
<th></th>
<th>LP5</th>
<th></th>
<th>Log(skatole)</th>
<th></th>
<th>Log(androstenone)</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Sire</td>
<td>Dam</td>
<td>Sire</td>
<td>Dam</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TNB</td>
<td>0.02 (0.01)</td>
<td></td>
<td>0.09 (0.01)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dam</td>
<td>0.36 (0.14)</td>
<td>0.09 (0.01)</td>
<td>0.70 (0.10)</td>
<td>0.17 (0.12)</td>
<td>0.02 (0.01)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LP5</td>
<td>0.43 (0.05)</td>
<td>0.58 (0.15)</td>
<td>0.38 (0.13)</td>
<td>0.06 (0.01)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Log(skatole)</td>
<td>0.05 (0.22)</td>
<td>0.06 (0.11)</td>
<td>-0.11 (0.18)</td>
<td>0.03 (0.13)</td>
<td>0.33 (0.04)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Log(androstenone)</td>
<td>-0.20 (0.27)</td>
<td>-0.14 (0.15)</td>
<td>-0.40 (0.22)</td>
<td>-0.20 (0.17)</td>
<td>0.41 (0.14)</td>
<td>0.59 (0.13)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- In general, weak genetic correlations between BT compounds and service-sire fertility

Littersize and BT: Duroc

- Bivariate models for TNB and boar taint

<table>
<thead>
<tr>
<th></th>
<th>TNB(dam)</th>
<th>TNB(S-sire)</th>
<th>Log(Andro)</th>
<th>Log(Ska)</th>
</tr>
</thead>
<tbody>
<tr>
<td>TNB(dam)</td>
<td>0.10 (0.01)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TNB(S-sire)</td>
<td>0.30 (0.11)</td>
<td>0.04 (0.01)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Log(Andro)</td>
<td>-0.08 (0.16)</td>
<td>-0.13 (0.19)</td>
<td>0.47 (0.08)</td>
<td></td>
</tr>
</tbody>
</table>

Model for semen and BT

- Combine Rep-model (1) with models (2, 3) for boar taint compounds

\[
\begin{align*}
\mathbf{y}_1 &= \begin{bmatrix} X_1 & 0 & 0 \end{bmatrix} \mathbf{b}_1 + \begin{bmatrix} Z_{pe} & 0 & 0 \end{bmatrix} \mathbf{p} \\
\mathbf{y}_2 &= \begin{bmatrix} 0 & X_2 & 0 \end{bmatrix} \mathbf{b}_2 + \begin{bmatrix} 0 & 0 & 0 \end{bmatrix} \\
\mathbf{y}_3 &= \begin{bmatrix} 0 & 0 & X_3 \end{bmatrix} \mathbf{b}_3 + \begin{bmatrix} 0 & 0 & 0 \end{bmatrix} \\
&+ \begin{bmatrix} 0 & Z_{c_2} & 0 \end{bmatrix} \mathbf{c}_2 + \begin{bmatrix} Z_{a_1} & 0 & 0 \end{bmatrix} \\
&+ \begin{bmatrix} 0 & 0 & Z_{c_3} \end{bmatrix} \mathbf{c}_3 + \begin{bmatrix} 0 & Z_{a_2} & 0 \end{bmatrix} \\
&+ \begin{bmatrix} 0 & 0 & 0 \end{bmatrix} \mathbf{c}_3 + \begin{bmatrix} 0 & 0 & Z_{a_3} \end{bmatrix}
\end{align*}
\]

- Standard assumptions

\[
\mathbf{p} \sim N(0, \mathbf{I} \otimes \mathbf{K}_p); \quad \mathbf{c} \sim N(0, \mathbf{I} \otimes \mathbf{C}); \quad \mathbf{a} \sim N(0, \mathbf{A} \otimes \mathbf{G}); \quad \mathbf{e} \sim N(0, \mathbf{I} \otimes \mathbf{R})
\]

Semen and BT

- Key genetic correlations

<table>
<thead>
<tr>
<th>Trait</th>
<th>( r_g(x, \text{Log(skatole)}) )</th>
<th>( r_g(x, \text{Log(androstenone)}) )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Volume</td>
<td>0.01 (0.13)</td>
<td>0.02 (0.18)</td>
</tr>
<tr>
<td>Concentration</td>
<td>-0.11 (0.13)</td>
<td>-0.24 (0.16)</td>
</tr>
<tr>
<td>Total sperm</td>
<td>-0.17 (0.13)</td>
<td>-0.13 (0.18)</td>
</tr>
<tr>
<td>Functional sperm</td>
<td>-0.16 (0.17)</td>
<td>-0.10 (0.18)</td>
</tr>
</tbody>
</table>

- High standard errors on genetic correlations

Semen quality and BT

- Multi-trait liability model for binary semen quality traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>$h^2$</th>
<th>$r_g(x, \text{Log(skatole)})$</th>
<th>$r_g(x, \text{Log(androstenone)})$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Normal/abnormal</td>
<td>0.08 (0.02)</td>
<td>0.09 (0.20)</td>
<td>-0.39 (0.25)</td>
</tr>
<tr>
<td>Motility low/high</td>
<td>0.21 (0.03)</td>
<td>-0.08 (0.15)</td>
<td>-0.38 (0.19)</td>
</tr>
</tbody>
</table>

- Lowheritabilities for semen quality traits
- Weak genetic correlations

Semen and BT: Duroc

- Bivariate repeatability models

<table>
<thead>
<tr>
<th>Trait</th>
<th>$h^2$</th>
<th>$r_{g(x, \text{Log}(Ska))}$</th>
<th>$r_{g(x, \text{Log}(Ind))}$</th>
<th>$r_{g(x, \text{Log}(And))}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Motility</td>
<td>0.14 (0.02)</td>
<td>-0.41 (0.22)</td>
<td>-0.25 (0.22)</td>
<td>-0.06 (0.13)</td>
</tr>
<tr>
<td>Volume</td>
<td>0.29 (0.02)</td>
<td>0.15 (0.20)</td>
<td>0.10 (0.19)</td>
<td>0.15 (0.11)</td>
</tr>
</tbody>
</table>

- Again, weak genetic correlations
Testosterone and semen

- Low Test. Line (LTL): 28 ng/ml testosterone
- High Test. Line (HTL): 44 ng/ml testosterone

<table>
<thead>
<tr>
<th>Traits</th>
<th>LTL (b)</th>
<th>SE</th>
<th>HTL (b)</th>
<th>SE</th>
<th>(P)-value (c)</th>
</tr>
</thead>
<tbody>
<tr>
<td>DSP/g, millions</td>
<td>2.89 (\pm) 2.47</td>
<td></td>
<td>2.72 (\pm) 1.50</td>
<td></td>
<td>0.55</td>
</tr>
<tr>
<td>TDSP, billions</td>
<td>1.62 (\pm) 0.17</td>
<td></td>
<td>1.42 (\pm) 0.11</td>
<td></td>
<td>0.34</td>
</tr>
<tr>
<td>SPM/g, millions</td>
<td>12.65 (\pm) 1.08</td>
<td></td>
<td>11.87 (\pm) 0.65</td>
<td></td>
<td>0.54</td>
</tr>
<tr>
<td>TTS, billions</td>
<td>7.08 (\pm) 0.76</td>
<td></td>
<td>6.23 (\pm) 0.46</td>
<td></td>
<td>0.34</td>
</tr>
</tbody>
</table>

\(r_p(\text{testosterone}; \ TTS) = 0.12\)


Outline

- Introduction
- Performance testing and preliminary results
- Genetic associations to production and reproductive traits
- Results from genome wide associations
- Concluding remarks
GWAS for skatole in Landrace

- Region - Chr. 14
- Top-SNP: SIRI0000194
- CYP2E1

Rowe et al. BMC Genomics 2014, 15:424
GWAS for skatole in Duroc

Top-SNP: SIRI0000194
GWAS for androstenone in Duroc

- Region: 47 – 53 Mb on Chr. 6
- Candidate genes:
  - SULT2A1
  - HSD17B
- Duijvesteijn et al. (2010)
Single-Step GWAS for androsteneone

\[ u = q D Z' [Z D Z']^{-1} a^{And} \]
Summary

- Selection against boar taint will have
  - Minimal impact on production traits
  - Minimal impact on litter size traits
  - Minimal impact on semen traits

- GWAS results points to previous mapped regions

- Breeding is an option
  - Effective online sorting and grading of carcasses
  - Determine the economic weight of the trait
  - Phenotyping costs must be dramatically reduced
  - Breeding will never guarantee 100% of carcasses, being perceived as free of boar taint