

Genetic association between male fertility and boar taint

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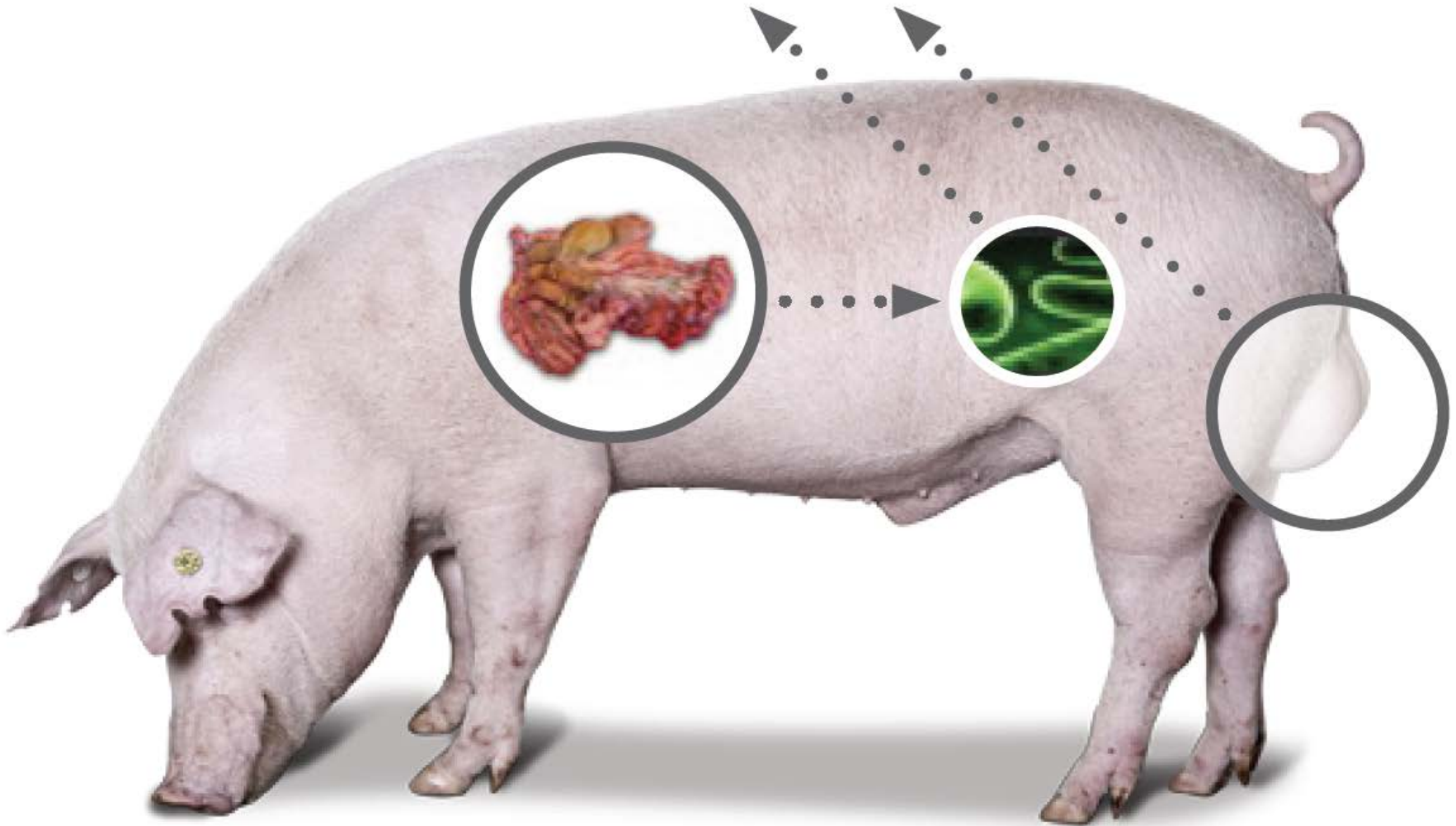
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Introduction

- Stop surgical castration by 2018
 - Improve animal welfare
- Boar taint problem!
 - Male fertility?

Deposition in back fat



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

Introduction

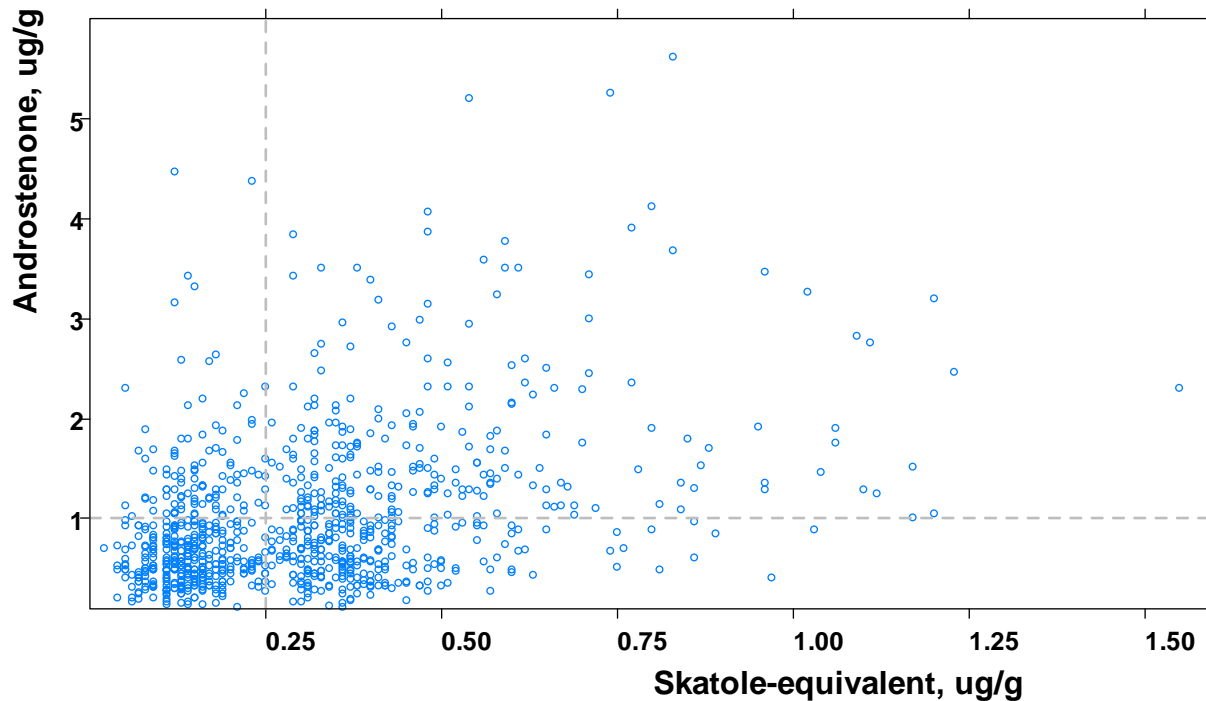
- Traits, representing male fertility
 - Serum testosterone and circulating steroid hormones
 - Unfavorable correlation to androstenone
 - Expensive to measure
 - Semen quality and quantity
 - Routinely collected at AI-stations, but rarely analysed
 - Litter size traits
 - Large data volume as part of genetic improvement
 - Service-sire component

Objective

To estimate genetic association between male fertility and boar taint in Danish Landrace

Boar taint data

- Boar taint data
 - Skatole(equivalents) – 6000 boars
 - Androstenone – 500 pairs of full sibs



BT Model and Results

Let \mathbf{y}_1 and \mathbf{y}_2 denote vectors Log(skatole) and Log(androstenone)

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_{a_1} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{a_2} \end{bmatrix} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_{c_1} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{c_2} \end{bmatrix} \begin{bmatrix} \mathbf{c}_1 \\ \mathbf{c}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix}$$

Where $\mathbf{b}_1 = [\mu, HYS, ASL, WSL]'$ $\mathbf{b}_2 = [\mu, HERD, ASL, WSL]'$
 $\mathbf{c} \sim N(\mathbf{0}, \mathbf{I} \otimes \mathbf{C})$; $\mathbf{a} \sim N(\mathbf{0}, \mathbf{A} \otimes \mathbf{G})$; $\mathbf{e} \sim N(\mathbf{0}, \mathbf{I} \otimes \mathbf{R})$

Parameter estimates and (SE)

Trait	h^2	r_g	r_p
Log(skatole)	0.33 (0.05)	0.37 (0.12)	0.26 (0.03)
Log(Androstenone)	0.59 (0.14)		

Semen data

➤ Data: 3145 boars and 95267 ejaculates

	Mean	SD	Min	Max
No. ejaculates per boar	30.3	23.1	5	126
Volume, ml	195	77.7	26.0	598
Concentration, 10^6 /ml	374	134	103	998
Total sperm, 10^9	67.8	26.2	7.20	199
Functional sperm, 10^9	60.3	23.4	5.76	179

➤ Prevalence of abnormal ejaculates (0/1): 5.8%

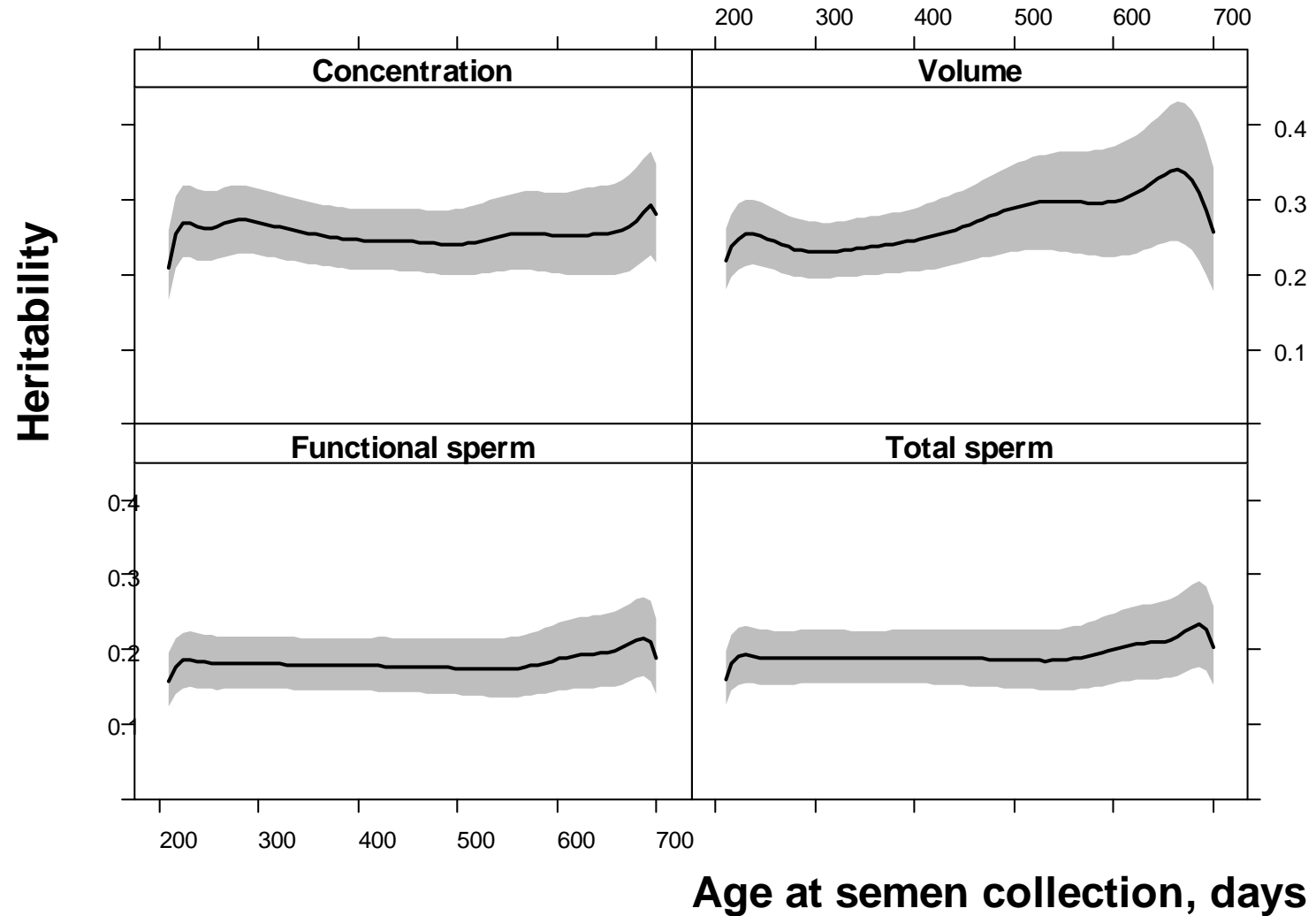
➤ Prevalence of low motility ejaculates (0/1): 9.9%

Random regression model

$$y_{ijklt} = AIsys_i + Int_j + Age_k + \sum_{n=0}^{kp} p_{l,n} \Phi_n(w_t) + \sum_{n=0}^{ka} a_{l,n} \Phi_n(w_t) + e_{ijklt}$$

- AI-station-year-season effect (310 classes): $AIsys_i$
- Interval between collections (9 classes): Int_j
- Age of boar in weeks (71 classes): Age_k
- Legendre polynomials (LP) of age:
 - Standardized time: $w_t = [-1, \dots, 1]$
 - kp and ka were the orders (up to 8) of LP
 - Random LP coefficients
 - Non-genetic animal effect, $p_{l,n}$
 - Additive genetic effect, $a_{l,n}$
 - Residual error term, e_{ijklt}

Heritability of semen traits



Model for semen and BT

- Combine “best” RR-model₍₁₎ with models_(2, 3) for boar taint compounds

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \\ \mathbf{y}_3 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{X}_3 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \\ \mathbf{b}_3 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_{pe} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \end{bmatrix} \begin{bmatrix} \mathbf{p} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix} \\
 + \begin{bmatrix} \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{c_2} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{Z}_{c_3} \end{bmatrix} \begin{bmatrix} \mathbf{0} \\ \mathbf{c}_2 \\ \mathbf{c}_3 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_{a_1} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{a_2} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{Z}_{a_3} \end{bmatrix} \begin{bmatrix} \mathbf{a} \\ \mathbf{a} \\ \mathbf{a} \end{bmatrix}$$

Non-existing residual covariances (co betw and BT compounds

- Standard assumptions

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

Semen and BT

➤ Key genetic correlations

Trait _x	$r_{g(x, \text{Log}(\text{skatole}))}$	$r_{g(x, \text{Log}(\text{androstenone}))}$
Volume	0.01 (0.13)	0.02 (0.18)
Concentration	-0.11 (0.13)	-0.24 (0.16)
Total sperm	-0.17 (0.13)	-0.13 (0.18)
Functional sperm	-0.16 (0.17)	-0.10 (0.18)

➤ High standard errors on genetic correlations

Semen quality and BT

- Multi-trait liability model for binary semen quality traits

Trait _x	h ²	r _{g(x, Log(skatole))}	r _{g(x, Log(androstenone))}
Normal/abnormal	0.08 (0.02)	0.09 (0.20)	-0.39 (0.25)
Motility low/high	0.21 (0.03)	-0.08 (0.15)	-0.38 (0.19)

- Low heritabilities for semen quality traits
- Weak genetic correlations

Litter size data

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

Trait	No	Mean	SD	Min	Max
TBN	35715	13.6	3.80	1.0	28.0
LP5	34991	10.5	3.45	0.00	22.0

Model Litter size and BT

- Let $\mathbf{y}_1, \mathbf{y}_2, \mathbf{y}_3$ and \mathbf{y}_4 denote vectors of Log(skatoles) and Log(androstenones) for the four offspring of a dam.

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \\ \mathbf{y}_3 \\ \mathbf{y}_4 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{X}_3 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{X}_4 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \\ \mathbf{b}_3 \\ \mathbf{b}_4 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_{ps_1} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{ps_2} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \end{bmatrix} \begin{bmatrix} \mathbf{p}_{s_1} \\ \mathbf{p}_{s_2} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix} + \begin{bmatrix} \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \end{bmatrix} \begin{bmatrix} \mathbf{c} \\ \mathbf{c} \\ \mathbf{c} \\ \mathbf{c} \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_{d_1} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{d_2} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \end{bmatrix} \begin{bmatrix} \mathbf{d}_1 \\ \mathbf{d}_2 \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix} + \begin{bmatrix} \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{Z}_{a_3} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{Z}_{a_4} \end{bmatrix} \begin{bmatrix} \mathbf{0} \\ \mathbf{0} \\ \mathbf{a}_3 \\ \mathbf{a}_4 \end{bmatrix} + \begin{bmatrix} \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \end{bmatrix} \begin{bmatrix} \mathbf{e} \\ \mathbf{e} \\ \mathbf{e} \\ \mathbf{e} \end{bmatrix}$$

Herd-year-quarter effects and regression on age at first mating

Non-existing residual covariances compounds

- with assumptions

$$\mathbf{p}_s \sim N(\mathbf{0}, \mathbf{I} \otimes \mathbf{S}_0), \quad \mathbf{c} \sim N(\mathbf{0}, \mathbf{I} \otimes \mathbf{C}_0), \quad \begin{bmatrix} \mathbf{s} \\ \mathbf{d} \\ \mathbf{a} \end{bmatrix} \sim N(\mathbf{0}, \mathbf{A} \otimes \mathbf{G}_0), \quad \mathbf{e} \sim N(\mathbf{0}, \mathbf{I} \otimes \mathbf{R}_0)$$

Litter size and BT

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

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

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

Conclusions

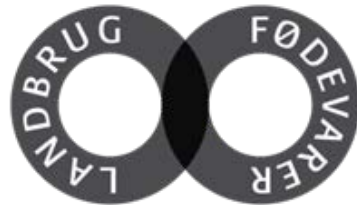
- Heritability of semen traits
 - Quantity: 0.18 to 0.28
 - Quality: 0.08 to 0.21 (liability scale)
- Genetic correlations to BT were low
 - Semen: -0.39 to 0.09
 - Litter size: -0.40 to 0.06
- **Minimal impact on semen and litter size traits**

Genetic parameters for male fertility and its relationship to Skatole and Androstenone in Danish Landrace Boars

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Acknowledgements

Videncenter for
Svineproduktion



The Danish National
Advanced Technology Foundation

