Genetic and genomic selection to reduce boar taint in Danish pigs

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Outline

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

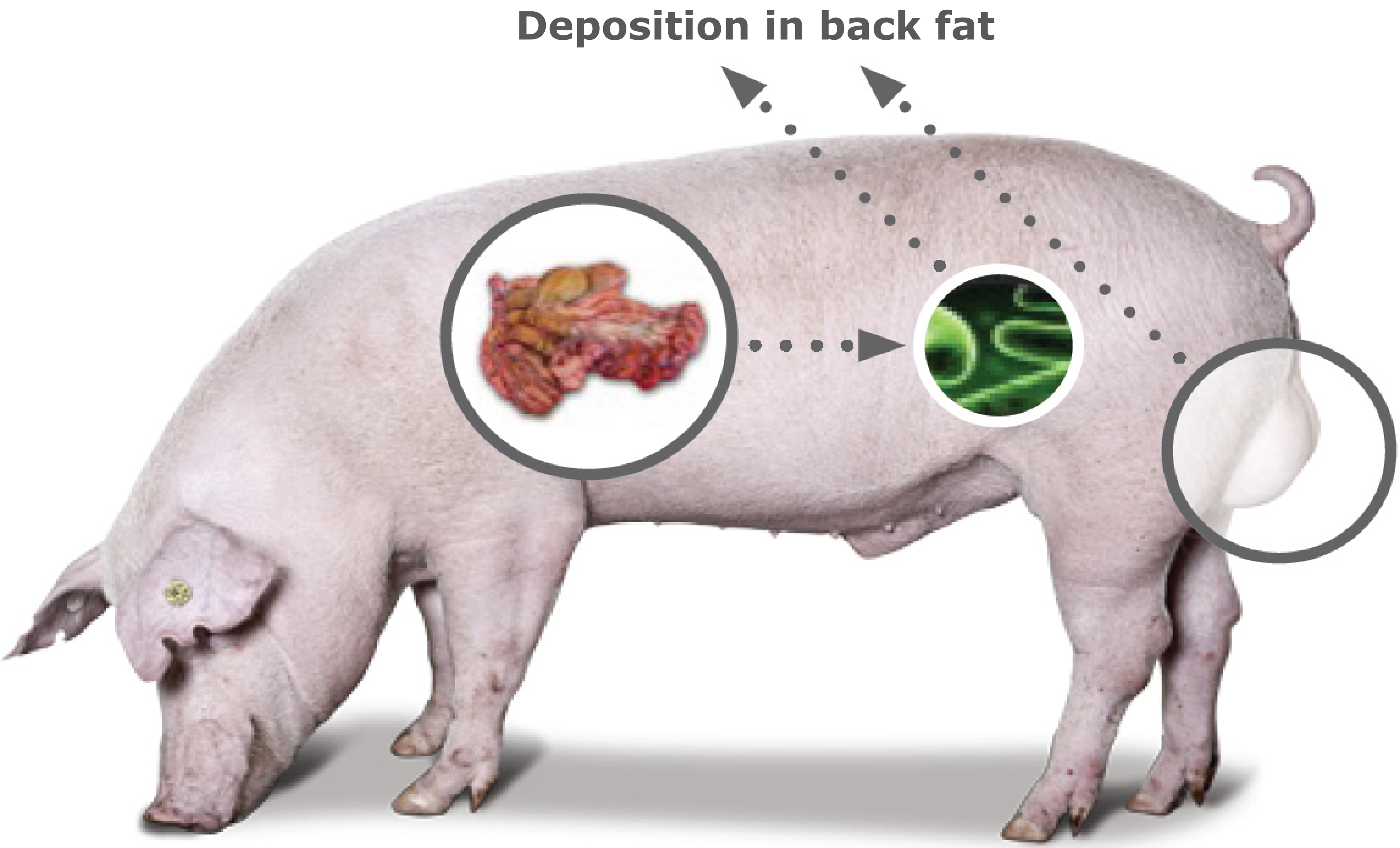
Introduction

- 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

Odours perceived by humans

Boar taint

Chemical/sharp

Sweat

Urine

Manure

Stable

Perfume

Spicy

Rancid/old

Soap

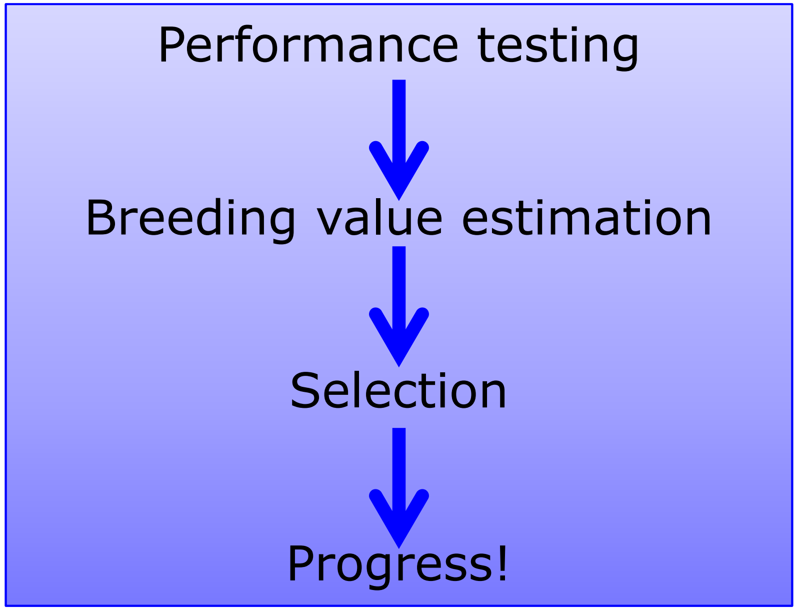
Danish Meat Research Institute (2013)

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


Performance testing

Breeding value estimation

Selection

Progress!

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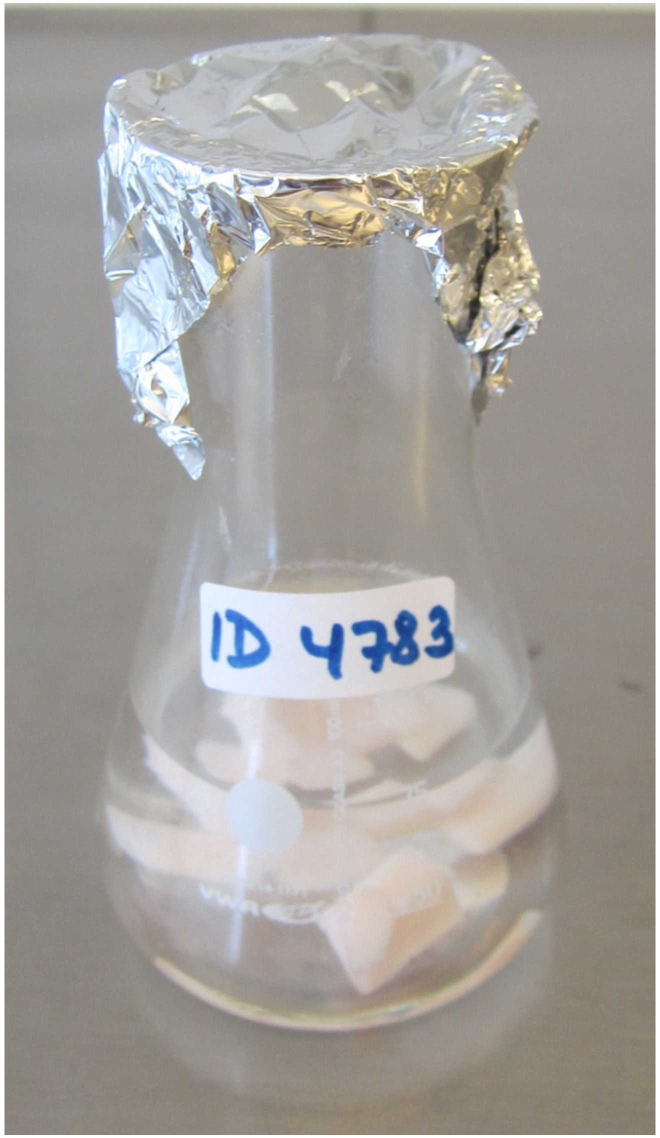
Performance testing

- 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 skatoleEq

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

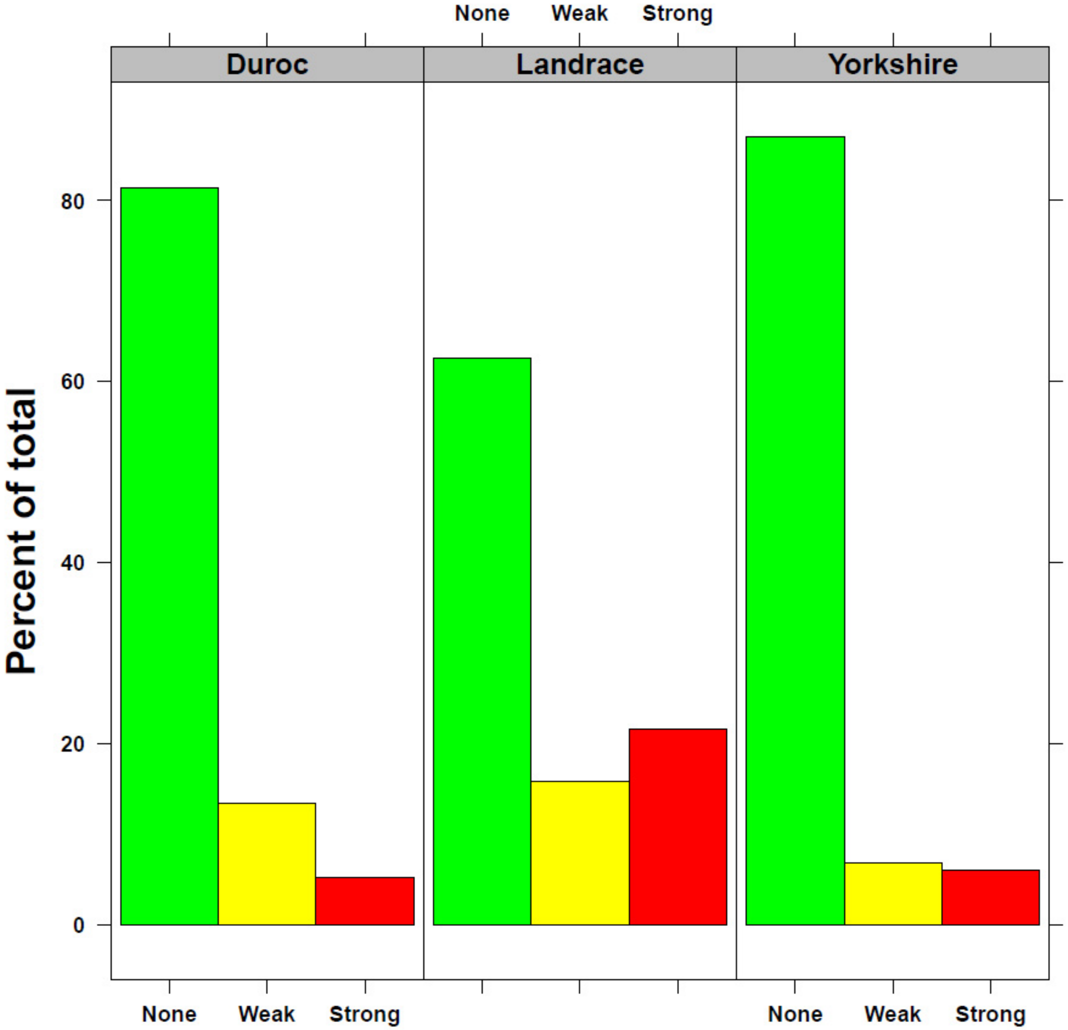
Human nose score



- 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:

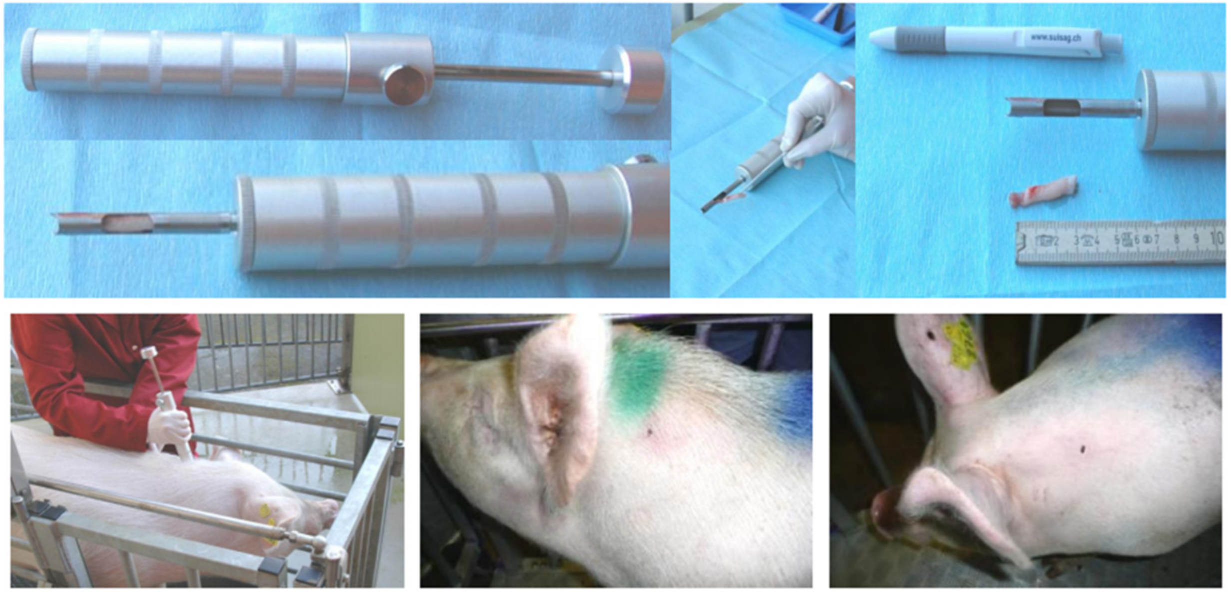
HNS = Sektion*Panel + Lwgt + Age + Slweek + Animal + e

(Fixed effects) **(Random effects)**

Breed	Estimate
Duroc	**0.08 (0.05)**
Landrace	**0.16 (0.07)**
Yorkshire	**0.09 (0.05)**

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 ={Log(Ska), Log(Ind), Log(And)}:

Log(BT_i) = Sektion + Lwgt + Age + Animal + e

(Fixed effects) (Random effects)

Duroc:

	Log(Ska)	Log(Ind)	Log(And)
Log(Ska)	**0.22 (0.07)**		
Log(Ind)	0.78 (0.20)	**0.23 (0.07)**	
Log(And)	0.28 (0.25)	0.21 (0.24)	**0.48 (0.09)**

Yorkshire:

	Log(Ska)	Log(Ind)	Log(And)
Log(Ska)	**0.37 (0.14)**		
Log(Ind)	0.85 (0.33)	**0.19 (0.11)**	
Log(And)	0.18 (0.26)	0.58 (0.38)	**0.53 (0.14)**

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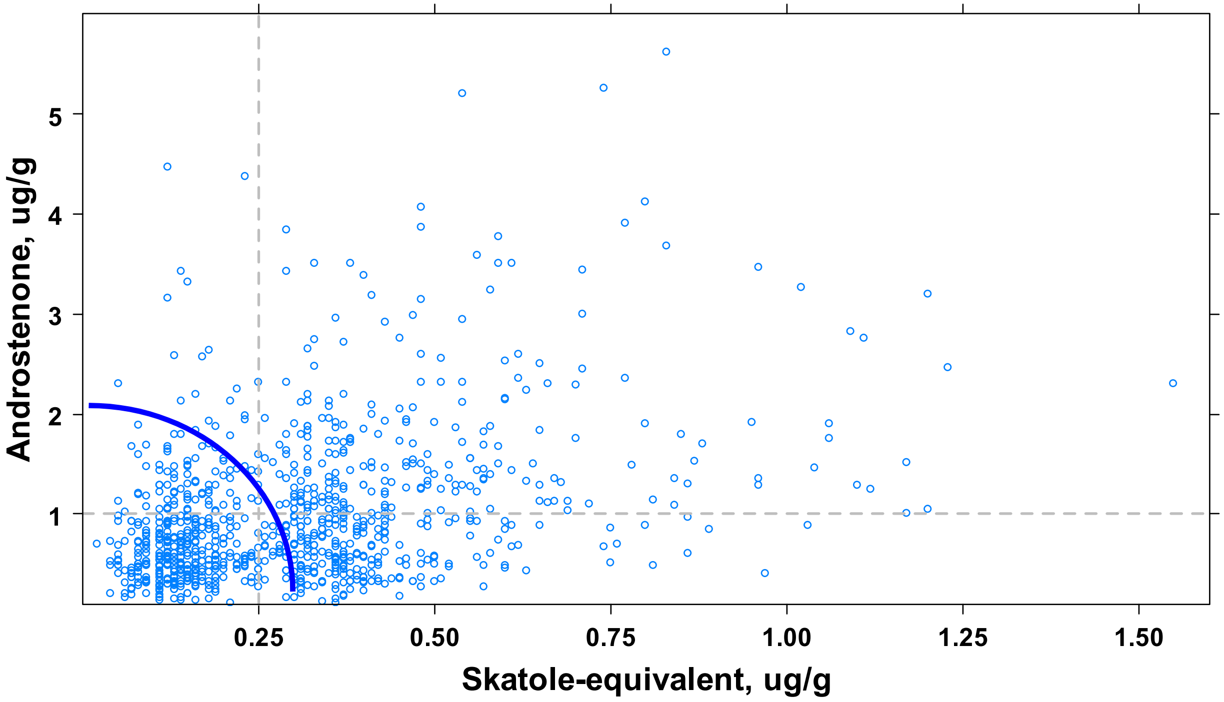
Danish Landrace

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



Genetic parameters for Landrace

Bivariate model:

Log(Skatole) = HYS + SLwgt + SLage + Litter + Animal + e
Log(Andro) = Herd + SLwgt + SLage + Litter + Animal + e

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)		

Strathe et al. J. Anim. Sci. 2013. 91:2587-2595

Production traits: Landrace

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

Trait_x	$r_{g(x,\ \text{Log(skatole)})}$	$r_{g(x,\ \text{Log(androstenone)})}$
ADG100	-0.04 (0.08)	0.10 (0.11)
Feed conversion ratio	0.18 (0.19)	-0.04 (0.26)
Meat percentage	-0.20 (0.07)	-0.18 (0.10)

- Low genetic correlations and largely favorable!

Strathe et al. J. Anim. Sci. 2013. 91:2587-2595

Production traits: Duroc

- Results from fitting bivariate models

Trait_x	**$r_{g(x,\ \text{ADG})}$**	**$r_{g(x,\ \text{Meat percentage})}$**
Log(skatole)	-0.28 (0.22)	-0.01 (0.18)
Log(Indole)	-0.24 (0.20)	-0.29 (0.18)
Log(Androstenone)	-0.17 (0.11)	-0.25 (0.10)
HNS	0.28 (0.33)	-0.33 (0.28)

- 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

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 vect
Log(skatole) and Log(androsten

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \\ \mathbf{y}_3 \\ \mathbf{y}_4 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{X}_3 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{X}_4 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \\ \mathbf{b}_3 \\ \mathbf{b}_4 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_{ps_1} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{ps_2} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \end{bmatrix} \begin{bmatrix} \mathbf{p}_{\mathbf{s}_1} \\ \mathbf{p}_{\mathbf{s}_2} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix} + \begin{bmatrix} & & & \\ & & & \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & & & \end{bmatrix} \begin{bmatrix} \\ \\ \mathbf{0} \\ \\ \end{bmatrix}$$

$$+ \begin{bmatrix} \mathbf{Z}_{d_1} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{d_2} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \end{bmatrix} \begin{bmatrix} \mathbf{d}_1 \\ \mathbf{d}_2 \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix} + \begin{bmatrix} \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{Z}_{a_3} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{Z}_{a_4} \end{bmatrix} \begin{bmatrix} \mathbf{0} \\ \mathbf{0} \\ \mathbf{a}_3 \\ \mathbf{a}_4 \end{bmatrix} + \begin{bmatrix} \mathbf{0} & \mathbf{0} & \\ \mathbf{0} & \mathbf{0} & \\ \mathbf{0} & \mathbf{0} & \mathbf{Z} \\ \mathbf{0} & \mathbf{0} & \end{bmatrix}$$

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

Non-existing residual covariances

s
ce-
BT
compounds

- with assumptions

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

Strathe et al. J. Anim. Sci. 2013.91:4659–4668

Litter size and BT: Landrace

- 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

Strathe et al. J. Anim. Sci. 2013.91:4659–4668

Littersize and BT: Duroc

- Bivariate models for TNB and boar taint

	TNB(dam)	TNB(S-sire)	Log(Andro)	Log(Ska)
TNB(dam)	**0.10 (0.01)**			
TNB(S-sire)	0.30 (0.11)	**0.04 (0.01)**		
Log(Andro)	-0.08 (0.16)	-0.13 (0.19)	**0.47 (0.08)**	

Strathe et al. J. Anim. Sci. 2013.91:4659–4668

Model for semen and BT

- Combine Rep-model$_{(1)}$ with models$_{(2,\ 3)}$ for boar taint compounds

$$\begin{bmatrix}\mathbf{y}_1\\ \mathbf{y}_2\\ \mathbf{y}_3\end{bmatrix}=\begin{bmatrix}\mathbf{X}_1 & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{X}_2 & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{X}_3\end{bmatrix}\begin{bmatrix}\mathbf{b}_1\\ \mathbf{b}_2\\ \mathbf{b}_3\end{bmatrix}+\begin{bmatrix}\mathbf{Z}_{\mathbf{pe}} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0}\end{bmatrix}\begin{bmatrix}\mathbf{p}\\ \mathbf{0}\\ \mathbf{0}\end{bmatrix}$$

$$+\begin{bmatrix}\mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{Z}_{c_2} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{Z}_{c_3}\end{bmatrix}\begin{bmatrix}\mathbf{0}\\ \mathbf{c}_2\\ \mathbf{c}_3\end{bmatrix}+\begin{bmatrix}\mathbf{Z}_{a_1} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{Z}_{a_2} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{Z}_{a_3}\end{bmatrix}\begin{bmatrix}\mathbf{a}\\ \mathbf{a}\\ \mathbf{a}\end{bmatrix}$$

(co
betw
and BT
compounds

Non-existing
residual
covariances

- Standard assumptions

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

Strathe et al. J. Anim. Sci. 2013.91:4659–4668

Semen and BT

- Key genetic correlations

Trait_x	$r_{g(x,\ \text{Log(skatole)})}$	$r_{g(x,\ \text{Log(androstenone)})}$
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

Strathe et al. J. Anim. Sci. 2013.91:4659–4668

Semen quality and BT

- Multi-trait liability model for binary semen quality traits

Trait_x	**h^2**	**$r_{g(x,\ \text{Log(skatole)})}$**	**$r_{g(x,\ \text{Log(androstenone)})}$**
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

Strathe et al. J. Anim. Sci. 2013.91:4659–4668

Semen and BT: Duroc

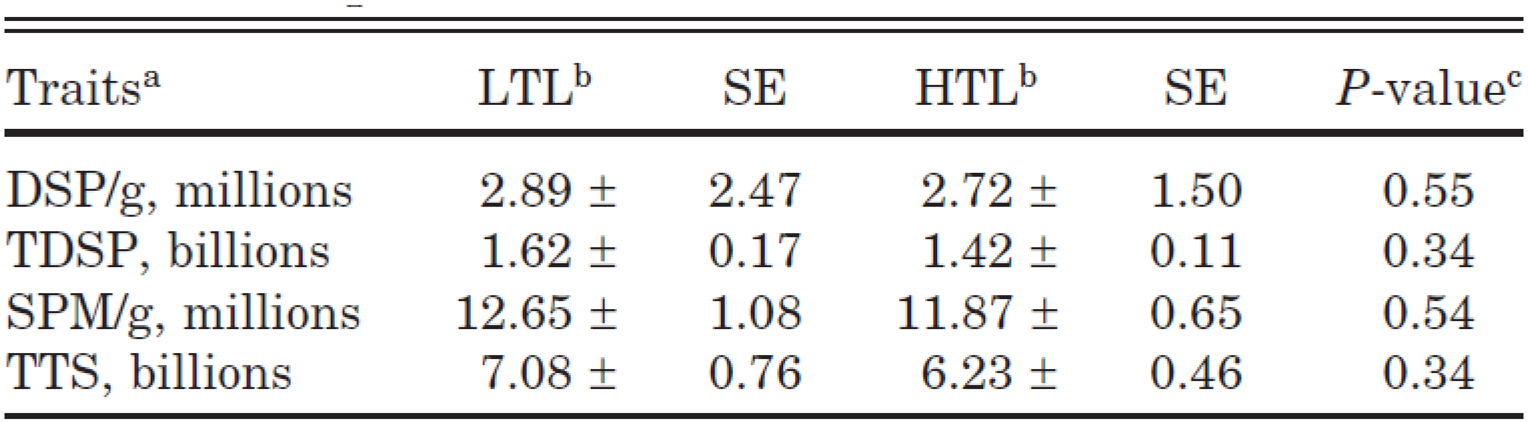
- Bivariate repeatability models

Trait_x	**h^2**	**$r_{g(x,\ Log(Ska))}$**	**$r_{g(x,\ Log(Ind))}$**	**$r_{g(x,\ Log(And))}$**
Motility	0.14 (0.02)	-0.41 (0.22)	-0.25 (0.22)	-0.06 (0.13)
Volume	0.29 (0.02)	0.15 (0.20)	0.10 (0.19)	0.15 (0.11)

- Again, weak genetic correlations

Testosterone and semen

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



Traits[a]	LTL[b]	SE	HTL[b]	SE	P-value[c]
DSP/g, millions	2.89 ±	2.47	2.72 ±	1.50	0.55
TDSP, billions	1.62 ±	0.17	1.42 ±	0.11	0.34
SPM/g, millions	12.65 ±	1.08	11.87 ±	0.65	0.54
TTS, billions	7.08 ±	0.76	6.23 ±	0.46	0.34

Walker et al. (J. Anim. Sci. 2004. 82:2259–2263)

- r_p(testosterone; TTS) = 0.12
  - Ren et al. (Reprod. Dom. Anim. 2009. 44:913–919)

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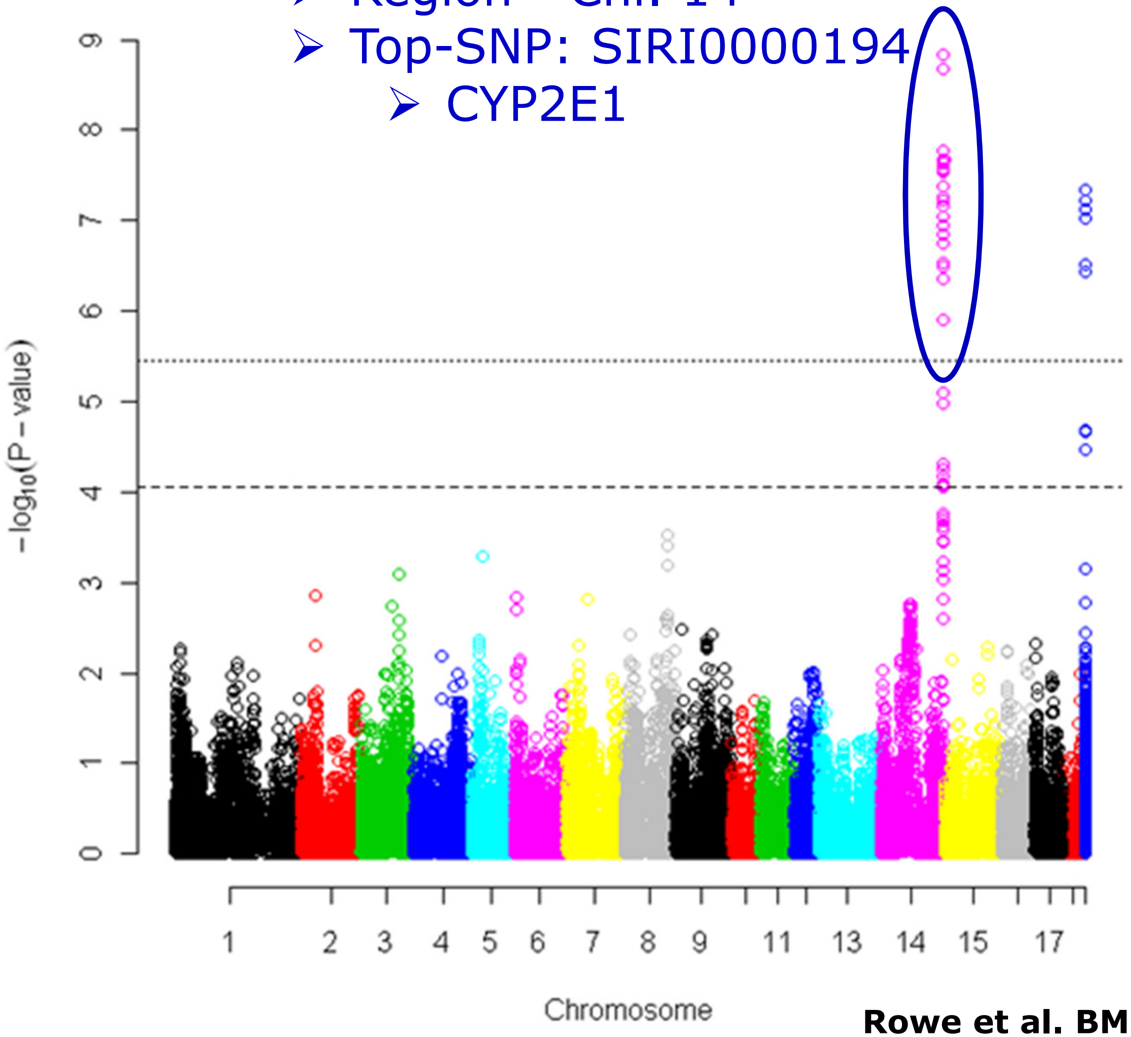
- **Results from genome wide associations**
- Concluding remarks

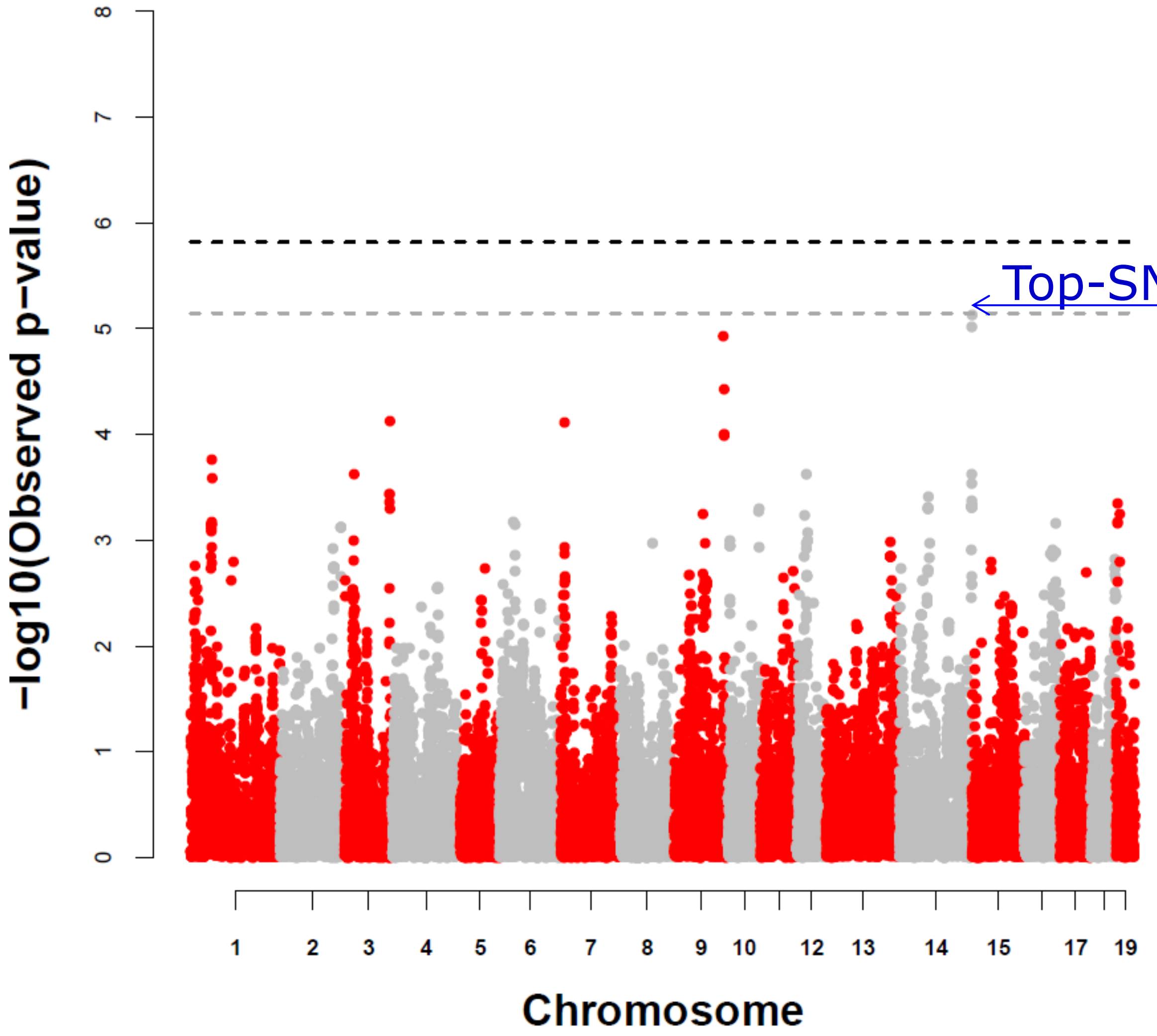
GWAS for skatole in Landrace

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



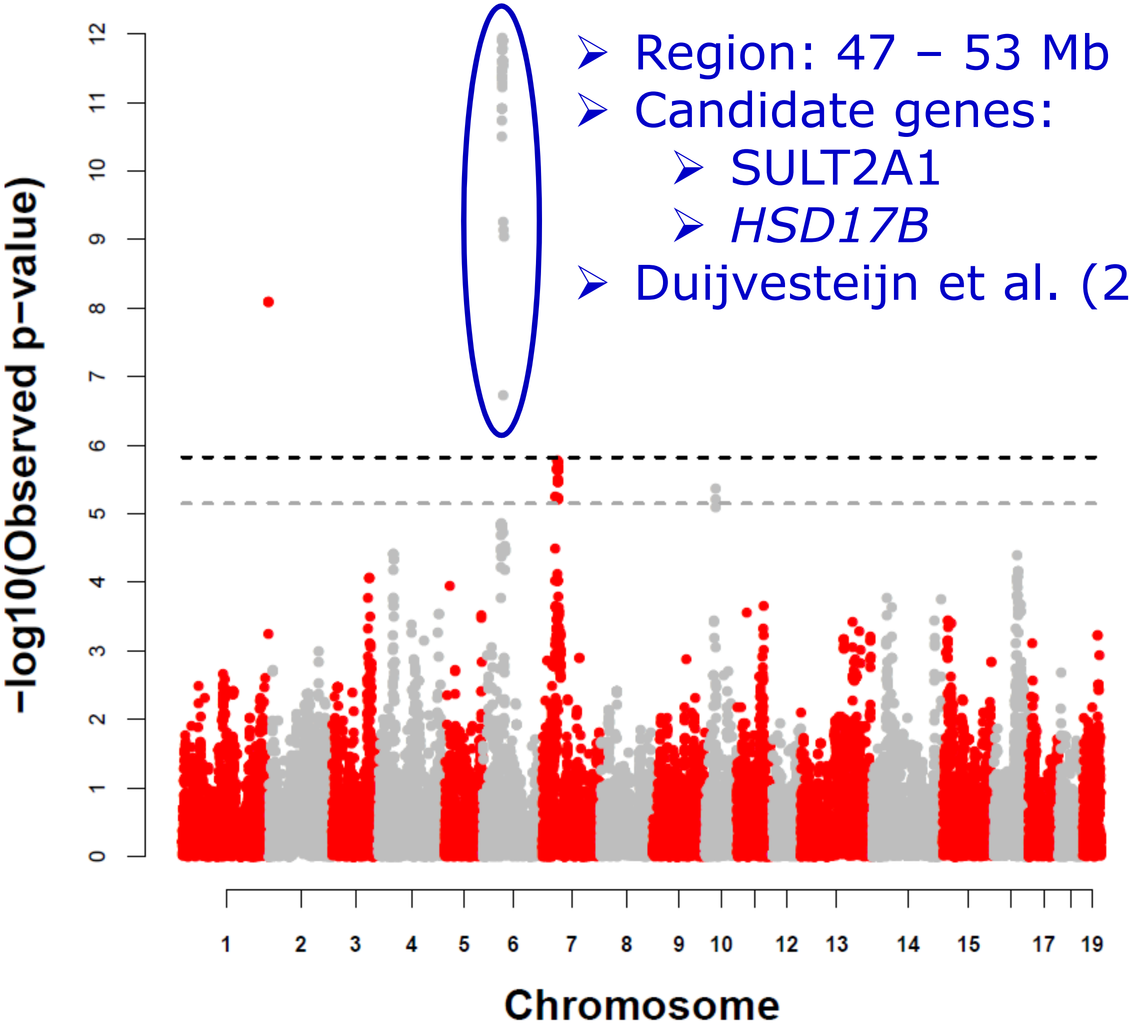
Rowe et al. BMC Genomics 2014, 15:424

GWAS for skatole in Duroc



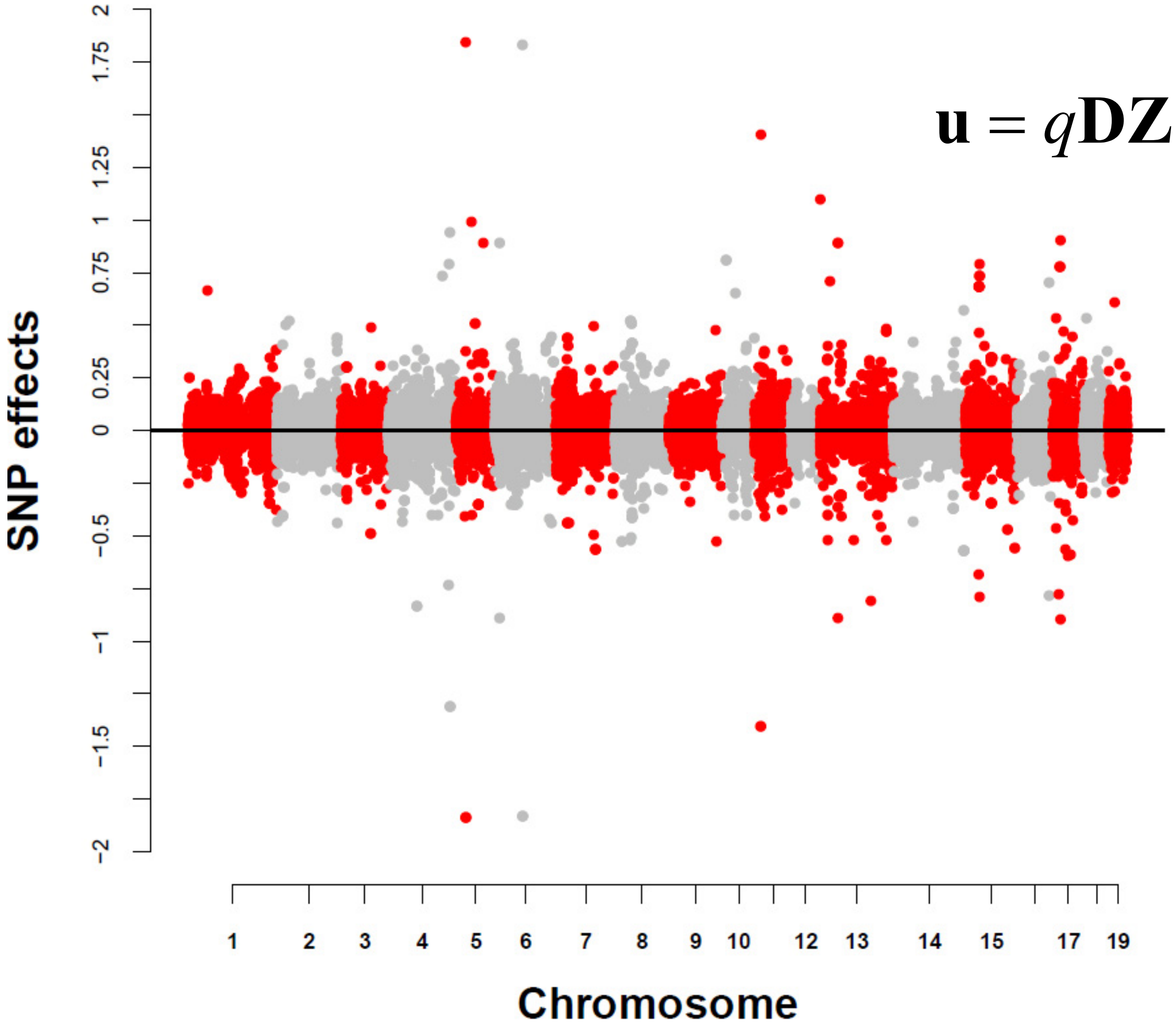
Top-SNP: SIRI0000194

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



$$\mathbf{u} = q\mathbf{DZ}'\left[\mathbf{ZDZ}'\right]^{-1}\mathbf{a}^{And}$$

Wang et al. Genet. Res. 2012. 94:73–83

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