# Genetics of tail-biting receipt in gilts from the Tai Zumu line

*Source: AXIOM*

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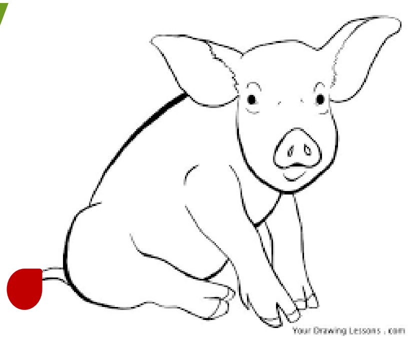
# Behaviour and trait under study



Tail-biting = damaging behaviour

Receipt of tail-bites = aberrant behaviour

Record: ≥ 1 bite fresh or healing - one single technician at control

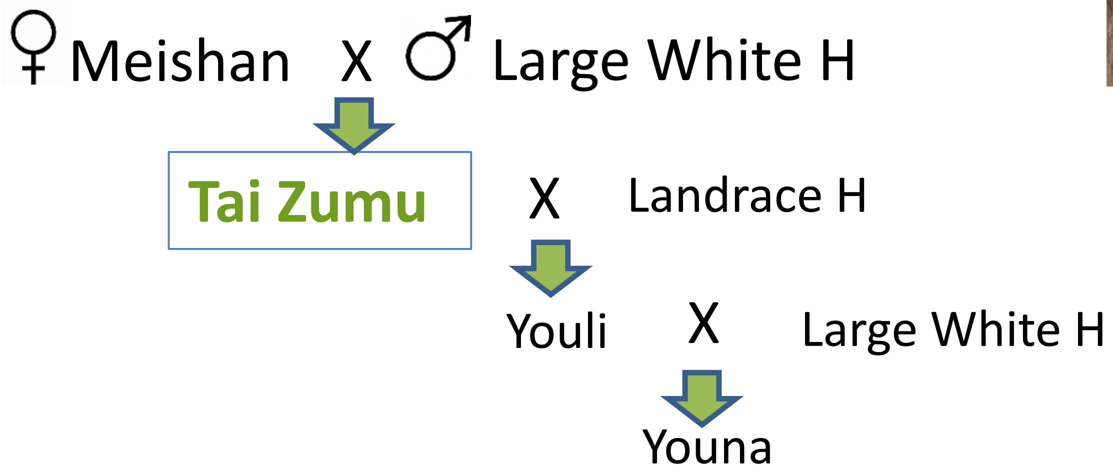
## Questions

- Magnitude of social effects in the prevalence of tail bites ?
- Influence of the farm environment
  on the genetic expression of this behaviour ?

# Population under study


Source: AXIOM

Composite line stabilized since 2001



♀ Meishan X ♂ Large White H

**Tai Zumu** X Landrace H

Youli X Large White H

Youna

H0 : females are more likely to tail bite than males

Confirmed <3.8% in males

⇨ focus on female population

# Data

- 33,266 fattening gilts 2,970 groups of 6 to 20 females
- Tail biting in 30% of groups : $\bar{x}$ = 2.8 pigs injured

TB receipt frequency differed between herds (p<0.0001)

| | Herd 1<br>2.8 % | Herd 2<br>6.6% | Herd 3<br>10.8% |
|---|---|---|---|
| Group size | 8.5 $_{1.0}$ $^{a}$ | 12.7 $_{1.9}$ $^{b}$ | 14.7 $_{3.9}$ $^{c}$ |
| Density (pigs / m²) | 0.78 | 0.82 | 0.85 |
| Feeding system | single trough | single trough | dry feeder |

# Difference in performance between bitten females and non-bitten females

1. Classic linear model – no genetic effect

Phenotypic value:

Bitten females are leaner

| | E1 | E2 | E3 |
|---|---|---|---|
| **Age at 100 kg (days)** | +0,29 | +0,19 | -0,06 |
| **Backfat thickness (mm)** | -0,62 *** | -0,32 *** | -0,15 ° |

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2. Classic linear model **with direct** genetic effect

Genetic value:

and have a higher genetic merit for growth and leanness

| | E1 | E2 | E3 |
|---|---|---|---|
| **Age at 100 kg (days)** | +0,52 | -0,63 ** | -1,33 *** |
| **Backfat thickness (mm)** | -0,16 | -0,20 ** | -0,29 *** |

*Asreml Software*

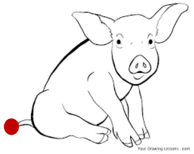
# Social linear model

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_D\mathbf{a}_D + \mathbf{Z}_S\mathbf{a}_S + \mathbf{Vg} + \mathbf{Wl} + \mathbf{e}$$

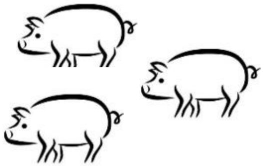
0/1 trait

$n$ group mates (H)YM

Direct genetic



Social genetic



Group

Litter

$$\sigma^2_{TBV} = \sigma^2_{A_D} + 2(\bar{n}-1)\sigma_{A_D,A_S} + (\bar{n}-1)^2\sigma^2_{A_S}$$

$$\sigma^2_P = \sigma^2_{A_D} + \sigma^2_g + \sigma^2_l + (\bar{n}-1)\sigma^2_{A_S} + \sigma^2_e$$

$$T^2 = \sigma^2_{TBV} / \sigma^2_P$$

1. All population
2. Sub-populations ⬄ 2 nucleus herds

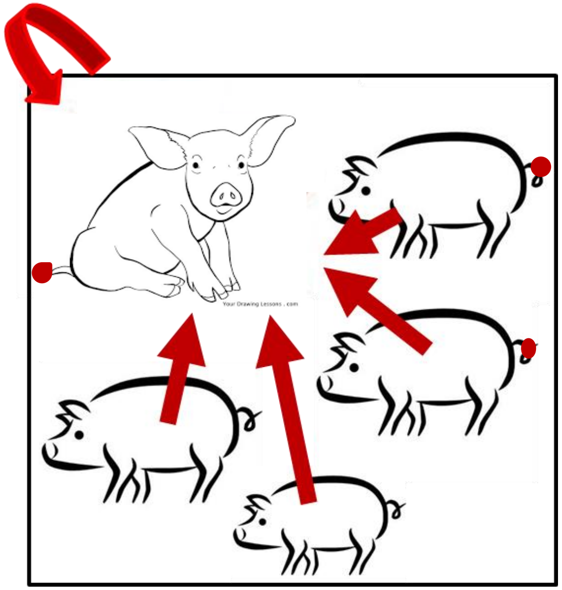
*Asreml software*

# Investigation of GxE

- Connectedness with use of common AI sires across herds
- 59 sires with ≥ 20 daughters measured for TB receipt in each herd

Sire by environment interactions

$$TBV_{ij} = DBV_{ij} + (n - 1)\ SBV_{ij}$$



Spearman rank correlations between DBVs, SBVs and TBVs

# Results 1 – social models

| | **All population** | | **Herd 2** | **Herd 3** |
|---|---|---|---|---|
| | | | | |
| **N** | 33266 | | 12375 | 11856 |
| $\sigma^2_{AD}$ | 0.353 0.049 | | 0.322 0.066 | 0.759 0.157 |
| $\sigma^2_{AS}$ | 0.032 0.0037 | | 0.012 0.0038 | 0.019 0.005 |
| $\sigma^2_{P}$ | 5.932 0.055 | | 5.753 0.087 | 8.94 0.157 |
| $\sigma^2_{TBV}$ | 4.749 0.529 | | 2.300 0.610 | 3.966 0.944 |
| $h^2_d$ | 0.06 0.01 | | 0.06 0.01 | 0.08 0.02 |
| $\hat{T}^2$ | 0.80 0.09 | | 0.40 0.11 | 0.44 0.11 |
| $r_{ADS}$ | 0.11 0.10 | | 0.19 0.19 | -0.13 0.18 |

Contribution of social effects to heritable variation

93% 86% 81%

*Variance estimates to multiply with a $10^{-2}$ factor*

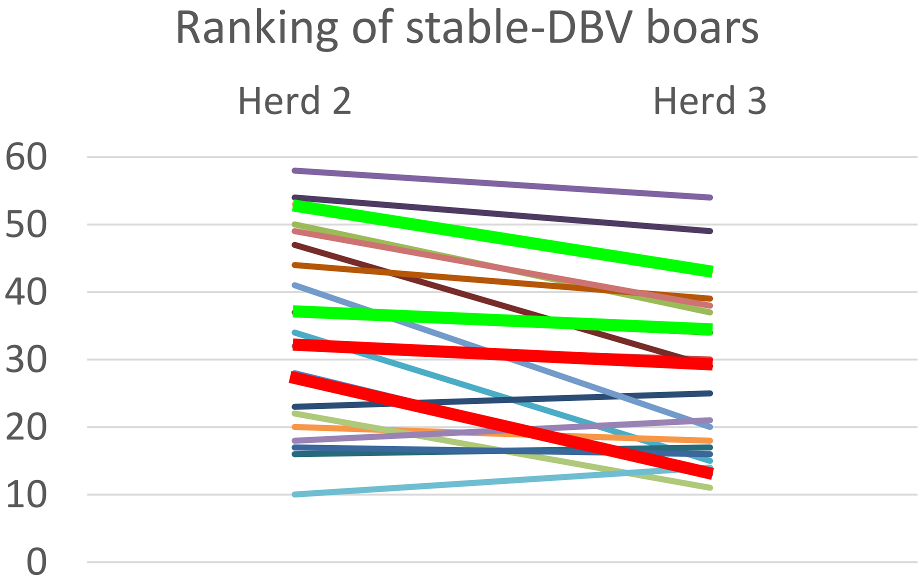
# Conclusion – social models

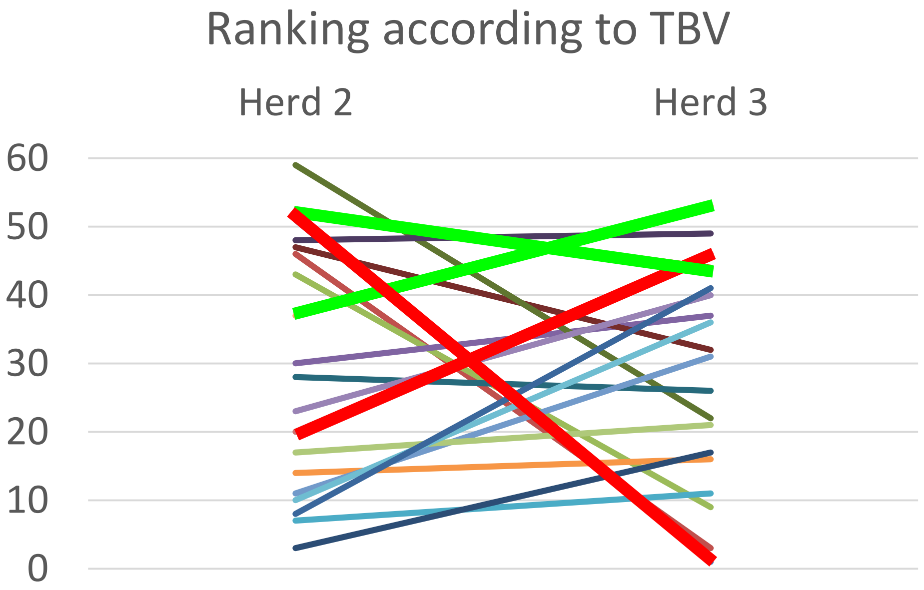
- Significant social effects with large genetic component on TB receipt

- Large expected gain on response to selection by including social genetic effects in models

# Results 2 – Sire ranking accross herds 2 and 3

| | Spearman rank correlation | p-value H0: r=0 |
|---|---|---|
| DBV | 0.09 | 0.49 |
| SBV | 0.12 | 0.37 |
| TBV | 0.13 | 0.32 |





# Conclusion – Sire x E

- Strong re-ranking across herds

- Selection based on TBV rather than DBV would either increase or attenuate the discrepancies in ranking between Herds 2 and 3

Recommendation

⇨ sires less sensitive to environmental conditions when implementing a selection against gilts with tail bitten

# Perspectives

- MODELLING
  Study genetic relations with growth + fatness
- SELECTION  limiting the impact of GxE
- New phenotyping technologies ⇨ behaviour

# *Thank you for your attention*

*Source: AXIOM*

# Modelling difficulties

**Binary trait**

- Threshold sire model
- Linear model ⇨ estimates for direct and social genetic effects

**Trait of low prevalence**

- Many individuals with 0 value
- 30% of informative groups (0 and 1 observations)

Genetic components not easy to estimate
but convergence and estimability correct

# Results – social models

| Herd | All population | Herd 2 | Herd 3 |
|---|---|---|---|
| | | | |
| N | 33266 | 12375 | 11856 |
| % TB receipt | 7.1 | 6.6 | 10.8 |
| $\sigma^2_{AD}$ | 0.353 0.049 | 0.322 0.066 | 0.759 0.157 |
| $\sigma^2_{As}$ | 0.032 0.0037 | 0.012 0.0038 | 0.019 0.005 |
| $\sigma^2_{P}$ | 5.932 0.055 | 5.753 0.087 | 8.94 0.157 |
| $\sigma^2_{TBV}$ | 4.749 0.529 | 2.300 0.610 | 3.966 0.944 |
| $h^2_d$ | 0.06 0.01 | 0.06 0.01 | 0.08 0.02 |
| $\hat{T}^2$ | 0.80 0.09 | 0.40 0.11 | 0.44 0.11 |
| $r_{ADS}$ | 0.11 0.10 | 0.19 0.19 | -0.13 0.18 |
| $\sigma^2_{g}$ | 0.519 0.049 | 0.717 0.077 | 1.323 0.143 |
| $\sigma^2_{l}$ | 0.235 0.027 | 0.103 0.037 | 0.467 0.076 |