Fine Mapping of QTL-regions for boar taint

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Topigs Norsvin

PROGRESS IN PIGS

Introduction

- Boar taint is unpleasant, problem can be avoided by castration, castration is unpleasant too, ethical issues, animal welfare, economical reasons, farmers' welfare, etc.
- Numerous QTL's have been defined on most of the pig chromosomes
- Earlier research in Norsvin Landrace and Norsvin Duroc indicated interesting regions on the genome:
  - On SSC7 at 74.7–80.5 Mb for skatol in both lines
  - On SSC5 at 22.6–24.8 Mb for androstenon in Norsvin Duroc
  - No simultaneous effect on the other sex steroids could make this interesting regions for selection against boar taint

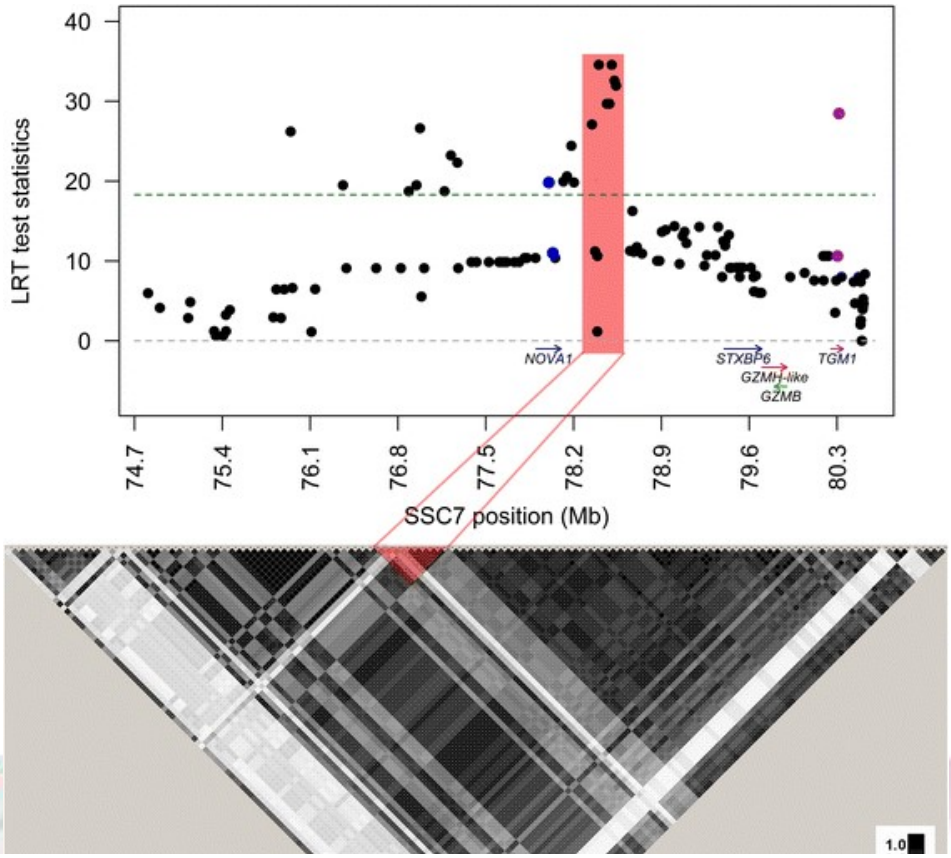
Objective of the study

- Fine map the most significant region affecting the level of skatole, found on SSC7 at 74.7–80.5 Mb for both Norsvin Landrace and Norsvin Duroc
- Fine map the QTL affecting the level of androstenone found at 22–25 Mb on SSC5 for Norsvin Duroc
- Scrutinize positional candidate genes for polymorphisms
- Identify causative mutations

What have we done

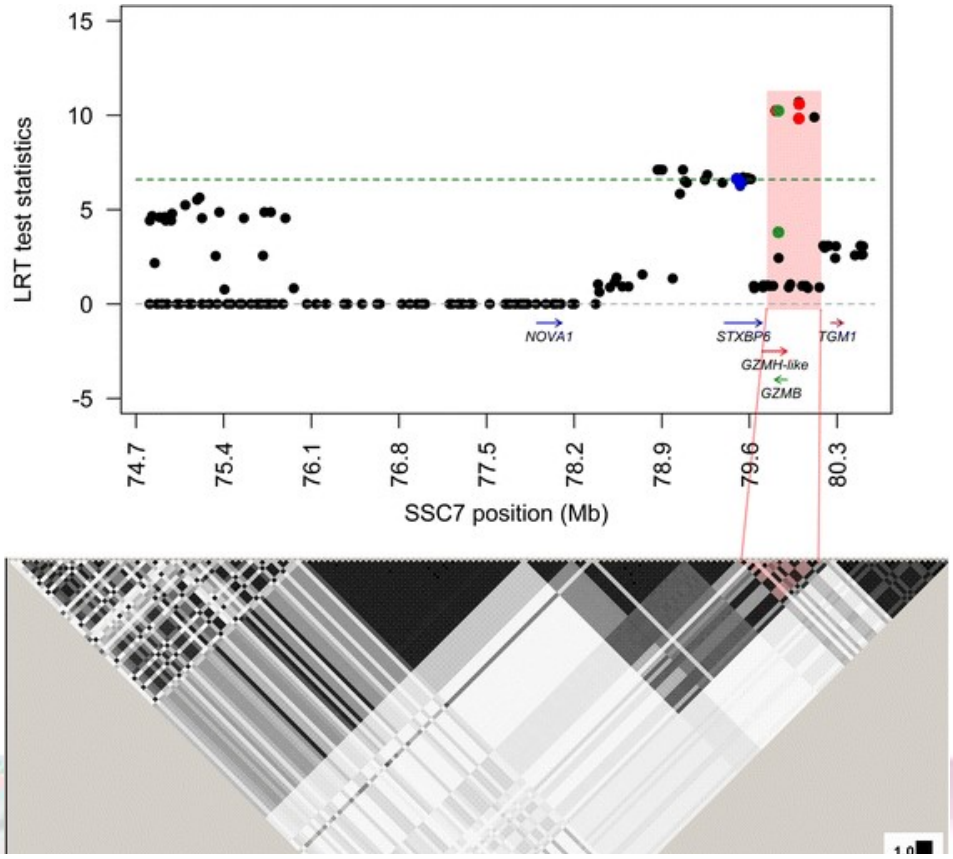
- Whole genome sequencing performed for 23 Norsvin Duroc and 24 Norsvin Landrace boars, frequently used AI-boars between 2010-2013, average per-animal coverage 9-17X
- 911 Norsvin Landrace and 767 Norsvin Duroc boars have been genotyped using 60k BeadChip (Illumina), for Landrace another 440 boars were available with 60k genotypes from a previous study
- All boars were reared under similar conditions up till 100 kg (156 days for Duroc, 143 days for Landrace) and slaughtered 15 days later
- Blood samples for DNA extraction were taken before slaughter, fat tissue samples for skatol and androstenone analysis were taken from the neck and collected in the slaughter line

Results – Landrace/Skatol



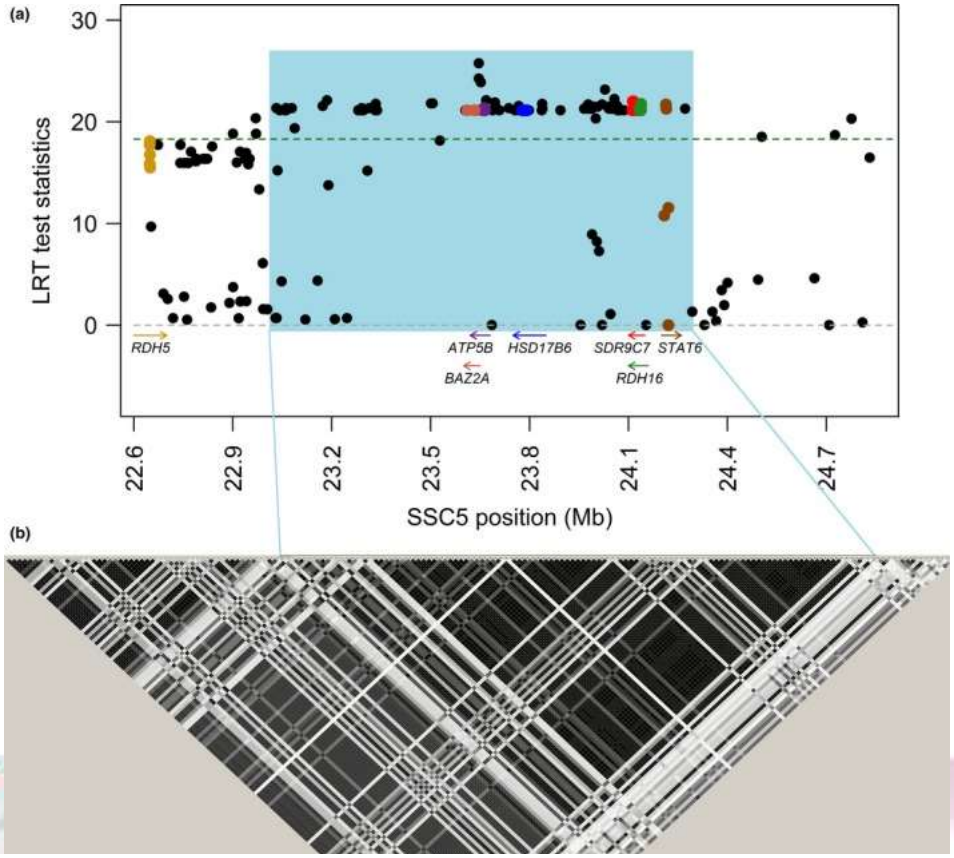
- Two SNPs located at 78.4 and 78.5 Mb in an intergenic region, explaining 5% of variation;
- In total, 21 SNPs significantly associated with skatol

Results – Duroc/Skatol



- Most significant SNP located at 80 Mb, explaining 2.6% of variation;
- In total, 18 SNPs significantly associated with skatol, but less significant compared to Landrace

Results – Duroc/Androstenone



- Two most significant SNPs in high LD with each other and physically linked (only 6 kb apart) at position 23,65 Mb in an intergenic region, explaining 5.4% of variation;
- In total, 94 out of 100 SNPs that are highly associated with androstenone are in a 1.24Mb extended block

Take-away message

- Using sequence data allowed us to narrow down the region of the QTLs
- Using sequence data did not, however, allow us to identify any causative mutation
- Each of the QTL regions, both in these two studies and others published, explain max 5 % of the genetic variance

In the meantime …

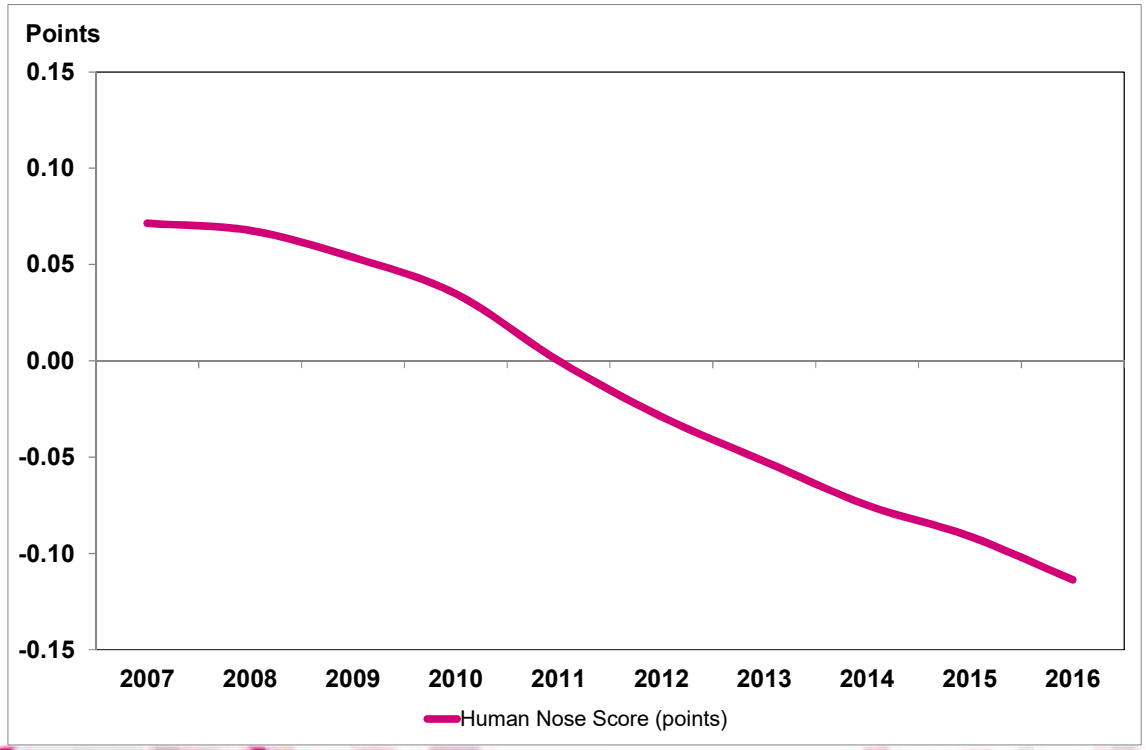
Human Nose Scores (HNS)

4	Strong penetrating odor
3	Penetrating odor
2	Abnormal odor
1	Slightly abnormal odor
0	Normal pork smell

Mathur et al. (2013) Meat Science. 91(4):414-22

"Closer to consumers' detection of boar taint then the boar taint compounds"

In the meantime …



- Genetic progress for full Topigs Norsvin product
- HNS range: 0.4 ~ 1.0, different by line
- Strongest improvement in reduction of the highest classes

Thank you for your attention!

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