

Lipogenic enzyme mRNA expression and fatty acid composition in relation to nutritional value of pork

Duncan T. Marriott^a, Joan Estany^b, Olena Doran^a

^aCentre for Research in Biosciences, University of the West of England, Bristol, UK

^bDepartament de Producció Animal, Universitat de Lleida, Lleida, Spain

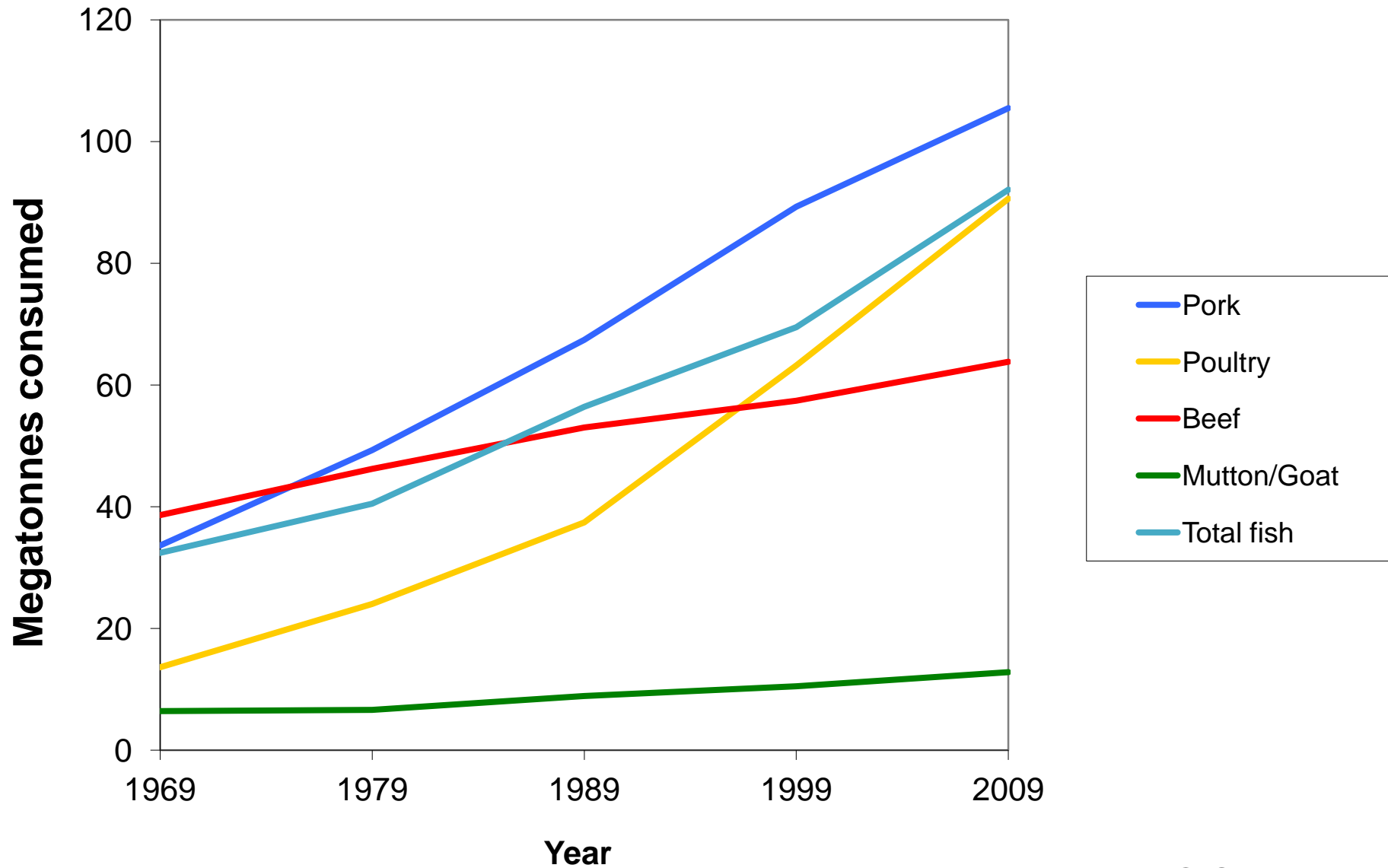
Background

- The composition of dietary fat has great importance for human health.
- Saturated fatty acids associated with cancer, CHD and obesity when consumed in high quantities.
- Consumption of unsaturated fatty acids has a number of health benefits.

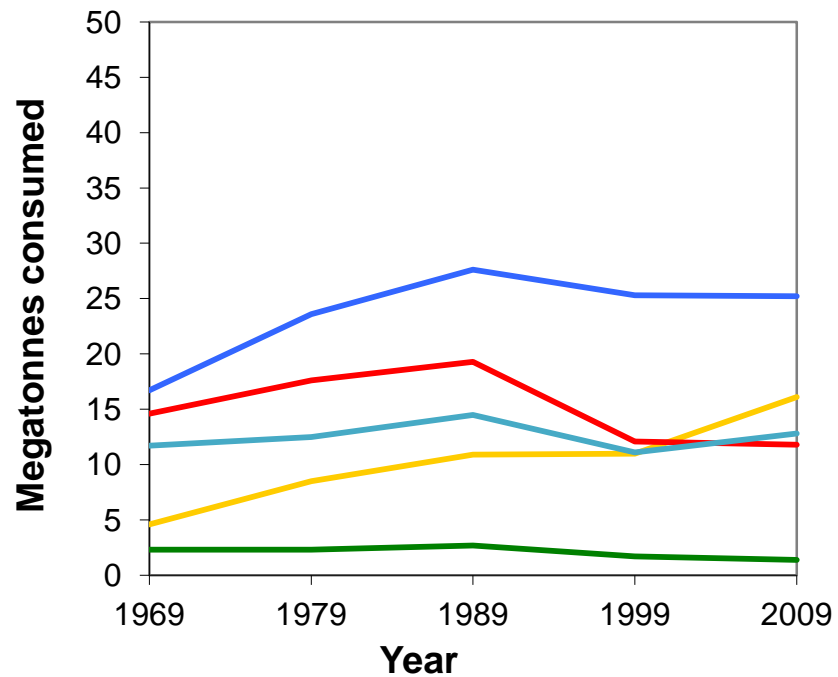
Ideal fatty acid composition

- Lower SFA
- Higher PUFA and MUFA
- Higher P:S ratio
- Lower n-6:n-3 ratio

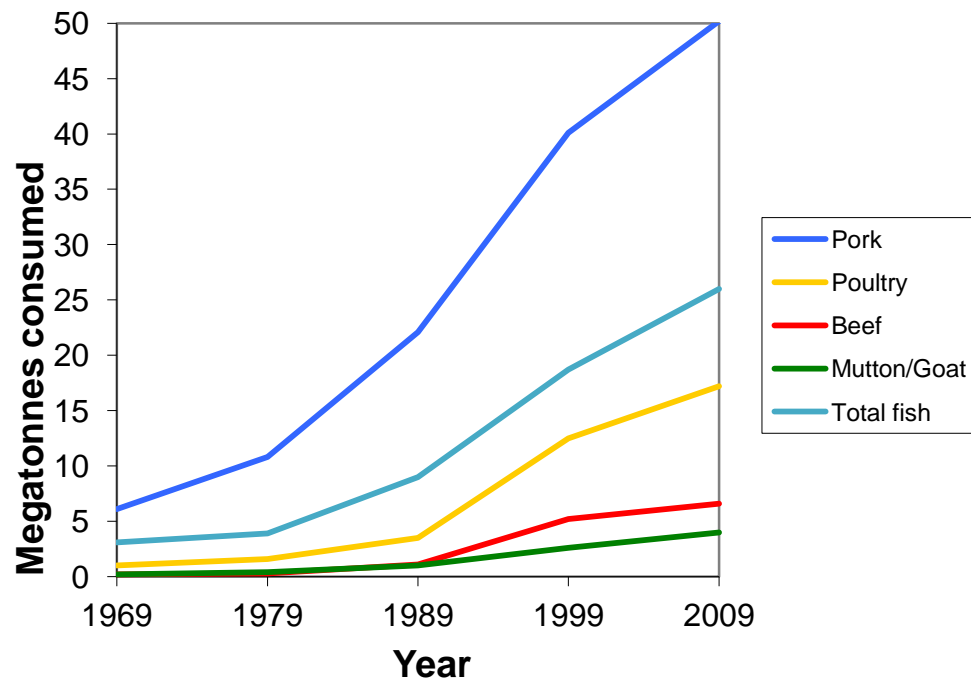
Global meat consumption 1969 - 2009



European meat consumption 1969 - 2009



Chinese meat consumption 1969 - 2009



- Subcutaneous fat (SF) - undesirable.
- Intramuscular fat (IMF) - desirable.

Genetic selection



Lower SF




Lower IMF



- Amount of fat and tissue distribution differs between breeds and individual animals within a breed.

Reduced protein diet  Increased IMF but not SF.

Doran et al, British J. Nutr., 2006

Reduced protein diet  Increased IMF in commercial breeds but not a traditional breed.

Wood et al, Meat Sci., 2004

- Implies genetic regulation of fat partitioning.

Lipogenic enzymes & fat deposition

- Stearoyl-CoA desaturase (SCD) → MUFA, IMF.
- Delta-6 desaturase ($\Delta 6D$) → PUFA, Breed-specific.
- Acetyl-CoA carboxylase (ACC) → SFA, ?

Candidate genes

Animals

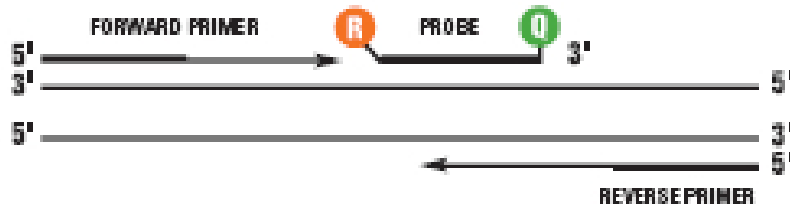
- 4 breeds, all barrows fed ad libitum.
 - Duroc 1 x Duroc 1 (D1xD1) n = 6
 - Duroc 1 x Duroc 2 (D1xD2) n = 7
 - Duroc 1 x Iberian (D1xI) n = 4
 - Large White x Landrace (LWxLr) n = 7
- Sampled for muscle and subcutaneous adipose tissue.

Methodology

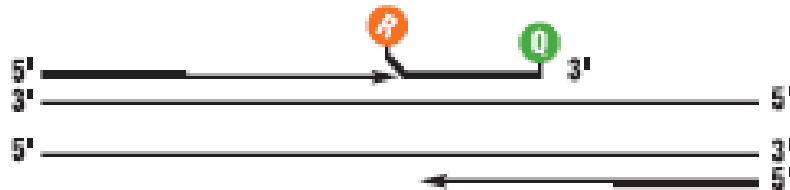
- Fatty acid composition – High Resolution Gas Chromatography
- mRNA analysis – TaqMan[®] real-time PCR
Gene expression assays

TAQMAN® PROBE-BASED ASSAY CHEMISTRY

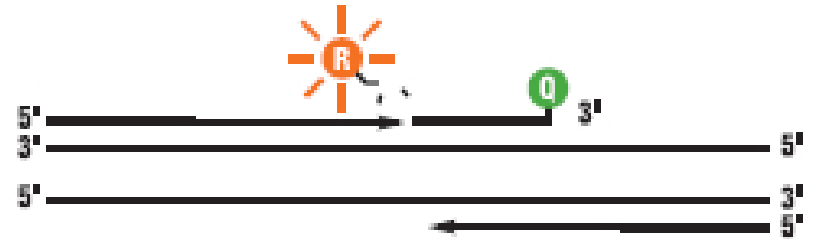
1. **Polymerization:** A fluorescent reporter (R) dye and a quencher (Q) are attached to the 5' and 3' ends of a TaqMan® probe, respectively.



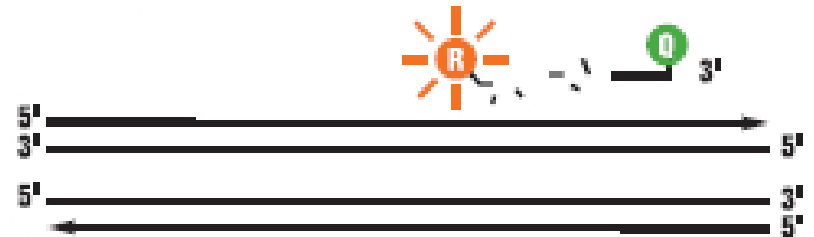
2. **Strand displacement:** When the probe is intact, the reporter dye emission is quenched.



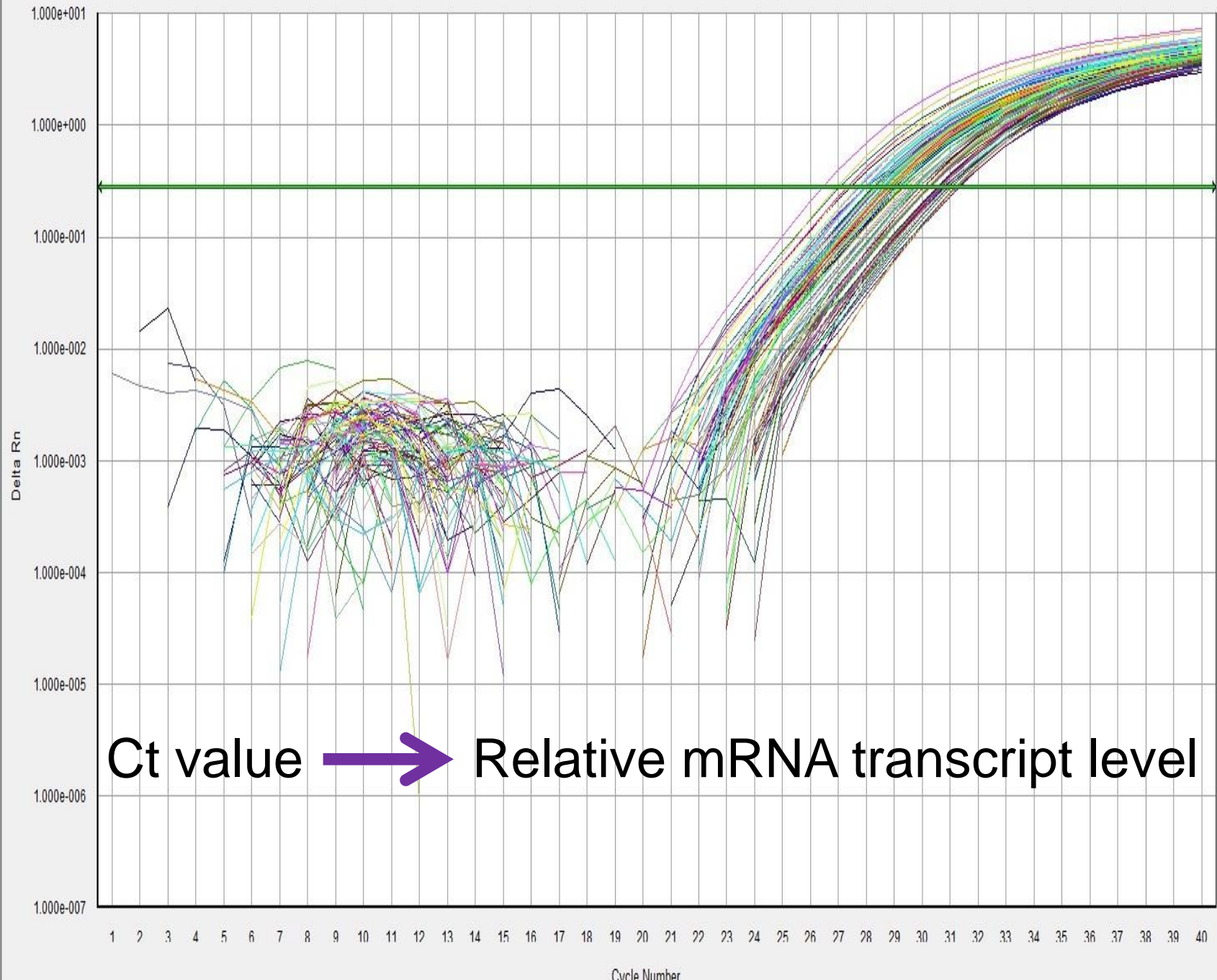
3. **Cleavage:** During each extension cycle, the DNA polymerase cleaves the reporter dye from the probe.



4. **Polymerization completed:** Once separated from the quencher, the reporter dye emits its characteristic fluorescence.



Delta Rn vs Cycle



Data: Delta Rn vs Cycle

Detector: All

Line Color: Well Color

Analysis Settings

Auto Ct

Manual Ct

Threshold: 0.279181

Auto Baseline

Manual Baseline:

Start (cycle): Auto

End (cycle): Auto

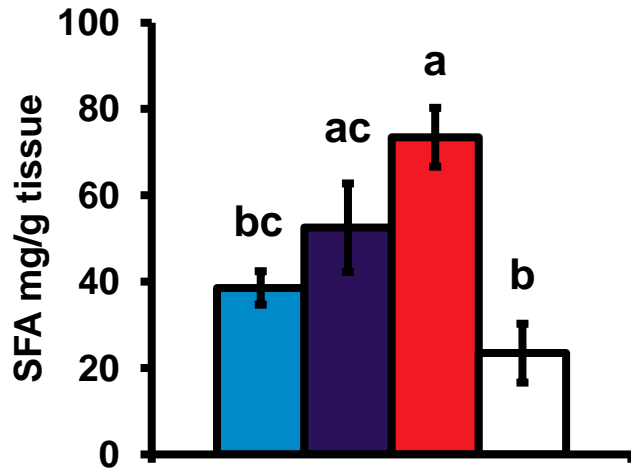
Analyze

Help

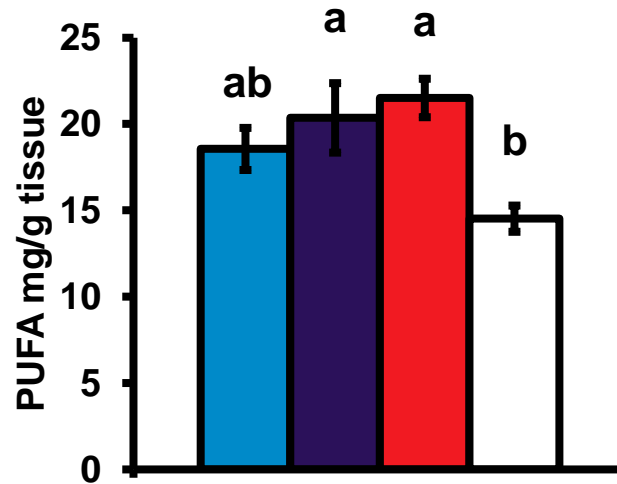
Ct value  Relative mRNA transcript level

Results – Fatty acid composition muscle

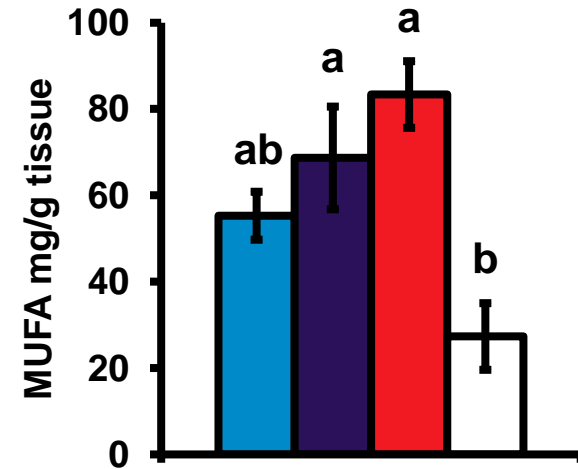
SFA in muscle



PUFA in muscle



MUFA in muscle



Legend

D1



D1xD2



D1xI

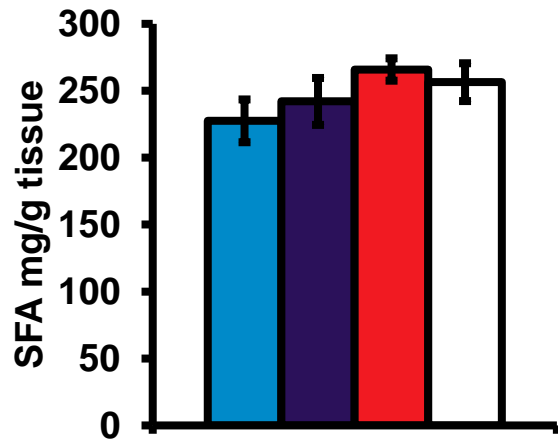


LWxLr

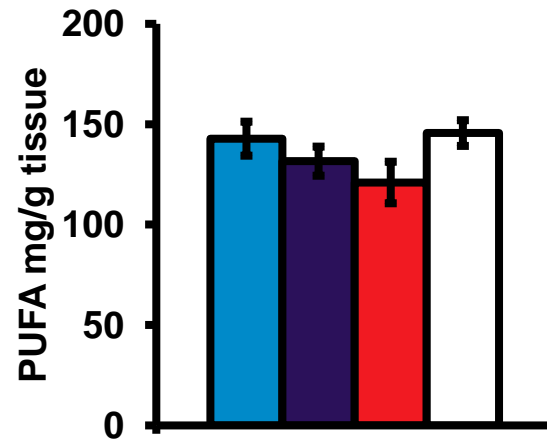


Results – Fatty acid composition adipose

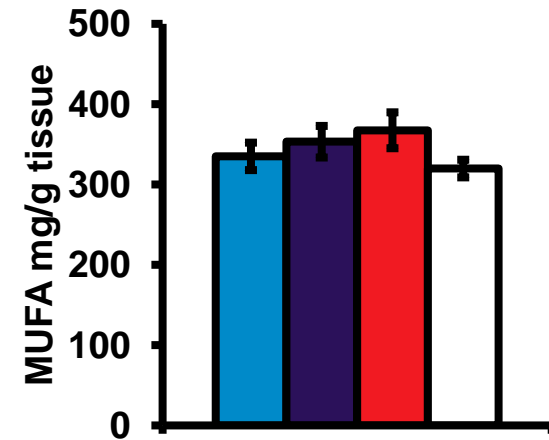
SFA in adipose



PUFA in adipose



MUFA in adipose



Legend

D1

D1xD2

D1xI

LWxLr



Results – SCD

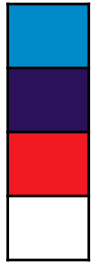
Legend

D1

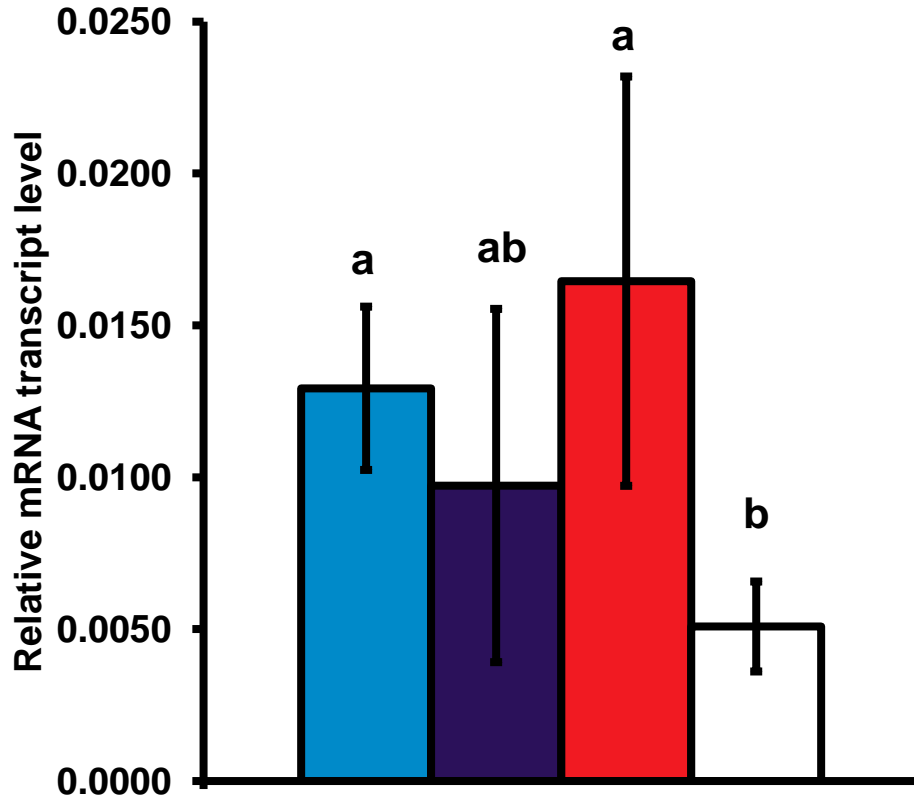
D1xD2

D1xI

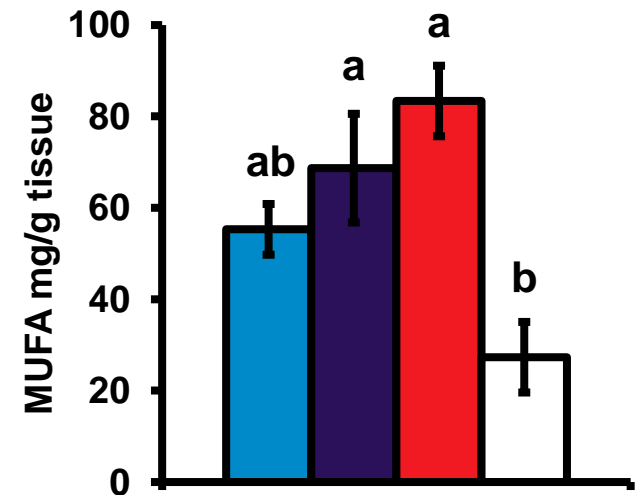
LWxLr



SCD mRNA expression in muscle



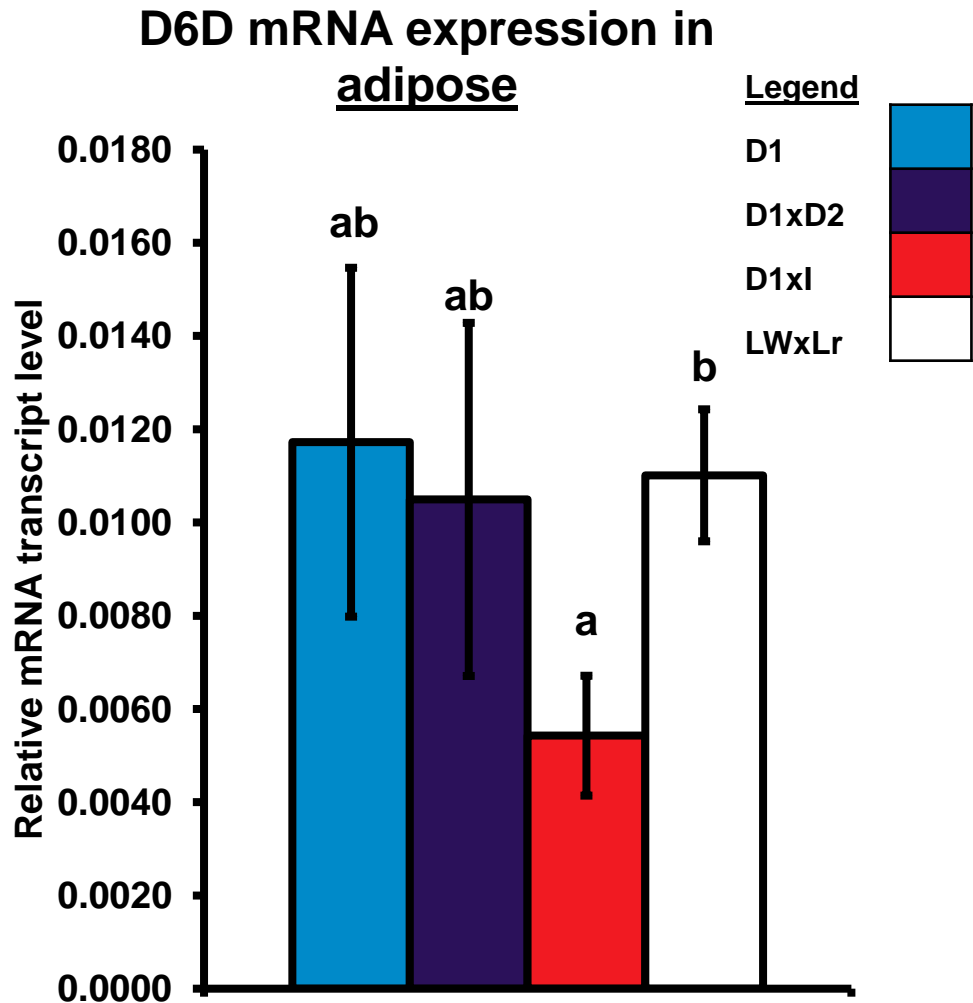
MUFA in muscle



• Adipose SCD mRNA and MUFA – both non-significant

Results – $\Delta 6D$

- Muscle $\Delta 6D$ mRNA
– all non-significant.
- Muscle PUFA
– D1xD2 and D1xI higher than LWxLr
- Adipose PUFA
– all non-significant.



Results - ACC

- Muscle ACC mRNA and SFA – both non-significant

- Adipose SFA – non-significant.

Legend

D1

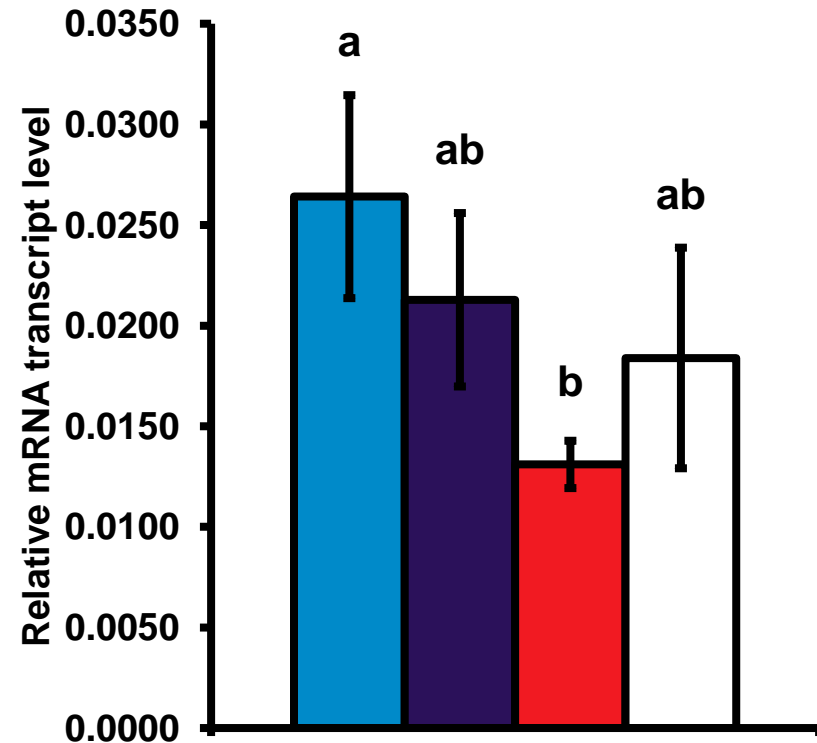
D1xD2

D1xI


LWxLr



ACC mRNA expression in adipose



Discussion

- Muscle MUFA: similar breed-differences to muscle SCD mRNA
 transcriptional regulation.
- Muscle PUFA: differences not explained by $\Delta 6D$ mRNA expression.

- Between-breed differences in adipose ACC and $\Delta 6D$ mRNA not accompanied by differences in SFA and PUFA content respectively.



Post-transcriptional regulation.

Conclusions

- Further evidence for both breed- and tissue-specific regulation of fat partitioning in pigs.
- MUFA content in muscle may be regulated by SCD at transcriptional level.
- SCD in muscle is a candidate for Single Nucleotide Polymorphism (SNP) discovery.

Acknowledgements

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Thank you for your attention



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