Breed effects on adipose tissue and muscle transcriptome in growing Iberian and Duroc pigs



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INTRODUCTION

Iberian pig production is based on both purebred Iberian and crossbred Duroc x Iberian pigs. Iberian and Duroc breeds show important phenotypic differences in growth, fattening, tissue composition and meat quality. The study of breed effects on gene expression, could explain phenotypic and metabolic differences between breeds.



Statistical March 19

AIM

The objective of this study was to evaluate breed effects on phenotype and ham subcutaneous adipose tissue and Biceps femoris muscle transcriptome in growing Duroc pigs with Iberian RNAseq and technology.

MATERIAL AND METHODS



PHENOTYPIC RESULTS

Higher subcutaneous fat thickness in Iberian			
24.1 <i>v</i> s 10.7 mm in loin <i>P</i> <0.001 27.8 <i>v</i> s 15.7 mm in ham P<0.001	ſ		
Higher average feed intake in Iberian	6		
2 <i>v</i> s 1.7 kg <i>P</i> <0.05	2		
Higher % IMF in <i>B.femoris</i> in Iberian			
3.7 vs 2.5 P<0.001			



TRANSCRIPTOMIC RESULTS

N° reads/sample: 38-55 millions % of mapped reads: 91-93 % Expression> 0.5 FPKM Fold change \geq 1.5 and **FDR<0.01**

SUBCUTANEOUS HAM FAT 349 DE genes 135 up-regulated in DUROC

BICEPS FEMORIS 347 DE genes 144 up-regulated in DUROC



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Higher ham weight in Duroc

4.5 vs 3.5 kg P<0.001

P*<0.05 ** *P*<0.01 **P*<0.001

Prediction Legend –

Prediction Legend

Increased measurement

edicted activation

Predicted inhibition

Predicted Relationships

Leads to activatior Leads to inhibitior

Decreased measurement (

ore extreme in dataset

Glow indicates activity when

nore confidence

DE genes upregulated in Duroc

DE genes upregulated in Iberian

FUNCTIONAL ANALYSIS

CANONICAL PATHWAYS ADIPOSE TISSUE



CANONICAL PATHWAYS BICEPS FEMORIS

positive z-score	□ z-score = 0	negative z-score	no activity pattern available	
-				
/				
6				





CONCLUSIONS

The results indicated a strong effect of the breed on gene expression in both tissues affecting relevant molecular functions related to the phenotypic differences observed. The bioinformatic analysis also allowed the prediction of potential regulators (such as ATF4, ERBB2, INS1 or TNF) for the expression differences observed.

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