

Genomic analysis of water holding capacity of meat in a porcine resource population



H. Heidt¹, M. Cinar¹, S. Sahadevan¹, C. Looft¹, D. Tesfaye¹, E. Tholen¹,
A. Becker², A. Zimmer², K. Schellander¹ and C. Große-Brinkhaus¹



¹Institute of Animal Science, Group of Animal Breeding and Husbandry, University of Bonn, Endenicher Allee 15, 53115 Bonn, Germany;
²Institute of Molecular Psychiatry, University of Bonn, Sigmund Freud Str. 25, 53127 Bonn, Germany; *eMail: cgro@itw.uni-bonn.de




Introduction

High losses of fluid in the form of drip may affect financial output, nutritional value, consumer appeal and technological properties of porcine meat. Combining genome wide association and expression analysis, it is possible to identify regulatory networks underlying the quantitative trait and localizing genomic variation.

Aim of this study: Identification of candidate genes related to drip loss by (1) analyzing the correlation of drip loss and transcript abundance and (2) combining genome wide gene expression profiling and genotyping.

Material & Methods



- Duroc × Pietrain resource population (DuPi):
 - 6 parental, 39 F₁, 169 F₂
 - Drip loss (bag method) 
- Gene expression profile: Affymetrix Porcine Genome Array
 - Samples from *M. long. dorsi* 
 - N = 100 F₂ DuPi
 - 32 Array data from a previous study¹
 - Normalization: plier²
 - Batch effect correction: ComBat³
- Genotyping: Illumina SNP porcine 60K chip 
- Quality control (QC):
 - call rate: 95 %, MAF > 5 %, missing rate per SNP: 2 %

Statistical analysis

- Correction of the expression value and drip loss using general linear model:
 - $y = \mu + \text{gender} + \text{season} * \text{place of slaughter} + \text{slaughter weight} + \text{slaughter age} + e$
- Pearson correlation coefficient for gene expression residuals and drip loss residuals
- Hyper geometric gene set enrichment test⁴
 - Overrepresentation of gene sets of particular KEGG-pathways
- Genome-wide association analysis : PLINK⁵
 - Simple linear regression of phenotype on genotype, permutation procedure to correct for family structure
 - False discovery rate⁶ (FDR) < 0.1
 - Transcript and SNP positions: *Sus scrofa* Build 10.2

¹ Ponsuksili et al. 2008, ² Affymetrix Technical Note 2005, ³ Johnson et al. 2007, ⁴ R package: Gostats, ⁵ Purcell et al. 2007, ⁶ Benjamini & Hochberg 1995

Results & Discussion

- 822 positive and 406 negative correlated ($p < 0.05$) gene transcripts with drip loss
- 8 significant enriched KEGG-pathways:
 - e.g. Glycolysis, pentose phosphate pathway & pyruvat metabolism
- 267 highly significant correlated ($p < 0.01$) transcripts were used for eQTL analysis
 - 1451 eQTL were identified (FDR < 0.1)
 - 8 eQTL were assumed to be *cis*-regulated (Table 1)
- AMBP is known to be involved in the formation of drip loss (Fig. 1, Cinar et al. 2012)
- SLC37A4 located on SSC9, trans eQTL on SSC18 where QTL for drip loss were identified (Fig. 2, Jennen et al. 2007)

Table 1: Potential *cis*-regulated eQTL (selected results)

SSC ¹	Gene name	Position of the transcript ²	SNP	Position of SNP ²	P-Value ³	Variance ⁴
1	ZNF79	301.85 – 301.87	ALGA0010677	303.48	5.10E-07**	0.175
1	AMBP	285.71 – 285.73	ASGA0007079	287.94	7.85E-06*	0.141
1	PCDH9	86.706 – 86.707	ALGA0004442	86.848	0.0001701**	0.102
10	RAB18	44.073 – 44.074	ALGA0058578	44.475	1.56E-06*	0.161
14	NEURL	124.31 – 124.39	ASGA0066211	124.32	5.73E-12***	0.303
14	NEURL	124.31 – 124.39	H3GA0042143	124.38	3.71E-05*	0.121

¹: *Sus scrofa* chromosome, Position of transcript and SNP in Mbp, ²: FDR<0.1, ³: FDR<0.05, ⁴: FDR<0.01, ⁴ gene expression variation expl. by the associated SNP

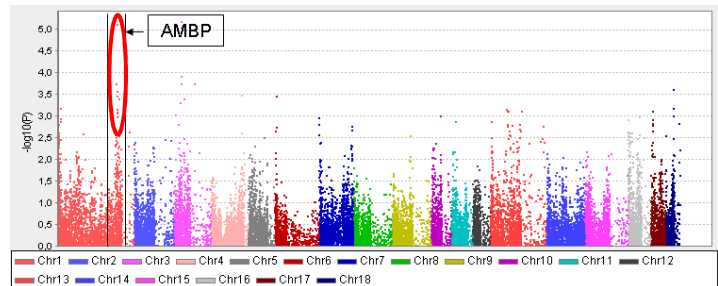


Figure 1: eQTL controlling expression of *polypeptide a-1-microglobulin/bikunin precursor* (AMBP), assumed *cis*-regulated

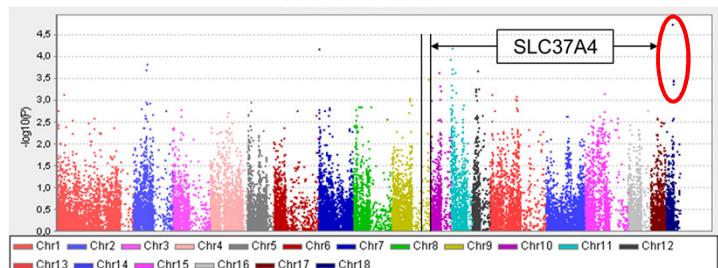


Figure 2: eQTL controlling expression of *solute carrier family 37, member 4* (SLC37A4), *trans*-regulated assumed

Conclusion

This approach supports to identify trait-associated SNPs and to understand the biology of complex traits. It was possible to identify new candidates and to confirm known candidate genes for drip loss. These promising candidate genes need further validation and the gene regulations have to be more closely investigated.

Acknowledgement

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