

feed efficiency in Hampshire sheep, but validation on a larger sample deserves further research efforts.

Gene <sup>1</sup> and Alleles	SNP ID <sup>2</sup>	Region	Genotypic Frequencies					
			Low RFI			High RFI		
			++	+-	--	++	+-	--
GHSR1a	A/C rs423156356	3' UTR	0.16	0.66	0.16	0.83	0.16	0
MBOAT4	A/G rs399405301	Coding	0.33	0.66	0	1	0	0
	G/A rs421869734	Intron	0.33	0.66	0	1	0	0
	A/T rs604106535	Intron	0.33	0.66	0	1	0	0
	G/A rs417836509	Intron	0.33	0.66	0	1	0	0
	G/A rs600356564	Coding	0.33	0.66	0	1	0	0
	G/A rs590893697	Intron	0.33	0.66	0	1	0	0

<sup>1</sup> GHSR1a = growth hormone secretagogue receptor 1a; MBOAT4 = membrane-bound O-acyltransferases 4

<sup>2</sup> dbSNP reference records

**Table 1.** Description of the markers mapping GHSR1a and MBOAT4 genes and the genotypic frequencies in Hampshire lambs with low and high residual feed intake

**Keywords:** ghrelin interaction network, nutritional status, RFI genetic markers

### PSXV-3 Genome-Wide Association Study for Sweat Gland Area in Multi-Breed Brahman-Angus Population.

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**Abstract:** Thermal stress in subtropical regions is a major limiting factor in beef cattle productions with around \$370 million being lost annually due to reduced performance. About 45% of beef cattle in the United States are in the southern and southeastern states where tropical and subtropical climates are most prevalent. Cattle utilize sweating to dispense most of their excess heat allowing them to return to their thermoneutral zone. The objective of this study was to conduct a genome-wide association study on sweat gland area in the Multi-breed Angus-Brahman herd of the University of Florida. Skin samples were collected along the shoulder from 337 cows of varying Brahman and Angus percentages. Cows were genotyped with the Bovine GGP F250k array. The biopsies were processed into histology slides and then ImageJ software was used to measure sweat gland area. A general linear model was used to test the significance of breed composition and age group on sweat gland area. Breed composition and age group had a significant effect on sweat gland area ( $P < 0.0001$  and  $P < 0.0001$ , respectively), with sweat gland area increasing with Brahman percentage. Quality control was conducted using BLUPF90 software including a call rate of 0.90 and a minor allele frequency of 0.01 which left 125,035 SNPs available for the single-step genome wide association analysis. BLUPF90 software was used to fit a single locus mixed model to test the effect of each marker. There were a significant SNPs located in the MINDY1 and

PRUNE1 gene, which are involved in cell proliferation and induction of cell motility. These results show that with selection on these SNPs, can improve the ability of cattle to adapt to thermal stress.

**Keywords:** Angus-Brahman, genome-wide association study, thermotolerance

### PSXV-7 Nutrient Digestibility Evaluation in Finisher Pigs from Diverse Feed Efficiency Groups.

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**Abstract:** Feed efficiency (FE) is a critical trait in swine production to improve the overall production efficiency and profitability and is an important goal for pig breeding companies. FE is a complex trait involving utilization and storage of dietary nutrients in different organs, and more especially in skeletal muscles. However, whether nutrient digestibility in the pig is altered by genetic selection for FE is less clear. Thus, this study investigated the variation in apparent total tract nutrient digestibility (ATTD) in finisher boars selected for high (HFE) or low (LFE) FE within a Large White dam and sire line. A total of 130 boars were selected at 23 wk of age based on their genomic-enabled breeding value for FE and fed ad libitum a corn-soybean meal-based diet using feeding stations that recorded individual feed intake and body weight. Fecal and diet samples were analyzed for dry matter, neutral detergent fiber, acid detergent fiber, crude protein (CP), energy, ash, phosphorus, and calcium to determine ATTD using acid-insoluble ash as an indigestible marker. There was no difference in ATTD values between genetic lines ( $P > 0.10$ ). However, HFE pigs had greater ( $P = 0.03$  ATTD of CP compared with LFE pigs. Based on the estimated protein deposition and the average feed intake one week before sampling, calculated dietary digestible lysine content diet met the requirements for the average pig. However, HFE pigs had a reduced feed intake, implying that they might have experienced a shortage of lysine in the diet. It is unclear whether the improved ATTD of CP was due to a lysine-shortage or differences in genetic merit for FE.

**Keywords:** acid-insoluble ash, feed conversion ratio, feed efficiency