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Data Article

Microarray analysis of subcutaneous adipose tissue from mature cows with divergent body weight gain after feed restriction and realimentation

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ABSTRACT

Body weight response to periods of feed restriction and realimentation is critical and relevant to the agricultural industry. The purpose of this study was to evaluate differentially expressed genes identified in subcutaneous adipose tissue collected from cows divergent in body weight (BW) gain after feed restriction and realimentation. We compared adipose samples from cows with greater gain based on average daily gain (ADG) during realimentation with samples from cows with lesser gain. Specifically, there were four comparisons including two comparing the high and low gain animals across each feeding period (feed restriction and realimentation) and two that compared differences in feed restriction and realimentation across high or low gain classifications. Using microarray analysis, we provide a set of differentially expressed genes identified between the high and low gain at both periods of nutrient restriction and realimentation. These data identify multiple differentially expressed genes between these two phenotypes across both nutritional environments.

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Specifications Table

Subject area	*Biology*
More specific subject area	*Livestock transcriptomics*
Type of data	*Table and figures*
How data was acquired	*Affymetrix Bovine 1.1ST Gene Array (Microarray technology)*
Data format	*Filtered, analyzed*
Experimental factors	*RNA isolated from adipose tissue collected from the same cows following exposure to two nutritional treatments; feed restriction and realimentation.*
Experimental features	*Transcriptomic analysis of subcutaneous adipose tissue from cows divergent in body weight gain following two nutritional treatments.*
Data source location	*USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE, USA*
Data accessibility	*Data is accessible through the NCBI GEO database. The series record ID is GSE94746 located at* https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE94746

Value of the data

- Body weight gain is a complex trait closely connected with feed efficiency; thus, identifying gene networks and metabolic pathways potentially involved in the divergence of weight gain may provide a platform for further investigation into some of the critical control points of feed efficiency.
- Adipose tissue is a highly metabolically active tissue and also is closely regulated by energetics of the animal. Gene networks identified in this tissue may provide insight into how, during extreme energy balance times, animals divergent in body weight gain, responds and adjusts to these nutritional extremes.
- Differentially expressed genes and pathways identified in these comparisons may be used in future experiments investigating response in adipose tissue to nutritional status and divergence in feed efficiency.
- Datasets evaluating the molecular mechanisms of feed restriction and realimentation in cattle are scarce; thus, these data may be useful for inclusion with additional sets of similar data for a meta-analysis of nutritional treatments.

1. Data

Microarray analysis comparing mRNA isolated from subcutaneous adipose of 12 cows (6 high ADG and 6 low ADG) collected at two nutritional stages (nutrient restricted vs. ad libitum). This results in four separate comparisons; 1) Feed-restricted treatment: high vs. low gain cows; 2) Ad libitum treatment: high vs. low gain cows; 3) Low gain cows: feed-restricted vs. ad libitum treatments; 4) High gain cows: feed-restricted vs. ad libitum treatments. A list of differentially expressed genes ($>$ 2.0-fold; nominal $P < 0.05$) was generated for each comparison (Supplementary material). Pathway analysis for the overrepresented down-regulated and up-regulated gene lists identified enriched pathways and relationships between pathways for each comparison (Figs. 1–8). For comparison 1, a total of 68 (61 annotated) down-regulated and 45 (39 annotated) up-regulated differentially expressed genes were used in pathway analyses with a total of 4 and 9 nodes identified containing 23 and 21 pathways, respectively (Figs. 1 and 2). In comparison 2, 27 (24 annotated) and 33 (30 annotated) differentially

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