

Summary of Adipose Genes Affecting Body Weight Gain in Mature Cows

-Lorianne Stevens

Most producers have asked at some point in their careers, how genetics affect average daily gain of an animal. To answer this question, Dr. Hannah Cunningham University of Wyoming Assistant Professor set out to determine the transcript abundance for metabolic regulation in fat tissue.

Feed costs tend to be the largest expenses on cow/calf operations. The better part of the feed provided goes to maintenance requirements. In times of drought or high feed costs, cows that are genetically predisposed to lower energy expenditure for maintenance are better able to support not only pregnancy and milk production but also greater average daily gain.

Over 700 quantitative trait loci have been identified in relation to average daily gain, however these may have only a small effect on gain. Fewer genes with possibly greater effect have been identified using feed restriction followed by reintroduction of *ad libitum* feed to represent true differences in response to energy state.

Genes affecting the degradation of the amino acid valine were associated with increased gains following a period of feed restriction. Valine degradation prevents buildup of toxic branched-chain amino acids. Any changes in amino acid degradation and synthesis can affect rate of gain.

The study also identified the LPS/IL-1 inhibition of the retinol x receptor function pathway in high gain animals. This pathway is responsible for inflammatory responses that can inhibit transcription. Cunningham believes that cattle with higher gains could respond to periods of nutrient restriction more favorably due to decreased maintenance costs by regulating pathways such as this.

This research was the first to examine the differences of gene expression in fat tissue between feed restricted and free-fed mature cows. This study paves the road for more research to discover key genes and their roles in fat tissue and how they influence weight gain and gain efficiency in mature cows.

Cunningham hopes one day that these genes will serve as genetic markers to be used by producers as selection tools for breeding cattle with greater feed efficiencies and abilities to respond more favorably to periods of nutrient restriction.