



## Monday June 26<sup>th</sup>: ADSA-USD Competition: Original Research Poster Presentations

### Molecular and gene expression changes in liver tissue from mid-lactation dairy cows supplemented with methionine during a subclinical mastitis challenge.

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#### POSTER1034M

The objectives were to assess molecular changes in the liver of cows supplemented with methionine during solely a subclinical mastitis challenge (SMC). Thirty-two multiparous Holstein cows (145±51 DIM) were enrolled in a randomized complete block design and assigned to either a basal diet (CON; n=16) or a basal diet supplemented with rumen-protected methionine (SM; n=16, Smartamine M 0.09% DM). The dietary treatment was administered at -21 days relative to a SMC, and data were collected from 0 to 3 days. At 0 d relative to SMC, the mammary gland rear right quarter was infused with 500,000 cfu of *Streptococcus uberis* (O140J). Blood samples were collected during SMC to assess inflammation, oxidative stress, and liver function biomarkers. Liver biopsies were taken -10 and 1 d relative to SMC. Genes related to methionine and glutathione metabolism, inflammatory response, and oxidative stress were analyzed via qPCR and western blots. Data were analyzed using the PROC MIXED procedure of SAS with TRT and TRT\*TIME interaction as an effect. Significance was declared at  $P \leq 0.05$  and trends at  $P \leq 0.10$ . There was no TRT\*TIME interaction for any of the evaluated genes. A trend ( $P = 0.07$ ) for greater milk yield (+0.9 kg) was observed in SM cows than CON. Methionine metabolism genes *MAT2A* and *PEMT* were upregulated ( $P = 0.02$ ) in SM cows compared with CON. *BHMT* was downregulated ( $P = 0.03$ ) in SM cows compared with CON. Compared to CON, a trend ( $P = 0.09$ ) was observed for upregulation of *MAT1A* in SM cows. Immune cell signaling gene *MYD88* was downregulated ( $P = 0.01$ ) in SM cows compared with CON. A trend ( $P = 0.06$ ) in haptoglobin (*HP*), a positive acute-phase response, was observed, where *HP* was downregulated in SM cows compared with CON. A transcription factor involved in antioxidant regulation, *NRF2*, was upregulated ( $P = 0.01$ ) in SM compared with CON. A trend

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( $P = 0.09$ ) was observed in glutathione synthetase (*GSS*), which directs the final step in glutathione biosynthesis, where *GSS* was upregulated in SM cows compared with CON. The lower reduction in milk yield in SM cows during the SMC could be associated with upregulation of antioxidant-related genes and downregulation of inflammatory-related genes.

Keywords: Methionine, Inflammation, Oxidative Stress

**Adisseo Message:**

Feeding methionine during the peripartum period is becoming a common practice in commercial herds. Cows fed Smartamine M during this period have shown increased DMI and milk production, have experienced lower incidence of post-calving metabolic disorders and have had higher plasma antioxidant status. This trial was designed to determine the metabolic response of cows fed Smartamine M infected by infusing *Streptococcus uberis* to the rear right quarter of the mammary gland. Methionine is not an antibacterial drug, but rather it is a required nutrient that has functional properties. The results of this work demonstrate how methionine affects metabolic pathways that impact antioxidant-related genes, and therefore provides meaningful insights that help to explain the better health and higher milk production of cows after calving.