

Abstract #M217

Section: [Physiology and Endocrinology](#)

Session: [Physiology and Endocrinology: Effects of nutrition and metabolism on ruminant reproduction](#)

Format: [Poster](#)

Day/Time: [Monday 7:30 AM–9:30 AM](#)

Location: [Gatlin Ballroom](#)  Find It

M217

Effects of rumen-protected methionine and choline supplementation on gene expression of follicular cells of the first postpartum dominant follicle.

[Diego A. Velasco Acosta](#)^{*1,2}, Ines M. Rivelli², Cassandra Skenandore², Daniel Luchini³, Marcio Corrêa¹, Felipe Cardoso^{2,1}, *Universidade Federal de Pelotas, Pelotas, Rio Grande do Sul, Brazil*, ²*University of Illinois, Urbana, IL*, ³*Adisseo NA, Alpharetta, GA*.

This study aimed to determine the effects of rumen-protected methionine and choline supplementation during the transition period on mRNA expression of follicular cells of the 1st postpartum dominant follicle in Holstein cows. Multiparous cows were assigned in a randomized complete block design into 4 treatments from 21 d before calving to 30 DIM. Treatments were: CON (n = 10, fed the close-up and fresh cow diets with a Lys:Met = 3.5:1), MET (n = 9, fed the basal diet + methionine, Smartamine M to a Lys:Met = 2.9:1), CHO (n = 9, fed the basal diets + choline 60 g/d, Reashure), and MIX (n = 12, fed the basal diets plus Smartamine M to a Lys:Met = 2.9:1 and 60 g/d Reashure). Follicular development was monitored via ultrasound every 2 d starting at 7 DIM until the first dominant follicle reached a diameter of 16 mm. Follicular fluid from each cow was aspirated and cells were retrieved immediately by centrifugation and stored at -80°C until RNA extraction. Statistical analysis was performed using the MIXED procedure of SAS. Gene expression of *LHCGR*, *STAR*, *3 β -HSD*, *P450 $_{\text{scc}}$* , *P450 $_{\text{c17}}$* , *CYP19A1*, *IRS1*, *IGF*, *MAT1A*, *SAHH*, *TLR4*, *TNF*, *IL1- β* , *IL8* and *IL6* was measured by real-time PCR. Treatments did not affect mRNA expression of *LHCGR*, *STAR*, *P450 $_{\text{scc}}$* , *CYP19A*, *SAHH*, *MAT1A* and *IL6* ($P > 0.05$) however, *3 β -HSD* expression was higher ($P < 0.05$) for MET (1.46 ± 0.3) and MIX (1.25 ± 0.3) than CON (0.17 ± 0.04) and CHO (0.26 ± 0.1). For *TNF*, *TLR4* and *IL1-B* mRNA expression was higher ($P < 0.05$) for CON (11.70 ± 4.6 , 21.29 ± 10.4 , 6.28 ± 1.4) than CHO (2.77 ± 0.9 , 2.16 ± 0.9 , 2.29 ± 0.7) and MIX (2.23 ± 0.7 , 1.46 ± 0.6 , 2.92 ± 0.8). There was higher ($P < 0.05$) *IL1- β* expression and a tendency ($P = 0.07$) for higher TNF expression in CON (6.27 ± 1.4 , 11.70 ± 4.6) than MET (3.28 ± 0.6 , 3.06 ± 0.8). There was no difference ($P = 0.43$) between CON and MET for *TLR4*. Expression of *IL8* mRNA was lower ($P < 0.05$) for CHO (0.98 ± 0.3) than CON (4.90 ± 0.7), MET (6.10 ± 1.7) and MIX (5.05 ± 1.8). In conclusion, supplementing Smartamine M and Reashure during the transition period changed mRNA expression in follicular cells of the 1st postpartum dominant follicle in Holstein cows.

Key Words: methionine, choline, gene expression