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Session 4 Poster 23

Saccharomyces cerevisiae fermentation products supplementation to dairy calves: effects on growth, metabolism, and immune status

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To evaluate the effect of supplementing Saccharomyces cerevisiae fermentation products (SCFP) on calf growth, metabolism, and immune status, 18 Holstein female calves were allocated to 2 treatments: control (CTR; n=9; no supplementation) or supplemented group (SCFP; n=9; 1 g/d of SmartCare®, Diamond V, in milk replacer plus 5 g/d of NutriTek®, Diamond V, from 5 to 70 d in the starter). Calves were weaned at d 60 and feed intake was recorded up to d 70. Body weight (BW) was measured until d 160, and blood samples were collected regularly until d 70 for the assessments of metabolic profile, plasma volatile fatty acids, and polymorphonuclear cells (PMN) phagocytosis. Data were analyzed using a mixed model for repeated measures. Compared with CTR, SCFP had increased post-weaning growth, with greater average daily gain from d 70 to 100 (+57%; P<0.01) and BW from d 100 to 160 (~9 kg more; P<0.04). SCFP tended to have greater plasma β-hydroxybutyrate at d 60 (P=0.06) and urea at d 70 (P=0.08) and had higher plasma concentration of acetate and propionate (P<0.05), suggesting an increased rumen activity. The latter might reduce weaning stress. Plasma myeloperoxidase was higher in SCFP at d 70 (P=0.04), as well as PMN phagocytosis at d 60 and 70 (P=0.03), indicating improved immune system functionality. In conclusion, supplementing SCFP improved the metabolic and immune status of dairy calves and supported the post-weaning growth.

Session 4 Poster 24

Effect of age, undernutrition and hydroxythyrosol supplementation on metabolic stress markers during the last third of gestation in beef cattle

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Undernutrition in late pregnancy is a common scenario in beef herds. Hydroxytyrosol (HT), a polyphenol present in olive leaves, has been shown to improve antioxidant capacity. The aim of this study was to assess the effects of undernutrition (100% vs. 60% of requirements) and HT supplementation (Control vs. HT, 178±36 mg/kg) during the last term of pregnancy on whole blood gene expression of redox and energy metabolism markers in beef cattle. Blood samples were collected from 56 cows at week 37 after mating. Gene expression of SOD1, CAT, GPX1, NRF2, ALOX5, SCD, and IGF-R was analysed by qPCR. A general linear model including fixed effects (nutrition, HT supplementation and cow age (<8 vs. ≥8 years)) and their interactions was used to compare gene expression with JMPro software. A higher SCD expression was observed in 100% than 60%-cows, while higher ALOX5 expression was observed in HT than control cows (P < 0.05). Lower SCD expression would indicate impaired lipogenic activity in 60%-cows, whereas ALOX 5 upregulation could imply the activation of a prompt termination of the inflammatory stress during the peripartum in HT cows. In <8-year-old cows, there was an increase in NRF2 and IGF-R expression, along with a decrease SOD1, CAT, and GPX1 expression compared to ≥8-year-old cows (P < 0.05). Our results suggest that older cows exhibit higher metabolic flexibility and higher antioxidant status than younger cows during peripartum period. Overall, cow age, undernutrition and HT supplementation influenced metabolic stress markers during peripartum period in beef cattle. Funded by PID2020-113617RR-C21/22.