Performance, whole-blood immune gene expression, and plasma metabolome of beef steers fed diet supplemented with a *Saccharomyces cerevisiae*-based direct-fed microbial

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INTRODUCTION

The feedlot-receiving period is characterized by several stressors caused by separation from the mother, commingling, transportation, vaccination, exposure to pathogens, and changes in diet and environment (Arthington et al., 2013). Research studies have focused on evaluating several nutritional strategies, including the use of DFM to optimize animal performance and immunity during the receiving period (McAllister et al., 2011). The objective of this study was to evaluate the effects of dietary supplementation of a blend of DFMs and their fermentation products on performance, immunity, serum biochemistry, and plasma metabolome of newly weaned beef steers during a 42-d receiving period.

MATERIALS AND METHODS

- Forty newly weaned Angus crossbred steers (7 days post-weaning; 210 ± 12 kg of BW; 180 ± 17 d of age) from a single source were stratified by BW into 4 weight blocks
- The steers were assigned to two treatments for a period of 42 d.
  - Diet with no additive (**CON**; n = 20)
  - CON + 19 g of Commence Additive (**PROB**; n = 20)
- Commence™ Feed Additive (PMI, Arden Hills, MN) is an optimized blend of 6.2 × 10^{11} cfu/g of *S. cerevisiae*, 3.5 × 10^{10} cfu/g of a mixture of *Enterococcus lactis, Bacillus subtilis, Enterococcus faecium, and L. case*i, and the fermentation products
- The quantity of feed offered to each steer was recorded daily. Diet refused (as fed) was also measured daily
- Body weights of steers were obtained before morning feeding on d 0, 21 and 42.
- 15 mL of blood was taken before the morning feeding on d 0, 21, and 42 for subsequent whole blood immune gene expression and plasma metabolome analysis.
- Expression of 84 genes related to innate and adaptive immune responses was analyzed using the RT2 Profiler™ cow innate and adaptive immune responses PCR Array (PABT-052ZA; Qiagen)
- In-depth untargeted metabolome profile of the plasma samples collected on d 42 was done using CIL/LC-MS-based technique

RESULTS

Table 1. Effects of a blend of *Saccharomyces cerevisiae*-based direct-fed microbial and fermentation products on the performance of steers during a 42-d receiving period

Item	CON	PROB	SE	P-value
Initial weight, kg	209	210	8.08	0.95
d 1 – 42				
Final weight, kg	260^{b}	270^{a}	2.67	0.01
ADG, kg/d	1.23^{b}	1.42^{a}	0.06	0.04
DMI, kg/d	5.86	6.11	0.15	0.24
Feed efficiency	0.209^{y}	0.232^{x}	0.01	0.10
d 1 – 21				
ADG, kg/d	1.24	1.32	0.10	0.56
DMI, kg/d	5.43	5.72	0.18	0.25
Feed efficiency	0.226	0.232	0.01	0.82
d 22 – 42				
ADG, kg/d	1.23^{b}	1.50^{a}	0.08	0.02
DMI, kg/d	6.30	6.50	0.17	0.41
Feed efficiency	0.196^{b}	0.230^{a}	0.01	0.05

CON = control; PROB = a blend of *Saccharomyces cerevisiae*-based direct-fed microbial and fermentation products fed at 19 g/steer/day.
^{a,b}Means with different superscript letters differ at $P \leq 0.05$
^{x,y}Means with different superscript letters differ at $0.05 < P \leq 0.10$

Table 2. Effects of a blend of *S. cerevisiae*-direct-fed microbial and fermentation products on blood immune gene expression in beef steers during a 42-d receiving period

Gene Name	Gene symbol	Day 21		Day 42	
		Fold change[1]	P- value	Fold change[1]	P- value
Toll-like receptor 2	TLR2	1.46	0.02	1.82	0.01
Toll-like receptor 6	TLR6	1.27	0.01	1.52	0.01
Tumor Necrosis Factor	TNF	1.22	0.05	1.53	0.02
Signal transducer and activator of transcription 6	STAT6	1.32	0.02	1.22	0.04
Caspase 1	CASP1	1.38	0.04	1.29	0.02
Interleukin 8	IL-8	0.43	0.01		
Intercellular adhesion molecule 1	ICAM1			1.29	0.02
Retinoic acid-related -related orphan receptor C	RORC			1.25	0.03
Transcription factor T-bet	TBX21			1.44	0.01
Toll-like receptor 1	TLR1			2.01	0.01
C-X-C motif chemokine receptor 3	CXCR3			1.20	0.02

[1]Fold change (relative to CON) = $2^{-\Delta\Delta Ct}$ = $[(CT_{\text{gene of interest}} - CT_{\text{reference genes}})_{PROB} - (CT_{\text{gene of interest}} - CT_{\text{reference genes}})_{CON}]$.
Only genes with both fold-change ≥ 1.2 or ≤ 0.83, relative to Control and $P \leq 0.05$ are shown.
CON = control; PROB = a blend of *Saccharomyces cerevisiae*-based direct-fed microbial and fermentation products fed at 19 g/steer/day.

RESULTS

Table 3. Identified peak pairs (tier 1 and tier 2) that were affected by dietary supplementation of a blend of *S. cerevisiae*-based direct-fed microbial and fermentation products.

Item	Normalized RT	FC	P-value	Identification level
5-Methylcytosine	529.1	1.20	0.02	Tier 2
Indole-acrylic acid	1247	1.26	0.002	Tier 1
5-Aminopentanoic acid	523.9	0.72	0.007	Tier 1
4-Methylaminobutyrate	553.6	0.79	0.001	Tier 2
3,4-Dihydroxyphenylethyleneglycol	636.0	0.80	0.001	Tier 2
Trans-2,3-Dihydroxycinnamate	841.9	0.81	0.01	Tier 2
2-Hydroxy-3-(4-hydroxyphenyl)propenoate	871.8	0.81	0.02	Tier 2

Normalized RT (retention time) shows the corrected retention time of the peak pair with Universal RT Calibrant data.
FC: fold change relative to Control;
P-value was calculated from student's t-test;
Tier 1 - Positive Identification (CIL Library);
Tier 2 - High Confidence Putative Identification (LI Library).

CONCLUSIONS

- This study demonstrated that PROB diet improved the growth and feed efficiency of newly weaned beef steers during the receiving period.
- The increased growth and feed efficiency was supported by increased expression of genes responsible for promoting the animal's immune response toward intracellular and extracellular pathogens.
- In addition, plasma untargeted metabolomic profiling of the steers fed PROB diet revealed an increase in the concentration of metabolites involved in protecting the animals against inflammation.

REFERENCE

- Arthington, J. D., R. F. Cooke, P. Moriel, N. Dilorenzo, and G. C. Lamb. 2013.
- McAllister, T., K. A. Beauchemin, A. Alazzeh, and K. Stanford. 2011.

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