BEEF & FORAGE CENTER

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UT BEEF AND FORAGE CENTER
Research and Recommendation Meeting
December 20, 2022

10:00 am EST	Welcome and Introductions	
10:10 – 10:40 am	UTIA focus on beef and forage work	UTIA administration
10:40 – 11:00 am	UT Smoking School	Gary Bates
11:00 – 11:20 am	New techniques to determine consumer preferences	Charlie Martinez
11:20 – 11:40 am	Alfalfa addition to grass pastures and hayfields	Renata Nave Oakes
11:40 – 12:00 pm	Research overview from CVM	David Anderson
12:00 – 1:00 pm	Lunch	
1:00 – 1:20 pm	Composting large livestock carcasses	Jennie Ivey
1:20 – 1:40 pm	Upper Cumberland Team Forage Webinar Series	Chris Hicks
1:40 – 2:00 pm	PLF equipment at MTREC	Kevin Thompson
2:00 – 2:20 pm	Cover crops as forages	Virginia Sykes
2:20 – 2:40 pm	New FDA rules on over-the-counter drugs	Lew Strickland
2:40 – 3:00 pm	Forage testing capabilities	David McIntosh
3:00 – 3:20 pm	BVD research	Andi Lear
3:20 – 3:40 pm	Water intake by growing cattle	Kyle McLean
3:40 pm	Wrap up	Gary Bates

Table of Contents

Research Reports

Abstracts

The effects of protein supplementation on growth and economic factors in developing replacement heifers.

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Take Home Message: *Replacement heifer development is one of the most critical components of cow-calf production and generally requires supplemental feeds to ensure the growth and maturation of heifers. However, protein supplementation above 10% did not impact reproductive maturation but did influence the cost associated with replacement heifer development*

Summary: The development of replacement heifers is one of the most critical components of cow-calf production. Most heifer development programs require supplemental feeds to ensure heifers are pubertal entering their first breeding season. Spring-born crossbred Angus heifers (n = 60) were blocked by BW and randomly assigned to one of 3 dietary supplements: 1) 10% crude protein (**CP**) supplement (**CON**), 2) 20% CP supplement (**P20**), or 3) 40% CP supplement (**P40**). Heifers were housed in groups of 5 heifers each resulting in 4 pens per treatment. To test the effects of differing protein supplementation levels on BW, BCS, and economic factors associated with heifer development, a mixed model ANOVA was completed via PROC GLIMMIX (SAS 9.4, Cary, NC). Final BW for CON group heifers (744.5 ± 9.74 lbs) was lower ($P < 0.01$) than both P20 and P40 (828.3 ± 9.74, 831.4 ± 9.74 lbs; respectively). Similarly, BCS was lower ($P=0.007$) in the CON heifers (5.57 ± 0.027) compared with the P20 (5.82 ± 0.027) and P40 (5.82 ± 0.027) heifers at the end of development. The total cost per heifer was greater ($P<0.001$) for the CON heifers ($109.22 ± 1.1) than the P40 heifers ($101.04 ± 1.1) which were also greater than the P20 heifers ($91.20 ± 1.1). In conclusion, protein supplementation above 10% is not necessary for reproductive maturation but can impact the cost associated with replacement heifer development

Introduction

There are nearly 6 million replacement heifers annually, development of these females is one of the most critical components in cow-calf production. Most heifer development programs require supplemental feeds to meet nutritional requirements. These supplements are typically energy and protein dense to help ensure that heifers entering their first breeding season have reached puberty and average 60 to 65% of mature BW (Patterson et al., 1992; Perry et al., 2012). Heifers that conceive earlier in the first breeding season have longer to recover after calving increasing the chance to rebreed the following breeding season. A review of the association between pre-breeding BW and heifer pregnancy reported opportunities to limit growth early during development to reduce costs per pregnancy (Endecott et al., 2013. However, in most cases, a longer breeding season (~15 days) or lower overall pregnancy rates (3-5%) occurred in the lighter BW heifers (Funston et al., 2012).

Protein is the first limiting nutrient in cattle production systems grazing low-quality forages. Supplementing feedstuffs high in protein has been demonstrated to help overcome these deficiencies and benefit reproductive function, usually via decreased age at puberty (Lalman et al., 1993; Funston et al., 2012). Economic advantages exist for producers to utilize low-input strategies via supplementing replacement heifers consuming primarily forage. Nearly $100 per head reduction in production costs was reported when supplementing replacement heifers grazing forages instead of rearing heifers in a more intensive, dry-lot system (Dickinson et a., 2019). The hypothesis of the current study was that supplemental protein would alter costs of development without influencing the maturation of replacement heifers.

Materials and Methods

Approximately one month after weaning, spring-born crossbred Angus heifers (n = 60) from the Middle Tennessee Research and Extension Center were grouped into 4 blocks based on BW and randomly assigned to one of 3 dietary supplements: 1) 10% crude protein (**CP**) supplement (**CON**), 2) 20% CP supplement (**P20**), or 3) 40% CP supplement (**P40**). All heifers had ad-libitum access to native grass hay (95.62% dry matter, 7.60% CP, and 1.97% fat). This resulted in diets with an estimated crude protein of 11, 15, and 19% for CON, P20, and P40 heifers, respectively. Heifers were housed in group pens of 5 heifers each resulting in 4 pens per treatment. To maintain similar energy levels (via controlled intake) between treatments, supplementation levels were adjusted every two weeks, targeting an average daily gain (**ADG**) of 1.50 lbs. per day for all treatments. To test the effects of differing protein supplementation on the BW, BCS, and economic factors associated with heifer development, a mixed model ANOVA was completed via PROC GLIMMIX (SAS 9.4, Cary, NC). Means were determined to be significantly different when $P > 0.05$ and a tendency when $P > 0.10$

Results and Discussion

The relationship between BW, BCS, and the economic impacts of protein supplementation during heifer development are reported in **Table 1**. The initial BW was not different ($P = 0.87$) between CON, P20, or P40 heifers (587.7 ± 4.07 lbs, 584.8 ± 4.07 lbs, and 586.9 ± 4.07 lbs; respectively).

Table 1. The effects of protein supplementation on body weight (BW) and body condition score (BCS) during heifer development.

TRT[1]	CON	P20	P40	SE	*P* – Value
Initial BW	587.7^a	584.8^a	586.9^a	4.07	0.87
Final BW	744.5^b	828.3^a	831.4^a	9.74	<0.01
ADG[2]	1.1^b	1.73^a	1.76^a	0.06	<0.001
Initial BCS	5.45^b	5.72^a	5.85^a	0.025	<0.01
Final BCS	5.57^b	5.82^a	5.82^a	0.027	0.007
Total Supp. (lbs.)[3]	758.6^a	608.1^b	631.6^b	3.38	<0.001
Supp. Cost[4]	288	300	320	---	---
Cost per Heifer ($)	109.22^a	91.20^c	101.04^b	1.11	<0.001

[1] TRT: is the protein supplementation given to heifers; CON – 10% protein, P20 – 20% protein, P40 – 40% protein

[2] ADG: average daily gain

[3] Total Supp. Is the total supplement consumed per heifer

[4] Supp. Cost is the cost per ton of supplement

However, final BW for CON group heifers (744.5 ± 9.74 lbs) was lower ($P < 0.01$) than both P20 and P40 (828.3 ± 9.74, 831.4 ± 9.74 lbs; respectively). The ADG also showed that.the CON heifers (1.1 ± 0.06) gained less ($P<0.001$) per day compared with both P20 and P40 (1.73 ± 0.06 and 1.76 ± 0.06 lbs/d; respectively; **Table 1**). While BW is certainly important to reproductive development, BCS is even more so influential to reproductive function. Minimizing mature BW did not have a negative impact on reproductive performance (Endecott et al., 2013). This supports our findings that BCS more accurately describes the body energy reserves of the animal, There has also been observed that there is a positive correlation between BCS and fertility, given that the heifer is not over conditioned (Utter et al., 1994). The Initial BCS shows that the CON group (5.45 ± 0.025) was less than (P<0.01) P20 and P40 (5.72 ± 0.025 and 5.85 ± 0.025; respectively). Similarly, the final BCS was lower (P=0.007) in the CON heifers (5.57 ± 0.027) compared with the P20 (5.82 ± 0.027) and P40 (5.82 ± 0.027) heifers (**Table 1**).

The objective of this study was to evaluate the economic impacts (feed consumed and development cost) of different protein supplementation levels on heifer development. The CON heifers (758.6 ± 3.38 lbs) consumed more ($P<0.001$) supplements than P20 and P40 (608.1 ± 3.38 lbs and 631.6 ± 3.38 lbs; respectively; **Table 1**). However, the P20 and P40 heifers consumed similar amounts of supplement throughout development. The cost per ton of each supplement was $288, $300, and $320 for CON, P20, and P40, respectively. The total cost per heifer was greater ($P<0.001$) for the CON heifers ($109.22 ± 1.1; **Table 1**) compared with the P20 heifers ($91.20 ± 1.1) whereas the P40 cost ($101.04 ± 1.1) was intermediate.

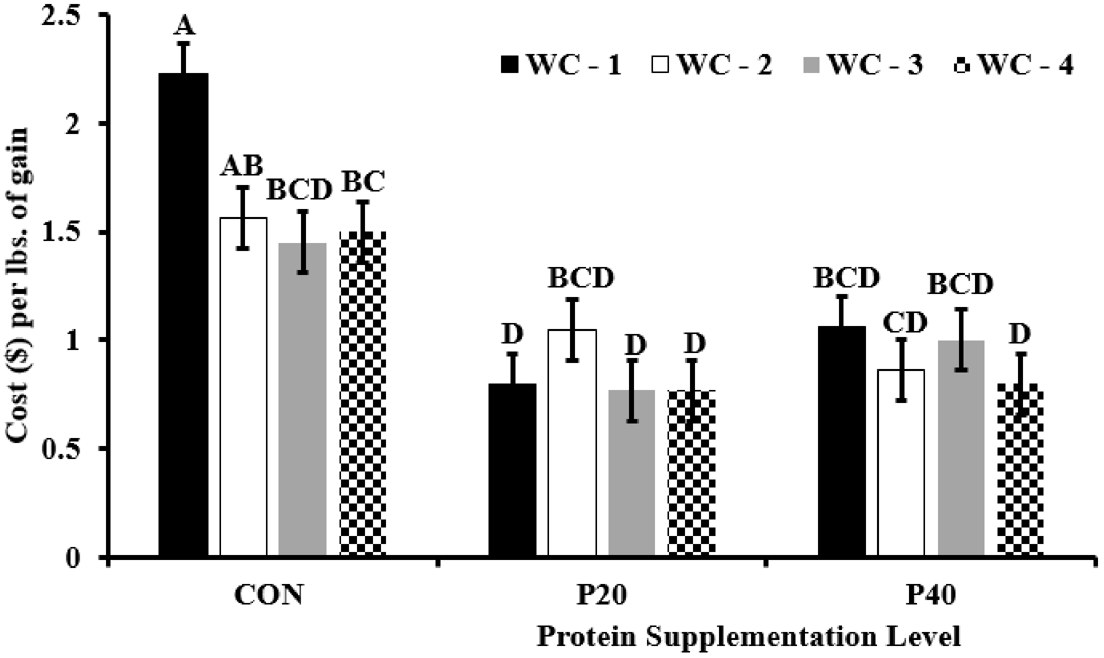

Figure 1. The effects of protein supplementation and weight class on the cost per lbs. of gain during heifer development.

The cost per pound of gain for the CON group (1.44-2.2 ± 0.14) was higher ($P<0.0001$) than P20 and P40. The cost per pound of gain for WC 1 (2.2 ± 0.14) was higher than the other three weight classes in the CON. The cost per pound of gain for WC 3 in CON (1.45± 0.14) was similar to that of WC 2 (1.05± 0.14) in P20 as well as WC 1 (1.06± 0.14) and WC 3 (0.99± 0.14) in P40. Weight class 1, 3, and 4 (0.79, 0.77, 0.76 ± 0.14, respectively) of P20 heifers and WC 4 (0.79± 0.14) of P40 heifers were similar (**Fig. 1**). Since BCS has been found to correlate with fertility and reproductive performance, and based on the data findings, the CON group was the least economically feasible, since the lower supplementation level led to more supplement required, making their maintenance the most expensive. As for P40, the combination of their decreased BCS and their more expensive maintenance compared to P20 shows that P20 was the most reasonable supplementation level. This means that to find the balance between protein supplementation level, cost, and reproductive efficiency, P20 was the most effective and reasonable option.

Acknowledgments

The authors would like to thank Kevin Thompson and the Middle Tennessee Research and Education Center staff for help in collecting samples and providing care for the animals used in the study. Additionally, the authors would like to thank the state of Tennessee through UT AgResearch, the Department of Animal Science, and the USDA National Institute of Food and Agriculture, Hatch Project No. 1019048 for providing funding and support

Literature Cited

Dickinson, S. E., M. F. Elmore, L. Kriese-Anderson, J. B. Elmore, B. N. Walker, P. W. Dyce, S. P. Rodning, and F. H. Biase. 2019. Evaluation of age, weaning weight, body condition score, and reproductive tract score in pre-selected beef heifers relative to reproductive potential. Journal of Animal Science and Biotechnology 10:18.

Endecott, R., R. Funston, J. Mulliniks, and A. Roberts. 2013. Joint Alpharma-Beef Species Symposium: implications of beef heifer development systems and lifetime productivity. Journal of Animal Science 91(3):1329-1335.

Funston, R., J. Martin, D. Larson, and A. Roberts. 2012. Physiology and endocrinology symposium: nutritional aspects of developing replacement heifers. Journal of animal science 90(4):1166-1171.

Lalman, D., M. Petersen, R. Ansotegui, M. Tess, C. Clark, and J. Wiley. 1993. The effects of ruminally undegradable protein, propionic acid, and monensin on puberty and pregnancy in beef heifers. Journal of animal science 71(11):2843-2852.

Patterson, D., R. Perry, G. Kiracofe, R. Bellows, R. Staigmiller, and L. Corah. 1992. Management considerations in heifer development and puberty. Journal of Animal Science 70(12):4018-4035.

Perry, G., E. Larimore, G. Bridges, and R. Cushman. 2012. Management strategies for improving lifetime reproductive success in beef heifers. Proceedings, Applied Reproductive Strategies in Beef Cattle 30:249-266.

Utter, S., P. Houghton, L. Corah, D. Simms, M. Spire, and M. Butine. 1994. Factors influencing first-service conception and overall pregnancy rates in commercial beef heifers.

The effects of growth rate on the economic factors in developing replacement heifers.

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Take Home Message: *Replacement heifer development is one of the most critical components of cow-calf production. Management strategies that meet thresholds for development are more important than the process; however, the economic impacts of how heifers are developed could impact the bottom line for producers.*

Summary: Replacement heifer development is one of the most critical and costly components of cow-calf production. Heifers that conceive early in the breeding season have longer to recover after calving and a better chance to rebreed the following year. Our hypothesis was that growth rates throughout development would impact the cost without changing production status at the onset of the first breeding season. Angus-crossbred heifers (n=48) were blocked by body weight (**BW**) and randomly placed in pens of 4 heifers. The pens (n=12) were then randomly assigned to one of 3 supplemental treatments resulting in 4 pens per treatment: 1) control (**CON**); targeted 1.5 lbs./day for the entire treatment period (120 d), 2) fast then slow (**F/S**); targeted 2.75 lbs./day for the first 57 d then 0.25 lbs./day for the last 63 d, and 3) slow then fast (**S/F**); targeted 0.25 lbs./day for the first 57 d then 2.75 lbs./day for the last 63 d. Initial and final BW as well as average daily gain were not impacted ($P \geq 0.31$) by growth rate. Initial and final BCS were different ($P \leq 0.05$) across the three treatment groups. The total amount of supplement consumed was the highest ($P < 0.001$) in the CON group (706.2±0.001) and the S/F group (612.7±0.001) was higher than the F/S (583.7±0.001). The supplement and overall gain to feed (**G:F**) were different ($P < 0.001$) between all three treatment groups but the G:F for hay was not impacted by growth rate ($P = 0.40$). The cost per pound of gain only tended ($P = 0.07$) to be impacted by growth rate with the CON group costing the most per lbs. of gain during development. The growth rate of heifers did not impact development but could impact the economics of heifer development and the foundation of cow-calf production.

Introduction

There are over 5 million replacement heifers entering the US beef herd annually. The development of these females is one of the most critical components of cow-calf production. Most heifer development programs require supplementation to meet nutritional requirements for development which may not be supported by forages alone. These supplements are typically energy and protein dense to help ensure that heifers entering their first breeding season are on a positive plane of nutrition (Patterson et al, 1992; Perry et al., 2002) and that a majority have reached puberty. Heifers that conceive earlier in the breeding season have longer to recover after calving and a better chance to rebreed the following year. Funston et al. (2012) reviewed the association between pre-breeding BW and heifer pregnancy and found opportunities to limit growth during development but in most cases, this required a longer breeding season (~15 days) or resulted in slightly lower overall pregnancy rates (3-5%).

One of the most important factors in early reproductive success is nutrition. Replacement heifers must be supplied enough energy to support both somatic development and reproductive function. Strictly monitoring the rate of gain is essential in the development of heifers. By maintaining a balanced diet, producers can encourage essential reproductive development while at the same time preventing over- and under-conditioning (Garret, 1988; Larson, 2007). Ultimately, studies have indicated that the rate of growth during heifer development is not as important as reaching a target body weight before the breeding season. However, the rate of growth may impact molecular mechanisms of reproductive efficiency (Cardoso et al., 2014) and the overall economics of heifer development. Therefore, our hypothesis was that increased growth rate diets will trigger a different inflammatory response in developing beef heifers compared with more moderate growth trajectories.

Materials and Methods

Weaned Angus-crossbred heifers (n=48; Average BW 712.27±3.87 lbs.) were blocked by BW and randomly placed in pens of 4 heifers. The pens (n=12) were then randomly assigned to one of 3 supplemental treatments resulting in 4 pens per treatment: 1) control (**CON**); targeted 1.5 lbs./day for the entire treatment period (120 d), 2) fast then slow (**F/S**); targeted 2.75 lbs./day for the first 57 d then 0.25 lbs./day for the last 63 d, and 3) slow then fast (**S/F**); targeted 0.25 lbs./day for the first 57 d then 2.75 lbs./day for the last 63 d. Heifers were offered ad libitum access to native grass hay (95.62% dry matter, 7.60% crude protein, and 1.97% fat), commercial trace mineral supplement (Tennessee Farmers', Cooperative; La Vergne, TN), and water. Grain supplements comprised of 75% dry distillers' grain and 25% corn were provided 4 times per week to maintain protein levels (Marston et al., 1995) and meet targeted gains. All G:F ratios were calculated using lbs of gain divided by total lbs of supplement, hay, or overall intake. Hay intake was estimated at 3% of BW. To test the effects of growth rate on the BW, BCS, and economic factors associated with heifer development, a mixed model ANOVA was completed via PROC GLIMMIX (SAS 9.4, Cary, NC). Means were determined to be significantly different when $P>0.05$ and a tendency when $P>0.10$.

Results and Discussion

The initial BW for the CON, S/F, and F/S (637.6±3.2 lbs., 630.3±3.2 lbs., and 645.9±3.2 lbs.) are all similar ($P=0.31$; **Table 1**). Similarly, final BW (831.2±4.88 lbs., 825±4.88 lbs., and 836.1±4.88 lbs.) and ADG were also not different ($P\geq0.76$; **Table 1**) for CON, S/F, and F/S (1.6±0.03 lbs./d, 1.63±0.03 lbs./d, and 1.58±0.03 lbs./d, respectively). These data confirm that the developmental programs were all successful even with the differential growth rates. We did not observe any reproductive differences in these animals (data not shown). This supports previous work that placed an emphasis on BW at the time of the first breeding season (Funston et al., 2012). However, initial BCS was different ($P = 0.05$) among the three treatment groups with controls starting at a greater BCS (5.5±0.06) compared with both S/F and F/S (5.3±0.06 and 5.35±0.06, respectively; **Table 1**). Body condition score at the end of the trial was also different ($P=0.04$) between treatments with the CON group (5.4±0.06) having a greater BCS than S/F (5.2±0.06) and the F/S group intermediate (5.3±0.06; **Table 1**).

Table 1. The effects of growth rate on body weight (BW) and body condition score (BCS) during heifer development.

TRT[1]	CON	S/F	F/S	SE	*P* – Value
Initial BW	637.6^{a}	630.3^{a}	645.9^{a}	3.2	0.31
Final BW	831.2^{a}	825^{a}	836.1^{a}	4.88	0.76
ADG[2]	1.6^{a}	1.63^{a}	1.58^{a}	0.03	0.92
Initial BCS	5.5^{a}	5.3^{b}	5.35^{b}	0.06	0.05
Final BCS	5.4^{a}	5.2^{b}	5.3^{ab}	0.06	0.04

[1] TRT: is the nutritional plane of heifers during development; CON – linear constant growth, S/F – slow then fast growth, F/S – fast then slow growth

[2] ADG: average daily gain

While these were significant due to the subjective nature of BCS and the lack of BW differences any physiological effects should have been limited

The total amount of supplement consumed (TC) was the highest (*P* < 0.001) in the CON group (706.2 ± 0.001) and the S/F group (612.7 ± 0.001) was higher than the F/S (583.7 ± 0.001; **Table 2**). Since all heifers were provided the same supplement at a cost of \$300 per ton the linear growth heifers (CON) would have cost the most to develop. To further elucidate the impacts of growth rate analyses of the G:F ratio for the supplement, hay, and overall was conducted. The supplement G:F was different (*P* < 0.001) for all three treatment groups. The CON was the lowest (0.27 ± 0.001) and the S/F group (0.32 ± 0.001) was lower than the F/S group (0.33 ± 0.001; **Table 2**).

Table 2. The effects of growth rate on gain to feed (G: F) and cost of developing replacement heifers.

TRT[1]	CON	S/F	F/S	SE	*P* – Value
TC[2]	706.2^{a}	612.7^{b}	583.7^{c}	0.001	<0.001
Gain: Sup[3]	0.27^{c}	0.32^{a}	0.33^{b}	0.001	<0.001
Gain: Hay	0.11	0.10	0.11	0.002	0.40
Gain: Feed	0.077^{c}	0.080^{b}	0.084^{a}	0.001	<0.001
\$/lb gain	2.8	2.39	2.26	0.07	0.07

[1] TRT: is the nutritional plane of heifers during development; CON – linear constant growth, S/F – slow then fast growth, F/S – fast then slow growth

[2] TC: Total supplement consumed per heifer over the course of the study

[3] Gain: Supplement ratio

This again supports the fact that the CON group required the most supplement during the development. However, the G:F ratio for hay was the same (*P* = 0.4) across the three treatment groups (0.10-0.11 ± 0.002; **Table 2**). This is due to the fact that hay intake was estimated at 3% of BW and BW were not impacted by treatment. Conversely, the overall G:F was similar to the G:F for the supplement, the CON group (0.077 ± 0.001) was the lowest (*P* <0.001) and the S/F group (0.08 ± 0.001) was lower than the F/S group (0.084 ± 0.001; **Table** 2). Interestingly, even with increased consumption and altered G:F the cost per pound of gain only tended (*P* = 0.07) to be impacted by growth rate. The CON group ($2.8 ± 0.07 per lbs.) was the highest and the F/S and S/F were similar ($2.39 ± 0.07 per lbs. and $2.26 ± 0.06 per lbs., respectively; **Table 2**). In conclusion, heifer development strategies can impact the lifetime production of the animal and the growth rate at which the heifer is managed from weaning to first breeding can impact the overall cost of replacement heifer development.

Acknowledgments

The authors would like to thank Kevin Thompson and the Middle Tennessee Research and Education Center staff for help in collecting samples and providing care for the animals used in the study. Additionally, the authors would like to thank the state of Tennessee through UT AgResearch, the Department of Animal Science, and the USDA National Institute of Food and Agriculture, Hatch Project No. 1019048 for providing funding and support

Literature Cited:

Cardoso, R. C., B. R. C. Alves, L. D. Prezotto, J. F. Thorson, L. O. Tedeschi, D. H. Keisler, C. S. Park, M. Amstalden, and G. L. Williams. 2014. Use of a stair-step compensatory gain nutritional 1 regimen to program the onset of puberty in beef heifers. Journal of Animal Science 92:2942-2949. doi: 10.2527/jas2014-7713

Dickinson, S. E., M. F. Elmore, L. Kriese-Anderson, J. B. Elmore, B. N. Walker, P. W. Dyce, S. P. Rodning, and F. H. Biase. 2019. Evaluation of age, weaning weight, body condition score, and reproductive tract score in pre-selected beef heifers relative to reproductive potential. Journal of Animal Science and Biotechnology 10:18.

Funston, R., J. Martin, D. Larson, and A. Roberts. 2012. Physiology and endocrinology symposium: nutritional aspects of developing replacement heifers. Journal of animal science 90(4):1166-1171.

Garrett, J. E., R. D. Geisert, M. T. Zavy, and G. L. Morgan. 1988. Evidence for maternal regulation of early conceptus growth and development in beef cattle. Journal of Reproduction and Fertility 84:437-446.

Larson, R. L. 2007. Heifer Development: Reproduction and Nutrition. Veterinary Clinics Food Animal Practice 23:53-68.

Marston, T. T., K. S. Lusby, and R. P. Wettemann. 1995. Effects of postweaning diet on age and weight at puberty and mild production of heifers. Journal of Animal Science 73(1):63. doi: 10.2527/1995.73163x

Patterson, D., R. Perry, G. Kiracofe, R. Bellows, R. Staigmiller, and L. Corah. 1992. Management considerations in heifer development and puberty. Journal of Animal Science 70(12):4018-4035.

Perry, G., E. Larimore, G. Bridges, and R. Cushman. 2012. Management strategies for improving lifetime reproductive success in beef heifers. Proceedings, Applied Reproductive Strategies in Beef Cattle 30:249-266.

Utter, S., P. Houghton, L. Corah, D. Simms, M. Spire, and M. Butine. 1994. Factors influencing first-service conception and overall pregnancy rates in commercial beef heifers. 672

IN PROGRESS: Forage Characteristics of Native Forbs and Legumes

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Take Home Message: *The objectives of this research were to evaluate 12 native forbs and legumes for various forage characteristics to determine suitability for beef pasture systems and insect pollinators. Species like cup plant and purple coneflower could provide critical floral resources and nutrient-dense forage in a pasture system.*

Summary: Pastures provide an opportunity to serve both growing beef cattle and critical pollinators by including a diverse set of native forbs and legumes. However, native forbs and legumes have not been evaluated for various forage characteristics. Therefore, the objectives of this study were to examine harvest response, blooming patterns, and nutritive composition of 12 forb and legume species in a small plot study. Twelve species were seeded in 2018 and monitored between 2020 and 2022. Plant heights increased (*P*<0.001) across the three years and were highest (*P*<0.001) earlier in the season. Most species had some tolerance of defoliation except for black-eyed susan, and all exhibited varying flowering periods. Most species met or exceeded the nutritional needs of a growing beef steer, suggesting that they could be beneficial in a pasture system.

Introduction

There are a wide variety of native forbs and legumes indigenous to the United States (U.S.), many of which are present across the Great Plains and much of the eastern U.S. Many native forbs and legumes are components of early successional communities and prairies, and provide wildlife with cover, nesting sites, and nutritional resources (Harper, 2007). Compared to deciduous shrubs and trees, and some grass species, forbs and legumes can provide higher concentrations of energy and crude protein (CP; Ulappa et al., 2020), which could make them valuable forages for livestock. In addition to mammals and birds, native forbs and legumes provide floral resources for critical pollinators, many of which are in grave decline across the U.S. due to pesticide and herbicide use, disease, and habitat loss (Potts et al., 2010; Shackelford et al., 2013; Weiner et al., 2014; Grab et al., 2019).

Pastures present an opportunity to support both vital pollinators and growing livestock in a dual-purpose system that incorporates forage production with native forbs and legumes. However, forage characteristics have not been documented for most native forbs and legumes. Therefore, the objectives of our research were to evaluate 12 native forbs and legumes for harvest response, blooming patterns and forage nutrient composition in a small plot experiment.

Materials and Methods

Research was conducted at the East Tennessee AgResearch and Education Center, Plant Science Unit in Knoxville, TN. The experiment was established on 16 July 2018 in a randomized block design with four replicates (**Table 1**; n = 48) in an 0.2-acre

Table 1: Seeding rates (PLS[1] lb. ac^{-1}) of native forbs and legumes planted in 150 ft^2 plots on 16 July 2018 at the East Tennessee AgResearch and Education Center, Plant Science Unit in Knoxville, TN.

	Common Name	Scientific Name	Seeding Rate PLS lb. ac^{-1}
Forb	Canada Goldenrod	*Solidago canadensis* L.	0.5
	Cup Plant	*Silphium perfoliatum* L.	7.9
	Maximilian Sunflower	*Helianthus maximiliani* Schrad.	3.7
	Oxeye Sunflower	*Helopsis helianthoides* (L.) Sweet	7.9
	Eastern Purple Coneflower	*Echinacea purpurea* (L.) Moench	6.9
	Lanceleaf Coreopsis	*Coreopsis lanceolata* L.	3.6
	Upright Prairie Coneflower	*Ratibida columnifera* (Nutt.) Woot. & Standl.	1.6
	Black-eyed Susan	*Rudbeckia hirta* L.	1.6
Legume	Illinois Bundleflower	*Desmanthus illinoensis* (Michx.) MacMill.	6.6
	Partridge Pea	*Chamaecrista fasciculata* (Michx.) Greene	9.5
	Purple Prairie Clover	*Dalea purpurea* (Vent.) Rydb.	2.6
	Showy Tick-trefoil	*Desmodium canadensis* (L.) DC.	4.7

[1] Pure live seed, PLS

field. Twelve forb and legume species were planted individually within 6 x 25' plots (**Table 1**). Native forbs and legumes were planted into a prepared seedbed at a depth of 0.4 inches with a Hege1000 plot drill (Hege Equipment Inc.). The field received P and K amendments based on annual soil tests. Plots received an annual application of 60 lb. ac^{-1} nitrogen in the form of urea each April from 2019 – 2021. The field was not irrigated. Due to forb and legume rosette persistence through winter and early spring, non-selective herbicides, semi-selective herbicides, and broadleaf-selective herbicides were not used during the study to control broadleaf weeds. Grasses were controlled using a grass-selective herbicide (Clethodium) annually as needed at a rate of 16.4 oz ac^{-1} through broadcast spraying. Broadleaf weeds were controlled by hand.

Plant heights were recorded weekly throughout the growing season except for the 1–3-week period following each harvest. Each plot was measured in five locations using a yard stick and plants taller than 36 inches were recorded at 37 inches. Maturity stage was recorded weekly in conjunction with height measurements. Maturity stages assessed were vegetative, actively reproductive (flowering), post reproductive, and deceased and each were scored on a scale of 0 (the plot did not exhibit a given maturity stage) to 100% (the entire plot exhibited that maturity stage). Plant heights and maturity composition were compared across three years, 2020–2022. Forage samples were dried in forced-air ovens at 130°F for 72 hours until they maintained a constant mass. Dried samples were ground to a fine particle size and were analyzed for forage nutrient composition using wet chemistry (Dairyland, Arcadia, WI). Specifically, forbs and legumes were analyzed for CP, neutral detergent fiber (NDF), and acid detergent fiber (ADF). Forage nutritive composition was analyzed across three harvests occurring in 2020: 22 June, 28 July, 2 September.

Analysis was conducted using R software (version 4.1.1) running RStudio (version 1.4.1717) and statistical significance was set at $P \leq 0.05$. Treatment differences were compared for each response variable (plant height, maturity, CP, NDF, and ADF) using ANOVA. Mixed linear models were used for each response variable where date, days since harvest, and plant species were fixed effects and plot was a random effect.

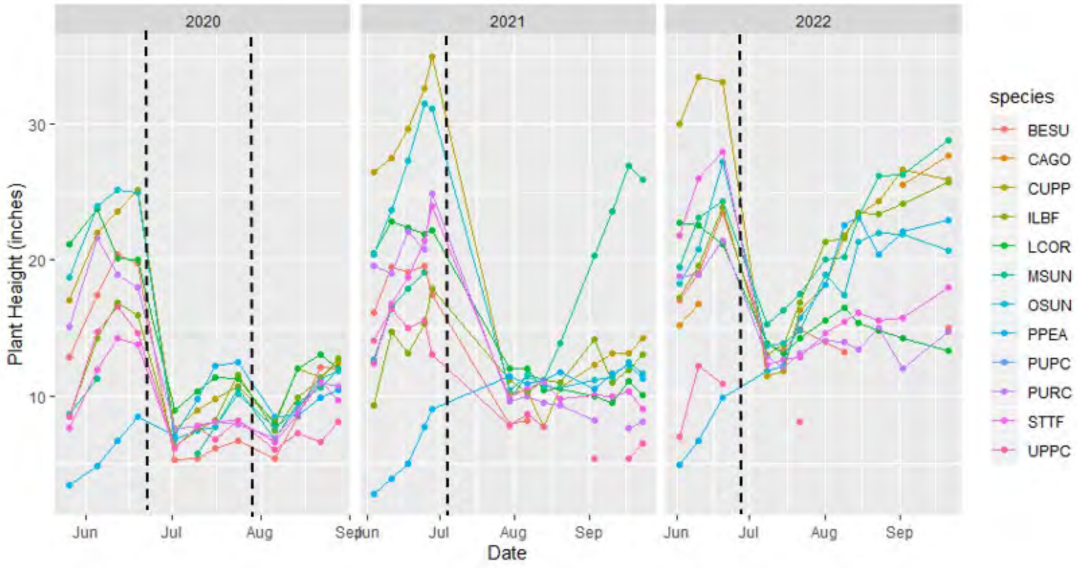

Figure 1: Plant height of 12 native species across three summers subjected to repeated defoliation in 2020–2022 at the East Tennessee AgResearch and Education Center, Plant Science Unit in Knoxville, TN. [1]black-eyed susan, BESU; Canada goldenrod, CAGO; cup plant; CUPP; Illinois bundleflower, ILBF; lanceleaf coreopsis, LCOR; Maximillian sunflower, MSUN; oxeye sunflower, OSUN; partridge pea, PPEA; purple prairie clover, PUPC; purple coneflower, PURC; showy tick-trefoil, STTF; upright prairie coneflower, UPPC [2]Harvests are marked with a vertical black line

Year was a repeated measure for plant heights. Mean separations were compared using Tukey's honest significant difference test.

Results and Discussion

Plant height by species was directly related to date and days since the last harvest (**Figure 1**; $P<0.001$) where plants were taller earlier in the season and were taller the further the date was from the last harvest or spring dormancy. Over the three years, plant height increased ($P<0.0001$) each year. Plant maturity was impacted by date and days since the last harvest ($P<0.001$) where species flowered during different times of the year (**Table 2**) and each responded differently to defoliation. Forage nutritive composition differed among species and harvest intervals (**Figure 2**; $P<0.001$). Crude protein was the greatest ($P<0.05$) for most species during the second or third harvest, and both fiber components decreased ($P<0.05$) between the first and later harvests.

Forage characteristics have not been documented for most native forb and legume species. Plant heights, as a measure of plant productivity after a harvest, may be a good indicator of a species' tolerance to defoliation. Yang et al. (2020) found that higher stubble heights allowed plants to produce more mass and height by the next harvest compared to plants with lower stubble heights. Although all plants in this study were harvested at an 8-inch stubble height, species with lower tolerance to defoliation, like black-eyed susan, grew shorter plants after harvest. Plants like Maximillian sunflower with moderate

Table 2: Flowering patterns and response to defoliation of 12 native forbs and legumes subjected to repeated defoliation in 2020–2022 at the East Tennessee AgResearch and Education Center, Plant Science Unit in Knoxville, TN.

Species	Predominant Flowering Window[1]	Response to Defoliation[2]
Cup Plant	Late Season	Tolerant
Eastern Purple Coneflower	Mid Season	Tolerant
Lanceleaf Coreopsis	Early Season	Tolerant[3]
Partridge Pea	Mid to Late Season	Tolerant[3]
Showy Tick-trefoil	Mid Season	Tolerant
Maximilian Sunflower	Late Season	Moderately Tolerant
Oxeye Sunflower	Mid Season	Moderately Tolerant
Illinois Bundleflower	Mid Season	Moderately Tolerant
Black-eyed Susan	Early to Late Season	Not Tolerant[4]
Canada Goldenrod	Late Season	N/A
Upright Prairie Coneflower	Mid Season	N/A
Purple Prairie Clover	Mid Season	N/A

[1] early season=May–June; mid season=June–mid August; late season=August–September

[2] tolerant=a majority of plants sustained after defoliation; moderately tolerant=some plants sustained after defoliation; not tolerant=a minority of plants sustained after defoliation; N/A=not applicable or not enough observations

[3] Laceleaf coreopsis tolerates defoliation, but is a prolific reseeder and can increase plant number despite mortalities

[4] Black-eyed susan does not tolerate defoliation, but can repopulate if allowed to reseed itself

tolerance often produced shorter plants after subsequent harvests, but to a lesser extreme than non-tolerant species. In addition to shorter regrowth heights, some low and moderate-tolerant species experienced plant mortality, especially in the case of black-eyed susan when harvested after flowering. Plant persistence is an important factor to consider when planning species to incorporate into a pasture system.

The flowering patterns of different species are also important to determine when support of insect pollinators is the objective. The lack of pollen-producing species desired by insect pollinators throughout the summer could add to pollinator decline (Shackelford et al., 2013) and providing consistent floral resources could be beneficial. Lanceleaf coreopsis and black-eyed susan were predominant early-season bloomers while purple coneflower and some legume species flowered during mid-season. Late-season floral resources are some of the most critical to insect pollinators (Lowe et al., 2022) as many must collect pollen to survive winter. Late summer and fall can also be the most pollen limiting given different climate conditions like droughts. Both Maximillian sunflower and Canada goldenrod, for example, flower starting in August and many goldenrod species can flower into early October, making them good choices to support pollinators later in the season.

Forage nutritive composition when incorporating diverse forages into a pasture system can impact cattle production. When consuming 1.5 to 2.5% of their body weight in forage each day, a growing steer requires about 13% CP (Nutrient Requirements of Beef Cattle, 2016) and fiber content should

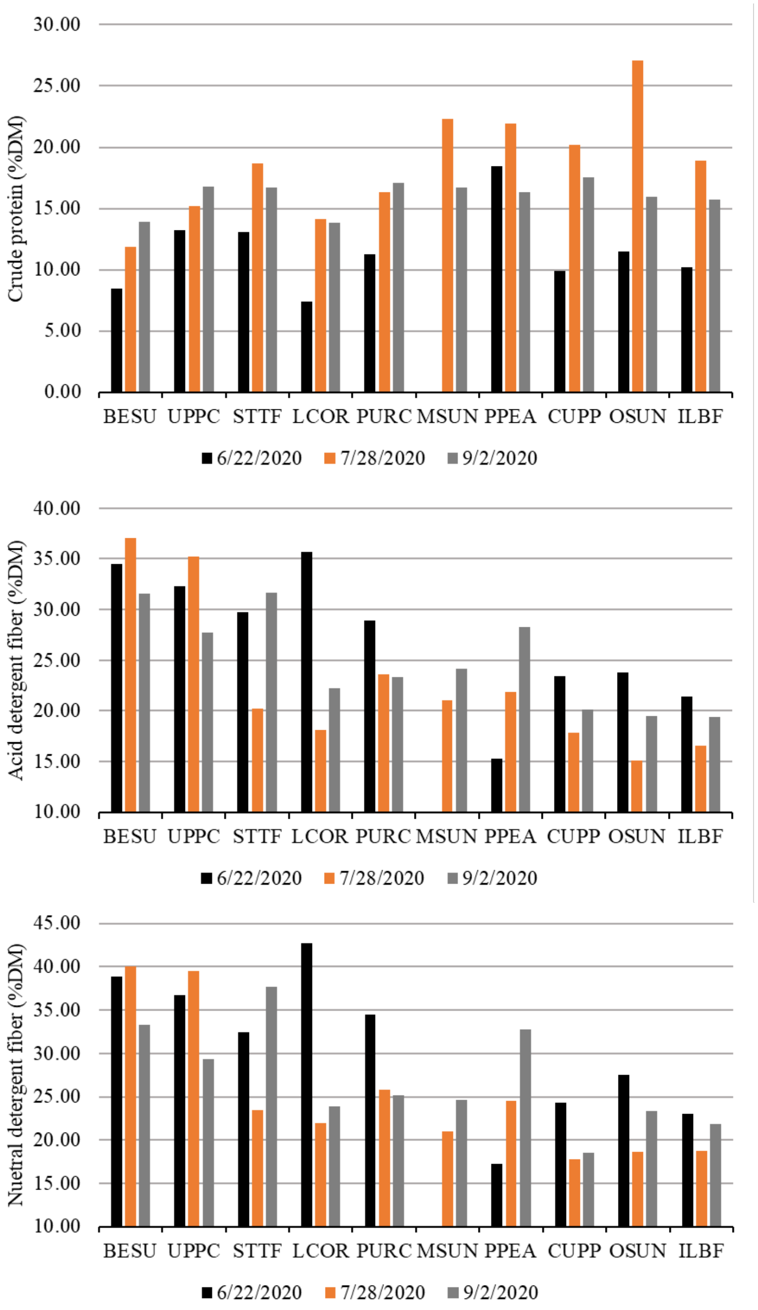

Figure 2: CP[1], ADF, and NDF composition of native forbs and legumes at different harvest periods in 2020 at the East Tennessee AgResearch and Education Center, Plant Science Unit in Knoxville, TN. [1]crude protein, CP; acid detergent fiber, ADF; neutral detergent fiber, NDF; black-eyed susan, BESU; upright prairie coneflower, UPPC; showy tick-trefoil, STTF; lanceleaf coreopsis, LCOR; purple coneflower, PURC; Maximillian sunflower, MSUN; partridge pea, PPEA; cup plant, CUPP; oxeye sunflower, OSUN; Illinois bundleflower, ILBF

not be excessive to where it provides a barrier to palatability or intake. Most forbs and legumes met or exceeded the CP requirement, particularly during the second and third harvests. Species like cup plant, Illinois bundleflower, and oxeye sunflower produced the least amount of fiber, suggesting that these species may not impact palatability or total intake based on fiber.

Conclusion

Native forbs and legumes are previously unexplored forage alternatives for beef cattle. Their variety and floral resources would increase biodiversity and pollinator assets when included into a pasture system. Although not every species tolerates repeated defoliation, lanceleaf coreopsis, purple coneflower, and cup plant, for example, could persist in a pasture system based on our results. Additionally, all twelve species produced a wide range of floral seasons that could help fill in nutritional gaps for at-risk pollinators. Lastly, most species met or exceeded the nutrient requirements of the growing steer and could improve forage nutritive composition within a grass pasture system

Literature Cited

Grab, H., M.G. Branstetter, N. Amon, K.R. Urban-Mead, M.G. Park, et al. 2019. Agriculturally dominated landscapes reduce bee phylogenetic diversity and pollination services. Science (80-.). 363(January): 282–284.

Harper, C.A. 2007. Strategies for managing early succession habitat for wildlife. Weed Technol. 21(4): 932–937. doi: 10.1614/wt-07-024.1.

Lowe, A., L. Jones, G. Brennan, S. Creer, and N. de Vere. 2022. Seasonal progression and differences in major floral resource use by bees and hoverflies in a diverse horticultural and agricultural landscape revealed by DNA metabarcoding. J. Appl. Ecol. 59(6): 1484–1495. doi: 10.1111/1365-2664.14144.

Nutrient Requirements of Beef Cattle. 2016. Eighth Ed. National Academy Press, Washington, D.C.

Potts, S.G., J.C. Biesmeijer, C. Kremen, P. Neumann, O. Schweiger, et al. 2010. Global pollinator declines: Trends, impacts and drivers. Trends Ecol. Evol. 25(6): 345–353. doi: 10.1016/j.tree.2010.01.007.

Shackelford, G., P.R. Steward, T.G. Benton, W.E. Kunin, S.G. Potts, et al. 2013. Comparison of pollinators and natural enemies: A meta-analysis of landscape and local effects on abundance and richness in crops. Biol. Rev. 88(4): 1002–1021. doi: 10.1111/brv.12040.

Ulappa, A.C., L.A. Shipley, R.C. Cook, J.G. Cook, and M.E. Swanson. 2020. Silvicultural herbicides and forest succession influence understory vegetation and nutritional ecology of black-tailed deer in managed forests. For. Ecol. Manage. 470–471(July 2019): 118216. doi: 10.1016/j.foreco.2020.118216.

vanEngelsdorp, D., J.D. Evans, C. Saegerman, C. Mullin, E. Haubruge, et al. 2009. Colony collapse disorder: A descriptive study. PLoS One 4(8). doi: 10.1371/journal.pone.0006481.

Weiner, C.N., M. Werner, K.E. Linsenmair, and N. Blüthgen. 2014. Land-use impacts on plant-pollinator networks: Interaction strength and specialization predict pollinator declines. Ecology 95(2): 466–474. doi: 10.1890/13-0436.1.

Yang, Z., H. Minggagud, T. Baoyin, and F.Y. Li. 2020. Plant production decreases whereas nutrients concentration increases in response to the decrease of mowing stubble height. J. Environ. Manage. 253(September 2019): 109745. doi: 10.1016/j.jenvman.2019.109745.

Poster Number: 701

US Cattle Producer’s Use of Price Risk Management Tools

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Beef cattle production is vulnerable to economic losses from various uncontrollable events like drought and disease, but volatile cattle prices have historically been the primary cause of economic losses to United States (US) cattle producers. Several tools are used to manage price risks, such as forward contracts, options, futures contracts, and livestock risk protection insurance. The purpose of this research is to find out the usage of price risk management tools among the United States cattle producers, their perceived effectiveness and understanding of these tools, the barriers to adopting these tools, the sources of risks related to cattle production, and which information about the market are more important to them. Moreover, this research aims to determine how hypothetical changes to Livestock Risk Protection would affect the adoption of the tools. A US survey of cattle producers was conducted where we found out that most producers never used any price risk management tools, and currently the most used tool is LRP (5.65%). Most of the respondents indicated they do not understand these tools' usage and effectiveness, which indicates the need for education for these tools.

Poster Number: 702

Using Novel Phenotypes to Understand and Predict Fertility Traits in Beef Cows

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Reproduction plays a major role in the production efficiency of livestock species. However, cow-centric reproductive traits are lowly heritable and show delayed expression, making phenotypic selection ineffective at generating genetic gain. Genetic progress can be made by focusing selection on the genetic component of reproductive traits using Expected Progeny Differences (EPDs). We used the American Simmental Association's performance and Total Herd Enrollment data, made up of 786,323 calving records from 339,835 females (199,798 cows and 140,037 heifers), 31,000 of which are genotyped, to develop two continuous and two discrete fertility phenotypes. We are analyzing calving interval (days between calves), calving date (cow's calving date relative to the start of the calving season), heifer pregnancy (did animal calve as 2-year-old), and discrete early calving (did animal calve in the first 30 days of the calving season) as distinct, but correlated measures of fertility. Pedigree-based heritabilities have been estimated to be lowly to moderately heritable for calving interval, calving date, heifer pregnancy, and discrete early calving. We are actively working to integrate genomics to improve heritability estimates and generate breeding values using single-step genomic best linear unbiased prediction (ssGBLUP). Additionally, we aim to better understand the underlying genetic variation that controls these traits by conducting a series of genome-wide association studies (GWAS). GWAS will use ~30 million imputed variants to identify loci significantly associated with each measure of fertility. Taken together, we expect that this work will deliver tools to producers that will enable more accurate sire selection for daughter fertility. Additionally, results from GWAS analyses will enhance our understanding of the genetic architecture of fertility traits while providing informative markers for genetic evaluations.

Poster Number: 703

Factors Affecting Chinese Beef Consumers' Purchase Frequency

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China is an emerging beef market and per capita consumption of beef increased by 48 percent over the past ten years (2011 to 2020). Given the importance of the Chinese beef market to domestic Chinese beef producers and foreign beef exporters, we evaluated the factors associated with Chinese beef consumers purchase frequencies. Using a 2021 survey of 560 Chinese consumers in the cities of Beijing, Shanghai, and Guangzhou, we found that among beef consumers, nearly 50% purchased beef at least two to three times a week. Results of an Ordered Probit Regression found that respondents who purchased steak, flank, shank, and brisket, those who purchased beef from wet markets and supermarkets, younger respondents, and those with higher wages were likely to buy beef more often. Similarly, respondents who consider country of origin and growth hormone-free production important factors when purchasing beef were likely to purchase beef more frequently. If consumers considered price and premium quality important factors when purchasing beef, they purchased beef less frequently. Our findings provide insights for domestic and foreign beef producers regarding the demographics and characteristics of Chinese beef consumers.

Poster Number: 704

Evaluation of Yield and Forage Nutritive Value of Stockpiled Tall Fescue in Alabama and Tennessee

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Beef cattle are a predominant agricultural commodity in Tennessee and rely heavily on grazed forages to support nutritional needs. Pastures in Tennessee comprise mainly tall fescue [*Schedonorus arundinaceus* (Schreb.) Dumort.], a cool-season perennial grass. Producers can utilize stockpiling to extend the grazing season (Fribourg and Bell, 1984). Stockpiling tall fescue consists of fertilization and accumulation of forage throughout the fall and delayed grazing beginning in the winter months. Although this practice has been proven to reduce hay needs (Poore et al., 2000), it is vital to maintain up-to-date recommendations and data from the southeastern US to inform grazing decisions. The objective of this study is to determine nutritive value and dry matter yield of tall fescue in fall and winter months throughout the southeastern United States. Twelve farms across Alabama and Tennessee were identified as sampling sites and split into two groups based on latitude. In September of 2021, three exclusion cages (1.3-m × 1.3-m) were constructed at each site and plots were fertilized at a rate of 67 kg nitrogen per acre. Samples were taken on a monthly basis. A 0.25-m^2 area within each cage was clipped to a 5-cm stubble height, weighed in the field to determine fresh weight, and taken to the lab to be analyzed for dry matter yield and nutritive value. Sampling occurred monthly from October through February, coinciding with months that cattle would typically graze stockpiled fescue. One year of sampling has been completed. Location did not have an effect of forage yield ($P = 0.1594$). Forage yield increased from October to February ($P < 0.0001$). Nutritive value analysis and the second year of data collection are currently underway. Results will be used to inform stockpiling recommendations used by producers to make management decisions that increase grazing days and reduce input costs.

Poster Number: 705

Using Embryos to Dissect Gene Expression Heterosis in Beef Cattle

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The impacts of heterosis through the utilization of crossbreeding are easily across traits in beef cattle. However, our understanding of how heterosis functions on a molecular level remains limited. Crossbreeding is one most underutilized tools in U.S. beef cattle production, with only 50% of operations leveraging the advantages of heterosis. Understanding the functional biology that underlies heterosis at the molecular level could enable the industry to better predict and harness the benefits of hybrid vigor in breeding programs. To quantify gene expression heterosis (i.e., differential expression in F1 compared with purebreds of same origin), we measure gene expression heterosis in *in vitro*-derived embryos. This allows us to largely regulate environmental conditions and observe molecular heterosis at a critical point in early development. Embryos will be generated via *in vitro* fertilization using abattoir-derived oocytes from Angus and Brahman cull cows, using Angus and Brahman sires in a diallel-like cross. We have performed bulk RNA-sequencing on 62 Angus x Angus and 33 Brahman x Angus embryos during sire testing. We remain in the early stages of data generation, thus a full diallel cross has yet to be performed. However, initial results suggest that different patterns of gene expression exist between purebred Angus and F1 embryos. Knowledge of misexpressed genes and important networks can aid in dissecting the molecular basis of heterosis in cattle while allowing us to understand transcriptional dynamics at an early point in mammalian development.

Poster Number: 706

Relationship of Placentome Vascular Perfusion and Circulating Pregnancy Associated Glycoproteins throughout Gestation in Pregnant Beef Heifers

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During pregnancy, blood flow to the uterus and placenta changes to support fetal demand. The placentomes serve as vascular attachment sites for exchange of gases, nutrients, and fetal metabolic products. In human and veterinary medicine, non-invasive methods of ultrasonography and biomarkers have been described to assess placental health and fetal viability. Pregnancy associated glycoproteins (PAGs) are produced by the ruminant placenta and detected in maternal circulation. Current literature suggests that changes in circulating PAG concentrations may be a useful biomarker for assessing placental health. The objective of this study is to determine the association between placentome blood perfusion and circulating PAG concentrations as they relate to the health of the developing fetal calf. The hypothesis states that placentome perfusion and PAG concentration will be positively correlated and associated with neonatal outcome.

A prospective, observational study was designed using 30 pregnant, nulliparous, Angus heifers and variables assessed throughout gestation.

Placentome blood perfusion was visualized monthly via transrectal Doppler ultrasonography with power flow function. Five placentomes, selected at random, were imaged per time point. Ultrasound images were analyzed using ImageJ software to determine the percent area of perfusion and integrated pixel densities. Mean blood flow was calculated from the five representative pixel images.

Venous blood was collected monthly via coccygeal venipuncture. PAG concentrations were determined via a commercially available serum PAG enzyme-linked immunoassay.

Following parturition, calving characteristics including, gestation length, sex, and weight were assessed.

Statistical analysis was performed using SAS 9.4. Mean blood flow and PAG concentrations were assessed via linear regression. Pearson correlation was used to compare blood flow and PAG concentration over time.

Results indicate that there is a positive linear relationship between circulating PAG concentration and placentome blood perfusion, validating the use of transrectal power flow Doppler ultrasonography as a non- invasive technique to determine placental blood flow morphometrics. This technique will guide future studies for understanding how compromised pregnancy alters placental blood perfusion and the overall health of the feto-maternal unit.

Poster Number: 707

Validation of a Minimally-Invasive Rumen Wall Sampling Method for Use in Beef Cattle

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The rumen microbiome converts low quality feedstuffs into usable energy and provides approximately 70% of energy required by its ruminant host. Epimural microbes interact directly with the rumen epithelium, acting as intermediary communicators between the rumen liquid fraction and the host. This subset of the microbiota is thought to differ in composition from the ruminal liquid microbiome and to perform unique roles within the rumen environment. However, methods to sample epimural communities from the rumen wall are limited and invasive, requiring animal fistulation or even animal harvesting. To characterize the epimural communities present on the rumen wall, a novel and minimally-invasive surgical method was developed to swab the epithelium of the ventral sac of the rumen. The objective of this study was to validate this sampling method by comparing epimural and liquid fraction bacterial communities. During a 70-day feed efficiency trial, Angus steers ($n = 45$) were sampled on day 35 using the novel surgery method and tubed on day 70 to sample rumen liquid content. Genomic DNA was used to generate amplicon libraries of the V4 region of the 16S rRNA gene and sequenced on an Illumina MiSeq. Analyses were conducted in R using packages ‘phyloseq’ and ‘dada2’ to identify amplicon sequence variants (ASVs). For beta diversity, a Bray-Curtis PCoA between rumen and epimural communities was tested using a PERMANOVA with 999 permutations ($P < 0.05$). The phylum Firmicutes was found in lower abundance in the rumen liquid fractions, while the genera *Mycoplasma*, *Lactiplantibacillus*, *Bibersteinia*, and *Succinovibrio* were of higher abundance (FDR < 0.05). These results demonstrate that the novel method of sampling from the rumen wall can be used to capture differences between epimural and ruminal fluid bacterial communities, thus facilitating studies investigating the interactions between epimural bacteria with the host.

This work is supported by the Agriculture and Food Research Initiative Competitive grant no. 2020-67015- 30832 from the USDA National Institute of Food and Agriculture.

Poster Number: 708

Predicting Immunization Status at Arrival in Tennessee Stocker Calves

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Bovine respiratory disease is a multifaceted disease with agent, host, and environmental factors. Stocker calves are at high risk of contracting the disease through many stressors. The projects purpose was to test if externally observed physical characteristics of calves on arrival at a stocker facility can be used to predict calfhood vaccination status determined based on antibody titer levels. Knowledge of highly correlated characteristics could allow stocker operators to reduce the occurrence of BRD through targeted management strategies, thus lowering morbidity, mortality, and treatment costs. Ear notches, blood, and visual characteristics were collected (n=408) from stocker calves at four farms in Tennessee. Each animal was tested for BVDV-PI status and titer levels for three known viral agents. Multiple visual characteristics were predictive of immunization status, including the presence of a prior ear tag (1.6 times), heifers (0.82 times), steers (1.26 times), polled cattle (4.8 times), BCS increasing by one (1.46 times) and possessing health records (2.2 times). When analyzed together, the calf factors of sex, tag, and health records remained most universally informative. When evaluating the predictive nature of multivariable models, predictability was generally low. Despite low model accuracy, this initial work creates a good foundation for further research focused on more robust data collection to build more robust models.

Additionally, we followed sixty calves through the stocker phase to ascertain the downstream impacts on health and production of preconditioning. We found that preconditioned calves had lower BRD incidence, higher presence of detectible titers, and gained more weight over 60 days than naïve cattle. However, many calves marketed as preconditioned did not have detectible titers on arrival. This work identifies practical solutions for stocker operations to make more informed purchasing and management decisions. It also lays the groundwork for future work identifying ways to deliver precision management to stocker cattle.

Poster Number: 709

Price Determinants of Graded Feeder Cattle Sale

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Over the last couple of decades, a great deal has been learned about how factors such as cattle characteristics, changes in corn price, lot size, and value-added programs following production protocols impact feeder cattle values. However, some local auction markets offer special monthly graded feeder calf sales where a USDA certified individual grades the cattle. The objective of this proposed research is to explore how factors such as sex, breed, lot size, weight, weaned, and USDA grades impact sale prices of feeder cattle. A hedonic pricing model will be estimated to show the direction and magnitude of these factors on sale prices using monthly sale data from 2019 to 2022 in Tennessee. The results will build on the literature and help inform producer education programs on adding value to feeder cattle. Primarily results show that weight negatively impacts sale price along with heifers selling for a lower price than steers. Grade was found to impact the price along with if the producer indicated the cattle were weaned. Further analysis is needed to control for seasonal effects and year effects. These results will be applicable to southern regional economists who research or do producer education for cattle production.

Poster Number: 710

Rumen Biogeographical Regions and Their Impact on Microbial and Metabolome Variation

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The rumen microbiome is a complex microbial network with the inherent ability to convert low-quality feedstuffs into energy for cattle. Many studies focus on sampling from the ventral sac due to ease of access and repeatability. However, anatomical musculature demarcates the rumen into five sacs which may support distinct microbial communities. The distinction among the microbes may generate functional variation among the rumen microbiome; thus, specialized tasks within different sacs. The objective of this study was to determine the rumen liquid metabolome and epimural, planktonic, and fiber-adherent bacterial communities among each rumen biogeographical region. It was hypothesized that differences in bacterial species and metabolome would occur due to differing anatomy and physiology associated with the respective regions. To assess this variation, epithelial and content microbial-associated communities were evaluated, as well as the metabolites among rumen biogeographical regions. A total of 17 cannulated Angus cows were utilized to examine the fiber-adherent (solid fraction), planktonic (liquid fraction), and epimural microbial communities from the cranial, dorsal, caudodorsal blind, caudoventral blind, and ventral sacs. Metagenomic DNA was extracted and sequenced from the hypervariable V4 region of the 16S rRNA gene. Reads were processed using packages ‘phyloseq’ and ‘dada2’ in R. Untargeted metabolomics were conducted on rumen liquid from each sac using UHPLC-HRMS and analyzed in MetaboAnalyst. Within the bacterial communities, neither alpha nor beta diversity determined significance against the rumen sacs ($P > 0.05$), although there was significance against the fraction types ($P < 0.05$) Utilizing MaAslin2, there were significant differential abundances found in fraction type × location ($P < 0.05$). Future projects focusing on either planktonic or epimural fractions, may need to consider multiple rumen sac sampling to obtain the most comprehensive analysis of the rumen. Defining these variabilities, especially among the rumen epimural microbiome, is critical to define host-microbiome interactions.

Poster Number: 711

Cow Manure-Based Bio-Formulations as a Plausible Approach to Rejuvenate Soil and Enhance Plant Growth

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Cow manure is an excellent and versatile fertilizer due to its balanced nutrient ratio. Cow dung is either applied as slurry or composted aerobically, anaerobically, or by vermicomposting. Growing interest in dynamic regenerative agricultural systems has sparked curiosity about the science behind the indigenous knowledge of using cow manure to create bio-formulations for agriculture. Cow manure bio-formulations contain diverse microorganisms that can promote plant growth by producing metabolites, enhancing nutrient cycling, and suppressing plant pathogens. However, little documentation exists on survival of inoculated bacterial and fungal species in the soil, and the impact of their release on soil's native microbiota. Additionally, the extent of the inoculation effect on subsequent crops is unknown in relation to the buffering capacity of the plant-soil-biota consortium. The goals of this project are to (i) analyze the effect of cow manure-based inoculations on plant growth, and (ii) classify and characterize the functionality of the bacterial and fungal taxa from organic formulations prepared from cow manure. Both seed treatment and plant-growth promoting formulations were prepared by aerobic fermentation of cow manure, cow urine and soil from a local certified organic land. Their effect on plant growth was determined in a greenhouse pot study using three replications of soybean, wheat, and corn plants treated with the following: (i) seed treatment and plant-growth formulations, (ii) plant-growth formulation only, and (iii) control (no treatment). Microbial characterization was done using Illumina MiSeq Next Generation sequencing on amplicon 16S rRNA and ITS genes. Significant differences in microbial compositions and wheat growth characteristics were identified among treatments 30 days after planting. This research demonstrated the viability of locally manufactured cow-manure organic formulations to stimulate plant growth and enhance soil health.

Poster Number: 712

Uterine Gene Activity in Response to in vivo and in vitro Produced Cow Embryos

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During bovine early pregnancy, endometrial cells secrete histotroph to support conceptus development. The conceptus responds by secreting interferon-tau (IFNT), the maternal recognition of pregnancy signal and inducer of interferon-stimulated genes (ISGs). Therefore, IFNT modifies endometrial gene expression and likely, histotroph. Using a conceptus-endometrial co-culture system, a recent study identified endometrial transcripts that differed in response to Day 15 *in vitro* produced (IVP) compared to *in vivo* derived (IVD) bovine conceptuses. However, the exact day of the estrous the endometrium was collected and extent by which co-culture effected the uterine histotroph was unknown. Thus, this study was designed to identify synchronized endometrial RNA and histotroph components in response to Day 16 IVP compared to IVD bovine conceptuses. Angus-Holsten heifers underwent fixed-timed estrus synchronization and were either bred by AI (to generate IVD conceptuses), received age and sire matched IVP bovine blastocysts by embryo transfer (ET), or remained open to generate Day 16 endometrial tissue. On Day 16, uteri were harvested, and three treatments were established in 1 mL of medium: 1) endometrium alone (Control; n=13), 2) endometrium co-cultured with IVD conceptus tissue (IVD; n=15) and 3) endometrium co-cultured with IVP conceptus tissue (IVP; n=13).). After 12 h, endometria were collected, and RNA was isolated and assayed by RT-qPCR. Relative expression was calculated, and data were statistically analyzed using a GLM. Compared to Control, endometrium treated with IVD and IVP had greater expression of ISGs *ISG15*, *MX1*, *OAS1* and *LGALS9* ($P < 0.001$)) as well as other pregnancy-related genes such as glycine transporter *SLC6A9* ($P < 0.01$) and *IL1B* ($P < 0.05$). In conclusion, synchronized endometrial gene expression, and possibly histotroph, is altered by IVP compared to IVD bovine conceptuses. By understanding how conceptus types vary, further research can be done to improve *in vitro* embryo production efficiency and outcomes.

Poster Number: 713

Plasma Metabolome Profiles to Predict Average Daily Gain in Weaned Heifers

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A high average daily gain (ADG) in calves during the weaning phase is critical for cattle producers' profitability. Development of methods to predict ADG in well managed, genetically similar animals during the first fifty days post weaning would improve producer's ability to select replacements or market feeder calves. We hypothesized that phenotypic records in well managed herds would be inadequate to predict day-48 postweaning ADG, and that metabolome profiles from plasma collected at weaning would discriminate animals with high or low initial post-weaning ADG. A study was performed with the objective to evaluate the relationship between day-48 postweaning ADG and both phenotypic records and serum metabolome profiles. Blood was collected at weaning from 60 heifers housed at the UT Highland Rim AgResearch and Education Center. We also collected weights at weaning and on day-48 postweaning to calculate postweaning ADG in all animals. The average day-48 post weaning ADG among all heifers was
1.505 lbs/day, and 18 heifers presented either a gain of >2 lbs/day (n=9; High Gain) or <1 lb/day (n=9; Low Gain). There was no difference in weaning weight, pre-weaning ADG, age, or dam age in high and low post-weaning ADG heifers ($p>0.05$). Plasma collected from the blood of high and low post-weaning ADG heifers was sent to the University of Tennessee Biological and Small Molecule Mass Spectrometry Core to analyze metabolome levels between the samples. We are currently completing an analysis of metabolome profiling and hypothesize detection of a small number of plasma metabolites that differ in abundance between high and low post weaning ADG heifers. Our results will serve as preliminary data for future studies to improve prediction of post weaning ADG in beef calves.

Poster Number: 714

Uterine Metabolites Dependent on Conceptus Origin in Cattle

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Bovine endometrial and conceptus secretions include metabolites that support conceptus development. Recent studies found the endometrial transcriptome responds differently to *in vitro* produced (IVP) compared to *in vivo* derived (IVD) conceptuses. The impact of this on uterine metabolites is unknown. We compared metabolites collected from cyclic uteri and uteri carrying IVP and IVD conceptuses on Day 16 of the estrous cycle and pregnancy, respectively. Angus-Holstein heifers underwent estrus-synchronization and were then divided in to 3 treatments after signs of estrus (Day 0): 1) artificial insemination (AI) on Day 0 (P-IVD; n=5), 2) embryo transfer (ET) with an age and sire matched IVP embryo on Day 7 (P-IVP; n=5), or 3) no AI or ET [Control (CONT); n=5]. On Day 16 the ipsilateral uterine horn was flushed with 20 mL of medium (RPMI). Uterine flush fluid (UFF) underwent metabolomic analysis (LC-MS/MS) and ElMAVEN was used to visualize and acquire peak intensities through an in-house metabolite library. Fold changes were calculated using each sample group's average intensity and differences calculated using a t- test. MetaboAnalyst was used during KEGG pathway analysis. Compared to CONT, 9 metabolites were greater in pregnant uteri (P-IVD and P-IVP data combined). Analysis of KEGG pathways revealed 5 of the 9 metabolites were associated with the pyrimidine pathway, including orotate, N-carbamoyl-L-aspartate and uridine ($P<0.05$, $FDR<0.05$). Upregulation of the pyrimidine pathway is correlated with rapid cell proliferation and could be related to conceptus elongation on Day 16. Compared to P-IVD, P-IVP UFF had greater concentrations of 6 metabolites including cystathionine and 3-methylthiopropionate ($P<0.05$), both associated with the methionine pathway. Methionine is a key methyl donor for DNA methylation, which is different between IVD and IVP embryos. Greater understanding of metabolites associated with IVP embryos may lead to strategies that mitigate reproductive failure related to *in vitro* fertilization technologies.

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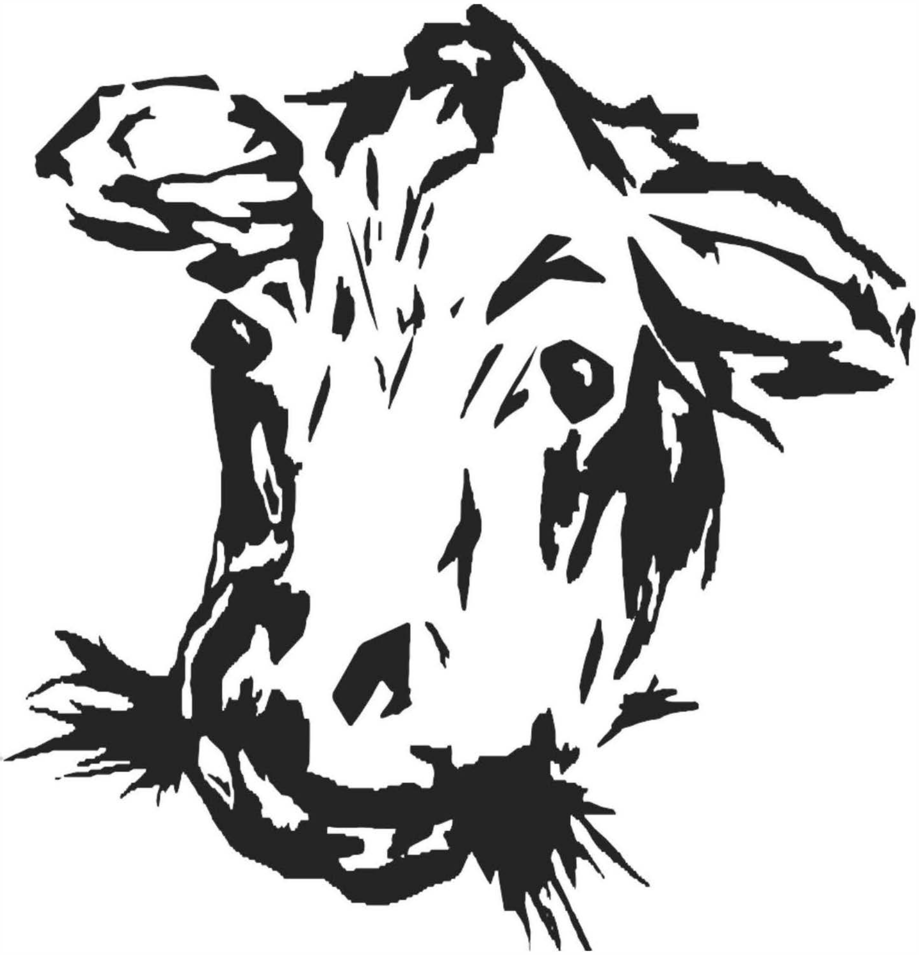

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