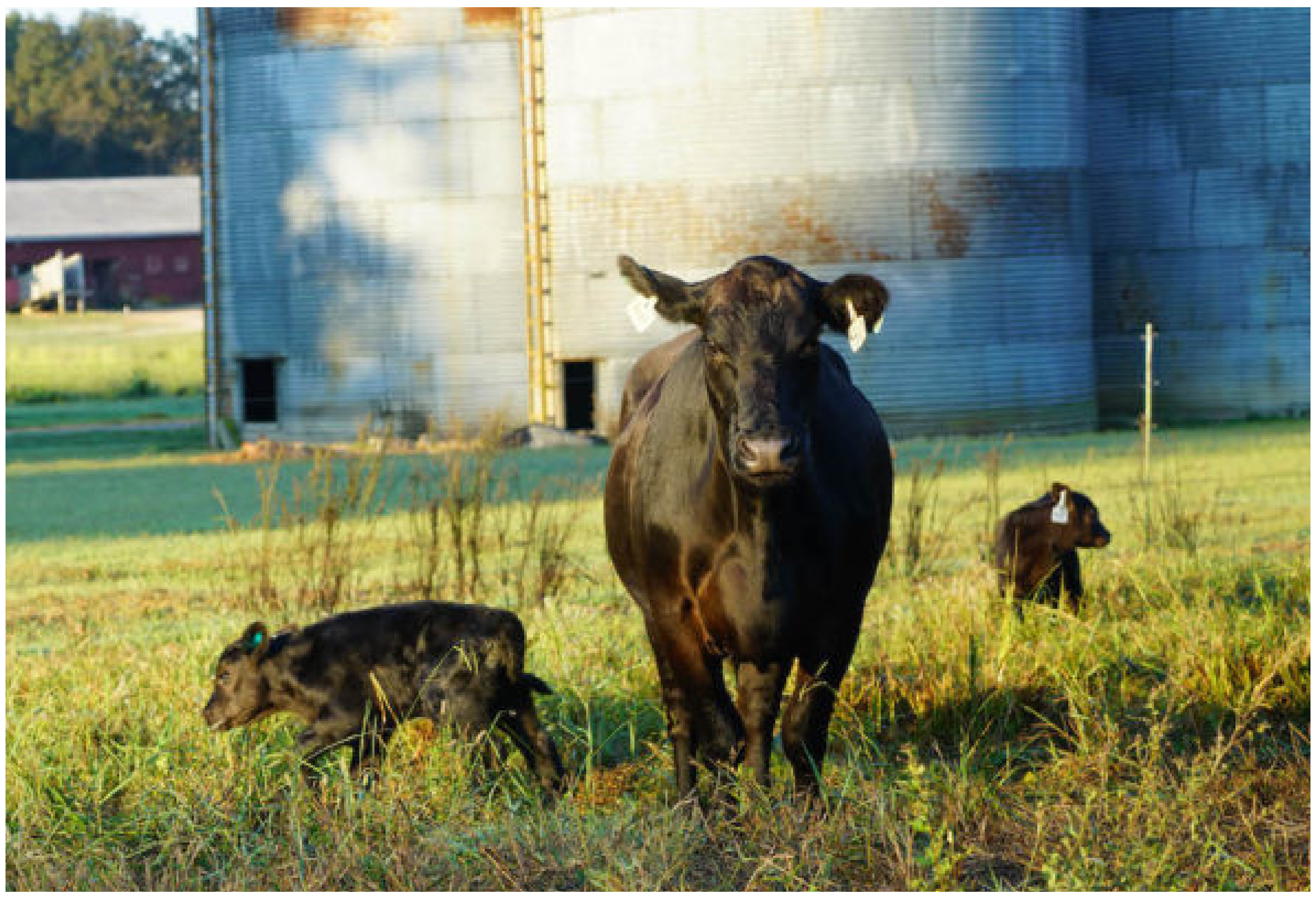

UNIVERSITY OF TENNESSEE INSTITUTE OF AGRICULTURE

BEEF AND FORAGE CENTER

ANNUAL RESEARCH REPORT

Facilitating Extension, research, and educational activities related to issues facing beef and forage systems in Tennessee and beyond

VOLUME 2, 2021

DOI: 10.6084/m9.figshare.17208854.v1

Contents

Research Reports

Poster Abstracts

Welcome

2021 UT Beef and Forage Center Annual Research Report

Welcome to the second volume of the UT Beef and Forage Center Annual Research Report. The mission of the Center is to facilitate research and communication of science-based information to advance the Tennessee beef and forage industry. The Center functions as an "information hub" serving all in the Tennessee beef and forage industries. The Center also serves as a focal point and catalyst for research, Extension, and teaching efforts related to issues facing beef and forage systems in Tennessee. The report aims to build on this vision by providing an opportunity to highlight the current work related to the Center to producers and stakeholders across the state. Volumes of the report will provide comprehensive material to convey new knowledge and technology to improve the management, efficiency, and production of high-quality beef cattle.

The Beef and Forage Center would like to thank Dr. Kyle McLean for his great effort in leading the development of this report so that we can produce a great statewide report. Also, thanks to the contributors to the report and to the staff and students who help with the research, teaching and Extension activities on beef cattle and forages. Finally, thanks to the funders of the grants that help fund the research projects and students/staff working on the projects. We truly appreciate your contributions to our research programs because without this support, the research would not be possible.

Should have any questions about the work reported in this report, please do not hesitate to contact the UT Beef and Forage Center or any of the authors of the individual reports. Thank you for your encouragement and support of beef and forage research in Tennessee.

Sincerely,

The University of Tennessee Beef and Forage Center

2505 EJ Chapman Drive, PBB 112
Knoxville, TN 37996-4561
utbeef@tennessee.edu
UTBeef.com

IN PROGRESS: Patch-Burn and Rotational Grazing Effects on Performance of Beef Heifers and Pasture Productivity

M. Berry[1], P. Keyser[1], R. Smith[2], and E. Bisangwa[3]

[1]Department of Forestry, Wildlife and Fisheries: University of Tennessee; Knoxville, TN
[2]Center for Native Grasslands Management, University of Tennessee, University of Kentucky
[3]Center for Native Grasslands Management, University of Tennessee
Corresponding Author: Dr. Patrick Keyser; pkeyser@utk.edu

Take Home Message: *Patch burn grazing can be an efficient management strategy to produce high quality forage in native warm-season grasses. While not commonly utilized in the tall fescue belt, patch burn grazing can produce results equivalent to other conventional forage management strategies.*

Summary: Patch-burn grazing (PBG; also known as pyric-herbivory) uses prescribed fire to distribute cattle grazing pressure within a pasture to foster heterogeneity, enhance biodiversity, and reduce management burden. This strategy has produced similar gains in cattle and forage mass as other traditional grazing methods (Scasta et. al, 2015). Still, PBG has not been explored in eastern forage systems such as the tall fescue belt. Therefore, we implemented an experiment at three sites, two in Kentucky and one in Tennessee, using either weaned or yearling heifers. These animals were randomly assigned to 25-ac pastures managed with either PBG or rotational (ROT) grazing; each divided into three patches or paddocks. Pastures had been seeded with a native warm-season grass mix [big bluestem (*Andropogon* gerardii) and indiangrass (*Sorghastrum nutans*)] in 2012, three years prior to the initiation of grazing. Cattle were weighed yearly before initial grazing and again after final removal. Forage samples (n = 16) were taken within actively grazed ROT paddocks and within PBG grazing paddocks; eight were taken from un-burned and eight from burned patches. Tiller counts (tillers per plant) were conducted yearly during mid-summer. Gains and grazing days were comparable between treatments. Forage mass declined through the summer at all locations and was comparable between treatments. Tiller counts declined at one site over the course of the study, but in no case differed between treatments.

Introduction

Native grasslands provide high quality forage for livestock along with essential wildlife habitat. Managing such pastures through PBG may produce prime pastures for grazing while simultaneously being advantageous for native wildlife as demonstrated by prior studies. In 2016, Ricketts and Sandercook reported that PBG contributed to improved structural heterogeneity and improved mammal biodiversity (Ricketts and Sandercook, 2016). In a separate study conducted by Winter et al. (2014), cattle performance did not appear to differ on pastures managed by PBG versus those managed with traditional techniques (Winter et. al, 2014).

Materials and Methods

We conducted our research at Middle Tennessee AgResearch and Education Center, Lewisburg, TN (MTREC); Robinson Center for Appalachian Resource Sustainability, Lost Creek, KY (QUICK); and Blue Grass Army Depot (BGAD), Richmond, KY. All sites were planted during May/June 2012 with a big bluestem

(*Andropogon* gerardii) and indiangrass (*Sorghastrum nutans*) mixture. Two grazing treatments, PBG and ROT, were assigned under a random block design, with three replicates at BGAD, two at MTREC and two at QUICK. Initial stocking rates were based upon site productivity. Weaned heifers (545.3 lbs) were assigned at QUICK, yearling heifers at BGAD (856.6 lbs) and MTREC (925.3 lbs). In 2015, approximately one-third of each PBG pasture was burned (BGAD, 11 Apri1; MTREC, 2 April; and QUICK, 24 April). The seven rotational grazing pastures were managed by rotational grazing and without burning. Grazing initiation dates were 1 May (MTREC, 4 weeks post-burning), 8 May (QUICK, 2 weeks post-burning), and 19 May (BGAD, 5 weeks post-burning). Cattle were permitted to graze freely on patch burn pastures and cattle were rotated approximately every 1-2 weeks contingent on canopy conditions. Cattle were weighed each year before moving onto pastures and weighed again when removed at summer's end. We clipped 0.25-m^2 quadrat forage samples (n=16) from each pasture monthly during the grazing season. Samples were taken within rotational grazing paddocks from the actively grazed paddock or the next paddock in the rotation. Samples were also obtained in patch burn grazing paddocks (eight from the un-burned and eight from the burned portion). In each clipping, two cuts were obtained – a cut from 2-11 inches was used to determine forage mass (FM). Samples were dried for a minimum of 72 hours. Tiller counts were conducted yearly during mid-summer by counting all tillers on a single plant (per paddock or patch). A repeated measures ANOVA was conducted via PROC GLIMMIX (SAS 9.4) for forage mass and tiller counts with treatment and sample period (FM) and year (tillers) as fixed effects. A mixed model ANOVA with year and treatments (fixed effects) was conducted for average daily gain (ADG), grazing days and gain per acre. Means were declared to be different at $P < 0.05$.

Table 1. Average daily gain, grazing days and gain per acre for patch burn grazing (PBG) and rotational razing (ROT) treatments in sites QUICK (Lost Creek, KY) and MTREC (Lewisburg, TN). Means followed by different letters within a site and model factor differ (P <0.05).

Trt	Average Daily Gain (lbs)		Trt	Grazing Days (per acre)		Trt	Gain (lbs per acre)	
	QUICK	MTREC		QUICK	MTREC		QUICK	MTREC
PBG	1.42	1.59	PBG	63^a	100^b	PBG	89.1^b	158.3
ROT	1.4491	1.5763	ROT	72.8119^b	91.2039^a	ROT	102.5^a	143.7
Year			Year			Year		
2015	1.57^a	1.50^b	2015	71^a	99^a	2015	106.1^a	149.1
2016	1.44^a	1.66^a	2016	65^b	92^b	2016	93.1^b	152.8
2017	1.29^b	N/A	2017	69^a	N/A	2017	88.3^b	N/A

Results and Discussion

The ADG was similar between PBG and ROT grazing treatments in both the MTREC ($P > .86$) and QUICK ($P > .66$) sites (Table 1). However, ADG varied ($P < .03$) between years at MTREC and declined ($P <. 006$) in the third year at QUICK (Table 1). relatively stable ($P < .001$; Fig. 1c).The ADG at BGAD interacted ($P < .01$) by treatment and year (Fig.1a). Grazing days differed by grazing treatment at both MTREC ($P < .05$) and QUICK ($P < .001$). With respect to year,

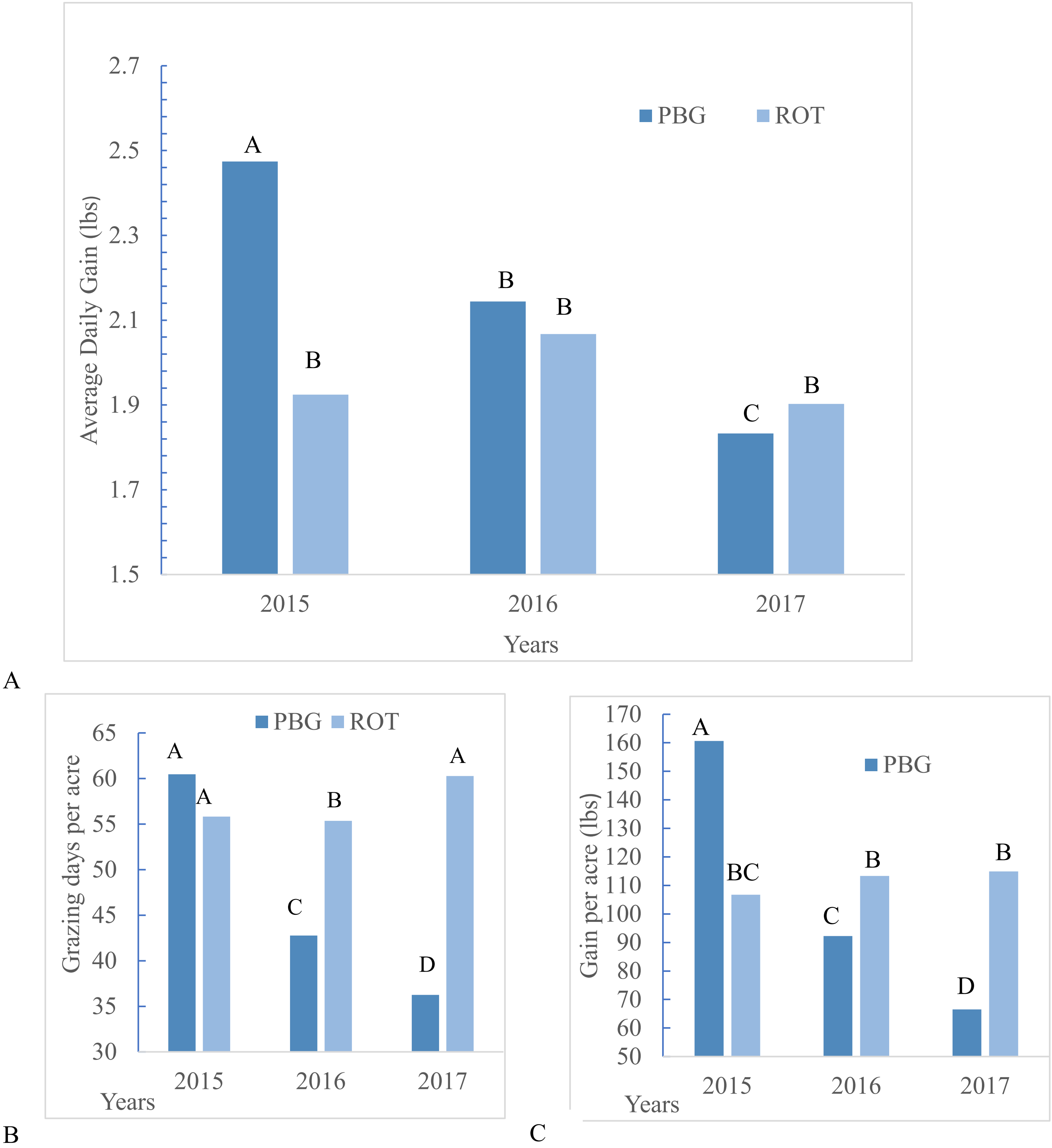

Figure 1: Average daily gain (A), grazing days per acre (B), and gain per ac (C) for BGAD (Richmond, KY) for patch-burn grazing (PBG) and rotational grazing (ROT) treatments. Letters show significant differences or overlap among treatments for subsequent years.

Table 2. Tiller counts for patch burn grazing (PBG) and rotational grazing (ROT) treatments in sites BGAD (Richmond, KY), MTREC (Lewisburg, TN) and QUICK (Lost Creek, KY). Means followed by different letters within a site differ.

Trt	Tiller Counts		
	BGAD	MTREC	QUICK
PBG	57.7	112.1	30.2
ROT	56.5	82.1	31.2
Year			
2015	87.8^{a}	107.7	27.5^{b}
2016	49.4^{b}	86.6	30.7^{ab}
2017	35.3^{c}	N/A	33.8^{a}

grazing days were reduced in the 2016 at MTREC (*P* < .001) and QUICK (*P* < .002). Grazing days declined (*P* < .001) in all three years at BGAD for PBG and fluctuated for ROT (Fig. 1b). There was no difference in gain per acre for either treatment or year at MTREC. Gain was higher (*P* < .005) in the rotational treatment and in the first year (*P* < .001) at QUICK. At BGAD, gain per acre followed a similar pattern as grazing days, declining all three years while for ROT, it remained Forage mass differed in treatments only at MTREC only (*P* < .05). All three sites showed reduced FM from the first to last sample dates (Table 3).

Table 3. Forage mass for patch burn grazing (PBG) and rotational grazing (ROT) treatments in sites BGAD (Richmond, KY), MTREC (Lewisburg, TN) and QUICK (Lost Creek, KY). Means followed by different letters within a site differ.

Trt	Forage Mass		
	BGAD	MTREC	QUICK
PBG	1,337	$2,141^{a}$	2,222
ROT	1,369	$1,224^{b}$	2,070
Sample Date			
August	$1,725^{a}$	$2,380^{a}$	$3,495^{a}$
July	$1,461^{ab}$	$1,981^{ab}$	$1,818^{b}$
June	$1,285^{b}$	$1,382^{ab}$	$1,769^{b}$
May	941^{bc}	986^{b}	$1,502^{b}$

Based on tiller counts, stands were weakened at BGAD during the three-year study, but did not appear to be treatment related; potentially as a result of grazing intensity (Table 2). Overall, patch-burn and rotational grazing produced comparable gains in cattle. While stands declined slightly, pastures were not impaired from PBG. Forage mass in patch burn grazing treatments was analogous to ROT grazing treatments.

Literature Cited

Ricketts, A. & Sandercook, B.K. 2016. Patch-burn grazing increases habitat heterogeneity and biodiversity of small mammals in managed rangelands. *Ecosphere.* Vol. 7, Issue 8.

Scasta, J.D., Thacker, E.T., Hovick, T.J., Engle, D.M., Allred, B.W., Fuhlendorf, S.D., & Weir, J.R. (2015). Patch-burn grazing (PBG) as a livestock management alternative for fire-prone ecosystems of North America. *Renewable Agriculture and Food Systems*. Vol 31, Issue 6.

Winter, S.L., Fuhlendorf, S.D. & Goes, M. 2014. Patch-Burn Grazing Effects on Cattle Performance: Research Conducted in a Working Landscape. Rangelands. Vol 36, Issue 3. pp. 2-7

IN PROGRESS: Animal Performance and Pasture Productivity of Weaned Steers Grazing Native Warm-Season Grass Pastures with and without Interseeded Native Forbs and Legumes

J.L. Prigge[1], E. Bisangwa[1], P.D. Keyser[1]

[1]Department of Forestry, Wildlife, and Fisheries; University of Tennessee Institute of Agriculture; Knoxville, TN 37996

Corresponding Author: Dr. Patrick Keyser; pkeyser@utk.edu

Take Home Message: *Pastures provide an unexplored opportunity to support both growing beef cattle and critical pollinator species that are in grave population decline. Our objectives were to evaluate animal performance and pasture productivity in native warm-season grass pastures with and without interseeded native, flowering forbs and legumes. This study documented similar ADG for steers when grazing both pasture types, though forage mass tended to be less in interseeded pastures. These results suggest that interseeding native forbs and legumes not only maintains beef production but could also provide valuable pollinator resources.*

Summary: The U.S. tall fescue belt is home to over 12.8 million grazing beef cattle (*Bos taurus*) on 306,000 farms (USDA-NASS, 2017) where pastureland provides an opportunity to increase forage biodiversity to support both growing cattle and pollinators. Insects such as bees and butterflies provide a variety of crucial ecosystem services and assist with the pollination of flora (NRC 2007). Due to environmental stressors such as insecticides and the increasing use of monocrops, many pollinators are in decline (Potts et al., 2010). Therefore, the objectives of this study were to evaluate animal performance and pasture productivity for steers grazing native warm-season grasses (NWSG) with and without interseeded native forbs and legumes (FORB). In spring 2021, four, 2.75-acre pastures were interseeded with an 18-species blend of native forbs and legumes. From May–August 2021, weaned beef steers grazed NWSG (n=4) and FORB (n=4) pastures. Average daily gain (ADG), total gain per acre, and forage mass were analyzed using linear regression models in R software (version 4.1.1). There was no difference (P = 0.35) in ADG between treatments for the 28-day intervals, or for the full grazing season (P = 0.42). Additionally, total gain per acre did not differ (P = 0.42) between pasture treatments. Among 28-day intervals, ADG declined ($P < 0.001$) as the season progressed. Total forage mass was less (P = 0.003) in FORB pastures and declined (P = 0.003) over the grazing season for both treatments. These similarities in ADG could be attributed to similarities in pasture composition between the treatments due to poor FORB establishment, a problem encountered in other studies of FORB establishment in NWSG. Further research should explore methods for improved FORB establishment into NWSG pastures.

Introduction

In the U.S. tall fescue belt, pasturelands support over 12.8 million beef cows (*Bos taurus*) on roughly 306,000 farms documenting annual farm receipts of over 866 million dollars (USDA-NASS, 2017). Unlike some crop systems, pastures have the capacity to be dual purpose and can support both production animals and wild species such as insects, birds, and rodents. Pollinator insects like as honeybees, bumblebees, and butterflies provide a variety of ecosystem services, and approximately 75% of crop species require assisted pollination provided by these insects and other animals (NRC 2007). Despite pollinators' vital roles in environmental health and seed production, both human-managed and native pollinators are in decline due to a variety of environmental stressors including pesticide use, changes in land use, and disease (Potts et al., 2010). Additionally, the use of herbicides and the increasing practice of monocrop production systems have considerably decreased the availability of floral resources, further reducing bee populations that have traditionally provided critical pollinator services (Shackelford et al., 2013). Pastures in the tall fescue belt present an opportunity to provide forage for beef cattle production as well as flowering forb species to support pollinator persistence. Despite this potential, there is a lack of research on the benefits of incorporating native flowering forbs and legumes (FORB) into beef grazing systems. Therefore, the objectives of this study were to evaluate animal performance and pasture productivity for steers grazing native warm-season grasses (NWSG) and NWSG pastures interseeded with native forbs and legumes.

Materials and Methods

Research was conducted at the East Tennessee AgResearch and Education Center, Holston Unit, in Knoxville, TN. Twenty-five acres of an established (2012), mixed NWSG pasture [big bluestem (*Andropogon gerardii*), indiangrass (*Sorghastrum nutans*), and little bluestem (*Schizachyrium scoparium*)] were divided into eight, 2.75-ac pastures. Four of the pastures were interseeded with an 18-species mixture (Table 1) of FORB in February

Table 1: Seeding rates (PLS[1] lbs. ac^{-1}) of FORB interseeded into an established NWSG stand and grazed by weaned Angus steers, May–August, 2021, Knoxville, TN.

	Forb or Legume Species	Scientific Name	Seeding rate (PLS lbs. ac^{-1})
Forbs	Canada Goldenrod	*Solidago canadensis*	0.10
	Cup Plant	*Silphium perfoliatum*	0.25
	Maximilian Sunflower	*Helianthus maximiliani*	0.25
	Oxeye Sunflower	*Helopsis helianthoides*	0.50
	Prairie Dock	*Silphium terebinthinaceum*	0.25
	Purple Coneflower	*Echinacea purpurea*	1.00
	Plains Coreopsis	*Coreopsis tinctoria*	0.01
	Lanceleaf Coreopsis	*Coreopsis lanceolata*	0.50
	Upright Prairie Coneflower	*Ratibida columnifera*	0.50
	Black-eyed Susan	*Rudbeckia hirta*	0.50
Legumes	Illinois Bundleflower	*Desmanthus illinoensis*	0.50
	Partridge Pea	*Chamaecrista fasciculata*	0.50
	Purple Prairie Clover	*Dalea purpurea*	0.60
	White Prairie Clover	*Dalea candida*	0.40
	Panicledleaf Ticktrefoil	*Desmodium paniculatum*	0.50
	Roundhead Bushclover	*Lespedeza capitata*	0.40
	Showy Ticktrefoil	*Desmodium canadensis*	0.50
	Slender Bushclover	*Lespedeza virginica*	0.25

[1] Pure live seed, PLS; native forbs and legumes, FORB; native warm-season grasses, NWSG

2021 and again in April 2021 (8 pure live seed lbs. ac^{-1} total). To assist in forb establishment, all pastures were sprayed with glyphosate (N-[phosphonomethyl]glycine; 1qt ac^{-1}) to control winter annual weeds in March 2021 prior to forb emergence. No nitrogen was applied to pastures during the study.

Weaned Angus steers (n=32; 549 ± 86 lbs.) were stocked four per pasture (799 ± 48 lbs. ac^{-1}) on 27 May 2021. Steers were weighed at stocking, after 28, 56, and 90 days on pasture, and when removed from the pasture on 28 August 2021. Weights were taken on two consecutive days prior to and following stocking of pastures. Steers had ad libitum access to minerals, water and shade while grazing. All animal care and experimental procedures were approved by the University of Tennessee Institutional Animal Care and Use Committee (protocol #2258).

To determine forage mass, 10, 2.7-ft^2 quadrats were sampled in each pasture every 28 days by harvesting the available forage to a 2-inch stubble height. Forage was sorted into NWSG and FORBs to determine botanical composition. Samples were dried in forced-air ovens at 130˚F until they maintained a constant mass (approximately 72 hours) to determine dry matter content.

Analysis was conducted using R software (version 4.1.1) running RStudio (version 1.4.1717) and statistical significance was set at $P \leq 0.05$. Mean separations were compared using Tukey's honest significant difference test. Treatment differences were compared for each response variable using ANOVA. Average daily gain (ADG) was calculated by dividing the weight gain by the number of grazing days during the interval of interest. Average daily gain measures were analyzed using linear mixed effect models, where treatment was set as a fixed effect and paddock and steer were random effects. Total gain (lbs. ac^{-1}) was represented by the multiplication of the paddock's ADG and the total grazing days per acre (130.9 d ac^{-1}). Total gain was analyzed using a linear mixed effect model where treatment was set as a fixed effect and paddock was a random effect. Differences in ADG between the three grazing intervals were analyzed using a mixed effect model where treatment and grazing interval were fixed effects and paddock and steer were random effects.

Table 2 Means and standard errors of animal performance (ADG[1]) and pasture productivity of weaned Angus steers grazing NWSG (Control) and FORB pastures, May–August, 2021, Knoxville, TN.

Treatment	ADG 28	ADG 56	ADG 90	Overall ADG	Gain
	——————lbs.——————				lbs. ac^{-1}
Control	$2.28 \pm 0.33^{a(x)2}$	$1.49 \pm 0.25^{b(x)}$	$0.79 \pm 0.19^{c(x)}$	$1.47 \pm 0.10^{(x)}$	$192 \pm 12.6^{(x)}$
FORB	$2.60 \pm 0.33^{a(x)}$	$1.76 \pm 0.25^{b(x)}$	$0.81 \pm 0.19^{c(x)}$	$1.59 \pm 0.10^{(x)}$	$207 \pm 12.6^{(x)}$

[1] Average daily gain, ADG; native warm-season grasses, NWSG; NWSG interseeded with native forbs and legumes, FORB; ADG during the first grazing interval, ADG 28; ADG during the second grazing interval, ADG 56; ADG during the last grazing interval, ADG 90

[2] Means within a row (a, b, c) or column (x, y, z) without a common letter differ based on Tukey's HSD test ($P \leq 0.05$).

Total forage mass was analyzed using linear models where the paddock and the interaction between treatment and grazing interval were fixed effects. Pasture composition for the FORB treatment was compared using a linear model including forage type, paddock and grazing interval as fixed effects.

Results and Discussion

Average daily gain did not differ ($P = 0.79$) between treatments over the first 28 days (Table 2), between days 28 and 56 ($P = 0.48$), between days 56 and 90 ($P = 0.94$), or over the entire grazing season ($P = 0.42$). Additionally, there was no difference ($P = 0.42$) in gain per acre between NWSG and FORB pastures. However, ADG declined ($P < 0.001$) as the grazing season progressed. The FORB treatment produced less ($P = 0.003$) total forage mass than the control (Figure 1).

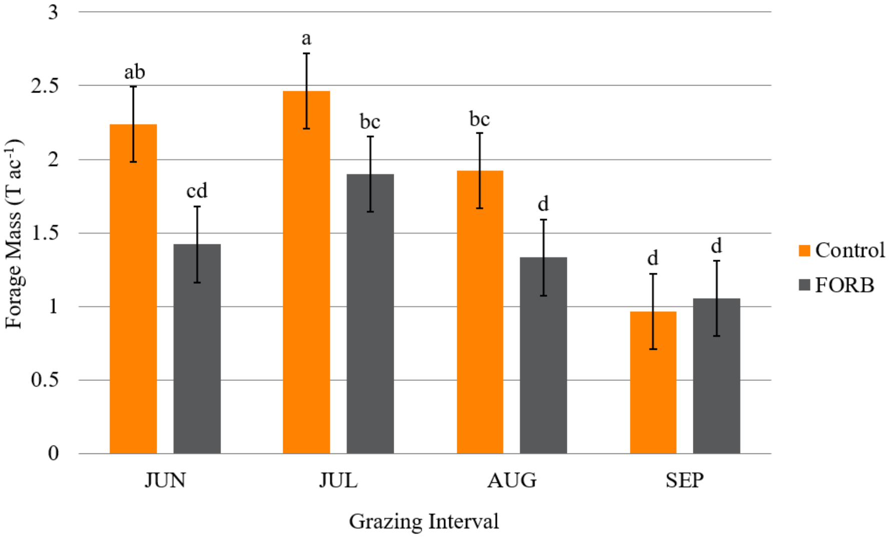

Figure 1 Average forage mass[1] produced throughout the grazing season in NWSG[2] (Control) and FORB pastures grazed by Angus steers, May–August, 2021, Knoxville, TN. [1]Values are presented as mean total forage mass and error bars represent 95% confidence intervals. [2]Native warm-season grasses, NWSG; NWSG interseeded with native forbs and legumes, FORB; June, JUN; July, JUL; August, AUG; September, SEP [a-d]Means without a common letter differ based on Tukey's HSD test ($P \leq 0.05$).

There was a significant interaction ($P = 0.003$) between total forage mass and grazing interval where the total available forage declined ($P = 0.003$) as the grazing season progressed for both treatments. Despite this difference, forbs and legumes made up minimal (< 1%; $P < 0.001$) forage mass compared to NWSG.

Similarly, Keyser et al. (2016) found no ADG differences when grazing bred dairy heifers on NWSG and NWSG interseeded with red clover. Keyser et al. (2016) attributed the similarity to the inconsistent establishment and poor competitiveness of red clover within the established NWSGs, leading the mixed stands to have limited amounts of red clover. The current study also exhibited poor establishment of secondary forages into NWSG and this challenge has been related to dense cover by the established NWSGs. For instance, Jung et al. (1985) observed that NWSG stands providing >75% cover greatly reduced the establishment rate of interseeded legumes, even during NWSG dormancy. Mason et al. (2019) also observed that interseeding cool-season grasses (CSG) and legumes into dormant NWSG stands produced poor CSG and legume mass. Season-long ADG and total gain were less in the current study compared to Backus et al.

(2017) who observed higher season-long ADG and total gain when grazing big bluestem and indiangrass. Although our pastures were relatively similar in composition and forage mass, the lack of nitrogen fertilizer application, the later grazing initiation in the spring of 2021, and the advanced maturity of the stands likely lowered ADG. Furthermore, the stocking rates were not altered during the grazing season in the current study, which may have decreased the gain per unit of land. Also, similar to the results reported by Keyser et al. (2016), ADGs were higher earlier in the grazing season compared to later in the season. These differences could be attributed to the reduction in forage quality as the stands matured over the grazing season and the reduction in forage mass as the season progressed.

Based on our preliminary results, NWSG pastures interseeded with FORB have produced similar ADG in growing beef steers and total gain per acre compared to NWSG pastures. These results suggest that interseeding FORB not only maintains beef production, but could also provide valuable pollinator resources. Despite these promising findings, it will be imperative to investigate and improve FORB interseeding into established NWSG stands to fully examine the benefits or detriments of these forages.

Acknowledgments

The authors gratefully acknowledge the assistance of D. Hopkins, B. Beavers, B. Simpson, and the staff of the East Tennessee AgResearch and Education Center for implementing this research. We also acknowledge the assistance of K. Beavers, A. Hanson, and H. Poole in collecting data. Financial support for this study was provided by USDA-NRCS Conservation Innovation Grant 423512-19D43 and USDA Hatch Project TEN00547.

Literature Cited

Backus, W. M., Waller, J. C., Bates, G. E., Harper, C. A., Saxton, A., McIntosh, D. W., Birckhead, J., & Keyser, P. D. (2017). Management of native warm-season grasses for beef cattle and biomass production in the Mid-South USA. *Journal of Animal Science 95*:3143-3153. doi:10.2527/jas2017.1488

Jung, G. A., Griffin, J. L., Kocher, R. E., Shaffer, J. A., & Gross, C. F. (1985). Performance of switchgrass and bluestem cultivars mixed with cool-season species. *Agronomy Journal, 77*(6):846-850.

Keyser, P. D., Holcomb, E. D., Lituma, C. M., Bates, G. E., Waller, J. C., Boyer, C. N., & Mulliniks, J. T. (2016). Forage attributes and animal performance from native grass inter-seeded with red clover. *Agronomy Journal, 108*(1):373-383. https://doi.org/10.2134/agronj2015.0198

Mason, K. M., Mullenix, M. K., Tucker, J. J., Muntifering, R. B., Angle, J. S., & Yeager, J. (2019). Overseeding eastern gamagrass with cool-season annual grasses of grass-legume mixtures. *Crop Science, 59*:2264-2270. doi: 10.2135/cropsci2019.02.0099

National Research Council (NRC). (2007). *Status of pollinators in North America*. Committee on the Status of Pollinators in North America. National Academy Press, Washington, DC, USA.

Potts, S. G., Biesmeijer, J. C., Kremen, C., Neumann, P., Schweiger, O., & Kunin, W. E. (2010). Global pollinator declines: trends, impacts and drivers. *Trends in Ecology & Evolution, 25*(6):345-353. https://doi.org/10.1016/j.tree.2010.01.007

Shackelford, G., Steward, P. R., Benton, T. G., Kunin, W. E., Potts, S. G., Biesmeijer, J. C., & Sait, S. M. (2013). Comparison of pollinators and natural enemies: a meta-analysis of landscape and local effects on abundance and richness in crops. *Biological Reviews, 88*(4):1002-1021. https://doi.org/10.1111/brv.12040

USDA-NASS. 2017. National Agricultural Statistics Service. Retrieved 10.8.21 fromhttp://www.nass.usda.gov/.

Poster Abstracts

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

C.C. Catrett, S.E. Moorey, J.E. Beever, and T.N. Rowan*

Department of Animal Science, University of Tennessee, Knoxville, TN

* Corresponding Author: trowan@utk.edu

Reproduction plays a major role in driving forward the production efficiency of livestock species. However, reproductive traits are lowly heritable, 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). Using the American Simmental Association's performance and Total Herd Enrollment (THE) data, we have 1,463,873 calving records from 827,157 cows, 31,000 of which are genotyped. With this data, we have calculated two continuous and two discrete phenotypes that we will use as measures of fertility. We will analyze calving interval (days between calves), calving dates (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). Using these phenotypes, we will identify individuals who have shorter calving intervals and consistently calve early each season. We will use this information to observe the genetic components of sustained cow fertility and calculate genomic predictions for fertility. The main objectives of the study are to determine the heritability of these traits and investigate their genetic correlations with other economically important traits. 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 imputated single nucleotide polymorphisms (SNPs) to identify loci significantly associated with each measure of fertility. The relevance of this work to the future is that it will enable producers to utilize EPDs to select more productive females. This research will also deliver a set of informative and interesting genetic markers that may be added to existing genomic tests for cattle.

Poster Number: 602

Genomic Determinants for the Rumen Microbiome: A Proposal

MT Henniger[1], JE Beever[1], TN Rowan[1], BH Voy[1], JE Wells[2], LA Kuehn[2], and PR Myer[1*]

[1] Department of Animal Science, University of Tennessee, Knoxville, TN
[2] U.S. Department of Agriculture, Agricultural Research Service, U.S. Meat Animal Research Center, Clay Center, NE

* Corresponding author: pmyer@utk.edu

The rumen microbiome converts low quality feedstuffs into usable energy for ruminants, providing approximately 70% of energy to the host animal. The critical role of the rumen microbiome is reflected in its impact on important production-relevant phenotypes, such as feed efficiency. The degree to which the host genome may determine features of the rumen microbiome is unknown. To identify host genetic factors that influence the rumen microbiome, approximately 400 Angus steers will be fed from a GrowSafe system for 70 days to measure individual feed intake. Body weights will be taken two days consecutively per month to calculate residual feed intake and other feed efficiency metrics. Steers will be fed a diet similar in fiber and protein content throughout the study with *ad libitum* access to water. On day 35, a surgical incision will be made to access the dorsal rumen via trocar insertion to swab the ventral rumen wall to collect microbial communities present on the wall, and blood will be collected from the tail vein. At the end of the feed efficiency trial, rumen fluid will be sampled from steers via orogastric tubing. Bacterial, archaeal, protozoal, and fungal communities will be sequenced from the rumen wall and rumen content. From blood collected, genomic DNA will be isolated and low-pass whole genome sequencing will be used to generate high-density genotype information. Untargeted metabolomics will be used for serum and rumen fluid to determine potential variation in metabolites associated with differences in host genotypes and phenotypes. With these data, genome-wide association studies will be performed to associate microbial phenotypes with host genetic variation. Discovering connections between the host genome and the rumen microbiome will allow for insights into improving the production efficiency of beef cattle.

Poster Number: 603

Pre-ovulatory Follicular Fluid and Serum Metabolome Profiles in Beef Cows with Thin, Moderate, and Obese Body Condition

E.J. Horn[1], C.C. Read[1], J.L. Edwards[1], F.N. Schrick[1], J.D. Rhinehart[1], R.R. Payton[1], S.R. Campagna[2], H.F. Castro[2], J.L. Klabnik[1], and S.E. Moorey[1*]

[1] Department of Animal Science, University of Tennessee, Knoxville, TN
[2] Department of Chemistry, University of Tennessee, Knoxville, TN

* Corresponding author: smoorey5@utk.edu

Acknowledgements: Emma Hessock, Alison Stokes, Samantha Roberts, Meredith Hinson

Extremes in body composition affect beef cow fertility and productivity. Overly thin or obese cows often experience decreased pregnancy rates. A key component of pregnancy establishment is ovulation of a developmentally competent oocyte. The oocyte is supported by the surrounding follicle and follicular fluid (FF) which provides it with substances needed to grow and mature. Variation in the metabolome of maternal serum may influence the follicular microenvironment and the oocytes' metabolic activity, directly influencing developmental capacity. FF and serum metabolome profiles were demonstrated to be influenced by body composition in women and dairy cattle; however, such information is lacking in beef cattle. Investigation of the impact of body composition on the circulating and FF metabolome during the pre-ovulatory time-period is essential to understanding how extreme body composition impacts fertility. We hypothesized that differences in the metabolome of FF and serum influences oocyte maturation and acquisition of developmental competence. This may contribute to reduced fertility when cattle experience extreme body composition. We designed a study to explore the relationship between body condition score (BCS) and the metabolome of FF and serum in beef cattle. We selected individuals with BCS 4(thin;n=14), BCS 6(moderate;n=18), or BCS >8(obese;n=14) for analysis. Metabolites were extracted from FF or serum and analyzed by UHPLC-MS. We identified metabolites using MAVEN program and identified differences using a multiple linear regression model utilizing least-squared means to detect metabolites that differed among thin, moderate, and obese animals (adjusted-$p<0.05$). MetaboAnalyst-4.0 was used for enrichment analysis of significant metabolites. We identified 38 metabolites in FF and 49 metabolites in serum. There were no significant differences in FF metabolite content among BCS classifications. There were 5, 22, and 1, serum metabolites differentially abundant between thin-obese, moderate-thin, and moderate-obese classifications, respectively. These metabolites were enriched in multiple processes including 'arginine biosynthesis' and 'arginine/proline metabolism' (FDR<0.04).

Poster Number: 604

Predicting Vaccination Status at Arrival in Southeastern Stocker Calves: A Proposal

C. Hunkler[1], A. Akter[1], B. Karisch[2], L. Strickland[1], M. Caldwell[3], and L. G. Schneider[1] *

[1] Department of Animal Science, University of Tennessee, Knoxville, TN
[2] Department of Animal and Dairy Sciences, Mississippi State University, Mississippi State, MS
[3] Department of Large Animal Clinical Science, University of Tennessee, Knoxville, TN

* Corresponding author: lschneider@utk.edu

Bovine Respiratory Disease Complex (BRDC) is a multifaceted respiratory disease that is associated with multiple viral and bacterial pathogens. Some of the viral pathogens that are recognized as major contributors to BRDC include are bovine respiratory syncytial virus (BRSV), bovine viral diarrhea virus (BVDV), infectious bovine rhinotracheitis (IBR), and parainfluenza 3 virus (PI3) and calves are often vaccinated against these viruses to reduce BRDC incidence. Stocker calves are at increased risk of BRD due to stress from handling, transportation, weaning, and comingling at sale barns. Additionally, calves' vaccination history is often unknown to the stocker producers. Therefore, we aimed at determining if physical characteristics of calves upon arrival at the stocker facility can be used to predict calfhood vaccination status. We will collect serum samples from newly purchased calves via jugular vein at commercial stocker operations in Tennessee (n=400) and Mississippi (n=200). Visual data collection will include castration status (fresh, healed, or intact), sex, coat score, body condition score, approximate weight, breed, horn status, presence of a prior ear tag, clinical signs of BRDC, and other predictors. Ear notches from each calf will be collected to test for persistent infection with BVDV. Serum samples will be used to assess antibody titers of three important respiratory viral pathogens (i.e., BVDV type 1, BRSV, and IBR (BHV-1)) via virus neutralizing test. Calves will be classified based on their vaccination status (likely vaccinated, likely currently exposed, and no titer (never exposed)). Descriptive statistics will be reported to explain the cattle sampled and logistic regression models (Proc LOGISTICS in SAS 9.4) will be developed to assess factors predictive of vaccination status. These data will offer researchers, veterinarians, and extension personnel with new understanding of stocker cattle production and health, leading to areas of outreach and education that can improve profitability and calf wellbeing.

Poster Number: 605

The Level of LCORL Expression in Muscle is Associated with Lean Growth Rate in Beef Cattle

L. Majeres[1], S. Moisa[1], A. Dilger[2], J. McCann[2], D. Shike[2], and J. Beever[1*]

[1] Department of Animal Science, University of Tennessee, Knoxville, TN
[2] Department of Animal Sciences, University of Illinois, Urbana, IL

* Corresponding author: jbeever@utk.edu

Previous studies have implicated genetic variation at the LCORL locus to be associated with increased lean growth characteristics in cattle and several other species. However, a definitive cause for what drives this change in phenotype has yet to be defined in any species except perhaps the dog. To shed light on this mystery, our goal was to investigate the impact of LCORL expression on phenotype, independent of genotype. To do this, we analyzed RNA isolated from the muscle tissue of 87 crossbred heifers and steers. For each animal, a biopsy of the longissimus dorsi muscle was collected at approximately 300 days of age and subsequently used for RNA isolation. Relative LCORL expression was quantified using quantitative polymerase chain reaction (qPCR) using beta-2 microglobulin expression as a reference. Relative LCORL expression varied by approximately 7-fold between animals with the lowest and highest expression. The relationship between relative expression and several performance traits were analyzed using a general linear model. LCORL expression was positively correlated with birth weight ($P=0.0012$), on-test weight ($P<0.0001$), yearling weight ($P=0.0060$), and harvest weight ($P=0.0067$), as well as hot carcass weight (HCW) ($P=0.0079$) and rib-eye area (REA) ($P=0.0205$). LCORL expression was also negatively correlated with kidney, pelvic, heart fat (KPH%) ($P=0.0182$). Our results indicate that increased LCORL expression is associated with increased lean growth and reduced adiposity in beef cattle.

Poster Number: 606

Pregnancy Influences on the Feed Efficiency and Rumen Environment of Angus Heifers in Producing a Quality Beef Product: A Proposal

M.G. Martin[1], B.A. Clemmons[1†], T.B. Ault-Seay[1], M.T. Henniger[1], L.G. Schneider[1], B.H. Voy[1], K.J. McLean[1], P.Y. Mulon[2], D.E. Anderson[2], and P.R. Myer[1*]

[1] Department of Animal Science, University of Tennessee, Knoxville, TN
[2] College of Veterinary Medicine, University of Tennessee, Knoxville, TN

[†] Present Affiliation: Department of Agriculture, Texas A&M University-Commerce, Commerce, TX

[*] Corresponding author: pmyer@utk.edu

With an expected increase in population by 2050, the demand for more animal protein will increase. To improve the sustainability of US cattle production, producers and researchers have historically focused on improving the feed efficiency of steers, producing a more marketable beef product. However, without a successful pregnancy, there would be no marketable animal to feed. The objective of this study was to examine the physiological changes that occur during pregnancy and their impact on the rumen microbial communities and resulting feed efficiency in Angus heifers. Utilizing 17 cannulated Angus heifers, feed efficiency data was previously collected by utilizing a GrowSafe to monitor feed intake for a 70d trial and weights were taken throughout the trial period to calculate residual feed intake. Following the trial, heifers were bred, and rumen fluid and content samples were collected every two weeks during gestation and four samples were collected after parturition. A total of 30-40mL of rumen fluid was collected during each sampling and rumen solid material was removed from the ventral sac. To analyze the microbial communities, DNA will be extracted from the rumen samples, sequencing libraries will be prepared targeting the bacterial and archaeal 16S rRNA gene and will be sequenced using an Illumina MiSeq. All microbial analyses will be analyzed in the R environment. With prior feed efficiency and microbiome data collected during a heifer development trial on the same cattle, we will compare and contrast differences and changes throughout gestation in bacterial communities within the rumen and their significance with feed efficiency and nutritional physiology. These data will aid in the development of management strategies to improve the sustainability of the cow-calf enterprise.

Poster Number: 607

Effects of Protein Concentration, Degradability, and Beta-Adrenergic Agonists on Ruminal Microbial Communities in Finishing Heifers

A.P. Pfau[1], K.L. Samuelson[2†], M.E. Hubbert[3], E.R. Oosthuysen[2], Z. Bester[2], C.A. Löest[2], M. T. Henniger[1], K.E. Hales[4], A.K. Lindholm-Perry[5], A. McLean[1], K. Mason[1], and P.R. Myer[1*]

[1] Department of Animal Science, University of Tennessee, Knoxville, TN
[2] Department of Animal and Range Sciences, New Mexico State University, Las Cruces, NM
[3] Clayton Livestock Research Center, New Mexico State University, Clayton, NM
[4] Department of Animal and Food Sciences, Texas Tech University, Lubbock, TX
[5] US Meat Animal Research Center, USDA-ARS, Clay Center, NE

[†] Present address: Department of Agricultural Sciences, West Texas A&M University, Canyon, TX

* Corresponding Author: pmyer@utk.edu

To improve animal performance and modify growth by increasing lean tissue accretion, beef cattle production has relied on use of growth promoting technologies such as beta-adrenergic agonists. These synthetic catecholamines, combined with the variable inclusion of rumen degradable (RDP) and undegradable protein (RUP), may improve feed efficiency and rate of gain in finishing beef cattle. However, the impact of beta-adrenergic agonists and protein level and source on the ruminal microbiome is limited. The objective of this study was to determine the effect of different protein concentrations and beta-adrenergic agonist (ractopamine hydrochloride; RAC) on ruminal bacterial communities in finishing beef heifers. Heifers (*n*=140) were ranked according to body weight and assigned to pens in a randomized complete design to 6 different treatments, containing 3 protein treatments (Control: 13.9% CP, 8.8% RDP, and 5.0% RUP; High RDP: 20.9% CP, 13.4% RDP, 6.1% RUP; or High RUP: 20.9% CP, 9.1% RDP, 10.4% RUP) and 2 RAC treatments (0 and 400 mg/day). Rumen samples were collected from heifers by oral lavage 7 days before harvest. The DNA from the samples were sequenced to identify bacteria based on the V1-V3 hypervariable regions of the 16S rRNA gene using the Illumina MiSeq. Sequences and data from the treatments was analyzed using the R environment and PROC MIXED in SAS 9.4 (SAS Inst.; Cary, NC). Beta diversity was analyzed using PERMANOVA based on PCoA Bray-Curtis distances and were significant among the treatments ($P < 0.05$). Alpha diversity metrics such as Chao1 and Shannon diversity indices were not significantly different ($P > 0.05$). Differences among treatments at variable taxonomic levels after analyses through DESeq2 were significantly different for the main effects of protein and RAC, as well as their interaction ($P < 0.05$). These results suggest possible effects on the microbial communities, potentially acting synergistically to improve performance.

Poster Number: 608

Animal Performance and Pasture Productivity of Weaned Steers Grazing Native Warm-Season Grass Pastures with and without Interseeded Native Forbs and Legumes

J.L. Prigge, E. Bisangwa, and P.D. Keyser[*]

Department of Forestry, Wildlife, and Fisheries, University of Tennessee Institute of Agriculture, Knoxville, TN

* Corresponding author: pkeyser@utk.edu

Insects such as bees and butterflies provide a variety of ecosystem services but are in a grave decline due to environmental stressors such as insecticide use and the increasing practice of monocropping (Potts et al., 2010). The U.S. tall fescue belt is home to over 6.5 million grazing beef cattle on 244,000 farms (USDA-NASS, 2017) where pastureland provides an opportunity to increase forage biodiversity to support both cattle and pollinator species. Therefore, the objectives of this study were to evaluate animal performance and pasture productivity for steers grazing native warm-season grasses (NWSG) with and without interseeded native forbs and legumes (FORB). In spring 2021, four, 1.1-hectare pastures were interseeded with an 18-species blend of native forbs and legumes. During May–August 2021, weaned beef steers grazed NWSG (n=4) and FORB (n=4) pastures. Average daily gain (ADG), total gain per acre, and forage mass were analyzed using linear models in R software (version 4.1.1). There was no difference ($P = 0.35$) in ADG between treatments for the 28-day intervals, or for the full grazing season ($P = 0.42$). Additionally, total gain per acre did not differ ($P = 0.42$) between pasture treatments. Average daily gain and forage mass declined ($P < 0.001$; $P = 0.003$, respectively) for both treatments as the season progressed. However, total forage mass was less ($P = 0.003$) in FORB pastures. These similarities in ADG could be attributed to similarities in pasture composition between the treatments due to poor FORB establishment. Further research should explore methods for improved establishment of FORB into mature NWSG pastures.

Poster Number: 609

Influence of Pre-Ovulatory Follicle Size on the Follicular Fluid Metabolome in Lactating Beef Cows

C.C. Read[1], J.L. Edwards[1], F.N. Schrick[1], J. D. Rhinehart[1], R.R. Payton[1], S.R. Campagna[2], H.F. Castro[2], J.L. Klabnik[1], E.J. Horn[1], and S.E Moorey[1*]

[1] Department of Animal Science, University of Tennessee, Knoxville, TN
[2] Department of Chemistry, University of Tennessee, Knoxville, TN

* Corresponding author: smoorey5@utk.edu

Induced ovulation of small pre-ovulatory follicles reduced pregnancy rates, embryo survival, day seven embryo quality, and successful embryo cleavage in beef cows undergoing fixed-time artificial insemination. RNA-sequencing of oocytes and associated cumulus cells collected from pre-ovulatory follicles 23 hours after gonadotropin releasing hormone (GnRH) administration to induce the pre-ovulatory gonadotropin surge suggested reduced capacity for glucose metabolism in cumulus cells of follicles ≤11.7 mm. We hypothesized that the follicular fluid metabolome in-fluences metabolic capacity of the cumulus-oocyte complex and contributes to reduced embryo cleavage and quality grade observed following induced ovulation of small follicles. Therefore, we performed a study to determine the correlation between pre-ovulatory follicle diameter and follicular fluid metabolome profiles in lactating beef cows (Angus, n=130). We synchronized the development of a pre-ovulatory follicle and collected the follicular contents approximately 20 hours after GnRH administration. We then performed UHPLC-HRMS metabolomic studies on 43 follicular fluid samples and identified 38 metabolites within pre-ovulatory follicles of increasing size. We detected 18 metabolites with a significant, positive correlation to follicle diameter. Individual and pathway enrichment analysis of significantly correlated metabolites suggest that altered glucose and amino acid metabolism likely contribute to reduced developmental competence of oocytes when small pre-ovulatory follicles undergo induced ovulation. This work is/was supported by the USDA National Institute of Food and Agriculture, Hatch project 1022068 and the state of Tennessee through UT AgResearch and the Department of Animal Science.

Poster Number: 610

Rumen Biogeographical Impacts on Host-Microbiome Interactions: A Proposal

M.P. Soltis, A.M. McLean, S.E. Moorey, L.G. Schneider, and P.R. Myer*

Department of Animal Science, University of Tennessee, Knoxville, TN

* Corresponding Author: pmyer@utk.edu

As the population continues to increase, the demand for high-quality protein increases as well. Beef cattle in the US are among the most efficient cattle in the world due, in part, to improvements in feed efficiency and genetics. While multiple factors can influence the feed efficiency of beef cattle, recent studies have investigated and established the significance of the rumen microbiome in modulating production-relevant impacts. Rumen microbial communities aid in converting feed into energy and this conversion provides opportunities for increasing productivity. Researchers have historically focused on the ventral sac when sampling within the rumen due to ease and repeatability. However, the rumen has multiple sacs that may be accommodating distinct microbial communities and supporting feed efficiency. This study aimed to determine the rumen wall and content microbial communities, tissue gene expression, and fermentation profiles among various rumen biogeographical regions. To address this, we took solid, liquid, and papillae samples from 17 cannulated Angus cows in each of the five rumen sacs. Microbial DNA sequencing will be performed with the samples using the hypervariable V4 region of the 16S rRNA gene. Gene expression analyses will be performed on the rumen epithelial papillae. Fermentation profiles will be determined using untargeted metabolomics. With this information, we will gain a deeper understanding of the interface between the host and rumen microbiota and why differences in the various rumen sacs occur. There is a crucial need to define the differences among the rumen biogeographical regions influencing host-microbiome interactions, which may ultimately impact feed efficiency. Without better defining these rumen physiological-based host-microbe relationships, efforts to identify the variation in feed efficiency will be limited.

UTBEEF.COM

UTIA.TENNESSEE.EDU