University of Alberta

Beef and Range Report

Prepared for the Roy Berg Kinsella Ranch Field Day by:

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Welcome to the 2014 Beef and Range Report

From 1921 to 1992, the Department of Animal Science at the University of Alberta published an annual "Feeders' Day Report". These reports were intended to provide an overview of the scope and breadth of research taking place in the discipline of Animal Science. Above all, these reports were intended to serve as a critical form of outreach to industry and practitioners, provincial and federal extension staff, non-government organizations, and members of the general public. In short, these reports enabled scientists to communicate the role of complex science in describing, in simple form, 'practical and relevant solutions to real world problems'.

In August 2014, the Kinsella Research Ranch will be formally re-named the Roy Berg Kinsella Research Ranch, in recognition of the critical role Dr. Roy Berg (pictured at the ranch, below), professor of beef genetics, former Chair of the Department of Animal Science and Dean of the Faculty of Agriculture & Forestry at the U of A, played in furthering the development of beef breed development in Canada and around the world. The intent of this document is to resurrect the Feeders' Report, albeit in a slightly different form.

Photo courtesy of Ruth Ball

This particular version includes articles chronicling and commemorating Dr. Berg's contributions to beef breeding, as well as cutting edge research on beef genomics. This report also includes however, a review of the evolving role of the Kinsella Research Station in supporting beef research in general, much of which over the last several decades has included a major focus on forage agronomy and rangeland management. In addition to significant work conducted by Dr. Arthur Bailey from 1966 to 1997, the last 15+ years have been witness to a marked increase in research on rangeland ecology, including the role of rangelands in providing a wide range of environmental goods and services (EG&S) to society, attributes that include forage and red meat production, but also biodiversity, clean water, and carbon storage, among others. Several articles in this report describe newly initiated or ongoing research, including their projected outcomes and benefits to industry and society.

An important recent development that has greatly expanded our capacity to conduct research on rangeland ecology, management, and beef production, is the establishment of the Mattheis Research Ranch 150 km south of Kinsella in the Mixedgrass Prairie. An introduction is provided to this facility, and to several research projects examining wide-ranging topics from beef production efficiency in extensive cow/calf systems, to rangeland ecology and the provisioning of environmental goods and services. In combination, these facilities provide a significant core land base to support initiatives of the Rangeland Research Institute, an organization established to promote research, education and outreach on the environmental and economic sustainability of rangelands around the world.

On behalf of all the contributors to this report, we hope you find its contents enlightening, stimulating and helpful, as we all work towards improving beef and rangeland management. As always, contributors to this report would be pleased to share additional information with those of you seeking more details. All the best for a great 2014.

Edward Bork
Mattheis Chair in Rangeland Ecology & Management
Director, Rangeland Research Institute

Berg's Bastards – Controversial research forever changed the Alberta beef industry

Michel Proulx[1]

[1]*Faculty of Agricultural, Life and Environmental Sciences, University of Alberta*

This article, written to recognize the contributions of Roy T. Berg upon his passing in May 2012, is reprinted from "Greenhouse" – the Alumni Magazine of the Faculty of Agriculture, Life and Environmental Sciences (ALES), Summer 2012.

It had been a glorious day. Thirty years after Roy Berg had begun his controversial research at Kinsella Ranch, he and his fellow researchers had showed assembled guests how they had been able to improve the productivity of beef cattle by up to 40 per cent. The 150 people gathered included the who's who of the beef cattle industry in Alberta and Canada, including then-deputy Prime Minister Don Mazankowski, who had grown up in the area.

"We were just about finished and an old farmer got up in the back," explains Mick Price, a long-time Berg collaborator who was emceeing the event. "He came walking down the middle and had a cranky look about him. He was mumbling as he was coming down the aisle and I thought, 'Oh geez, there's always trouble.'

"He asked me if I was finished because he wanted to say a few words. He told me, 'I was one of the people who opposed this ranch from the very start.' So he got to the micro- phone and asked the crowd if they minded if he said a few words. I mean, what can I do?"

"I'd like to say now that I was wrong," said the old farmer. "Roy Berg has done more good for the beef industry than everybody else combined!"

Roy Torgny Berg grew up on a farm in Millicent, Alberta, one of nine children. He graduated from the University of Alberta with a BSc (Ag) in 1950, earned an MSc and PhD from the University of Minnesota and then, in 1955, returned to the U of A as an assistant professor in the Department of Animal Science.

Together with the head of his department, L.W. McElroy, they began planning for the creation of a beef cattle breeding facility. Eventually, they received funding from the provincial government through the Horned Cattle Trust Account and the search for an adequate site began in earnest.

It didn't take long before Berg settled on a 5,500-acre ranch in Kinsella, Alberta, two hours east of Edmonton. "This ranch had everything we wanted," Berg is quoted as saying in *Agriculture and Forestry Bulletin* in 1980. "It had native grass, shelter, (and) water with a rolling topography. It was ideal for cattle."

As an animal geneticist, Berg sought to improve fertility in females and growth in males. Specifically, he wanted to show that selective cross-breeding of beef cattle – passing on desirable traits from a variety of breeds and capitalizing on hybrid vigour – could improve production. You'd have thought he wanted to outlaw ranching in Alberta, given the uproar it caused.

"There were tremendously strong feelings about it," explains Price. "Ranchers thought that by crossbreeding, we would ruin the herds. They used the word 'mongrelized.' They thought that once you mongrelized the breed, you'd never get back the beauty that was the Alberta herd and everybody would be ruined." The opposition to his research was so ferocious, producers dubbed the cross-bred cattle "Berg's bastards" and "Roy Burgers." Editorials denouncing the research were published. A group of producers even went so far as to try and have him fired from the university. Their efforts were quickly rebuffed by then-president Walter H. Johns. "He pointed out that (Berg) had tenure and there was no possible way of getting rid of him for doing what he consciously believed was the right thing," said Price.

Yet Berg also had his supporters, a handful of producers who believed in what he was doing. They were a small but influential group that included, among others, members of the Copithorne family, a big ranching family in Alberta, Bert Hargrave, the federal MP for Medicine Hat, and Neil Harvie, one of Berg's students, who ran Glenbow Ranching. His father had founded the Glenbow Museum and the Glenbow Foundation.

In 1970, they and others including Sherm Ewing and John Stewart-Smith founded Beef Boosters, a company that revolutionized the bull breeding industry by following similar hybrid breeding techniques as those used by Berg. It's still in business today. "(Roy) often said to me that without them, he would have given up," said Price.

"You have to have some friends out there, because if there's no one listening to you, you have no impact," Berg said in a 1999 *Folio* article. "You could do your research and demonstrate some things, but if you haven't got an audience then nothing will happen. It'll get in the scientific literature, and that's where it'll stay."

Berg had the tenacity to see his research through, despite the brutal opposition. "He was a very complex man," says Price, who worked with Berg for decades. "There's no easy way to describe him. He would say controversial things. He'd tell people that their cattle were too fat. He went straight for the jugular. If he believed that hybrid breeding was the best way to produce cattle, he wouldn't compromise; he just wouldn't back down."

In a 1989 *Folio* article, Berg says he was just being himself. "I had colleagues in other institutions saying, 'You shouldn't be spouting off like that or you're going to get in trouble.' But I couldn't help it," says Berg. "I never had enough sense to realize this was a danger."

Thanks to Berg's research program, Kinsella Ranch became one of the most successful cattle breeding research operations in the world. He bred two hybrid lines, according to Price. The first was 30 per cent more productive while the second was 40 per cent more productive.

To begin his research, Berg took a pure bred Hereford group of cows, as the breed was the standard cattle in Alberta at the time, and developed a three-way hybrid by crossing Angus, Charolais and Galloway cattle. Using the exact same criteria – fertility in females and growth in males – he compared the two groups to see which one improved the fastest.

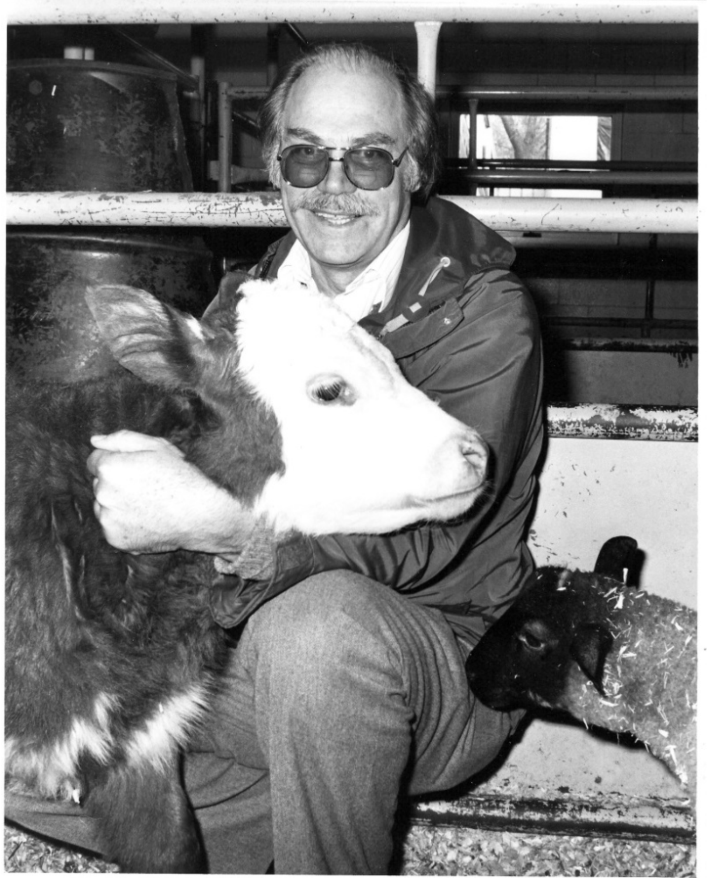

Photo courtesy of Ruth Ball

The fertility criterion he used for females was having a calf at two years old, not three as was typical at the time, and another calf every year from then on. If they didn't, they were no longer part of the herd. For the males, they underwent the 140-day test, which consisted of being fed for 140 days after being weaned. Whichever bulls grew the fastest under those conditions were used as sires for the next generation. The others weren't. "You had to be a bloody good cow to stay in this herd," says Price.

At the time, according to Price, people accepted the notion that if you cross-bred cattle, there would be an immediate increase in fertility for females and growth in males through hybrid vigour. "But many in the industry would say that you get this one jump up and from then on, it's all downhill," explains Price. "That was what many people felt. From a genetic point of view, that's total nonsense. Genetically, the more genes you've got, the faster your progress will be."

And so it was. Berg's hybrids kept getting more productive and the gap in productivity between his new line and the purebred Herefords was increasing. "No geneticist in the world was even the slightest bit surprised," says Price.

It took Berg and his colleagues 10 to 15 years to convince the cattle industry of the merits of his hybrid breeding and the economic advantages it would provide producers. But eventually, with the evidence being overwhelming, cross-breeding became the norm in the beef cattle industry.

Today, when travelling on Alberta highways and seeing the various herds, travelers are hard pressed to find a purebred commercial herd. It happened to the late Frank Jacobs, the long-time editor of *Canadian Cattlemen* magazine, who after driving from Edmonton to Medicine Hat and back again in 1980, wrote about the trip in the magazine.

"I counted three solid black herds, four straight-bred red cattle with white face and two all-white herds. The rest were rainbow herds – crossbreds of various kinds. Why all the crossbred cattle?

Well, one reason is that research work at Kinsella indicates that selective cross-breeding, combined with realistic selection, will increase production by more than 30 per cent over conventional one-breed systems. Try to estimate what that could mean in an industry which generates $1.1 billion in the province in 1979."

"Just think what that means today," says Price. Indeed.

The University of Alberta beef breeding project after 30 years – A review

Roy T. Berg, M. Makarechian, P. F. Arthur

This article is reprinted from the "69th Annual Feeders' Day Report", published by the Faculty of Agriculture and Forestry, University of Alberta, Edmonton, May 31, 1990. It provides a summary of 30 years of the ground-breaking research on cattle breeding and livestock genetics conducted by Dr. Roy Berg and his students and Post-Doctoral Fellows at the Kinsella Ranch.

Beef cattle breeding research has been carried out at the University ranch at Kinsella, Alberta, since the ranch was acquired in 1960. The ranch is now in its 31st year of operation and the major objective of the breeding program has been selection for performance and productivity under commercial management conditions similar to typical beef operations in Alberta. In addition to the breeding program, the ranch has served as an invaluable research facility for other aspects of animal research in Animal Science and other departments of the University, Alberta Agriculture, the Veterinary Infectious Diseases Organization and the livestock industry. Over 600 scientific publications and extension articles have been published on research emanating from the Kinsella ranch over its 30 years of operation. The ranch has also served as a model and demonstration farm for beef producers in Alberta.

Eleven progress reports and many related studies, using cattle from Kinsella, have been published in past Feeders' Day Reports. Hence those wishing to have detailed information on the history and operation of the ranch are directed to those reports. The purpose of this report is to provide an update of the performance of the beef lines maintained at Kinsella from 1960 to 1989.

Summary

- Prior to 1982, calf crop percentages born and weaned were higher for the synthetic lines (SY1 and SD) than for the Herefords (HE). Beginning in 1982, the HE line was merged into a crossbred Hereford line to evaluate its response to cross breeding and subsequent breed synthesis. The conversion of the HE to a synthetic (SY2), resulted in an almost complete catchup of that line and now all three synthetic lines are very similar at 81% for calves born and 75% for calves weaned.
- Up to 1982, cow productivity based on weight of calf weaned per cow exposed to breeding was 30% higher for SY1 and 42% higher for the Dairy Synthetic (SD) compared to the HE line. Following conversion of HE to SY2, the superiority in cow productivity in the SY1 and SD lines compared with the SY2 line dropped to 5% and 13%, respectively.
- Birth weights in all lines increased up to 1982. From 1982, birth weights have remained constant in SY1 (-0.04 kg/year) decreased in SD (-0.59 kg/year) and increased moderately in SY2 (0.24 kg/year).
- For 180-day weights, increases per year since 1982 have been high for SY2 (4.41 kg/year for males and 2.82 kg/year for females). Increases for SY1 and SD have been more modest, ranging from 1.46 kg/year for SY1 males to -0.36 kg/year for SD females.
- Yearly increases in 365-day weights, since 1982, were 8.50 kg/year for SY2, 4.21 kg/year for SY1 and 8.50 kg/year for SD.
- Increases per year in 540-day weights of heifers were rather modest in all lines up to 1982 (0.78 to 1.46 kg/year) but showed high to moderate increases from 1982 (5.68, 2.61 and 3.07 kg/year from SY2, SY1 and SD, respectively).

Breeding populations

Two breeding populations were established in 1960: the purebred Herefords (HE) and the Beef Synthetic (SY). The purebred HE line has served its mission as a control population for comparison with the SY. The HE line was low in productivity compared to SY mainly due to low reproductive performance and growth rates.

Beginning in 1982, the HE line was merged into a crossbred Hereford line to evaluate its response to cross breeding and subsequent breed synthesis. The new synthetic is named Beef Synthetic #2 (SY2); its breed composition is shown in Table 1. It has been made up of approximately 60% Hereford breeding over the last four years (1986-1989).

With the development of this new synthetic line, the original Beef Synthetic line has now been called Beef Synthetic #1 (SY1). The percentages of the contributing breeds in SY1 have stabilized since 1970 at approximately 33% each of Angus and Charolais, 20% Galloway, 5% Brown Swiss and small amounts of other breeds (Table 1).

A Dairy Synthetic (SD) population was started in 1967, and it has stabilized at approximately 60% dairy breeds; Holstein, Brown Swiss and Simmental, and 40% beef breeds primarily; Angus, Hereford, Charolais and Galloway (Table 1).

In addition to these three main breeding populations, other small experimental populations have been developed at Kinsella, such as the Pee Wee breed group, which is made up of beef breeds and selected for low body weight, and the Double Muscled breed group, which is used in studies on muscling and carcass leanness.

Management and selection

The plan from the beginning was to manage the ranch as a low cost commercial operation comparable with beef production ranches in Alberta. The breeding herds are on the range year round and depend on natural grazing except for 3-4 months in the winter when supplementary feed is provided. The level of supplementary feed depends on the pasture conditions and severity of the winter. Cows are bred in July and August each year; selection of sires within each breed group being based on pre-and post-weaning (test) gain. Bulls are selected and used for breeding as yearlings and about 25% are used again in the next year. Breeding is usually in single sire groups of about 25 cows to a bull, but the SD line has generally been bred as a multiple sire group in a single pasture. Occasionally multiple sire groups have been used in the other lines. Calving is in April and May; heifers calving for the first time are closely supervised.

Calves are weaned in the fall and following a 28-day adjustment period they are put on a performance test for 140 days. Bull calves are full fed on a high energy feedlot diet and heifers are limited to a 2.3 kg concentrate and 2.3 kg hay per day. Straw bedding is available at all times.

Females are selected with emphasis on reproductive performance. All sound heifers have been exposed to a bull at approximately 14 months of age for up to 60 days during the breeding season. Since 1986, however, the length of the breeding season has been restricted to 35 days for heifers and 45 days for cows. Heifers which fail to conceive are culled and fed out to slaughter. Thereafter, cows are required to produce and wean a calf each year to remain in the breeding herd. In addition, cows are periodically culled for low productivity, poor udders, body condition, lameness, physical disability and temperament.

Selection for growth rate in the two original synthetic lines (SY1 and SD) had increased calf birth weight and consequently the incidence of difficult calving. The selection program was, therefore, modified in 1982 to consider birth weight of the bull in addition to his weaning weight and post-weaning gain indices. The objective was to study the rate of progress in growth when bulls with high birth weights were culled.

Cow reproduction and production

Calf crop percentages born and weaned, based on the total number of cows and heifers exposed to breeding and overall cow productivity (weight of calf/cow exposed) for the three lines are shown in Table 2. In most years up to 1982, the two synthetic lines were a few points ahead of the HE line in calf crop born and weaned. However, overall calf crop born and weaned up to 1989 were similar among the three lines with averages of 81% and 76%, respectively. Losses from birth to weaning, which include stillbirths, are minimal and are influenced by weather and disease, particularly calf scours.

Table 1. Average breed percentages in calves born at Kinsella from 1962-1988

Breed	1962	1970	1974	1978	1982	1984	1986	1988
Beef synthetic #1								
Angus	41.4	37.6	36.0	35.7	36.8	36.9	36.2	35.6
Brown Swiss	-	4.7	4.2	4.5	5.2	5.0	5.3	5.7
Charolais	16.8	35.1	34.4	34.7	34.1	33.7	32.3	31.4
Galloway	40.3	20.3	21.4	21.7	20.6	20.7	20.1	20.9
Others	1.5	2.3	4.0	3.4	3.3	3.7	6.1	6.4
Beef synthetic #2								
Angus	-	-	-	-	11.1	10.0	15.3	12.1
Charolais	-	-	-	-	9.4	7.8	8.8	8.0
Galloway	-	-	-	-	7.4	4.4	6.7	5.1
Hereford	-	-	-	-	65.0	69.5	59.8	60.1
Others	-	-	-	-	7.1	8.3	9.4	14.7
Dairy synthetic (SD)								
Brown Swiss	-	17.5	30.1	27.3	22.5	23.7	22.7	25.8
Holstein	-	63.4	34.4	27.4	30.5	23.0	24.5	22.1
Simmental	-	-	-	9.4	7.2	12.1	8.9	6.1
Beef breeds[z]	-	19.1	35.5	35.9	39.8	41.2	43.9	46.0

[z] Includes mostly Angus, Galloway, Hereford and Charolais

Table 2. Cow reproduction and production by breed, 1962-1989 Kinsella

Trait	Line	1962	1966	1970	1974	1978	1982	**Avg. to 1982**	1984	1986	1988	1989	**Avg. from 1982-1989**	**Over-all avg.**
No. of cows exposed	HE/SY2[z]	71	124	122	108	77	94	**77**	52	159	189	263	**142**	**118**
	SY1	79	164	164	172	197	176	**207**	215	225	196	205	**210**	**193**
	SD	-	-	28	40	47	65	**119**	131	135	160	142	**137**	**101**
Calf crop born (%)	HE/SY2	75	64	73	73	90	78	**79**	85	78	76	77	**83**	**81**
	SY1	86	78	79	86	90	83	**86**	77	82	74	84	**78**	**81**
	SD	-	-	79	80	85	82	**75**	81	86	69	87	**81**	**82**
Calf crop weaned (%)	HE/SY2	69	59	72	68	84	71	**74**	83	73	75	71	**78**	**75**
	SY1	82	74	76	74	84	77	**77**	73	79	70	76	**73**	**75**
	SD	-	-	79	75	80	78	**68**	74	78	67	82	**76**	**77**
Avg. age at weaning (days)	HE/SY2	144	168	160	169	164	159	**151**	171	170	160	157	**164**	**162**
	SY1	150	172	163	173	170	163	**154**	160	170	158	156	**163**	**163**
	SD	-	-	151	172	164	162	**156**	161	172	158	158	**163**	**163**
Avg. calf weight, October (kg)[y]	HE/SY2	127	169	163	161	172	166	**172**	172	202	210	207	**194**	**180**
	SY1	161	191	198	196	210	196	**195**	203	207	225	219	**216**	**206**
	SD	-	-	206	210	226	214	**200**	213	215	226	222	**224**	**219**
Weight of calf/ cow exposed (kg)	HE/SY2	88	100	117	110	145	118	**127**	143	147	146	148	**150**	**134**
	SY1	131	141	151	146	177	151	**151**	148	164	158	170	**158**	**155**
	SD	-	-	162	157	183	167	**136**	158	167	151	181	**170**	**169**

[z] Since 1982, the Hereford and Hereford crossbred lines have been developed into a synthetic line; Beef Synthetic #2 (SY2)

[y] Actual weights taken at weaning in October

The conversion of the HE line into a synthetic line, SY2, since 1982, has resulted in significant increases in calf crop born (6.4%), calf crop weaned (9.9%), calf weaning weight (16.8%) and overall cow productivity (27.1%) in that herd. The increase in cow productivity in the HE/SY2 line was primarily due to increases in percent calves born and weaned since the development of the SY2 line. Cow productivity was estimated at 128% for SY and 142% for SD compared with HE controls at 100% up to 1982. With the development of the SY2 line, however, the SY1 and SD advantage over SY2 in cow productivity has reduced to 105% and 113%, respectively. Thus hybridization of HE to SY2 eliminated all deficiencies in the calf crop percentages and most of the deficiency in cow productivity compared to the original synthetics.

Growth and performance of calves

Weights at birth, at 180 days (adjusted for age of calf and age of dam), at 365 days and at 540 days for each line are given in Table 3. Weights of calves, born from 1982 to 1989, at various stages of growth are plotted in Figures 1-3.

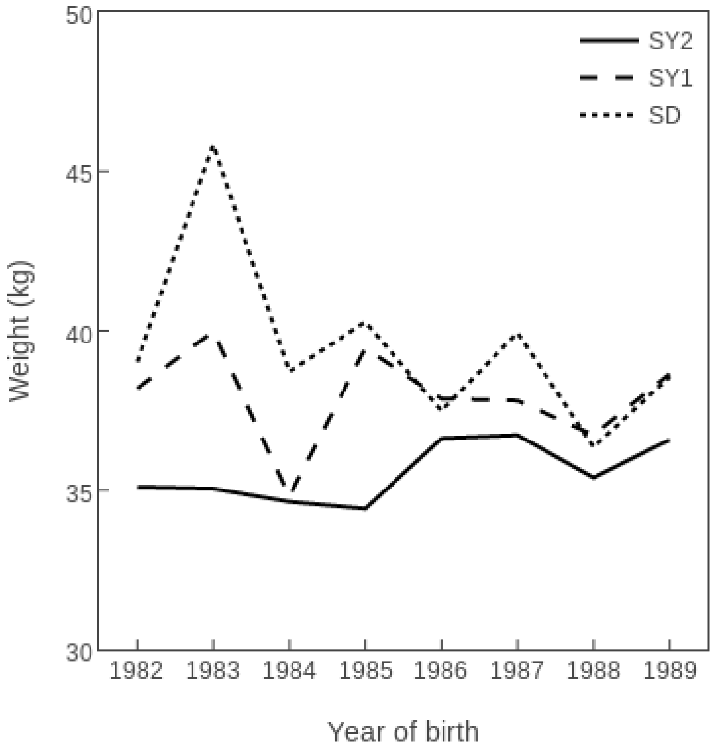

Figure 1. Average birth weight of calves (sexes combined): 1982-1989, Kinsella

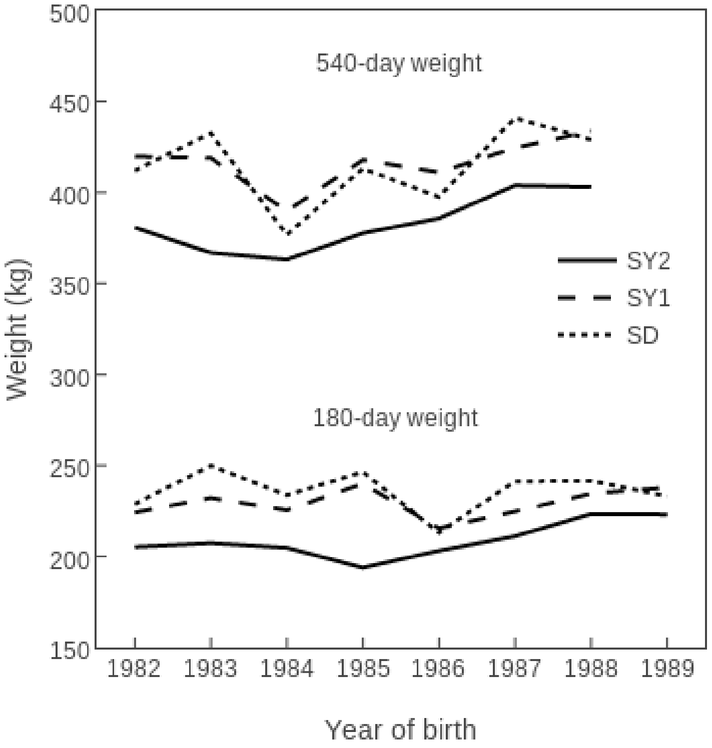

Figure 2. Average weights of females at 180 and 540 days of age: 1982-1989, Kinsella

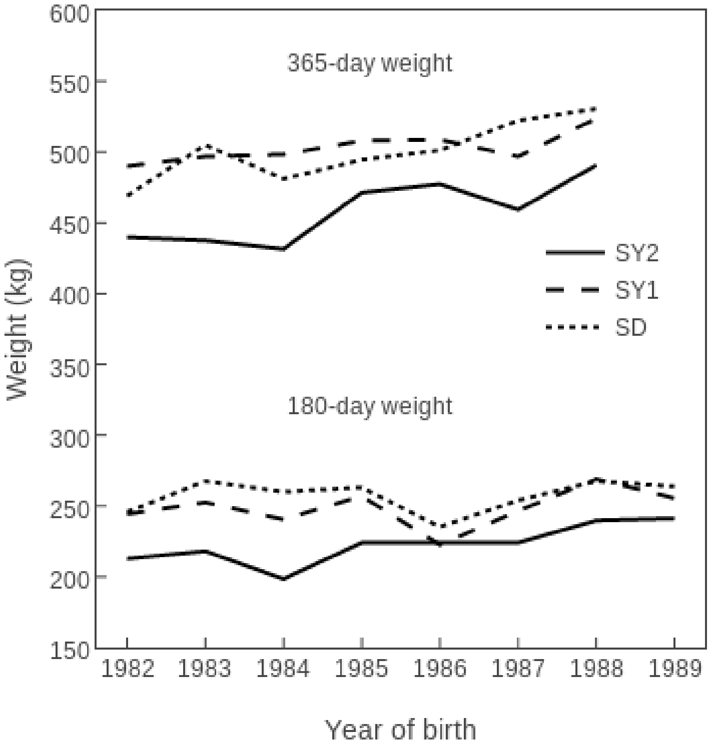

Figure 3. Average weights of males at 180 and 365 days of age: 1982-1989, Kinsella

Up to 1982, birth weight shows a trend to increase in all lines. However, from 1982 to 1989, birth weight in the SY1 line has remained relatively constant while that in the SD line has shown a decrease (-0.59 kg/year). This change could be the result of efforts being made in recent years to reduce calving difficulty by selecting bulls with high post-weaning growth rates but low birth weights. The SY2 line has, however, shown an increase in birth weight (0.24 kg/year) which is the result of the continuing development of the original purebred HE line (with low birth weights) into the new synthetic group which involved the introduction of relatively large breeds into the line. This effect has also been reflected in subsequent weights in this line.

From 1982 to 1989 increases in adjusted 180-day weights have been highest in the SY2 line (4.41 and 2.82) followed by the SY1 line (1.46 and 2.92) then the SD line (0.68 and -0.36) kg/year for males and females.

Improvements in 365-day weight per year in males prior to and following 1982 was maintained in the SY1 line (4.36 vs. 4.21 kg/year) but increased in the SY2 line (2.02 vs. 8.50 kg/year) and the SD line (5.18 vs. 8.50 kg/year), respectively.

Heifer 540-day weights showed modest increases over the years with larger increases occurring between 1982 and 1988. Up to 1981, the HE, SY and SD lines had increases of 0.78, 1.40 and 0.46 kg per year, respectively, but between 1982 and 1988 increases were 5.68, 2.61 and 3.07 kg per year for SY2, SY1 and SD lines, respectively.

Acknowledgements

Financial support from grants from Alberta Cattle Commission, Agriculture Canada, the National Sciences and Engineering Research Council of Canada, the Farming for the Future program of the Agricultural Research Council of Alberta and Pitman-Moore Inc. are gratefully acknowledged.

Gary Minchau, the ranch manager has been at the ranch since its beginning. Sincere thanks to him and his staff for managing the ranch and data collection.

Table 3. Weights and adjusted weights of calves from 3 lines, 1962-1989 Kinsella

Trait	Breed	1962	1974	1978	1982	1984	1985	1986	1988	1989	Trend 1962-83	Trend 1982-90
		kg									kg yr^{-1}	
Birth weight, male & female	HE/SY2	31.8	33.1	35.1	35.1	34.6	34.4	36.6	35.3	36.6	0.17	0.24
	SY1	33.1	35.8	37.8	38.1	34.6	39.5	37.8	36.6	38.9	0.25	-0.04
	SD	-	38.6	41.4	39.0	38.6	40.3	37.4	36.3	38.6	0.34	-0.59
Adjusted 180-day weight, male	HE/SY2	155	181	195	212	197	223	221	238	239	2.20	4.41
	SY1	207	217	237	243	239	256	221	267	252	2.23	1.46
	SD	-	239	266	243	259	261	232	265	259	0.94	0.68
female	HE/SY2	166	178	188	206	205	194	204	224	224	1.89	2.82
	SY1	190	211	223	224	226	240	215	234	238	2.07	0.92
	SD	-	218	237	229	234	247	213	241	233	0.92	-0.36
365-day weight, male	HE/SY2	238	348	418	440	430	470	476	490	-	2.02[y]	8.50
	SY1	296	401	488	489	496	506	507	526	-	4.36[y]	4.21
	SD	-	405	531	467	478	493	499	528	-	5.18	8.50
540-day weight, female	HE/SY2	336	308	343	381	363	377	385	402	-	0.78	5.68
	SY1	365	363	385	419	389	417	410	433	-	1.40	2.61
	SD	-	375	396	412	375	413	397	428	-	0.46	3.07

[z] Since 1982, the Hereford and Hereford crossbred lines have been developed into a synthetic line; Beef Synthetic #2 (SY2)

[y] Calculated from 1966-1981

[x] Calculated from 1982-1988

Development and utilization of genomic tools to exploit genetic diversity and heterosis in Canadian beef cattle populations

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Heterosis, or hybrid vigour, refers to the superiority of hybrid individuals over the average of their corresponding purebred parental breeds. The concept of heterosis has been utilized in beef production to enhance fertility, longevity, growth and meat quality traits in commercial herds through various cross-breeding systems. However, the genetic basis of heterosis in beef cattle still remains elusive. Understanding the genetic mechanisms underlying heterosis will not only improve our knowledge of this phenomenon, but will also create new opportunities to develop genomic tools and technologies that could be used in beef production to increase profitability.

Genetic diversity is required to maintain the basis for future sustainable genetic improvement, to enable selection of genetically superior individuals so as to meet current production needs in various environments and to respond to changing environments and breeding objectives (e.g., customer demands). Genetic diversity among different breeds also provides materials to generate heterosis through cross-breeding. Despite the importance of genetic diversity, beef breeds are under intensive selection for increased productivity but these continuous selections may lead to substantial reduction of genetic diversity.

The populations of cattle at the Kinsella Research Ranch represent an important resource to explore these questions. Along with herds from other locations we have accumulated genotype data (Illumina BovineSNP50 [50K]) and phenotypic records on growth and carcass merit traits for over 10 000 purebred and hybrid cattle. These data provide a great resource for the study of heterosis and genetic diversity in Canadian beef populations using genomic approaches.

Objectives

This project will utilize genomic tools to assess the extent of genetic diversity in beef cattle in Canada and to investigate the genomic mechanisms of heterosis for growth and carcass traits to improve productivity and profitability.

The ultimate goal is to improve genetic merits of Canadian beef populations and to increase profits for Canadian beef producers by providing the beef industry with enhanced genomic tools for genetic evaluation, optimal mate selection, and prediction of hybrid performance. Knowledge of the extent of genetic diversity in Canada's beef cattle is important to ensure that the beef cattle populations in Canada are well able to adapt to changing environments and breeding objectives to meet the world's demand for food now and in the future.

The proposed research will deliver the following main outcomes related to:

Genetic diversity

- A good understanding of the extent of genetic diversity in beef cattle in Canada
- Recommendations for maintenance and improvement of genetic diversity to ensure the long-term sustainability and value of Canada's beef breeds
- Utilization of genetic diversity in production, especially in mate selection to improve productivity by addressing both additive and non-additive effects

Heterosis

- New knowledge about genetic mechanisms of heterosis for growth and carcass merit traits in beef cattle
- New technology of using genomics to predict heterosis in beef cattle

- Improved genomics tools for more accurate prediction of breeding values in beef cattle;
- Enhanced mate-selection approaches using genomics tools
- Enhanced genomics tools for more accurate prediction of hybrid performance
- Demonstrated long-term benefits of exploiting heterosis using genomics tools

Current progress and future work

The "heterosis and diversity project", is funded by the Alberta Livestock and Meat Agency and Beefbooster Inc. and will be completed in 2016. At this early stage of the project, we are assembling data from various sources. The main data are coming from the ongoing Canadian Cattle Genome Project and other Livestock Gentec projects. We are using 50K genotypes and phenotypic information on growth and carcass merit traits. The Kinsella composite population (established by Roy Berg), together with the Angus and Charolais purebred herds which are now co-located at the Kinsella Research Ranch, have contributed around 3000 of the records. Additional genotype data will also be obtained from other Canadian breeds, including Galloway, Blonde, Highland and Shorthorn, for the analysis of genetic diversity which is planned to begin the second year of this project.

A small-scale data analysis has been conducted to examine the additive and dominance genetic variance components within the purebred Angus population. Initial results showed that dominance has a low to moderate effect on growth and carcass traits (Table 1). A short paper based on these results has been accepted for publication in the proceedings of the upcoming 10th World Congress of Genetics Applied to Livestock Production to be held in Vancouver, BC, Canada in August 2014. Further studies will be conducted using larger data sets and will also seek to include epistatic genetic effects.

Next, genome-wide association studies will be conducted to try to identify individual loci influencing heterosis, using data from within and across populations. Heterosis will be predicted using genome-wide markers and the predicted performance will be evaluated by comparing the predicted heterosis with those estimated from the phenotypic observations. Methodologies that take into account non-additive genetic effects will be developed and evaluated for genomic prediction of breeding values of purebred and crossbred seed stock animals, genomic prediction and selection of bulls and dams for mating, and genomic prediction of hybrid performance for better management in feedlot sorting programs. Both linear and non-linear models will be evaluated and compared, and the non-additive genetic models with also be compared with additive genetic models.

Genetic diversity will be assessed both within and between populations / breeds and between herds from different geographical regions in Canada. Relationships between the populations or regions will be estimated by calculating the geometric and genetic distances between all pairs of individuals in the study. These relationships will be expressed using classification and/or ordination methods. Results from molecular studies and from other types of data (e.g., geographical or phenotypic) will be compared. Classification or clustering (of phylogeny) can be used as a way of communicating results and providing initial tools to exploit diversity.

Genetic diversity assessed simultaneously with heterosis will allow recommendations to be made on which pairs of alleles should be 'mated' to establish allele combinations that will result in optimum productivity. This could be implemented through mate selection software or recommended menus for sire teams etc. The project will recommend an optimum genomic selection strategy to achieve a maximum long term genetic gain in Canadian beef herds by considering genetic diversity and heterosis. The project will also try to provide information to help manage the genetic health of beef breeds in Canada, particularly the smaller breeds, and is therefore of interest to the Canadian Beef Breeds Council. Overall, we hope the project will contribute to achieving a more competitive and sustainable Canadian beef sector, and represent another way in which the Kinsella Ranch has impacted our industry.

Table 1. Estimates of additive and dominance variance components for growth and carcass traits in Angus population

Traits	σ_a^2	σ_d^2	h_a^2	d^2
Birth weight	67.65 ± 14.43	36.73 ± 19.01	0.44 ± 0.08	0.24 ± 0.12
Weaning weight	853.69 ± 240.13	259.92 ± 361.47	0.31 ± 0.08	0.10 ± 0.13
Average daily gain	0.0095 ± 0.0033	0.0094 ± 0.0077	0.25 ± 0.08	0.25 ± 0.20
Hot carcass weight	764.1 ± 184.3	72.1 ± 297.4	0.37 ± 0.08	0.03 ± 0.14
Lean meat yield	6.92 ± 1.31	1.73 ± 2.00	0.50 ± 0.08	0.14 ± 0.16
Marbling score	0.05 ± 0.01	0	0.26 ± 0.07	0
Rib eye area	16.15 ± 4.30	2.16 ± 8.38	0.34 ± 0.08	0.05 ± 0.18
Average backfat	8.67 ± 1.71	1.84 ± 2.61	0.51 ± 0.08	0.11 ± 0.15

σ_a^2 = direct additive genetic variance; σ_d^2= dominance genetic variance; h_a^2= direct heritability; d^2 = proportion of phenotypic variance explained by dominance

Acknowledgements

Thanks to the Alberta Livestock and Meat Agency and Beefbooster Inc. for funding, and to co-investigators John Basarab (Alberta Agricultural and Rural Development), John Crowley (University of Alberta), Tom Lynch Staunton (Livestock Gentec), and Zhiquan Wang (University of Alberta).

The Canadian Cattle Genome Project

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The Canadian Cattle Genome Project (CCGP) is a large-scale $8.2M project currently underway at the University of Alberta and funded through Genome Canada. The project is collaborative in nature, involving researchers and data sets from Ireland, Scotland, USA, Australia and New Zealand. The overall aim of the CCGP is to apply genomic selection to Canadian beef cattle, with emphasis on economically important traits that are difficult to measure and therefore difficult to improve using conventional breeding strategies. More specifically, the project has created a large database of sequence, genotype, and phenotype information on Canadian cattle breeds and crossbred animals. The database will be used in the development of prediction equations, which will be used to identify genetically superior animals for a variety of traits, including residual feed intake (RFI). Through the application of these equations and continued genotyping, the project stands to reduce the costs and environmental impacts of raising cattle while accelerating the improvement of key production traits.

Sequencing and genotyping

The project is working with 10 breeds / populations including the major breeds (Angus, Charolais, Gelbvieh, Hereford, Limousin, Simmental and Holstein) and three composite populations (Beefbooster®, Guelph composite and Alberta composite). Pedigree analyses were conducted for each breed / population to identify animals that have made significant genetic contributions to the current Canadian herds. Included in the project are key animals that contributed to the herds at the Kinsella Research Ranch. The top-ranked animals were then sequenced and genotyped. Some of these animals are key historic bulls. Figure 1 shows an animal chosen for sequencing from each of the major breeds and indicates the number of progeny and the number of descendants for that animal.

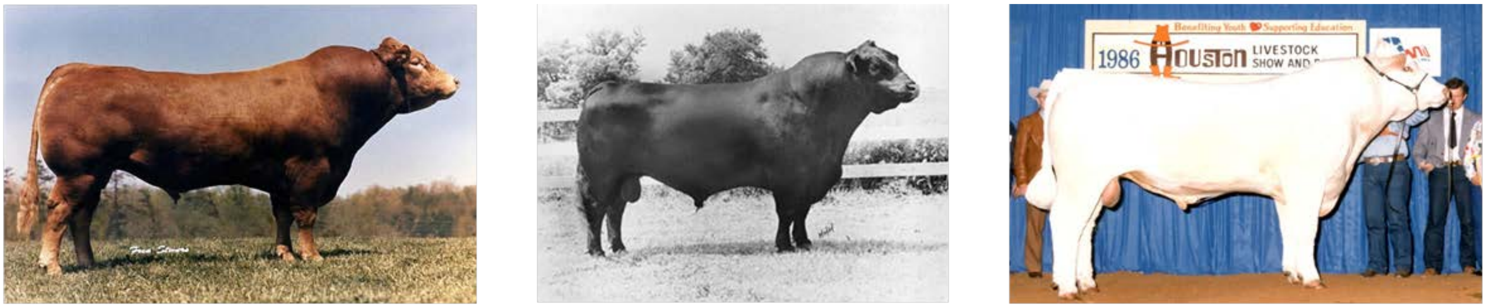
The project has completed sequencing of 315 animals and high density genotyping (770K and 50K) for over 10 000 animals. Through the collaboration with our partners and the 1000 Bull Genomes Project, we have access to more than 1000 complete genome sequences and thousands of additional genotypes. In-depth analyses of the sequence data have identified millions of variable sites in the bovine genome, most of which were previously unknown. Table 1 shows the number of Single Nucleotide Polymorphisms (SNPs) and Insertions and Deletions (InDels) identified in each breed. These variable sites may hold the key to the discovery of genes that contribute to complex animal traits.

Table 1. Number of Single Nucleotide Polymorphisms (SNPs) and Insertions and Deletions (InDels) identified in each breed included in the Canadian Cattle Genome Project

Breed / population	Number of animals sequenced	Number of SNPs	Number of InDels
Angus	30	12 763 637	1 435 544
Charolais	30	16 447 566	1 571 903
Hereford	30	13 015 145	1 444 096
Limousin	30	13 296 742	1 198 388
Simmental	30	12 672 405	1 059 884
Gelbvieh	29	14 801 190	1 610 967
Holstein	48	13 314 502	1 544 219
Beef Booster	29	16 048 035	1 674 345
Alberta	29	16 168 957	1 682 164
Guelph	30	15 309 508	1 545 919

Development of imputation tools and prediction equations

The data described above will now be used for two critical goals: 1) to develop improved imputation tools; and 2) to link genotypes with phenotypic traits, in order to develop prediction equations that can be used by industry for selection of purebred and crossbred animals.



Limousin, Seven Forty Seven
Born: 1978
Progeny: 461
Descendants: 228 792

Angus, Ankonian Dynamo
Born: 1970
Progeny: 462
Descendants: 1 144 106

Charolais, Roxy's Jack Dempsey 63R
Born: 1983
Progeny: 1,896
Descendants: 251 309

Simmental, Signal
Born: 1969
Progeny: 4 396
Descendants: 563 711

Hereford, Remitall Keynote
Born: 1988
Progeny: 1 103
Descendants: 89 855

Gelbvieh, Belgrad 62837
Born: 1971
Progeny: 172
Descendants: 109 271

Figure 1. Key historic bulls from nine major breeds included in the Canadian Cattle Genome Project, showing the number of progeny and the number of descendants (as of early 2012) for each bull. These bulls were sequenced at 20X coverage.

The development of imputation tools is important because they allow us to fill in the SNPs missing from inexpensive low-density genotypes. The process involves comparing the complete genome sequences to the low-density genotypes, to identify segments of DNA shared between the sequenced and genotyped animals. The detailed sequence information for such segments is then copied from the sequenced animals to the genotyped animals. In this way, we take advantage of the relationships among the animals to infer genomic information at a reduced cost. CCGP researchers from the University of Guelph have developed and tested improved algorithms for imputation from 50K (i.e. 50 000 SNPs) up to the 770K level and the sequence level (nearly 30 million SNPs). Imputation in beef cattle is challenging because of the wide range of breeds and populations used in the beef industry. However, high imputation accuracies can be achieved through the use of larger reference populations with animals from a variety of breeds.

The pipelines for imputation are now in place so that "imputed" sequence genotypes can be generated quickly for any animal for which a low-density genotype is available. These imputed sequence genotypes will then be combined with extensive phenotypic information from the same animals, to build prediction equations. The use of imputed sequence genotypes, rather than a lower density genotype is important because this will allow the prediction equations to give more accurate estimates of genetic merit.

In order to predict breeding values, phenotypes as well as genotypes are needed. To this end, the project has amassed an impressive collection of phenotypic measurements on more than 8000 animals. Traits collected include RFI, carcass quality and meat quality. RFI measurements from Kinsella animals are a critical part of this database. Figure 2 shows the distribution of RFI values for animals in the dataset—the animals on the left side of the distribution (i.e.

with negative values) are the efficient animals. Once the genetic data is linked with the RFI data through the development of genomic predictions, we can select for low-RFI animals with increased accuracy and reliability. Two methods for generating genomic predictions, GBLUP and Bayesian-type methods, will be tested and compared. Predictions will be generated for RFI and several additional traits including dry matter intake, average daily gain, live weight, back fat, residual gain and residual intake and gain.

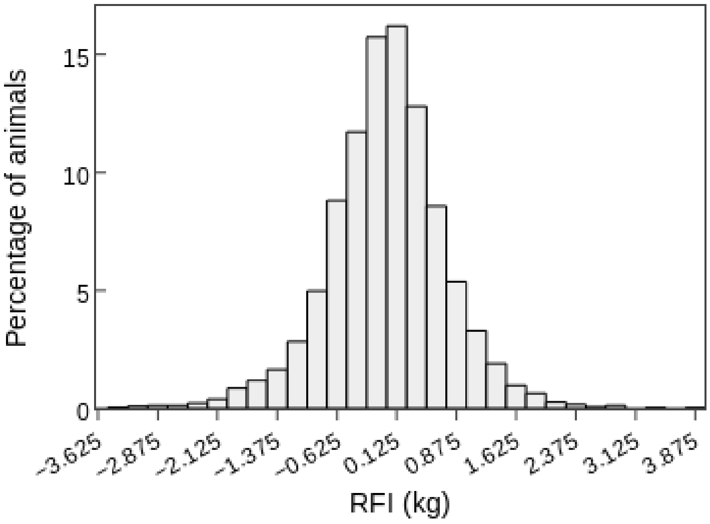


Figure 2. Distribution of residual feed intake (RFI) estimated across animals in the Canadian Cattle Genome Project's phenotypic database

Future directions

The Kinsella Research Ranch is poised to capitalize on the data and the tools developed through the Canadian Cattle Genome Project to further their efforts to develop tools for Canadian breeders and producers. A project recently funded by the Alberta Livestock and Meat Agency will use the Kinsella composite and purebred breeding herds to demonstrate how to build a feed-efficient cowherd with improved carcass quality. This will be done using genomics and multi-trait selections tools, while at the same time maintaining other important production traits. This project involves many of the Livestock Gentec team and is coordinated by Dr. Carolyn Fitzsimmons of Agriculture and Agri-Food Canada under guidance from an Industry Steering Committee. The overall goal is to increase industry adoption of RFI and genomics by successfully demonstrating the value of these tools to improve returns across the beef value chain. To this end, sequence and genotype data from the CCGP have been used to choose sires with high genetic merit for RFI. Replacement heifers will be chosen based on a multi-trait maternal index including genomic predictions to create an efficient herd. A control herd will be selected without the use of genomic predictions so that at the end of the project, genetic gain of RFI can be compared between the two herds to demonstrate the value. This project is just one example of how the resources from the CCGP can and will be used in the future. For more specific information on this project, refer to the article by Dr. Fitzsimmons that follows.

The Canadian Cattle Genome Project is laying the groundwork through sequencing, genotyping and imputation so that immediate benefits from genomics can be achieved by Canada's beef producers. The large genomic and phenotypic database, and the tools generated, will provide the Canadian beef breeds with a valuable resource that can be utilized now and in the future for the development of a variety of new genomic tools to increase efficiencies, sustainability and profitability across the beef industry.

Acknowledgements

The following agencies are gratefully acknowledged for their support for the work described here: Genome Canada, Genome Alberta, Alberta Livestock and Meat Agency Ltd., Western Economic Diversification and all our collaborators and partners.

The Kinsella Project

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Sustaining profitability in the Alberta beef industry in the face of decreasing agricultural land requires innovations in efficiency. The aim of this project is to demonstrate and to act as a catalyst to increase the uptake of residual feed intake and genomics[1] as a means to increase profit for cow-calf and feedlot producers. Genomics will aid selection of a feed-efficient beef herd, and its profitability will be compared to a herd selected without genomic input. In the feedlot, steers will be managed to reach specialized end-points based upon genomic potential to reduce inefficiencies stemming from non-conformity.

Background

Opportunities – residual feed intake (RFI)

- Feed costs account for 50-70% of the production costs of cow-calf operation (Alberta Agriculture and Rural Development 2005)
- 50-70% of greenhouse gas production from beef cattle is generated from mature cows (Basarab et al., unpublished data)
- One generation of selection for low RFI improves feed to gain ratio by 2.5% in feeders and replacement heifers and is worth $15 to $26/head/year in feed savings and $1.50-2.00/head in carbon credits
- No adverse effects on carcass quality, productivity and fertility

Opportunities – marker-assisted management

- Feeder cattle come from many genetic and environmental backgrounds resulting in considerable carcass variation even after traditional sorting
- The 2005 National Beef Quality Audit suggested that $270/carcass was left on the table due to over fat, over weight and inconsistent carcasses
- A combination of live animal evaluation with genomic information can lead to better management decisions and improve carcass consistency; Kolath (2009) used marker-assisted management to increase USDA % Choice from 40 to 77.4%

Kinsella Project

Objectives

a) Design a breeding-herd and feedlot program to demonstrate the use of genomic technologies in beef cattle production focusing on:
    - improving cow feed efficiency using RFI molecular breeding values (MBVs);
    - integrating carcass MBVs to help sort feeder cattle into more uniform groups for slaughter; and
    - partnering with industry to determine economics of using genomic technologies;

b) provide training for interns, students and industry personnel on the use of genomic information for the betterment of beef production, especially seed-stock producers; and

c) continue to accumulate phenotypic and genotypic data future application of genomic selection.

Current progress

The “Kinsella Project” as we have fondly come to call it, has just completed one full year of implementation. Within the Kinsella Composite (KC) cattle population,

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[1] Genomics in this case is the use of information on DNA variation to identify the genetic potential of a very young animal – samples can even be taken at birth. Typically hair samples or ear notches are collected during routine handling, sent to a laboratory (in our case Delta Genomics in Edmonton) for the genotype of the animal to be determined which is then blended with other information on the animal to help predict its EPD or breeding value.

equal base cattle groups for the "efficient" and "control" herds were established in spring 2013. Feed-efficient yearling bulls and replacement heifers, tested in GrowSafe Systems® to determine their residual feed intake (RFI – a measure of feed efficiency), were added to the efficient herd, while young breeding animals unselected for RFI were added to the control herd for the 2013 breeding season. Calves born from both herds in 2013 were genotyped soon after birth on the 50K SNP chip to determine their molecular breeding value (MBV) for dry matter intake, RFI, average daily gain, lean meat yield, rib-eye area, average fat, and carcass marbling. This information has been used to sort feedlot steers into specific carcass outcome groups. As more phenotypic (trait) information was acquired, it was melded with the MBVs to produce genomic enhanced breeding values (GEBVs) for potential replacement bulls and heifers that would enter the breeding herds in spring 2014. Determinants of economic profitability (current feed, cattle prices, etc.) were obtained from industry and used to establish an economic weighting on key traits that would maximize profitability in both the feedlot and cow-calf levels of production. This in turn was combined with the herd-specific phenotypic and genomic information to produce two selection indexes for this year's breeding animals: a Feedlot Profitability Index (FPI) and a Maternal Productivity Index (MPI). Both indexes score animals with low RFI (more efficient) animals higher in the index, but also take into account other traits that should promote both profitability and productivity. The maternal profitability selection index was applied to the KC-Efficient replacement bulls and heifers for 2014, while for the KC-Control herd replacements were selected using phenotypic information only, with no emphasis on RFI.

The purebred Angus and Charolais herds located at the Kinsella Research Ranch are also a part of the Kinsella Project. Since these herds are smaller than the KC herd, there is no control group – all cattle will be selected with the help of genomics, and with an emphasis on RFI (Fig. 1). Breeding goals for these two breeds are different; for purebred Angus, the emphasis is on maternal productivity, and for Charolais, feedlot profitability. Progress realized on trait selection in the Angus and Charolais herds using genomics will be monitored by comparing phenotypic information measured in the calves from one generation to the next, whereas for KC cattle, calves of the Control and Efficient herds will be compared both within and between generations. The entire project will continue for at least five years.

Figure 1. Angus heifers being fed in GrowSafe Systems® to determine their residual feed intake (RFI). Photo by C. Fitzsimmons.

Researchers involved in this project are not only interested in investigating the use of genomics in breeding animal selection, but also in the positive and negative effects of selection for RFI on other economically important traits. Many other projects that investigate various aspects and/or causes of differences in RFI utilize the calves produced by the Kinsella Project. The large team that oversees this work is made up of researchers from Agriculture and Agri-Food Canada, Alberta Agriculture and Rural Development, the University of Alberta, Livestock Gentec, and AgResearch (New Zealand)[2]. The resource at Kinsella will also act as a pull to attract international collaboration to this effort. We also have the benefit of consulting on an industry steering

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[2] Project Team consists of: Graham Plastow, John Basarab, Carolyn Fitzsimmons, Changxi Li, Liuhong Chen, Lisa McKeown, Barry Irving, Tom Lynch-Staunton, Lynda Baker, Michael Vinsky, Steve Miller, Zhiquan Wang, John Crowley, Marcos Colazo, Divakar Ambrose, Manuel Juarez, Heather Bruce, and Kinsella Staff: Vernon Erickson, Dave Crawford, Dale Paterson, Peter (Sarge)

committee made up of representatives of Alberta Beef Producers, the feedlot and cow-calf sectors and the meat-packing industry. The research team invites the public, especially cattle producers, to come to the Kinsella Ranch to view that cattle herds and progress made within the Kinsella Project – we appreciate any feedback!

Acknowledgements

This project is funded by both the Alberta Livestock and Meat Agency, and the Beef Cattle Research Council under the federal Growing Forward 2 Program. The purebred Angus and Charolais cattle at Kinsella are owned by CALRT (Canada-Albert Livestock Research Trust), who generously donate the use of these herds to support beef cattle research. This project and the Kinsella Research Ranch also represent the spirit of collaboration found within the beef research community, and their desire to investigate and deliver functional genomics tools to benefit cattle production in Canada.

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Genomic prediction for feed efficiency and carcass traits in Angus and Charolais beef cattle

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Feed efficiency is of particular importance as feed provision represents the single largest variable cost (50-70%) in the beef production system. However, measuring feed efficiency of individual animals is relatively difficult and costly, which hinders the genetic improvement of traditional phenotype-based genetic evaluation and selection.

Genomic prediction is an emerging genetic selection method that uses a reference population of individuals with both phenotypic and DNA marker information to estimate DNA marker effects, and subsequently, to predict the genetic merit of selection candidates based on their DNA marker genotypes. Therefore, genomic prediction offers an opportunity to select genetically superior cattle at birth without having to measure any phenotypic traits, which will accelerate genetic improvement rates, especially for difficult or costly-to-measure traits such as feed efficiency. Genomic prediction can also help enhance genetic improvement progress for carcass quality as phenotypes of carcass merit traits are collected by sacrificing potential breeding candidates.

For the past 15 years, a purebred Angus herd of approximately 185 cows and a purebred Charolais herd of 125 cows owned by the Canada-Alberta Livestock Research Trust Inc. (CALRT) have been maintained by Agriculture and Agri-Food Canada (AAFC) to support its beef genomics program. In 2007, the Angus and Charolais herds were transferred from the Onefour Sub-station (AAFC) to the University of Alberta's Kinsella Research Ranch. AAFC scientists and collaborators have been measuring feed efficiency and carcass merit traits on the Angus and Charolais animals since 2001, with the objectives of understanding the genetics of feed efficiency and developing genomic prediction tools that will enable the industry to select more efficient beef cattle with superior carcass merit to reduce production costs and to improve carcass quality.

Key results

As of 2013, feed efficiency and carcass merit traits were measured on approximately 1100 Angus and 910 Charolais steers. These animals were also successfully genotyped on the Illumina BovineSNP50 Beadchip containing 54 609 single nucleotide polymorphisms (SNP). Key results included:

There are substantial variations in residual feed intake (RFI), a measure of feed efficiency, in both Angus and Charolais steer populations, with a range of -2.47 kg of dry matter (DM)/day (more efficient) to 1.90 kg of DM/day for Angus and -1.60 kg of DM/day to 1.69 kg of DM/day for Charolais. The heritability estimates for RFI were 0.47±0.12 for Angus and 0.68±0.14 for Charolais, indicating a great potential to improve feed efficiency in both the Angus and Charolais populations.

The accuracy of genomic prediction for RFI based on the Illumina BovineSNP50 SNP genotypes ranged from 0.29 to 0.58 for Angus and from 0.38 to 0.62 for Charolais, depending on the relativeness of selection candidates with the Kinsella Angus and Charolais reference populations. The highest accuracy was achieved when the selection candidates were immediate offspring of the Kinsella Angus or Charolais population.

Accuracy of genomic prediction for carcass merit traits were from 0.32 (lean meat yield) to 0.37 (carcass marbling score) in the Angus population and for Charolais the genome prediction accuracy for carcass traits ranged from 0.24 (rib-eye area) to 0.46 (carcass backfat thickness).

Implications

The genomic prediction equations for RFI and carcass merit traits have provided a preliminary tool to predict and select efficient bulls with improved carcass merit at young age in Angus and Charolais. The genomic prediction for carcass merit traits has also provided a tool to predict and sort feeder cattle into more uniform groups for slaughter to improve carcass consistency. The genome prediction accuracy will be further improved with more representative Angus and Charolais bulls bred with cows at Kinsella to increase its genetic relativeness with selection candidates. Meanwhile, the Angus and Charolais data has become part of a joint data set to develop genomic prediction tools of RFI and carcass traits for multiple breeds and crossbred beef cattle populations.

Acknowledgements

This work is funded by the Agriculture and Agri-Food Canada (AAFC) Livestock Genetics and Genomics Program, the AAFC A-base peer-reviewed research projects (RBPI-1139, RBPI-1752), Beef Cattle Research Council Beef Cluster project (FDE.05.09), the Canadian Cattle Genome Project, the Canadian Angus Association, and the Canadian Charolais Association.

Methane emissions from beef cattle bred for low residual feed intake (RFI)

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Alberta is among the largest beef producing regions in North America, containing 42% of the beef cows and 70% of the beef feeding capacity in Canada. Alberta is also the only jurisdiction in North America that has an active carbon trading registry[1]. Three beef cattle greenhouse gas (GHG) reducing protocols have been registered, namely: 1) reducing days on feed; 2) reducing age at harvest; and 3) selection for low residual feed intake. It has been estimated that reducing age at harvest in Alberta's 2.4 million feeder cattle by one month would reduce GHG emissions by 681 000 tonnes of equivalent carbon dioxide (CO_2e) annually. Similarly, after 25 years of selection for low residual feed intake (RFI), the HOLOS whole farm model estimated that GHG emissions were 0.844 tonnes CO_2e/cow/year lower compared with the average herd, or 1.64 megatonnes CO_2e/year lower for Alberta's 1.95 million beef cows and bred heifers. However, these model estimates are not based on rigorous emission measurements in real-world conditions.

The accurate measurement of methane emissions from cattle can be labour intensive and expensive, and are difficult to interpret when animals are subjected to atypical management conditions during measurement. Such "unnatural" situations alter the behavior of the animals and change their methane emissions. To further complicate the problem, cattle methane emissions are not uniform over time and vary within and between days and seasons. This project will use a variety of techniques to measure the greenhouse gas-mitigation potential of low-RFI selection of beef cattle in a real-world setting. The work will help to advance Alberta's leadership role in GHG mitigation, and it could open the door to pursuing a type of ruminant that has lower methane emissions.

Project activities

The project is funded and supported by Climate Change and Management Corporation, Alberta Innovates Bio Solutions and the Alberta Meat and Livestock Agency, and consists of three coordinated trials.

Figure 1. Measuring methane (CH_4) using Boreal laser at the Lacombe Research Centre. Photo by V. Baron.

Figure 2. Measuring CH_4 using Open path Fourier Transform Infrared Spectrophotometers (OP-FTIR), Lacombe Research Centre. Photo by T. Flesch.

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[1] See: http://esrd.alberta.ca/focus/alberta-and-climate-change/regulating-greenhouse-gas-emissions/alberta-based-offset-credit-system/

Objectives

Trial 1

a) Measure methane (CH_4), feed intake, RFI and various biometrics in yearling beef heifers during winter feeding (confinement) and summer grazing at two locations; and

b) quantify the relationships of CH_4 and CO_2 emissions with feed intake, RFI and various biometrics.

Over three years (2015-2017), high- and low-RFI replacement heifers will be monitored using techniques that include laser-based OP-FITR for continuous measurement of gases, the GreenFeed™ system for "spot" measurements of methane, and the GrowSafe Beef® system to measure various biometrics.

Trial 2

a) Measure CH_4 emissions, feed intake, RFI and various biometrics in heifers and mature beef cows at two locations under confined feeding and swath grazing conditions; and

b) quantify the relationships of CH_4 with feed intake, RFI and various biometrics.

In each of two years (2015-16 and 2016-17), high- and low-RFI cows will be monitored using all of the techniques employed in Trial 1.

Trial 3

a) Compare and validate CH_4 emissions from high- and low-RFI beef heifers using GreenFeed compared with respiration chambers.

Future work

This work, conducted at the Lethbridge Research Centre, will monitor high- and low-RFI beef heifers for methane emissions, using the GreenFeed system in a group pen (with feed intake monitored with GrowSafe Beef) and in individual animals placed in open-circuit respiratory chambers. The two methane measurement techniques will be compared.

The GreenFeed system is essentially an instrumented portable fume hood into which an animal, identified by its RFID (ultra-high frequency [UHF]), places its head. Feed, water or mineral (bait) is delivered to a feed tray designed around a gas intake manifold. While the animal is consuming the "bait", a fan pulls air at a specific mass flow rate over the animal's head and nostrils, through the intake manifold and into the air-flow monitoring system. Proximity sensors detect the position of the animal's nose in relation to the air intake manifold, and CH_4, CO_2 and air flow rate are recorded every second. A tracer gas is routinely released into the feeder for calibration purposes. In addition the GreenFeed system includes web-based software tools for real-time data review, graphics and a webcam to watch cattle at the feeder.

The study will be guided by the White Paper on "Consensus methods for breeding low methane emitting animals" prepared by the international working group of the Animal Selection, Genetics and Genomics Network, and will provide samples to Livestock Gentec for genotyping, imputation to higher density genotypes and SNP association analysis. Data from this project would also be available for international collaboration. For further information, contact the corresponding author, Dr. John Basarab.

Acknowledgements

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Association between rumen microbiome and cattle feed efficiency

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The importance of improving cattle feed efficiency has been emphasized recently, owing to the increasing demand for beef production, increasing feeding cost, higher transportation fees, etc. Raising cattle with higher feed efficiency is favorable to the industry. Much research has been conducted to develop novel methods to improve cattle feed efficiency from different aspects such as changing dietary formulas, altering management, selecting animals with specific genetic markers, and so on. Because these studies focused on the host animals, the rumen microbiome, which serves as the main digester to decompose the ingested feed and supply host with nutrient and energy, has not been well studied. The roles of the rumen microbiome in impacting host performance have not been well documented. Our research aimed to illustrate the association between the rumen microbiome and cattle feed efficiency, and to supply solutions for farmers to improve cattle feed efficiency from the microbial aspect. To achieve our goals, crossbred beef steers from the Kinsella Research Ranch were selected according to their feed efficiency (residual feed intake [RFI]). Rumen samples were collected and subjected to the downstream analyses on the rumen micriobiome. Our research mainly focused on two major types of microorganisms: bacteria and methanogenic archaea.

Rumen bacteria are the largest component of the rumen microbiome, which is responsible for both primary breakdown and secondary fermentation of the ingesta. Bacteria are the major energy and nutrient supplier to the host animals, thus understanding the correlation between rumen bacteria and host feed efficiency is crucial to illustrate the roles of rumen microbiota on host performance. Samples collected from cattle fed both a growing diet and a finishing diet were analyzed. In cattle consuming the growing diet, butyrate was found to be positively correlated with daily dry matter intake, and tended to have higher concentration in high-RFI animals, while isovalerate was associated with host RFI. Bacterial profiles did not cluster according to host RFI class. However, five bacterial phylotypes were associated with high-RFI animals while four phylotypes were associated with low-RFI animals. In cattle consuming the finishing diet, the bacterial profiles of the same RFI class were more similar than those of different RFI class. In low-RFI animals, *Succinivibrio sp*. was correlated with dry matter intake and average daily gain. In high-RFI animals, *Robinsoniella sp*. was correlated to host RFI. The *Eubacterium sp*. population significantly differed between high- and low-RFI animals. Four phylotypes were low-RFI associated, and seven phylotypes were high-RFI associated. Total bacteria abundance was similar among animals irrespective of host RFI class or diet. Based on these results, it could be speculated that particular bacteria and their metabolism in the rumen, instead of the total bacteria population, may contribute to the differences in host feed efficiency.

The major role of rumen methanogens is to convert the hydrogen produced during microbial fermentation into methane gas, so as to maintain low hydrogen partial pressure and to ensure the continuity of the normal fermentation process within the rumen. Although methanogenesis is necessary, it leads to dietary energy loss to the host animals, thereby reducing host feed efficiency. It has been reported that animals with higher feed efficiency (lower RFI) produced less methane. Our studies on the rumen methanogens mainly aimed to reveal the differences in the rumen methanogenic communities between high- and low-RFI steers, to understand the linkage between cattle feed efficiency and rumen methanogen communities, and to reveal the association between methanogenic communities and enteric methane production. Similar to the studies on rumen bacteria, animals receiving both growing and finishing diets were examined. In cattle fed the growing diet, the main methanogen was

Methanobrevibacter ruminantium regardless of the host RFI class. The methanogenic communities of high-RFI animals were more complex than that of low-RFI animals. Although 18 different methanogen phylotypes were shared by both high- and low-RFI steers, four phylotypes were exclusively observed for low-RFI animals while nine phylotypes were restricted to high-RFI animals. In addition, two methanogen phylotypes, *Methanosphaera stadtmanae* and *Methanobrevibacter sp*. AbM4, were more prevalent in high-RFI animals. In cattle fed the finishing diet, the composition of methanogens changed significantly, with the main phylotype(s) being *Methanobrevibacter smithii*, and/or *Methanobrevibacter sp*. AbM4, and/or *Methanobrevibacter ruminantium*. Although major phylotypes varied among animals, the microbial profiles were more similar within animals of the same RFI class compared to that of different RFI class.

It has been reported that microorganisms of different species or strains may display different metabolic characteristics, and produce different end products. Therefore, we speculate that the different methanogenic communities between high- and low-RFI animals may lead to a variation in the available energy and substrates to the host, which further influencing host feed efficiency. In addition, total methanogen population was similar between high- and low-RFI animals, and between the two diets. These results suggest that the microbial composition may be more important than the population in affecting host performance.

Our research has supplied fundamental understanding on the differentiation of the rumen microbiome between high- and low-RFI animals under different dietary conditions, suggesting that the varied functions of different microbial species may have different impacts on the host rumen fermentation process. These results have emphasized the importance of further investigation of particular microbial phylotypes in addition to analyzing the whole microbiome. Currently, we are applying advanced sequencing technologies to study the microbial metagenome, metatranscriptome, and metabolome, to obtain a more comprehensive understanding of the entire rumen microbiome together with insights regarding each species. With these techniques, not only bacteria and archaea, but also protozoa, fungi, and phages are being studied, so the real mechanisms of how microbial metabolism affects host feed efficiency can be revealed.

Acknowledgements

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Epigenetics and fetal programming – Are your cattle what their mothers ate?

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Gestation length in cattle – roughly 285 days – is a long time for calves to spend in utero and be solely dependent upon their mothers' nutrition and physiology to grow and develop, and become ready for life on the "outside". In utero they are relatively safe from the effects of minor fluctuations in maternal diet, or are they? Research conducted at the University of Alberta's Kinsella Research Ranch is investigating the role that maternal pre-natal nutrition plays in the post-natal life of the beef calf. The primary objective of this research is to determine the impact of reduced access to feed (e.g., because of scarce feed resources, conditions that make it challenging to obtain feed, or other stressors such as being low in the pecking order as compared with older cows) has on the quality of cattle's offspring. The effect of selection for residual feed intake (RFI) – a measure of feed efficiency in cattle – as an interacting factor, is also being investigated.

RFI has been intensely studied over the past 10 years, mainly during the feedlot stage of beef production. Fewer studies have been conducted on breeding females, and the consequences, whether positive or negative, of selection for RFI upon fertility, health, and longevity both of the heifers / cows themselves and subsequent generations of calves. Selection for RFI in cattle involves changes in the ways animals acquire, metabolize, and distribute energy that are far from understood. Therefore, it is important to investigate other economically important traits that may be linked with selection for low-RFI animals.

Maternal nutrition during pregnancy has been shown to permanently affect metabolism in other mammals, and evidence of this does exist in cattle. Therefore, pre-natal nutrition may influence some of the same biological processes as selection for RFI. Raising cattle that are of a more consistent quality involves breeding (genetics), and proper care and nutrition after birth. The latter has become highly evolved in the feedlot stage; however, more precise manipulation of the maternal diet during pregnancy, and investigation of its influence on post-natal growth and development of the calf have only just begun. Determining and then optimizing the impact of maternal nutrition during pregnancy may give producers another tool in providing more consistent, quality products to consumers.

Objectives

a) Determine if plane of nutrition during the first half of gestation in beef heifers affects the post-natal health status, growth, sexual development, RFI, and carcass and meat characteristics of their calves;
b) determine if low-RFI (efficient) heifers yield better quality calves than high-RFI (inefficient) heifers when subjected to different planes of nutrition during the first half of gestation;
c) examine the changes in gene expression and DNA methylation in tissues of calves from high- and low-RFI dams exposed to different planes of nutrition during early pregnancy; and
d) investigate whether pre-natal nutrition during the first half of pregnancy can change the expression of genetic potential for RFI in calves.

Project progress

Before the breeding season in 2012 and 2013, purebred Angus yearling heifers at the Kinsella Research Ranch were tested for RFI in the GrowSafe® automated feed recording system. Subsequently, heifers were divided into high- and low-RFI groups, which in turn were mated to high- and low-RFI bulls, respectively, by artificial insemination to produce genetically high- or low-RFI fetuses. On day 30 of pregnancy, heifers entered one of two diet treatments:

they either received a ration formulated to allow gain of 0.5 kg/day, or 0.7 kg/day. Rations were fed until 150 days of pregnancy, and were adjusted periodically to account for heifer and fetal growth as well as decreasing fall temperatures. After day 150 of pregnancy, heifers were grouped together and offered free-choice hay. While receiving the diet treatment and before calving, cattle were monitored for weight gain and ultrasound rib and rump fat changes.

Figure 1. Angus heifers produced at the Kinsella Research Ranch to have genetically high and low residual feed intake (RFI). Photo by C. Fitzsimmons.

The calves born in 2013 have been monitored from birth to puberty or slaughter for growth and health phenotypes, muscle and fat development, RFI, female fertility, and carcass characteristics to determine if there are any effects of selection for RFI, pre-natal nutritional treatment, or their interaction, on any of these economically important traits (Fig. 1). Calves from the second year of heifers, born in spring 2014, will be monitored for growth phenotypes, muscle and fat development, RFI, male fertility, and carcass characteristics.

To date, information collected from the project has revealed some very interesting preliminary results. Analysis of the first-year diet treatment data has shown that low-RFI heifers exhibit different feeding behavior and eat less on average than high-RFI heifers on both the high and low diets – and this is in the absence of a difference in weight gain or measurements of rib and rump fat both during and after the diet treatment. Gestation length, as well as calf birth and weaning weights, appear not to be affected by either maternal diet, RFI, or their interaction. Some indicators of early innate immunity, as well as expression of genes known to be affected by pre-natal nutrition, measured in muscle biopsies collected soon after birth, are affected by RFI classification, or maternal diet, or both.

Serial blood serum collections in the heifer calves have been performed since post-weaning until the end of May 2014 to measure progesterone levels in order to predict puberty. Heifer calves have also completed their own GrowSafe test and analysis of effects of maternal diet on subsequent RFI measurement in the calves is underway. During summer 2014, the steer calves will also be tested for RFI in GrowSafe, and will be sent for slaughter at the Lacombe Agriculture and Agri-Food Canada abattoir for collection of detailed carcass and meat characteristics, as well to contribute to carcass composition data collection and calibration of AAFC Lacombe's new DEXA (Dual-energy X-ray absorptiometry) machine, which measures total body composition and fat content with a high degree of accuracy.

In conclusion, the initial results from this study indicate that although no gross differences in calf phenotype such as weight or growth have been detected, subtle differences in other important traits are present, and these warrant further investigation.

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Testing residual feed intake in extensive cow-calf systems and evaluating behavioral aspects of efficiency

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Current efforts to increase profitability of the beef industry have targeted production efficiency and cost reductions. Residual feed intake (RFI) of beef cattle, or the difference between actual and expected feed requirements given a specific body size and production level, has been identified as an important attribute of efficiency (Fig. 1). Low-RFI cattle require less feed to reach marketable weight and can lead to lower environmental impacts such as greenhouse gas (GHG) emissions. While improvements to RFI are a key component of industry competitiveness, most previous research on RFI has been conducted in drylot using higher energy diets under restricted choice feeding conditions.

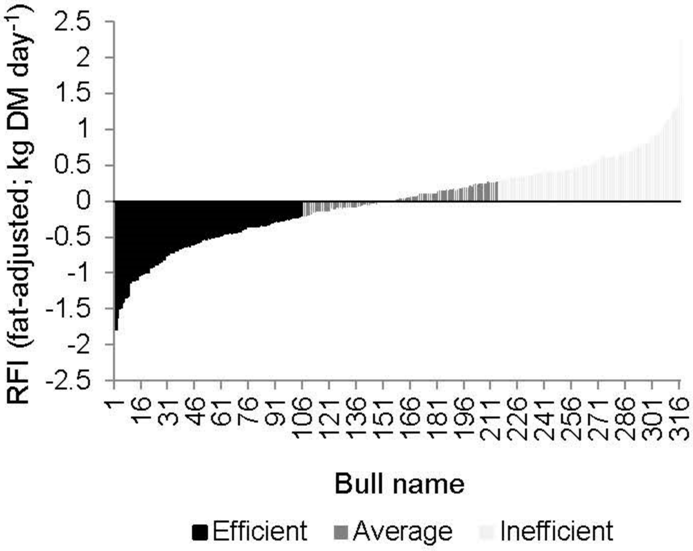

Figure 1. Established range of residual feed intake (RFI$_{fat}$) for Hereford bulls tested in 2012-2013. Efficient bulls (*n*=106) had an average RFI of -0.65 kg dry matter [DM] day^{-1}, and average daily gain of 1.37 kg day^{-1}; average bulls (*n*=107) had an average RFI of 0.03 kg DM day^{-1}, and average daily gain of 1.36 kg day^{-1}; and inefficient bulls (*n*=107) had an average RFI of 0.61 kg DM day^{-1}, and average daily gain of 1.37 kg day^{-1} (J. Basarab, unpublished data).

It is unclear, however, if cattle with low RFI in drylots are similarly efficient in extensive cow-calf systems, where efficiency and associated environmental footprint is influenced by mobility, maternal characteristics, habitat and forage conditions, as well as dietary preferences and intake under free-choice foraging (Fig. 2). Testing the repeatability of RFI under extensive grazing is the goal of this research. These results will have implications for improving beef production efficiency and environmental sustainability in Alberta.

Figure 2. Cattle grazing in open rangeland are faced with many decisions on where and how to forage, with significant variation possible in the quantity and quality of forage intake achieved, as well as the energy expended obtaining that forage. Photo by E. Bork.

With support from the Alberta Livestock Meat Agency, the Climate Change and Emissions Management Corporation and Delta Genomics, we are testing the relationship between beef cattle production efficiency within a cow-calf production system under open range grazing, and predicted RFI as determined using GrowSafe® feed intake data and/or DNA marker panels. To accomplish this, we will:

1. Determine whether cattle previously identified as low RFI exhibit favorable performance when tested in a cow-calf production system (extensive open rangeland) with free choice selective foraging, and whether cattle with high RFI are less efficient under the same conditions. To do so, we will quantify changes in body weight and composition, rebreeding ability and offspring pre-weaning growth, of cows selected for high and low RFI under open range foraging.
2. Test the performance of offspring from bulls previously identified as low- or high-RFI in an extensive cow-calf production system, including quantifying subsequent forage intake of yearling heifers with known differences in performance (efficiency or RFI) and behavior in free-choice grazing.
3. Evaluate different methods for assessing efficiency in extensive cattle production.
4. Utilize an open range environment to identify and test behavioral mechanisms responsible for influencing RFI in cow-calf pairs, including habitat type and availability, animal habitat selection, biomass availability and use, forage quality and selection, and cow movement.

This study will be conducted at the 5,000–hectare [ha] Mattheis Research Ranch in the Mixedgrass Prairie, 40 km north of Brooks, Alberta. To accomplish our objectives, we will use the genotypes from a 400+ cow-calf commercial cattle herd and at least 20 bulls. After initial genotyping using 50K marker panels, animals will be divided into low-RFI (i.e., ~50 efficient cows) and high-RFI (i.e., ~50 inefficient cows) based on their molecular breeding values (MBVs) or genotype expected breeding values (GEBVs) in the spring of 2014 for the upcoming breeding season. These values will incorporate RFI information where available. Low- and high-RFI cows will be crossed with low- and high-RFI bulls, respectively, to create as large a range as possible in efficiency of cow-calf pairs following calving in the spring of 2015. Remaining cows (~300 head) will be crossed with bulls having a range of breeding values. All calves born in 2015 will be tested for parentage to verify sire progeny.

In the subsequent test of cattle performance, cow-calf pairs of different RFI lineage will be grazed together during 2015 under open-range (free choice) grazing. All animals will be grazed together to ensure equal access to the same foraging conditions (water, plant communities, forage species, etc.) throughout the grazing season, thereby avoiding confounding effects in the interpretation of cattle responses. Cattle will be grazed at moderate stocking rates in a rotational grazing system, consistent with widespread management practices across Alberta.

To assess animal performance, the following metrics will be measured:

- Cow condition at or after calving on all cattle, and again in the fall at weaning;
- Calf birth weights, weaning weights and season-long weight gain;
- Calving ease and cow calving interval;
- Cattle movement and spatial distribution on a subset of high and low efficiency cows in 2015 to determine energy expenditure and habitat use, using a variety of measurement tools (including GPS locational ear tags and pedometers);
- Dietary forage (plant species) composition within a subset of high and low RFI cattle will be assessed in 2015 using fecal histological analysis (i.e. microscopic dissection of plant species in cow patties); and
- Replacement heifer feed intake and dietary composition.

To address the last point, above, a subset of replacement heifers (born in 2015) with hypothesized high- and low-RFI will be tested for intake on pasture and in drylot during 2016, similar to work being done in Lacombe (Fig. 3). Ten heifers from each group will be enclosed in small (~2 ha) pastures and hand-fed pellets containing alkanes twice a day for up to 15 days. Fecal samples will be collected twice daily from days 8-15 to assess alkane dissipation curves and associated forage biomass intake. These heifers will also be tested for RFI in drylot to validate molecular breeding values based on maternal and paternal lines.

Figure 3. Heifers being tested for intake on monoculture pasture using controlled doses of alkane markers. Photo by J. Basarab.

Anticipated outcomes of this research include the testing and cross-validation of existing RFI selection criteria for application to cow-calf systems. In addition, results of this study will facilitate recognition of those factors (animal or forage constraints) controlling the identity of efficient/inefficient cattle under open-range grazing production systems. Finally, insight into RFI application may lead to the development of new measurement tools for RFI in cow-calf production systems, or alternatively, insight into how existing criteria may require refinement for enhanced applicability to extensively managed cow-calf systems. Performance metrics will reflect the relationship between predicted and measured efficiency by breeding cows, offspring and replacement heifers.

Ultimately, our long-term goal is to explore the performance of current selection methods and the need for alternative approaches to optimize feed efficiency and RFI for extensively managed cow-calf producers grazing rangelands in Alberta. Results of this research will provide much needed information on how current genetic improvement programs for beef cattle may impact cow-calf production and associated profitability. More importantly, any benefits arising from current genetic selection programs for cow-calf producers will be quantified by establishing strategies that lower costs at existing production levels, or increase cow-calf weight gain at the same costs. Results of this study are also expected to identify additional needs and opportunities within existing beef selection programs that would directly aid cow-calf producers by further reducing RFI during extensive grazing.

This is one of the latest additions to the portfolio of research being undertaken on feed efficiency here in Alberta. These include work at Olds College, the Lacombe Research Station, and the Kinsella Research Ranch, along with other academic and industry partners. Lessons and approaches are shared across projects when appropriate with the principle of making the best use of the animal resources available. We may see additions to the protocol here such as analysis of the rumen microbiome and testing or validating new methods of collecting data, as well as the confirmation of results from this project in other environments across the province and Canada.

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Canadian consumers' preferences for beef produced using genomic information in selective breeding

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The Canadian beef industry faces many challenges that include extremely thin margins in many years. At a global level the industry is often described as a significant source of greenhouse gases (Steinfeld et al. 2006, U.S. Environmental Protection Agency [EPA] 2014). The cattle farming industry may be able to benefit from new applications of genomics that allow cattle breeders to select for more feed-efficient cattle which could reduce greenhouse gas (i.e., methane [CH_4] and nitrous oxide [N_2O]) emissions.

Enhancing feed efficiency in cattle could have the effect of making beef production more environmentally and economically sustainable. Other possible methods of changing the rumen to reduce greenhouse gases include vaccinating cattle (Wedlock et al. 2013). Producer adoption of genomic information to be used in selective breeding (or vaccination) could be influenced by their perceptions of the public acceptability of the use of technology. Whether the public understands or does not understand the processes currently used in breeding cattle (e.g. selecting on phenotypic information), they may either approve or disapprove of the use of genomic information in selective breeding. This approval/disapproval could be partially driven by their perceptions of the importance of feed efficiency and/or reducing greenhouse gas emissions.

Public investment in the development of the genomics technology is significant and society will benefit if producers adopt the technology. Understanding public perceptions and preferences is essential for producers to decide whether or not the use of genomics is acceptable, and whether or not the potential profit can outweigh the additional costs of using vaccination or genomic information in breeding.

Methods

The aim of this study is to describe Canadian consumers' preferences for steak that is produced from cattle bred to be more feed-efficient using either vaccination or genomic information. Data used is from an online survey conducted in 2012 in Canada. Respondents were general household shoppers and they were asked questions that allowed us to determine their preferences for steaks that are produced from cattle bred to be more feed-efficient (no technology identified) and bred to be more feed-efficient using genomic information. Stated preference (SP) experiments were used to evaluate consumers' attribute preferences. To explain variations in preferences across survey respondents, explanatory variables including price of steak, socio-demographic variables (such as age, gender, level of education, level of income, presence of children under 18 in the household), general trust in people, living in rural areas or not, whether or not they had heard about genomics prior to the survey, their extent of knowledge about science and technology development, to what extent they thought science and technology would make their lives better off or worse off, and a measure of their attitudes towards animals (Herzog et al. 1991) were used.

Two levels of steak prices ($15.39 and $30.78 per kg) were offered, and respondents were asked initially to select either a conventional steak or a steak that was produced from animals that were more feed-efficient (producing between 10 and 20% less methane). The respondents were then provided with a brief explanation about feed efficiency, methane emissions, economically sustainable beef production and the use of genomics. After the description of genomics, in a second set of questions, respondents were asked to choose between two steaks. Both steaks under consideration were from cattle raised on a farm where animals produce 10-20% less methane, by different methods – either by being vaccinated to change the microbes in the rumen, or by being bred using genomic information to be more feed-efficient. Respondents could not choose both steaks.

To estimate the probability that each respondent would choose first the more feed-efficient animal and second the more feed-efficient animal produced with genomics, a random parameter logit (RPL) model was used to account for the preference heterogeneity across the sample of respondents.

Results

For the first question – probability of preferring a steak that is more feed-efficient – older people chose meat from more feed-efficient animals. People from Ontario were less likely than people from the rest of Canada to choose meat from more feed-efficient animals. Respondents who have pro-animal welfare attitudes, who believe science and technology will make society better off, and who have higher than average self-assessed knowledge about scientific and technological developments chose steaks from animals with lower methane emissions/higher feed efficiency.

For the second set of questions – wherein respondents chose between steak from more feed-efficient cattle bred by genomics versus vaccination – people with higher incomes and people who believe scientific advances will make our society better off chose the feed-efficient steak produced by genomic information used in selection. People who live in Ontario were less likely to choose the meat from animals produced using genomic information in selective breeding. There were no significant differences in respondents' preference for genomics versus vaccination based on their personal attitudes towards animals.

The willingness-to-pay measures from the RPL model showed that a representative Canadian consumer[1] is willing to pay between $8.28 and $9.25 per kg for the steak with higher feed efficiency, without any information provided on the process used to enhance feed efficiency. This is a premium over the normal price of steak. The representative consumer is also willing to pay between $7.16 and $7.28 per kg more for steaks with higher feed efficiency produced with genomic technology introduced as the application which improves the feed efficiency/methane emissions, as opposed to the same steak produced from using vaccination. In each case, there is a distribution of responses across the population of respondents (Fig. 1), with a small group of people so strongly opposed they would need to be compensated to purchase the products, if they knew the processes involved. That small group does not see feed efficiency (or feed efficiency produced with genomic information in selective breeding) as important.

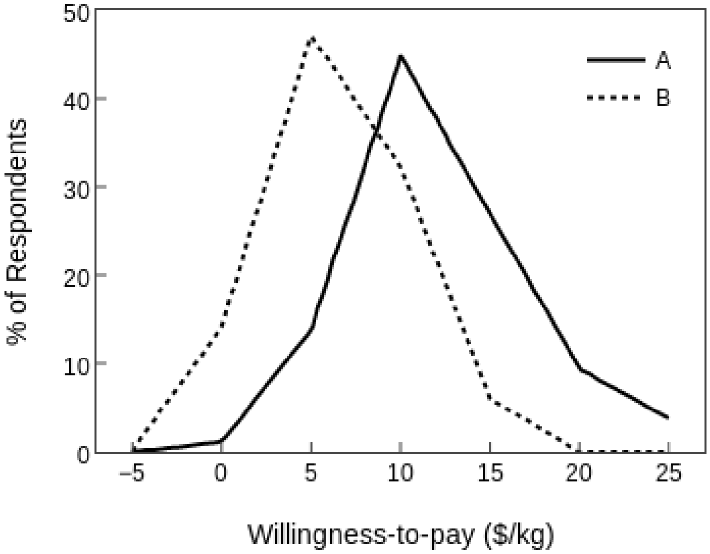

Figure 1. Distribution of Canadian consumers' willingness-to-pay for steak with (A) lower methane per animal production/higher feed efficiency (solid line) and (B) genomics application (lower methane production/higher feed efficiency; dotted line), as determined by random parameter logit regression analysis

Implications

The results show that some socio-demographic characteristics are important in shaping consumers' preferences in this context. In the steak choice models, it appears that a positive attitude towards science and technology and/or higher levels of self-assessed

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[1] The arbitrarily selected respondent is a 45 year old man who lives in a rural area with no children under 18 in the home, who has heard about genomics prior to the survey, of average education and income, and who believes other people cannot be trusted, with an animal attitude score at mean level of 42.

knowledge of science are important in respondents' views towards beef that involves the application of genomics. Attitudes towards animals were also shown to be important in explaining preferences for more feed-efficient animals, but not in the preferences for the method of producing more feed-efficient animals.

Although the technique used here is stated preference, which uses hypothetical choices made by survey respondents, the results are predictive to a certain extent of the possible reactions of the public when such products are introduced into the market place. Clearly, the attribute of feed efficiency (described in this survey as improving producer livelihood and reducing greenhouse gases) is not yet of interest to all of the Canadian population. However, there is a positive premium for the use of genomics to achieve feed efficiency over the use of vaccination to achieve the same ends. In general, the population – particularly those individuals with higher levels of science understanding and belief in the positive social outcomes from science – is more positive about this (and other) uses of technology.

The lack of interest in more feed-efficient/reduced greenhouse gas emission beef shown by some respondents may be due to the complexity of the greenhouse gas/climate change story, the debates by scientists around the issue and the perceptions this leaves with the public that immediate behavioural change is not necessary to reduce greenhouse gases.

Acknowledgements

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Genetic influence of host animal on fatty acid profile in beef

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Beef can be an excellent source of protein in the human diet and also contains many essential vitamins and minerals. However, more consumers are demanding healthier beef due to increasing awareness that atherosclerosis and other cardiovascular diseases are correlated with fat intake. While some saturated fatty acids (SFA) are considered to have harmful cardiovascular effects, other types of fatty acids such as mono and polyunsaturated fatty acids (MUFA and PUFA) including Omega-3 and conjugated linoleic acids (CLA) are believed to benefit human health.

Improvement of beneficial fatty acids in beef can be achieved, to some extent, by designed diet supplements. However, significant variation of fatty acid content has been observed among beef steers fed a typical western Canadian finishing diet. This variability indicates a great potential to further improve fatty acid profiles by capitalizing on the natural genetic differences among animals through genetic selection. In contrast to diet management, genetic improvement of fatty acid composition is perpetual, which will benefit both the beef steers and beef cows in a cattle herd without adding extra costs associated with designed diet supplements. However, genetic evaluation and selection for fatty acids has not been practiced in beef, due to the high cost of accurate measurement of fatty acid composition in various beef cuts and lack of understanding on host genetic controls of fatty acids. In 2010, the research project “Identifying DNA markers for enhancing beneficial fatty acids in beef” was initiated with objectives to: 1) examine the genetic variation and estimate genetic parameters, i.e. heritability of each fatty acid in striploin and subcutaneous fat tissues, as well as phenotypic and genetic correlations between fatty acids; 2) estimate phenotypic and genetic correlations between different fatty acid components with growth, fat deposition, carcass merit, and meat quality traits; 3) identify DNA markers of host genes that are significantly associated with concentrations of fatty acids in the animal tissues; and 4) develop genomic prediction equations to predict concentrations of fatty acids in animal tissues based on DNA markers.

Key results

Longissimus lumborum muscle (striploin) and subcutaneous adipose tissues of 1366 beef cattle were collected in conjunction with the Alberta Livestock and Meat Agency-funded “Phenomic Gap” project (led by Dr. John Basarab), and the team has successfully quantified 83 individual and groups of fatty acids in the muscle and 81 fatty acids in the adipose tissue. The animals were also successfully genotyped on both the bovine 50K single nucleotide polymorphism (SNPs) chip (i.e., 54 609 SNPs) and a panel of 1536 gene SNPs. Key findings included:

- Variations of fatty acid concentrations in animal tissues exist among animals fed a feedlot finishing diet typical to western Canada with a potential to increase contents of beneficial fatty acids 11t-18:1, sumCLA, PUFA, Health Index by 37.3%, 20.3%, 33.3% and 14.8%, respectively, and to reduce SFA by 6.4% in striploin (Health Index=Total MUFA + Total PUFA) / (4 x C14:0+C16:0).
- Most fatty acids had low estimates of heritability (<0.25) including trans vaccenic acid 11t-18:1, sumCLA, PUFA in striploin. However, some monounsaturated fatty acids 9c-14:1, 9c-18:1, 13c-18:1, 9c-16:1 and Health Index of meat were found to be moderate to moderately highly heritable (0.45-0.69) in striploin.

- DNA markers of multiple genes were found to be significantly associated with contents of fatty acids in the beef tissues. However the identified DNA markers had relatively small effects, accounting for less than 10% of phenotypic variance for most of fatty acids including beneficial fatty acids 11t-18:1, sumCLA, PUFA and Health Index. However, for fatty acids C14:0, 9c-141 and 13c-18:1, the identified DNA markers explained a larger proportion of phenotypic variance (10.9% to 30.99%), indicating stronger host gene direct effects on these fatty acids.
- Accuracy of genomic prediction for most of the fatty acids, including beneficial fatty acids 11t-18:1, sumCLA, MUFA and PUFA, were at the lower end (<0.30). Moderate to moderately high accuracy of genomic prediction (0.35-0.53) were obtained for individual fatty acids C14:0, 9c-14:1, 9c-16:1, 13c-18:1 and Health Index in striploin.
- Improving contents of beneficial fatty acids 11t-18:1, sumCLA, and Health Index in striploin and adipose tissue had no significant effects on carcass merit traits. However, the results confirmed that improving the content of Omega-3 PUFAs in striploin could lead to a decrease in marbling as PUFA are found in the cell membranes, not in the triglycerides found in the marbling fat.
- Improving contents of beneficial fatty acids sumCLA, MUFA and Health Index in the striploin will also improve beef flavor and tenderness. However, improved contents of PUFA in striploin were correlated with a higher drip loss, and reduced tenderness and flavor. Therefore, a multiple trait economic selection index method and/or Vitamin E supplement to the animal's diet may mitigate the antagonistic correlations of improving contents of PUFA on carcass and meat quality traits.

Implications

This study represents the first of its kind in Canada to investigate genetic controls of host animal genes on fatty acid concentrations in beef tissues. The heritability estimates, correlations of fatty acids with carcass and meat quality traits, the SNP markers associated with fatty acids and genomic prediction equations for fatty acids have laid a foundation for future investigations into how host genes influence contents of fatty acids. The genomic prediction equations for the fatty acid contents may also be incorporated with genomic prediction for other important traits such as feed efficiency so that animals with healthier fatty acids in meat may be selected to meet consumer demands. However, more studies are required to elucidate how rumen microbes interact with host genes in determining contents of fatty acids in beef tissues in order to enhance the genome prediction accuracy and to facilitate gene-based diet management to further improve contents of beneficial fatty acids in beef.

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Can potential for dark cutting be predicted by phenotype? Relationship between gender, carcass characteristics and the incidence of dark cutting beef

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Carcasses from cattle under 30 months of age that have a purple or dark red rib eye muscle 20 minutes after "ribbing" at the 12th-13th rib are considered dark cutting and are graded Canada B4. Dark cutting carcasses are downgraded because they usually have a meat ultimate pH greater than 5.8, which encourages the growth of spoilage bacteria (Aberle et al. 2001). As a result, dark cutting carcasses are discounted and there is a direct financial loss to producers. Although a well-recognized meat quality defect with well-known causes, dark-cutting continues to occur, with its annual incidence increasing in Canada within the last 10 years from 0.8 to 1.3% (Beef Cattle Research Council 2013). The persistence of dark cutting in the beef industry despite prevention strategies such as not mixing cattle suggests that the causes of this meat quality defect are manifold and changing. The purpose of this study was to relate the effect of gender, carcass conformation and animal phenotypic characteristics to the frequency of dark cutting beef in order to test the hypothesis that the likelihood of a beef animal producing a Canada B4 (dark cutting) carcass can be predicted from live animal measurements.

Materials and methods

Data

Data used in this study were drawn from an existing set of records for 845 cattle with production and carcass measurements available. Data within this data set were collected from cattle studied from 2003 to 2011 on three farms (Farms A, B and C). Cattle within the database were sired by purebred Black or Red Angus, Charolais and Hereford sires and composite (BeefBooster®, Calgary, Alberta). Dams of cattle were Hereford-Angus, purebred Charolais or composite (BeefBooster) breeding. A sub-set of data from one farm (Farm A, $n = 41$) with complete live animal and carcass data was used for detailed analysis of the relationships between gender, carcass and production phenotypes and the frequency of dark cutting. The Farm A data set (steers $n = 23$; heifers $n = 18$) was created by selecting carcasses that graded Canada A ($n = 9$), AA ($n = 11$) and AAA ($n = 10$), matched as closely as possible within same-sex slaughter lot by date of birth, to Canada B4 carcasses ($n = 11$).

Production and carcass data included dry matter intake (DMI, kg DM day^{-1}), average daily gain (ADG, kg gain day^{-1}), feed conversion ratio (FCR, kg DMI kg^{-1} gain), residual feed intake (RFI, kg feed day^{-1}), ultrasound rib eye area (uREA, cm^2), ultrasound subcutaneous fat depth (uSFD, mm), ultrasound marbling score (uMS), carcass weight (CarWt, kg), grade fat depth (gFD, mm), grade rib eye area (gREA, cm^2), and grade marbling score (gMS). Ultrasound and carcass subcutaneous fat depth, marbling score and rib eye areas were measured at the Canadian beef grading site (12-13th rib interface). Both ultrasound and post mortem rib eye muscle marbling scores were categorized using the United States Department of Agriculture scoring system (USDA, 1997) where Canada A, AA, AAA and Prime quality grade marbling corresponded with traces (300-399), slight (400-499), small to moderate (500-799), and greater than or equal to slightly abundant (800-1099), respectively. These categories equated to ultrasound marbling scores between 1.00 to 3.99, 4 and 4.99, 5 to 7.99, and 8 to 11, respectively.

Table 1. Influence of grade on animal performance and carcass characteristics of beef cattle on an Alberta farm, 2003 to 2011

	Least square means, by grade				
Measurement	A (*n*=9)	AA (*n*=11)	AAA (*n*=10)	B4 (*n*=11)	Pr > F[z]
Average daily gain (kg day^{-1})	1.39	1.29	1.35	1.31	0.7298
Dry matter intake (kg day^{-1})	8.97	8.62	8.87	8.50	0.7694
Feed conversion ratio	6.54	6.86	6.53	6.56	0.8331
Age at finishing (days)	342.50	341.10	347.80	340.60	0.3157
Finishing days	136.70	135.30	121.50	138.90	0.6208
Age at slaughter (days)	478.60	475.90	469.00	478.90	0.9276
Ultrasound fat depth (mm)	6.39	6.72	9.53	7.14	0.0545
Ultrasound marbling score[y]	4.82*b*	4.94*b*	5.77*a*	4.90*b*	0.0042
Ultrasound rib eye area	69.40	66.77	65.39	70.98	0.3298
Carcass weight (kg)	244.34	235.69	227.09	226.36	0.4322
Grade fat depth (mm)	6.99*b*	9.04*b*	11.97*a*	8.57*b*	0.0102
Grade marbling score[x]	383.33*c*	442.17*b*	555.00*a*	436.00*b*	<0.0001
Grade rib eye area (cm^2)	83.39*a*	75.86*ab*	72.39*b*	71.84*b*	0.0370

[z] Probability of the F test, with significance at $P < 0.05$

[y] Ultrasound marbling score: 1-3.99=traces; 4-4.9=slight, 5-7.9= small to moderate; and 8-11=slightly abundant

[x] Grade marbling score: 300-399=traces; 400-499=slight; 500-799=small to moderate; and 800-1099=slightly abundant

a–c For each measurement, values lacking a common letter differ at $P < 0.05$

Statistical analyses

Statistical analyses performed on animal and carcass data included analysis of variance, and binomial and multinomial logit regression. Data were analyzed using the MIXED procedure in the Statistical Analysis Software (SAS) package (SAS Institute Inc., Cary, NC) with gender, grade and their interaction as fixed sources of variation and block designated random. Differences between means were identified using least square means, with significance at $P < 0.05$. For binomial logit regression, data for cattle that produced Canada A, AA and AAA carcasses were combined into one category (NORMAL) and compared to the data of cattle that produced Canada B4 carcasses (DARK) and the probability of being dark (yes or no) was modeled. For multinomial logit regression, the response variables were the four grades (A, AA, AAA and B4) and animal and carcass parameters were analyzed separately with gender as the treatment effect.

Results and conclusions

Dark cutting (Canada B4) carcasses had marbling scores and fat depths similar to those of the Canada AA carcasses but lower than that of Canada AAA carcasses (Table 1). Also, the average gREA of dark cutting carcasses was similar to that of Canada AAA and AA carcasses but less than that of Canada A carcasses. Grade had no effect on other animal or carcass characteristics (Table 1), although a significant interaction between gender and grade for live weight, showed that steers producing dark cutting (Canada B4) carcasses had a greater mean live weight than steers producing Canada AAA carcasses, while heifers that produced Canada B4 carcasses had a mean live weight less than that of heifers that produced Canada A grade carcasses (Fig. 1). Multinomial regression of live animal measurements showed that uFD tended to describe 25% of the variation in grade and indicated that cattle that cut dark were most likely to have an uFD similar to that of cattle that produced a Canada AA carcass. Results also showed that the highest probability of a Canada B4 or AA carcass occurring was associated with cattle with an uFD between 5 and 10 mm (Fig. 2), while at uFD above 10 mm a Canada AAA carcass was most likely to result. Multinomial logistic regression analysis of carcass data indicated that gMS ($P = 0.014$) described 72% of the variation in grade. This result was not unexpected, as grade is determined using marbling score; however these results (Fig. 3) substantiated that dark cutting carcasses were most likely to have a gMS similar to Canada AA carcasses (400 to 500).

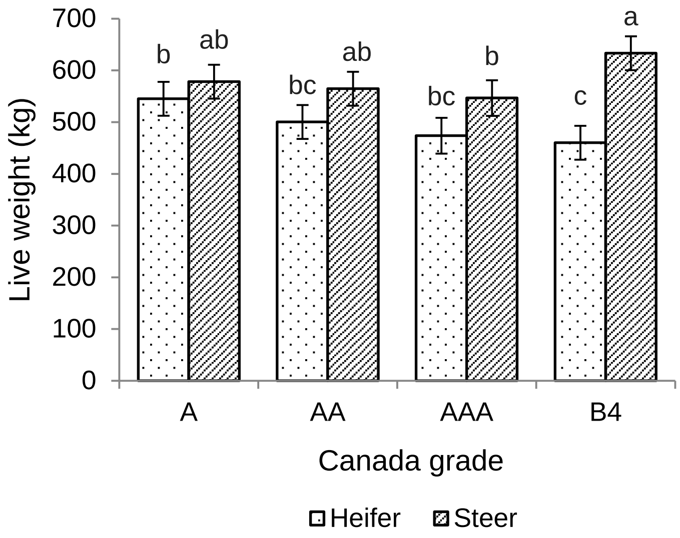

Figure 1. Influence of the interaction between grade and gender on live weight (kg) of cattle on three Alberta farms, 2003 to 2011. Within each grade, values with different letters differ at $P < 0.05$.

From the present study, we concluded that cattle that produced Canada B4 carcasses were most similar in live animal and carcass measurements to cattle that produced Canada AA carcasses. Subcutaneous fat depth was the most important live animal indicator of dark cutting risk but it did not adequately describe all incidences, substantiating that multiple factors contribute to dark cutting. Incorporation of weather conditions, growth hormone use, estrus activity, pre-slaughter handling, breed and gender into statistical models will likely improve prediction accuracy. Notably, the current study results indicated that finishing cattle to at least 10 mm back fat at the 12-13th rib to ensure a grade of Canada AAA will minimize the likelihood of dark cutting.

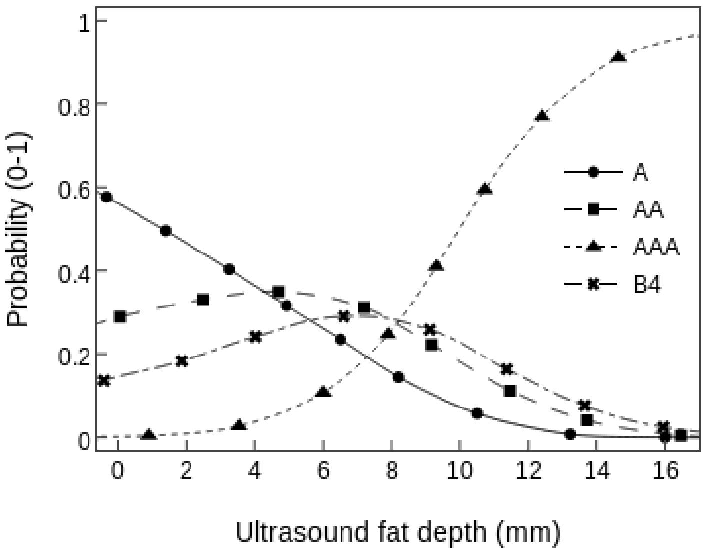

Figure 2. Predicted probabilities from multinomial logistic regression by grade describing the incidence of dark cutting (grade B4) as it relates to ultrasound fat depth (mm)

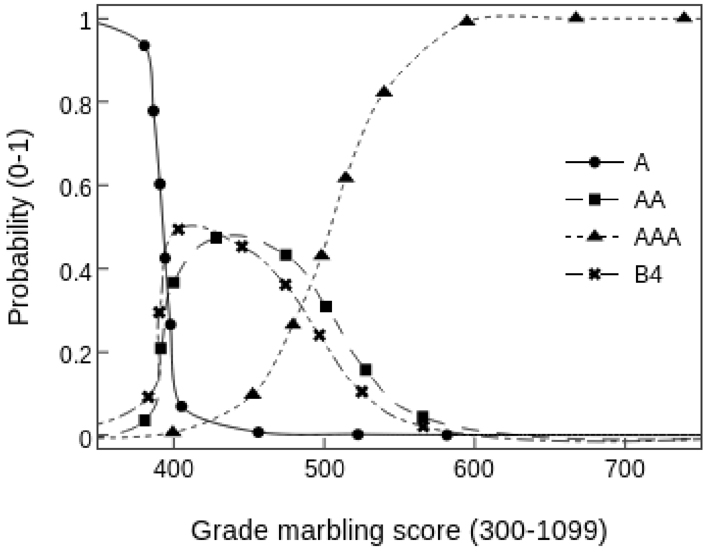

Figure 3. Predicted probabilities from multinomical logistic regression by grade describing the incidence of dark cutting (grade B4) as it relates to grade marbling score

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An abbreviated history of range management research, Kinsella Ranch: first 20 years, 1966-1986

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In 1961, Dr. Bill Corns, Head of the Department of Plant Science, was the first plant scientist at the new research ranch starting in 1961 applying herbicides to aspen forest. The writer arrived as a 27-year-old new Ph.D. graduate in June 1966. He had no experience in Canadian prairie rangelands, and was immersed in research within a week of arrival.

This writer started his research at Kinsella by being assigned a brush control project by Dr. Corns. From that first experiment he began to explore other options for managing brush emphasizing the use of natural grassland and woodland forages without having to eradicate them by the popular method of clearing and breaking. First, it required the development of an understanding of the grassland and forest ecosystems on the Kinsella Ranch (rangeland ecology), and second it required research into the various options for managing brush: herbicides, prescribed fire, and a combination of fire and grazing. Within a decade the primary emphasis focused upon the development of prescribed fire and grazing.

Kinsella as a practical field laboratory for teaching and research

From the beginning, research was the primary function of the Kinsella Ranch, but so also was teaching. This ranch is a living field laboratory for students. This is where students, regardless of the degree (bachelor's, master's, Ph.D., or Postdoctoral Fellow), could learn about the real world of rangeland ecology. Over the first 30 years, about 1200 students enrolled in the introductory range management class visited the ranch to spend a day learning about plant species, forage yields, carrying capacity and possible range improvements. The advanced range class, totaling about 250 students, went on to participate in a range ecology field exercise on the "471 hill", learning about the sequence of plant communities and associated soils, plant species, forage productivity, clipping plots and digging soil pits.

Early range research: range ecology, herbicides, fire and grazing to manage brush

Research into the ecology of plains rough fescue grasslands, snowberry shrublands and aspen forest ecosystems were studied over the period 1969-1974.

The coverage (%) of aspen and balsam poplar recorded on 26 one-mile transects at the Kinsella Ranch is presented in Table 1. Results from these repeatedly sampled transects associated with legal land surveys as early as 1903 showed average tree cover on the ranch increased from 7% in 1903 to 52% by 1963. The average annual rate of increase in tree encroachment per mile was 0.75% during the sixty year period since first settlement.

Table 1. Coverage of aspen and balsam poplar on one-mile transects at the Kinsella Research Ranch in 1903 and 1963 (Scheffler and Bailey 1972)

	1903 Legal Land Survey	1963 Aerial Photographs
Number of transects	26	26
Percent (%) coverage of trees	7	52
% of transects having trees	62	92

Why had aspen forest replaced so much rough fescue grassland at Kinsella? The first legislation passed by the new Northwest Territories government was the establishment of strict fire control regulations (Nelson and England 1971). Ottawa bureaucrats required that free land must be plowed, and fire does not travel far on plowed land.

Table 2. Average herbage production and livestock utilization within areas treated with herbicide and control areas in three vegetation types at the Kinsella Research Ranch, 1968-1969 (Hilton and Bailey 1972, 1974)

	Grassland		Small Aspen		Large Aspen	
	Herbicide	Control	Herbicide	Control	Herbicide	Control
Herbage (kg ha^{-}	1 220	1 138	1 166	273	760	108
Grazing use (%)	54	52	37	49	52	35

Aerial application of herbicide to manage aspen forest

Early attempts to control tree encroachment exploited what tools were readily available. A study on the effect of the repeated aerial application of 2,4-D and 2,4,5-T on the aspen parkland was initiated in July 1966 (Bailey and Hilton 1971), with the herbicide being applied in both 1966 and 1968. Mean herbage production and livestock utilization rates collected in 1968 and 1969 and are shown in Table 2. Notably, herbage production and livestock use remained the same in fescue grasslands. In both Small (i.e. young) Aspen and Large (i.e. older) Aspen communities, however, much more herbage was produced and consumed in sprayed areas, highlighting the competitive effects of trees on forage and cattle production. In 1969, the density of woody stems remained high in all three vegetation types. While herbicide treatment was successful in opening up the forest canopy, continued presence of a high density of brush remained a challenge.

Rangeland fire ecology and prescribed burning research

In November 1792, Peter Fidler left Buckingham House and passed near Kinsella travelling southwest by horse over upland grassland vegetation (Fidler 1793). During the winter of 1792-93, while living with his aboriginal hosts, he observed their management of grasslands. Their practices included frequent use of controlled burning. As a typical European, the use of broadcast burning alarmed him (Bailey and Bailey 1994). For many centuries, plains people had maintained grasslands by burning, and these habitats provided vital winter nourishment to the vast herds of bison that wintered in fescue grasslands of both the parkland and southwestern Alberta. All northern plains aboriginal tribes depended upon bison for food and shelter. However, to white European explorers and the settlers that followed, this was a very unwanted form of land management. Widespread use of fire had died out in Europe more than 2000 years ago. Thus, neither Peter Fidler, nor the Ottawa politician, nor the prairie homesteader, looked upon the use of prairie fire with favour.

Prescribed burning research began at the Kinsella Ranch in 1967 and continued for decades. The first few years of experimental burning were used to develop the skills and knowledge necessary to start, understand, manipulate, and extinguish the fires necessary to achieve management objectives. Initial fires were small and surrounded by firebreaks. It was soon learned that firebrands from burning woody shrubs and aspen were dangerous when the relative humidity (RH) was low. Firebrands from brush could ignite spot fires in dry grass many meters away, depending mostly upon wind speed and RH (Bailey 1979, Wright and Bailey 1982). Rarely would a firebrand cause a spot fire when the RH was above 45%. Relative humidity, wind, and fuel moisture content were critical factors regulating when and where prescribed burns could be safely undertaken. Inevitably, prescribed burning does carry risks that are not always accepted in some influential circles. Prescribed burning requires permits from local authorities, and much personal knowledge to manage and suppress the fire as needed (Bailey 1978, Wright and Bailey 1982).

During this time, significant progress was made on our understanding of fire ecology. Herbage of plains rough fescue grassland harvested in late summer after being burned in early spring was often the same as in unburned areas (Bailey and Anderson 1978). If the burn or mowing occurred in late spring however, when grass was growing rapidly, first year forage yield declined (Sinton-Gerling et al. 1995).

Bailey and Anderson (1980) found that fire temperatures were about twice as high (398°C) in snowberry shrub patches and aspen forest compared to in fescue grasslands (186°C; Table 3). In the 1980s, some aspen forests were completely burned to counteract widespread aspen expansion from the 1970s – a result of a climatic cycle of long winters, late springs and higher precipitation.

Table 3. Fire temperature, fuel loads and area burned in plains rough fescue grassland, western snowberry and aspen forest at the Kinsella Research Ranch in the 1970s (Bailey and Anderson 1980)

	Grassland	Snowberry shrubland	Aspen forest
Fire temperature (°C)	186	398	393
Total fuel (kg ha^{-1})	5 085	18 255	13 436
Standing fuel (kg ha^{-1})	657	11 017	1 732
Area burned (%)	90	100	53

Table 4. Comparison of biomass, soil organic matter (0-15 cm) and percent cover of plant species in unburned and burned aspen parkland grassland and shrubland at CFB Wainwright, 1976 (Anderson and Bailey 1980)

	Treatment	
Response	Unburned	Burned
Biomass (kg ha^{-1})		
Litter	4 502*	262
Shrub	3 217*	173
Grass	1 408*	719
Forb	117	295
Total living	4 742*	1 200
Soil organic matter (%)	8.1	11.5*
Plant species cover (%)		
Rough fescue	36*	18
W. porcupine grass	15*	11
W. snowberry	31*	2
Silverberry	4*	2
Wheatgrass	3*	1.2
Goldenrod	1.7	27*
Blunt sedge	1.1	18*
Buffalo bean	0.7	3*
Sandgrass	0.7	41*

*Indicates a significantly higher value at $P < 0.05$

At CFB Wainwright, an 8000-hectare [ha] area has been burned annually in very early spring since 1950. This practice limited summer wildfires caused by live firing in military exercises. This management kept aspen cover at similar levels to the 1903 legal land survey at Kinsella. The Camp Wainwright burned area was compared with adjacent unburned rough fescue grassland (Table 4). Biomass by category was significantly greater in unburned areas. Soil organic matter under this burning regime was greater in the top 15 cm of soil than in unburned areas.

It took this writer and Henry Wright of Texas ten years to prepare their fire ecology textbook (Wright and Bailey 1982). Much of the research information relevant to the Northern Great Plains in Chapters 1, 2, 5, and 16 originated from research and experience at the Kinsella Ranch. The burning prescriptions presented in Chapter 16 for burning rough fescue grassland and aspen forests are quite similar to prescriptions used today.

Prescribed burning and prescribed grazing to manage the aspen parkland

In a 1978 pilot study, a two-year old burned aspen forest produced 6270 kg ha^{-1} of woody sprouts, forbs, grasses and sedges. The area was fenced and when steers grazed all available palatable biomass, they removed 4140 kg ha^{-1} of forage leaving behind 2130 kg ha^{-1} of standing woody stems. In another test comparing prescribed burning alone to a combination of burning and grazing, native understory herbage produced 625 kg ha^{-1} the year after the spring burn in the absence of grazing. In the presence of cattle, herbage doubled to 1110 kg ha^{-1} from the first to the second year (Table 5). This study illustrates the marked influence of a short-duration heavy grazing treatment, followed by rest from grazing for the remainder of the year, in facilitating forage increases. In contrast, areas burned but not grazed initially were returned to forest by year four and herbage yield fell to 200 kg ha^{-1}.

On May 15, 1979, a prescribed burn was conducted to further study the use of prescribed burning to top-kill aspen and shrubs (Table 6). It was followed by broadcasting seed into the ash seed bed (Fitzgerald and Bailey 1984). Heavy grazing took place in early July for the “early graze” treatment and in late August for the “late graze” treatment. After the 1979 late grazing treatment, an unusually warm period lasted through September, and aspen sprouted and grew until early October when severe frosts probably killed aspen suckers and their root system. Thus aspen regrowth biomass for the late grazing treatment was very low the following year compared to the early grazed treatments (Table 6), an anomaly that has never been repeated.

Table 5. Forage and brush regrowth production (kg ha^{-1}) for four years following burning in aspen forest at the Kinsella Research Ranch (Bailey 1979)

	Years since burning				
Regrowth	1	2	2[z]	3	4
Herbage	520	625	1 110	600	200
Woody	1 380	3 070	1 200	7 900	12 540

[z] Heavily grazed by cattle/whitetail deer three months after burning (in Year 1)

Table 6. Yield (kg ha^{-1}) of grasses and forbs, aspen, western snowberry and wild rose following a May 1979 prescribed burn, and early (E) or late (L) grazing by cattle at the Kinsella Research Ranch

	May 1980		August 1980		July 1981	
Species	E	L	E	L	E	L
Grass + forbs	381	175	1 117	791	1 191	1 031
Aspen	615	70	953	56	1 640	136
W. snowberry	417	631	524	1 364	792	1 394
Wild rose	210	466	224	605	435	865

Wagon Wheel Study: Comparison of Spray & Burn vs Clear & Break

In the 1980s, an experiment designed to compare three contrasting management systems for aspen management was initiated at the Kinsella Ranch. Management approaches were to: 1) leave the landscape as it was (Control); 2) remove all vegetation, disc and reseed to establish an agronomic mix (Clear and Break); and 3) top-kill aspen trees with herbicide and fire, and establish an understory of forage and browse (Spray and Burn). The study site was subdivided into 20-ha paddocks in a wagon wheel arrangement to compare Spray and Burn (S&B; *n* = 3), Clear and Break (C&B; *n* = 3), and two untreated fields in a field scale experiment (Bailey et al. 1985). The three S&B fields had an aerial application of 2,4-D applied June 1980, and were then burned on April 22, 1981. A few days after the fire, a seed mixture of tame grasses and alfalfa was applied by helicopter. Bulldozers cleared the three C&B fields in March 1980, followed in summer by breaker disc to till the land. In spring 1981 the C&B fields were drill seeded with a mixture of grasses and alfalfa. Heavy short duration rotational grazing was applied in each field to each treatment from 1981 through 1983.

Live weight gain of calves ranged from 1.0-1.3 kg day^{-1} in all treatments. Browse constituted 77, 54 and 33% of cattle diets in S&B paddocks in 1981, 1982, and 1983, respectively. Also in the S&B treatment, 42% of aspen trees were dead or dying following the 1981 fire; by 1983, the total number of dead or dying aspen had risen to 74%.

Forage yield data are presented in Table 7. On average, the Control produced about 2000 kg ha^{-1} of total herbage and browse each year. C&B started out in 1981 with 6000 kg ha^{-1} and declined to 3500 kg ha^{-1} by 1983, the S&B produced 2500 kg ha^{-1} in 1981, and leveled off at 5400 kg ha^{-1} in 1982 and 1983. The estimated cost of treatments in 1981 was: Control = 0; Clear & Break = \$390/hectare; and Spray & Burn = \$130/hectare.

Overall, the S&B method offered an effective alternative method for converting aspen forest into more productive rangeland for livestock, while preserving some rough fescue grasslands and native species within the modified aspen groves. It is likely that the herbicide application contributed little to this experiment.

Table 7. Comparison of herbage and browse production (kg ha^{-1}) in Spray and Burn, Clear and Break and Control brush management treatments, followed by heavy rotational grazing at the Kinsella Research Ranch, 1981-1983

	Control			Spray and Burn			Clear and Break		
Year	Herb	Browse	**Total**	Herb	Browse	**Total**	Herb	Browse	**Total**
1981	400^{z}	1600^{z}	**2000^{z}**	400	2100	**2500**	5200	800	**6000**
1982	400	1600	**2000**	2400	3000	**5400**	3500	900	**4400**
1983	400	1200	**1600**	2800	2600	**5400**	2700	800	**3500**

^{z}Estimated in 1981

Closing thoughts

Professors are expected to be research leaders to benefit society. Sometimes our studies are not popular with certain parts of society. Research into the use of prescribed burning and the maintenance of natural vegetation on parkland rangelands falls into that category, as did Roy Berg's cross-breeding experiments in the 1960s.

Only a cross-section of the range research completed from 1966-1986 is presented here. Studies into the response of plains rough fescue grasslands to grazing intensity and season, the benefits of rotational grazing vs continuous grazing of brome-alfalfa (forage yield, animal gains and contributions of certain key minerals), as well as several studies of silverberry – a nitrogen fixing shrub – await another time to be added to the history of range research at the Kinsella Ranch.

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Introducing the University of Alberta's Mattheis Research Ranch

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The University of Alberta acquired the Mattheis Research Ranch, located approximately 40 km north of Brooks, Alberta, following the generous donation of the property by U of A alumni Edwin and Ruth Mattheis in 2010. Much like the broader southern Alberta landscape in which it is embedded, the ranch encompasses a diversity of ecosystems that are managed for multiple uses, including cattle grazing, biodiversity and wildlife conservation, mineral extraction and irrigation agriculture. The ranch represents a significant opportunity for researchers to explore various phenomena underlying important issues facing ranchers and other land managers throughout the region. Further, this new facility complements the Kinsella Research Ranch by giving researchers the opportunity to replicate their work in two distinct environments (Aspen Parkland and Mixedgrass Prairie), and significantly bolsters the University of Alberta's overall capacity to address today's key questions about the ecology and management of rangeland systems. Having access to a variety of physical environments is particularly important for researchers looking to identify beneficial management practices that are generalizable to all rangelands. The recent closure of the Agriculture and Agri-Food Canada Onefour and Stavely research sub-stations in Alberta makes the Mattheis Research Ranch even more important for supporting ongoing rangeland research, education and technology transfer.

Natural and human history

Located on the banks of the Red Deer River, the Mattheis Research Ranch covers approximately 5000 hectares [ha], which includes about 300 ha of irrigated land and 700 ha of tame pasture, with the balance being native rangeland. Vegetation diversity is particularly high across the property. Alluvial floodplains with cottonwoods adjacent to the Red Deer River give way to steep river breaks, and eventually to uplands dominated either by loamy Mixedgrass Prairie plant communities or extensive stabilized sand dune formations (Fig. 1).

Figure 1. Ecosystem types represented within the Mattheis Research Ranch (clockwise from top left): alluvial floodplains, Red Deer River coulees, loamy Mixedgrass Prairie uplands and vegetated sandhills

A variety of riparian areas are present throughout the ranch, some of which are supplemented by an influx of water on the southwestern edge of the property by overflow irrigation water. This moisture supply contributes significantly to vegetation development, aiding woody species establishment and the persistence of a variety of wetlands, which range from permanent lakes to ephemeral ponds and meadows. A relatively shallow water table across much of the property also allows plant species characteristic of more mesic environments to persist throughout, contributing to high overall diversity. Dominant grass species on the property's uplands include needle-and-thread grass, (*Hesperostipa comata*), western wheatgrass (*Pascopyrum smithii*), Junegrass (*Koeleria macrantha*), blue grama (*Bouteloua gracilis*) and sand grass (*Calamovilfa longifolia*). Plant communities also include a rich variety of forbs, as well as shrubs such as prickly rose (*Rosa acicularis*), western snowberry (*Symphoricarpos occidentalis*) and thorny buffaloberry (*Shepherdia argentea*). Wildlife on the ranch includes pronghorn antelope, mule and whitetail deer, elk and moose, Sprague's pipit and many other prairie songbirds, and migratory waterfowl. More than 90 species of birds were documented on the property as part of a recent research project.

The variety of habitat types present within the Mattheis Research Ranch not only support a diversity of flora and fauna, but likely also contributed to the site's rich human history. Prior to European settlement, there is evidence that the area was used extensively by First Nations people for both travel and hunting, with archaeologists having documented several Medicine Wheels, tipi rings and cairns on and around the property, as well as a bison kill site at the south end of the ranch along Matzhiwin Creek. Later, the famous cowboy John Ware chose the site as the new location of his Three Walking Sticks Ranch. Having driven cattle eastward from his original homestead near Millarville in 1900, Ware lived and worked on and around what is now the Mattheis Research Ranch until his death following a riding accident in 1905. In 1977, Edwin and Ruth Mattheis purchased the ranch and continued to manage it primarily for cattle production, as had been the case since the property was originally settled by Ware.

Over time, the human footprint on the ranch and surrounding area has increased. In the 1940s, Ducks Unlimited Canada began constructing a complex of irrigation-fed wetlands to create habitat for waterfowl and other migratory birds. This network of constructed wetlands now covers thousands of hectares in southern Alberta, and approximately 400 ha of the western portion of the Mattheis Research Ranch (Fig. 2). Water circulates through these wetlands before being delivered to the rest of the ranch via pumps, conveyance ditches, and shallow earthen dikes. Such infrastructure is commonly found throughout southern Alberta, as irrigation agriculture has proliferated across the region. Energy infrastructure is also prevalent; several high voltage transmission lines and a network of oil and gas infrastructure are present on the Mattheis Research Ranch, including over 100 active well leases, in addition to numerous compressor stations, pipelines and access roads.

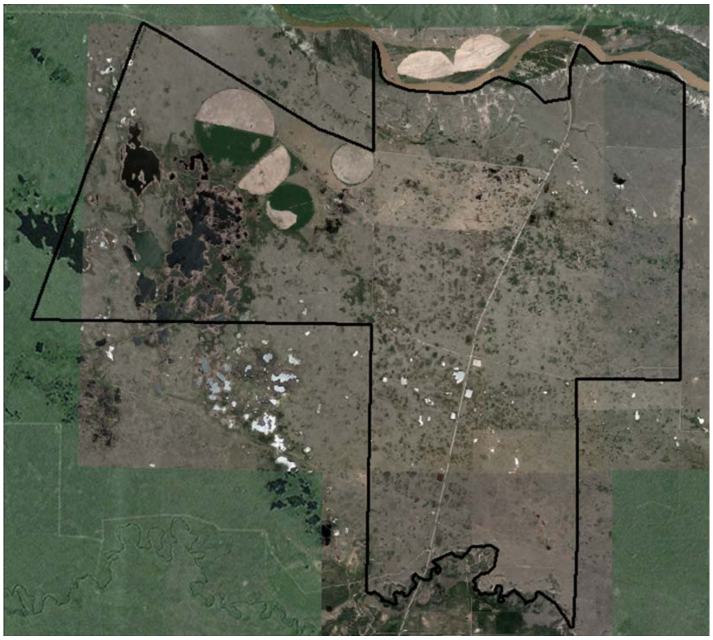

Figure 2. Aerial view of the University of Alberta's 5000-hectare Mattheis Research Ranch, with black line indicating property boundary. The ranch is bisected by Alberta Highway No. 36, and abuts the Red Deer River in the north and Matzhiwin Creek in the south. The western portion of the ranch encompasses Ducks Unlimited Canada's Verger Project, part of a larger network of irrigation-fed wetlands in southern Alberta. Imagery courtesy of Alberta Environment and Sustainable Resource Development.

Emergence as a key facility for rangeland research

The expansion of cultivated acres, energy development, urban sprawl and rural subdivision all contribute to fragmentation of Alberta's native prairie landscapes. Recognizing that their ranch was a unique part of a large, contiguous tract of native rangeland, Edwin and Ruth Mattheis set out to conserve its ecological value by protecting the property from further cultivation or subdivision, while simultaneously ensuring that it be used to advance knowledge and understanding of rangeland ecology and management, including sustainable cattle production.

The Mattheis family's donation to the University of Alberta has created significant opportunities for researchers and students of Western Canadian rangelands. The Mattheis Research Ranch continues to be managed as a working ranch, and is therefore an ideal location for conducting long-term research and monitoring with real-world applications. Researchers are currently investigating a wide variety of topics, from the implications of climate change on grassland ecosystem function, to beef cattle efficiencies and the effects of various land management practices on plant and animal diversity, as well as rangeland productivity (Fig. 3). Furthermore, industrial development on the property offers many opportunities to assess various re-vegetation and reclamation practices following disturbance.

Figure 3. Edwin and Ruth Mattheis give the author a tour of the Mattheis Research Ranch, June 2013 (top); Drs. Edward Bork and Cameron Carlyle work with students Ruth Greuel and Greg Boorman to harvest biomass samples, June 2012 (bottom). Photos courtesy of R. Gruel and T. Broadbent.

A newly emerging area of research that is actively being pursued on the Mattheis Research Ranch is the quantification of environmental goods and services (EG&S) from rangelands. EG&S are benefits provided by rangelands to society, and include things such as water storage and purification, biodiversity conservation, carbon storage and greenhouse gas mitigation, and the maintenance of habitat for consumptive and non-consumptive wildlife. Valuation of EG&S has the potential to provide significant revenue diversification from rangelands, and in the process, may increase profitability of ranchers, particularly during times of economic uncertainty associated with the beef industry.

Finally, people of all ages and backgrounds are benefiting from the university's acquisition of the Mattheis Research Ranch. Undergraduate and graduate students use the property to learn everything from basic ecology, to the practical considerations of managing for multiple uses in working rangeland landscapes. The site is also being used for technology transfer to producers and other industry professionals, and has attracted visitors from across the country and around the world who are interested in the ecological, economic and social sustainability of rangelands.

In acknowledgement of the magnitude of the Mattheis' gift, and the opportunities it represents, the University of Alberta established the Rangeland Research Institute in 2011. The institute now serves as a key mechanism bringing together expertise from within the university and beyond to conduct groundbreaking research and teaching on the Mattheis Research Ranch, the Kinsella Research Ranch, and at other facilities throughout Alberta. You can stay apprised of the institute's work by visiting rri.ualberta.ca.

Seasonal availability of cool and warm-season herbage in Northern Mixedgrass Prairie

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Figure 1. Comparison of typical loamy (left) and sandy (right) Mixedgrass Prairie range sites (largely stabilized dune complexes) found across the Mattheis Research Ranch. Photos courtesy of C. Carlyle and A. Tastad.

A key challenge in managing beef production from rangelands is matching natural changes in the seasonal availability of herbage production with ongoing grazing activities throughout the growing season. Ideally, changes in seasonal growth and associated forage supply provide a steady supply of nutrition that coincides with all phases of the beef production cycle, including spring green up, peak lactation in early to mid-summer, and late summer when cattle begin putting on energy reserves in preparation for winter. However, forage supply is variable in space and time, being regulated by changes in soil conditions, including resource availability (water and nutrients), combined with associated changes in plant species composition.

Among the critical soil factors altering rangeland productivity is texture, which has a profound impact on moisture infiltration, water holding capacity, nutrient availability, and plant rooting opportunities. While sandy soils tend to have lower water- and nutrient-holding capacity than clay soils, sandy soils allow for deeper root penetration, which can facilitate water use from sub-soil layers, including moisture that may have accumulated over the preceding dormant season. In addition, sandy soils have the benefit of facilitating rapid water entry into soil, allowing moisture to promptly escape evaporation, a process that remains particularly important when rainfall events are small.

Variability in herbage production over time is regulated largely by changes in growing conditions, which in the case of the Northern Mixedgrass Prairie, is primarily precipitation and the extent of moisture deficit during the growing season. Moisture deficits frequently constrain forage production and grazing opportunities in the Mixedgrass Prairie of Western Canada (Willms and Jefferson 1993). Although the majority of precipitation (60%+) occurs during the summer and fortuitously coincides with peak water demand, dormant season precipitation contributes positively to soil moisture recharge and subsequent years plant growth (Smoliak 1986).

Little information exists quantifying seasonal herbage availability during the growing season in the Northern Mixedgrass Prairie, including how changes in range site conditions (namely soil texture) and plant composition alter these patterns. As grasslands in this region include a mix of cool- and warm-season species, forage availability may be further modified by localized changes in vegetation composition. Grasslands dominated by cool-season grasses typically experience a pulse of early spring growth, while those dominated by warm-season grasses may produce disproportionately more biomass in mid to late summer, collectively altering opportunities for cattle grazing.We quantified changes in forage availability throughout the growing season across four Northern Mixedgrass sites at the Mattheis Research Ranch, situated 40 km north of Brooks, AB. Specific objectives were to: 1) compare and contrast total herbage production and seasonal forage dynamics throughout the growing season; 2) quantify the contribution of cool and warm-season grasses to seasonal production; and 3) identify implications for cattle grazing.

Methods

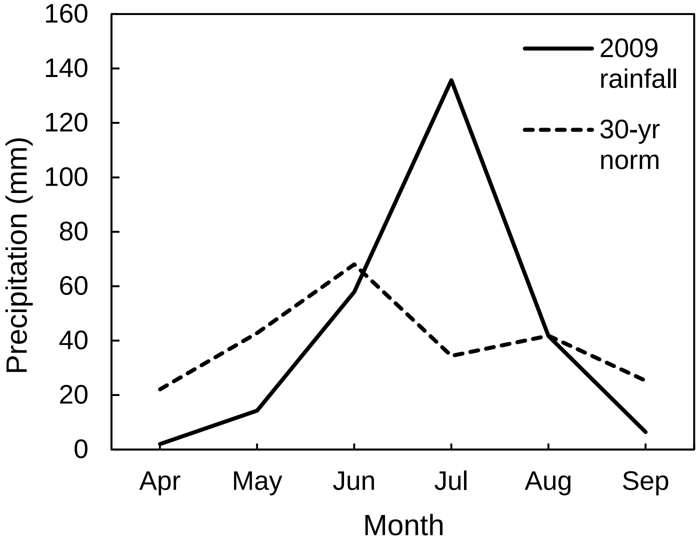


Figure 2. Rainfall patterns at the Mattheis Research Ranch in 2009 and comparison with the 30-year long-term averages (1980-2010)

Seasonal production was quantified at each of two loamy prairie and two sandy prairie sites in 2009 (Fig. 1). In early May, plots were set up in a randomized complete block design, with five plots harvested at each site on a monthly interval from early June through early September, inclusive. Cool-season grasses were largely needle-and-thread grass (*Hesperostipa comata*) and western wheatgrass (*Pascopyrum smithii*), with lesser amounts of other grasses such as junegrass (*Koeleria macrantha*). Warm-season grasses were comprised primarily of blue grama (*Bouteloua gracilis*) and sandgrass (*Calamovilfa longifolia*). Rainfall was below average in spring of 2009, near normal in June and late summer of that year, but remained well above-average in July (Fig. 2).

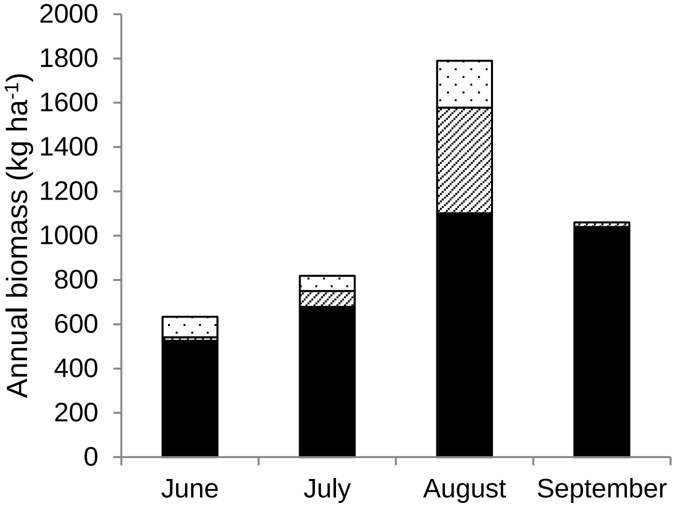
Plots were 50 cm x 50 cm in size and harvested to ground level, sorted to litter (carryover growth from the previous year), broadleaf forbs, cool-season grasses and warm-season grasses. Samples were dried, weighed and converted to kg ha^{-1}. Total biomass and the biomass of each vegetation component were analyzed using an analysis-of-variance with range site and sampling month as fixed factors to characterize spatial and temporal variation in productivity. To isolate the additive effect of litter on production, litter biomass was included as a covariate in the initial analysis, and subsequent regressions were performed between litter levels and grass biomass.

Results and discussion

Peak herbage production did not differ between the loamy (1707 kg ha^{-1}) and sandy (1461 kg ha^{-1}) range site, reaching a maximum during August for both (Fig. 3). However, temporal patterns of current annual growth over the growing season were dissimilar between sites. During early June, loamy and sandy sites had reached 39% and 48% of their peak annual biomass, respectively. By early July, this proportion had increased only modestly to 52% on the loamy soil, but risen sharply to 87% of peak biomass on the sandy sites; the latter therefore experienced more rapid plant development and provided greater late spring and early summer grazing opportunities. In contrast, biomass on loamy sites increased rapidly in July prior to early August sampling (Fig. 3). By early September, available biomass declined to 62% and 74% of peak biomass on the loamy and sandy sites, respectively, suggesting that opportunities for livestock production had universally begun to decline.

Broadleaf forb biomass did not differ between range sites, and comprised less than 16% of biomass at all sampling times, regardless of range site (Fig. 3). Forbs rapidly disappeared during late summer (August), highlighting their inability to provide late season forage. Cool-season grasses formed the majority of biomass available (60-61%), and did not differ between range sites (Fig. 3), starting at 502 kg ha^{-1} in June, increasing to 708 kg ha^{-1} in July, and peaking at 953 kg ha^{-1} in August.

A. Loamy Sites ($n = 2$)



B. Sandy Sites ($n = 2$)

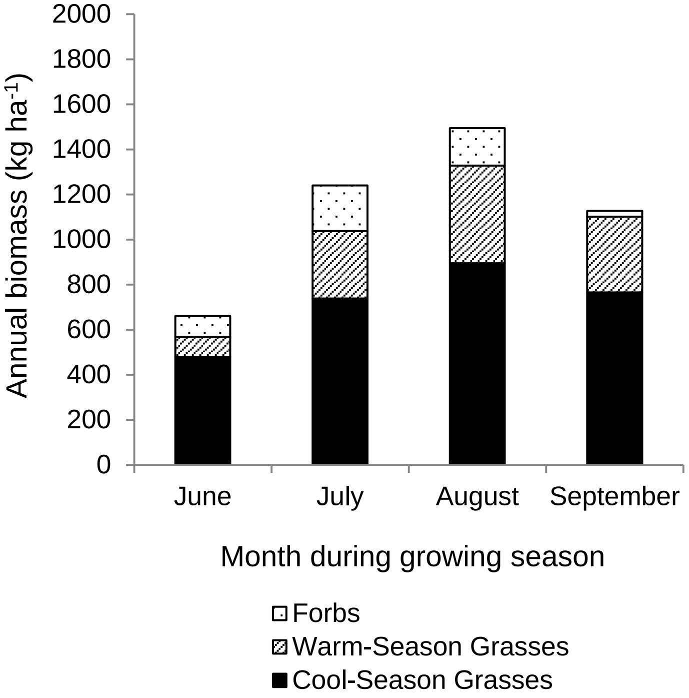


Figure 3. Comparative contribution of forbs, cool-season grasses and warm-season grasses, to total production at each of the (A) loamy and (B) sandy range sites at the Mattheis Research Ranch, 2009

Warm-season grasses contributed much less biomass than cool-season grasses (27-29% of total biomass) in our assessment (Fig. 3), despite low spring rainfall that likely impeded early-season growth of the latter. Moreover, high July rainfall should have been favorable for warm-season grasses, and more normal precipitation may be expected to favor cool-season grasses to an even greater extent. Unlike cool-season grasses, warm-season biomass also differed with soil conditions. Mean monthly warm-season grass production on the sandy sites (290 kg ha^{-1}) was greater ($p = 0.09$) than that on loamy range sites (146 kg ha^{-1}), a pattern that did not vary with sampling time throughout the growing season ($p = 0.44$). Warm-season grass biomass did persist better into September on the sandy range site than the loamy counterpart (Fig. 3), likely due to a greater contribution of tall-statured sandgrass rather than blue grama, the latter of which can occupy a large area but contribute limited biomass in Mixed Prairie grasslands (Smoliak 1965).

Notably, the inclusion of litter as a covariate in the analysis of biomass was significant for several vegetation components. While litter was positively associated with total herbage ($p = 0.048$), litter was particularly important for increasing cool-season grass ($p = 0.0009$) rather than forb ($p = 0.75$) biomass. Inclusion of litter by sampling time effects in our analysis of cool-season grass biomass ($p = 0.004$) indicated that although litter impacts were consistently positive ($R^2 \geq 0.12$), they were more apparent during August and September ($R^2 = 0.17$ and 0.23), the second half of the growing season (Fig. 4). This is not surprising, as litter is known to conserve moisture and increase opportunities for plant growth (Willms et al. 1986; Deutsch et al. 2010), thereby extending the growing season. While no overall effect of litter was evident on warm-season grass biomass ($p = 0.27$), this response did vary somewhat over time, with warm-season grasses weakly declining with more litter, particularly in July (data not shown). Although the reason for this surprising response remains unknown, excess litter may have impeded green-up of warm-season grasses that rely on high temperatures for favorable growth. As cool-season grasses supply the majority of biomass in these grasslands, and were positively influenced by litter, we emphasize that the maintenance of litter should remain an important objective for rangeland managers. Finally, litter levels also differed between range sites ($p = 0.006$), being 25% greater in the loamy sites (2109 kg ha^{-1}) than the sandy areas (1684 kg ha^{-1}). No litter by range site effects were detected.

Implications

Overall, these results provide clarification of the relative contribution of different vegetation components to seasonal grazing opportunities in the Northern Mixedgrass Prairie, including the key role of cool-season and warm-season grasses, and the positive influence of litter in maintaining forage production. Specifically, our findings indicate that cool-season grasses provide the majority of grazing opportunities in the Northern Mixedgrass Prairie, and should be a priority for conservation when developing grazing plans. Similarly, moderate stocking rates will promote litter retention, aid water cycling, and help maintain cool-season grass production.

Acknowledgements

This study would not have been possible without the cooperation and support of Edwin and Ruth Mattheis, whose generosity and inspiration will be the source for many transformative changes to rangeland management in the years to come. Additional support was provided by the University of Alberta.

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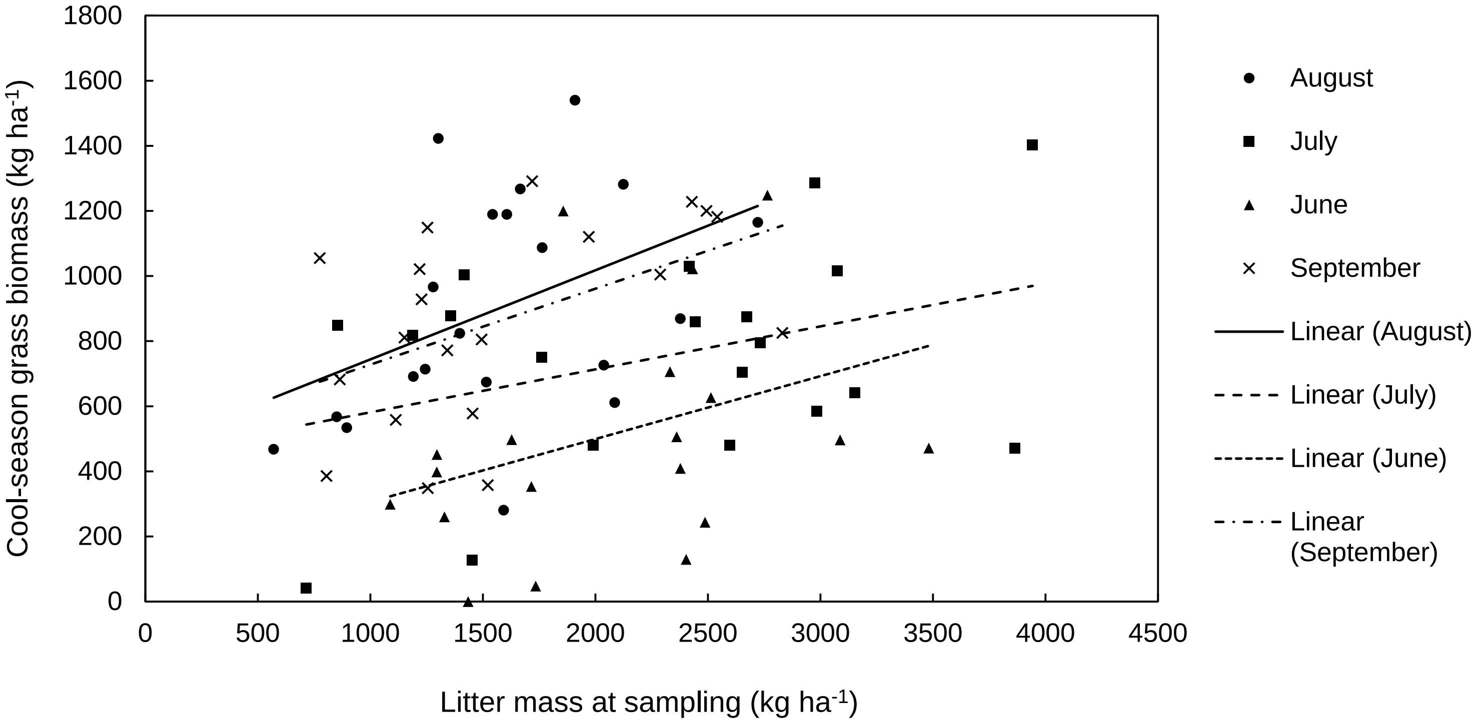

Figure 4. Total cool-season grass production at the Mattheis Research Ranch was positively related to litter mass at all four sampling times, particularly August and September of 2009 (top two lines)

Pasture forage and compositional dynamics in response to defoliation regime and moisture

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Controversy exists over the benefits of rotational grazing in facilitating increases in herbage growth in support of livestock production. Recent synthesis studies have suggested the perception that rotational grazing enhances plant growth relative to continuous grazing may not be justified (Briske et al. 2008). However, more recent reviews have provided alternative explanations for how and when rotational grazing may benefit livestock producers (Teague et al. 2013). In any case, strategies of rotational and time-controlled grazing (the latter being a key component of holistic resource management; Savory 1999) continue to be used by many cattle producers, necessitating answers to questions such as: "When, where and how can intermittent defoliation assist forage growth?".

To address this question in central Alberta, we conducted investigations into patterns of grass growth and yield response in relation to varying intensities and frequencies of defoliation, in combination with two levels of available moisture supply. Our premise was that increases in moisture may increase the potential for plant regrowth following defoliation, and that bunchgrasses may be less likely to benefit from regrowth opportunities compared to sodgrasses. Therefore, our working hypothesis was that when abundant moisture is made available to sodgrasses that are highly tolerant of defoliation and have a high capacity for regrowth, this will enhance opportunities for plant growth and increase forage yields. Here we provide a summary of select results of a more detailed report outlined by Broadbent (2013).

Methods

We used a combination of two studies, including greenhouse and field investigations, both of which controlled defoliation intensity and frequency, in combination with moisture. The greenhouse investigation allowed tight control over all growing conditions, including removing the influence of neighboring vegetation, thereby isolating the influence of the primary treatments. The greenhouse study compared the influence of defoliation frequency (every three vs every six weeks) and cutting height (3 vs 15 cm) on accumulated grass yield under both high and low soil moisture. In 'high' treatments, moisture was sustained near field capacity, while 'low' treatments were subject to intermittent reductions in moisture to levels likely to impede plant growth. Defoliation regimes included HIHF (high intensity–high frequency, representing continuous grazing), HILF (high intensity–low frequency, representing mob grazing), LIHF (low intensity–high frequency, representing short duration grazing), and a deferred treatment where grasses grew undisturbed until the end of the study.

In the greenhouse investigation, grasses from eight species, representing natural pairs based on phylogenetic associations or similarities in geographic home ranges, were tested. A total of four bunchgrasses (meadow brome [*Bromus riparius*], foothills rough fescue [*Festuca campestris*], western porcupine grass [*Hesperostipa spartea*], and needle-and-thread grass [*Hesperostipa comata*]) and four sodgrasses (smooth brome [*Bromus inermis*], plains rough fescue [*Festuca hallii*], western wheatgrass [*Pascopyrum smithii*], and northern wheatgrass [*Elymus lanceolatus*]) were grown from seed, then transplanted four plants per pot, and exposed to the eight moisture and defoliation treatment combinations described above for 12 weeks. Five replicates of each treatment combination were grown in deep pots (46 cm) enabling largely unimpeded root growth. Measurements included accumulated shoot biomass through final harvest, root biomass at harvest, and changes in tiller demography (i.e., vegetation reproduction) throughout the trial. Here we limit our presentation of data only to root and shoot biomass of four species.

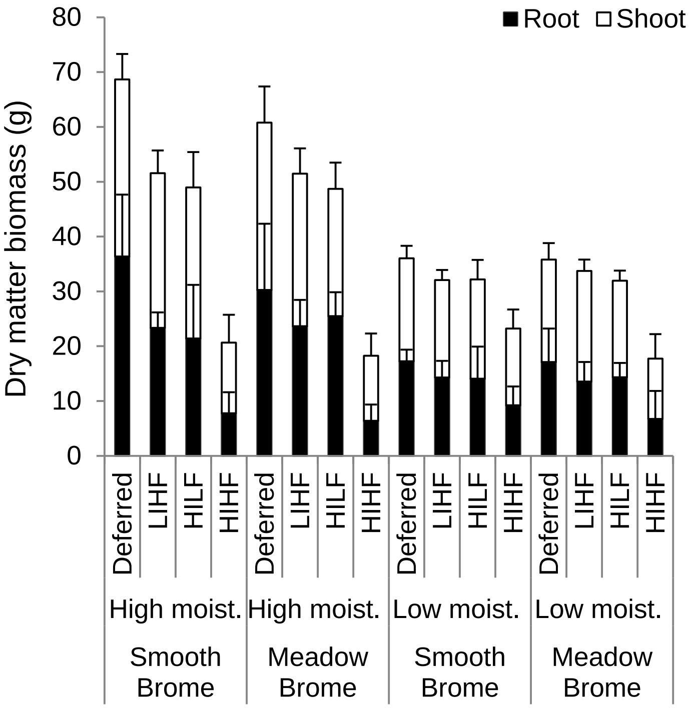

Figure 1. Accumulated shoot and final root biomass in smooth brome (*Bromus inermis*) and meadow brome (*Bromus riparius*) relative to high and low moisture, and various defoliation regimes (deferred, low intensity–high frequency [LIHF], high intensity–low frequency [HILF], and high intensity–high frequency [HIHF] defoliation)

In the associated field study, we examined the impact of defoliation and moisture regimes throughout the growing season in replicated plots within each of two study sites at the Mattheis Research Ranch situated in the Mixedgrass Prairie of southeast Alberta. Sites differed modestly in composition and soil conditions, with one being a more mesic community dominated by needle-and-thread grass and western wheatgrass on a loam soil, while the other was a community with more blue grama grass (*Bouteloua gracilis*), and less needle-and-thread and wheatgrass on a sandier soil (Coupland 1961). Defoliation regimes were similar to those implemented in the greenhouse study, but were applied to all vegetation within 1 m x 1 m permanent plots. To eliminate moisture as a limiting factor for growth, monthly summer (May through August) moisture was increased to 150% of normal in half of the plots. Measures taken in each of three successive years (2010-2012) included: accumulated plant biomass by growth form throughout the growing season; vegetative reproduction (tillering) in needle-and-thread and western wheatgrass, and their biomass; plant community composition at peak growth (August); and environmental conditions (light, soil moisture; Broadbent 2013). Here we again concentrate on plant biomass responses.

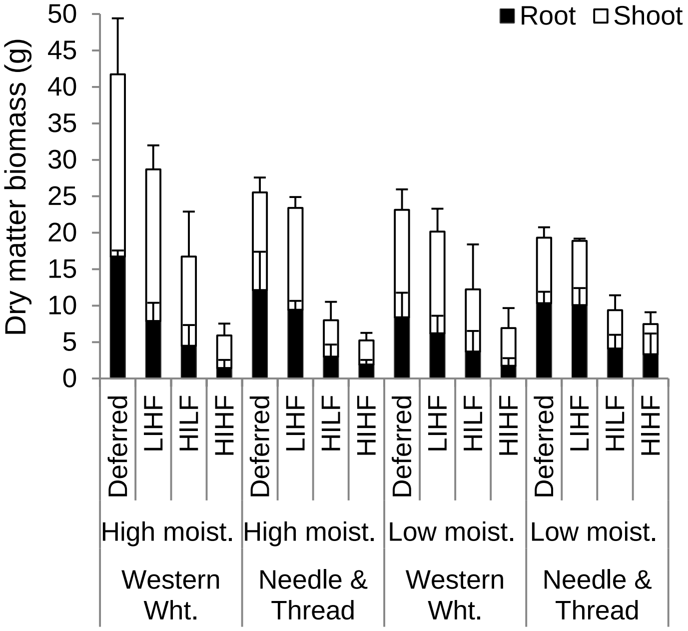

Figure 2. Accumulated shoot and final root biomass in western wheatgrass (*Pascopyrum smithii*) and needle-and-thread grass (*Hersperostipa comata*) relative to high and low moisture, and various defoliation regimes (deferred, low intensity–high frequency [LIHF], high intensity–low frequency [HILF], and high intensity–high frequency [HIHF] defoliation)

Results and discussion

Greater grass biomass yields were produced in the greenhouse study under high moisture, a pattern consistent across all plant species, including introduced agronomics common in the Aspen Parkland (brome grasses; Fig. 1) and those native grasses critical for supplying forage in the Mixedgrass Prairie (Fig. 2). Similarly, while deferred defoliation consistently maximized grass biomass due to uninterrupted expansion of plant growth throughout the study period, increasing defoliation intensities and frequencies reduced biomass, with plants experiencing HIHF defoliation demonstrating the lowest forage yields. Additionally, defoliation frequency had a more negative impact on accumulated grass shoot yield than intensity within the greenhouse environment, as grasses subject to HILF defoliation produced more biomass than those exposed to LIHF defoliation, particularly under high moisture (Figs. 1 and 2).

Under field conditions, biomass yields of needle-and-thread grass did not differ with moisture addition, highlighting the relatively fixed (i.e., pre-determined) growth habit of this species. In contrast, western wheatgrass increased significantly in biomass from 120 g m^{-2} to 178 g m^{-2} with water addition over the three growing seasons ($P < 0.05$). Notably, patterns of accumulated biomass for each of the two focal grass species exhibited a trend in the field study similar to that in the greenhouse investigation, being maximized under deferred defoliation, and declining through the HILF, LIHF and then the HIHF defoliation regimes (Fig. 3).

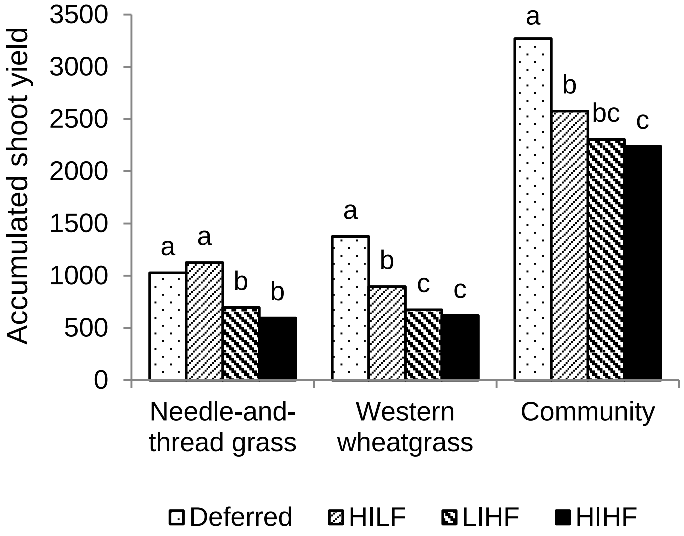

Figure 3. Comparison of accumulated shoot yield of needle-and-thread grass (*Hersperostipa comata*; mg $plant^{-1}$) and western wheatgrass (*Pascopyrum smithii*; kg ha^{-1}) averaged across both study sites, and total plant community biomass (kg ha^{-1}) within the lowland site, in relation to the various defoliation regimes (deferred, low intensity–high frequency [LIHF], high intensity–low frequency [HILF], and high intensity–high frequency [HIHF] defoliation). Within a response variable, means with different letters differ at $P < 0.05$.

Consistent with expectations, total community biomass increased significantly with water addition from 1272 kg ha^{-1} to 2196 kg ha^{-1} on the upland site, and from 2192 kg ha^{-1} to 3012 kg ha^{-1} on the lowland site. While community biomass remained relatively stable among the four defoliation regimes on the upland site, suggesting other species (e.g., broadleaf forbs) compensated for biomass reductions under defoliation, marked differences in accumulated biomass remained apparent among the defoliation treatments of the lowland site (Fig. 4). Once again, the HIHF defoliation regime was associated with the lowest forage yield, with the deferred treatment greatest in yield.

Implications

Overall, our results indicate that both defoliation frequency and intensity, together with moisture supply, have the ability to regulate grass growth responses, leading to sharply contrasting forage production and associated potential to support livestock grazing. These results help explain how and when rotational grazing may lead to more favorable plant production in select grasslands and production systems. Further research is needed to more fully test the forage growth dynamics and production responses likely to occur under operational grazing systems at the practical ranch 'scale' (Teague et al. 2013).

Acknowledgements

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How will climate change affect grazing resources and plant diversity in the Canadian prairies?

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Climate variability has long been a challenge for ranchers relying on native prairie to support their beef herd. Unfavorable weather conditions, such as drought, can have serious financial ramifications for producers. Forecasts of future climate in the Canadian prairies predict increased extreme weather events, as well as warmer average temperatures and altered summer rainfall. Rather than take a “wait-and-see” approach, we used experiments to better understand how changes in climate affect native prairie and associated grazing resources.

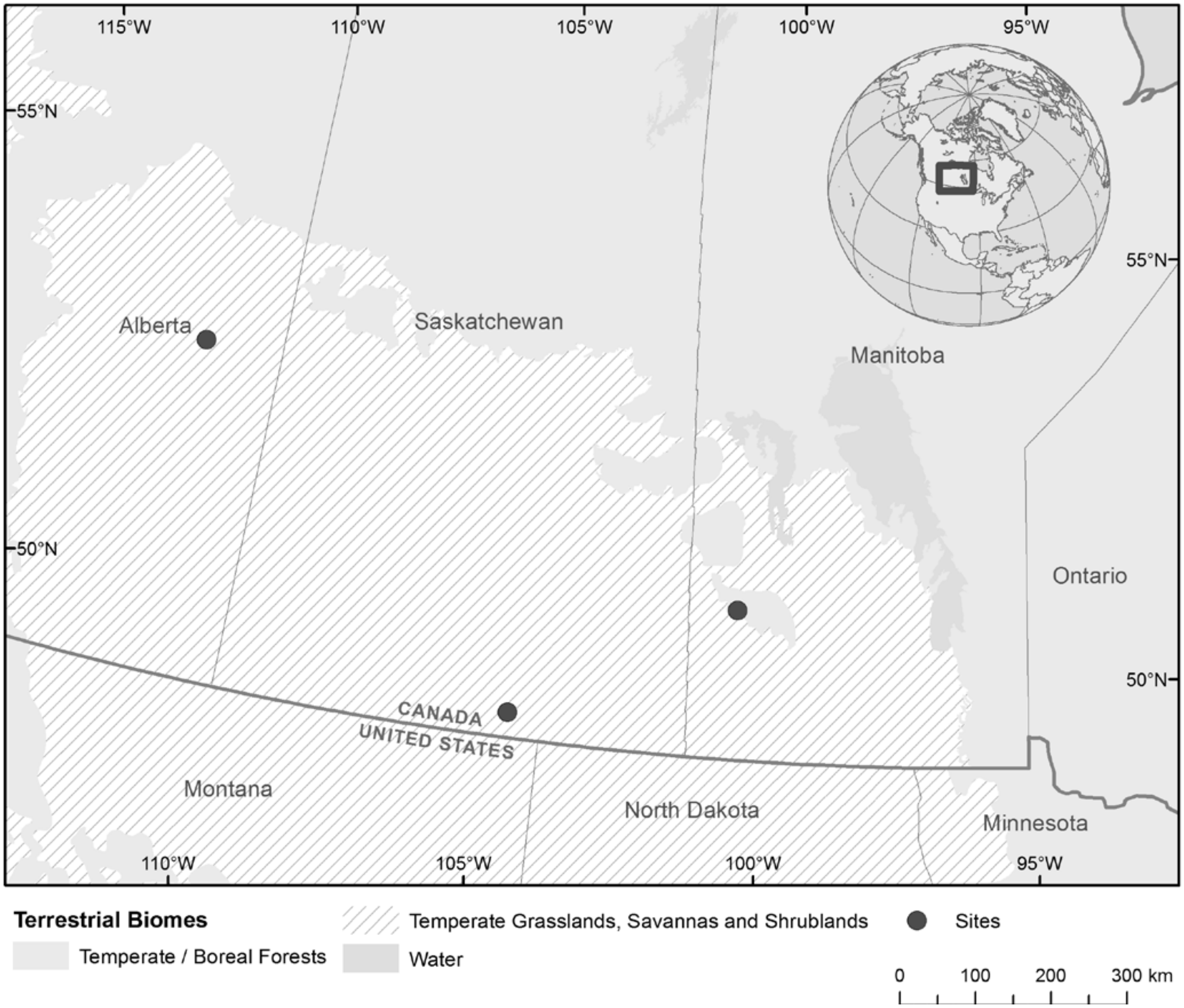

Figure 1. Map of experimental sites in Alberta, Saskatchewan, and Manitoba in relation to the northern extent of grasslands in North America.

Methods

We set up experiments to simulate increased temperatures and altered precipitation at three native grassland sites across the prairie provinces (Fig. 1). The main site was at the University of Alberta's Kinsella Research Ranch, with additional sites at the Gap PFRA community pasture in southern Saskatchewan, and Riding Mountain National Park in southern Manitoba. At each site, we increased summer air temperature at half of the plots by approximately 3°C using fibreglass open-top chambers (OTCs); this warming is within the moderate range predicted under climate change scenarios for 2050 across the prairies. We also used rain-out shelters to decrease precipitation in half the plots by 60%; at the Alberta site only, an added precipitation treatment was included to assess increases in precipitation, as some climate change models predict this could occur in Western Canada.

Weather can affect rangelands in a variety of ways, and thus a suite of response variables were measured. Of direct relevance to livestock producers, we assessed the amount and quality of both season-long accumulated and regrowth forage produced, as well as the proportion of plant growth consisting of broadleaf forbs versus grasses. We also monitored belowground plant responses, such as root biomass and the ratio between shoot and root biomass. Finally, since the diversity of plant species in rangeland can affect productivity and other key ecosystem services, we monitored changes in plant diversity. To interpret vegetation responses, we measured an array of environmental variables (e.g., litter and nitrogen) that can be controlled by weather conditions or management practices, and are known to affect both rangeland productivity and diversity.

Importantly, grazing intensity is known to influence plant community composition, and can interact with climate to affect rangelands in ways that climate on its own would not do. For example, Klein et al. (2004) found that plant species loss with warming was dampened under grazing. Unlike weather, grazing intensity is controlled by livestock producers and can be modified using specific grazing management practices. Thus, we added a third treatment in our research to test how grazing intensity interacts with climate to affect rangeland productivity and diversity. We simulated low- and high-intensity grazing by clipping all plants within our experimental plots to 7 cm and 3 cm, respectively, in mid-June. All treatments (warming, altered precipitation, and clipping) were fully crossed, and replicated five times for each combination, resulting in a total of 210 plots. The experiment ran for three years.

Results and discussion

Summer precipitation and clipping were the main determinants of total forage production (grass and forb components combined), while warming had a lesser role (White et al. 2014). Season-long accumulated forage decreased with lower precipitation (-25%) and more severe clipping (-13% under low clipping; -32% under high clipping), as did warming, but to a smaller extent (-8%). Similarly, end of summer regrowth biomass following mid-summer clipping declined sharply with reduced precipitation but had a limited decline with warming, highlighting the impact of moisture reductions on late season grazing opportunities. Results also varied by site and year; notably, the reduction in accumulated forage with reduced precipitation was not evident in Saskatchewan, the driest site (Table 1). Warming also acted in concert with other treatments; at the Alberta site, the combination of warming and drought increased accumulated forb biomass, but under ambient precipitation, warming decreased forbs. A distinct trade-off was observed between grass and forb biomass under warming, indicative of marked shifts in plant community composition. In contrast, a positive relationship existed between these two variables without warming.

To further compound the problem, reduced precipitation and warming both decreased forage quality, specifically crude protein concentrations. Not surprisingly, clipping increased forage quality. These results indicate losses in forage production under climate change (both drought and warming) may be further exacerbated by decreases in forage quality. Declines in forage production and quality with warming were evident across the three prairie provinces, suggesting producers should take into account warming as well as drought when planning future use of their grazing resources. These effects may be made even worse by evidence that the preferred forage group (grasses) appeared to be more sensitive to climate change than forbs (many of which are weedy opportunistic species that increased with grass decline).

Despite immediate reductions in forage quality and quantity, total plant biomass was remarkably stable in relation to our treatments, mostly due to a persistently large root mass and even increases in root biomass in some situations (e.g. warming in combination with clipping). These results demonstrate that rangeland plants change growth allocation to roots and shoots in response to climatic factors. The implications of this result for long-term sustainability of forage production are unknown, and highlight the need for further research.

We took a unique approach to evaluating grassland diversity responses to the treatments (White et al., in press). It is well known that climate can affect the plant community via a multitude of direct and indirect pathways. For example, warming can affect plants directly if the new temperature is outside the optimal range for the species, or indirectly through mechanisms such as reduced soil moisture brought about by increased evaporation. Thus, we used multivariate path modeling to simultaneously assess the network of direct and indirect effects linking clipping, warming, and precipitation, to plant community diversity (including richness [number of species] and evenness [consistency in distribution of species]). Warming directly led to plant species loss in all three grasslands (Table 1). This finding of widespread, directly-controlled plant diversity loss with warming is consistent with global concerns about declining biodiversity under ongoing climate change.

Both precipitation and clipping acted mainly via indirect pathways. At all sites, clipping reduced plant diversity (Table 1). We showed this negative effect of clipping on diversity was controlled by shoot biomass and any disturbance effects on the latter. For example, clipping decreased shoot biomass, that in turn, decreased diversity. We observed a similar pattern with precipitation; decreased shoot biomass due to reduced precipitation depressed diversity. However, this negative effect of reduced precipitation on diversity was only evident in Alberta and Manitoba (Table 1). At the driest site in Saskatchewan, shoot biomass was maintained despite substantial reductions in precipitation, and thus diversity remained stable.

Identifying shoot biomass as a key driver of diversity across study locations is one of the key findings emerging from this study. Evenness was generally more stable in relation to the treatments than diversity, with no consistent responses being recorded across sites.

Implications and future work

Our results reinforce the need to plan for biodiversity conservation and altered grazing resources across western Canada under future climate conditions, particularly reduced precipitation, but also warming, as well as the need for further research. To address variability in precipitation responses, a group of global researchers, including several from the University of Alberta, are planning a coordinated drought experiment that will assess sensitivity to drought across a broad range of ecosystems. We are also working to expand on our findings related to reduced plant diversity, and better understand shifts among plant species and community level responses under altered climatic conditions and management regimes. In collaboration with researchers at the University of Tübingen, Germany, we are developing a predictive understanding of shifts in grassland community composition in response to the integrated experimental treatments described here. To do this, we are using information on plant species' ranges from the Alberta Biodiversity Monitoring Institute to group species according to their climatic tolerance and guide hypothesis-testing for shifts in species composition within different experimental treatments. Finally, we are pursuing opportunities to integrate our results with those from similar experiments performed globally to develop a broader understanding of rangeland responses to climate change.

Table 1. Summary of responses in plant species diversity and season-long accumulated forage production to reduced precipitation, warming, and clipping

	Treatments		
Study Site	Reduced Precipitation 	Warming	Clipping 
Alberta	Diversity decreased Forage decreased	Diversity decreased Forage decreased	Diversity decreased Forage decreased
Saskatchewan	Diversity stable Forage stable	Diversity decreased Forage decreased	Diversity decreased Forage decreased
Manitoba	Diversity decreased Forage decreased	Diversity decreased Forage decreased	Diversity decreased Forage decreased

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Legume restoration in pastures following broadleaf weed control

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Legumes are an important component of pastures in the Aspen Parkland, where they are responsible for increasing forage yield and quality through the benefits of nitrogen (N) fixation and resulting enhanced fertility. Legume species that are common throughout the Parkland include alfalfa (*Medicago sativa*) and white clover (*Trifolium repens*), which occur as seeded forages, or in some cases, as legumes naturally establishing from the soil seed bank.

The Alberta Weed Control Act mandates that action must be taken to prevent the spread and limit the presence of noxious weeds. This action has the added benefit of reducing yield losses associated with these weeds, which can reach levels as high as 2 kg ha^{-1} of forage for each 1 kg ha^{-1} of Canada thistle (*Cirsium arvense*), for example (Grekul et al. 2004). While broadleaf herbicides have proven effective for weed control, many herbicides simultaneously remove legumes from the sward and thereby reduce forage yield and quality. The prompt recovery of legumes is therefore an important management outcome for ranchers operating in the Parkland.

Legume re-establishment in the Parkland is likely constrained by the rate of herbicide degradation in soil, in combination with the presence of legume seed in the seed bank and the environmental conditions known to regulate legume growth, including the availability of soil moisture, light and competition from neighboring vegetation. Studies examining the degradation of herbicides with residual effects on legumes in pastures are rare, even more so in northern temperate grasslands, where a short-growing season and relatively cool temperatures may slow degradation compared to studies conducted routinely in warmer regions of the southern United States.

We initiated investigations to experimentally test legume abundance and recovery following: 1) rates of herbicide degradation of two broadleaf herbicide bioactives (aminopyralid [AMP] and aminocyclopyrachlor [AMCP]); 2) variation in environmental factors such as moisture, light and competition, as regulated by intermittent defoliation; and 3) contrasting influences of management factors (grazing regime, fire, fertilization, manure application, etc.). Our goal is to gain a better understanding of how these factors regulate legume abundance in the seed bank, and provide grazing managers with beneficial management practices intended to facilitate the return of legumes.

Methods

To achieve our objectives, we used a combination of short-term herbicide dose trials, together with long-term herbicide field trials and accompanying greenhouse herbicide bioassays (Miller 2013). In addition, we conducted retrospective surveys of pasture seed bank composition within a large sample of randomly selected fields distributed across the Parkland of central Alberta.

In the short term dose trial, AMP and AMCP were sprayed at rates of 1x, 0.5, 0.25, 0.125, 0.0625, and 0x the suggested application rates for these bioactives, to simulate progressive degradation associated with successive half-lives (i.e., representing a 50% decline in herbicide bioactive presence). Study areas were broadcast-seeded with 15 kg ha^{-1} of alfalfa and clover prior to spraying. Full (1x) herbicide rates were 120 g a.i. ha^{-1} of AMP and 60 g a.i. ha^{-1} for AMCP. These trials were conducted in four site-years (each of 2010 and 2011 at the Ellerslie and St. Albert Research Stations). Additionally, treatments were combined with mowing to assess the role of neighbor competition on short-term legume recovery.

Long-term forage biomass trials were conducted at five locations in central Alberta between May 2010 and September 2012. At each site, legume recovery, forage biomass and weed control were assessed for up to three years after spraying of AMP and AMCP at full rates, both with and without mowing to simulate grazing. Legume recovery was further assessed under natural recovery (no seeding), and in areas over-seeded to alfalfa or white clover. Legume counts were done in June and August/September of each year. Forage biomass was similarly assessed at peak growth in late July/early August, sorted to grass, legume and weed components, dried and weighed. To supplement legume demography data, we conducted soil bioassays in the spring (early May) and fall (early September) of each year. Soil cores were removed from 1x and 0x herbicide treatments in non-mowed plots, and frozen until greenhouse bioassays were run. A total of 3328 cells were analyzed, half of which used treated field soil, and half used non-sprayed soil from Ellerslie to standardize all legume responses in sprayed plots. Responses included plant density (# cell^{-1}, to a maximum of three) and biomass per live legume plant after growing for six weeks (mg live plant^{-1}).

Last, we conducted a comprehensive survey of 102 randomly selected pastures in the Edmonton region to assess the potential for natural legume recovery. For each pasture, once permission had been obtained from the landowner, an interview was completed to collect information on the history of the pasture, including age (i.e., time since last cultivation), grazing history (number, animal type, and timing of grazing), herbicide application (product and target species), manure or fertilization application, fire history, and other disturbances. This was followed by a field survey of the pasture. In each pasture, 53 soil cores (3.25 cm x 6 cm deep) were removed and subsequently grown out in the greenhouse to determine seed bank diversity and composition. Dominant vegetation composition was also assessed, along with range health for tame pastures. Multivariate analytical tools (NMDS Ordination, and Indicator Species Analysis) were used to evaluate the relationship between seed bank composition and management history.

Results and discussion

Alfalfa and white clover seedlings were similarly sensitive to AMP and AMCP during establishment within the short-term dose trial, with legume plant density remaining depressed at exposure to herbicide rates indicative of up to 4 half-lives (Fig. 1). Legume densities were lower under all rates, with even the 0.125 rate leading to 39-68% less legume than in non-sprayed plots. Closer examination of our results suggested the half-lives of these bioactives may be about 50 days during the growing season, considerably longer than the 28-32 days found in the southern US. More importantly, approximately 200 days of degradation under favorable conditions (i.e., soil thawed and microbially active) appear necessary for sufficient herbicide degradation to facilitate legume re-establishment in central Alberta. These findings have implications for producers seeking to promptly re-establish legumes within pastures sprayed for weed control in temperate regions of North America.

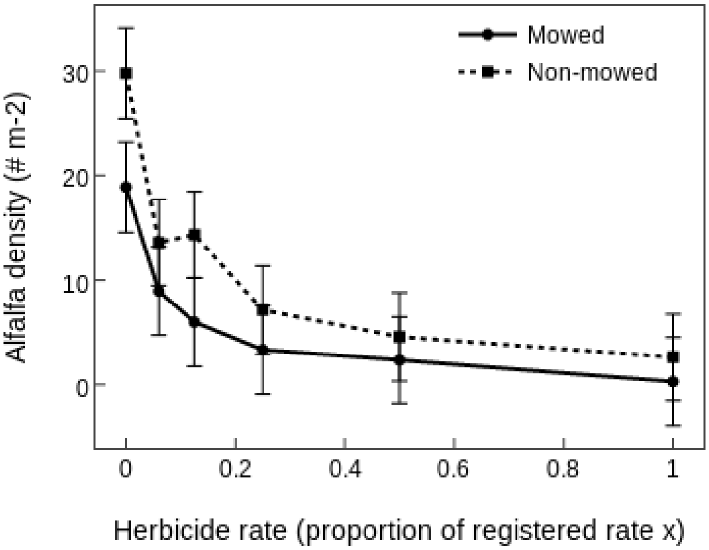

Figure 1. Sensitivity of alfalfa seedlings to herbicides (aminopyralid [AMP] and aminocyclopyrachlor [AMCP]) in mowed and non-mowed plots, St. Albert Research Station. Herbicides were applied to soil at doses emulating the herbicide rate after degradation. Alfalfa was extremely sensitive to AMP and AMCP. It is estimated that herbicides would be required to degrade to less than 10 % of the recommended rate (or four half-lives) before seedlings could establish. Depending on the temperature and moisture, microbial degradation may require 200 days when the soil is not frozen.

In the long-term recovery trials, legume densities remained lower in sprayed field plots than their adjacent controls, with recovery failing to occur until 23 months after spraying for white clover, and not occurring at all for alfalfa through 26 months after spraying. Notably, greenhouse bioassays performed on soil removed from these plots indicated that withdrawal periods for legumes were shorter than in field trials (14 months), potentially the result of more favorable conditions for herbicide degradation in the greenhouse. These results suggest that caution should be exercised when using greenhouse bioassays to assess soil suitability for legume establishment, and we recommend that legumes should not be seeded into treated pastures until the second full year after spraying (i.e. 24 months after treatment).

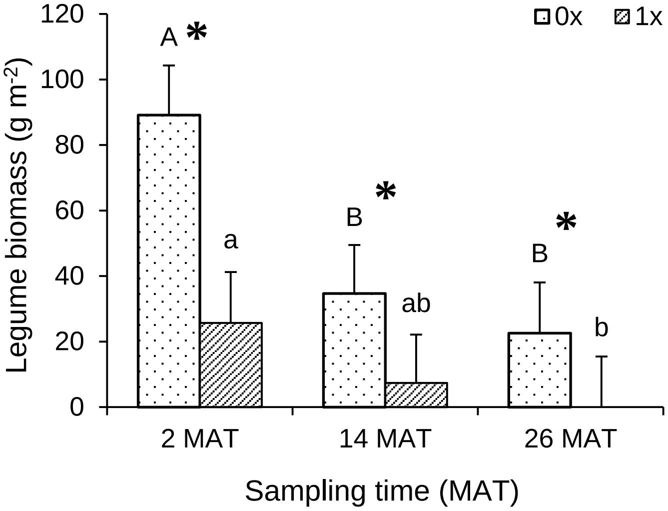

Figure 2. Mean (±SE) legume biomass in central-Alberta pastures measured at peak growth during each of three successive years (2010-2012), within 0x and 1x herbicide plots. Within a given herbicide rate, sampling time means with different letters differ based on a Tukey HSD test ($P < 0.05$). Within sampling times, pairs of herbicide rates with an asterisk differ ($P < 0.05$).

AMP and AMCP residues had similar functional impacts on sward composition based on peak annual biomass, reducing legumes by 71-100% across the three years, equivalent to 63.4 to 22.6 g m^{-2} from year 1 to 3, respectively (Fig. 2). Although grass biomass did not change with herbicides, net reductions in total forage were limited to 6.8% (28 g m^{-2}) over the study period despite legume decreases. Legume biomass was also greater following over-seeding but only in non-sprayed controls, which then decreased over time, likely due to competition from grasses thriving under a deferred defoliation regime. In contrast, biomass of non-legume forbs and the cover of dandelion (*Taraxacum officianale*), the predominant weed, were lower following herbicide application, but reached levels similar to non-sprayed controls by the second growing season. Defoliation also influenced sward composition, favoring dandelion recovery following herbicide application.

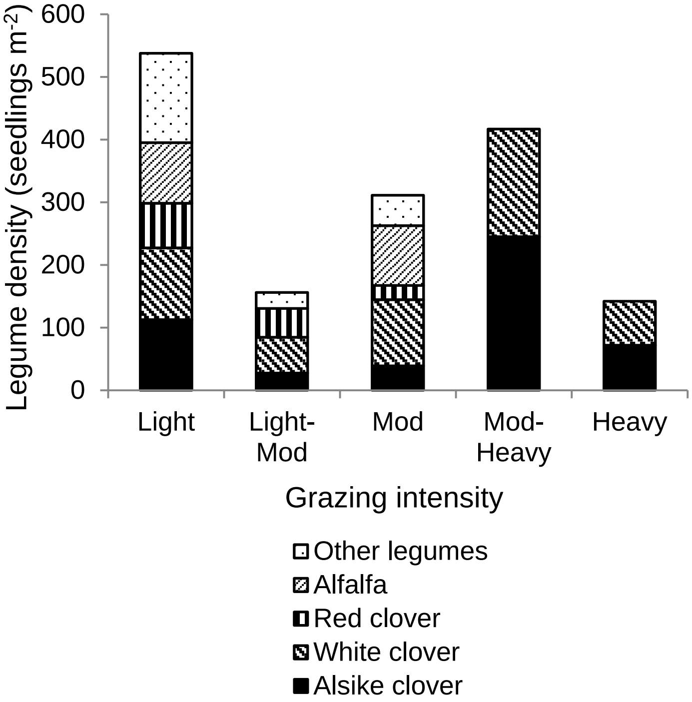

Figure 3. Summary of legume densities found emerging in central Alberta pastures ($n = 44$) associated with different grazing intensities in 2012

In the pasture seed bank survey, germinable legume abundance was affected by the type of grazing system ($p = 0.026$) and grazing intensity ($p = 0.017$) employed by the producer. Pastures deferred during the spring had greater legume seed abundance than grazed pastures, with continuously grazed pastures having the least potential for legume recruitment. Legumes peaked at low and moderate-high grazing intensities (Fig. 3), but for different reasons. Low-intensity grazing allowed a greater variety of legumes to accumulate in the seed bank, including alfalfa and red clover, together with minor amounts of pea vine, vetchling (*Lathyrus spp.*) and cicer milkvetch (*Astragalus cicer*), while moderate-high grazing favored low-statured, grazing tolerant legumes, specifically white and alsike clovers (*Trifolium repens* and *T. hybridum*, respectively). Legume abundance was also positively affected by manure application ($p = 0.026$). Manure piles are now being sampled for the presence of legume seed. Herbicide treated pastures had seed banks with the potential for legume re-establishment, although there was a non-significant trend for sprayed pastures to have fewer legumes ($p = 0.143$), which warrants further investigation.

Implications

Our results provide more definitive information for understanding the impact of broadleaf herbicide application on legume recovery in pastures, and the role of the seed bank in assisting legume recovery after broadleaf herbicide application, including the potential for natural legume recovery. Minimum withdrawal periods after spraying for AMP and AMCP are 23-26 months in northern temperate pastures, with even low doses of herbicide capable of reducing legume establishment in the short-term. While existing pastures contain significant potential for legume recovery, many factors dictate seed bank composition, and legume re-establishment will ultimately be controlled by factors such as grazing activities.

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Encroachment of thorny buffaloberry (*Shepherdia argentea*) into the Mixedgrass Prairie and implications for cattle production

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Encroachment by woody species into open grasslands has been observed worldwide and is capable of significantly impacting ecosystem function. Woody plant invasion can change plant community composition, including grassland biodiversity, alter soil properties, and reduce the potential of these areas to support various land uses, including livestock grazing. The encroachment of woody species and subsequent competition it imposes can sharply reduce forage production and lead to economic losses for livestock producers. While shrub and tree encroachment are more common within the central parkland (Bailey and Wroe 1974) and foothill regions (Burkinshaw and Bork 2009) of Alberta, woody species encroachment is less common in the Mixedgrass Prairie. This is because water availability typically limits woody species abundance in this region (Willms and Jefferson 1993), thereby restricting the ability of shrubs to spread across these normally arid landscapes. However, at the Mattheis Research Ranch, 40 km north of Brooks, Alberta, the native shrub thorny buffaloberry (*Shepherdia argentea*) has gained a significant foothold into the mainly mixedgrass environment of the 5000-hectare [ha] ranch property (Fig. 1).

The Mattheis Research Ranch is situated within the Eastern Irrigation District, and has significant influences from overflow irrigation water, which may be responsible for increases in shrub. In light of concerns over thorny buffaloberry (TBB) encroachment across the property, we conducted a study to: 1) assess changes in the spatial coverage of TBB over the last five decades; 2) evaluate the impact of TBB presence on rangeland forage production, native grassland biodiversity, and associated soil properties; and 3) quantify the degree to which cattle will enter and occupy TBB stands, including livestock impacts on the understory. Finally, these data were used to derive the collective loss in carrying capacity for cattle across the property.

Figure 1. Contrasting shrubland and neighboring grassland habitats found interspersed across much of the Mattheis Research Ranch. Photo by R. Dahl.

Methods

To assess changes in TBB presence, we obtained aerial photography of the ranch from 1949, 1970, 1991 and 2012. After georectifying the images, individual shrub patches were visually identified and traced in ArcGIS. The area of shrub was quantified at each time point.

To evaluate the impact of shrub encroachment on grasslands, we characterized vegetation and soil conditions in the summer of 2013 using a paired-plot design, with plots situated inside and adjacent to each of 30 shrub patches randomly selected across the Mattheis Research Ranch. A pairwise configuration was used to compare vegetation and soil conditions inside the shrub patch and outside, within the adjacent grassland, at a distance of no more than 15 m. Each pair was situated on the same ecosite (elevation, slope, drainage) to minimize confoundment with other physical conditions capable of altering vegetation.

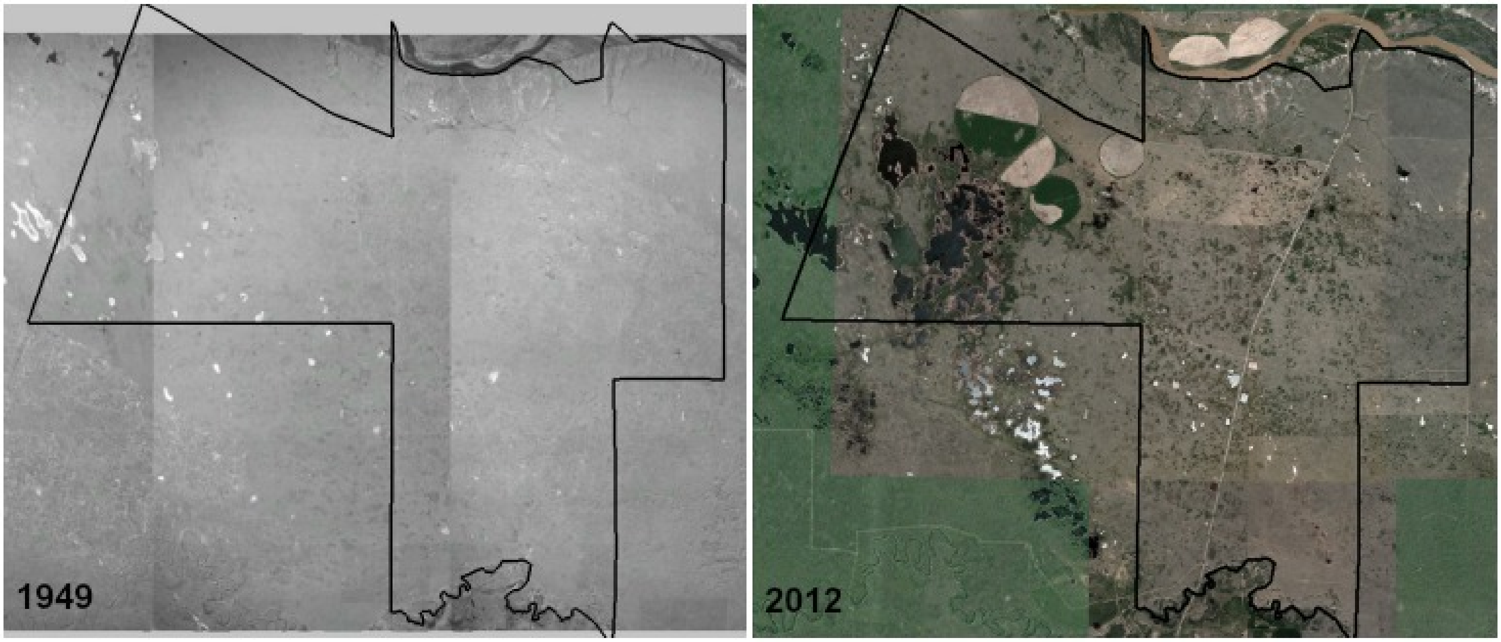

Figure 2. Comparison of aerial photos from 1949 and 2012 showing the extent of vegetation change, including shrub encroachment, across the Mattheis Research Ranch. Imagery courtesy of Alberta Environment and Sustainable Resource Development.

Vegetation assessment was done by identifying all plant species present and quantifying their cover within a 1 m x 1 m quadrat randomly located within each paired plot. Additionally, herbage (grass and forb) biomass was harvested to ground level, dried and weighed to quantify forage availability. Within each quadrat, two 10-cm soil cores (3.18 cm in diameter) were extracted and bulked to assess soil properties (LFH depth, bulk density, salinity, pH, organic matter, nitrogen and carbon content).

Within each stand of TBB investigated, an additional assessment was done to evaluate the extent to which cattle occupied these shrublands. Where stands were occupied by cattle, estimates were made of the proportion of the stand disturbed by cattle (as evidenced by cattle trails, defecation and shrub breakage). A total of 19 shrub stands had evidence of cattle presence, allowing pairwise comparison of the additive impact of cattle use on TBB shrubland characteristics using an additional pairwise comparison. Understory vegetation and soil conditions were therefore sampled independently for both cattle-disturbed and undisturbed areas. Finally, shrub cover and density were estimated within the shrub encroached areas.

Results and implications

Results of the aerial mapping revealed that since 1949, a total of 77 ha of the Mattheis Research Ranch has been encroached by TBB. Almost no visible signs of TBB were evident in the earliest photo (Fig. 2), suggesting the entry of TBB occurred relatively recently. Historical records indicate that the entry of overflow water began on the property in 1952 with a wetland construction project initiated by Ducks Unlimited (DU), and this may have been the catalyst initiating shrub encroachment. Moreover, the current distribution of shrublands is concentrated around the DU-constructed wetlands on the west side of the Mattheis Research Ranch, with limited TBB around ephemeral wetlands on the east side of the property. Trajectories of TBB abundance remained relatively low in 1972, only to increase rapidly through 1991 and 2012 (Fig. 2). It is unknown just how abundant TBB may become over the next several decades.

Field data indicated that shrub encroachment was associated with a sharp reduction (-94%) in herb biomass compared to adjacent grasslands (Fig. 3). Of the 30 TBB stands assessed, 11 had no evidence of cattle activity (36%). Moreover, within those stands having any evidence of cattle, an average of only 23% of the area within these shrublands was occupied by cattle. The decrease in herb biomass associated with intense competition from encroaching shrubs, together with the reduction of area accessed by cattle, has collectively led to a loss of 140 animal-unit-months of annual cattle grazing at the Mattheis Research Ranch. While total herb biomass (grass + forb) declined markedly with even small increases in shrub cover (Fig. 4), shrublands disturbed by cattle and having reduced canopy cover were associated with an increase in herb biomass (Fig. 3), presumably due to the increase in light with reduction in shrub presence. Results of the soil assessment showed limited differences, although areas occupied by cattle did have greater bulk density, likely the result of cattle trampling and hoof action.

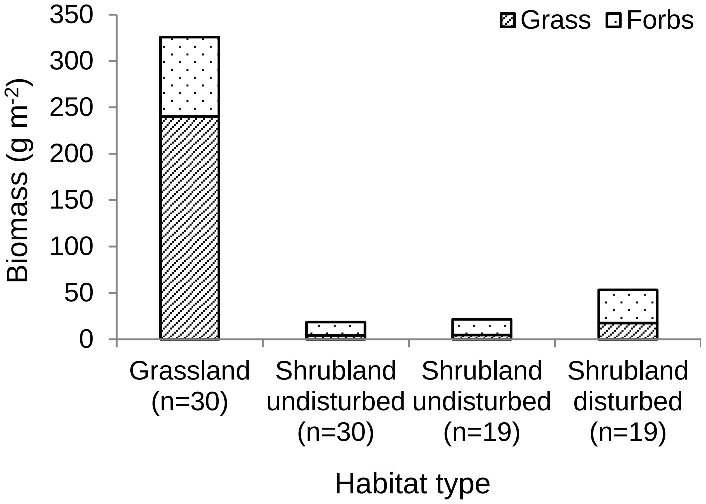

Figure 3. Grass, forb, and total herb biomass in grassland and shrubland habitats found at the Mattheis Research Ranch in 2012 (shrubland undisturbed = thorny buffaloberry plots with no evidence of occupation by cattle; shrubland disturbed = thorny buffaloberry plots with evidence of occupation by cattle)

Additional changes were observed in the composition of the understory, as native plant species richness and diversity were markedly lower in shrublands compared to neighboring grasslands. In contrast, shrublands were associated with an increase in the abundance of introduced plant species, many of which were weeds.

Our results highlight the marked impact that an invasive shrub such as TBB can have on grassland composition and productivity. Although this shrub offers unique habitat for a number of wildlife species in this region of the Mixedgrass Prairie, and is known to input nutrients through nitrogen fixation, the increase in TBB over the last several decades may be cause for concern in the future, particularly with respect to its impact on cattle grazing opportunities. Other than altering the amount of overflow water distributed to wetlands, control options for this particular shrub may be limited, as prescribed fire is not as feasible an option for woody plant control in the Mixedgrass Prairie as it is elsewhere in the province. Future research will attempt to understand the impact of water availability (amount and timing) in regulating abundance of this shrub, which in turn, may identify prescriptive management strategies capable of containing this woody invader.

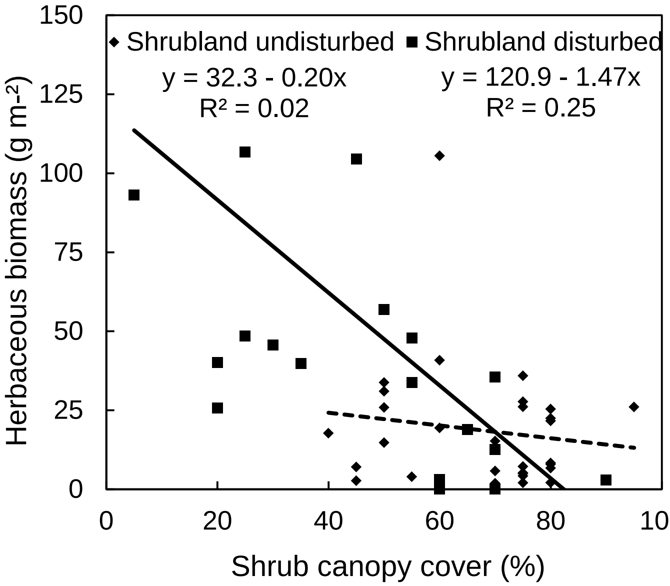

Figure 4. Relationship of total herb biomass (dry matter) and shrub canopy cover for each of the undisturbed (no evidence of occupation by cattle) and disturbed (evidence of occupation by cattle) shrubland habitats. Biomass is significantly related to cover ($P < 0.01$) only in disturbed areas.

Acknowledgements

Funding and in-kind support for this research was provided by the University of Alberta and Rangeland Research Institute. We thank Adrienne Tastad and Jamie Kalla for assistance with field work, Rick Pelletier for GIS support, and Don and Sandra Armitage, along with Ruth and Edwin Mattheis for their hospitality and support.

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Understanding the ecological impacts of the smooth brome (*Bromus inermis*) invasion into Alberta's native grasslands

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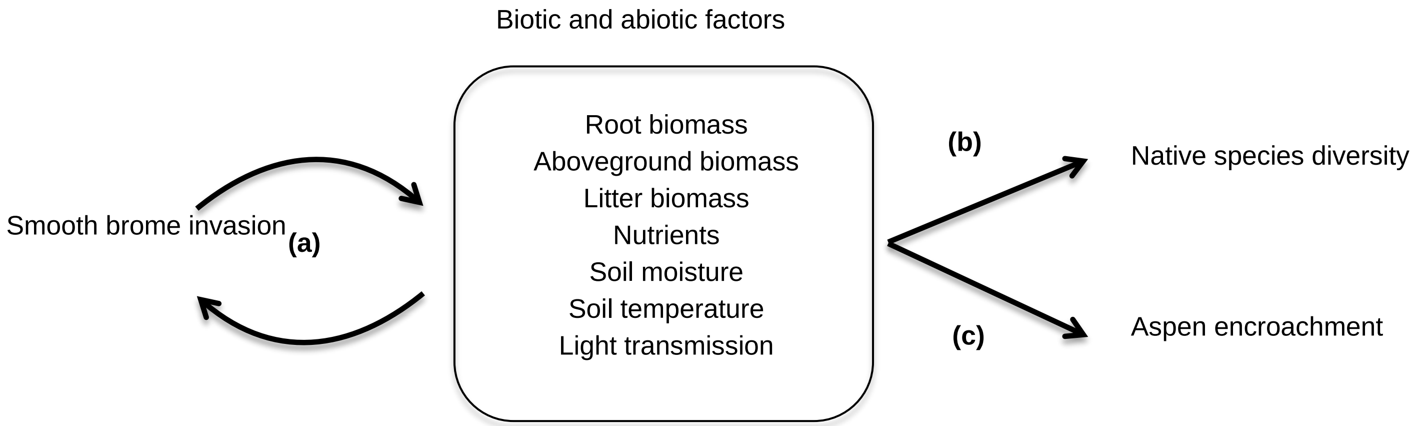

Figure 1. Mechanisms behind smooth brome invasion (a) and impact on native communities (b,c). Smooth brome invasion can be determined by abiotic and biotic factors, but it may also be driving its own invasion by modifying the conditions where it invades (a). Through the modification of biotic and abiotic conditions, smooth brome can have a strong impact on native species diversity or it can be facilitating aspen encroachment into native grasslands (c).

Smooth brome (*Bromus inermis*) is a perennial grass introduced to North America in the 1800s as a forage crop (Romo and Grilz 1990). It is widely planted and actively bred in Canada (Otfinowski et al. 2007). However, this species often escapes cultivated areas and has been found invading native habitats in every Canadian province (Otfinowski et al. 2007). In Alberta, smooth brome is invading many protected and relict areas of the Mixed Prairie and Aspen Parkland, including fescue grassland (McClay et al. 2004, Otfinowski et al. 2007). Where established, it forms dense mono-specific patches, and is associated with a decline in native plant diversity (Otfinowski et al. 2007, Fink and Wilson 2011). Declines in native biodiversity can be associated with changes in many ecological services, including a reduction in the quality of dormant season grazing for livestock. Impacts on wildlife (e.g., pollinators, nesting birds, etc.) are less well understood (but see Wilson and Belcher 1989, Bunnell et al. 2004). Due to its widespread distribution and potential to dominate sites, it is necessary to evaluate the threats smooth brome poses to native plant communities.

Smooth brome is typically found occupying nutrient-rich, moist sites and its invasion is favored by disturbance (Fig. 1; Blankespoor and Larson 1994, Blankespoor and May 1996, Larson 2003). By understanding which conditions facilitate or prevent smooth brome expansion and its impacts, we can help target management strategies to specific areas. However, smooth brome could also be driving its own invasion by altering conditions where it invades (Fig. 1). For example, there is evidence that smooth brome alters soil conditions (e.g., nutrient and moisture regimes) following invasion (Vinton and Goergen 2006, Jordan et al. 2008). Such soil-based changes can result in a cascade of disruptive impacts on the dynamics of native grasslands.

Brome-induced changes in soil conditions may be of particular importance in the Parkland Ecoregion, where native prairie is interspersed with patches of trembling aspen (*Populus tremuloides*). Smooth brome appears to recruit inside /adjacent to forest patches, even without disturbance. Growth and vegetative reproduction can result in near monocultures of brome, with expansion into the adjacent grasslands (Fig. 2a). One of many characteristics of smooth brome invasion is a rapid buildup of soil moisture and nutrients (Fig. 1; Fink and Wilson 2011) – two factors known to limit the expansion of aspen in the Parkland Ecoregion (Köchy and Wilson 2001, Lieffers et al. 2001, Fraser et al. 2002). Thus, it is possible that smooth brome poses a threat to native grasslands not only through its own invasion, but also through soil-mediated facilitation of aspen encroachment. Information on brome-aspen interactions, with a particular focus on soil conditions, is therefore of urgent need.

2a (above) and 2b (below)

Figure 2. Smooth brome invasion into native habitats in Alberta. Photo A illustrates a common transition from aspen forest stand (in the back) to a smooth brome invaded area (light green) to native community (light brown, in the front). Photo B shows a transect set up to monitor smooth brome expansion. The white arrow in the back shows where the transect starts, in the smooth brome-invaded area, and the white arrow at the front shows where the transect ends in the native area. To the left side of the transect is where above and belowground biomass were sampled. Photos by G. Stotz.

Our first research goal is to understand the conditions that facilitate or limit smooth brome invasion and impact throughout grasslands of Alberta, and understand the degree to which smooth brome alters soil conditions. Second, we will explore whether smooth brome is facilitating aspen encroachment. This information will help identify priority areas where the consequences of smooth brome invasion have the most detrimental effects on the native communities, as well as areas of presumed decreased risk.

Methods

To determine the rate of expansion of smooth brome and its impact, we set up transects within nine sites across Alberta, at Writing-on-Stone Provincial Park (PP), Police-Outpost PP, Cypress Hills PP, Dry Island Buffalo Jump PP, Big Knife PP, Kleskun Hill Natural Area, Saskatoon Island PP and at the University of Alberta’s Kinsella and Mattheis Research Ranches. These sites represent most of the area known to be undergoing invasion by smooth brome in Alberta (Otfinowski et al. 2007). Biotic and abiotic (i.e., growing) conditions were measured along the transects at 0, 30, 60, 120 and 200 cm moving away from the edge of invasion in both directions (into each of the native and brome areas; Fig. 2b). Biotic variables measured included root biomass and aboveground biomass (sorted into shrub, forb, smooth brome, other grass, and litter biomass). Abiotic conditions measured were nutrients, soil moisture, soil temperature and light transmission.

At the Kinsella Research Ranch, located in the Parkland Ecoregion, we are also monitoring aspen encroachment into the native prairies by measuring brome impacts on the establishment of aspen seedlings and subsequent growth of aspen saplings. By experimentally modifying the competitive environment, we can begin to separate brome effects on soil conditions from direct effects on plant competition. Such information is critical for the development of effective brome management plans, including restoration efforts.

Preliminary findings and interpretation

Even though sites included in this study were not seeded with smooth brome, at all locations smooth brome was found to be invading native grasslands. Brome invasion appears to be associated with up to a 75% reduction in local native plant diversity. More generally, we found only one-third of the species within regional species pools appear able to persist within a smooth brome stand.

Although results presented here are preliminary, we have evidence that smooth brome is rapidly expanding into native grasslands across sites. Expansion rates vary across the province likely due to site conditions; we found slower expansion in the southern, most nutrient-poor and driest site, and greater expansion in the northern, most nutrient rich and moist site. Linear expansion rates of brome fronts during the growing season, at sites ordered from south to north (mean ± standard error) were: Mattheis Ranch = 0.14 ± 0.03 cm day^{-1}; Dry Island Buffalo Jump PP = 0.20 ± 0.04 cm day^{-1}; and Kinsella Ranch = 0.30 ± 0.04 cm day^{-1}. These results indicate that smooth brome invasion may be of less concern on southern, less productive sites, and management efforts may be better concentrated on northern, more productive sites. Future results from this study will allow us to determine which biotic and abiotic factors facilitate or prevent smooth brome expansion and impact. This information will allow us to allocate management efforts to sites where smooth brome poses a greater threat to native grasslands.

Results on whether smooth brome is facilitating aspen encroachment are pending. However, we have data indicating that nutrient availability is greater within smooth brome invaded areas compared to adjacent native communities. Nitrate, potassium and phosphorus were significantly higher, while total nitrogen and ammonium did not differ between invaded and native areas. High nutrient availability has been shown to increase aspen growth and encroachment (Köchy and Wilson 2001, Fraser et al. 2002). If smooth brome is facilitating aspen encroachment through the modification of soil conditions, brome invasion will not only lead to biodiversity losses, but also to a loss of grassland in general.

Smooth brome is an important forage crop in Canada, but also poses threats to biodiversity and overall grassland conservation. We need to better understand its impact and spread if we want to make informed decisions on how to manage this species in an effective way. We recognize there are a large number of potential research questions to be asked and that many others are interested in the management of this species. We welcome feedback, ideas, and critiques as this project moves forward.

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Impact of an invasive legume (*Astragalus cicer*) on ecosystem goods and services in the dry mixed prairie

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Grasslands provide a range of ecosystem goods and services (EG&S). Foremost is the provision of forage for livestock, but grasslands are increasingly being recognized for other important services. Grasslands can sequester and store carbon, which offsets carbon dioxide emissions that are altering the climate. Additionally, grasslands are important for conserving biodiversity and serve as critical habitat for some endangered species. Ultimately, these EG&S are driven by plant growth, but human activity can alter the abundance and identity of plant species on the landscape. The spread of invasive plants is a growing global concern for diversity and ecosystem function (Pejchar and Mooney 2009). In grasslands, non-native plants are a major concern when they reduce the quantity or quality of forage production, but they can also impact hydrology, nutrient cycling, erosion, soil chemistry and diversity.

Figure 1. Cicer milkvetch at the University of Alberta's Mattheis Research Ranch. Photo by C. Carlyle.

Cicer milkvetch (*Astragalus cicer*, Fig. 1) is an agronomic plant often used in hay fields or tame pasture in Alberta, but we have recently observed it invading the dry mixed prairie in Alberta. Cicer milkvetch is a long-lived perennial legume that is valued as forage because it does not cause bloating in cattle and has high protein content. It is cold-tolerant and therefore well-adapted to the Canadian prairie, but has hard seeds, which causes slow germination and establishment. Recently, work has been done to increase the germination and establishment rate of cicer milkvetch (Acharya et al. 2006), which could increase the risk of this species spreading into native grasslands in the future. As a legume, this plant is capable of fixing nitrogen, a process that can increase soil fertility and lead to other ecosystem changes. Because of its large size, cicer milkvetch may also be competitive with native plants. The objective of this study was to examine the effects of cicer milkvetch on multiple EG&S, in particular, forage quantity and quality, soil carbon and plant diversity.

Methods

To examine the impact of cicer milkvetch on EG&S, we conducted a study at the University of Alberta's Mattheis Research Ranch, located in the dry mixed grass prairie, 40 km north of Brooks, Alberta, Canada. Annual precipitation is approximately 350 mm and elevation is approximately 720 m above sea level. Soils are a coarse-textured Orthic Brown Chernozem. We quantified different measures of EG&S in 25 randomly selected cicer milkvetch patches within an approximately 4 km^2 area. Individual patches were at least 20 m apart. To make comparisons to grassland without cicer milkvetch, we also sampled the area immediately adjacent to the patches and a location 5 m away from the patch that was on the same ecosite (i.e., same drainages, slope and elevation), for a total of 75 study plots. In each 20 cm x 50 cm plot, we measured the cover of all plant species and collected live plant material. Plant biomass was dried and weighed and a sample ground to measure nitrogen content (LECO Truspec CN Analyser), which was converted to crude protein. We also collected two types of soil cores; a single large core was used to measure soil bulk density (6-cm diameter, 15-cm depth), and four smaller cores (3.25-cm diameter, 15-cm depth) removed from each plot were combined, dried, hand sorted to remove roots, and then ground to a fine powder for carbon analysis (LECO Truspec CN Analyser). We used a multivariate ordination to examine patterns between plots and EG&S and found that EG&S were associated with different plant community types (Fig. 2).

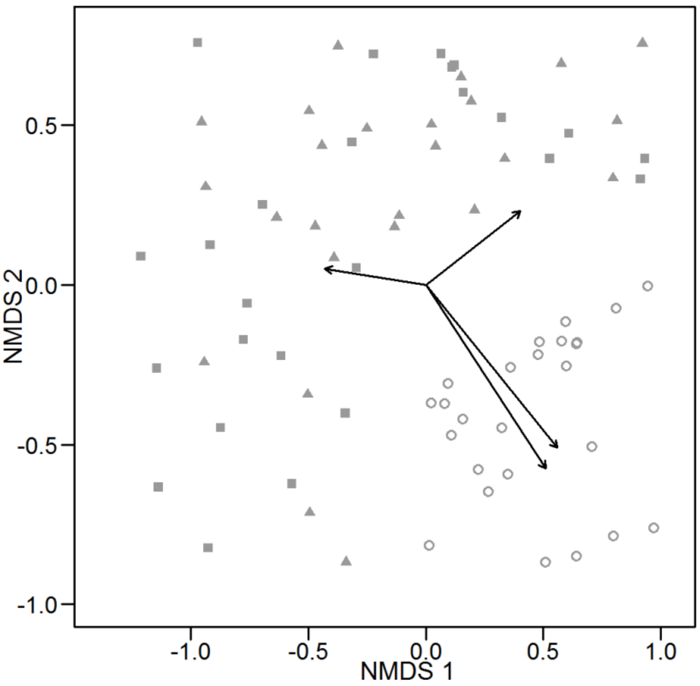

Figure 2. Ordination of plots (non-metric multi-dimensional scaling) and an overlay of ecosystem goods and services measured at the Mattheis Research Ranch. Open circles represent plots with cicer milkvetch, triangles and squares represent plots beside and distant from cicer milkvetch patches (no significant difference between these groups in ordination space). Arrows indicate association of ecosystem goods and services (forage quantity and quality, soil carbon and plant diversity) with plots.

Results and discussion

Cicer milkvetch plots had more available forage, 694 g m^{-2} compared to 177 g m^{-2} in uninvaded plots, and more available crude protein, 138 g m^{-2} compared to 22 g m^{-2}. Soil carbon was associated with plots that had greater cover of Kentucky bluegrass (*Poa pratensis*), but did not vary significantly among our three plot types, which averaged 3310 g m^{-2} in the top 15 cm of soil. Finally, there were fewer plant species in cicer milkvetch plots, 3.3 species $plot^{-1}$, compared to uninvaded plots, which had an average of 4.7 species $plot^{-1}$. Plots dominated by the native needle-and-thread grass (*Hesperostipa comata*) tended to have higher plant diversity.

Our results show that a single plant species, cicer milkvetch, can alter EG&S in the dry mixed prairie and that there are trade-offs between different services. In contrast to many other invasive plant species in rangelands (e.g., downy brome [*Bromus tectorum*]), cicer milkvetch increased the quantity and quality of available forage at our study sites, which may be considered beneficial. However, we also observed an associated decline in plant species diversity where cicer milkvetch was growing. We found no change in soil carbon with milkvetch presence, but note that milkvetch invasion is relatively recent and changes in soil properties can require decades to manifest. Nitrogen is often a limiting resource in grasslands; if nitrogen increases it could alter nutrient cycling and lead to changes in the carbon balance of this ecosystem. This will require a longer-term study of soil carbon in this ecosystem. Other questions also remain, since we only examined the impact of cicer milkvetch at a small scale. Anecdotal evidence suggests that the landscape cover of cicer milkvetch is increasing, so the question remains whether plant diversity has been reduced at larger scales and what the consequences of more widespread cover of this plant will be at the landscape level. To fully understand the consequences of plant invasion multiple EG&S should be examined.

Acknowledgements

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Quantifying carbon stores in perennial grasslands across Alberta and its relation to grazing

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Alberta contains nearly 10 million hectares of grazing land, of which about 70% is privately owned. This land is a critical resource supporting the provincial beef industry, which at 1.8 million head of breeding cattle, is the largest in Canada. Despite the vast amount of land dedicated to beef production, and the critical economic role of this industry (primary sales circa $4B per annum), net incomes of beef producers have fallen over the last decade. Increased profitability may come about via new sources of income, or reduced costs. However, the latter may be difficult to achieve given the global increase in energy costs. Similarly, animal production efficiencies being explored to aid the cattle industry rely heavily on increasing feed efficiency, which is mostly being examined in the context of confined feeding rather than extensively grazed rangeland and pasture.

Figure 1. Grasslands are known for storing carbon, particularly belowground. Up to 85% of plant biomass in the Mixedgrass Prairie (pictured here) is found in roots, leading to favorable long-term soil organic matter accumulation. In contrast, cultivation can lead to the loss of 20-60% of soil C.

As producers depend heavily on the ability of cattle to convert an otherwise unusable natural resource (i.e., coarse forage) into commodities (e.g., red meat), economic diversification from grazing lands remains an important way to increase profit margins. Rangeland ecosystems are known for providing environmental goods and services (EG&S), which benefit all of society. Examples of EG&S include filtering water, providing wildlife habitat, maintaining biodiversity, and sequestering and storing carbon (C), which can offset atmospheric CO_2. While direct markets to reward ranchers for these services remain undeveloped, C storage in perennial grasslands is a benefit that can be readily quantified and is consistent with the provincial and national mandates to reduce greenhouse gases.

Perennial grasslands are widely recognized for their potential to store large amounts of C, both in vegetation (root and shoot mass), and especially in soil organic matter (Fig. 1). Because a large proportion of the C is belowground, it remains relatively stable and resistant to release in the short-term, even with abrupt changes to aboveground vegetation (e.g., due to grazing or surface fire). Additionally, C pools in perennial grassland are known to be greater than in cropland, where cultivation has reduced C by 20-60% (Lal 2002). Despite the key role of rangelands in storing C, little is known about the overall size and stability of C pools in the grasslands of Alberta, including how they vary regionally (with agroclimate). Previous studies have typically examined only a few localized sites under a narrow range of conditions, and thus, do not provide a comprehensive regional and provincial accounting of C stores. Furthermore, studies examining the impact of grazing on rangeland C are highly variable; some studies indicate that grazing increases C, with others showing the opposite or no effect (Derner and Schuman 2007).

In 2012, with support from the Alberta Livestock Meat Agency, we started an investigation to: 1) quantify the size and stability of C pools in rangelands across Alberta; 2) characterize the distribution of biological C pools in ecosystem components, including live vegetation (shoots and roots), litter and mulch and various soil fractions; and 3) evaluate the impact of grazing and other land uses (such as conversion to tame pasture and annual cropping) on C pools.

Carbon benchmarking in grasslands

In 2012, working in partnership with the Range Management Branch of Alberta Environment and Sustainable Resource Development (AESRD), the University of Alberta began sampling a large network of Rangeland Reference Area sites currently maintained and monitored by AESRD. A total of 120 sites throughout the Mixed Prairie, Aspen Parkland (*n* = 63), as well as the Foothills Fescue and Montane (*n* = 57) Natural Sub-regions were included. These reference sites are well suited to the assessment of C pools because they have existing long-term data on both community composition and forage production, both with and without grazing, the latter within fenced cattle exclosures approximately 10 x 20 m in size (Fig. 2). Working with AESRD staff, we have been collecting vegetation, litter and soil samples from each plant community. Within every community, 10 soil cores, each 3.25 cm in diameter, are being sampled to 30-cm depth in 15-cm intervals. An additional 10-cm diameter core was taken to assess soil bulk density for adjusting C to a volumetric mass basis. In addition to these sites and where opportunities exist to do so, sampling will be conducted on adjacent tame pasture and annual cropland to facilitate comparisons of C profiles between contrasting land uses.

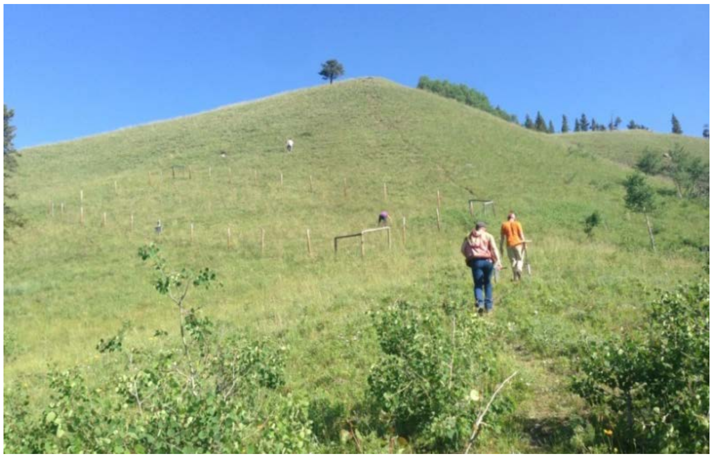

Figure 2. Example of a long-term Rangeland Reference Area sampled for carbon in the foothills of southwest Alberta

Soils will be assessed for physical (texture, bulk density) and chemical properties (pH, salinity, electrical conductivity, soil organic carbon and total organic matter, total C and N, inorganic C). Concentration and mass of C and N will be determined for live vegetation shoots and roots, litter, mulch and soil. The latter will also be assessed for the whole soil and by fractions (<53 µm or fine, 53-250 µm or medium, and >250 µm or coarse fractions) to assess C stability.

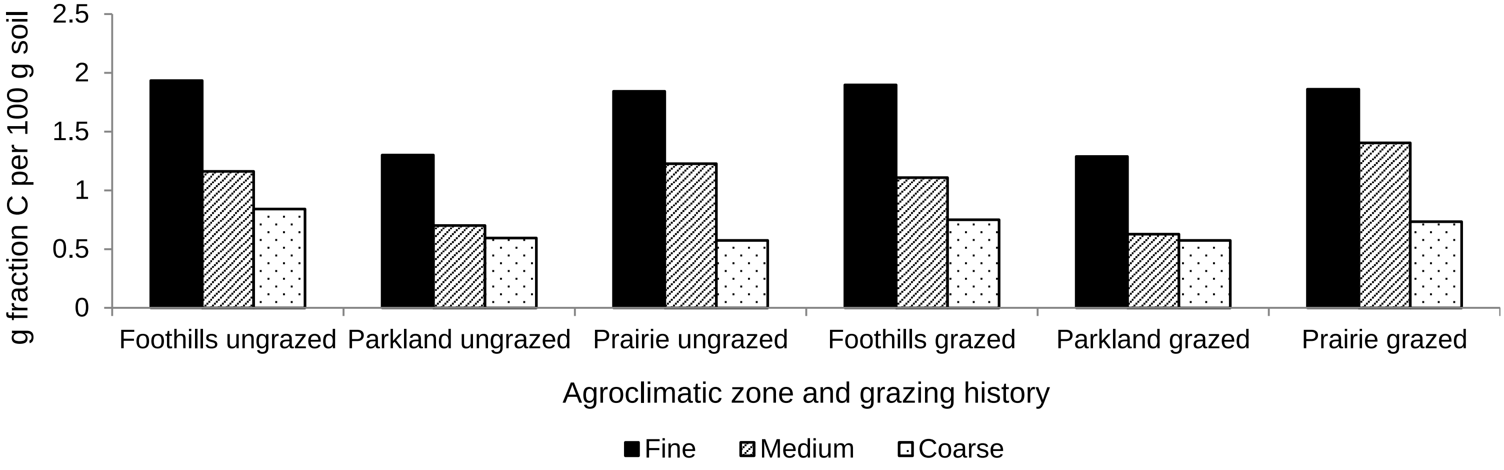

Figure 3. Preliminary carbon stores (on a soil mass basis) found within the fine (<53 µm) medium (53-250 µm) and coarse (>250 µm) size fractions and associated with different agroclimatic zones and grazing histories. A large proportion of carbon in Alberta grasslands is found in the fine fraction, which tends to be more resistant to decomposition.

Carbon stored in the fine fraction is generally considered to be more stable due to this fraction's increased resistance to breakdown. Our preliminary results suggest large differences exist in the C pool size among agroclimatic zones, with less variation attributed to grazing (Fig. 3).

Data analysis will include correlating standing C pools to soil, vegetation and climatic parameters from across sampling sites. Second, C pools will be compared among agroclimatic zones and areas with different grazing histories. Third, the size and stability of C pools will be interpreted using disturbance (i.e., land use) history and plant composition using multivariate analytical tools. Finally, we will use the collective results to develop an inventory of provincial C pools within perennial grasslands.This will be done by linking measured C concentrations to high resolution spatial maps of grassland distribution for the province (the Grassland Vegetation Inventory, developed by AESRD).

Understanding the role of grazing

This study is being expanded to investigate potential mechanisms that account for when, where and how grazing may alter grassland C. Our working hypothesis is that by altering species composition of the dominant grasses, cattle grazing may accelerate or slow down plant litter turnover, which in turn, would account for whether net C pools increase or decrease over time (Fig. 4). To examine this, we are using a subset of 12 exclosures (four in each of the Mixed Prairie, Parkland and Foothills) to examine rates of litter decomposition over an 18-month period. In addition to quantifying the decay of community litter, we will examine the decomposition rates of major grass species known to increase or decrease under grazing, as well as two other standardized controls. We will also use eco-enzyme assays conducted in both soils and litter to determine rates of organic C, N, and P turnover within these grasslands. Finally, at each of three additional locations, we will compare litter decomposition and nutrient cycling under three contrasting grazing treatments, including management-intensive rotational grazing, conventional set stocking, and no grazing. Collectively, these investigations will provide novel insights into the specific conditions under which grazing may increase C pools.

Figure 4. Cattle are known to alter plant species composition through selective grazing. If the species that increase in abundance decompose more slowly, this may lead to net carbon accumulation over time.

Implications

Comprehensive information on the size and stability of carbon pools, and how these are affected by cattle grazing, is necessary to promote the establishment of progressive policies to reward ranchers for C offsets in grasslands. Although policy instruments that promote C storage have existed for annual crop producers in Alberta for some time (e.g., C offsets for reduced tillage), no similar mechanisms are in place to reward beef producers for storing C in perennial grasslands. Ultimately, this research aims to provide the information needed to inform regulators and policy makers on the critical role of grasslands in providing the key ecological service of C storage and stabilization, and to direct future strategies for valuing new and existing C stored in rangelands by beef producers.

Acknowledgements

This project is funded by the Alberta Livestock and Meat Agency and Alberta Innovates – Bio Solutions, and has involved several collaborators from Alberta Environment and Sustainable Resource Development, including Mike Alexander, Craig DeMaere, Darlene Moisey, Jennifer Richman, Tennille Kupsch, Tanner Broadbent, and Laura Blonski.

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Agroforestry systems and grazed pastures play key role in storing carbon in Alberta

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Atmospheric greenhouse gas concentrations are rising and have been linked to changes in climatic conditions, including air temperatures and the timing and amount of precipitation. As a result, significant attention is being paid to strategies that reduce atmospheric greenhouse gases (GHGs), including biological sequestration. This natural process involves the use of live vegetation to convert atmospheric carbon into organic carbon pools, which may remain stable for time scales ranging from years to decades or even centuries (Christensen 2001). Soils represent one of the largest pools of terrestrial carbon, stored primarily as soil organic matter, the size and stability of which is directly impacted by changes in land use practices (Six et al. 1999). Agricultural management practices that increase soil carbon by some combination of increased plant growth and/or reduced carbon losses (via decomposition and/or erosion) are likely to be more effective in reducing GHGs (Paustian et al. 2000).

Agriculture has often been implicated for its role in increasing GHGs. Within agricultural landscapes, maintaining areas of forest may be an important strategy to increase soil carbon storage. Agroforestry is a land use that deliberately combines agricultural and forest land uses to achieve integrated benefits for farmers and ranchers (Lassoie and Buck 2000). Common examples of agroforestry in Alberta include the planting of shelterbelts and retention or promotion of natural hedgerows adjacent to annual cropland, or the grazing of forested bush pasture comprised of aspen groves intermixed with grassland. While many benefits of forests within these systems are well known, such as their role in reducing erosion, trapping snow, providing shelter to livestock, and promoting biodiversity and wildlife (see Kort et al. 2001), the benefits of these systems for increasing soil carbon and reducing GHGs remains unclear.

In this study supported by the Agriculture Canada – Agricultural Greenhouse Gases Program, we evaluate three agroforestry systems commonly found across central Alberta, and examine the contribution of the agricultural and forest land use components for their role in carbon storage and GHG reduction.

Methods

We sampled 36 randomly selected agroforestry systems, including 12 cropland-shelterbelts, 12 cropland-natural hedgerow systems, and 12 aspen forest-pasture complexes (i.e., silvopastures; Fig. 1), across a 270-km long (Athabasca to Lacombe) and 120-km wide (Stoney Plain to Wainwright) area in central Alberta. Study sites covered an agroclimatic gradient (encompassing variation in precipitation and temperature), and included a range of soils from Black and Dark Gray Chernozems, to Gray Luvisols. At each site, we quantified the size and stability of the soil carbon (C) pool along transects up to 50-m long in both forested and agricultural components of the landscape. Transects were on the same ecosite (slope, aspect, drainage) and separated by one mature tree length (30 m+). Ten, 3.2-cm wide soil cores were collected systematically along each transect. Cores were stratified into shallow (0-10 cm) and deep (10-30 cm) layers, and after preparation, samples were assessed for whole carbon concentration in the lab. To assess C stability, the whole soil was further separated into fine (< 53 μm), medium (53-250 μm), and coarse (250-2000 μm) fractions. Carbon in the fine fraction is less likely to decompose and be released to the atmosphere. Consequently, the fine fraction is considered more stable in the long-term and hence, is more important for reducing atmospheric C levels through biological sequestration in agricultural landscapes. Here we report on the soil C masses in the top (0-10 cm) layer only.

Figure 1. Typical silvopasture found in central Alberta, including a mix of grazed forest and adjacent grassland. Photo by M. Baah-Acheamfour.

Results and implications

Across all areas, 48.4%, 28.5% and 23.1% of soil organic carbon (SOC) was found in the fine, medium and coarse fractions, respectively. Mean SOC in the whole soil was greatest in the silvopasture, followed by the hedgerow and shelterbelt systems (Fig. 2). Similarly, the size of the soil C pool in most size fractions was greatest within the silvopasture, followed by the natural hedgerow and shelterbelt systems (Fig. 2), the lone exception being in the fine fraction, which did not differ between the hedgerow and silvopasture. Within each agroforestry system, the forested land use component consistently had more total SOC than the herbaceous agricultural component, a trend that applied to all fractions examined (Fig. 3). SOC was particularly low in the annual cropland (i.e. cultivated) components of the agroforestry systems.

Our results demonstrate the potential for trees, and grazed agroforests in particular, to increase soil C sequestration where they are maintained or established as agroforestry systems. Integrating trees with agricultural lands has potential to store more C than land managed for a single agricultural use, particularly those under monoculture crop production. Cropland tended to have the lowest SOC levels among all Agroforestry x Land Use combinations investigated, likely a result of the combined effects of soil C reductions due to crop removal, ongoing erosion of exposed soil and physical destruction of soil aggregates during cultivation, and net C loss due to elevated microbial activity created by the altered microenvironment under periodic cultivation (i.e., warmer, well aerated soil favors decomposition).

Most SOC in the shallow soil layer was in the fine fraction across the regional study sites, followed by the medium and coarse fractions, regardless of the agroforestry system studied. Carbon in the fine fraction is more stable than the coarse fraction. As the silvopasture and hedgerow systems had greater fine fractions of C, increased use of these systems may promote long-term storage of SOC compared to storage within shelterbelts. In this particular investigation, aspen forest and hedgerows were more diverse in plant composition and structure (i.e., they typically included trees, tall shrubs, low shrubs, and a variety of understory herb layers). This diversity may promote both understory production and associated SOC accumulation.

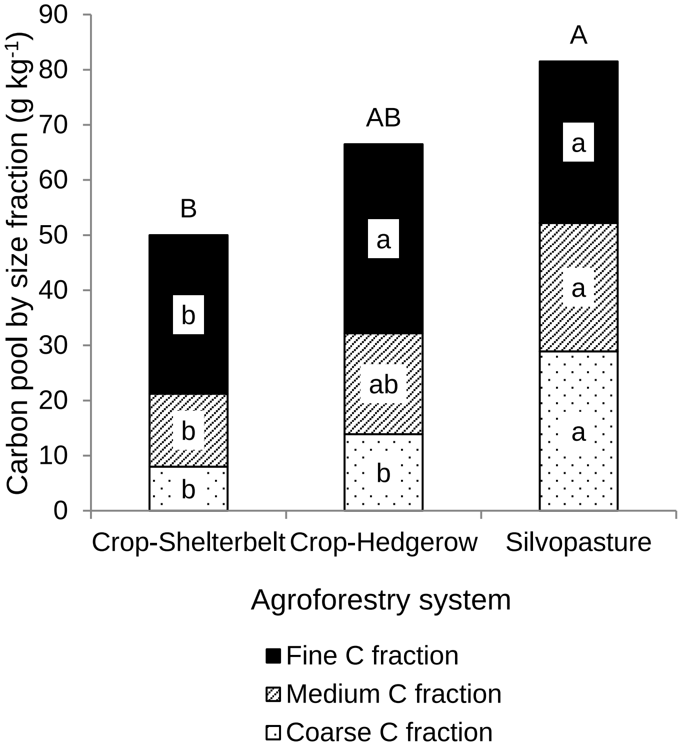

Figure 2. Distribution of soil organic carbon (SOC) in fine (< 53 μm), medium (53-250 μm), and coarse (250-2000 μm) soil fractions in each of three agroforestry management systems. Data represent the top 10 cm of soil. Total SOC values with different uppercase letters differ, at $P < 0.10$. Within each soil fraction, SOC values with different lower case letters differ, at $P < 0.10$.

The forested component of agroforestry systems is particularly important for C storage given that these areas contain greater SOC concentrations compared to adjacent herbaceous agricultural land uses, including larger pools of SOC in the more stable fine fraction. The fact that such favorable amounts of C can be stored by integrating trees and crops through agroforestry is important in the context of mitigating increases in atmospheric CO_2.

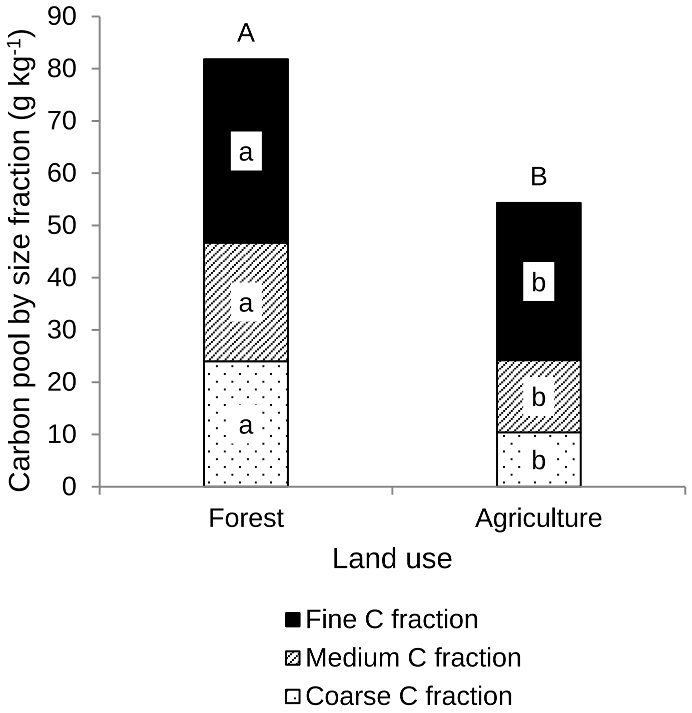

Figure 3. Mean soil organic carbon (SOC) in fine (< 53 µm), medium (53-250 µm), and coarse (250-2000 µm) soil fractions within the top 10 cm of soils associated with the forest and agricultural management systems sampled across central Alberta. Total SOC values with different uppercase letters differ, at $P < 0.10$. Within each soil fraction, SOC values with different lower case letters differ, at $P < 0.10$.

Although the data reported here exclusively consider C resources in the surface soil, when one includes the aboveground and belowground C stocks held in biomass (which can be substantial for woodland and perennial grassland communities), our results suggest that silvopastures may store the most C. Ongoing research will quantify the role of above- and belowground vegetation components in regulating SOC storage. This work is being further supplemented with direct measures of seasonal fluxes of GHGs (CO_2, N_2O and CH_4) and microbial activity within the agroforestry systems described here. Collectively, this information will lead to an improved understanding of the role of agroforestry, including silvopastures, for storing C and reducing GHG in the future, and is expected to help develop alternative C offset markets for farmers and cattle producers in Alberta.

Acknowledgements

This project was funded by the Agricultural Greenhouse Gas Program (AGGP) of Agriculture and Agri-Food Canada. We are grateful to S. Banerjee for participating in field data collection, to the many agricultural field men for helping find study sites, and to the numerous landowners across central Alberta who allowed us access to their farmlands to conduct this investigation.

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A new look at rangeland health and productivity

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- Is a more diverse rangeland healthier and more productive than a less diverse one?
- Can rangelands be used to sequester carbon and help stabilize our climate?
- Can these questions be addressed with automated instrumentation and satellite technology as a basis for long-term monitoring?

These questions are being addressed with a variety of remote sensing (non-contact) observational methods coupled with field measurements. Based on several years of study within grassland sites of Alberta and the United States, the answers emerging are generally positive. A key goal of the research is to develop operational methods of rangeland monitoring using remote sensing and automated field methods that can be readily and broadly used to detect changing patterns of vegetation productivity and address practical management questions. Given that rangeland performance varies widely in space and time in response to natural and anthropogenic drivers, these methods have several advantages over traditional field monitoring methods.

One aspect of the research involves testing new remote sensing technologies that can be deployed on light aircraft. From these platforms, imaging spectrometers are used to depict detailed vegetation patterns. Ground calibration using additional, automated instruments and biomass harvesting is used for validation (Fig. 1). These methods are being tested at the Mattheis Research Ranch in southern Alberta, as well as at various other locations around the world.

By combining remotely sensed imagery with ground measurements, we can develop calibrations that can be used to map spatial and temporal patterns of vegetation health, productivity and biodiversity. In this work, satellite time series of vegetation greenness (NDVI) are also compared to ground measurements (Fig. 2), including biomass (Fig. 3). Good agreement between these methods allows accurate estimation of rangeland yield and carbon uptake from satellite and airborne remote sensing. Automated field sensors are being tested for ongoing validation.

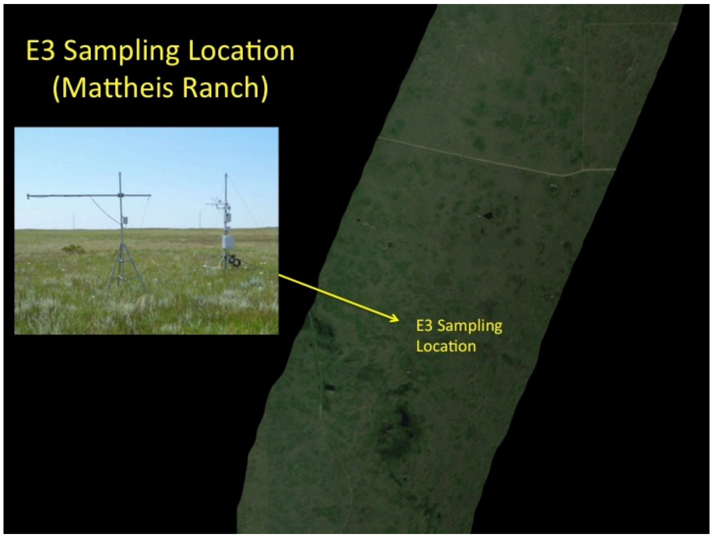

Figure 1. Airborne imagery (right) is validated and calibrated by ground instrumentation (insert on left). Shown here are instruments for measuring carbon uptake and vegetation reflectance.

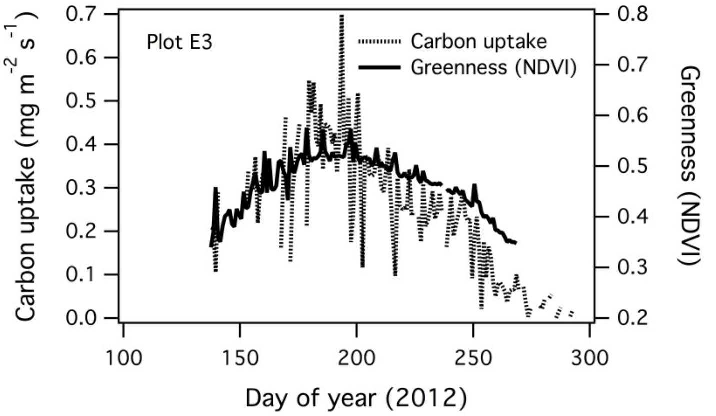

Figure 2. Ground instrumentation provides continuous time series of carbon uptake (dotted line) and vegetation greenness (Normalized Difference Vegetation Index [NDVI]; solid line) at the Mattheis Research Ranch. These "raw" data are subsequently corrected for aberrant effects of rain or other weather events, removing dips and spikes shown above, and

revealing broad seasonal trends. Both methods show maximum C uptake at midsummer when photosynthetic activity peaks. These seasonal patterns vary from site to site and from one year to the next showing dynamics in carbon uptake.

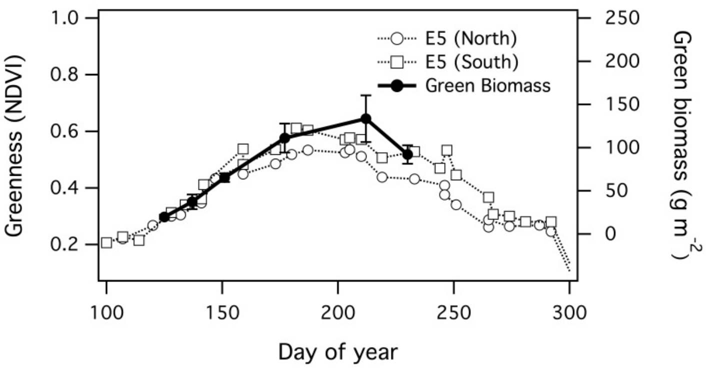

Figure 3. Satellite greenness (NDVI) measurements for two sites at Mattheis Research Ranch (dotted lines) compared to biomass harvests (solid line) for the ranch. Both greenness and the amount of biomass peak in mid-summer, with seasonal trends varying from year to year and site to site because of variability in site properties and growing conditions.

While addressing basic questions of rangeland health and productivity, these methods can also be used to evaluate practical management issues. For example, early impacts of drought or other climate-related stresses can be easily detected, and this can be used to inform rangeland insurance (e.g., forage shortfall and rainfall deficit) programs. These approaches can also assist in the determination of appropriate stocking rates and other "best practices" for maintaining overall rangeland health and productivity, while providing economic benefits (e.g., carbon credits) for good rangeland management. It is possible that effective rangeland carbon uptake and storage can help stabilize climate while providing these practical benefits. By integrating this research into a working cattle ranch (the Mattheis Research Ranch), ongoing studies being conducted at the University of Alberta are geared towards addressing these topics. Related research at other locations is currently addressing the role of biodiversity and species composition in overall health and productivity for prairie sites. Together, these methods provide a rich set of tools for maintaining the long-term sustainability of productive rangelands.

Acknowledgements

Funding for this work has been provided by the University of Alberta, the Rangeland Research Institute, NSERC, the Canadian Foundation for Innovation, and iCORE/AITF. Beginning in 2014, additional funding has been provided by US agencies (National Science Foundation and NASA) for remote sensing of biodiversity at other prairie sites. Additional thanks to Don Armitage, Saulo Castro, Chris Wong, Gilberto Pastorello, Li Hitao, Enrica Nestola for field assistance, to Donnette Thayer for data analysis, and to VeriMap Plus for assistance in airborne data collection.

Native pollinators in Alberta's agricultural landscape

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Insect pollinators, such as bumble bees and honey bees, provide a critically important ecosystem service (Vanbergen et al. 2013). Plants produce nourishing nectar and protein-rich pollen that bees use as a food source, and in return bees fertilize flowers so that they can produce seeds. Bees are responsible for pollinating most flowering plants and 35% of food crops worldwide (Klein et al. 2007). This ecosystem service ensures plant reproduction and a continuous supply of fruits and vegetables for human consumption while supporting a multi-billion dollar agricultural industry.

Figure 1. A native bumble bee pollinating an important forage crop, cicer milkvetch. Photo by C. Carlyle.

Insect pollinators are successful and highly efficient at pollination due to their ability to fly long distances and transport pollen. There are typically two types of bees: 1) commercial bees that are maintained by humans in artificial hives or colonies and relocated to pollinate crops; and 2) native bees (Fig. 1) that are wild and occur in natural settings where they pollinate native plants and crops at no cost. World pollination services are valued at approximately CDN $227B annually (Gallai et al. 2009). Unfortunately, the health and abundance of commercial bees is declining (Cameron et al. 2011) due to a myriad of factors generically referred to as Colony Collapse Disorder (CCD). There is still no defining cause of CCD but several factors in combination, including chemical pesticides and pathogens, are considered to be the underlying cause of bee mortality. In order to ensure the success of commercial crops, interest in native pollinators is increasing. In Alberta, there is little information about the current status of native bees, including their relative abundance and diversity, despite their critical importance for natural ecosystems and some annual crops. We are initiating three projects with support from the Alberta Livestock and Meat Agency (ALMA), the Alberta Biodiversity Monitoring Institute (ABMI) and the University of Alberta's Rangeland Research Institute (RRI) to examine the current status of native pollinators in Alberta and identify management strategies for pollinator conservation in Alberta's agricultural landscape.

Characterizing pollinators in rangelands

In our first study, supported by ALMA, we will survey Alberta's native grasslands to provide an inventory of pollinator diversity and abundance. We will relate this information to indicators of rangeland productivity and health. Most bees do not construct their own nests; instead they rely on abandoned underground burrows of other animals and grass tussocks to establish colonies (Kells and Goulson 2003). Consequently, native grasslands are likely important habitats for bees compared to cultivated lands where nesting sites are limited by mechanical soil disturbance (Kells and Goulson 2003). By facilitating flowering plant diversity and abundance through pollination, native pollinators can contribute to the quantity and quality of forage for livestock. The results from this project will help establish the role of rangelands in supporting bee diversity, and to inform grazing management practices that could benefit bee populations and enhance forage yields.

Bees and crop production

Our second project, supported by ABMI, will focus on linking canola production and crop management with pollinators. Bees are the dominant pollinators of canola in Alberta. Although the majority of canola planted in Alberta (*Brassica napus*) is self-compatible, seed yield can be improved by pollination (Hayter and Cresswell 2006, Bommarco et al. 2012). This study will determine which bee species are using canola and will identify factors affecting the diversity and abundance of these species, including landscape factors and agricultural practices. With these data, we plan to identify management strategies that can increase crop yields through support of native pollinator communities.

Alberta's agricultural landscape is a patchwork of rangeland and annual crops and bees are far ranging insects capable of travelling up to 3 km from their nests in search of food. Consequently, we will also examine if landscape factors predict bee communities and whether they are regionally correlated across different landscape types (e.g., rangeland, cropland). Rangelands provide suitable nesting habitat for pollinators (Kimoto et al. 2012) and early season floral resources that sustain pollinators until other floral resources become available. Later in the growing season, flower rich agricultural crops can provide abundant pollen and nectar to bees. Data from the rangeland and canola projects will allow us to examine how bee community composition varies in these landscapes and how proximity and variation in landscape characteristics alter pollinator diversity. In understanding how landscape factors affect native pollinator populations, community assemblages and abundance, we can make suggestions for future management and conservation of native pollinators in Alberta.

Cattle grazing and pollinators

The third project we have initiated is supported by the RRI and will examine the complex relationship between cattle, pollinators and native and invasive plant species. Native grasslands are subject to disturbances such as grazing by cattle and the introduction of non-native plants, which may alter floral resources and habitat available to native insect pollinators (Kimoto et al. 2012). Cicer milkvetch (*Astragalus cicer*) is a large European legume that is invading the dry mixed prairie of southern Alberta. Cicer milkvetch is a valuable forage plant, but due to its larger size and abundant flower production, it may compete with native flowering plants for pollinators. Furthermore, grazing of cicer milkvetch by cattle may affect invasive and native plant growth and allocation to floral resources. Influences of large herbivores on the fitness of forage species and subsequent pollinator responses are not well understood. Thus, we are taking a first step to unravelling these complex relationships in order to better manage environmental goods and services provided by grasslands.

Implications

At the completion of these projects we will have measured the relative abundance and diversity of bee pollinators in Alberta's rangelands and canola fields, and hope to understand some of the mechanisms affecting these measures. Further, we will be able to link pollinator communities to the quality and quantity of economically important plant systems such as forage species and canola yields. These projects are some of the first studies of their kind to be implemented across Alberta and our surveys will provide new insight into pollinator populations. The results will allow us to suggest management practices for the ranching and agricultural sectors that aid in the crucial conservation of native pollinators.

Acknowledgements

We thank the Alberta Livestock and Meat Agency, the Alberta Biodiversity Monitoring Institute and the University of Alberta Rangeland Research Institute for their support of these projects.

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Putting Alberta's ecosystem services on the map: focus on rangeland

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There has been recent attention on utilizing an ecosystem services (ES) approach to guide integrated regional planning, and enhance environmental outcomes through market-based instruments. However, connecting ES valuation information to policy action has proven challenging, with most programs still in the proof-of-concept phase. Accurate, spatially explicit information on ES value is necessary when incorporating ES approaches in policy. Although ES in Canada are estimated to be worth more than twice those of the U.S. (Sutton and Costanza 2002), the U.S. has significantly more information on ES value, including in grasslands, an ecosystem in which Canadian ES knowledge is conspicuously lacking (Molnara and Kubiszewskib 2012). Globally, grasslands are the most threatened ecosystem; they are also biodiversity hotspots and provide a host of ES, ranging from cultural values and pollination benefits to adjacent crop fields, to water catchment for downstream users.

The Alberta Biodiversity Monitoring Institute (ABMI) is addressing this lack of spatially-explicit, accurate information on ES in Alberta, through the Ecosystem Services Assessment Project, funded by the Alberta Livestock and Meat Agency and Alberta Innovates-Bio Solutions. Using a simulation-modeling approach, a series of ES including pollination, timber production, biodiversity, carbon storage and forage production, are being assessed at the provincial scale. Data are drawn heavily from ABMI's biodiversity, land use and land cover data, as well as other freely-available sources. Here we focus on two ES highly pertinent to grasslands: rangeland forage production and soil organic carbon (SOC) storage.

In efforts to curtail climate change due to rising atmospheric greenhouse gas concentrations, there is increasing interest in the benefits provided by SOC storage and sequestration, in terms of consequent climate regulation or climate change mitigation. Globally, soils store more than four times as much carbon as does the atmosphere, and SOC storage in grasslands exceeds that of other terrestrial ecosystems. Grasslands also provide significant SOC storage as compared to annual crops; in their meta-analysis, Guo and Gifford (2002) estimated 59% of SOC is lost in conversion from pasture to crop. Although its value is already represented in the economic market, another important ES provided by grassland is forage production on rangeland for grazing livestock. However, in Canada there has been an ongoing shift in land use activity evidenced by decreasing grasslands for livestock production, and towards increasing cultivated lands for crop production. This shift is bolstered by strong crop prices among other factors.

Methods

As our study area we used the agricultural extent of the province of Alberta, as defined by the Agricultural Region of the Alberta Soil Inventory Database[1]. We used ABMI's wall-to-wall Land Cover map to delineate native grassland areas. For our biophysical plant production and SOC model we used CENTURY, a model for SOC and nitrogen dynamics developed primarily for application in grassland systems (Parton et al. 1988). Minimum datasets to run the model include monthly rainfall and minimum and maximum temperature, soil texture, latitude, soil depth, nitrogen inputs, and fire and management regime. CENTURY has been widely used to estimate soil carbon and plant production across systems worldwide, including Canadian applications.

We extracted soil data from native soil types in the AGRASID database, across 26,105 polygons. For each polygon, we also extracted fine-scale climate data from ClimateWNA (Wang et al. 2012). The CENTURY model is designed to be run for single sites, thus we

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[1] See: http://www1.agric.gov.ab.ca/$department/deptdocs.nsf/all/sag3249

coupled CENTURY with i_Century[2], a model control system designed to allow simultaneous runs of Century for multiple sites. Linking these point-based results to their polygons essentially allows for spatially-explicit CENTURY model output.

The CENTURY model has been extensively validated and test under various soil, climatic and agricultural practices, and most of the internal parameters in CENTURY were based on experiments in Great Plains grasslands, of which Alberta rangeland is a northern extension. For initial C:N ratio in litter and mineral soil we obtained estimates from the literature to apply to all sites. For plant production, we chose parameters developed in CENTURY for temperate, cool-season grassland, and modified as necessary for our system. All other parameters were left to default values or, in the case of initial soil organic matter (SOM), established through equilibrium. To allow time to establish equilibrium SOM pools, we specified an equilibrium period of 4900 years. Management events can also be added in CENTURY; for the equilibrium period, we specified bison grazing and fire; for the recent period of the last 100 years, we specified cattle grazing according to local grazing practices, but removed fire events.

Preliminary results

Here we depict aboveground biomass removed by grazing as forage production (Fig. 1), and total SOC, including belowground structural and metabolic components as SOC storage (Fig. 2). We estimate total SOC storage in the top 20 cm across Alberta's native grassland to be 812 891 tonnes, and total forage production to be 29 017 153 kg. Another important question we are exploring with the use of the CENTURY model is the effect of grazing intensity on forage production and SOC (results not shown).

The Ecosystem Services Assessment project is working to further couple these results with the suite of ES within a scenario-modeling perspective, enabling projections of ES provision under varied land use scenarios. Applications of this information include regional planning, developing market approaches for enhancing ES, and sustainability and conservation reporting.

Acknowledgements

This project is supported by the Alberta Livestock and Meat Agency and Alberta Innovates-Bio Solutions.

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[2] See: http://www.card.iastate.edu/environment/interactive_programs.aspx

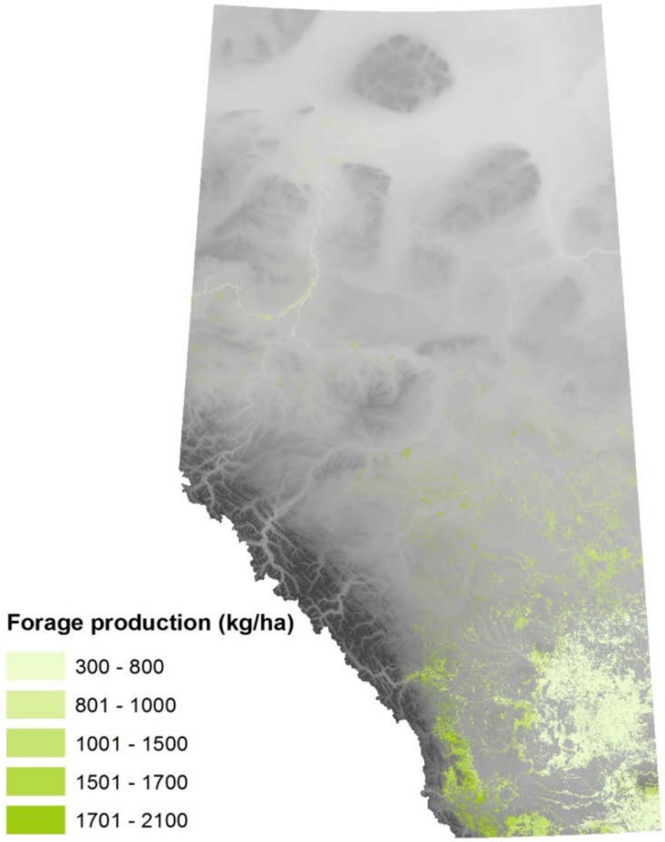

Figure 1. Estimated average annual forage production (kg ha^{-1}) across Alberta native grassland. Black areas indicate non-grassland.

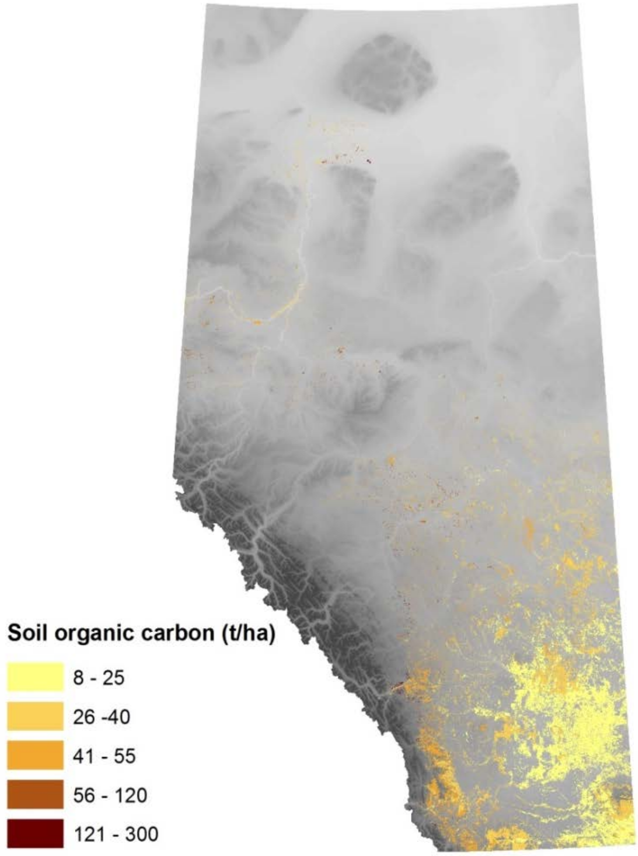

Figure 2. Estimated soil carbon storage (t ha^{-1}) across Alberta native grassland. Grey areas indicate non-grassland.

Cow-calf producers’ self-perceptions and the theoretical risks of sustainable development

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Two conflicting accounts of the environmental impacts of beef production can be found in both popular culture and academic literature. One tells a story of stewards of the land and ranchers who care deeply about the environment and rely on it for their families’ livelihoods (Ellis 2013). The other presents worrying data on environmental impacts from cattle production. These include degraded soil, water, and habitat and contributions of up to18% of global greenhouse gas (GHG) emissions (Capper 2011). Many authors suggest that additional research is needed to more thoroughly understand beef producer practices within their social contexts (Burton 2004, Ellis 2013). This study seeks to understand the space in which these conflicting accounts can simultaneously be true. To do so we consider the narratives that cow-calf producers draw upon to understand their role vis-a-vis the natural environment and the food production system of which they are a part. We then consider the impact those self-perceptions have on environmental management practices. As an example of a stewardship practice, we ask about producers’ thoughts on the use of genomics in selectively breeding for increased feed efficiency to reduce methane emissions from cattle. We consider these views relative to producers’ current environmental management perspectives. Overall, we find that producers understand themselves as doing what is good for nature by applying their local expertise through impactful management decisions. Sustainable development narratives are often drawn upon to come to this understanding. Applying critiques of sustainable development shines light on decision-making practices that may inadvertently result in adverse environmental impacts.

Methods and research paradigm

This study uses a focused ethnography, an approach that examines in-depth and personal insights into the practices and beliefs of sub-population of society (Knoblauch 2005). In this case, I focused my research on cow-calf producers because they make important decisions about local environmental matters as well as breeding. These breeding decisions may or may not be related to the use of genomics to enhance feed efficiency as a means of environmental improvement (Basarab et al. 2013). In total, 17 individuals in decision-making positions within cow-calf operations shared their time and stories by participating in semi-structured, qualitative interviews. Interviews took place in person ($n = 13$) and by phone ($n = 4$) and lasted one hour on average. Interviews were recorded, transcribed, and then coded using thematic analysis (Braun and Clarke 2006).

This research is informed by theories regarding sustainable development. We have focused on and applied key aspects of discussions regarding tensions between economic and environmental aspects of sustainable development. Sustainable development has become a widely accepted concept and strategy and it assumes that the wellbeing of environment and the economy do not conflict (Lele 1991). While this has opened some opportunities by reconciling a variety of interests, at times when the environment and development are in conflict this assumption may facilitate economic interests being prioritized at the expense of the environment (Robinson 2004, Seghezzo 2009). Certain qualities of sustainable development further encourage this, such as a focus on human rather than ecological needs, promotion of growth, and ambiguity (Seghezzo, 2009). Understanding how sustainable development mindsets may, in theory, result in prioritization of economic factors at the expense of the environment can help shed light on the positive and negative implications of producers’ self-perceptions.

Results and implications

As noted above, there are three key aspects to participants' explanations of themselves and their work relative to the natural environment and the food system they are a part of: being good for nature; holding local expertise; and impact of management decisions. Firstly, it was clear that many producers take pride in doing what they see as good for nature. Many participants explained how they were improving nature, such as increasing soil organic matter, and how they were making use of otherwise marginal areas. The majority of participants saw ranching as a natural fit on the landscape by their cattle filling the ecological niche of bison and requiring low resource inputs. Many producers felt they ought to be compensated for environmental outcomes but that the publically held misperceptions of the beef industry prevented this. With respect to genomics, producers generally believed that GHG contributions from their cattle were relatively low compared to other industries. At the same time, producers were excited by the prospect of cattle requiring lower resource inputs. This could, for example, reduce grazing pressures or feed purchases. While there are benefits to be gained from these pro-environmental values, to some extent economic development is seen by producers as necessary to protecting the environment. As we have learned from critiques of sustainable development, in situations where the economy and environment conflict this mindset may justify prioritizing the economy over the environment or may allow for negative impacts to be dismissed as natural. Further, this self-perception applies only to the land on which individuals operate and may not take into account the effects of even relatively small negative contributions to the big picture.

Secondly, producers saw themselves as the holders of local expertise. Real world experience and intimate knowledge of the unique qualities of their land made them capable decision makers. Subsequently, when making decisions about environmental management, participants felt well equipped to modify practices to suit their environmental and business needs. Many producers pursued environmental management practices they could custom fit and avoided rigid requirements for accreditation or funding. Extension programs and seminars were used to some extent for getting ideas but many individuals favoured smaller community groups of like-minded people. With respect to genomics, this aspect of producer self identity made many hesitant to adopt. Many producers felt they would have insufficient knowledge and power when selectively breeding using genomics. Further, some questioned the applicability of genomics on their particular landscape. Overall, we noted that producers' local expertise is bounded, applying to their own land. This again may ignore cumulative effects. Additionally, this expertise may often apply to altering environmental management practices to suit human needs specifically. Producers' self-perceptions as local experts could thereby further facilitate compromising environmental wellbeing, even unintentionally.

Lastly, participants emphasized the importance of management. Participants did not consider environmental and other operational management as separate. Further, most participants recognized that environmental harm could occur through cow-calf production but saw these risks as a matter of management, rather than inherent to production. For the most part, all possible environmental impacts were considered to be within the power of producers to control. However, producers frequently noted that many practices are expensive and costs were top of mind when making decisions. Overall, participants believed that through proper management, win-win situations were inevitable. Some producers saw GHG emissions as a matter of proper feeding management and therefore saw little need for genomics for this purpose. Tensions between the economy and the environment are especially apparent in this aspect of producer identity. Participants noted some environmental management practices are cost prohibitive and profitability must be prioritized. Also, understanding environmental issues as solely management issues may deny the degree of degradation occurring so as to justify further production (Goldman and Schurman 2000). Additionally, this perspective may lead producers to be mistakenly optimistic regarding their environmental mitigation abilities.

In summary, the mindset of sustainable development is used broadly and in some cases includes circumstances where economic growth is pursued at the cost of the environment in many situations world-wide. Aspects of this mindset are present in the descriptions that producers have of their own work and in their connection to the environment. These perspectives help us understand how accounts of environmental degradation and accounts of environmental caring from producers can co-exist with legitimacy. Importantly, this shines light on where producer mindsets and self-perceptions need to be considered so as to help the beef industry avoid the shortcomings of economic development at the expense of environmental sustainability.

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