National Program for Genetic Improvement of Feed Efficiency in Beef Cattle

US Consortium for the Genetic Improvement of Feed Efficiency in Beef Cattle

www.beefefficiency.org

Genetic Improvement of Feed Efficiency in Beef Cattle

Select cattle that are feed efficient, thereby reducing feed resources required to produce beef

BEEF EFFICIENCY
RESEARCH · EDUCATION · EXTENSION

Producers can
- Develop a cowherd that will produce progeny that are more efficient at converting nutrients to beef.
- Select animals for the feedlot that will use less feed to produce quality protein.

NIFA Funded Study
Provides a genetic selection tool that allows producers to select animals on profit when the output is growth and the intake is feed.
Includes:
- data from 8,000 animals (8 breeds)
- 18 scientists from 11 institutions

Study will genotype animals to generate MA-EPDs* for feed efficiency:
- feed intake
- growth
- carcass traits

* marker-assisted expected progeny differences

A 1% improvement in feed efficiency has the same economic impact as a 3% increase in rate of gain. Genomic predictors enable earlier selection decisions based on feed efficiency.

PROGRAM PARTICIPANTS
University of Missouri
Dr. Jerry Taylor, Project Director
Dr. Monty Kerley
Dr. Robert Schnabel
GeneSeek,
a Neogen Company
Dr. Elisa Marques
Iowa State University
Dr. Dorian Garrick
Dr. Stephanie Hansen
Dr. Dan Loy
Kansas State University
Dr. Robert Weaber
Texas A&M University
Dr. Chris Seabury
University of Illinois
Dr. Jon Beever
Dr. Dan Shike
University of Minnesota
Dr. Scott Fahrenkrug
University of Nebraska
Dr. Matt Spangler
Washington State University
Dr. Kris Johnson
Dr. Holly Neibergs
USDA – Beltsville, Maryland
Dr. Tad Sonstegard
USDA – Meat Animal Research Center
Dr. Harvey Freetly
Dr. John Pollak

USDA United States Department of Agriculture National Institute of Food and Agriculture

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OBJECTIVES

Research:
- Assemble DNA samples, individual animal FI, growth and carcass composition data for 8,000 animals representing 8 major US beef cattle breeds
- Genotype 2,400 animals from 6 breeds and develop and validate across-breed molecular expected progeny differences (MEPDs) for FI, growth and carcass traits
- Sample animals from the tails of the FE distribution from large groups (≥300) of Angus, Hereford, Gelbvieh and composite breed cattle with individual FI data for basic studies of GHG emissions, gut microbiome composition and tissue-specific gene expression/network studies
- Test an approach to rapidly identify FE causal mutations
- Develop and maintain DNA, RNA and phenotype repositories for project samples and publicly distribute these to the international research community
- Examine roles of mitochondrial complex I and III proteins on FE of 600 animals from 3 breeds (Angus, Simmental and Gelbvieh)
- Perform grain $\times$ forage and grow $\times$ finish feeding trials to quantify genotype $\times$ feeding regimen (nutritional environment) interactions on 900 Charolais steers and heifers with individual FI data
- Provide research experiences for undergraduates at CoPD universities to attract these students to graduate school and prepare the next generation of well-trained, diverse scientists with expert skills and breadth of knowledge to address sustainable beef production

Extension:
- Develop and deliver to a national industry-wide stakeholder audience the resources, tools, information and educational activities that will enhance their understanding of the: a) importance of FE to farm economics and resource use, b) emerging technologies for genetic improvement in FE and component traits (FI, growth, carcass composition), and c) options to use marker assisted management (MAM) systems to sustainably improve profitability
- Conduct a field demonstration project to demonstrate the utility of MEPDs for FE and component traits and "push" the technology into the beef industry
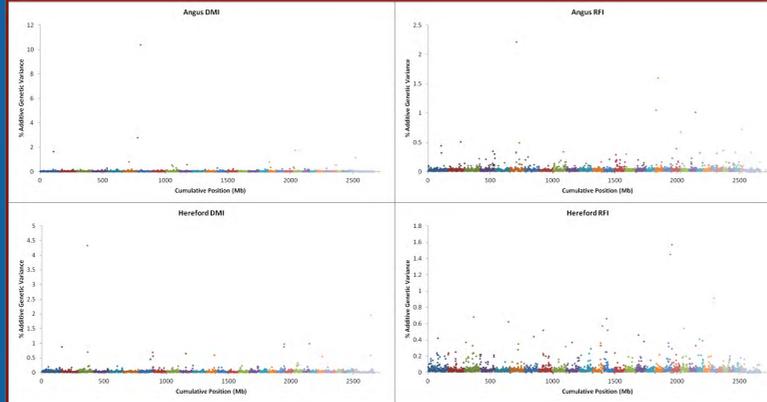- Deploy GS based on MEPDs for FE and component traits to the beef industry

Fig 1: GWAS for DMI and RFI in Angus (N=1,579) and (N=847) Hereford steers

Genomic Selection/GWAS

Table 1: Samples collected, genotyped and analyzed by breed

Breed	SNP50	HD	#Animals	#SNPs[1]	2013 Animals[2]	Total Animals[2]
Angus	1,093	510	1,603	747,473	435	2,038
Charolais		24	24	N/A		24
Charolais×Ang					450	450
Commercial Xbred					220	220
Gelbvieh		369	369	N/A		369
Hereford	361	491	852	684,458	300	1,152
Limousin		37	37	568,501	45	82
Normande					3	3
Pied×Ang×Simm	236		236	N/A		236
Red Angus		155	155	694,847	3	158
Simm×Ang	2,251	589	2,840	690,184	909	3,749
Wagyu		35	35	N/A	150	185
Total	**3,941**	**2,210**	**6,151**		**2,515**	**8,666**

[1] 50K imputed to HD using Beagle
[2] Does not include possible data exchanges with TEAGASC, the Canadian Feed Efficiency Consortium or USMARC

Table 2: BayesB(π=0.9995) analyses of DMI and RFI in Angus and Hereford

Breed	Trait	σ_G^2 (lb[2])	σ_E^2 (lb[2])	h^2	Largest QTL % σ_G^2	Largest 10 QTL % σ_G^2
Angus (N=1579)	DMI	4.12	7.51	0.35	10.39	21.02
	RFI	1.30	4.76	0.21	2.21	9.11
Hereford (N=847)	DMI	3.23	4.57	0.41	4.33	12.58
	RFI	1.57	1.94	0.45	1.57	8.04

GWAS Conclusions:
- Additive genetic variance similar between Angus and Hereford
- Larger residual variance for Angus (and lower heritability) probably reflects feeding at two different locations using Calan Gates versus GrowSafe systems
- Largest effect QTLs appear to differ between Angus and Hereford (Fig 1). Either different genes/mutations underlie variation in these closely related breeds or allele frequencies differ greatly affecting QTL allele substitution effects and ability to detect them via linkage disequilibrium
- Identification of causal mutations will need to be performed both within and across breeds (Fig 2)
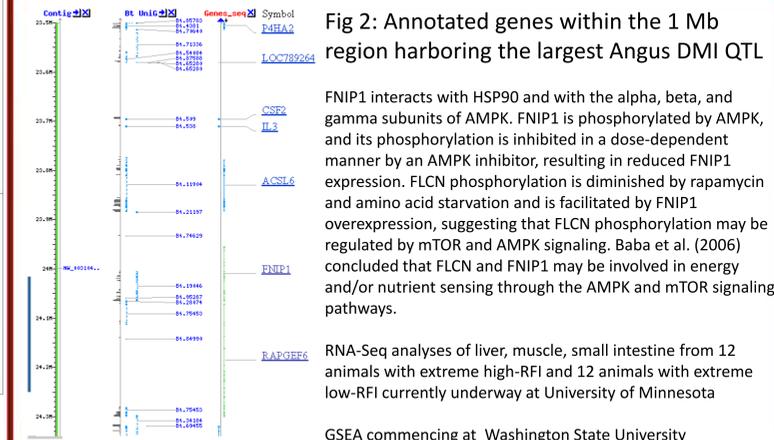

Fig 2: Annotated genes within the 1 Mb region harboring the largest Angus DMI QTL

FNIP1 interacts with HSP90 and with the alpha, beta, and gamma subunits of AMPK. FNIP1 is phosphorylated by AMPK, and its phosphorylation is inhibited in a dose-dependent manner by an AMPK inhibitor, resulting in reduced FNIP1 expression. FLCN phosphorylation is diminished by rapamycin and amino acid starvation and is facilitated by FNIP1 overexpression, suggesting that FLCN phosphorylation may be regulated by mTOR and AMPK signaling. Baba et al. (2006) concluded that FLCN and FNIP1 may be involved in energy and/or nutrient sensing through the AMPK and mTOR signaling pathways.

RNA-Seq analyses of liver, muscle, small intestine from 12 animals with extreme high-RFI and 12 animals with extreme low-RFI currently underway at University of Minnesota

GSEA commencing at Washington State University
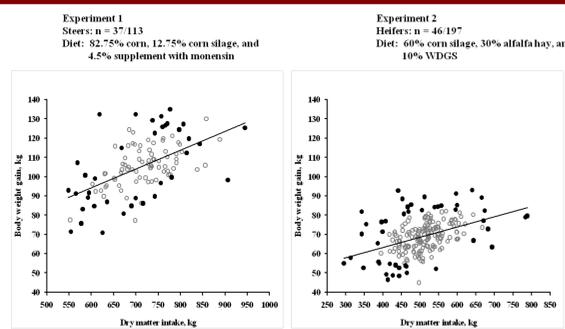
Methane Emissions

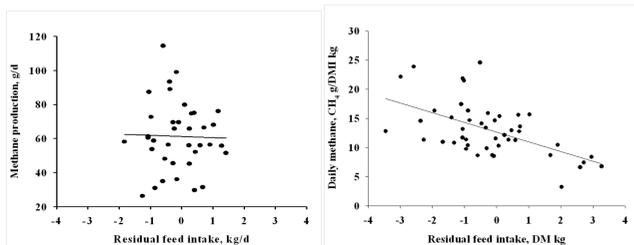Fig 4: Growth of individually fed animals selected for methane emission analysis

Fig 5: Relationship between RFI and methane production in steers (left) and heifers (right)

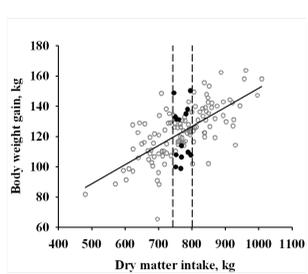$DMI = (0.126 \pm 0.013)DMI + 25.68 \pm 9.91; R^2 = 0.43$

Fig 6: Sampling of N=7 positive and N=7 negative residual gain steers at the same level of dry matter intake from 132 individually fed crossbred steers

Methane ctd

Table 3: *In vitro* methane production/unit dry digesta of steers differing in residual gain (mmol·min-1·g-1)

Residual Gain	Rumen	Cecum	SE
Positive (n = 7)	50.81×10^{-5}	3.529×10^{-5}	7.258×10^{-5}
Negative (n = 7)	51.11×10^{-5}	3.585×10^{-5}	7.258×10^{-5}

Methane Conclusions:
- Rumen is a much greater source of methane in ruminants than is the cecum (as expected)
- Animals that more efficiently convert feedstuffs into growth do so with higher levels of methane emission than do less efficient animals (reduced methane production in high efficiency animals in published studies primarily driven by reduced feed intake)
- *Speculation:* Animals with higher FE have higher digestion rates (rumen fermentation rates) and passage rates which lead to higher amounts of methane production rather than lower amounts as previously suggested
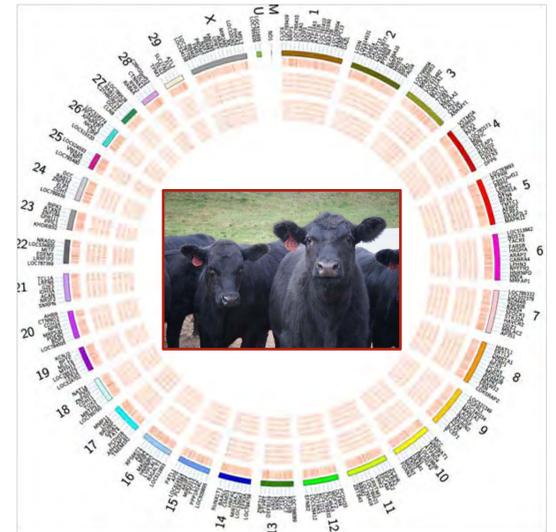

Fig 3: RNA-Seq of liver samples from 4 high- and 4 low-RFI Angus steers

Extension/Demonstration Project

- Advisory Board meeting held March 4-5, 2011 in Kansas City
- Project stakeholder conferences held June 21-22, 2011 and June 27-28, 2012 at USMARC. Audience ~120 seedstock and commercial producers including the Weight Trait Project participants and academic/USDA scientists. Presentations are at www.beefefficiency.org
- Youth Meeting—Junior members (9) of the breed associations involved in the Field Demonstration Project attended the annual meeting and also toured Neogen and USMARC
- Youth Beef Industry Congress held February 2012 in Nashville. Audience ~125 junior board members from all of the major US beef breed associations and several state cattlemen's associations
- Cattlemen-to-Cattlemen Programming - Three video segments produced for the National Cattlemen's Beef Association's Cattlemen-to-Cattlemen program. Latest two aired on RFD TV Sept 11 and 19, 2012. Segments provided an overview of importance of FE and the role of genomics in genetic improvement. A fourth segment will be produced in 2013
- Stakeholder Survey - Developed a nationwide stakeholder survey on feed efficiency, genetics and genomic concepts in collaboration with USDA NASS. Anticipate February 2013 mailout
- Website: Developed project web site, www.beefefficiency.org including activation of a Q&A Section, a comprehensive page overviewing the producer demonstration project, hotlinks to investigator pages, videos of annual meeting presentations, and links to segments broadcast on NCBA's Cattlemen-to-Cattlemen on RFD-TV.
- Plans for 2013 include a display in the NCBA trade show convention and beginning the development of a fact sheet series for producers
- Demonstration project – 700 animals 50K and 70 animals 780K genotyped in 24 seedstock herds representing 7 breeds. ~220 sire identified steers produced from mating collaborating producer herd bulls and commercial cows owned by our commercial ranch partner sent to MU to collect individual animal feed intake data. ~400 steers and heifers produced from mating collaborating producer owned bulls with crossbred cows at USMARC weaned and sire identified. 750 cows bred via AI at USMARC to collaborating producer owned bulls in 2012 using semen donated by the producers and will calve in 2013