



Genomic Approaches to Improve Grazing Distribution

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Status of Large Animal Genome Sequence and Tools

Item	Cow	Horse	Sheep	Goat	Yak
Reference genome	✓	✓	✓	✓	✓
Additional animals sequenced	✓	✓	✓	✓	
50K SNP-chip	✓	✓	✓	✓	
HD SNP-Chip	✓	✓			
Other SNP-Chips	✓				
Functional information on SNP-Chip	✓				



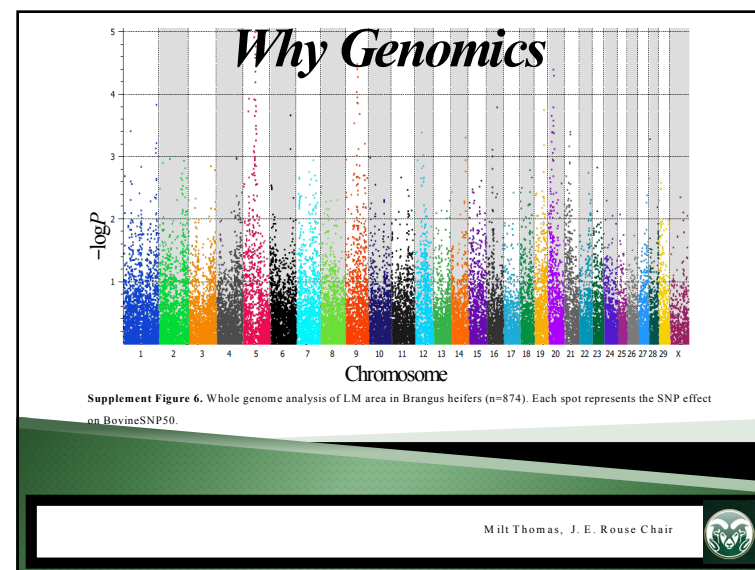

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Evolution of EPD models for beef cattle:

1. Animal (pedigree)
2. Multi-trait
3. Multi-breed
4. gEPD (genome enhanced)
 - a. Molecular breeding value
 - b. Genomic relationship matrix

± Value (accuracy)

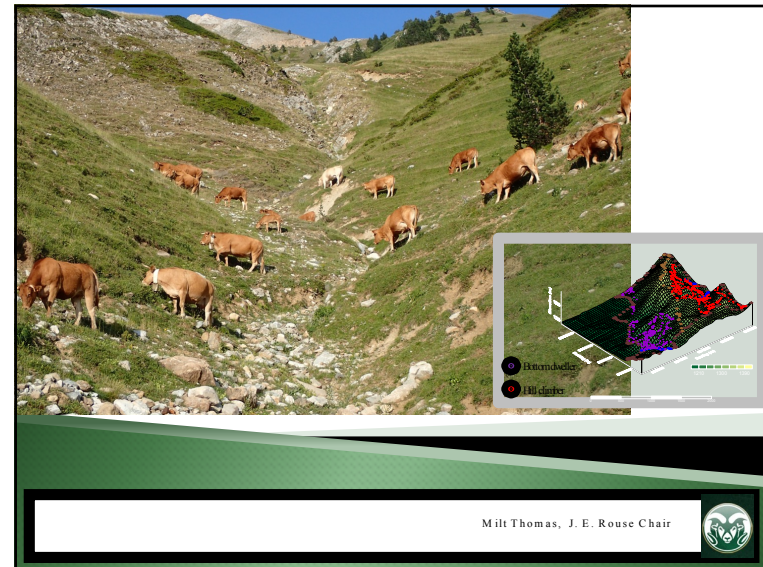
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Beneficial use of DNA technology will primarily be for genetic improvement of *traits difficult to measure*:

- a. Feed efficiency
- b. Fertility
- c. Health traits
- d. Grazing distribution
- e. Consumption traits
- f. etc.

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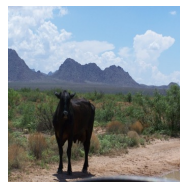
Two terrain-use indices (Bailey et al. Range Ecol. Mgt. 68:142-149; 2015)

Rough Index = Slope + Elevation

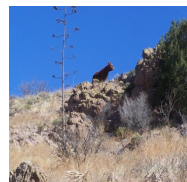
Rolling Index = Slope + Elevation + Distance from Water



Bottom dweller
(<100)

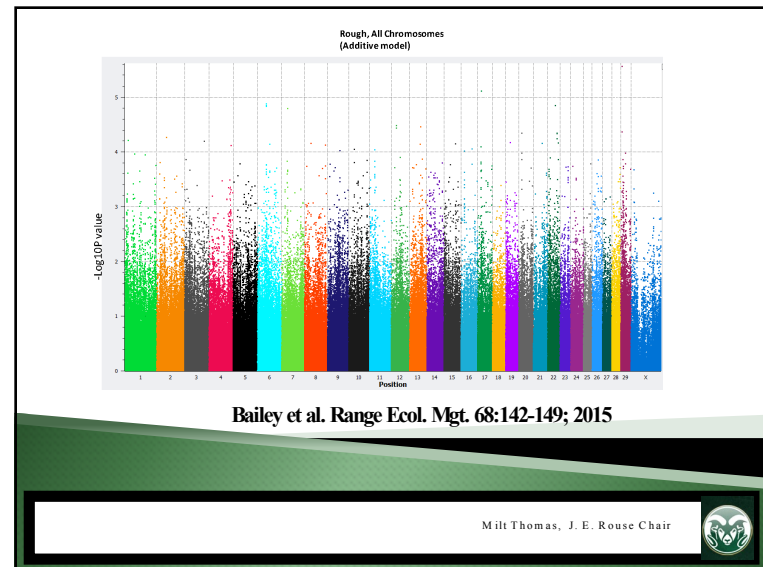


Average
(=100)



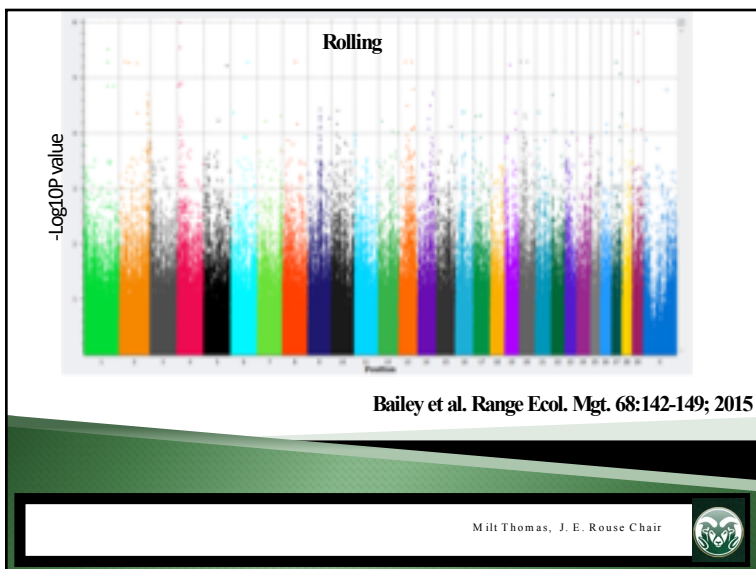
Hill climber
(>100)

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Candidate Genes from GWAS of Rough and Rolling Indexes

Chromosome	Gene	Function
29	GRM5	Locomotion, motivation, and spatial memory
17	MAML3	Regulation of neurogenesis, myogenesis, etc.
8	RUSC2	Regulation of intracellular transport
4	SDHAF3	Gluconeogenesis and carbon assimilation
12	SUPT20H	Autophagy, gastrulation, and regulation of ER stress

Bailey et al. Range Ecol. Mgt. 68:142-149; 2015

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Implementation of Genetic Selection for Grazing Distribution to Make Cattle Grazing in the Western US More Sustainable (SW15-015)

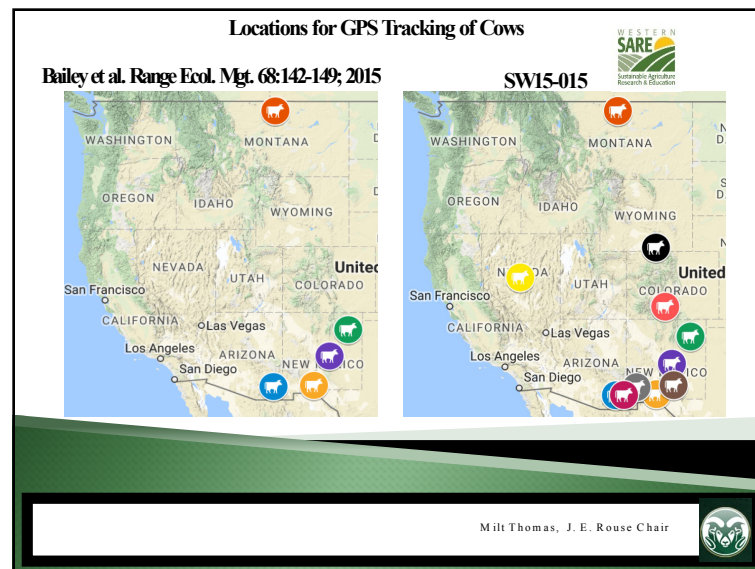
NMSU = Derek Bailey, Michael Millard, Tatjana Mercardo, Maggie Gannon, Colt Knight (U of Maine – extension)

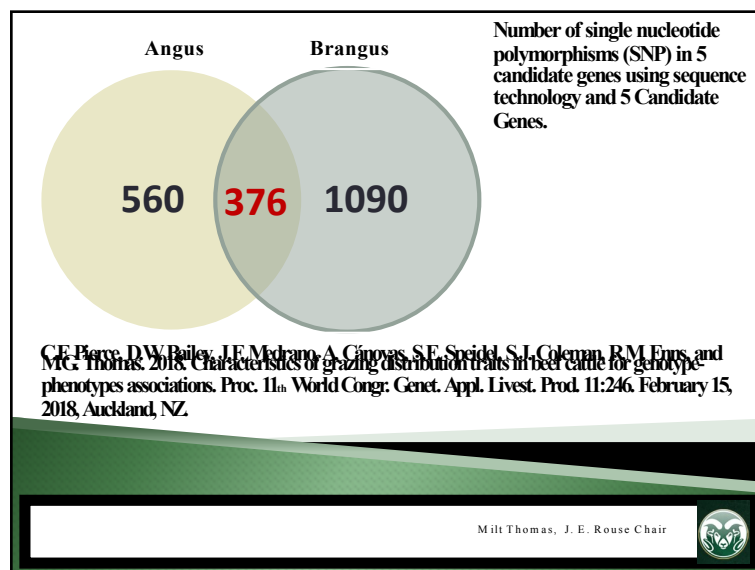
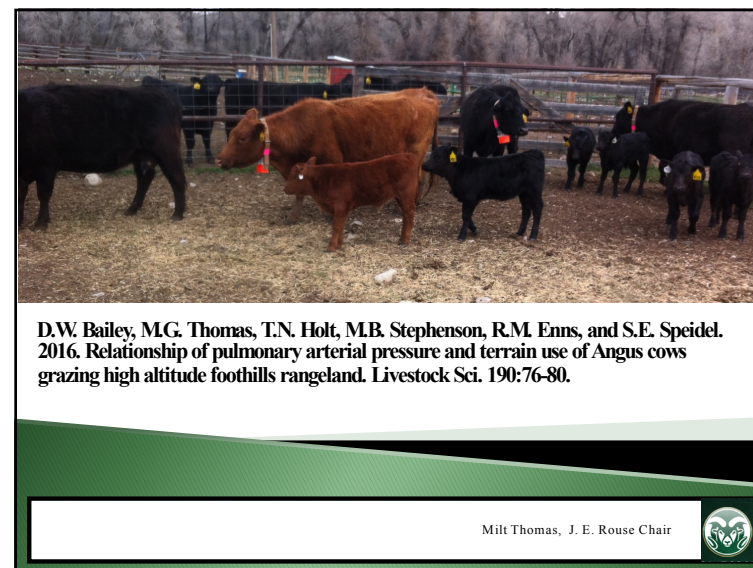
CSU = Courtney Pierce, Scott Speidel, Mark Enns, Milt Thomas

UC-Davis = Juan Medrano, Angel Canovas (Guelph)

UA = Larry Howery

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Why Bayesian statistics?

Simple Linear Regression	Bayesian Approach
Test individual SNP	Test all SNP simultaneously
Explain small fraction of genetic variance	Account for larger portion of genetic variance
Power of detecting associations is inversely related to the number of SNP tested	Power of detecting associations isn't inversely related to the number of SNP tested

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Results: Rough Index

CHR	SNP1	Posterior Inclusion Probability	Distance from Previously Identified SNP (Mb)	Did We Validate?
4	BovineHD0400028256	1.6%	86.3	No
12	BovineHD1200012572	2.1%	20.8	No
17	BovineHD1700005311	2.1%	-	Yes
29	BovineHD2900007615	2.2%	18.9	No

1Single nucleotide polymorphism with highest posterior inclusion probability

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Results: Rolling Index

CHR	SNP1	Posterior Inclusion Probability	Distance from Previously Identified SNP (Mb)	Did We Validate?
4	ARS-BFGL-NGS-63223	1.5%	28	No
17	BovineHD4100013008	2.1%	12	No
29	BovineHD2900006334	2.3%	15	No

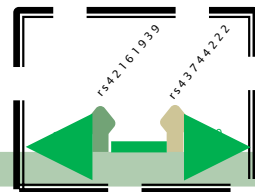
1Single nucleotide polymorphism with highest posterior inclusion probability

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Region of Interest

- Issues obtaining accurate results when # of observations is small in comparison to # SNP (Van den Berg, 2013; Yazdani and Dunson, 2015)
- Truncate the data to reduce # of markers
- Chose CHR29 because of gene function
- # of markers: 13,902 → 50



GRM5

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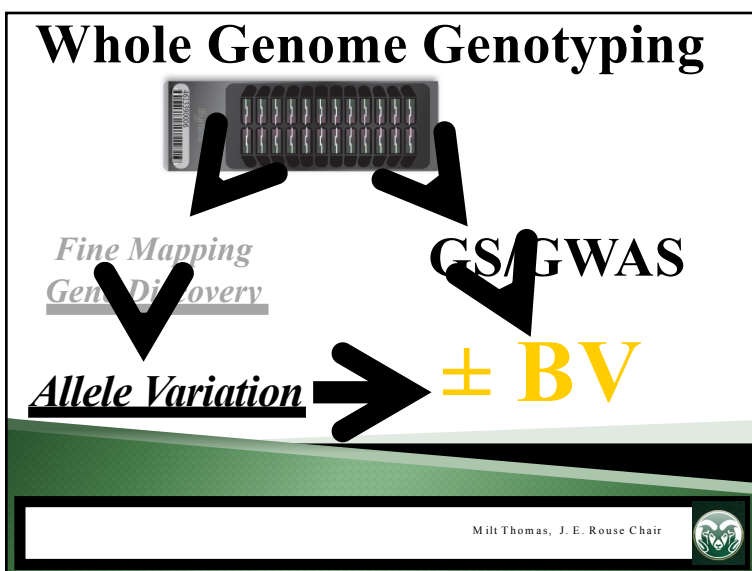
Results: region of interest

CHR	SNP1	Posterior Inclusion Probability	Distance from Previously Identified SNP (Mb)	Did We Validate?
29	BovineHD2900001972	54.9%	-	Yes
29	BovineHD2900001982	21.6%	-	Yes

1Single nucleotide polymorphism with highest posterior inclusion probability

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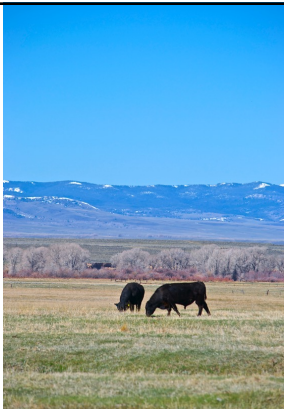
Conclusions:

1. Genetics of grazing distribution is complex (i.e., many traits, distance, slope, elevation).
2. Polygenic.
3. Lots of work to do to translate genomic tools to industry!



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Questions and Discussion



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