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Current Design of the Germplasm Evaluation Project

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Goals of the Transition to a New Structure

- Provide information that serves the current needs of the beef industry as efficiently as possible.
- Develop a population that provides the resources to respond to future needs of the beef industry as rapidly as possible.
  - Design the project in such a way that it can adapt rapidly to changing needs or better ideas.

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Current Primary GPE Objectives

- Characterization of Genomic Variation in Germplasm Representative of the Beef Industry
  - Linkage Disequilibrium
  - Linkage

- Estimation of Differences Among Breeds Used by the U.S. Beef Industry
  - Multi-breed Genetic Evaluation
  - Breed Differences for New Traits

- Evaluation of Exotic Germplasm

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Secondary GPE Objectives

- Estimation of heritabilities and genetic correlations
  - Especially between new physiological indicator traits (e.g., gene expression, proteomics, metabolomics) and economically relevant traits.
  - Among the full spectrum of economically important traits
- Estimate breed-specific heterosis

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Trait Categories Evaluated

Calving
- Dystocia
- Survival

Growth
- Gestation Length
- Birth Weight
- Weaning Weight
- Postweaning growth
- Mature weight, height, and condition

Maternal
- Birth Weight
- Dystocia
- Survival
- Weaning Weight
- Milk Production

Carcass & Meat Quality
- Shear force
- Cutability
- Yield Grade factors
- Marbling
- Color Stability

Efficiency
- Feed utilization of finishing steers
- Feed utilization of pre-breeding heifers
- Mature cow maintenance requirements
- Rumen microbial composition

Reproduction
- Heifer age at puberty
- Heifer pregnancy rate
- Cow pregnancy rate
- Fetal death loss
- Postpartum interval
- Male fertility

Longevity

Disease Resistance

Adaptation

… and many more.

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Sires Sampled Since 2006

98	Angus	36	Beefmaster
75	Hereford	33	Maine-Anjou
69	Simmental	38	Brahman
58	Charolais	32	Santa Gertrudis
54	Red Angus	34	ChiAngus
56	Limousin	34	Salers
48	Gelbvieh	31	Braunvieh
36	Shorthorn	14	South Devon
38	Brangus	10	Tarentaise

794 Total

Sire Sampling Process

- Aim is to sample high accuracy sires that are as influential in their breeds as possible.
- We greatly appreciate the cooperation, support, and patience of the breed associations, bull owners, and AI industry.
- We do our best to sample each breed as fairly as possible.
- And then, we do our best to adjust out any remaining sampling differences in the analyses.
- We produce roughly 10 progeny per bull sampled.

New Population Structure

AI Sires:
AN, HH, SM, CH, AR, LM, GV, SH, BN, BM, MA, BR, CI, SG, SA, BV, SD, TA

Dams:
AN, HH, SM, CH, AR, LM, GV, SH, BN, BM, MA, BR, CI, SG, SA, BV, SD, TA

PB & F_1 Steers   PB & F_1 Bulls   PB & F_1 Heifers
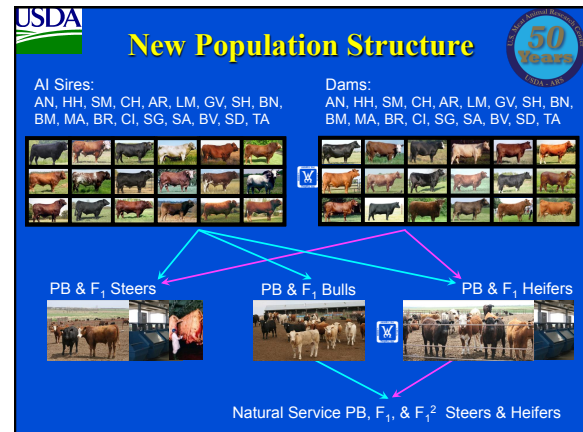
Natural Service PB, F_1, & F_1^2 Steers & Heifers

Calves Produced by Year

Birth Year	AI 1/2	3/4	7/8	15/16	PB	Nat. Serv.	Total
2007	277	38				21	336
2008	629	204			42	1379	2254
2009	345	227	6		123	1548	2249
2010	415	204	27		128	1585	2359
2011	434	308	82	2	115	1369	2310
2012	488	274	115	8	122	1284	2291
2013	318	302	145	36	127	1553	2481
2014	388	153	73	20	46	1248	1928
Spring	2050	1148	323	47	512	8247	12327
Fall	1244	562	125	19	191	1740	3881
Total	3294	1710	448	66	703	9987	16208

AI-sired Calves Produced

Breed	1/2	3/4	7/8	15/16	PB	Total
Angus	246	135	26	2	167	576
Beefmaster	224	66	5			295
Brahman	204	56				260
Brangus	243	67	6		1	317
Braunvieh	209	73	17	1		300
Charolais	141	97	27	7	191	463
Chiangus	216	77	33	1	11	338
Gelbvieh	143	162	79	12		396
Hereford	194	114	19	1	184	512
Limousin	134	180	69	18		401
Maine Anjou	240	90	20			350
Red Angus	143	166	68	17		394
Salers	202	94	14			310
Santa Gertrudis	204	81	22	2		309
Shorthorn	246	109	19	1		375
Simmental	205	110	23	4	149	491
South Devon	47	13				60
Tarentaise	53	16				69
Total	3294	1706	447	66	703	6216

TABLE 2: BREED OF SIRE MEANS FOR 2012 BORN ANIMALS UNDER CONDITIONS SIMILAR TO USMARC

Breed	Birth Wt.	Weaning Wt.	Yearling Wt.	Maternal Milk	Marbling Score[a]	Ribeye Area	Fat Thickness
Angus	87.0	574.3	1051.3	563.3	6.10	13.19	0.639
Hereford	91.3	568.6	1017.2	540.4	5.34	12.92	0.580
Red Angus	88.0	558.1	1018.4	558.8	5.67	12.83	0.598
Shorthorn	93.5	551.3	1018.0	563.2	5.44	12.92	0.485
South Devon	91.1	564.1	1020.9	564.6	5.89	13.18	0.503
Beefmaster	91.8	573.4	1012.6	547.7			
Brahman	97.9	587.0	1000.4	569.2	4.76	12.72	0.489
Brangus	90.3	565.9	1014.0	552.5			
Santa Gertrudis	92.3	570.4	1014.0	552.5	4.93	12.68	0.527
Braunvieh	90.2	542.1	979.6	574.2			
Charolais	94.4	589.8	1052.0	553.7	5.20	13.97	0.416
Chiangus	91.1	545.2	990.4	550.4	5.39	13.25	0.494
Gelbvieh	89.3	571.4	1033.6	570.5	5.27	13.81	0.447
Limousin	90.6	571.4	1009.9	554.9	4.88	14.35	
Maine-Anjou	91.8	546.1	1001.7	552.3	5.09	13.81	0.401
Salers	88.9	562.1	1020.8	561.9	5.71	13.56	0.422
Simmental	90.8	584.1	1044.9	563.5	5.32	13.93	0.420
Tarentaise	88.9	573.0	1004.2	565.0			

[a]Marbling score units: $4.00 = SI^{00}$; $5.00 = Sm^{00}$

Philosophy

- It is more efficient to concentrate the collection of extensive and expensive phenotypes on populations that can be used for multiple objectives.
- We have moved beyond cycles into continuous evaluation.

Slide 1 — Emphases of Genomics Research

Calving
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- Survival

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Slide 2 — Emphases of Genomics Research

Multi-breed Prediction

PB & F$_1$ Steers   PB & F$_1$ Bulls   PB & F$_1$ Heifers

Natural Service PB, F$_1$, & F$_1$² Steers & Heifers

Slide 3 — Sequenced Bulls

PB	F$_1$	Breed		PB	F$_1$	Breed
24	6	Angus			1	Brangus
21	13	Hereford				Beefmaster
20	12	Simmental			4	Maine-Anjou
19	12	Red Angus		2	4	Brahman
22	15	Gelbvieh			4	Chiangus
19	14	Limousin			5	Santa Gertrudis
23	5	Charolais			7	Salers
	6	Shorthorn			3	Braunvieh
180	**81**	**Total**				

Slide 4 — Imputation of Genomic Sequence to Thousands of Descendants

- An approach to determining genomic sequence of many individuals at low cost per animal.

Sequenced

Slide 5 — Imputation of Genomic Sequence to Thousands of Descendants

Color indicates chromosomes with identical genomic sequence

Color of diamonds indicates DNA markers with different states

Gray background indicates region containing a crossover in which origin (and hence sequence) cannot be inferred unambiguously

No region of unambiguity around crossover in sequenced animal

The gray chromosome segments represent DNA inherited from ancestors that have not been sequenced. Currently about 25%. Will decrease in future.

Sequenced

In practice, there will be far more descendants genotyped (at low cost per animal) than ancestors sequenced (at higher cost per animal)

Slide 6 — Challenging Assumptions of Animal Breeding

- As we have started estimating breed-specific heterosis effects, the most interesting result is that the model we have been using to estimate heterosis retention in composites may be underestimating heterosis retention somewhat.

Adjust the Project Design as We Learn Which Assumptions Need to be Tested

- So, we are exploring ways to adjust the population design to test long-standing assumptions about heterosis.
- I believe we can do this without increasing the cost of the project and with minimal impact on other objectives of the project.

Conclusions

- I am confident that we utilize your tax dollars more effectively by using the same cattle to address multiple objectives simultaneously than would be possible with a number of smaller projects, each focused on only one objective.

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For More Information:

www.ars.usda.gov/Main/docs.htm?docid=6238

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