Current Status of Genotyping and Discovery Work at USMARC

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Beef cattle **Genotyping and Discovery at USMARC** has been impacted tremendously by the release of the 50K marker chip (Illumina® BovineSNP50 Beadchip) by Illumina in 2008 (Figure 1). This product introduced a new realm of research possibilities by providing a platform where animals could be genotyped for over 50,000 **DNA markers** at one time. These markers are distributed evenly across the entire **genome**. As a result, these DNA markers are dramatically more likely to explain the variance in economically relevant traits caused by **genes** on any chromosome. The application of this panel has already significantly changed genetic evaluations for dairy cattle. However, beef cattle have several challenges that have slowed application (many more breeds, less artificial insemination, and an interest in traits that are not routinely evaluated in **national cattle evaluation**). Research at USMARC is focused on overcoming these challenges.
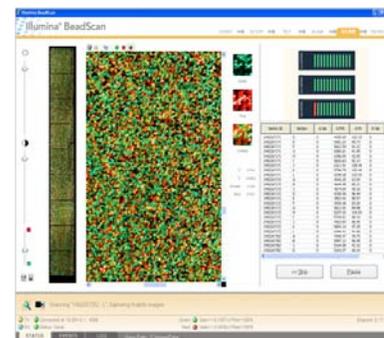

Figure 1. Processing of 50,000 markers on the Illumina BovineSNP50.

Development of Marker Panel for the Weight Traits Project (WTP): USMARC has **genotyped** over 6,000 animals using the 50K marker chip. Approximately 3,000 of these animals were calves born at USMARC with birth, weaning and yearling weights. From these records, 192 markers that explained the highest amount of genetic variation in weaning and yearling weight were selected to add to the WTP panel (in combination with a weight panel and parentage markers from Igentity®). Markers were selected on a genomic region-by-region basis to maximize genetic variation explained.

2,000 Bull Project: USMARC genotyped over 2,000 bulls in collaboration with the 16 largest US breed associations that have a genetic evaluation (Figure 2). The purpose of this project was to evaluate the effectiveness of producing marker tests from a discovery population (USMARC) and exporting these genomic predictions to an industry representative set of animals. Correlations between USMARC predicted **molecular breeding values** and industry **expected progeny differences (EPD)**

Angus	402	Brangus	68
Hereford	317	Beefmaster	64
Simmental	253	Maine-Anjou	59
Red Angus	173	Brahman	53
Gelbvieh	136	Chiangus	47
Limousin	131	Santa Gertrudis	43
Charolais	125	Salers	42
Shorthorn	86	Braunvieh	27
			2026

Figure 2. Number of bulls sampled in the USMARC 2,000 Bull Project.

have not been high (in the range of 0.10 to 0.40 across traits); however, it is important to remember that these correlations are limited by the accuracy of EPD. Also, it has led researchers at USMARC to begin looking at methods to evaluate breed specific effects of markers in our crossbred populations. The 2,000 Bull Project has had additional benefits

including the delivery of resulting genotypes to the participating breed associations and the development of tests for breed composition in crossbred animals.

Breed Composition Test: Based on the frequencies of each marker for each breed in the 2,000 Bull Project, breeds can be shown as genetically distant from one other (Figure 3). Although some of the distances are inflated due to biases from the discovery source of the DNA markers on the 50K chip (e.g., Hereford origin vs. Angus origin), these distances can be exploited to determine breed composition of animals with unknown pedigree. Using a relatively simple procedure, scientists at USMARC were able to accurately predict the (known) breed composition of a set of 4-way cross cattle that had been genotyped using the 50K chip. Accuracy of this prediction averaged well over 90% (Figure 4) and at least some of the drop in accuracy was likely due to pedigree errors. This methodology is likely not cost effective for use in determining breed composition in non-source verified commercial animals, but it may be useful in determining the average breed composition of groups of animals using a pooled DNA sample.

AN: Angus GV:Gelbvieh
BM: Beefmaster LM: Limousin
BN: Brangus MA: Maine Anjou
BR: Brahman RA: Red Angus
BV: Bruanvieh SA: Salers
CA: Chiangus SG: Santa Gertrudis
CH: Charolais SH: Shorthorn
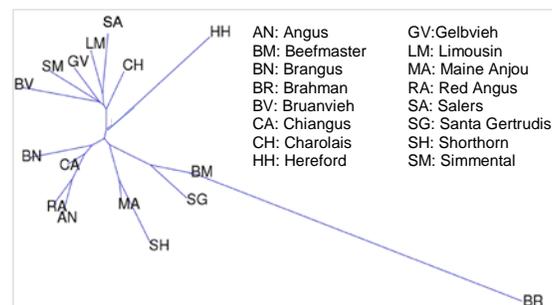HH: Hereford SM: Simmental

Figure 3. Approximate genetic distance between breeds using data from the 2,000 Bull Project.
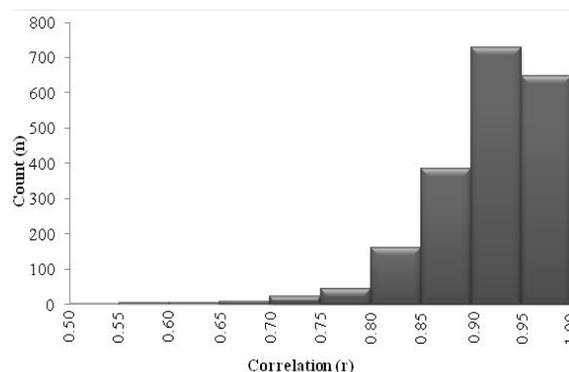

Figure 4. Accuracy of breed prediction in a 4-way cross using the marker frequencies from the 2,000 Bull Project.

Fine Mapping Efforts: Molecular geneticists at USMARC are working toward finding causal variation in genomic regions that have been identified by analysis of the 50K chip data. One success from this effort, in cooperation with scientists from the University of Illinois, led to a test for Osteopetrosis (Marble Bone Disease), a recessive genetic disease that had been identified in Red Angus. Current research is focusing on new genetic markers/mutations indicative of feed efficiency and fertility. These efforts allow us to develop markers that are more robust across populations of cattle and can help identify biological processes that underlie genetically caused variance we observe.

Table 1. Current number of AI progeny produced for each breed in the GPE Program

Breed	1/2	3/4	7/8	PB	Total
Angus	74	29	1	75	179
Beefmaster	41	3			44
Brahman	120	11			131
Brangus	44	5	1		50
Braunvieh	143	16			159
Charolais	69	28		94	191
Chiangus	159	17			177
Gelbvieh	59	96	5		160
Hereford	84	10		70	164
Limousin	63	88	6		157
Maine Anjou	130	10			140
Red Angus	54	101	9		164
Salers	136	14			150
Santa Gertrudis	143	18			161
Shorthorn	152	21			173
Simmental	93	30	7	60	190
Total	1564	497	29	300	2390

The USMARC Germplasm Evaluation (GPE) Program: The USMARC GPE Program samples industry relevant sires in order to estimate breed differences and genetic parameters (**heterosis, genetic correlations**) for economically relevant traits and to provide a resource for genomics work. The GPE Program has been in the process of producing purebred herds of the breeds sampled to help meet these objectives (see current status in Table 1). An additional advantage of developing these purebred populations is an improved capacity to estimate breed-specific marker effects.