WS Marvel 8M

Simmental

- True power and glory in one of the most physically imposing and genetically valuable packages ever in the Simmental breed.
- Massive for performance and phenotype, he maintains wonderful structure and balance, especially for a bull with his level of growth.
- Marvel ranks in the top 1 or 2% currently for ten diverse and economically crucial trait EPDs, including YW, MWW, Doc., and Marbling REA.
- All of these breed-leading projections place him at a rare level of calculated profit for both $API and $TI.

ASA# 4363941 • PB SM • Homozygous Black • Homozygous Polled

Bridle Bit Eclipse E744
Sire: Hook`s Galileo 210G
Hook`s Evita 18E

LCDR Favor 149F
Dam: WS Sweet Katch K4
WS Sweet Sixteen F16

Semen available from ABS. Call for pricing.
800-ABS.STUD • www.absbeef.com

Trait	CE	BW	WW	YW	ADG	DMI	$Gain	MCE	Milk	MWW	Stay	DOC	CW	YG	Marb	Fat	REA	Shr	API	TI
EPD	13.1	.2	103	167.2	.4	1.59	.06	8.5	31	82.4	19.7	18.4	58.2	-.34	.98	-.051	1.3	-.34	201.9	118.3
ACC	.45	.48	.50	.51	.51	.35	.40	.28	.23	.31	.37	.45	.44	.36	.43	.39	.42	.03		
%	30	30	2	1	1	99	30	15	10	1	10	2	2	70	1	80	2	55	1	1

EPD as of 2.21.25

Aaron Schlenker
Woonallee Simmental

J/C Simmentals

Miller Simmental

ABS

All Beef
Marty Ropp
406-581-7835

Getting a Clearer Picture with the Help of Genomics

by Dr. Troy Rowan, University of Tennessee

Genomics has become one of the most powerful tools in the cattle industry over the last decade, but the technology is often misunderstood. Genomics is a major part of nearly all seedstock genetic evaluations (i.e., EPD calculations), but is beginning to see more use in commercial settings. My goal here is to help dispel some myths and confusion around the use of genomics.

Genomic tests are not the same thing as "gene tests."

Much of the industry's first exposure to genomics was in the form of single-gene tests for carcass traits. These tests were designed to identify an animal's genotype for a handful of large-effect DNA variants involved in marbling and tenderness. These single-gene tests were generated to identify mutations believed to have an outsized effect on traits of interest. These associations were highly dependent on the population of animals being tested, and many failed to be validated by follow-up analysis.

Contemporary genomic tests are very different in design compared to these early single-gene versions. Current tests are less interested in genotyping known mutations that affect specific traits. Instead, they aim to characterize the landscape of an animal's three billion-plus DNA bases. Genomic tests take advantage of the fact that DNA is inherited in large chunks called haplotypes. As such, a single marker is sufficient to characterize the likely state of large areas of the genome. Current tests use between 30,000 and 100,000 evenly spaced markers in categorizing the entirety of the cattle genome rather than a handful of places.

In genetic evaluations, genomics increase EPD accuracy.

EPD are our best statistical guesses of an animal's actual genetic merit. The ultimate goal of EPD calculations is to help identify which DNA, good or bad, an animal inherited fromits parents. The random sampling of genetics that an animal receives from each parent can lead to considerable differences in genetic merit between siblings. EPD use information on relatives and progeny to understand whether an animal received good or bad samples of parental genes. As the information supporting an EPD increases (i.e., progeny records, pedigree relative progeny records), our confidence that the prediction represents the animal's actual genetic merit also increases.

We usually choose from bulls with low or no progeny information. This is true of commercial herds purchasing young bulls and seedstock operations that use the newest generation's genetics to drive progress. Historically, this lack of progeny information in EPD meant low accuracy in young animals. With the addition of genomics, we can directly identify which genetics an animal inherited from its parents rather than relying on progeny information to resolve these differences. The result is EPD that are more accurate for unproven animals. Depending on the trait, accuracy increases from a genomic test can be the same that ten to 30 calves would generate.