IPU Red Reserve 65L

- High-selling bull at 2024 LaBatte Simmentals in Canada. Outcross pedigree with excellent performance; strong maternal power bull.
- Dark red, polled, non-dilutor.
- Powerful maternal cow family.
- The sire, Mader Walk the Line, has sired breed-leading genetics for powerful growth and high maternal traits.

ASA# 4484939 • PB SM • Red • Polled

Mader Walk This Way 224B	IPU 2Y Dillinger 80B
Sire: Mader Walk The Line 92J	**Dam: IPU Ms Red Dakota 6H**
IRCC Darlin` 613D	IPU Ms Red Dakota 104F

Semen: $50/unit
Semen available through owners.

Trait	CE	BW	WW	YW	ADG	DMI	$Gain	MCE	Milk	MWW	Stay	DOC	CW	YG	Marb	Fat	REA	Shr	API	TI
EPD	10.3	2.7	100.2	147.5	.3	1.50	.02	8.1	30.1	80.1	13.3	9.6	35	-.42	-.04	-.091	.93	–	121.2	86.9
ACC	.20	.23	.21	.21	.21	.31	.35	.14	.12	.16	.13	.19	.19	.14	.14	.12	.16	–		
%	70	80	3	10	20	–	–	20	10	2	75	75	30	30	90	20	35	–	70	30

EPD as of 2.25.25

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The Crucial Role of Phenotypic Data in Genetic Predictions

by Ryan Boldt, PhD, IGS Lead Geneticist

In the age of genomic testing and genomically enhanced EPD, do we really need to collect phenotypes? This question is asked often, and it is a good one. For those wanting a summary, the answer is yes. The collection of phenotypic information is still necessary and arguably more necessary now than prior to the incorporation of genomics into single-step genetic evaluations.

To show an example of EPD prediction and the impact of genomics, some statistics were pulled from the IGS database to compare the average accuracy based on the amount of information included in the genetic evaluation. For this analysis, weaning weight (WW) was used as the example trait.

Data Available on Non-Parent Animals	Avg. WW EPD Accuracy
Pedigree information only	0.14
Pedigree and individual phenotypic information only	0.25
Pedigree information and a genomic test (no phenotypes)	0.41
Pedigree information, genomic test, and phenotypic information	0.44

The preceding table displays the effect on the WW EPD accuracy of non-parent animals with various combinations of data available to the genetic evaluation.

As shown, the accuracy of the EPD increases as more data is added. However, a common misconception is that genomics alone can replace phenotypic data. Previous studies have shown that if we do not continue to supply the evaluation with both genomic and phenotypic information, the accuracy of the genomic portion of the EPD calculation quickly diminishes. The ability of genomic data to predict and improve EPD accuracy is dependent on the amount of the variation that can be explained by the markers included in the model.

In terms of genetic prediction, the types of variation that are most important are phenotypic and genetic variation. Phenotypic variation is the amount of variation that is seen in the measurements that are collected on animals, or the total amount of variation. This variation is influenced by the genetics of the animal and the environment that the animal experiences. When it comes to genetic prediction and genetic improvement, the amount of variation that can be explained due to differences in inheritable genetics is known as additive genetic variation. The important distinction here is that we want to focus on the genetics that can be inherited from one generation to the next. In terms of genomics being the only source of data used for genetic prediction, then the genotype would be