

Improving Selection through NALF Genomic-Enhanced EPDs (GE-EPDs)

Limousin breeders and their commercial customers benefit greatly from new breeding and selection tools. The North American Limousin Foundation (NALF) has launched genomic-enhanced EPDs (GE-EPDs) with the fall 2015 international cattle evaluation. This provides GE-EPDs for all Limousin and Lim-Flex® animals that have completed DNA testing for genomic profiles.

A recalibration in cooperation with GeneSeek® and the Canadian Limousin Association has supplied genomic profiles on more than 4,500 Limousin and Lim-Flex animals. Molecular breeding values from either a high- or low-density genomic profile test are then blended into EPD calculations to produce GE-EPDs. This recalibration has led to the doubling of the number of animals included, the number of traits enhanced, and the genetic correlations.

GE-EPDs provide more precise EPDs based on a combination of pedigree, phenotype, and DNA. One major benefit is risk reduction through increased accuracy value on many traits - equivalent to having 8-20 progeny. This saves time when assessing young breeding stock and delivers commercial customer confidence when buying seedstock.

GE-EPDs also give the chance to collect data on economically important traits, which are expensive or difficult to measure.

The information from the genomic data can be as informative as a bull's first calf crop or a cow's lifetime production record. Since the genomic data is incorporated directly into the EPDs, cattle producers will not have to learn how to interpret the new data.

Animals that are genomic-enhanced will have the NALF GE-EPDs displayed on their animal detail screen and performance reports in the NALF-DigitalBeef platform. Traits that are genomic-enhanced are highlighted in yellow on these reports.

For more information visit www.NALF.org or call 303-220-1693.



MAJOR BENEFITS OF GE-EPDs

- Risk reduction through improved accuracies
- Value of time to assess breeding stock at a younger age
- Increased rate of genetic progress
- Getting data on economically important traits, which are expensive or difficult to measure
- Combination of pedigree information, individual performance data, and genomics into one easy to understand number

Table 1. Effective progeny counts for interim EPD derived from differing combinations of pedigree, performance and genomic data

Trait	Heritability	BIF Accuracy				Effective Progeny Counts			
		PE	PE+GE	PERF	PERF+GE	PE	PE+GE	PERF	PERF+GE
CED	0.19	0.04	0.40	0.27	0.47	1	34	16	50
BW	0.37	0.04	0.46	0.26	0.51	0	24	8	32
WW	0.29	0.04	0.26	0.28	0.39	1	10	11	21
YW	0.23	0.04	0.41	0.26	0.47	1	30	13	42
MILK	0.16	0.04	0.34	0.04	0.34	2	31	-	-
CEM	0.15	0.04	0.37	0.04	0.37	2	38	-	-
CW	0.23	0.04	0.42	0.28	0.49	1	32	15	46
REA	0.46	0.02	0.40	0.27	0.47	0	13	6	20
MB	0.54	0.03	0.60	0.30	0.63	0	33	6	39
FAT	0.35	0.02	0.46	0.30	0.53	0	25	11	36

PE = Pedigree estimate interim EPD; PE+GE = Pedigree estimate plus genomic data; PERF = Performance record included in interim EPD calculation; PERF+GE = Performance record included in interim EPD calculation plus genomic data

Source: Dr. Robert Weaber, Kansas State University, 2015