

TECHNICAL SUMMARY

July 2010

**Dollar Molecular Value Prediction Index –
Feedlot (\$MVP^{FL}) — The beef industry's first
genomic-based economic selection index.**

Key points

- The Dollar Molecular Value Prediction Index – Feedlot (\$MVP^{FL}) predicts differences in genetic merit for net return during the feeding phase and related to carcass value.
- Genetic merit for growth and quality grade are key drivers of the index, which is expressed in units of dollars and breeding value — half of which is passed on to progeny.
- The \$MVP^{FL} index is part of the High-Density (HD) 50K for Angus offering developed by Pfizer Animal Genetics and includes components of growth, dry matter intake, carcass weight and grade (quality and yield) when carcasses are valued on a CAB-like grid.
- Of the three categories of traits that contribute to the \$MVP^{FL} variation in growth traits, carcass traits and dry matter intake account for 53%, 34% and 13% of the variation in the \$MVP^{FL} respectively.
- Evaluation of 1,115 progeny carcass records from sires grouped according to HD 50K \$MVP^{FL} demonstrated a compelling relationship between the index predictions and observed actual progeny carcass value.
- Selection based on \$MVP^{FL} is anticipated to yield reliable improvement in the genetic merit for the complex of feedlot and carcass traits related to profitability when cattle are marketed on a quality-grade oriented grid.

Introduction

Ultimately, cattle breeding would be more rewarding if selection decisions could be simplified and based on truer predictions of the genetic value of animals across combinations of traits according to their overall economic impact on production.

With this goal in mind, Pfizer Animal Genetics developed the Dollar Molecular

Value Prediction Index – Feedlot (\$MVP^{FL}) as part of its High-Density (HD) 50K for Angus offering. The objective of this technical bulletin is to provide more detailed information about the interpretation, use and efficacy of \$MVP^{FL} — the beef industry's first genomic-based economic selection index.

Interpreting \$MVP^{FL} predictions

The \$MVP^{FL} index estimates differences in the net return of animals based on genetic merit to gain and convert feed to pounds of carcass weight with a desirable CAB quality and yield grade.

For Angus breeders accustomed to using the Dollar Beef (\$B) index, \$MVP^{FL} integrates the same traits and assumptions, with two main differences: 1) \$MVP^{FL} includes predictions of dry matter intake; and 2) \$MVP^{FL} values are expressed in units of breeding value rather than expected progeny difference. One-half of the difference in parent breeding value is transmitted to offspring.

As an example, consider Sires A and B below with \$MVP^{FL} values of \$75 and \$125, respectively. The difference in their \$MVP^{FL} is \$50, and half of this difference, or \$25, is passed on to offspring.

This means that if the two sires were mated to similar cows, Sire B is expected to produce progeny that generate \$25 per head more net return as compared with offspring of Sire A. Assuming each sire produces 20 head of fed and harvested progeny per year for four years, \$MVP^{FL} indicates that progeny of Sire B would produce approximately \$2,000 more net income.

\$MVP ^{FL} Example:	
Sire A \$MVP ^{FL}	\$ 75
Sire B \$MVP ^{FL}	\$125
\$MVP ^{FL} (breeding value) difference	\$ 50
Average progeny difference (½)	\$25
Calves sired per year	20
Sire used for four years	x 4
	\$2,000

Index efficacy

To determine the efficacy of \$MVP^{FL} for sires as predictors of value differences in fed and harvested offspring, Pfizer Animal Genetics evaluated 1,115 purebred Angus progeny carcass records from Summitcrest Angus collected over a 12-year period.

The 1,115 progeny were produced from 21 different sires with HD 50K MVPs. All sires represented by greater than 10 progeny were included in the analysis. In general, progeny were harvested in groups when an average fat constant end-point of just over 0.5 inch of subcutaneous fat thickness was achieved. The analysis used actual data, with no adjustment of individual progeny records for age, end-point or contemporary group effects.

For the purpose of evaluating the extent to which differences in sire \$MVP^{FL} translate into value differences observed in progeny, carcass value was computed using carcass weight and grade information, along with grid prices (included in Table 1).

Table 1 – Carcass quality and yield grade pricing used in index evaluation.

Quality Grade	Yield Grade				
	1	2	3	4	5
Prime	\$166.45	\$164.95	\$163.45	\$145.95	\$143.44
Upper Choice	\$161.92	\$160.42	\$158.92	\$141.42	\$138.92
Choice	\$157.40	\$155.90	\$154.40	\$136.89	\$134.39
Select	\$147.00	\$145.50	\$144.00	\$126.50	\$124.00
Standard	\$133.00	\$131.50	\$130.00	\$112.50	\$110.00

Average progeny carcass performance from the 10 highest-ranking sires for \$MVP^{FL} (n=553) was contrasted against progeny of the 11 sires with the lowest-ranking \$MVP^{FL} (n=562). The highest-ranking sires had an average \$MVP^{FL} of \$174.02, while the lowest-ranking sires had an average \$MVP^{FL} of \$98.74.

Summary statistics for average progeny performance from these two groups, as well as sire MVP and EPD information for selected traits, are provided in Tables 2, 3 and 4. Given the magnitude of their \$MVP^{FL} values, these sire groups are identified as high and moderate \$MVP^{FL} sires in the tables and discussion that follows.

Table 2 – Comparison of average actual progeny performance and sire predictions for carcass merit.

	Number of Progeny	Progeny Actual Carcass Weight	Progeny Actual Fat Thickness	Progeny Actual Ribeye Area	Progeny Actual Yield Grade	Progeny Actual Marbling Score	Sire Average Marbling Score MVP	Sire Average Marbling Score EPD
High \$MVP ^{FL} Sires (n=10)	553	800	0.515	12.30	3.35	6.58 (Modest 58)*	0.93	0.67
Moderate \$MVP ^{FL} Sires (n=11)	562	781	0.512	12.35	3.27	6.34 (Modest 34)*	0.40	0.35
Difference		19	0.003	-0.05	0.07	0.24	0.53	0.32
Expected Progeny Difference							0.26	

*Modest 50 is the mid-point of Average Choice

Table 3 – Comparison of sire mean MVPs for growth and feed efficiency.

	Number of Progeny	Sire Average Weaning Weight MVP	Sire Average Daily Gain MVP	Expected Accumulated 180-Day Gain ¹	Sire Average Dry Matter Intake MVP	Expected 180-Day Intake ²
High \$MVP ^{FL} Sires (n=10)	553	28.6	0.40	72	0.19	34.2
Moderate \$MVP ^{FL} Sires (n=11)	562	24.2	0.30	54	0.16	28.8
Difference		4.5	0.10	18	0.03	-5.4
Expected Progeny Difference		2.25	0.05		0.015	

¹Average Daily Gain MVP * 180 days

²Dry Matter Intake MVP * 180 days

Table 4 – Comparison of sire predictions and progeny carcass value.

	Number of Progeny	Progeny Actual Carcass Value/cwt	Progeny Actual Carcass Value	Sire Average \$MVP ^{FL}	Sire Average \$B
High \$MVP ^{FL} Sires (n=10)	553	\$159.37	\$1,275.15	\$174.62	\$50.92
Moderate \$MVP ^{FL} Sires (n=11)	562	\$158.43	\$1,237.61	\$98.74	\$37.37
Difference		\$0.94	\$37.54	\$75.89	\$13.55
Expected Progeny Difference				\$37.94	

Index components

\$MVP^{FL} includes genomic predictions for seven traits that are key drivers of feedlot profitability:

Growth

- Weaning weight
- Average daily gain

Feed efficiency

- Dry matter intake

Carcass traits

- Carcass weight
- Fat thickness
- Ribeye area
- Marbling score

Evaluating the results

The average fat thickness, ribeye area and yield grade of progeny from the two sire groups were similar (Table 2), while the average carcass weight of progeny from high \$MVP^{FL} sires was 19 pounds heavier. Presumably, this is at least partially explained by slightly higher sire MVP values for weaning weight and average daily gain (Table 3), as well as carcass weight.

Sires from the high \$MVP^{FL} group possessed an average MVP for marbling score that indicated an expected 0.26 difference, or just over one-quarter of a quality grade advantage in progeny — which corresponded closely to the 0.24 observed difference in average progeny marbling score (Table 2) between the two groups.

Progeny of the high \$MVP^{FL} sire group produced carcasses that were \$37.54 more valuable than progeny of the low \$MVP^{FL} sire group. This aligns strongly with the expected difference of \$37.94 predicted by the average difference in \$MVP^{FL} for the two sire groups. Remember, half the \$75.89 difference in \$MVP^{FL} for the two sire groups is transmitted to progeny, which in this demonstration equated to more than \$20,000 difference in total value.

Conclusions

As the beef industry's first genomics-based economic selection index, \$MVP^{FL} gives producers a valuable new tool for making accurate genetic selection decisions.

Producers can use the index to help differentiate between young animals with limited or low accuracy genetic predictions. Demonstrated efficacy of the \$MVP^{FL} index is an important prerequisite for integration of genomic predictions along with EPDs, in future indexes that include both sources of genetic information.

