High-Density (HD) 50K MVPs—The beef industry’s first commercially available Molecular Value Predictions from a High-Density panel with more than 50,000 markers.

Key Points

- High-Density (HD) 50K provides genomic predictions for black Angus cattle for a suite of 14 production, efficiency, yield and quality traits, including the beef industry’s first DNA-based economic index.
- HD 50K Angus is the first DNA diagnostic test using more than 50,000 single nucleotide polymorphisms to maximize precision of selection.
- HD 50K was developed using 5,101 black Angus animals from industry relevant populations.
- HD 50K explains genetic variation for a greater number of traits and delivers higher reliability, ultimately expanding selection opportunities.
- The economic selection index, $MVP^{\text{FL}}$, simplifies appropriate multiple-trait selection for growth, efficiency and carcass merit traits that contribute to profitability in the U.S. feedlot industry.
- Simulation of added $ value from a more-informed selection decision by the seedstock producer results in added profitability for the commercial bull customer through genetic improvement in the marketed product.

Introduction

Until recently, genetic tests available for quantitative traits of economic importance have been based on relatively few markers (e.g., early versions of GeneSTAR®). Then, in early 2009, Pfizer Animal Genetics launched genomic predictions for feed efficiency, marbling and tenderness based on a 56-marker panel. The next stage in the evolution of DNA technology for livestock, namely the commercial application of high-density genotyping, is described here.

DNA technology in livestock has evolved dramatically in recent times. In order for producers to receive maximum information and harness the ability to grow and evolve with the technology, we have introduced the first commercial DNA diagnostic for quantitative traits in black Angus cattle using a high-density genotyping product. Traits of economic interest in livestock tend to be controlled polygenically (meaning many genes), where many loci (genes) each explain a small amount of the genetic variation in the trait. Because of the nature of complex genetics, the utility of using small numbers of markers for prediction of genetic merit is limited. High-Density 50K technology allows the limitations of using small panels of DNA markers to be overcome. This
is achieved by considering the total effect of informative markers spread more densely across an individual’s genome. The informative markers are derived by genotyping large numbers of animals using the Illumina® Bovine SNP50 BeadChip and associating the changes in the traits of interest. The end result is the new product that provides Molecular Value Predictions (MVPs) for individual animals from Angus seedstock operations.

Table 1 – Definitions of traits included in the High-Density 50K for Angus product.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Units</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Birth Weight (BW)</td>
<td>lbs.</td>
<td>The weight of a calf taken within 24 hours after birth</td>
</tr>
<tr>
<td>Calving Ease Direct (CED)</td>
<td>%</td>
<td>Predicts differences in genetic merit for the likelihood of unassisted births when mated to first-calf heifers, with calving ease considered as a trait of the calf</td>
</tr>
<tr>
<td>Adjusted Weaning Weight (WW)</td>
<td>lbs.</td>
<td>205-day adjusted weaning weight as defined by BIF (2006): (Adj. 205-Day Wean Wt. = ((Wean Wt. – Birth Wt.)/Weaning Age) X 205) + Birth Wt. + Age-of-Dam Adj.), measured from 160 to 250 days of age</td>
</tr>
<tr>
<td>Average Daily Gain (ADG)</td>
<td>lbs. /day</td>
<td>Average lbs. of liveweight gain during the testing period, calculated as lbs./day on an unfasted basis. The standard test period is 70 days. Growth data was computed for each animal by regressing bi-weekly weights on number of days on test</td>
</tr>
<tr>
<td>Dry Matter Intake (DMI)</td>
<td>lbs. /day</td>
<td>Weight of feed (lbs. dry matter) consumed per day by an animal during a 70-day test period while in a feedlot. Feed composition was fixed within the trial¹</td>
</tr>
<tr>
<td>Net Feed Intake² (NFI)</td>
<td>lbs. /day</td>
<td>The difference between an animal’s actual and expected feed intake based on its body weight and growth rate in lbs., calculated from the residual after fitting DMI = ADG + MTW⁰.⁷⁵ + CG, where DMI is dry matter intake, MTW is mid-test weight, and CG is contemporary group</td>
</tr>
<tr>
<td>Hot Carcass Weight (CW)</td>
<td>lbs.</td>
<td>Weight of carcass, prior to chilling, adjusted for age</td>
</tr>
<tr>
<td>Fat Thickness (FAT)</td>
<td>inches</td>
<td>Fat thickness measured at ¼ the lateral distance across the longissimus dorsi from the spine at carcass split between 12th and 13th ribs, adjusted for age</td>
</tr>
<tr>
<td>Ribeye Area (REA)</td>
<td>inches²</td>
<td>Longissimus dorsi cross-sectional area at carcass split between the 12th and 13th ribs, adjusted for age</td>
</tr>
<tr>
<td>Marbling Score (MS)</td>
<td>USDA system</td>
<td>USDA marbling score converted to numeric units from 100 – 1000 as per BIF (2006), adjusted for age</td>
</tr>
<tr>
<td>Tenderness (TND)</td>
<td>lbs.</td>
<td>Peak force from a standard Warner-Bratzler Shear Force (WBSF) test for a ½-inch core of longissimus dorsi, lbs. (aged for 14 days)</td>
</tr>
<tr>
<td>Calving Ease Maternal (CEM)</td>
<td>%</td>
<td>Predicts genetic differences in the likelihood of unassisted births in first-calf heifers when calving ease is considered as a trait of the dam</td>
</tr>
<tr>
<td>Milking Ability (MA)</td>
<td>lbs.</td>
<td>Maternal contribution to progeny weaning weight expressed at 205 days of age</td>
</tr>
<tr>
<td>$MVP Feedlot ($MVPFL)</td>
<td>$</td>
<td>Molecular Value Prediction – Feedlot ($MVPFL) economic index gives an estimate of differences in the profitability, in dollars, based on net genetic merit (MVPs) to produce valuable carcasses when sold on a Certified Angus Beef (CAB) grid</td>
</tr>
</tbody>
</table>

¹ On a dry matter basis the ration contains: Crude Protein: 13.0%; ADF (Acid Detergent Fiber): 23.9%; Net Energy – Gain (Mcal/lb): 0.50. Note: This is a bull test ration consisting of: 7% corn; 8% wheat midds/oats; 20% chopped hay; 63% silage, 2% supplement. ² NFI and RFI are used synonymously in the industry and represent the same trait.
Product Description

The HD 50K black Angus product provides beef producers with MVPs for 13 key traits including: calving ease traits — calving ease direct and birth weight; early growth traits — weaning weight and postweaning average daily gain; efficiency traits — dry matter intake and net feed intake; maternal traits — calving ease maternal and milking ability (maternal weaning weight); carcass traits — hot carcass weight, fat thickness and ribeye area; and quality (palatability) traits — marbling score and tenderness (shear force). In addition to the traits, the first DNA-based economic index is introduced. Labeled as $MVP^{FL}$, this economic index includes traits contributing to profitability in the U.S. feedlot industry. For trait and index definitions, see Table 1.

The MVPs are based on prediction equations developed through a comprehensive whole genome analysis using Aberdeen Angus populations and genotypic data generated from the Illumina Bovine SNP50 BeadChip (SNP50). The SNP50 technology generates genotypes for 54,001 single nucleotide polymorphisms (SNP) evenly spaced across the cattle genome (Matukumalli, et al. 2009). The development of the SNP50 was a major step in increasing the efficiency of discovery for the underlying molecular variation for production traits in cattle.

Genomic predictions for the thirteen traits are expressed as estimated breeding values called Molecular Value Predictions (MVPs), with an associated reliability value for each trait. The reliability value is the standard for assessing the predictive power of the MVP. It is based on the correlation (r) between the MVP and the animal’s genetic value (i.e., breeding value). The reliability value is expressed as a percentage of the maximum accuracy attainable and is a useful indication of how much additional information may be added in the future. Reliability values will continue to increase as more animals with phenotypic values are genotyped and as higher-density marker platforms become available for research and development.

Development of High-Density 50K for Angus Predictions

The development of HD 50K for Angus predictions from the Pfizer Animal Genetics Research and Development pipeline brings together the most recent advancement in genotyping technology (SNP50), with traits from populations representing relevant industry genetics. A proprietary methodology used to develop the MVPs included training and internal validation analyses. This was followed by an external assessment using data from animals that were not used for training and internal validation. In total, 5,101 Angus (black) animals representing populations from multiple production environments and geographical regions were used in the development of this product.

For all traits, subsets of the 5,101 animals were used, based on available trait measures for each animal. Populations described here are designated by a capital letter that coincides with the traits used in the development of genetic predictions (Table 2).

A – Angus yearling bulls evaluated for growth performance and feed intake comprised of six different test groups fed over three years from multiple sources across the U.S.—used in training and internal validation.

B – Bulls from populations that are independent of animals in A were used for independent external assessment. Specifically, approximately one-third of the pens of bulls from each test period were withheld and used for external assessment. This process was repeated for all test groups over the three years of data collection.

C – Angus yearling heifers with individual feed intake data (relatively high roughage diet) from a northern U.S. test facility used for external assessment.

D – Angus yearling bulls with intake data collected from the Western region of the U.S. and used for external assessment.

E – 22 groups of Angus steers with WBSF data, from five different sources, representing multiple regions of the country
over a 3-year period, used in training and internal validation.

**F** – Steers withheld from population E prior to discovery, training and internal validation. Entire groups (approximately one-third on a pen basis) were selected randomly and withheld for external assessment.

**G** – Industry A.I. sires and Angus bulls with EPDs and associated accuracies purchased from the American Angus Association (AAA).

**H** – Young Angus bulls with low accuracy EPDs from the AAA that were used for independent external assessment.

The sub-sampling for training versus validation was done on a trait-by-trait basis using EPD accuracy values, with the top two-thirds of animals as represented by higher accuracies used for training, and the bottom one-third of animals as represented by lower accuracy younger bulls used for validation. Animals with only pedigree index EPDs, and no individual record for a given trait, were excluded from the analysis.

In-house EBVs were calculated for ADG, DMI, NFI and TND using a model similar to that used by beef breed associations in their National Cattle evaluations (NCE). Expected progeny differences and associated accuracies were supplied by the American Angus Association for the other traits. In total, 2,495 animals with AAA registration numbers were available for analysis.

Animals used to generate feed intake EPDs were evaluated in commercial testing facilities operated in a manner consistent with the Beef Improvement Federation Uniform Guidelines (BIF, 2006) for feed intake testing programs. All animals were fed for 90 to 120 days—with the final 70 days used in the calculation of ADG, DMI and NFI.

Genomic predictions for traits using EPD information from the AAA were derived using a population of registered animals that consisted of a combination of Angus animals with individual and progeny records (n = 1,800) and relatively high accuracy Angus sires (n = 470).

The core development tool used for derivation of genomic predictions was the GenSel analysis software developed at Iowa State University (Fernando and Garrick, 2009). This software has been used by a number of organizations, and shown to yield robust predictions across a number of livestock species.

In addition to GenSel, a proprietary discovery and validation methodology was developed by the Pfizer Animal Genetics Research and Development group to help eliminate over-prediction in the training and development of prediction equations. Over-prediction has been previously observed from high-density genotype information, due to bias in family and pedigree structure. The analysis combined discovery and simultaneous internal validation resulting in prediction equations referred to as calibrations. This procedure used two-thirds of the available animals for a trait for the discovery and internal validation process where the training data was sub-divided into five cross-validation groups. The remaining one-third of animals, with the lowest accuracy, was used as an external assessment and validation of the resulting MVPs. The proprietary methodology employed in the development of the HD 50K Angus MVPs was reviewed by an external panel of experts during the development of this product and was deemed to be scientifically appropriate.

The efficacy of the development strategy is demonstrated in the regression values that resulted from the training and validation analyses (Table 2). For ADG, DMI, NFI and TND, additional populations were used for external assessment. The increased precision of the HD 50K predictions was supported by the number of traits with regression coefficients near the expectation of 1. Estimates of the percentage of genetic variation explained for each trait were calculated as the square of the correlation (r) between the MVP and either the EBV or EPD, for the associated trait. This correlation is the estimate of the reliability for each trait prediction.

In the decision to bring a high-density genotyping platform to commercialization for the industry, an analysis was conducted that looked at the number of markers needed for a given trait to maximize accuracy of prediction through assessment of correlations between the MVPs and EPDs.
Using marbling as an example, the top 200, 400, 2,500 and 50K DNA markers were used to build the predictions for marbling. The resulting correlations between marbling MVPs and EPDs were .30, .38, .47 and .77 respectively (Figure 1). The use of maximum information from the 50K platform allows for the greatest accuracy in predictions and the ability to evolve with the addition of new traits and updated predictions for those that already exist.

Descriptive statistics for MVPs including the mean, minimum, maximum, standard deviation (percentile ranking table available in other materials), the percent reliability and percent genetic variation for all 13 traits and the index are listed in Table 3. Reliability values range from 33 to 63 percent. As the correlation between the MVP and the animal’s breeding value, the reliability impacts the accuracy and associated risk associated with a selection decision. It is useful to approximate the number of progeny records that equate to given reliability values. For example, reliability values in the 50 – 65 percent range equate to 5 – 9 progeny records for a moderately heritable trait such as ribeye area (Van Eenennaam, 2009). Correlation between MVPs for all traits and the index are listed in Table 4.
Table 2 – Summary of populations and results used for development of HD 50K Angus MVPs.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Population</th>
<th>Animals</th>
<th>r</th>
<th>Regression</th>
<th>SE²</th>
<th>%GV¹</th>
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<td>ADG</td>
<td>A</td>
<td>1254</td>
<td>0.58</td>
<td>1.00</td>
<td>0.09</td>
<td>34</td>
</tr>
<tr>
<td>ADG</td>
<td>B</td>
<td>646</td>
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<td>0.81</td>
<td>0.05</td>
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<td>C</td>
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<td>0.82</td>
<td>0.08</td>
<td>30</td>
</tr>
<tr>
<td>ADG</td>
<td>D</td>
<td>64</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DMI</td>
<td>A</td>
<td>1254</td>
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<td>1.08</td>
<td>0.15</td>
<td>16</td>
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<tr>
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<td>10</td>
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<tr>
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<td>0.97</td>
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<td>17</td>
</tr>
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<td>14</td>
</tr>
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<td>1.07</td>
<td>0.13</td>
<td>9</td>
</tr>
<tr>
<td>NFI</td>
<td>C</td>
<td>262</td>
<td>0.36</td>
<td>0.98</td>
<td>0.16</td>
<td>13</td>
</tr>
<tr>
<td>NFI</td>
<td>D</td>
<td>58</td>
<td>0.41</td>
<td>1.14</td>
<td>0.34</td>
<td>17</td>
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<tr>
<td>TND</td>
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<td>0.71</td>
<td>0.09</td>
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<td>TND</td>
<td>F</td>
<td>641</td>
<td>0.53</td>
<td>1.02</td>
<td>0.07</td>
<td>28</td>
</tr>
<tr>
<td>MS</td>
<td>G</td>
<td>1143</td>
<td>0.77</td>
<td>1.08</td>
<td>0.06</td>
<td>59</td>
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<tr>
<td>MS</td>
<td>H</td>
<td>610</td>
<td>0.49</td>
<td>0.74</td>
<td>0.05</td>
<td>24</td>
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<tr>
<td>FAT</td>
<td>G</td>
<td>1097</td>
<td>0.70</td>
<td>1.02</td>
<td>0.07</td>
<td>49</td>
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<td>FAT</td>
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<td>REA</td>
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<td>CW</td>
<td>G</td>
<td>1100</td>
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<td>1.01</td>
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<tr>
<td>CW</td>
<td>H</td>
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<td>BW</td>
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<td>0.85</td>
<td>0.06</td>
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<td>WW</td>
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<td>WW</td>
<td>H</td>
<td>499</td>
<td>0.53</td>
<td>0.90</td>
<td>0.07</td>
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<tr>
<td>CED</td>
<td>G</td>
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<td>0.89</td>
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<td>CED</td>
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<td>444</td>
<td>0.41</td>
<td>0.86</td>
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<td>0.97</td>
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<td>29</td>
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<td>CEM</td>
<td>H</td>
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<td>45</td>
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<td>MA</td>
<td>H</td>
<td>504</td>
<td>0.43</td>
<td>0.69</td>
<td>0.07</td>
<td>19</td>
</tr>
</tbody>
</table>

¹See Table 1 for trait descriptions. Based on 5,101 animals.
²Details about the populations and letter designations can be found in the Development of the High-Density 50K for Angus Predictions section of the summary.
³Standard error of the regression coefficient.
⁴Percent of additive genetic variation accounted for by variation in the MVPs.
Table 3 – Descriptive statistics for High-Density 50K Angus MVPs, percent reliability and percent genetic variation for each trait.¹

<table>
<thead>
<tr>
<th>Trait</th>
<th>Unit</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Std Dev</th>
<th>Reliability² (%)</th>
<th>Genetic Variation² (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CED</td>
<td>%</td>
<td>5.0</td>
<td>-17.3</td>
<td>20.3</td>
<td>4.1</td>
<td>47</td>
<td>22</td>
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<tr>
<td>BW</td>
<td>lbs.</td>
<td>-0.0</td>
<td>-8.6</td>
<td>7.4</td>
<td>1.8</td>
<td>53</td>
<td>28</td>
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<tr>
<td>WW</td>
<td>lbs.</td>
<td>27</td>
<td>-25</td>
<td>89</td>
<td>9.8</td>
<td>57</td>
<td>32</td>
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<tr>
<td>ADG</td>
<td>lbs./day</td>
<td>0.34</td>
<td>-0.33</td>
<td>1.13</td>
<td>0.12</td>
<td>55</td>
<td>30</td>
</tr>
<tr>
<td>DMI</td>
<td>lbs./day</td>
<td>0.01</td>
<td>-2.31</td>
<td>2.48</td>
<td>0.49</td>
<td>33</td>
<td>11</td>
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<tr>
<td>NFI</td>
<td>lbs./day</td>
<td>-0.20</td>
<td>-1.00</td>
<td>1.04</td>
<td>0.20</td>
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<td>CEM</td>
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<td>lbs.</td>
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<td>-20</td>
<td>51</td>
<td>6.3</td>
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<td>lbs.</td>
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<td>-21</td>
<td>75</td>
<td>8.4</td>
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<td>29</td>
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<td>FAT</td>
<td>inches</td>
<td>0.00</td>
<td>-0.12</td>
<td>0.17</td>
<td>0.03</td>
<td>63</td>
<td>40</td>
</tr>
<tr>
<td>REA</td>
<td>inches²</td>
<td>0.16</td>
<td>-0.84</td>
<td>1.23</td>
<td>0.19</td>
<td>54</td>
<td>29</td>
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<tr>
<td>MS</td>
<td>Marbling score</td>
<td>0.42</td>
<td>-0.32</td>
<td>1.73</td>
<td>0.25</td>
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<td>34</td>
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<tr>
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<td>lbs.</td>
<td>-0.57</td>
<td>-1.22</td>
<td>0.97</td>
<td>0.16</td>
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<tr>
<td>$MVPFL$</td>
<td>$</td>
<td>$115</td>
<td>$-28</td>
<td>$276</td>
<td>$33</td>
<td>n/a</td>
<td>n/a</td>
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</table>

¹ See Table 1 for trait descriptions. Based on 5,101 animals.
² Weighted averages that include discovery/internal validation and external assessment.

Table 4 – Correlations between MVPs for all traits.

<table>
<thead>
<tr>
<th></th>
<th>CED</th>
<th>BW</th>
<th>WW</th>
<th>ADG</th>
<th>DMI</th>
<th>NFI</th>
<th>CEM</th>
<th>MA</th>
<th>CW</th>
<th>FAT</th>
<th>REA</th>
<th>MS</th>
<th>TND</th>
<th>$MVPFL$</th>
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Genomic-based Economic Selection Index Development

In order to help simplify appropriate multiple trait selection for growth, efficiency and carcass merit, the Molecular Value Prediction – Feedlot ($MVP_{FL}$) economic selection index has been developed. The index accounts for the amount of variation explained by the component MVPs and their economic impact as described by a profit function derived from a set of assumptions related to economic and production parameters.

MVPs for the following traits were included: weaning weight (WW), average daily gain (ADG), dry matter intake (DMI), carcass weight (CW), ribeye area (REA), fat thickness (FAT) and marbling score (MS). The resulting index provides an estimate of differences in economic return based on genetic merit (MVPs) to consume, convert, gain and produce carcass weight and grade (quality and yield) – valued on a quality-grade grid (Table 5) and a base carcass price of $145/cwt.

\[
\text{profit} = b_{DMI} MVP_{DMI} + b_{CW} MVP_{CW} + b_{MS} MVP_{MS} + b_{REA} MVP_{REA} + b_{FAT} MVP_{FAT} + b_{WW} MVP_{WW} + b_{ADG} MVP_{ADG}
\]

A bioeconomic model was used to estimate the profitability of each animal. The economic weightings for each of the trait MVPs were calculated using a set of HD 50K MVP-results (n > 1,800) and a blend of time (days on feed), fat and weight constant endpoints. The model assumed that animals deviated from the average genetic merit by the value of their MVPs. The economic return for each animal was based on its carcass value minus the feed it was predicted to have consumed. The relative economic weight of each of the MVPs was estimated by regression according to the equation above, where \( b \) is the index weight on the MVP for trait \( i \). The proportion of variation in $MVP_{FL}$ index value that was explained by variation in the different components of production was: growth – 53 %; DMI – 13 %; carcass merit – 34 %.

Demonstration of Return on Investment in High-Density 50K for Angus Testing

To demonstrate the potential return on investment (ROI) in HD 50K testing, a gene flow model was used to assess the economic impact of improved accuracy and increased scope of selection when used to enhance available EPD information (Figure 2). The model assumed that the investment in HD 50K genotyping was made at the seedstock level for a one-time selection decision of two herd sires—that were then used to produce a portion of the seedstock herd’s progeny.

The return on investment by the seedstock breeder was then realized by commercial

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Table 5 – Quality Grade price grid derived from the American Angus Association and U.S. Premium Beef.
bull customers through retained ownership and grid marketing of progeny from the sons of sires that were selected using HD 50K and EPDs, as compared to using available EPD information alone. The simulation revealed that the added information from HD 50K for Angus predictions, when incorporated along with EPDs into an index for net merit and used for selection, resulted in increased profitability through enhanced animal performance.

In the model scenario, EPD information used for selection included predictions for birth weight, weaning weight, yearling weight, carcass weight, fat thickness, ribeye area and marbling score. The Molecular Value Predictions (MVPs) derived from HD 50K genotypes that were used to enhance selection included predictions for weaning weight, average daily gain (postweaning), dry matter intake, carcass weight, fat thickness, ribeye area and marbling score. Additional assumptions that were modeled as part of this effort included:

- The Angus seedstock herd consisted of 120 cows
- An 85% calf crop, with approximately two-thirds of the bull crop marketed annually
- A total of six herd sires used annually by the seedstock breeder
- The one-time selection of two new herd sires (one-third of the bull battery) was based on EPD and MVP information from HD 50K for Angus tests performed on bulls evaluated for sale in a given year (33 bulls tested)
- In a given year, the two specially selected seedstock herd sires produced approximately 12 sons (six per sire) that were marketed and exposed to 30 cows by commercial customers
- Each son of the specially selected sires produced a total of 105 progeny over the useable lifetime of five calf crops for commercial producers
- All progeny of the sons of specially selected seedstock sires were retained through the feedyard and grid marketed, assuming: $3.75/bushel corn, $135/cwt carcass price, $7 Choice – Select spread, and typical yield grade premiums as well as discounts for nonconforming carcasses
The modeled economic return was based on the marginal benefit received by commercial customers who purchased sons of the selected bulls resulting from an HD 50K-enhanced selection decision. The marginal value of the progeny of the marketed bulls was predicted by the model—with improved gain, feed efficiency and increased value of carcasses identified as key drivers of increased net return. When the marginal benefit was expressed as the ROI in HD 50K testing, the ratio of return to investment cumulative over three years of commercial production was 3:1.

The projected value gained at the commercial level for the offspring of sons of specially selected sires was $3.80 per head. Given the assumptions of retained ownership, this equated to nearly $400 of added value per bull (son) purchased by commercial customers from added progeny feedlot and carcass performance. The direct benefits to the seedstock breeder from retained daughters with improved genetic merit, as well as from enhanced marketing and more appropriate commercial use of unselected HD 50K-tested bulls, were not included in the ROI calculations. These results have been validated by two independent experts who specialize in modeling the economics of livestock production and the impact of genetics.

Reporting High-Density 50K for Angus Results to Customers

The genetic predictions derived from HD 50K genotypes are expressed in the form of breeding values called Molecular Value Predictions (MVPs). Fundamentally, MVPs are expressed in units of the given trait and serve to rank animals for additive genetic merit. As such, the MVP and associated Percent Rank are both reported to customers.

Percent Rank values indicate the “top” position of the animal in the population, with lower values indicating higher and generally more desirable rank for most traits. The reference population for determination of Percent Rank is the 5,101 Angus animals with HD 50K genotypes and MVPs included in the Pfizer Animal Genetics global database. Reported Percent Ranks are rounded to the nearest top 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50, 60, 70, 80 and 90 percentiles.

Molecular Value Predictions, Percent Ranks and summary statistics from HD 50K for Angus diagnostics for core traits are electronically reported to customers via e-mail, with four associated attachments including:

- A letter to the customer explaining the attached document and reports
- The Reading HD 50K Angus MVP Reports document which provides explanatory information about how to interpret reports, MVPs and Percent Ranks for use in selection and marketing
- The HD 50K for Angus MVP Report, in PDF format, includes animal MVP information, summary statistics and opportunity for authorization for release of results
- The HD 50K for Angus MVP Report, in Microsoft Excel format, presents information in all-inclusive and print-ready layouts, including summary statistics

The HD 50K for Angus MVP Report (Figure 3) in PDF format includes reference to the version of the equations used for computing reported predictions under the following convention: HD 50K / Angus / 01. These elements identify the genotyping platform (HD 50K), breed or population (Angus), and version number (01) for the prediction equations applied to the markers used to compute the predictions. As the database of HD 50K genotypes and performance information expands, more advanced versions of prediction equations are planned.
Summary statistics included in the PDF and Excel reports provide average, minimum and maximum MVPs for Angus animals included in the Pfizer Animal Genetics global database, benchmarked against animals included in this reported job. The average reliability value associated with the MVP for each trait is also reported.

The option for authorization by the customer for release of all results in a given job to the identified breed association and/or permission for public display of individual animal results on the Pfizer Animal Genetics Web site is included on sample submission forms and on the PDF version of the HD 50K for Angus MVP report. The vision of Pfizer Animal Genetics is for MVP information to be communicated to the designated breed association for inclusion in the respective performance program, genetic evaluation (EPDs and accuracies) and economic indexes, as well as decision-support applications.

Conclusions and Implication for Use

The HD 50K Angus product produces Molecular Value Predictions for 13 traits and the first molecular-based index in the industry. Producers now have greater opportunity to increase the probability of making more accurate genetic selection decisions than in the past. HD 50K Angus allows producers to differentiate between young animals with limited information—examples include young sire prospects that are full-sibs and elite females to be used as donor dams. Additionally, HD 50K Angus allows more accurate information to be realized on the female side of genetic selection than was possible in the past. This innovative approach allows the producer to continue to evolve and grow with the technology at the present and as it goes forward into the future.
References

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