

DNA MARKER PANEL VALIDATION UPDATE BY NATIONAL BEEF CATTLE EVALUATION CONSORTIUM



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The National Beef Cattle Evaluation Consortium (NBCEC) is an organization of researchers, educators, producers and industry leaders focused on genetic evaluation of beef cattle. Its mission is to advance U.S. beef genetics, increase the sustainability and competitiveness of the beef industry, and provide consumers with affordable and healthy beef products. NBCEC shows this commitment through research, animal evaluation, genetic test validation, industry collaboration and outreach, and professional development.

Current Projects – NBCEC conducts comprehensive, innovative and science-based beef cattle genetic research. Learn about the variety of their current projects.

Sire Selection Manual – This comprehensive manual features a variety of NBCEC research and genetic technology that producers can apply to their farms and ranches

Genetic Test Validation – NBCEC provides independent, unbiased, third-party validation of genetic tests for the beef cattle industry. See a variety of test results and the validity of the claims.

BIF Annual Meeting – Attend the Beef Improvement Federation's Annual Research Symposium and Annual Meeting, April 30 – May 3 in Sacramento, CA.

Commercial genetic test validations



The purpose of the NBCEC commercial DNA test validation is to independently verify associations between genetic tests and traits as claimed by the commercial genotyping company using phenotypes and DNA from reference cattle populations

The validation process is a partnership of the owners of DNA and phenotypes (e.g., breed associations) and genomics companies, facilitated by the NBCEC

Commercial genetic test validations

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Summary of NBCEC validations for commercially-available DNA-tests for complex (quantitative or multigenic) traits in beef cattle (note: validations do not include tests for "simple" traits such as coat color, horned/polled, AM status etc.)

| Company | Test Name | Trait | Date of validation |
|---|-------------------------------|--|--------------------|
| Igenity www.igenity.com | Profile® | Fat Thickness | 12/2008 |
| | Profile® | Marbling Score | 12/2008 |
| | Profile® | Quality Grade (% ≥ Choice) | 12/2008 |
| | Profile® | Rib Eye Area | 12/2008 |
| | Profile® | Yield Grade | 12/2008 |
| | Profile® | Average Daily Gain | 12/2008 |
| | Profile® | Tenderness | 12/2007 |
| | Profile® | Residual Feed Intake (RFI) (for <i>Bos indicus</i> influenced cattle) | 12/2007 |
| | Profile® | Residual Feed Intake (RFI) (for <i>Bos taurus</i> cattle) | 6/2008 |
| | Profile® | Dry matter intake (DMI) (for <i>Bos indicus</i> influenced cattle) | 12/2007 |
| | Profile® | Heifer Pregnancy Rate | |
| | Profile® | Stayability (longevity) | |
| | Profile® | Maternal Calving Ease | |
| | Profile® | Docility | |
| Pfizer Animal Genetics (Bovigen) www.bovigen.com | GeneSTAR® Tenderness MVP | Tenderness | 2/2009 |
| | GeneSTAR® Marbling MVP | % IMF (Feedlot cattle) | 2/2009 |
| | GeneSTAR® Feed Efficiency MVP | Net Feed Intake (NFI) | 2/2009 |
| MMI genomics www.metamorphixinc.com | Tru-Marbling™ | Marbling Score and Quality Grade | |
| | Tru-Tenderness™ | Tenderness | |

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Commercial genetic test validations

Summary

The GeneSTAR Tenderness MVP^[1] was found to be significantly associated with a decrease in Warner-Bratzler shear force (WBSF) measurements (i.e. increased tenderness) at 14 d postmortem in two *Bos taurus* sample populations. Additionally this test was found to be significantly associated with a decrease in Warner-Bratzler-shear force measurements at day 1 d postmortem, but not 14 d postmortem, in a *Bos indicus*-influenced population of 390 animals.

Significance of the GeneSTAR Tenderness MVP* (Molecular Value Prediction)

| Population | TRAIT | Panel | b** | F | p | N |
|--|---|------------|-------|-------|---------|-----|
| North American <i>Bos taurus</i> "Pfizer A" validation population | WBSF*** Tenderness (day 14 postmortem;kg) | Tenderness | 0.665 | 4.2 | 0.021 | 462 |
| North American Angus validation population | WBSF Tenderness (day 14 postmortem;lb) | Tenderness | 0.328 | 14.33 | 0.00008 | 760 |
| North American <i>Bos indicus</i> -influenced "Pfizer C" validation population | WBSF Tenderness (day 1 postmortem;kg) | Tenderness | 0.358 | 6.227 | 0.007 | 390 |
| | WBSF Tenderness (day 14 postmortem;kg) | Tenderness | 0.037 | 0.189 | 0.332 | 388 |

* Molecular prediction values (MVP) were provided by Pfizer Animal Genetics based on their 56 SNP panel for Marbling Score, Tenderness and Net Feed intake (residual feed intake).

Commercial genetic test validations

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Summary

There was no significant association of this test with the trait of Marbling Score in any of the validation populations. However, the GeneSTAR Marbling MVP^[1] was found to be significantly associated with percent intramuscular fat (%IMF) in a *Bos indicus*-influenced, and one of two *Bos Taurus* populations. Additionally this test was found to be significantly associated with the quality grade (% choice or better) in the *Bos indicus*-influenced population of 394 animals, but not the *Bos taurus* "B" validation population.

Significance of the GeneSTAR Marbling MVP* (Molecular Value Prediction)

| Population | TRAIT | Panel | b** | F | p | N |
|--|-------------------|----------|--------|------|-------|-----|
| North American <i>Bos taurus</i> "Pfizer A" validation population | Marbling score*** | Marbling | -0.267 | 3.15 | 0.961 | 595 |
| | % IMF | Marbling | 0.193 | 1.76 | 0.094 | 282 |
| North American <i>Bos taurus</i> "Pfizer B" validation population | Marbling score | Marbling | .120 | 1.1 | 0.147 | 723 |
| | % Choice | | -0.032 | 0.1 | 0.624 | 723 |
| | % IMF | | 0.312 | 5.26 | 0.011 | 785 |
| North American <i>Bos indicus</i> -influenced "Pfizer C" validation population | Marbling score | Marbling | 0.367 | 1.73 | 0.096 | 392 |
| | % Choice | | 0.276 | 3.68 | 0.028 | 392 |
| | % IMF | | 0.659 | 9.83 | 0.001 | 394 |

* Molecular prediction values (MVP) were provided by Pfizer Animal Genetics based on their 56 SNP panel for Marbling Score, Tenderness and Net Feed intake (residual feed intake).

Commercial genetic test validations

Summary

The GeneSTAR feed efficiency MVP^[1] was found to be significantly and positively associated with residual feed intake (RFI) in a North American population of 671 *Bos taurus* cattle. No significant association was found between this MVP and feed efficiency in a North American population of 395 *Bos indicus*-influenced cattle.

Significance of the GeneSTAR Feed Efficiency MVP* (Molecular Value Prediction)

| Population | TRAIT | Panel | b** | F | p | N |
|--|--|--------------------|--------|-------|------|-----|
| <i>Bos taurus</i> "Pfizer A" validation population | Residual Feed Intake (RFI;kg) ^{***} | Feed Efficiency | 0.4 | n/a | 0.02 | 671 |
| <i>Bos indicus</i> - influenced "Pfizer C" validation population | Residual Feed Intake (RFI;kg) | Feed Efficiency | -0.019 | 0.017 | 0.55 | 395 |

* Molecular prediction values (MVP) were provided by Pfizer Animal Genetics based on their 56 SNP panel for Marbling Score, Tenderness and Net Feed intake (residual feed intake).

Commercial genetic test validations

[IGENITY Carcass Composition and Average Daily Gain](#)[IGENITY Tenderness](#)[IGENITY Maternal Traits](#)[IGENITY Docility](#)[IGENITY Feed Efficiency](#) for Bos indicus-influenced cattle[IGENITY Feed Efficiency](#) for Bos taurus cattle[Peer-reviewed studies](#)[Company website](#)

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Igenity profile Carcass Composition and Average Daily Gain



Summary

The IGENITY profile was found to be significantly associated with marbling score, back fat thickness, quality grade, ribeye area, and yield grade carcass traits and average daily gain in a commercial predominately *Bos taurus* sample population of 1364 animals. This test was not evaluated on a *Bos indicus*-influenced or purebred *Bos indicus* population.



Significance* of the Igenity Molecular Breeding Values for Carcass Traits and Average Daily Gain

| Breed | TRAIT | Panel | b** | F | p | N |
|----------------------------------|---|-----------------|------|-------|-----------|------|
| Commercial Validation population | USDA Marbling Score | MBS | 0.76 | 28.6 | 0.0000001 | 1354 |
| | Backfat Thickness | BFAT | 0.81 | 12.46 | 0.0002 | 1354 |
| | Quality Grade ¹ (% \geq Choice) | % \geq CHOICE | 0.73 | 14.06 | 0.00009 | 1364 |
| | Ribeye Area | REA | 1.01 | 10.99 | 0.0005 | 1354 |
| | Yield Grade | YG | 1.16 | 21.98 | 0.000002 | 1354 |
| | Average Daily Gain | ADG | 0.61 | 14.69 | 0.00007 | 1364 |

* Molecular breeding values (MBVs) for each trait were provided by Igenity based on the various SNP panels for each trait.

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IGENITY profile Feed Efficiency for Bos taurus cattle SUMMARY

The IGENITY TAURUS feed efficiency MBVs were inconsistently associated with residual feed intake in the validation populations. In two populations there was a significant positive association of the MBV with the trait (North American Bos Taurus, CRC Temperate), but in the remaining four populations there was no significant effect and in both Angus populations the estimated association was negative, meaning that the results were associated in the opposite direction.

For further information on this validation contact Dr. John Pollak (607) 255-2846.

| TEST DATASET | Trait | PANEL | b | P | N |
|---|-------|--------|--------|-------|------|
| TEMPERATE ¹ (CRC1) | RFI | TAURUS | 0.309 | 0.04 | ~546 |
| SHORTHORN ¹ (CRC) | RFI | TAURUS | 0.393 | 0.17 | ~189 |
| ANGUS (CRC) ¹ | RFI | TAURUS | -0.426 | 0.95 | ~327 |
| NORTH AMERICAN BOS TAURUS ² | RFI | TAURUS | 0.351 | 0.005 | ~706 |
| NORTH AMERICAN CHAROLAIS ³ | RFI | TAURUS | 0.022 | .443 | ~393 |
| NORTH AMERICAN ANGUS ³ | RFI | TAURUS | -0.217 | 0.89 | ~436 |

¹ Data analyses for these validation populations were performed by Dr. David Johnston, Animal Genetics and Breeding Unit, University of New England, Armidale, Australia (6/2008).

² Data analyses for this validation population was performed by Gordon VanderVoort, Dr. Matt Kelly, Duc Lu and Dr. Stephen Miller, University of Guelph (6/2008)

³ Data analyses for these validation populations were performed by Dr. Denny Crews, Agriculture and Agri-Food Canada (6/2008)

Publishing traditional EPDs and marker information separately, as is currently the case, is confusing and can lead to incorrect selection decisions when marker scores predict only a small proportion of the genetic variance.



An increasingly relevant question in evaluating commercial DNA tests is "*What proportion of the additive genetic variation in the target trait is accounted for by the test?*"

Estimation of the Proportion of Genetic Variation Accounted for by DNA Tests.

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**Advancements in Genetic Prediction Technical Keynote Session,
Tomorrow (Saturday) afternoon in Room 203, Convention Center**



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DNA markers



Professor Mike Goddard
Beef CRC Chief Scientist
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The CRC for Beef Genetic Technologies is heavily focussed on gene discovery.

This has come about as a result of the 'Bovine Genome Project' which identified the DNA sequence of every gene in the bovine chromosome.

However, the problem we now face is understanding which particular trait or productive process each genetic sequence controls.

The priority of the Beef CRC is to link all this new genetic information to the traits of interest to beef businesses -

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Australian beef DNA results

As part of its role in delivering DNA markers to the Australian beef industry, Beef CRC has agreed to independently test new panels of DNA markers as they are commercialised by companies such as Pfizer Animal Genetics, Igenity /Meril and Metamorphix Inc.

Results of all independent testing of commercially-available DNA markers undertaken by Beef CRC will be presented on this site, outlining the size and direction of effect and the amount of genetic variation that is accounted for by each panel of markers for the different traits (e.g. marbling, feed efficiency, tenderness etc).

Additional information is provided to help beef businesses interpret the results for themselves to determine the value to their own businesses from an investment in the particular panel of DNA markers.

Those decisions very much depend on the individual business' attitude to risk and can only be made effectively by the individual business.

It is possible that the panel of markers has also been independently evaluated in North American herds by the US National Beef Cattle Evaluation Consortium, so for further information on the size and direction of effect of the markers in those populations, please visit <http://www.ansci.cornell.edu/nbcec/>

[Pfizer GeneStar results](#)

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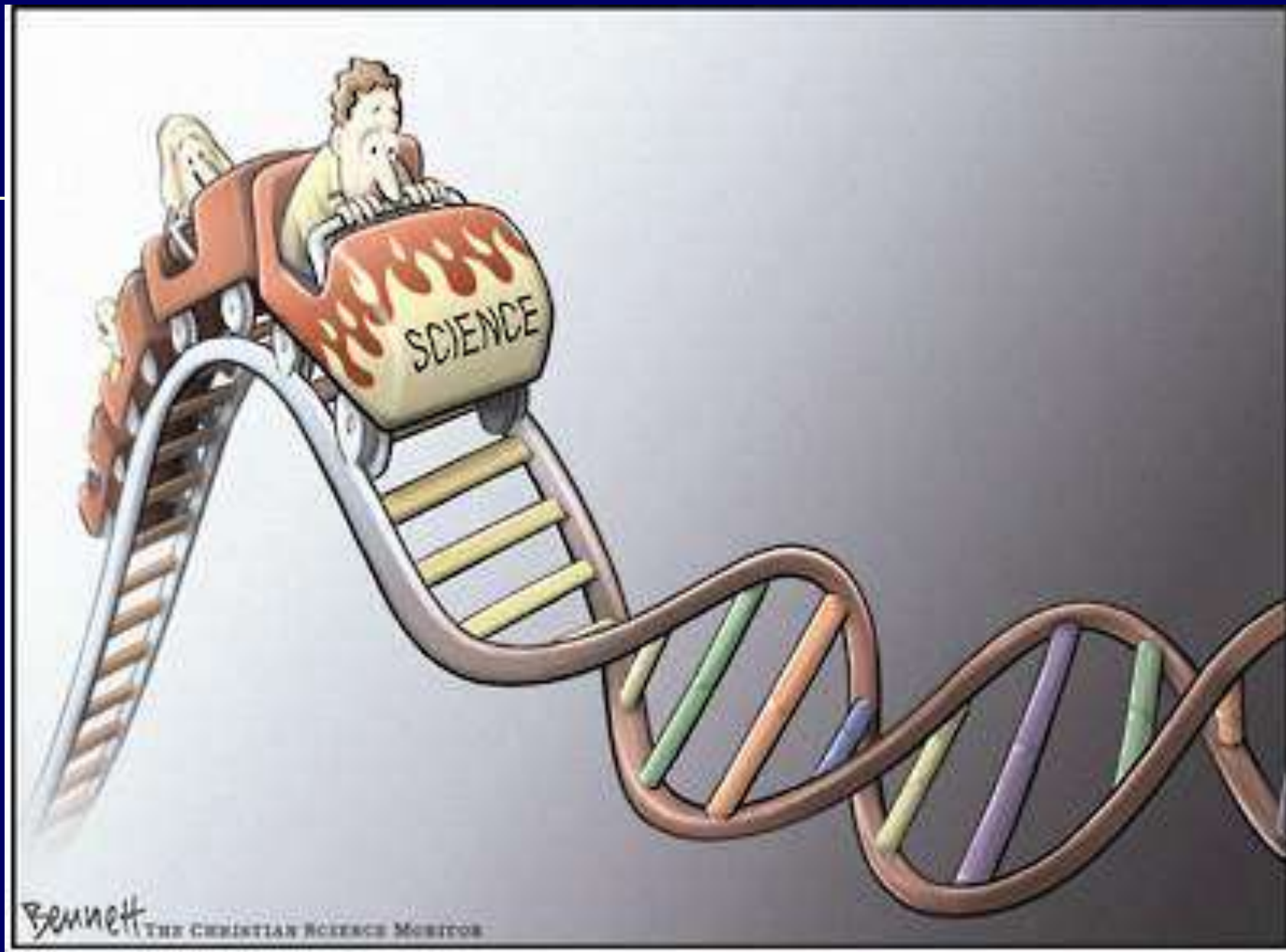
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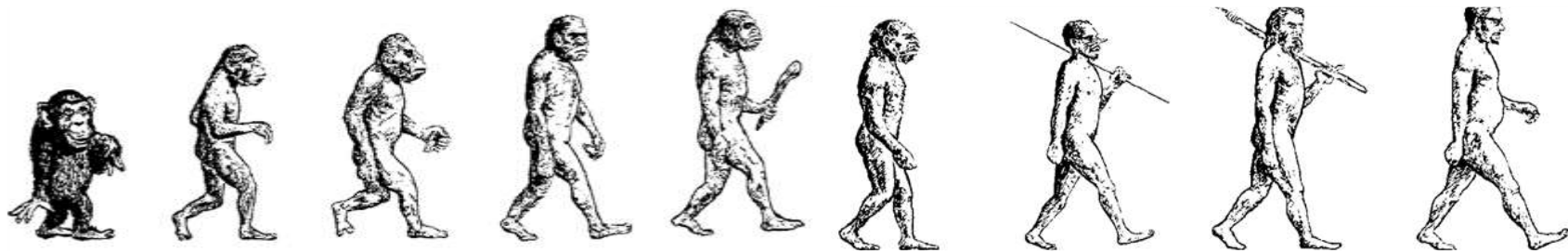
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Table 3: Bivariate animal model results using all phenotypes and GeneSTAR MVPs from the 56 marker pane Version January 2009. Results are from a data combining breeds and fitting breed in the model. The residual effect for the MBV was fixed at 0.001 and the residual correlation at 0.0. σ_p^2 = phenotypic variance of the observed data after fitting the models, h^2 = heritability of the trait, note MVP have a heritability of very close to 1.0, r_g = genetic correlation between MVP and target trait, r_g^2 = % genetic variance explained by marker, b = regression coefficient of MVP on phenotype has been calculated as ratio of covariance over variance of MVP. Standard errors of estimates are in brackets.

| Test | Trait | Data | N | σ^2_P | h^2 (se) | r_g (se) | r_g^2 | b (se) | |
|-------------------------------|-----------|------|-------------------|--------------|----------------|-------------|---------------|--------|---------------|
| Pfizer MVP Marbling | IMF | 1 | Phenot = MVP = | 3,594 703 | 2.035 0.035 | 0.39 (0.06) | 0.054 (0.07) | 0.3 | 0.255 (0.30) |
| | | 2 | Phenot = MVP = | 3,524 668 | 0.978 0.027 | 0.37 (0.06) | 0.064 (0.07) | 0.4 | 0.231 (0.24) |
| | | 3 | Phenot = MVP = | 876 253 | 0.767 0.026 | 0.23 (0.10) | 0.011 (0.13) | 0.0 | 0.028 (0.33) |
| | | 4 | Phenot = MVP = | 878 225 | 0.717 0.022 | 0.37 (0.11) | 0.121 (0.11) | 1.5 | 0.415 (0.39) |
| Pfizer MVP Marbling | MSA MS | 1 | Phenot = MVP = | 1,454 710 | 0.281 0.035 | 0.35 (0.09) | 0.131 (0.12) | 1.7 | 0.218 (0.20) |
| | | 2 | Phenot = MVP = | 1,808 670 | 0.236 0.027 | 0.37 (0.08) | 0.096 (0.08) | 0.9 | 0.171 (0.15) |
| | | 3 | Phenot = MVP = | 594 253 | 0.211 0.026 | 0.31 (0.13) | 0.016 (0.14) | 0.0 | 0.024 (0.22) |
| | | 4 | Phenot = MVP = | 636 225 | 0.229 0.022 | 0.19 (0.11) | 0.189 (0.17) | 3.6 | 0.262 (0.23) |
| Pfizer MVP Tenderness | LDSF | 1 | Phenot = MVP = | 3,322 659 | 0.433 0.088 | 0.08 (0.04) | 0.170 (0.14) | 2.9 | 0.109 (0.09) |
| | | 2 | Phenot = MVP = | 3,254 585 | 0.612 0.160 | 0.30 (0.06) | 0.283 (0.08) | 8.0 | 0.301 (0.09) |
| | | 3 | Phenot = MVP = | 785 253 | 0.658 0.142 | 0.26 (0.10) | 0.126 (0.14) | 1.6 | 0.137 (0.16) |
| | | 4 | Phenot = MVP = | 762 225 | 0.871 0.142 | 0.31 (0.10) | 0.547 (0.13) | 29.9 | 0.747 (0.18) |
| Pfizer MVP Feed Efficiency | NFI | 1 | Phenot = MVP = | 785 706 | 0.840 0.079 | 0.14 (0.11) | 0.248 (0.15) | 6.2 | 0.300 (0.13) |
| | | 2 | Phenot = MVP = | 687 671 | 0.687 0.056 | 0.21 (0.13) | 0.232 (0.11) | 5.4 | 0.366 (0.15) |
| | | 3 | Phenot = MVP = | 254 253 | 1.110 0.082 | 0.21 (0.25) | -0.044 (0.16) | 0.2 | -0.074 (0.27) |
| | | 4 | Phenot = MVP = | 215 225 | 0.958 0.056 | 0.37 (0.26) | -0.053 (0.14) | 0.3 | -0.131 (0.33) |





2003

2008

2013

2020

- single marker/
single trait
- reported
genotypes
- single
marker
accounted
for very
small
amount of
genetic
variation
- limited
adoption
- technology
oversold

- multimarker tests
for a few traits
reported in a
variety of formats
- no tie between
DNA test results
and national
genetic evaluation
- tests accounted
for small
proportion of
additive genetic
variation
- limited validation
- technology not in
a form producers
could use

- panels with
hundreds of markers
for many traits
- results reported in
units of the trait
- incorporation of
DNA information into
national genetic
evaluation
- DNA-based
evaluations improve
accuracy of EPDs
- large numbers of
genotyped
populations are
available for
validation

- universal marker
panel used by
worldwide beef
cattle community
- mandatory,
seamless
submission of
genotype data to
national genetic
evaluation/breed
associations
- cost is low and
industry uses DNA
information for
herd management
feedyard sorting,
and breeding.