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# AHA Releases Updated GE-EPDs

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The American Hereford Association (AHA) has released updated genomic-enhanced expected progeny differences (GE-EPDs) based on updated and much stronger correlations that provide more accurate genomic predictions.

Since the first release of GE-EPDs in August, there have been an additional 2,000 bulls 50K genotyped, and a large percentage of those are high accuracy bulls. With this additional information, beef cattle geneticists Dorian Garrick and Mahdi Saatchi have re-calibrated the genomic predictions, and, there is a tremendous improvement in the correlations (see Tables 1 and 2).

The AHA Board of Directors met by conference call and voted unanimously to update the correlations as soon as possible in order to give breeders the most current information to make breeding decisions this spring. These quick changes can be made because of the approach the AHA has taken to develop its specific Hereford panel and incorporate the genomic information with pedigree and phenotypes.

It is important to remember that genetic testing is a tool that complements and enhances, but does not replace, conventional pedigree and performance recording. It is still important for breeders to collect phenotypic information including ultrasound. The entire range of phenotypic measurements will be needed as the AHA moves forward to continually retrain the Hereford panel to further improve predictive ability.

You can find these animals by utilizing the EPD search on the *Hereford.org*. This work has been done in cooperation with the National Beef Cattle Education Consortium (NBCEC) and GeneSeek Inc., and made possible, in part, by contributions to the Hereford Research Foundation.

### Videos, fact sheet available

If you have any questions about DNA collection or GE-EPDs, visit *Hereford.org*, and look under "Latest News." To request DNA kits or for more information, contact Toni Shapiro at 816-842-3757 or tshapiro@hereford.org. HW

**Table 1: Original correlations**

| AHA trait | EPD acc. (BIF) | MBV & EPD correlation | MBV heritability | Trait heritability | Initial true acc. | Enhanced true acc. | Enhanced BIF acc. | Effective progeny |
|---|---|---|---|---|---|---|---|---|
| CE | 0.12 | 0.33 | 0.92 | 0.10 | 0.47 | 0.53 | 0.15 | 4.8 |
| BW | 0.12 | 0.40 | 0.94 | 0.43 | 0.47 | 0.56 | 0.17 | 1.6 |
| WW | 0.12 | 0.34 | 0.94 | 0.20 | 0.47 | 0.54 | 0.16 | 2.5 |
| YW | 0.12 | 0.33 | 0.96 | 0.36 | 0.47 | 0.54 | 0.16 | 1.2 |
| MM | 0.12 | 0.21 | 0.91 | 0.10 | 0.47 | 0.50 | 0.13 | 1.8 |
| MCE | 0.12 | 0.18 | 0.76 | 0.10 | 0.47 | 0.49 | 0.13 | 1.3 |
| SC | 0.12 | 0.25 | 0.88 | 0.37 | 0.47 | 0.50 | 0.14 | 0.7 |
| FAT | 0.12 | 0.43 | 0.76 | 0.30 | 0.47 | 0.54 | 0.16 | 2.8 |
| REA | 0.12 | 0.25 | 0.88 | 0.26 | 0.47 | 0.50 | 0.14 | 1.0 |
| MARB | 0.12 | 0.41 | 0.89 | 0.26 | 0.47 | 0.55 | 0.17 | 2.9 |
| Avg: | | 0.31 | | | | | | |

**Table 2: Updated correlations**

| AHA trait | EPD acc. (BIF) | MBV & EPD correlation | MBV heritability | Trait heritability | Initial true acc. | Enhanced true acc. | Enhanced BIF acc. | Effective progeny |
|---|---|---|---|---|---|---|---|---|
| CE | 0.12 | 0.68 | 1.00 | 0.10 | 0.47 | 0.73 | 0.32 | 33.5 |
| BW | 0.12 | 0.68 | 1.00 | 0.43 | 0.47 | 0.73 | 0.32 | 7.1 |
| WW | 0.12 | 0.52 | 0.98 | 0.20 | 0.47 | 0.63 | 0.22 | 7.0 |
| YW | 0.12 | 0.60 | 1.00 | 0.36 | 0.47 | 0.68 | 0.27 | 5.7 |
| MM | 0.12 | 0.37 | 1.00 | 0.10 | 0.47 | 0.56 | 0.17 | 6.2 |
| MCE | 0.12 | 0.51 | 1.00 | 0.10 | 0.47 | 0.63 | 0.22 | 13.7 |
| MCW | 0.12 | 0.64 | 0.98 | 0.38 | 0.47 | 0.70 | 0.28 | 6.6 |
| SC | 0.12 | 0.43 | 1.00 | 0.37 | 0.47 | 0.58 | 0.19 | 2.2 |
| FAT | 0.12 | 0.48 | 1.00 | 0.30 | 0.47 | 0.61 | 0.21 | 3.7 |
| REA | 0.12 | 0.49 | 1.00 | 0.26 | 0.47 | 0.61 | 0.21 | 4.5 |
| MARB | 0.12 | 0.43 | 1.00 | 0.26 | 0.47 | 0.58 | 0.19 | 3.3 |
| Avg: | | 0.53 | | | | | | |