Trait Reference Sheet

November 2020

Feed Saved (FSAV)

INTRODUCTION DATE

December 1, 2020, and then in all subsequent weekly, monthly and triannual evaluations

BENEFITS OF TRAIT

- Feed costs can make up over half of the total costs on a dairy farm[1]. Selecting for more feed-efficient cows can reduce these costs and improve profitability.
- Improving the efficiency of dairy cows will help reduce the amount of natural resources and energy needed to produce and process the feed required.
- Several studies have shown that cows that are more feed-efficient also produce lower methane emissions[2,3].
- Genetic selection for feed efficiency supports industry goals to reduce the environmental footprint of dairy production.

DESCRIPTION OF TRAIT

Genetic and genomic evaluations for Feed Saved (FSAV) are provided for Holstein males and females. Evaluations are expressed in pounds of feed saved per lactation above or below the breed average.

Trait definition:
The FSAV predicted transmitting ability (PTA) represents the expected pounds of feed saved per lactation based on body weight composite (BWC) and residual feed intake (RFI) evaluations. Larger, positive values are more favorable.

Unit of measurement: Pounds of dry matter intake

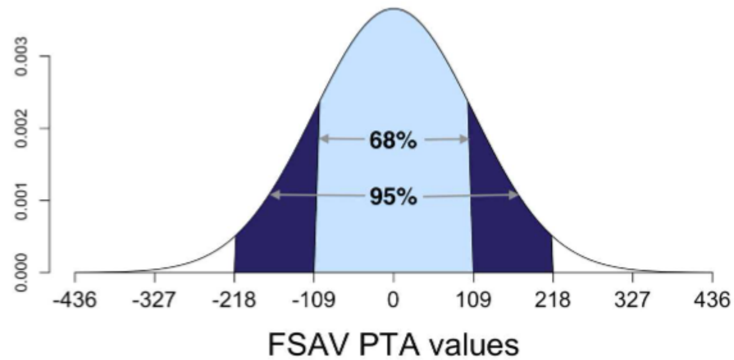
For example, daughters of a Holstein bull with a FSAV PTA of +200 pounds per lactation are expected to consume an average of 200 pounds of feed less than expected based on production and body size. Daughters of a Holstein bull with a FSAV PTA of -300 pounds per lactation are expected to consume an average of 300 pounds of feed per lactation more than expected based on production and body size.

Breeds: Initially, Feed Saved evaluations will be available only for Holstein animals. As more data become available, evaluations can be provided for additional breeds.

Data source: CDCB FSAV evaluations were developed using data collected by researchers involved in grants to study feed efficiency in dairy cows, from National Institute for Food and Agriculture (NIFA) in 2010 and Foundation for Food and Agriculture Research (FFAR) and CDCB grant in 2019. The majority of data were collected from herds located at the University of Wisconsin-Madison, Michigan State University, Iowa State University, University of Florida, and the Animal Genomics and Improvement Laboratory, ARS, USDA[4].

The CDCB national cooperators database includes over 650,000 daily intake records to calculate residual feed intake for approximately 6,200 Holstein cows (November 2020).

Range of population:
The standard deviation (variation) for FSAV PTA is 109 pounds per lactation. Because one and two standard deviations normally include 68% and 95% of observations, respectively, we assume about 68% of bulls will have a FSAV PTA between -109 and +109 percentage points while 95% of the bulls will range from -218 to +218 percentage points.



FSAV PTAs range from 594 more pounds of feed per lactation to 453 less pounds of feed per lactation in evaluated Holstein bulls with FSAV PTA reliabilities ≥50% (December 2020).

Reliability range: Young genomic bulls are expected to have reliabilities averaging 28% for Feed Saved, and progeny tested bulls are expected to have genomic reliabilities averaging 38%. As additional data are accumulated, reliabilities will increase.

Heritability: Estimated heritability is 14% for Residual Feed Intake (RFI). Estimated heritability for body weight composite is 40%.

Use in Net Merit indices: This trait will not be incorporated into Net Merit indices at launch. Inclusion of Feed Saved in Net Merit indices is expected at the next revision planned for April 2021.

It is suggested that producers continue to rely primarily on a composite economic index appropriate for the farm's milk payment situation and management system. Until Feed Saved is included in the indices, producers might consider avoiding those service bulls having low predictions for the trait.

PTA correlations: Correlations between residual feed intake (RFI) with yield traits are effectively zero by definition. Small correlations of less than 10% have been calculated during the testing phase with other traits such as Daughter Pregnancy Rate, Productive Life, and the disease resistance traits.

FUTURE DEVELOPMENTS

Data is being continually collected through the FFAR/CDCB project and will be added to the current database as available. International collaborations will also allow more data to be incorporated in the Feed Saved evaluation. Research around feed efficiency and Feed Saved is very active.

RELATED PUBLICATIONS

Tempelman, R.J., Spurlock, D.M., Coffey, M., Veerkamp, R.F., Armentano, L.E., Weigel, K.A., de Haas, Y., Staples, C.R., Connor, E.E., Lu, Y., VandeHaar, M.J., 2015. Heterogeneity in genetic and nongenetic variation and energy sink relationships for residual feed intake across research stations and countries. J. Dairy Sci. 98, 2013–2026. https://doi.org/10.3168/JDS.2014.8510

VandeHaar, M.J., Armentano, L.E., Weigel, K., Spurlock, D.M., Tempelman, R.J., Veerkamp, R., 2016. Harnessing the genetics of the modern dairy cow to continue improvements in feed efficiency. J. Dairy Sci. 99, 4941–4954. https://doi.org/10.3168/jds.2015-10352

VanRaden, P.M., O'Connell, J.R., Connor, E.E., Vandehaar, M.J., Tempelman, R.J. and Weigel, K. A. 2018. Including feed intake data from U.S. Holsteins in genomic prediction. Page 125 in Proc. 11th World Congress on Genetics Applied to Livestock Production, Vol. Biology–Feed Intake and Efficiency 1. World Congress on Genetics Applied to Livestock Production, Auckland, New Zealand

Li, B., VanRaden, P.M., Guduk, E., O'Connell, J.R., Null, D.J., Connor, E.E., VandeHaar, M.J., Tempelman, R.J., Weigel, K.A., Cole, J.B. 2020. Genomic prediction of residual feed intake in US Holstein dairy cattle. J. Dairy Sci. 103, 2477–2486. https://doi.org/10.3168/jds.2019-17332

CITATIONS

[1]United States Department of Agriculture – Economic Research Service. 2018. Milk cost of production estimates. http://www.ers.usda.gov/data-products/milk-cost-of-production-estimates/.

[2]de Haas Y, Windig JJ, Calus MPL, Dijkstra J, de Haan M, Bannink A and Veerkamp RF. 2011. Genetic parameters for predicted methane production and potential for reducing enteric emissions through genomic selection. J. Dairy Sci. 94, 6122–6134.

[3]Waghorn GC and Hegarty RS. 2011. Lowering ruminant methane emissions through improved feed conversion efficiency. Animal Feed Science and Technology 166, 291–301. doi:10.1016/j.anifeedsci.2011.04.019

[4]United States Department of Agriculture, Agricultural Research Service