

**2018 Beef Improvement Federation**

**“New IGS EPDs are really better”**

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Loveland, CO  
June 21, 2018

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An unprecedented collaboration between progressive breed associations to enhance beef industry profitability



**1997 Multi-Breed Genetic Evaluation**





**2010**

**Building Better Beef... Red Angus**  

Created long-term working relationship in which ASA provides genetic evaluation services and both associations direct and share equally in technological advancement





International Genetic Solutions



IOWA STATE UNIVERSITY  
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International Genetic Solutions:



CANADIAN  
SIMMENTAL  
ASSOCIATION



SimGenetics  
PROFIT THROUGH SCIENCE



AMERICAN  
GELBVIEH  
ASSOCIATION



Hybrid  
Advantage



SIRE  
EPD



SIRE  
EPD

Today, IGS is a collaboration of 12 progressive breed associations that have put self-interest aside to focus on the needs of the commercial cattle producer.

World's largest multi-breed genetic evaluation

~17 million animals

400,000 new/year

135,000 genotypes



TEAM  
WORK



Red Angus



Gelbvieh Association



Canadian Gelbvieh Association  
www.gelbvieh.ca



LIMOUSIN



LIMOUSIN



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What is EPD?

- EPD is the expected difference in future progeny performance of one individual relative to another individual(s).

| WW, lb | Bull A | Bull B |
|--------|--------|--------|
| EPD    | +0     | +10    |





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Genetic Evaluations



Sire



+60 lb  
+30 lb  
-20 lb  
+10 lb  
+20 lb

Sire EPD +12 lb

(EPD is "shrunk")

Progeny +20 lb



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Traditional Genetic Evaluations

Performance & (CG)

Pedigree

Genetic Evaluation Model

EPD

$$y = Xb + Zu + e$$
$$\begin{bmatrix} X'X^{-1} & X'Z^{-1} \\ Z'X^{-1} & Z'Z^{-1} + G^{-1} \end{bmatrix} \begin{bmatrix} y \\ u \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$
$$\text{var}(u) = G, \text{ e.g., } A_0 \oplus G_0, (MT) \text{ or } A_0 \oplus (ST)$$

Selection Decisions, BIF 2018, Loveland, Colo.

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DNA: A new genetic information

**MODERN TOOLS**  
for  
Plant Genetic Improvement

www.psgsc.wisc.edu

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Modern Genetic/Genomic Evaluations

The first step is to estimate the effects of DNA markers through a process called “training” or “calibration”. These effects are then used to calculate molecular expected progeny difference (MEPDs) on genotyped animals.

Two-step

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Modern Genetic/Genomic Evaluations

Two-step

Single-step

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Why Single-step GE-EPDs?

- GE-EPD are available only for genotyped animals while in the single-step the DNA has impact on all the relatives of the genotyped animals.
- Improved accuracy and removed bias in estimation of blending parameters.
- Avoids the double counting problem (high EPD animals turns to get high MBV and vice versa)!

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Types of Single-step models:

➤ SS-GBLUP is a breeding value model:

$$\begin{bmatrix} \mathbf{X}\mathbf{X} & \mathbf{X}\mathbf{Z} \\ \mathbf{Z}\mathbf{X} & \mathbf{Z}\mathbf{Z} + \mathbf{H}^{-1}\lambda \end{bmatrix} \begin{bmatrix} \mathbf{b} \\ \mathbf{u} \end{bmatrix} = \begin{bmatrix} \mathbf{X}\mathbf{y} \\ \mathbf{Z}\mathbf{y} \end{bmatrix}$$

where

$$\mathbf{H}^{-1} = \begin{bmatrix} \mathbf{A}^{11} & \mathbf{A}^{12} \\ \mathbf{A}^{21} & \mathbf{A}^{22} + (\mathbf{G} + \mathbf{I}\mathbf{F}\alpha)^{-1} - \mathbf{A}^{21}\mathbf{A}^{11} \end{bmatrix}$$

Uses all the markers to adjust relationships and assumes all markers have the same impact.

➤ SS-SHM is a marker effect model:

$$\begin{bmatrix} \mathbf{X}^T\mathbf{X}^* & \mathbf{X}^T\mathbf{W} & \mathbf{X}_1^T\mathbf{Z}_1 \\ \mathbf{W}^T\mathbf{X}^* & \mathbf{W}^T\mathbf{W} + \mathbf{I}_{n_2}^{-1}\sigma_w^2 & \mathbf{W}_1^T\mathbf{Z}_1 \\ \mathbf{Z}_1^T\mathbf{X}_1 & \mathbf{Z}_1^T\mathbf{W}_1 & \mathbf{Z}_1^T\mathbf{Z}_1 + \mathbf{A}^{11}\sigma_u^2 \end{bmatrix} \begin{bmatrix} \beta \\ \mathbf{d} \\ \mathbf{u} \end{bmatrix} = \begin{bmatrix} \mathbf{X}^T\mathbf{y} \\ \mathbf{W}^T\mathbf{y} \\ \mathbf{Z}_1^T\mathbf{y}_1 \end{bmatrix}$$

Squeeze more information from DNA by weight markers differently (ranging from a large to no impact) leveraging the biological fact.

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RESEARCH ARTICLE

Open Access

Why SS-SHM?

Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds

Mahdi Saatchi<sup>1</sup>, Robert D Schnabel<sup>2</sup>, Jeremy F Taylor<sup>2</sup> and Dorian J Garrick<sup>1,3\*</sup>

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Hybrid model - Accuracy:

Average Prediction Error Variance (PEV) for birth weight from BLUP and Hybrid Model with Bayes C0 and Bayes C by BLUP PEV group for genotyped animals.

Courtesy of Dr. Bruce Golden, Theta Solutions, LLC.

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Previous IGS EPDs:

➤ A multi-step blending approach:

• Molecular expected progeny differences (MEPD) are calculated (using GenSel software) separately from the traditional multibreed international cattle evaluation (MB-ICE) using Cornell Software.

Performance & (CQ)

Pedigree

DNA

EPD

MEPD

GE-EPD

$$\text{GE-EPD} = w_1 * \text{MEPD} + w_2 * \text{MB-ICE}$$



# IGS Multi-breed EPDs powered by BOLT

Theta Solutions: Sarrick & Golden

BOLT

Hyde Saatchi Spangler McGuire Shafer

**It is based on Single-step Super-hybrid model runs weekly since 5/5/2018.**

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## Are new IGS EPDs really better?

- Ran a same data set (pedigree, performance, genomics) for growth traits through both genetic evaluation software (BOLT and Cornell).
- Removed the performance records of animals born in 2015 and later from the evaluations to be used as progeny performance records for validation purposes.

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## Validation study (BOLT vs Cornell system):

Table 1- The correlations between BOLT vs. Cornell EPDs with progeny performance of non-genotyped sires for birth, weaning and yearling weights.

| Trait           | N of Sires | BOLT | Cornell |
|-----------------|------------|------|---------|
| Birth weight    | 29,154     | 0.34 | 0.27    |
| Weaning weight  | 21,571     | 0.29 | 0.19    |
| Yearling weight | 10,849     | 0.26 | 0.20    |

Table 2 - The average progeny performance of non-genotyped sires ranked based on either BOLT or Cornell EPDs.

| Trait | N of sires | BOLT   |           |            | Cornell |           |            | BOLT vs Cornell |
|-------|------------|--------|-----------|------------|---------|-----------|------------|-----------------|
|       |            | Top 1% | Bottom 1% | Difference | Top 1%  | Bottom 1% | Difference |                 |
| BW    | 29,151     | 95.9   | 74.2      | +21.7      | 92.8    | 76.0      | +16.8      | +3.1            |
| WW    | 21,571     | 655.3  | 546.2     | +109.1     | 638.5   | 558.6     | +79.9      | +16.8           |
| YW    | 10,849     | 1151.5 | 915.8     | +235.7     | 1111.3  | 895.6     | +215.7     | +40.2           |

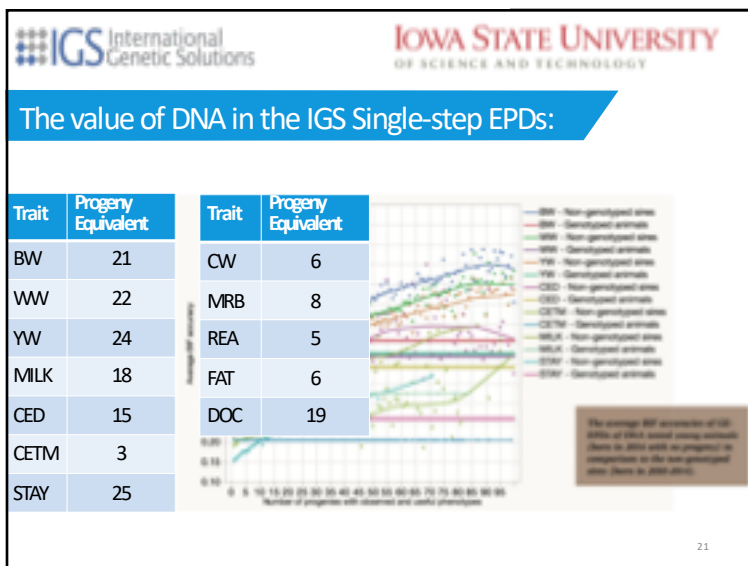
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## The value of DNA in the IGS Single-step EPDs:

| Trait | Progeny Equivalent |
|-------|--------------------|
| BW    | 21                 |
| WW    | 22                 |
| YW    | 24                 |
| MLK   | 18                 |
| CED   | 15                 |
| CETM  | 3                  |
| STAY  | 25                 |

The average EPD accuracy of 100 sires of each breed across various traits (BOLT vs. Cornell) is compared to the non-genotyped sires (BOLT vs. Cornell).

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### ASA's Cow Herd DNA Roundup Project:

*Her Biological Clock is Ticking!*

- ASA research project in collaboration with GeneSeek to improve genomic predictions for beef maternal traits by increasing number of female genotypes.
- Requires to submit DNA on their entire cow herd (reduce the biases due to selected samples).

**50K DNA Tests for just \$15/cow**  
Limited time only

**Adding a DNA test to your decision is like knowing...**

- 15 Calving ease scores
- 20 Birth weights
- 22 Weaning weights
- 25 Stayability records

**CHRYX**  
For more information, contact your local ASA rep or visit [cowherdna.com](http://cowherdna.com)

**SimGenetics**

Available to all academic and commercial members — regardless of breed type or breed makeup.  
\$15/sample requires both cow weights and body condition score (otherwise \$20/sample).  
Partnership included.  
Limited time only — samples must be submitted by 12/31/18. There is a cap on budget for projects, so don't delay!  
Collaborative research project with GeneSeek.

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### ASA's Carcass Merit Program:

- ASA young sire progeny testing program started in 1997 to collect more actual carcass data to increase the accuracy of EPDs.

**CMP ASA**  
CARCASS MERIT PROGRAM

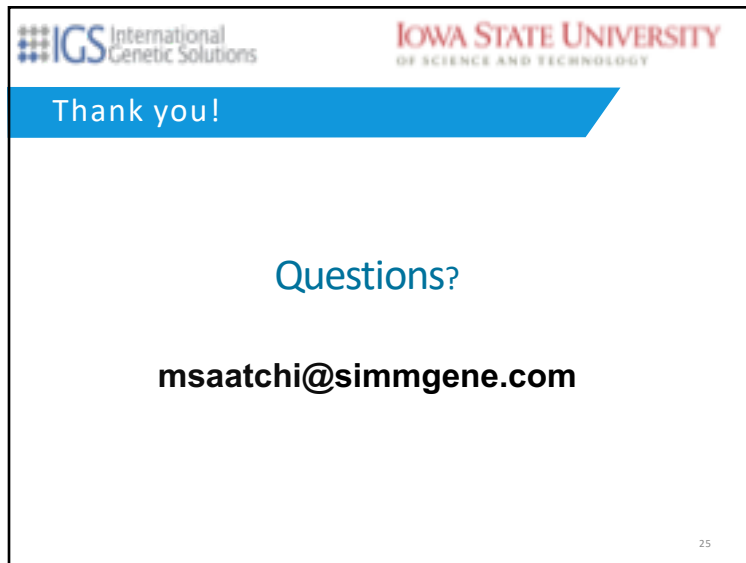
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### Conclusions:

- The need for improving EPD accuracy drives genetic/genomic evaluation model innovations.
- Single-step Super Hybrid Model (SS-SHM) is a breakthrough genomic model in accuracy improvement.
- We (IGS) are dedicated to use the best available technology to deliver more accurate genetic tool (GE-EPD) to improve commercial beef profitability.
- We showed that the new IGS EPDs are more accurate than previous IGS EPDs for growth traits. We will continue our validation study for all other traits.

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The slide features a header with two logos: 'ICS International Genetic Solutions' on the left and 'IOWA STATE UNIVERSITY OF SCIENCE AND TECHNOLOGY' on the right. Below the logos is a blue diagonal banner with the text 'Thank you!'. The main body of the slide contains the text 'Questions?' and the email address 'msaatchi@simmgene.com'. A small page number '25' is located in the bottom right corner of the slide frame.

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Thank you!

Questions?

**msaatchi@simmgene.com**

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