



ABS Global Genomic Enhanced Future

ABS TECHNOLOGY MILESTONES

- 1953 ABS produces the first living calf born in the U.S. from frozen semen
- 1988 ABS is the first A.I. company to successfully clone bulls from embryo splitting
- 1996 ABS implements DNA Marker Assisted Selection
- 1997 ABS produces the first clone born from a single somatic cell using proprietary NT technology
- 2008 ABS incorporates genomic results into Sire Acquisition

ABS – The World Leader in Bovine Genetics

ABS Global maintains its bovine industry leadership position through an extensive commitment to applied research in science and technology. Genomics demonstrates a new phase in ABS innovation. As the world's largest A.I. company, dairy and beef producers globally count on ABS to offer the finest and most diverse genetics available to improve the production of milk and protein. ABS is literally helping you feed the world!

In 1998, ABS, USDA, and six other A.I. organizations in North America joined together to form a DNA bank for genomic-related research. This resource enabled more in-depth genomics research by ABS, USDA, and the rest of the A.I. industry. The result of these monumental research accomplishments is a world-wide first for the dairy industry – published genetic evaluations that include a genomic contribution when predicting genetic merit of cows and bulls.

Genomic Evaluations will be published by USDA-AIPL with the release of the January 2009 Sire Summary for both unproven and proven sires in the Holstein and Jersey breeds. Genomic Evaluations incorporate daughter information, genomic information, and traditional pedigree contributions. Thus, the Real World Data® of progeny remains the gold standard by which genetic progress is made. Genomic information provides early insight on bulls with no or few daughters and provides another valuable tool in the toolbox that ABS uses to identify genetically elite sires like DIE-HARD, BOLIVER and SHOTTLE. The company's 20 Ph.D. Geneticists are working to ensure that ABS products continue to deliver benefits that exceed ABS customer expectations.

What are Genomic Evaluations and Where Do They Come From?

What are Genomic Evaluations?

Accurate genetic evaluations require a blending of different pieces of information to compute a bull's proof. In traditional evaluations, we combine pedigree contributions plus information from daughters. Genomic Evaluations incorporate the same principles as traditional evaluations and so also require blending of different pieces of information to compute proofs. In the case of Genomic Evaluations, the pieces include genomic (DNA-based) information plus any remaining pedigree contributions plus information from daughters.

How are we able to determine the predicted genomic contribution for bulls?

Chromosomes comprise two strands of the thread-like structure known as DNA. The two individual strands of DNA are held together by base pair molecules of which there are four different types. For cattle, their 30 different chromosome pairs contain roughly 3 billion DNA base pairs. Technology has enabled us to obtain DNA from a blood, hair,

Genetic Basics

- **What is DNA:** DNA provides the set of instructions that a cow needs in order to grow, produce milk, breed back, resist diseases, etc. Some parts of the DNA define what protein is made – an example of this is the genes that control red or black coat color. Other sections of DNA tell genes when to turn on or turn off.
- **What is a gene:** Genes are the basic unit of inheritance and comprise DNA. For a small handful of traits like horned/polled and coat color (red/black), one or two genes determine the animal's phenotype or performance. For most traits like production, reproduction, conformation, longevity, health, etc., many, many genes are involved and these genes interact with each other and with the environment in very complex ways to yield animals' phenotypes.
- **What is a SNP:** SNP or Single Nucleotide Polymorphisms are base pairs sites in DNA where genotyping has identified that animals can differ. When a base pair differs for animals, it presents one of three scenarios: 1) there is no impact or association with performance differences, 2) there is an association with performance differences but this difference does not hold up over time with subsequent generations, and 3) there is an association with performance differences that does hold up across generations. Most base pair differences result in little or no perceptible difference in performance because in nature, large differences typically are undesirable for animals.

tissue, or semen sample and from this DNA determine which of the four different bases are located at each of approximately 40,000 base pair sites. This process is referred to as genotyping. We would like to know the sequence of bases at each and every one of the 3 billion base pair sites because differences in bases found at these sites may influence characteristics of the animal, but determining all 3 billion base pairs is too costly today so instead we are looking at this subset of bases. By genotyping a large number of sires which have highly accurate and reliable proofs, we can now begin to look for associations between the genotypes and the proofs of these bulls. These associations between progeny test proofs and sires' genotypes at each of the 40,000 base pair sites are used to define the genomic information which contributes to bulls' genomic proofs.

What traits currently are predicted using a Genomic Evaluation?

The USDA looks at 29 traits: 5 yield traits (milk, fat, protein, fat %, protein%), 7 health traits (PL, SCS, DPR, SCE, DCE, SSB and DSB), 16 conformation traits (PTAT and 15 linear type traits), and Net Merit. In addition, Holstein Association USA plans to use Genomic Evaluation results to compute genomic TPI labeled as GTPI for bulls and cows that have been genotyped.

What will Genomic Evaluation Results look like?

Genomic evaluation results will look like

traditional PTAs for yield, Type, and management traits and like traditional STAs for linear traits. Genomic proofs will be identified by Holstein Association USA using the term, GTPI for Genomic TPI.

What causes genomic proofs on cows and bulls to change over time?

Genomic Evaluation results on young and proven animals alike will change over time as new information is added. Each of the three pieces of information, that is blended for the Genomic Evaluation – 1) genomic information, 2) any remaining pedigree contributions, and 3) information from daughters – will change as new information is added. Adding new genotyped proven bulls and their respective daughter information impacts genomic information for all bulls that share some of those same genotypes. Adding new daughters also influences proofs for their sires. Both of these factors will influence pedigree components. Ultimately, all of these additions of new information will impact genomic evaluations over time.

ABS Cornerstone®

How accurate are Genomic Evaluation results for young sires?

When genomic information and any remaining pedigree contributions are blended (providing a genomic-enhanced Parent Average), the resulting realized reliabilities average 50% across the traits predicted. This is more reliable than a traditional PA, but not nearly as high as the reliability that results from a progeny test (around 90%). Actual milking daughters remain the gold standard for predicting genetic merit for bulls and cows.

Will genomic information replace progeny testing?

Milking daughters are the true measure of a bull's transmitting ability! Further, progeny test information determines genomic contributions, so progeny test data are required to

Table A
Example of differences in a full-brother group

Bull	Evaluation type	Milk	Fat	Prot	PTAT	UDC	PL
Litter	Traditional PA	1151	46	45	2.4	2.12	3.8
A	ge-PA	1176	27	34	1.5	1.13	3.6
B	ge-PA	1395	43	42	2.1	1.74	1.6
C	ge-PA	1230	73	56	2.8	2.51	3.3

Advantages of Genomics

- Provides additional early information about the predicted genetic merit of young bulls
- Provides additional early information for traits like Productive Life where more time is required to collect actual daughter data.
- Provides a relatively accurate and reasonably low cost method for validating parentage including sire and dam if these are genotyped also.
- Allows us to look directly at the DNA and more accurately assess levels of inbreeding and genetic relationship.
- With additional ABS research, we expect that in the future genomics can be harnessed to improve mating decisions in GMS®.

continually update and improve the predictability of genomic information. Actual daughter data always are more reliable than pedigree predictions but genomic data will help us determine earlier which bulls to progeny test through the ABS Cornerstone program.

Is ABS genotyping all young bulls?

Yes, for the past several months, ABS has been testing bulls on farm before they come to ABS. **Table A** above is a quick example of a litter of 3 full brothers (A, B and C) each with his genomic-enhanced PAs (ge-PA) and traditional PAs.

In this case, even though A has the highest PL (3.6) and B has the highest Milk (1395), the selection is C, for his combination of several traits.

How is ABS using genomic information in sire acquisition?

There are many factors that go into making a great bull: he must be genetically unique, he must be physically sound, he must meet specific health qualifications, and he must produce ample quantities of fertile semen. As shown in the example (**Table A**), when we have to choose between three full brothers, Genomic Evaluations can give us an early clue about who likely inherited the most promising gene combinations and is yet another tool to help ABS identify which bulls to progeny test. Because we know that genomic information alone cannot accurately predict individual bulls, we must maximize our selection by using all of the tools in our toolbox. The toolbox also includes: traditional genetic evaluations, pedigree analysis, cow inspections, and most importantly, 'good cow sense'.

Will ABS test fewer bulls per year?

The ABS Cornerstone progeny test program has been growing in recent years to meet our expanding global market demand. Our goal is to accurately identify and market the finest genetics in the industry. We expect that Genomic Evaluations will improve our success rate. However, we will continue to progeny test even more bulls in order to offer proven sires of the highest quality! Ultimately, the ABS Cornerstone progeny test program will continue to be needed in order to identify the new and unique combinations of genes that result in the next generation of elite ABS sires like DIE-HARD, BOLIVER and SHOTTLE.

How are the Primetime Genetics bulls selected?

All Primetime sires have been carefully selected using all of the tools in the toolbox that are important to dairy producers. Each hand picked sire has a genomic-enhanced PA to ensure that all available genetic information is in place. We compliment the ge-PA by requiring leading cow families, reliable calving ease data, and published semen fertility data. Finally, only sons of highly reliable second crop sires are considered. The 2009 Primetime sires are sons of SHOTTLE and BOLIVER!

Proven Sires

Are bull rankings the same with traditional evaluations and Genomic Evaluations?

Some re-ranking will occur as new information is added to the breeding value. In general, first crop bulls will have a similar ranking. However, the added information and reliability of the Genomic Evaluations mean that some bulls will move up and some will move down.

Second Crop ABS Diamond Sires are the most accurately proven sires in the industry and therefore have the most stable proofs.

How will I know if a bull has a genomic proof?

Holstein Association USA plans to use Genomic Evaluation results to compute genomic TPI labeled as GTPI for bulls and cows that have been genotyped. A.I. companies in Holland and New Zealand also calculate genomic proofs and may use a different designation. All actively marketed bulls in the January 2009 ABS Dairy Profit Power will have a genomic evaluation unless otherwise noted. It is the ABS policy to test and publish genomic proofs for all proven sires unless otherwise noted.

How will the international bulls and proofs be handled?

Genomic Evaluation results from the USDA will apply to their U.S. proof only. The PTA data that goes to Interbull for international publication will contain only the traditional PTA data. There is no mechanism in place currently at Interbull to handle the Genomic Evaluations being published by USDA. Equally, Interbull has no procedures in place to handle Genomic Evaluations being calculated by A.I. companies in Holland and New Zealand. As a result, international bulls with MACE proofs and no U.S. genomic proof that are marketed in the U.S. will use their traditional PTAs only. ■

For more genomics information go to: www.absglobal.com and www.aipl.arsusda.gov



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Introducing the **NEW** absglobal.com

Designed with you in mind, the new ABS Global website features:

- More direct access to country-specific information
- Easy navigation
- Spanish language option
- Valuable resources and articles
- Customer testimonials

ABS will be holding a grand prize drawing for individuals visiting the new site. Register to win one of three MVE semen tanks, and be one of the first 1,000 visitors to receive a poster featuring elite ABS dairy and beef sires from around the globe.



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