

## BREEDERS HAVE LEGITIMATE CONCERNS ABOUT GENOMIC EVALUATIONS

We cannot recall a genetic evaluation run from the USDA Animal Improvement Programs Laboratory (AIPL) that has created as much concern and frustration among breeders as this run in April, only recently completed as we write this, reported on elsewhere in this issue. It certainly appears to our layman's eyes that there are at least two factors at work here, combining to create changes in values and rankings that breeders did not expect and cannot understand.

AIPL researchers have explained that genomic values were "imputed" (read, "estimated," our word) for animals that have not been tested for genomics and secondly that "adjustments" were made (read, "lowered," our word) for females with high values so that supposedly they are more comparable to the values for bulls and therefore, supposedly, more accurate. And by the way, we're told that females with genomic values cannot be compared with females that have only parent averages.

Some geneticists tell us that these problems affect primarily only elite females, and that evaluations for bulls are by and large satisfactory. Again, based on feedback we've had, there are individual bulls that have been assigned numbers that seem to make little sense, with seemingly no correlation between earlier genomics and new proofs with live daughters. We've also been told that some bulls with genomic value that were contracted after the January run now, with April results, are no longer wanted. Bulls less than a year old with no change in parentage! This situation too hits breeders right where they live.

The experts can try to reassure us that overall, for the whole population, we're facilitating genetic progress with these changes. But that's the difference between population geneticists and breeders... the breeders live and die with individual animals... cows and bulls... making individual matings. And when the rules that affect individual values are changed without warning, and seemingly without common sense, there is a huge impact on the value of what we thought were some of our best cattle... or at least some of our highest value animals.

We are reminded of the days 20 years ago when the "Breeders' Majority" rose up and said, "Enough!" The numbers don't match what we're seeing in our barns... the numbers are not correctly identifying the best animals.

In this issue along with our regular coverage, we lay out some of these issues, we include comments from very frustrated breeders and we also publish the explanations provided to the industry by AIPL.

Of course, everyone can and should come to his or her own conclusions. But we echo the thoughts of Holstein Association CEO John Meyer, quoted here, and we say the process of including genomic information in the genetic evaluations of U.S. dairy cattle has received a serious set-back. □

### STATEMENT FROM HOLSTEIN ASSOCIATION USA

Unfortunately, the prospect of calculating and publishing information on genotypes derived by imputation for genomic predictions on females never got to me or the Holstein Association Board of Directors. This is extremely disappointing, and I feel badly about any and all hardships it may have caused Holstein breeders.

From my perspective, the genomics phenomena has gone too far too fast without adequate research. We need to slow the genomic train down because we cannot expect people who breed good cattle and milk cows for a living to be able to keep up with the constant changes. I'm finding some of the scientists who suggested the changes never considered the potential negative consequences of them.

Bottom line, any credibility genomics may have had has been severely damaged by the most recent genetic evaluation.

-John Meyer, CEO

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# APRIL GENETIC EVALUATIONS CREATED EXCITEMENT

By Dr. David Selner



**Some have said that these multiple evaluations each year were not creating enough excitement.** That all changed in an instant on April 9, 2010. The phone lines were humming and e-mails were flying across the country with instant reaction and dismay. Breed leading animals dropped in uncharacteristic ways across the board. Previously active sires with daughters dropped an average of 46 pounds of milk, 2 pounds of fat, over 1 pound of protein and \$14 NM. While the genomic group of sires for sale previously dropped -202 pounds of milk, -8 pounds of fat, -6 pounds of protein, -0.2 PL, -0.1 DPR and \$58 NM. Naturally their genomically tested sisters and mothers dropped similarly. I have heard of cases were females

dropped over 600 points in CTPI.

What appeared to be a simple announcement released by AIPL on March 30, 2010, turned out to be a much bigger adjustment than was anticipated. (Announcement printed elsewhere) Most prior adjustments, except for base changes, have shown small swings and minor re-ranking of the top lists. However this adjustment created very substantial changes at the top end. The breeder reaction was swift and very vocal. When the rules of the breeding world change dramatically those with substantial money invested are going to react. The AIPL scientists have responded to the expressions of outrage by issuing a statement after the run on April 9th and another explanatory statement on April 14th. The bottom line is that genomic tested females and males were adjusted downward to more nearly reflect their ability to predict the outcome of their son's genetic evaluations. This resulted in increased accuracy which is usually a positive step. However since non-genomically tested cows were not adjusted, there is now an unequal playing field between the two groups. A devaluation of the superior females in regards to their less valuable herd mates has created a lot of confusion. These actions will greatly affect the embryo and daughter sales of all affected females negatively for the next four months.

Further enhancing this controversy was the decision to compute genomic evaluations on animals that had no real DNA test but could be imputed from their genomic tested offspring. Suddenly cows that have never been tested were labeled and also dropped. This really added to the anger. Many breeders have asked the question as to who owns the DNA and can you legally label an animal without the owner's approval?

The reaction from the bull studs has been rather mild. They are organized to buy and kill a lot of bulls so whether this bull graduates or that bull, it really does not affect them at all. Additionally since 99+% of the bulls are genotyped they have a level playing field.

Certainly over the next several months the genetics industry will try to resolve some of these concerns for the future. I think all involved have learned a lesson of not communicating enough.

The highlights of the evaluation run have both negative and positive factors. I will try to be explanatory of both sides of this ledger. On the low side, the breed leading sire Shottle dropped by 232 TPI points. The adjustments for the Productive Life trait (Announced elsewhere) had a substantial effect on his information. Since many of his older daughters are in foreign countries and culling data takes time to develop, he needed to be adjusted. Having made that comment he is still in the top 3 TPI sires and one of the great bulls of the breed. Remember these evaluations are a ranking of sires and not absolute values. Forget the drop and focus on a very predictable top ten TPI sire.

The other past sire of note is Golden Oaks ST Alexander. Alexander ranked number 39 TPI last time and has been getting rave reviews on his growthy heifers in the pens. This time he added 1 more daughter and dropped -149 TPI points and is no longer in the TOP 100. Stud officials have offered no explanation for the dramatic change. My observation is that the Productive Life trait dropped from +2.1 to +1.2 in this interval. Since there is such heavy weighting on this trait in the new TPI formula much of the drop can be attributed to this change. It

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## MONITOR METRITIS TO HELP MAXIMIZE REPRODUCTIVE PERFORMANCE



Dr. Staley

The days following freshening bring potential for profitability, but also pose great risk for loss. One of the hazards threatening early lactation cows is metritis, a widespread and costly fresh cow disorder.<sup>1</sup>

Without prompt treatment, this uterine bacterial infection can permanently alter reproductive performance and shrink milk production. The total cost per diagnosed case can reach up to \$300.<sup>2</sup>

Risk factors for metritis include dystocia; retained fetal membrane; stillbirth; and twinning. These events can stress the cow's uterus and leave her susceptible to infection.

"Metritis usually impacts the animal during the first 10 days of lactation but in some cases the effects linger for weeks or even months," says Gavin Staley, DVM, DiplACT, senior fresh cow reproductive manager, Pfizer Animal Health. "Numerous reproductive setbacks can occur, increasing days open, services per conception, calving interval and days to first service."<sup>1</sup>

Staley adds that metritis losses can extend beyond the transition period — even after the infection has cleared and the cow appears normal.

"Severe metritis infections can scar the cow's fallopian tubes, making breeding difficult or impossible," Staley says.

To arm against reproductive consequences, Staley recommends an approach that includes prevention protocols and immediate treatment if symptoms appear.

"Keep the immune system strong by ensuring adequate dry matter intake prior to freshening and maintaining proper hygiene during calving," Staley says. "After freshening, spot the signs of metritis early and treat the cow as quickly as possible."<sup>2</sup>

Staley suggests that dairy producers respond immediately to the signs of metritis, such as fever, and foul-smelling and watery vaginal discharge. To minimize losses, treat with an approved antibiotic to reduce the infection's severity and duration.

Reducing the risk for metritis during the transition period and treating clinical cases early can help boost your herd's reproductive performance.

## SIRE SUMMARY



29HO13366 BEACON  
MINERAL KING BEACON 5181-GRADE  
Owned by Neil Zwart, Visalia, CA



1HO8784 FREDDIE  
O'HARROW'S FREDDIE 7023  
Owned by O'Harrow's Family Farm LLC,  
Oconto Falls, WI

seems to me that many of the fluctuations on index hinge around this. Maybe it is time to look at Productive Life all alone instead of using all the adjustment factors to calculate the current version. The genomic prediction may be even more accurate for a single trait than today's multi-trait value.

In spite of all the negative vibes about the run there are some new exciting sires that jumped to the top of the leader board. The highest new entrant is the Genex sire Badger Bluff Fanny Freddie at +2298 TPI, the new Number 1. Freddie is an O-Man son from a VG-87 Die Hard with over 39,000 pounds of milk, 1352 fat and 1163 protein. The next dam is a Cubby Metro with 33,000 pounds of milk, 996 fat and 919 protein. The next dam is an O-Bee RC Matt Reflector daughter that was entered in the Holstein grade up program. Freddie is a 99%NA sire. This is the first time that I can remember a sire that is less than 100% being this high on the list. Freddie is an all around sire with no holes for production and very high for health traits. The Freddie daughters are not tall, open or very dairy looking but they have excellent feet and legs with great mobility. The udders show strong attachments with average center support. He is a sire that has been utilized for contract matings for the future.

The new number 6 sire is the ABS graduate End-Road Beacon. He is one of the early Shottle sons and comes from the excellent cow family of End Road Farms, Falmouth Michigan. The dam is a VG-88 GMD DOM daughter of BW Marshall with 34,600 of milk, 1267 fat and 1137 protein. The next dam is a Marty daughter scored EX-91 with 40,000 milk, 1493 fat and 1270 protein. Next, the Mathie dam of Boliver named Big Bang and the two great brood cows both GMD and DOM, Leadman Banjo and Royalty Bingo.

Beacon sires milk, plus components, easy calving and long lived daughters. The type pattern has no holes with long bodied, wide-rumped daughters that have excellent feet and legs. The udders are superbly attached. Beacon is a new hot sire of the breed.

Two other new TOP 20 sires are the Alta

graduate UFM-Dubs AltaEsquire at 2001 TPI and the Select Sires graduate Langs Twin B Minister at 1978 TPI. Esquire is an O-Man son from an EX-90 2E GMD-DOM Sam followed by an EX-90 Patron. The Esquires have extremely high fat and protein percents and breed improving health traits. The daughters are taller and stronger with wide rear udders. Minister is a Shottle son from Debut Jess, then Tesk Terry June and then Jezebel, the dam of O-Man. Long lived, healthy, money-making, daughters of average stature describes the breeding pattern of Minister. He is also a calving ease sire. Both of these sires will

see a lot of use in the coming months.

The April genetic run is final, but the building of communication lines and trust between the scientists and the breeders has to be worked on for the future. Hopefully the August evaluations will bring everything back in perspective. □

## AIPL NOTICES OF CHANGE

Changes to evaluation system (April 2010)

Posted March 30, 2010

### Cow adjustments in genomic evaluation

By George Wiggans, Tabatha Cooper, and Paul VanRaden

Traditional predicted transmitting abilities (PTAs) are inputs for genomic evaluation, but cows with high traditional PTAs for yield traits may be overevaluated. Adjustments were developed to rescale cow PTAs for yield traits to be more comparable to bull PTAs. Resulting genomic evaluations were more accurate when the rescaled cow PTAs were included in estimation of marker effects. Genomic evaluations for the top cows, top young bulls, and top heifers decreased by about 250 pounds for milk, 8 pounds for fat, and 5 pounds for protein, whereas genomic evaluations for the top bulls with daughters decreased only by about 70 pounds for milk, 3 pounds for fat, and 2 pounds for protein. Adjustments were largest for foreign bulls with a high proportion of genotyped daughters. The population average of all bulls with daughters decreased slightly by 40 pounds for milk, 1.5 pounds for fat, and 1.5 pounds for protein; standard deviations also decreased slightly by about 1%. Correlations between genomic evaluations before and after the adjustment were 0.997 for bulls with daughters and 0.990 for cows and young animals. Net merit decreased by as much as \$40 for many of the top cows and young animals because of the yield trait adjustments. Only yield and component percentage traits were adjusted because non-yield traits had less variance in females than males and did not benefit from applying these same methods for PTA adjustment. [See Wiggans et al. (2010) for further documentation of methods.]

March 30 update: A new edit was introduced for multitrait PL of cows. Previously, correlated traits measured during first lactation received credit when calculating genomic PTAs of genotyped cows. For a few prominent sires, this created an upward bias in PTA PL because many live, genotyped daughters received credit in marker effect estimation before information from any of the culled daughters entered the sire's traditional PL evaluation. The new edit includes only multitrait PL of genotyped daughters after they reach 36 months of age so that records from living and culled daughters enter equations at the same time.

**QUICK FACT:** The uterus is an ideal environment for bacterial growth. During the first week postpartum, at least 90 percent of cows incur bacterial contamination of the uterus.<sup>3</sup>



<sup>3</sup>Belschner A. Protect your cows from the damaging effects of metritis. Available at: <http://www.linco-spectin.com/PAHimages/pdfdocs/EX-US-DA-protect-EN.pdf>. Accessed March 8, 2010.

# GENOMIC EVALUATIONS DROP — BREEDERS OUTRAGED

By David Selner

**The April 2010 genetic evaluation** release will go down in history as one of the most contentious evaluations of all time. The reaction of breeders from all over the country has been enormous, emotional and defiant. The AIPL staff has already reacted to the discourse by issuing an explanatory message after the run to try to relieve some of the misunderstanding of the predictive model adjustments that were made. I cannot remember a time of such impassioned commentary since the very early days of sire evaluations in the early 1970s.

How did we get to this point where breeders do not believe the science, the AI industry appears unphased and many scientists seem to ignore the breeder's complaints? Numerous breeders have expressed the disbelief

in the reduction of their breeding assets overnight with no apparent reason. They have invested in high genomic animals with increased reliability and wham! They now own "just cows." The AI industry, which is totally structured to weather the variances in genetic fluctuations, seems to have no complaints about the new values. While the scientific community believes that all of the genomic evaluations are more accurate and correct.

Since there is already enough finger pointing and negative comments being made about "in the cloud" scientists or dairymen that just don't understand, I will try to add some new perspective to this volatile situation. I am a person who believes in science and has been trained that way. Yet my up-raising on a dairy also allows me to appreciate the opinions of

the dairyman. A quote I have made all over the world is that "Science generally will prove what a dairyman already intuitively knows, but now we will know the reason why." The modern evaluations of calving ease data were based on a scientist trying to prove that there was nothing to the inheritance of calving difficulty. To that scientist's credit when he did the research, he published the findings that proved him wrong. The US industry gained and we became a leader in the world for genetic improvement.

So I would caution anyone that when a group of dairymen, who are the greatest observers of minute details in the world, has a strong opinion they should be listened to. It has been exciting to see the entrance of the

*Please turn to page 36*

## Haplotypes used for imputing genotypes

By Paul VanRaden, George Wiggans, and Jeff O'Connell

New methods were used for imputing missing genotypes in genomic evaluation. About 1% of marker genotypes are missing in initial data, and previously about half of those were imputed using gene content of relatives and an algorithm that did not use neighboring markers or map location on the chromosome. Program findhap.f90 was developed to determine the paternal and maternal haplotypes that sum to the animal's genotype. Simulation results indicated that the initial rate of 99.0% for correct genotypes was increased to 99.95% after imputing the missing values with haplotypes. The same methods will allow imputing the much higher proportions of missing data that will result when lower or higher density marker sets are mixed with current data containing 50,000 markers. More than 1,000 nongenotyped cows had at least 90% of their single nucleotide polymorphisms (SNPs) correctly imputed using genotypes from multiple progeny (usually 5 or more). Those imputed genotypes are included in SNP estimation, and such cows will be listed in evaluation files with the genomic indicator set to 1 and will have a sample identification of "imputed" in the XML file. [See VanRaden (2010) and VanRaden et al. (2010) for further documentation of haplotyping methods.]

## Improved reliability for genomic evaluations

By George Wiggans and Paul VanRaden

The contribution to reliability from genomics was modified to consider the sum of genomic relationships of the animal with each animal in the

predictor population weighted by the reliability of that predictor animal's evaluation. Previously, the contribution to accuracy from genomics was assumed to be the same for each animal within a breed. The standard deviation of the change in reliability was about 2 for young bulls and heifers and 1 for bulls that had daughters included in their traditional evaluations. [For more information on the genomic reliability approximation, see Wiggans and VanRaden (2010).]

## High-Ranking Cows with Genomic Information

By Duane Norman, George Wiggans, and Paul VanRaden

The dairy industry has expressed concern that the April 2010 adjustment to improve accuracy of predicted transmitting abilities (PTAs) of Holstein and Jersey cows with genomic information (reported or imputed) decreased yield PTAs for those cows compared with other cows. The adjustment makes evaluations of genotyped males and females comparable, thus improving the contribution of cow information to genomic evaluations. The subsequent average gain in reliability of yield evaluations for young bulls was 3 percentage units for Holsteins and 9 percentage units for Jerseys.

Comparability of PTAs among cows might be improved further by decreasing heritability of yield traits or applying adjustments to all cows, and additional research is ongoing. More cows are being genotyped, especially those of interest as bull dams, and the demand for PTAs of genotyped females is increasing. A list of the top cows (registered and grade) with genomic information (reported or imputed genotype) for net merit now is provided for Brown Swiss, Holsteins, and Jerseys. All cows included on the list met screening requirements for elite or high-ranking grade status.

**QUICK FACT: Dry matter intake (DMI) prior to calving can be a significant indicator for metritis. In one study, metritis diagnosis increased three fold for every 2.2 pound decrease in DMI.<sup>2</sup>**



<sup>2</sup>The value of uterine health: the diseases, the causes and the financial implications. Dairy Cattle Reproduction Council. Available at: [http://www.dairyherd.com/drcr/uterine\\_health.pdf](http://www.dairyherd.com/drcr/uterine_health.pdf). Accessed March 8, 2010.

## Genetic Evaluations Drop - Breeders Outraged *continued from page 35*

breeding industry of young college educated producers who already operated good businesses but now are starting to invest in the genetic side of the industry. Since they have a business approach and the genetic estimates are more reliable, they should be able to operate their business with even more profit potential. Sadly from many of the comments I have heard about disasters, these people will no longer be investing in genetic improvement because it's too fickle and too dangerous to make a business model from unless you have the resources of an AI company. This should concern scientists and particularly the Holstein Association as these breeders will quit registering and making breed improvement, and go back to being good money-making dairymen. It is impossible to invest in an industry that will devalue itself overnight and the over-all impact is that less genetic progress will be made in the USA.

How did we get into this situation of mistrust, misunderstanding and a lack of cooperation between all segments of the genetic industry? As in the majority of crises the failure is in lack of communication, apathy, and a system that seems to have been ineffective in developing cohesion. The ruling advisory organization to the AIPL staff is the Council of Dairy Cattle Breeding that officially gives direction, advice and counsel to the geneticists. They meet twice a year and are composed in three equal parts by representatives of the National Association of Animal Breeders, the Breed Associations and Dairy Herd Improvement organizations.

In the area of genetics the representatives of the AI studs have been the most focal and involved. The Breed Associations have supplied some input as well. The DHI group has opinions but has been less vocal in issues that do not directly affect their business, like genomics. So in the absence of input the AI studs have taken the lead in filling the void. They have done a good job of directing the research but maybe without the checks and balances that have been previously successful.

This has led to the controversial agreement between USDA and NAAB to keep all genomic sire information out of the public domain. I truly believe that the more eyes scrutinizing new research the better the end results will be. In this case, that has not happened. So much of the concern is that all of this development has been done behind closed doors without the glare of

public debate. Unlike anything we have ever done before. In defense of NAAB they have invested huge amounts of money in this endeavor and should have some protections but it surely seems there could have been other ways to achieve this. The end result of these circumstances is that the majority of genetic research has been driven by the AI industry and AIPL personnel have less appreciation for the passionate breeder who lives and breathes cows every day of his life.

Now you as a breeder have also been very negligent in your role as a counter balance to all of these events. Have you stood up at your local AI, DHI or breed meeting and expressed any concerns before this? Have you lobbied your board of directors or voted for board members who reflect your positions? Were you one of the ecstatic breeders who had cows at the top of some list who were generally inflated in value? A wise, old genetics professor taught me early on that no cow should rank higher than the highest bull. We have had that situation for years. Additionally many breeders protested that these young genomic bulls were too high. Now when someone is trying to bring that in balance we quickly forget that we asked to bring them down evidently thinking their sisters and dams would somehow be unaffected. The average genomic bull dropped 202 pounds of milk, 8 pounds of fat, 6 pounds of protein and 58\$ Net Merit. Sometimes you have to be careful what you ask for and simply accept the reality of the facts. So nobody is blameless in this situation.

The final piece of the puzzle is the unreal expectations of the genomic estimates. They have been highly over hyped for accuracy and were never intended to be utilized in the manner that people have used them. It cannot be denied that genomics is not real, because it has worked so well in other species and plants. But most of that has been done in tight control of a large company of experienced personnel.

Now, we in dairy have proclaimed the advantages of the genomic prediction so well that the casual observer has accepted the concept with unbelievable fervor. We are still talking about a genetic estimate that combines several pieces of information in a scientific manner but is not a value set in stone. I know there are people that truly believe they will see a significant difference between cow number 20 for some index and cow number 100. That is just a falsehood because we are not that accurate. What is worse is that somehow these estimates have gained tremendous

financial worth. I am sure AIPL scientists would have never believed that overnight they will have devalued millions of dollars of net worth for US breeders. Likewise breeders have put too much value on this one number. We have to get back to the basics of valuing the animals to their worth but without the hyperbole.

Another example of the mis-use of these values is the perception that the differences between the parent average and the genomic value of several offspring can be a negative or positive trait of a specific cow family. That is not true. It has already been proven that any offspring can be shown to inherit anywhere from 40% to 60% percent of the performance genes from either parent. So if they all received 52% from the sire why is that cow suddenly better? This is just sampling variation. The best genetic estimate of a cow is still her genetic estimate not a genetic estimate with added value for difference from genomic adjustments. It is human nature to develop lists and tools to rank animals but do not put unreal value on simple ranking or auxiliary numbers.

The genetic researcher has to understand the principles of population genetics, inheritance and breeding. But remember the ultimate value of the genetic estimate and its use or power is not getting the population right but identifying the top end correctly to make major use of this tool. Do not just rely on rank correlations but what happens in the real world.

The AIPL scientist has to understand that the ultimate believability of genomics is not on how well they can predict young sire proofs, but how well those granddaughters milk in the tank, how many are in the hospital pens or how they look in the lots. The success will be judged on daughter deviations of production, type and health traits, not their sire's proofs. This is the way it has worked in hogs, chickens and seed corn and will not be different here. You can see the difference between 95 day corn and 105 day corn. For believability it will always be that way.

So what's the next step? We all have to start communicating a lot more and have a greater appreciation for each other's point of view. Scientists have to realize that the concerns of producers are real, not just sour grapes and that there are too many discrepancies to the logic. They must address those concerns in a serious, respectful manner. The industry groups all have to do a little better job of asking their membership about future goals, wants and needs, then express that col-

**QUICK FACT: Data shows cows diagnosed with metritis produce 15 pounds less milk per day in the first 30 days of lactation.<sup>2</sup>**



<sup>2</sup>The value of uterine health: the diseases, the causes and the financial implications. Dairy Cattle Reproduction Council. Available at: [http://www.dairyherd.com/drcr/uterine\\_health.pdf](http://www.dairyherd.com/drcr/uterine_health.pdf). Accessed March 8, 2010.

lective opinion in a proper manner. Finally, dairymen have to be less apathetic about what is going on in the world until a crisis happens. Get involved. Do your homework. Do not look for evil intent when something goes wrong. The scientists at AIPL are all honest, honorable people who truly care

about the dairy industry. No, they may not know how to pull a calf in the middle of the night, but that doesn't mean they have no ability or intellect.

If we do not unify as an industry we will surely not succeed in the genetic world. We are on the edge of determining the genetic fu-

ture of our US population. Working together we will prosper. Working against each other will ultimately lead to our purchasing semen and embryos from other countries. Our world domination of genetics cannot continue, unless we all work hard to improve this situation. □

## LETTERS TO THE EDITOR

### MYSTICAL MATH, VODOO CALCULATIONS... GENOMICS DESERVES BETTER

Several years ago, I was asked by our Holstein Association to supply genetic material on several heifers and cows to be used in a research phase of genomic testing. When the results were received it seemed there were no major surprises, some cows up slightly and some down slightly from their PTAs. It all seemed like an interesting little science project, but I didn't know what was to come.

My next exposure to genomics was on April 10, 2008. This is when I received a genomic report on a cow for which I had never submitted hair samples. The cow named Elsa had results that closely matched her current PTA. Elsa's milk in fact was within 4 pounds of her official PTA... 1330 vs. 1334.

Then the trouble began...seven days later, on April 17, 2008, I received another genomic evaluation on Elsa. I was told they made a mistake on the previous input data. The new values dropped Elsa's value for production about 30%. Who knows what is correct at this point? Over the next several Index runs, Elsa slowly worked her way up, in fact higher than the original results.

That was until this last Index run in April where "certain" cows were assigned an "imputed genomic" index because they had five or more genomic tested offspring. Over 1000 cows were assigned an "imputed genomic" index in April 2010. Elsa's dam, Elsie, was one of those fortunate (?) individuals, causing Elsie and the other 1000+ cow indexes to crash. Elsie by the way had been 90+% reliable for several years.

In the meantime in the real world, Elsa had four of the top seven genomic tested cows in Europe in January 2010. In April, Elsa's grandson is the #3 bull in Germany and in the Top 10 in Canada. At Select Sires, Elsa's son has been near the top of the list for udders and overall type. Elsa's Oman son is in the Top 10 protein bulls of the breed.

The problem seems to be that high producing cows and high producing herds give too much milk for this evaluation system. So the system feels that every cow is created equal so that cows that deviate must be lowered, perhaps so the lower milk cows do not have their feelings hurt.

When this new technology was introduced I told Tom Lawlor (Research Director at Holstein Association USA), and anyone else who would listen, that we needed to run a dual system for at least five years so that we could idiot proof and fraud proof this new technology.

I also said we needed complete transparency of the raw data so that many different eyes could view it and have input. This is not what has happened at all. Rather, we have restricted access to the raw data for both type and production and we have proceeded to adopt an untested secretive system that the American dairy industry is forced to accept at face value. It is a system that continues to be changed and manipulated to fit the needs of whoever is making the adjustments.

I truly believe that the people who are doing the tinkering behind

closed doors have no concept of the results of their careless and possibly fraudulent actions to achieve their misconceived goals of trying to make all cows average.

To further consider the pedigree on My 1326, the new world record holder for milk production. The index on My 1326 dropped substantially after making this milk record because her production must have offended her herd mates! My 1326's index is below parent average now. Her full sister who produced 30,000 pounds less milk and is scored 6 points lower now has a HIGHER index.

When genomic proofs were proposed, we were told that this would be a stabilizing force in the industry and that we would be able to rely on the results and data provided. Nothing could be further from the truth. PTA values based on genomics have moved around without rhyme or reason and without valid explanations. A cow, heifer or bull has valuable genetics one day and the next day has no genetic merit at all, according to this system.

I believe the dairy industry was devalued by well over \$1,000,000,000---yes, one billion dollars!! This was done by the April Index release. I personally invested \$40,000 in new genetics this past month. Now these very same genetics, according to AIPL have NO genetic value. All of these individual animals were genomic tested and were of elite genomic value before the April run.

I will not make this mistake again, nor will I advise young people or anyone else to invest in an industry so unstable! Remember, the genetic SNPs did not change, only the manipulation of the data!

I am not against science or new technology. I have always tried to embrace innovation and new advancements in science and management. This has served me well. And I do not think that genomic testing is without value.

But, as breeders and dairymen, we should not stand idly by and watch the most admired, time tested system of measuring the value of Holstein genetics be replaced by mystical math, misconceived assumptions and voodoo manipulation of facts to reach a pre-conceived conclusion.

Well over a century of dedicated effort has gone into the fantastic dairy breed WE have developed. Let's not let the scientists and AI folks, no matter how well intended, ruin what WE have developed as a group effort. The biggest mistake these people make is to assume that their intelligence and insight exceeds the collective intelligence and insight of the AMERICAN DAIRYMAN!!! Genomics to date has created NOTHING! It is only trying to measure what dairy breeders have spent their lifetimes developing.

**Concerned for the Future of the Dairy Breeding Industry**

**Tom Kestell**

**Waldo, WI**

**QUICK FACT: Cows with metritis are more likely to leave the herd within the first 60 days in milk.<sup>2</sup>**



<sup>2</sup>The value of uterine health: the diseases, the causes and the financial implications. Dairy Cattle Reproduction Council. Available at: [http://www.dairyherd.com/dcrc/uterine\\_health.pdf](http://www.dairyherd.com/dcrc/uterine_health.pdf). Accessed March 8, 2010.