

April Genetic Evaluation Observations

By David Selner

Many have questioned the genetic estimates that were published in the April genetic evaluations. This criticism is coming from breeders, a group that usually is not very vocal in their complaints and interestingly not normally consulted in national genetic evaluation discussions. Breeders feel that they are not being given due consideration and believe that their livelihoods are being affected by the decisions of A.I. studs and others without regard to their interests. These feelings could grow into animosity if the leaders in the industry do not take action to address their legitimate concerns. To help initiate change someone has to provide concrete examples of genetic values that appear to be questionable or very hard to understand to the scientists doing the research. Positive change can only happen when legitimate concerns are expressed and valid problems are identified. I will attempt to point out some of the concerns that have been expressed to me.

Genetic Values for Milk

The first area of concern is in the genetic values for milk on very high reliable influential sires. Since milk production is one of the more highly heritable traits it should be predicted rather easily. It has been the normal expectation of the breeders that when you reach thousands of daughters the actual genetic value mirrors the real observed differences fairly closely. Breeders always want to know at what level of reliability or number of daughters, does the amount of real information on daughters, exceed the need for any adjustment factors or values in the genetic estimates. Most breeders still relate to the previous genetic evaluation formulas where reliability gave an indication of

the amount of real data versus pedigree data. The methodology used today is different so you cannot make the same statements about the amount of daughter information versus the amount from pedigree or genomics adjustments. **However the expectation of the genetic evaluations mirroring the actual daughter deviations at high numbers of daughters is still the common belief among all dairymen.**

Bull	# Dtrs	Dtr Dev	Genetic Eval	Difference
O-Man	58474	724	841	+117
Goldwyn	33777	340	471	+131
ToyStory	21636	1246	1238	-8
Die Hard	52062	501	476	-25
Potter	23883	839	811	-28
Shottle	23128	1430	1399	-31
Jet Stream	10600	1042	979	-63
Boliver	24722	945	839	-106
Sharky	7993	1961	1835	-126
Lou	7199	1287	1075	-212
Bolton	7870	2202	1975	-227

Table 1 shows several popular second crop sires with over 7,000 daughters. It lists the number of daughters in the genetic evaluation, the average daughter deviation, the April genetic evaluation for milk and the difference between the genetic evaluation for milk and the average daughter deviation. The two sires O-Man and Goldwyn have very favorable genomic adjustments for milk production. (The last calculation to be done is the adjustment for genomics.) Now maybe 100 pounds doesn't sound like much but in the case of these two sires it equals a 15 to 30% increase over the true daughter deviations.

Before the beginning of the genomic adjustments to genetic evaluations I had never seen this high a discrepancy when looking at evaluations on sires with over 30,000 daughters. The daughter deviations for Toystory, Die Hard, Potter, Shottle, and

Jet Stream are very close to the genetic estimates. The comparisons for Boliver, Sharky, Lou and Bolton show a negative bias of the genomic adjustments to the real daughter deviations. Even if the genetic value says that the genome estimate is more correct than 58,000 daughters for O-Man or 24,000 daughters for Boliver **no dairyman will believe that this is right**. Because they will never see this extra milk from O-Man in their bulk tank but they will experience the extra milk in the tank for Boliver. This will lead to the inevitable belief that genetic estimates do not work because they do not reflect the real world.

That is why there is an outcry on these results. Why are some highly used and influential sires higher than their daughter deviations, some similar and some downgraded by the genomic adjustments. Since there is no consistent pattern many believe there is some sort of bias being introduced by the genomic adjustments. Now I have only looked at milk because it is easy to talk about, you can see it in the bulk tank and it is highly heritable. But there are similar values in other non-type traits. Clearly these occurrences should be examined to see if this difference from the real world and the unpredictable differences between sires can be solved.

Genetic Evaluations for Cow Families

Secondly let's examine the changes in genetic evaluations for cow families where the biggest complaints have come from. The genomic adjustments and imputed values have really been confusing to the average breeder. These problems have already been discussed with the challenge of two different genetic bases and the wide swings in unannounced genetic evaluations this time. But clearly the scientists have to see examples of cow families that have been questionably evaluated by this system

before they can see what needs to be corrected. I will use the example of a cow I know very well Ra-Mar-Land Lorelei. She has five sons with proofs at major bull studs. All of these sons are over +1000 pounds of milk for their official April 2010 genetic evaluation. Her January index for milk was +1579. Her new April index adjusted for an imputed genome effect (she died before the test was available) is +1225 or minus 354 from her last index. This is quite a drop for a cow that has done so well at producing high milk sons. Table 2 displays a more complete view of her son's information.

Sire #	#dtrs	Parent Ave	Dtr Dev	Pta Milk
H8058	73	1136	1767	1719
H5177	87	1033	774	1017
H8991	79	1033	2693	1398
H13204	117	1270	2211	1753
H8905	57	1270	-61	1118
Weighted Total	413	475386	664286	593235
Weighted Ave		1151	1608	1436
Simple average	82.6	1148	1477	1401

Those 413 granddaughters (dtrs of her sons) weighted average for PTA Milk is +1436. This PTA is +285 pounds more than the weighted average of the parent averages. This clearly indicates that the granddaughters out-performed their pedigree values. What is even more curious is that the real deviation of the daughters is still another 172 pounds higher than the PTA. Thus the daughters out-performed their pedigree by +457 pounds.

Now Lorelei's January index of +1579 is very near the average of her granddaughter's real deviation. This would make me feel that this is fairly correct in predicting her transmitting ability. But her April genomic imputed index dropped to +1225 for PTA Milk. So the real differences of the granddaughters superiority in

production over parent average was of no weighting in estimating what a cow like Lorelei can transmit. This just does not make sense.

Now I know that Lorelei's sons because of genomic adjustments are all over plus 1000 but in reality one of the sons is a bad bull (minus daughter deviations), one of the sons is close to the real daughter deviations for milk, but three of the sons (all by different sires) are under evaluated for what their daughters are producing and one by almost 1300 pounds. This genomic downward bias is hard to understand when compared to real records on granddaughters all over the United States. This family has been significantly higher than contemporaries for six generations. Because of genomics a Lorelei daughter has developed into one of the top 100 cows of the breed in April for GTPI and one of the sons of a daughter was a Top 20 sire for GTPI when he was released for sale last fall. So we have seen some of the positive effects of genomics. Yet the majority of the family has been devalued due to genomic adjustments. It is hard to figure out on one hand the family is great while on the other hand it is average. In my opinion this is due to a strong genomic sire effect (high or low bias) and very little real emphasis on the real deviations of milk. Since we have tried to keep this somewhat of an outcross family we have suffered a negative genomic effect. Yet there are generations of high real deviations that appear to influence the genetic evaluations by very little. This is really hard for a breeder to comprehend.

Since I knew of these two sons that deviated due to genomics over 1100 pounds plus and 1290 pounds minus from their real daughter averages, I thought I would examine other newly proven sires in April 2010 with genomic information from April 2009.

Table 3: Comparison of newly proven sires with their genomic values

Bull #	April 2010 #dtrs	April 2010 PtaM	April 2010 UnOff PtaM	Apr 2010 Dtr Dev	April 2009 Genomic no dtrs	2009 2010 PTA Dif	Apr09 Gen Apr10 DDev Dif
H8905	57	1118	358	-61	1315	-197	-1376
H8991	79	1398	2388	2693	1189	+209	+1504
H9161	68	+599	-631	-1165	2416	-1817	-3581
H13405	120	-35	-254	-459	1437	-1472	-1896
H8840	57	-4	-838	-1293	1364	-1368	-2657
H5192	88	+29	-346	-646	1442	-1414	-2089
H9103	56	+41	-551	-928	1068	-819	-1996
H9684	103	+55	-316	-594	1388	-1333	-1982
H9211	40	+869	+145	-349	2251	-1382	-2600
H1165	62	-349	-988	-1504	965	-1314	-2469
H13474	33	+297	-131	-777	1537	-1240	-2314
H9207	49	+663	+395	+22	2097	-1434	-2075
H9494	120	2029	2266	3577	1311	+718	+2266
H9575	118	1836	2406	2629	1404	+432	+1225

The first two bulls are sons of Lorelei that have official April Pta's for milk of +1118 and +1398. Their unadjusted unofficial PTA's for milk (no genomics) are +358 and +2388. The actual daughter deviations of their daughters are -61 pounds and +2693 pounds. Their genomic information in April of 2009, just one year ago with no milking daughters yet were +1315 and +1189. The next column is the difference between their published April 2009 genomic value and their actual April 2010 genetic value. The last column is the difference between their April 2010 actual daughter deviations with their April 2009 genomic value with no daughter information.

The last two sires along with the one from our cow family are examples of one of the potential types of genetic loss from a misevaluation, bulls with lower genomic

adjustments values but high real daughter performance values. These bulls if they were born today would be slaughtered and never given a chance to prove their genetic worth. They may have been able to contribute something. Interestingly there are only 10 sires of this kind. But what a loss to the industry when high bulls can be underestimated this much and are being slaughtered without a chance.

In the middle group of sires I selected some of the worst examples of sire prediction so you could quickly see the differences. In every case for this middle group of bulls the current genetic evaluation is much lower than last year's genomic predicted value. Secondly by looking at the current daughter deviations these bulls could go even lower. By examining the April 2010 traditional genetic evaluation (unofficial & unpublished) without genomics you can see that this value is much closer to the real daughter deviation than the published genomic adjusted value of today. Because the genomic information is pulling these sires upward and giving a false sense of what the real performance is going to be. Why is there such little influence on the real values when genomic adjustments are made?

Evaluation of Young Sires

The data set used has over 450 Holstein young sires with no daughter data but having genomic values in April 2009 and all values have been adjusted for the base change. The difference between the published genomic value of 2009 one year ago with the actual genetic evaluations of the bulls today is disappointing in my opinion. Here is a closer view on some of these sires using only these two values.

Table 4: Comparison Genomic Values with First Proofs

<u>Bull #</u>	<u>#dtrs</u>	<u>April 2010 PtaM</u>	<u>April 2009 Genomic PtaM no dtrs</u>	<u>2009 2010 PTA Dif</u>
H9161	68	+599	2416	-1817
H13405	120	-35	1437	-1472
H8840	57	-4	1364	-1375
H5192	88	+29	1442	-1414
H9684	103	+55	1388	-1333
H9211	40	+869	2251	-1382
H1165	62	-349	965	-1314
H13474	33	+297	1537	-1240
H9207	49	+663	2097	-1434

-Source: Request Ltd., Verona, WI

In this study there are over 430 bulls that have a value of -500 pounds or more and 119 of those are over -1000 pounds of milk. The biggest example is a sire that lost 1800 pounds of milk on his April 2009 official genetic estimate at 74% reliability. This difference is unacceptable in my opinion. Having 430 bulls too high by a volume of hundreds of pounds of milk would not be confidence building to any breeder I know.

If high genomic young sires like these are used the results will be very disappointing. When the breeder uses a high ranking sire and a year later he has a calf on the ground for a contract from a buyer or just as a herd replacement that is a genetic disaster who suffers the consequences? The buyer walks away and says it is not our fault but these genetics no longer qualify for our program. Now you have just another bull to market. In the worst case you now have a female from your best family that is virtually worthless as an income producer from a breeding standpoint. Breeders that have spent a lifetime building up their cow families cannot afford to have these types of

disasters happen ever. The financial future of many breeders cannot be treated with statements that the new values of today are now better than those you saw before. Breeders cannot operate like A.I. studs because they have to milk their mistakes they cannot just kill them.

So what does genomic adjustment really do? In the published genetic evaluations it can overwhelm the real data on sires with over 20,000 daughters. In other cases it can force sires too low or more commonly it raises sires too high. Generally it has not been as accurate as assumed by many in predicting real performance for milk. We need more predictable evaluations over years so that breeders can actually use these values with confidence and not suffer dire consequences.

Older Cows: Why Low Genetic Values?

The other concern expressed on the cow index is the extremely low genetic values obtained by older cows when compared to young cows and especially to these heifers today. If you look at the dams of these highly reliable sires you wonder where the genetics is inherited from.

<u>Bull</u>	<u>PTA Milk</u>	<u>Dam PTA Milk</u>
O-Man	+ 841	-468
ToyStory	+1238	-221
DieHard	+ 476	-850
Potter	+ 811	+102
Baxter	+1682	+213
Jet Stream	+ 979	+303
Boliver	+ 839	+ 79
Sharky	+1835	+982
Lou	+1075	-221
Bolton	+1975	+916

Surely these dams contributed something to these famous sons. In most cases we are looking at sons that exceed their dams by over +1000 pounds of milk. If it is true that genomics can show what was inherited from the dam or the sire it could be proven which parent contributed to this outstanding offspring. I find it hard to believe it only came from the sire side. It just seems that some of these cows that are older now drop off too fast in genetic value as compared to the younger unproven females. I believe there is just a little too much negative bias in the age factors when it comes to evaluating a females own performance. Why should it be almost automatic that these high daughters exceed their dams by so much?

Where to Find Outcross Genetics

The final point I would like to address is the lack of finding true outcross genetic breeding families. One of the brightest hopes of many breeders for genomics would be the ability to identify a high genetic value family that has not been tapped by the industry to create some more outcross genetics. These families are just not showing up. Now maybe we haven't done enough females to identify that family. But I am beginning to believe that our current system will not find those outlier families.

Everyone who has tested females for genomics knows that daughters of certain sires are treated more favorably by genomics than daughters of other sires. Many advise breeders not to sample certain daughters because they automatically will come out lower than you expect, because of a negative sire affect. (See the first chart with O-Man and Goldwyn versus Bolton and Lou) As we move along in the generations of animals tested it appears there are always some sires that genomically have a higher positive test factor than their performance indicates and some that have a lower

genomic factor than perceived. The current theory of some scientists is that cow families are so polluted with preferential treatment that nothing can be gained from studies of their genetics. Therefore there is more emphasis on the sires. But if we only look at sires, the only high cows will be Freddies, out of Planets, out of Goldwyns, out of Shottles, out of O-Mans. This just cannot be always right and will certainly ruin the breed by inbreeding.

Cow families do exhibit outstanding traits that can be traced by generation. We have to find these families to aid the development of the breed. I will again look at the family I know well. For eight generations this "L" family has produced females with superior milk production. No matter what the sire, all of her daughters that have calved in with four normal quarters have exceeded + 4000 on the DHI sheets. I believe that Lorelei with three sons by three different sires that all have daughters that deviate at +2000 pounds of milk should be a source of milk. The best daughter we have at home was starting out on an awesome two year old record for our herd. At about 90 days in milk she suddenly developed an infection that settled into her hock region and really created havoc. Near death we took her to the university hospital to see if we could save her. A month later we were told they were probably going to put her down but wanted to use some experimental drugs to see if they would work. About three weeks later she came home, very thin, not milking anything, but for us gloriously alive. She eventually started to milk again and peaked at over 90 pounds. She scored Very Good – 86, ended up over 8000 to her DHI contemporaries and milked for 800 days in her first lactation. Now certainly this ordeal cannot be confused as preferential treatment. So we decided to genomic test this cow as she had to be a genetic wonder for milk. Bad idea! She is from the wrong sire, one who actually is minus for PTA milk. Even with high brothers,

high sisters, a mother that was +10,000 to the herd and her own performance of +8000 to her contemporaries she dropped severely. Her current genomic value for milk is +486 and her overall GTPI of +1484 does not meet normal standards for Holstein embryo flush cows. We will continue to breed this family for their great performance but it would be nice to see that they would rank consistently in this area of genomics. Now maybe this family is not that great but surely in the entire Holstein population there has to be families that excel for certain traits that could enhance the breed. Breeders are continuing to complain about the inaccuracy of the female genetic evaluations and how they relate to their milk deviations from contemporaries on the DHI records. I believe it is time to do more research on the actual production record deviations, and the within herd variance differences among and between herds. The use of regional variance adjustment factors alone to standardize these differences does not seem to be consistent with what dairymen believe. There are too many females that do not seem to get enough credit for their performance and other average females that get too much credit for their performance. It is hard for a breeder to accept that one of his poorest performing cows is one of his best genetic index cows.

Legitimate Concerns

I hope that genetic researchers take a very close look at some of the concerns I have shared for others. These are very serious concerns because the faith of the breeder in these genetic values is clearly in doubt by the type of observations described here. The feeling that the system is geared to help the A.I. studs with little regard for the breeders who are the backbone of the genetics industry and supply all of the data that is used for genetic evaluations is real. There is getting to be less incentive for breeders to

supply this information if their concerns are unheeded. The A.I. studs demand speed and want to turn generations as fast as possible and that is what the system is supplying. However the breeder demands accuracy over speed and he is being ignored by the direction of the current breeding evaluations. It is impossible to make a long term financial commitment to purchase breeding stock, if before you have a chance to merchandise any products from your purchase the value of the animal has changed to make her useless as an income source. The A.I. studs can move on to other animals the breeder is stuck with what he owns. This breach of faith must be restored before the industry can make maximum genetic progress.

In my opinion the United States genetic evaluation system has been the Gold standard for the rest of the world for many years. I traveled the world and felt very confident that the genetic values I was promoting truly would show up in the bulk tanks of dairymen anywhere in the world. From the popularity of US genetics that surely has been the truth. But now with genomics adjusting genetic evaluations to the degree that does not necessarily show up in the bulk tank, the free stalls or the hospital pens I have concerns.

New research has shown that the current level of predicting lactation production from parent average is not as high as it used to be. Previously this was a value of near 1.0. Thus a very accurate prediction of lactation yield could be made. Expectations of production followed the parent average. Now the latest studies show this regression has dropped to roughly 0.6 to 0.9 instead of one. This means that the genetic parent average will not show up in the bulk tank as well as previously expected. This only adds to the bewilderment of the breeder who is trying to make a living breeding superior genetics.

I believe we have the best researchers in the world and we will find the solutions to these concerns in this new era of genomics. However if we ignore the need to have our genetic estimates be very transparent to the dairyman (seen in the tank) and make logical sense to the serious breeder. I fear we will have reduced use of the genetic tools available. The lessening of breeders using all of the best genetic tools available will be a detriment to the entire industry. This should be a concern of everyone in the US breeding industry.

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