

Genomic Testing and Method \mathcal{R} Variance Components Theory of Dairy Cattle

A Senior Project

presented to

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Bachelor of Science

By

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Abstract

The objective of this study is to determine the change in reliability from non genomic evaluations or Parent Averages to genomic evaluations. Due to recent industry popularity of genomic evaluations the California Polytechnic University, San Luis Obispo, decided to participate in the genetic movement of the dairy cattle industry. Genomic evaluations of both Holstein and Jersey cows at the Cal Poly dairy were chosen based on genetic superiority in order to possibly generate more income for the dairy and increase the herd's popularity. Leading genomic companies such as Pfizer Animal Health, and GenSeek made genomic evaluation of the Cal Poly herd affordable by donating genomic sampling kits. Using the BovineSNP50 Bead Chip and BovineSNP6 Bead Chip, hair and blood samples were taken from the Cal Poly cows and heifers and were sent to the respected companies to generate official genomic evaluations. The data that this project focused on was the change in reliability of health traits such as Productive Life, as well as type and production traits including Net Merit Dollars, Cheese Merit Dollars, Genomic Total Performance Index, and Predicted Transmitting Ability for Type. Increases from traditional parent averages reliabilities to genomic evaluations reliabilities were obtained for all 6 core traits that were evaluated from the tested animals. In 59 Jersey's that were tested, average reliabilities scores increased from an average of 45% to 69.61%. In addition the 51 tested Holstein females reliabilities raised from 43% to 74%. The genomic evaluations also suggest that the Cal Poly herd is genetically superior, they have two cows in the California top 100 GTPI cow and heifer lists for their respected breed. The gain in reliability of core industry traits and development of genetically superior animals of the Cal Poly herd has in turn increased their popularity of their herd, as well as potentially generating more income from its superior cows and heifers. A genomic based breeding program that Cal Poly has installed will speed up genetic progress of its herd by two years for each generation. The genomic evaluations of the Cal

Poly herd will be used as a breeding tool to generate superior genomic bulls and heifers for potential future income.

The algorithm that is used for estimating the variance of genetic components is called Method \mathfrak{R} , and it will be used to analyze the correlation between Traditional Total Performance Index (TPI) to the Genomic Total Performance Index (GTPI/GJPI). The algorithm Method \mathfrak{R} , must equal 1 regardless of the sample size in order for the theory to be true (Reverter, 1994). If the computed \mathfrak{R} is greater than 1, then the variance component ration or slope is underestimated, but if it is less than 1 it is overstated (Reverter, 1994). Moreover the Method \mathfrak{R} algorithm will essentially prove that if the newly designed, chromosome based, genomic predictions are correlated with the traditional parent averages.

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Introduction

Genetic progress in there dairy cattle is what every dairymen hope to achieve in order to generate income. With the release of genomic evaluations dairymen can achieve that goal even faster. Recently with the introduction of genomics dairymen are allowed to genetically enhance their herd faster, more efficiently, and select the best genetics for their individual herd requirements. With the use of genome mapping and generating genetic markers dairymen and A.I. industry companies are allowed to select superior genetic cows, heifers, and bulls to market.

Traditionally, young bulls, heifers, and cows were selected and deemed superior based on their parent averages (PA's). Now with the use of genomic evaluations dairymen and A.I. companies can see exactly what traits a cow, heifer, or bull has inherited from their parents (Dr. Weigel, 2011). Genomic evaluations are not 99% reliable as of yet, but they offer a powerful tool to help dairymen and A.I. companies predict results from matings (Dr. Weigel, 2011). Mendillian genetics is the basis of inheritance and traditionally states that offspring shall receive approximately 50% of its genes from each parent, 25% from each grandparent, and 12.5% from each additional great grand parent, as seen in figure 1 (Dr. Weigel, 2011). That is true when looking at a large group of offspring, but it isn't true when looking at an individual cow, heifer, or bull. Under newly innovated genomic evaluations dairymen and A.I. companies can look at each individual chromosome and see how much of a particular trait an individual inherits from each generation, as seen in figure 2 (Dr. Weigel, 2011).

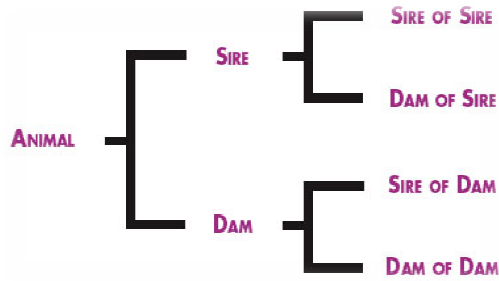


Figure 1. Traditional Mendelian genetics model.

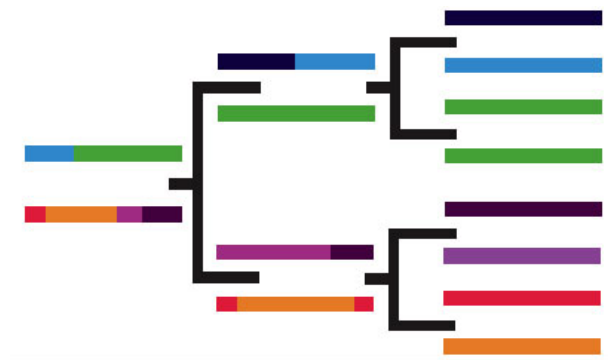


Figure 2. Inheritance from ancestor's individual chromosomes seen through genomic evaluations.

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Overall genomic evaluations provide dairymen and A.I. companies with a significant improvement in accuracy over PA values (Dr. Weigel, 2011). Genomic evaluations also allows for younger animals to be used as parents, therefore reducing generation intervals to enhance genetic gain (Dr. Weigel, 2011). The background surrounding genomic evaluations is focused on advancing genetic gain in a shorter amount of time.

The objective was to determine the change in prediction accuracy as reliability increases advancing from non genomic or PA's to genomic evaluations agrees with the theory. By using genomic evaluations as a management tools for genetic advancement it may be possible to

identify superior genetic females to use in marketing to increase farm income in the struggling dairy industry of the west coast.

Literature Review

QTL Mapping and History

Genome projects have been completed by scientist and under the supervision of the United States government to explore the genes and genomic progress. Prior to 1935 there was no known national program for evaluating dairy cattle breeding and no set real genetic progress was made (Hayes, 2007). Over the past 72 to 75 years there have been various programs or traits that have been introduced through the genome project, thus increasing the rate of genetic progress in different amounts of reliability, thus generating a better understanding on how to quickly improve the progeny of future dairy cattle. The induction of genomic evaluations on dairy cattle has been predicted to be one of the largest impacts on genetic gain for the dairy cattle industry, and ultimately assisting dairy producers to generate the “Genomic Giant” (Hayes, 2008).

To generate a better understanding of genomic evaluations reviewing an article by Dr. Ben Hayes from Victoria, Australia helped tremendously. Dr. Ben Hayes has provided an exceptional understanding of genomic evaluations in his designated short course textbook, “QTL Mapping, MAS, and Genomic Selection” that was copywrited in 2007 at Iowa State University. Dr. Hayes is a geneticist that maintains a superior understanding of exactly how genomic evaluations originated and how they are used, which is what I used to gain a better understanding of genomic evaluations. Dr. Hayes expresses that there has been a recent change in how dairymen and scientist identify the most superior genetically advance female or male to be produced and that is because of the ability to locate specified loci and chromosomes that will genetically alter an individual’s genetic index. There is now believed to be a finite number of loci that alter or mutate the quantitative traits in the genome. Research suggests that specified

genes will have a large effect on the animal and some genes that have a small effect and are hidden (Hayes, 2007). Traits that have an effect on a large distribution of traits are often times called quantitative trait loci or QTL, for example different allele's combinations may generate one total published value or number in an individual cow's index. Researchers dealing with genomic evaluations in dairy cattle look to QTL mapping to uncover exactly which chromosome regions are associated with variations among genetic traits and phenotypic traits.

Deoxyribonucleic acid (DNA) markers are the backbone or markers for what genomic evaluations identify for associations between alleles and QTL's (Hayes, 2007). Gene mapping allows for exact locations of a particular chromosome that is identified and can be monitored and mutated for further years.

Genomic Reliability

Genomic reliability is derived from the amount of information of a particular individual that is already logged into the USDA data base, based on prior testing of family decedents, to compute an overall confidence in the outcome of an individual's performance. Reliability is based on a combination of daughter evaluations, parent averages, and information derived from traditional evaluations or PTA's (Cassell, 2011). The reliabilities in December of 2010 for PTA milk yield for genomic evaluations were 74-81% for most cows and bulls (Wiggans, 2010). Reliabilities for NM\$ evaluations were greater than 70% in Holstein females and males (Cassell, 2011). The reliabilities of young bulls with first crop daughters increased 30%, which allowed semen companies to release bulls semen at 1 year of age rather than holding on to him until his daughters were analyzed at 2 years of age, thus spending more money feeding a bull that wasn't going to get released until he is 3 years old (Cassell, 2011). The reliabilities for bull proofs also increased for traits such as PL, Somatic Cell Score(SCC), and Daughter Preg Rate(DPR).

Factors affecting Reliability

Base change. As of April 1st, 2011 there was a base change in which genomic evaluations are computed. The new base for genomic evaluations is perdomately more accurate than the old base and prior genomic inflation has settled back true numbers of tested females and males (Cassell, 2011). Bennet Cassell, a writer for Hoards Dairyman, states "ultimately everyone who makes a living with dairy cows benefits form more accurate and publically available genetic evaluations," (Cassell, 2011). Genomic evaluations serve no purpose if they're not accurate and needed to be changed before the April 1st proof. Recalling inflated PTA's to improve accuracy on Holstein and Jersey females is what the USDA was eager to do when they

reformulated the genomic evaluations. Before the base change or recall numerous Holstein and Jersey females had emerged as the genomic freaks, boasting unheard of genomic index numbers that seemed at one time unheard of (Cassell, 2011). If the USDA hadn't changed the base of genomic evaluations the Holstein and Jersey breeds would not be developing new superior genomic females and males, therefore the genomic predictions will crumble. The most helpful tool of dairy cattle genetic advancement has been genomic evaluations and it is here to stay around if the base evaluations are correct.

Table 1. Numbers of genotyped animals by breed and evaluation date

Breed	Evaluation date	Bulls	Cows	Young bulls	Heifers	Imputed	All animals
Holstein	April 2009	7,600	2,711	9,690	1,943	-----	21,944
	August 2009	8,512	3,728	12,137	3,670	-----	28,047
	January 2010	8,974	4,348	14,061	6,031	-----	33,414
	April 2010	9,770	7,415	16,007	8,630	1,471	41,822
	August 2010	10,430	9,372	18,652	11,021	2,029	49,475
	Dec. 2010	11,293	12,825	21,161	18,336	2,172	63,615
	January 2011	11,194	13,582	22,567	22,999	2,282	70,342
	February 2011	11,196	13,935	23,330	26,270	2,350	74,731
	March 2011	11,713	14,382	24,505	29,926	2,463	80,529
	April 2011	12,152	11,733	25,204	36,047	2,342	85,136
	May 2011	12,429	11,834	26,139	40,996	2,442	91,398
Jersey	February 2010	1,977	479	1,172	197	-----	3,825
	April 2010	2,072	637	1,250	202	97	4,161
	August 2010	2,145	792	1,376	258	152	4,671
	Dec. 2010	2,217	2,189	1,754	1,924	178	8,084
	January 2011	2,209	2,316	1,868	2,130	186	8,523
	Feb. 2011	2,209	2,407	1,956	2,364	192	8,936
	March 2011	2,213	2,557	2,036	2,616	197	9,422
	April 2011	2,265	2,775	2,096	2,884	183	10,020
	May 2011	2,279	2,966	2,198	3,630	188	11,073

The traditional genomic evaluations before the base change were a combination of pedigree, performance, and progeny traits, but the new base change allowed females to escalate to the top of the charts. The males were more favorable under the old genomic base evaluations, even though some had the same genetic makeup as females. With the new genomic base evaluations in place, genomic accuracy rose about 3% when applied to both male and female Holsteins (Cassell, 2011). The accuracy of Jersey genomics under the new base change was more drastic boasting a nearly 9% improvement in reliability for yield traits (Cassell, 2011).

Genomic reliability evaluations have also improved as much as being able to impute untested animals based on the number of progeny they have tested. The new method of imputing individuals may be done if the dam is sired by a bull that has been 50K SNP tested and the combination of progeny tests based on amount of information provided by the dam when tested (Cassell, 2011). The ability to impute untested genomic females has allowed dairymen that have been heavily involved with genomic evaluations to receive a free genomic test with 95% accuracy (Cassell, 2011).

Currently genomic evaluations are running on average a 75% reliability of yield traits for young bulls and heifers (Wiggans, 2011). The 50 K SNP genomic evaluations are based on 42,503 SNP's from technology available in 2007 (Wiggans, 2011). The first genomic evaluations were published in 2009 for Holstein, Jersey, and Brown Swiss males and females and its popularity has taken off since (Wiggans, 2011). Genomic evaluations have allowed the dairyman, sire analyst, and semen companies to gain reliability in bulls and potential bull mothers from 2.7% to 47.6% units for Holsteins and 9.6% to 29.2% for Jersey's on the average (Wiggans, 2011).

Table 2. Reliabilities for both Holstein and Jersey traits going from parent averages to genomic evaluations.

<u>Breed</u>	<u>Trait2</u>	<u>August 2006 REL, %</u>			<u>R^2</u>			
		<u>Parent average</u>	<u>Genomic evaluation</u>	<u>Gain^3</u>	<u>Parent Average</u>	<u>Genomic evaluation</u>	<u>b</u>	<u>Basis^4</u>
Holstein	Milk, kg	38.1	67.5	29.4	19.4	41.1	0.91	-4
	Fat, kg	38.1	73.1	35	17.5	43.3	0.96	-0.9
	Protein, kg	38.1	63.7	25.6	20.3	39.1	0.88	0.6
	Fat, %	38.1	85.7	47.6	26.9	62.1	1.02	0
	Protein, %	38.1	77.9	39.8	29.5	58.9	0.9	0
	PL, mo	31	64.2	33.2	16.4	31.4	1.04	-1.5
	SCS	33.9	60.4	26.5	15.8	31.7	0.88	0
	DPR, %	29.8	46.8	17	21.8	29.4	1.08	-0.2
	Sire CE	27.1	40.9	13.8	20.5	28.2	0.79	1
	Daughter CE	26.2	44.3	18.1	10.1	17.7	0.93	-1
	Sire SB	22.7	29.8	7.2	7.6	10.2	0.87	2.1
	Daughter SB	26.6	29.3	2.7	9.3	10.2	0.89	0.3
Jersey	Milk, kg	39.5	53.9	14.3	38.9	49.2	1.03	89.8
	Fat, kg	39.5	49.9	10.4	30.7	38.1	0.88	5.8
	Protein, kg	39.5	49.1	9.6	34.2	41	0.94	3.4
	Fat, %	39.5	64.9	25.3	40.2	58.1	0.97	0
	Protein, %	39.5	61.4	21.8	36.7	52.6	0.96	0
	PL, mo	24.2	50.8	19.1	10.6	19.2	0.97	-0.4
	SCS	18.7	48.9	13.8	10.4	18.3	0.7	0.1
	DPR, %	24.1	60	29.2	9.9	22.7	1.3	-0.1

Genomic SNP Chip Size

In 2010 a low density and affordable genomic SNP chip called Bovine3K was available for dairymen seeking to genomic test their cows and heifers. In September of 2010 there were nearly 33,800 bovine animals that were 3K chip genotyped. The accuracy of genomic evaluations is based on the type of testing that is performed. Its density of SNP will be sensitive to the amount of SNP's that are being looked at for a particular genomic test. There have been multiple genomic test evaluations that will give the dairyman and genetic companies an accurate reading for an individual cow or bull, but the question is what test is worthy to use under certain circumstances. The Holstein Association and Pfizer have made multiple levels of genomic evaluations available to dairyman. The dairyman then selects a test based on how much information they are inquiring at an affordable rate. Recently the 6K SNP test has been developed for dairymen and it allows the user a sizeable increase in reliability as compared to the original 3K test. The accuracy of the 6K test is higher because they are looking at 6,000 SNP's instead of 3,000 SNP's as in the traditional 3K tests (Holstein USA, 2012). The 6K test also has a better readability and will increase reliability 5 percent over the 3K test (Holstein USA, 2012). Holstein USA believes that the 6K test will provide the greatest benefit or greatest increase in accuracy for its customers, especially if both the sire and dam have been 50K genomic tested, but if the dam isn't 50K tested the 6K test will give you a higher reliability than the traditional computed parent average scores that they received before being genomic tested. If an animal that has both its dam and sire 50K tested and she is genomic tested with a 6K test it will act as

though she was nearly 50K tested, and it is at an affordable price with increased accuracy (Holstein USA, 2011).

The 50K SNP test measures nearly 50,000 SNP's and is most desirable for semen companies that are testing potential bulls to use for potential semen collection and progeny testing. The 50K SNP test is 72% reliable and it will identify if a Holstein or Jersey female are carriers for three haplotypes that impact fertility and reproductive disorders (Holstein USA, 2011). Often in heifers and cows that come out high on their 6K test dairymen will retest them in order to increase their reliability in hopes of increasing their index numbers as well but this might not be the case for all animals retested. Some cows may see an increase in their index and some may see their index decrease, thus losing popularity and marketability.

The most advanced genomic test is the 800K (HD) SNP test. There aren't many cows and bulls that are 800K SNP tested because of its inflated and undesirable price but it is available. A company named Illumina released the 800K (HD) SNP in July of 2010 and it analyzes 777,962 SNP's in the bovine genome. The 800 (HD) SNP high density chip is not economical because it identifies possible crossbreeding or inbred heritage that is not acceptable to breed industries. Those that believe that their cow or bull is worthy of a 800K (HD) SNP must communicate with their breed association and speak with the quality assurance department to see if a 800K (HD) SNP test is what they desire (Holstein USA, 2011).

Materials and Methods

I. Animal Selection.

In order to obtain my first objective, I had to generate a group of dairy cattle to be genomic tested from the California Polytechnic herd. The Cal Poly herd is one of the most prestige college herds in the nation and has developed into an exceptional herd with the help of students, faculty, staff, and alumni. Cal Poly milks both Holstein and Jersey's and their Holstein herd is currently ranked second in the nation on Holstein Association USA's Progressive Breeders Registry for 54 qualifying years. Cal Poly's herd is the last remaining herd in San Luis Obispo County, which was at one time the leading dairy county in California from the start of World War I to 1940. Cal Poly currently is milking 109 Holstein cows with a mature equivalent rolling herd average at two times per day milking of 29,478 lbs. of milk, 1,043 lbs. of fat, and 883 lbs. of protein with a 106.1 Breed Age Average score. The Jersey's currently rank very high as well with 116 cows milking in the herd with 19,930 for milk, 983 for fat, and 704 for protein. Cal Poly has held true to their vision statement which is "to provide 'hands on' learning at the best university dairy in the United States", and with a learn by doing philosophy. They have developed an extensive and prestigious embryo transfer and progeny marketing program with the help of Cal Poly alumni dairyman. The Cal Poly dairy herd has sold numerous high caliber animals and embryos locally, nationally, and internationally, including potential future sales to the Dominican Republic and Brazil. Cal Poly's educational backbone is proven by their mission statement and that is,

"To enhance educational opportunities for students. To maintain fiscal accountability while providing educational opportunities, maintaining high production and high quality

registered animals. To support departmental and university recruitment and research. To provide leadership in demonstrating new technology in the dairy industry.”

Cal Poly dairy provides optional part time jobs available to Cal Poly students year round that will enhance student’s work ethic and education. They provide a four tier management system at Cal Poly Dairy with a Department head at the top, followed by a herd manager, faculty supervisor, and student managers that manage specified duties at the dairy such as herd manager, milk quality manager, feeding manager, calf manager, and cow comfort manager. Other student job opportunities include daily milker's, feeders, and calf feeders.

In order to fulfill my objective I selected 50 high performing animals within Cal Poly’s herd. In addition 89 cows were selected at random by the Dairy Science department head Dr. Bruce Golden, who received a grant to compile 89 head of genomic evaluations for the company GeneSeek. Dr. Golden extracted the DNA from his selected animals on the farm with the assistance of a Cal Poly student. Multiple types of DNA samples were used including nasal swabs, blood tests, and follicular hair extractions. Once the genomic evaluation materials were extruded they were sent to GeneSeek to be processed. Then with the help of Dr. Stan Henderson, professor of Dairy Science at Cal Poly, received a grant from Pfizer Pharmaceutical Company to provide 50 6K samples. Pfizer is one of the leading pharmaceutical companies in the agriculture industry and has recently been granted the rights by USDA to do genomic evaluations. Animals that were selected were thought to be most marketable to the Cal Poly herd. Current donor cows, potential donors, and offspring from the extensive embryo enterprise program of Cal Poly’s herd were selected. The embryo enterprise of Cal Poly dairy is a growing enterprise driven by faculty advisors and students, including Dr. Henderson, Rich Solaci, as well as RuAnn Dairy embryo transfer staff. RuAnn Dairy of Riverdale, California is owned by the

Maddox Family and is currently managed by Mr. Steve Maddox. Thanks to RuAnn Dairy's on staff embryo technician (ET), Dr. Daniela Demetrio, Cal Poly has generated a prestige embryo enterprise. The donor cows, potential donor cows, and offspring of donor cows are the most superior animals at Cal Poly dairy. We decided to do genomic evaluations of 50 genetically superior cows from Cal Poly Dairy. The genomic evaluations were collected in the form of hair samples for animals greater than three months of age. Test strips and blood samples were taken from calves that were less than three months of age materials were provided by Pfizer genomic sales representative, Flavio Silvestre.

II. Data Collection

In order to identify animals to run genomic tests on, the Cal Poly dairy collected samples from the top five animals within the Cal Poly Corporation herd that were deemed genetically superior based on the print outs provided by the Holstein Association USA. The Holstein Association sends a Genetic Herd Report to each individual dairy based on how often they classify their animals through the Holstein Association. Classification occurs at Cal Poly dairy twice a year and it is performed by a Holstein Association classifier who reports to farms and analyzes their cows based on previously identified physical attributes. The cow is analyzed, numbers are calibrated and entered into a computer data base and a final score from 50 to 100 is produced. Animals that score 90 to 100 are considered to be in the breeds top 10 percentile. The final score is then reported to Holstein USA. With the inclusion of official DHIA records and milk test a value known as Cows Total Performance Index (CTPI) is computed. The CTPI is a combination of genetic evaluations, physical evaluation and overall production performance. With the help of the CTPI list provided by the Holstein Association, 5 individuals were chosen

worthy of genomic testing based on a combination of Milk index, Productive Life, Sire stacks, and CTPI.

After receiving adequate feedback on the initial first five genomic evaluations Dr. Golden, Dairy Department Head at Cal Poly, gathered an additional 89 Jersey and Holstein individuals that were genomic tested. The genomic evaluation collection process that Dr. Golden elected to do was through the GenSeek Company, who is one of the leading genomic testing companies in the dairy cattle industry. The genomic tests that were provided by the GeneSeek Company were of the standard nasal swab sampling. The cows to be genomic tested were selected with the assistance of Rich Solaci, herd manager of Cal Poly dairy.

After multiple petitions and phone calls Cal Poly received materials to genomic test all animals within their embryo enterprise project. The funding was awarded by Pfizer pharmaceutical company, one of the top 5 leading pharmaceutical companies that have recently tapped into the genomic evaluation field. They are able to run their own genomic tests through their own labs but the only downfall of genomic tests through Pfizer is that they cannot release their genomic information until two months after you submit the tests. The Holstein Association and Jersey Association have allowed Pfizer to limit the publishing of Pfizer's genomic results. Pfizer genomic tests are 5 percent cheaper than Holstein and Jersey Association tests, so they are therefore considered to be more popular because of their rebates. Flavio Silvestre is the Pfizer representative that discussed terms and conditions of genomic testing. Animals to be tested had to have individual information gathered to be electronically submitted on a Pfizer spreadsheet template. The information that was needed included; cow number, identification number (RFID or registration number), date of birth, sire registration number, dam registration number, and sample number. All of the needed information for properly filling out the spreadsheet were

generated and received through a newly created report on the Cal Poly DHIA herd report. The information needed to successfully fill out the electronic spreadsheet were collected and submitted through Pfizer's Microsoft Excel spreadsheet using a multiple step process including;

1. Entering ID ear tag numbers of animals on separate excel spreadsheet and copy-paste them to the electronic Pfizer spreadsheet.
2. Selecting vlookup option and entering data collected from DHIA custom report from Cal Poly DHIA records.
3. Entering the sample numbers of individual genomic testing kits either hair or blood samples.

The collection process was next. Collection of the 35 live previously selected animals was performed. All animals that were 3 months of age and above were sampled through follicular hair samples that were pulled from their tails. It is important to collect a nice clean hair sample that is manure free and has at least 20 hair follicles. Those cows that were younger than three months were genomic tested through blood samples. These blood sample kits were provided by Pfizer and administered. The collection process for hair samples and blood tests are as follows;

- Hair samples
 - Peel back protective clear cover and discard non adhesive sheet
 - Grab tail of identified individual and isolate a group of clean and dry hairs at the end or near the end of cow's tail and tear off.
 - Twist extracted hair follicles and place into center of test kit with hair follicles facing up.

- Place adhesive cover strip over hair sample in a downward motion- making sure no air is in test packet.
- Tightly seal sample and cut off excessive hair
- Write ID of cow on test packet and place in zip-lock bag.



Figure 3. Clarified hair samples kit.

- Blood samples
 - Identify cow to extract blood from
 - Grab tail and elevate to find coddle vein and insert 14 gauge needle
 - Make sure needle is in coddle vein and receive blood to place on test strip- at least 80 percent of test strip needs to be covered
 - Allow test strip to dry before sealing

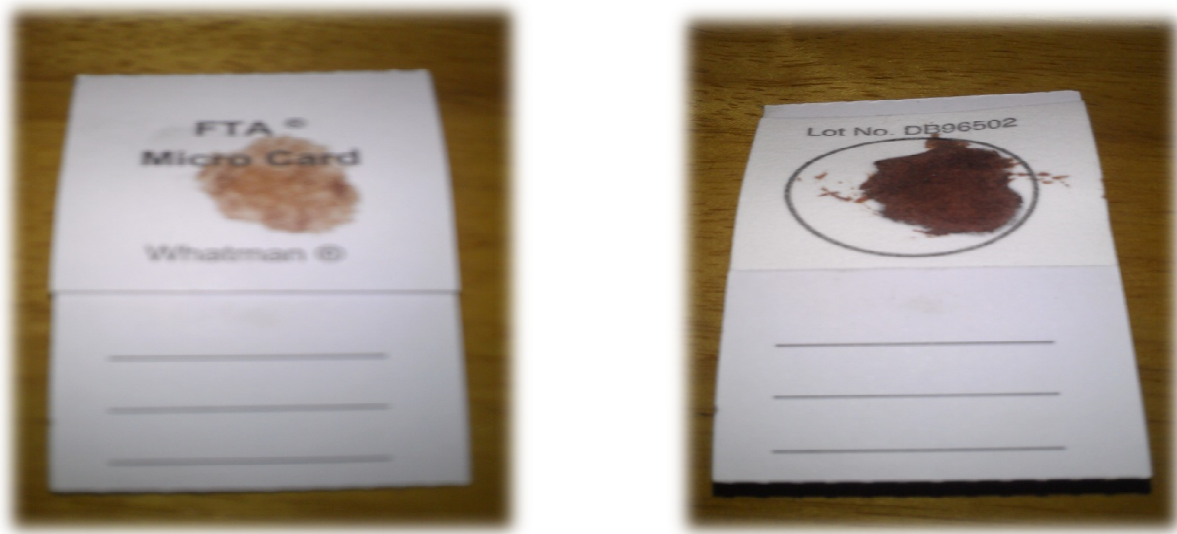


Figure 4. FTA micro card blood sample kit

The remaining calves to be tested were done in December 2011 because they were from calves at Fernandes Dairy in Tulare, California. These calves were embryo transfer calves that were inseminated into Fernandes Dairy recipients. These calves were blood sampled and sample numbers were collected and sent into Pfizer through their electronic submission spreadsheet. Additional hair samples from donor cows at RuAnn Dairy were collected as well and sent in with the blood samples from the December blood tests to Pfizer.

III. SNP Size and Marker Types

For this particular project the most realistic genomic test to use was the 6K through Pfizer mainly because it was more desirable because the Cal Poly herd hasn't had any known genomic superior animals within the herd and if identified those animals that were exceptionally high would be retested using the 50K SNP. On the other hand the genomic test that was done through Gene Sink was 50K SNP's. There wasn't much difference in the index's of the cows tested and the only effected area that changed the most was the reliability of the 50K SNP's because they are running a 72% reliability on average.

IV. Data Processing

The genomic evaluations from both GeneSeek and Pfizer were available in mid January for 110 out of 139 combined Holstein and Jersey females. The genomic evaluations that are missing were ran in the February genomic evaluation run because they were sent in mid December and they were released two months after they were turned in. The genomic evaluations were then analyzed based on specific breed leading popular traits for overall genetic value of the individual animals, and these categories included; Breed Performance Index, Percent Reliability, Net Merit, Final Score for Type, and Productive Life. The genomic evaluations were then placed in sub-categories based on the sire of the animal, and donor dam's progeny.

Breed Performance Index (GTPI for Holstein or GJPI for Jersey) is a computed value based on differences in animals on the overall total performance value by combining multiple genetic factors including; milk yield, conformation scores, health traits, longevity, and management traits compared to other animals in their specified breed. The calculation for GTPI and JPI varies for each individual cow and is calibrated from both maternal and paternal

bloodlines (Holstein USA, 2012). Breeds GTPI and GJPI are similar to the computed Total Performance Index for cows and Potential Total Performance Index for heifers but GTPI and GJPI are more accurate because it is computed based on individual genetic values. An animal's GTPI or GJPI is one of the most important values because it is what semen companies are looking for when picking out potential bull mothers, so the higher the GTPI or GJPI value the more popularity of the cow based on the leading genetic trends for the dairy cattle industry.

The next most important category is currently Net Merit dollars (NM\$ for Holsteins) or Cheese Merit dollars (CM\$ for Jerseys). The NM\$ is an index that expresses the overall expected life profit of an individual female compared to the breed average (Holstein USA, 2012). NM\$ is a combination of economically relevant traits that are related to milk yield, health, longevity, and calving ease (Holstein USA, 2012). Other specific traits included in the NM\$ index include fat and protein yield, productive life, daughter pregnancy rate, udder composite, somatic cell score, feet and leg composite, calving ability (including stillbirth information), and body size (Holstein USA, 2012). All of these are contributing factors that are combined to generate an animal's NM\$ value. Net Merit Dollar values in the Holstein breed can be as low as zero to as high as over 1,200. Cheese Merit Dollars is a value mostly related to breeds like Jersey and Brown Swiss because they are paid a premium for high fat and protein values. Cheese Merit Dollars is an index that focuses on the same traits as NM\$ but has a greater emphasis on protein and fat percentage index scores, thus making CM\$ values most useful for producers selling their milk in the cheese market.

The next index that was looked at was Productive Life. A Productive Life index score is on an individual basis per animal and can be different between full siblings. Productive Life index's are derived from specified health traits in an individual cows overall determined

computed genomic evaluation based on specified chromosomes within the animals genome (Pfizer, 2012). The PL index value is given based on the predicted cow's genetic ability to stay in the particular herd that she is being tested in and also accounts for specified characteristics that make an individual cow more sustainable for the dairy operation. The overall number value given for PL index is an expression of the predicted months in milk that a cow will have relative to the breed average, meaning that if a cow has a PL value of 6.0 that cow is predicted to have 6 more months in lactation than the breed average. Almost all bulls that are sampled will drop two points on PL once they have had a proof released. Productive Life index values are a great tool to use when dairymen are trying to optimize their cow's total performance and lifetime production to make sure that they exceed the breed average and live to pay for them.

V. Statistical Analysis

Once the genomic evaluations were received from the lab an electronic version of the results were analyze and submitted to a Microsoft excel spreadsheet in descending order and grouped by breeds starting with the oldest Jersey cows followed by the oldest Holstein cows. The basic analysis was to calculate a mean of the highlighted industry leading values (GTPI or GJPI, PL, NM\$ or CM\$, Reliability, and TYPE) and can be viewed in the appendix tables 1.

$$\text{Mean} = \frac{\text{sum of all data values in data set}}{\text{Number of data values}}$$

The individual cows genomic results were then compared to their TPI or PTPI indexes for all of the previously stated index values and an average of the two official index's were computed.

After finding the mean the animals were grouped by breed and SNP marker size. An analysis of covariance was then computed in order to generate a correlation between the traditional TPI/JPI or Y and the GTPI/GJPI or X for this example.

$$\text{Covariance (X, Y)} = (X' - E(X)) (Y' - E(Y))$$

Or

$$\text{Covariance (Genomic GTPI/GJPI)} = (\text{Genomic GTPI/GJPI} - E(\text{Gen. GTPI/GJPI}) \times (\text{Traditional TPI/JPI} - E(\text{Trad. TPI/JPI}))$$

After finding the covariance compute the variance using the following equation:

$$\text{Variance} = \text{var} (Y' - E(Y))^2$$

Or

$$\text{Variance} = \text{var} (\text{traditional TPI} - E(\text{traditional TPI}))^2$$

After finding the variance then calculate the correlation coefficient using the following equation:

The correlation coefficient should be equal to 1 if the theory is true.

$$\text{Correlation coefficient} = \frac{\text{COV (X, Y)}}{\sqrt{\text{VAR(X)} * \text{VAR (Y)}}}$$

The equation to find the slope of the regression is-

$$\text{Slope} = \text{ratio} \frac{\text{COVARIANCE GTPI}}{\text{VARIANCE Traditional TPI/JPI}}$$

If the Method R Variance component theory is proven the ratio should be equal to 1 to 1.

Results and Discussion

Results from genomic evaluations were collected in mid-January and February to be analyzed. The overall outcome of the genomic evaluations were very beneficial for the Cal Poly herd for they now have over 75% of their total milking herd genomic tested and genetic advancement can now be improved based on industry leading evaluations that are needed for improvement on an individual animal basis. Herd evaluations also allows for the quickest advancement of genetic improvement within the Cal Poly herd and a new criteria for bull selections can be properly made based on needed herd improvements.

Individual results for both Holstein and Jersey genomic evaluations can be found in Appendix I. Important index's including GTPI or JPI, \$NM, \$CM, PL, Reliability, and GPTA, were analyzed and cows and heifers were found in each respected area. The importance of high testing genomic cows and heifers is because of their increase in overall net worth. Cows and heifers that are leaders in each of the highlighted compared categories will increase in value to the Cal Poly herd. Cows and heifers that are genomic leaders also allow Cal Poly to focus on them for future possible donor cows and heifers. The biggest impact on the present donor cows in the Cal Poly ET enterprise will allow Cal Poly dairy staff to reanalyze their donor cows overall worth and possibly decrease the expenses on unworthy flush cows. Genomic evaluations will allow Cal Poly to focus on individual cows and heifers for genetic advancement as well. Based on individual breakdowns of cows and heifers genomic evaluations Cal Poly will be more able to mate cows and heifers for genetic advancement rather than going backwards in genetic progress. The following cows and heifers were selected as Cal Poly's most superior individuals in the herd based on GTPI and JGTPI.

Table 3. Top 5 GTPI and JGTPI computed results from 50K and 6K results

GTPI/GJPI	ID
2013	2356- POLY GOLDWYN CHERI-ET
2008	2498- POLY TIME SHAE
1914	2438- POLY ATLANTIC BARBIE
1867	2478- POLY TIME REGINA
1860	2476- POLY GOLDWYN JELIE
169	475- POLY VALENTINO ADREA
168	505- POLY TBONE AUDS
152	428- POLY VICTORY HONEY
150	356- POLY JUNIPER HATTIE
140	376- POLY IATOLA JEAN

Genomic breakdowns for tests were calibrated and averages for both Holstein and Jersey breeds were calculated. The high overall females were also listed to compare the overall averages to the most desirable individuals in the Cal Poly herd. Females that were deemed genetically superior shall now be the main focus for Cal Poly dairy in order to generate more profit and gain in overall genetics for the Cal Poly herd.

Table 4. Averages of REL%, CM\$, NM\$, PL, and GJPI/GTPI values for overall tested female compared to top GTPI/GJPI individuals

Avg. Females Indexes	REL	CM\$	NM\$	PL	GJPI/GTPI
59 Jersey females	70	200	183	1.9	69
POLY VALENTINO ADREA	57	488	439	3.8	169
51 Holstein females	74	---	134	.8	1575
POLY GOLDWYN CHERI-ET	78	---	437	4.0	2013

Table 5. Increase total SNP analyzed from GTPI/JPI testing combined with traditional TPI/JPI

Gain in SNP from Genomic Evaluations	Traditional SNP	Genomic SNP	
Milk	8	25	33
Fat	8	25	33
Protein	8	25	33
PTAT	6	20	26
Productive Life	24	56	80
Daughter Pregnancy Rate	46	102	148
			353 Total SNP analyzed

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The increase in reliability of animals from genomic evaluations is due to the correlations of SNP markers that the genomic tests detect. Genomic tests with higher reliabilities identify and mark more SNP's such as the 50K tests. Reliability will increase when more family members are genomic tested because more genetic markers will become available. The accuracy of the 6K test is higher because they are looking at 6,000 SNP's instead of 3,000 SNP's as in the traditional 3K tests. The 6K test also has a better reliability, and will increase reliability 5 percent over the 3K test. Holstein USA believes that the 6K test will provide the greatest benefit or greatest increase in accuracy for its customers, especially if both the sire and dam have been 50K genomic tested, but if the dam isn't 50K tested the 6K test will give you a higher reliability than the traditional computed parent average scores that they received before being genomic tested. If an animal that has both its dam and sire 50K tested and she is genomic tested with a 6K test it will act as though she was nearly 50K tested, and it is at an affordable price with increased accuracy (Holstein USA).

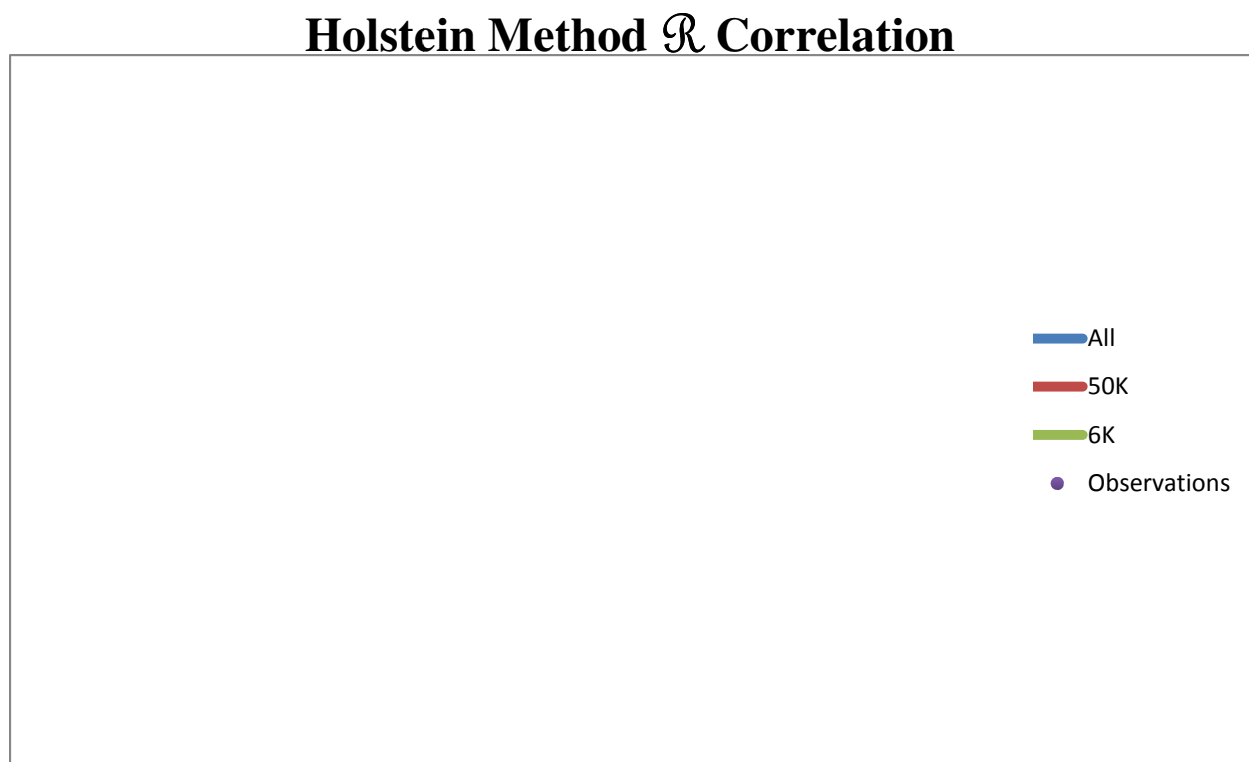
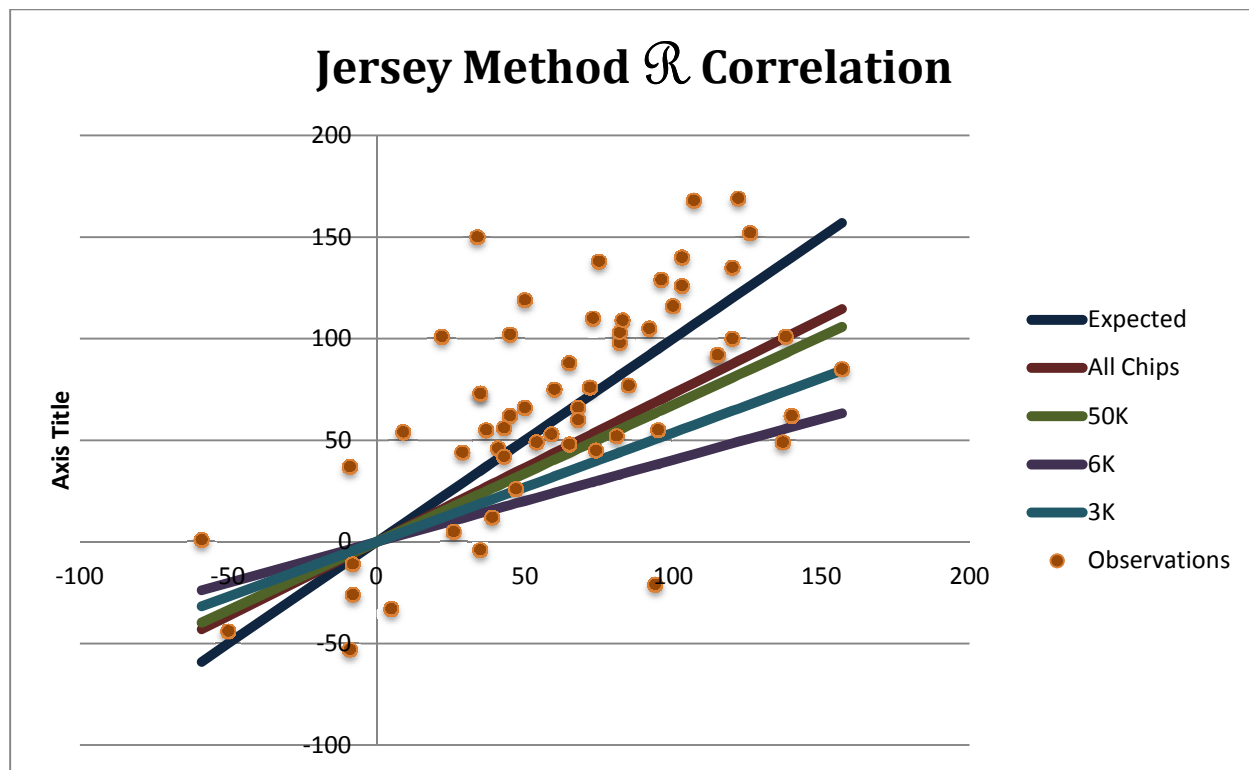


Figure 5. The change in prediction as reliability increases going from traditional PTPI to GTPI/GJPI agrees or disagrees with the overall theory.

The overall genomic evaluations on Cal Poly's herd generate multiple advantages within their herd. Cal Poly is always looking for new opportunities to advance the net worth on their cows and heifers to create popularity, recruitment opportunities, and student involvement. Leading Select Sires bull progeny analyzer Steve VerBeek presented a superior genomic presentation at this year's California State Holstein Convention in Petaluma, California, and he listed various advantages of genomic testing within every herd and they include:

- Opportunity and competition
- Better predictor than traditional Parent Average
- Remove environmental bias
- Add significant value to animals
- work with new families in A.I. industry
- determine genetic potential earlier
- improves mating decisions
- aids in herd management progress
- more affordable every year
- better options (6K and 50K)
- identified more recessive genes
- accuracy improves
- competitive on global market

All of the stated advantages of genomic testing in true for the Cal Poly herd and they will help open new doors for opportunity and possible increased sales of Cal Poly cows and heifers.

Performing a study of 139 genomic evaluations gave Cal Poly a reliable outside and totally unbiased review of the overall herd performance. Cal Poly can now take the information provided and reanalyze their reproduction program and continue to breed and generate superior genomic animals like they currently have. The study may be different than other genomic studies that have been done because it is based on individual SNP's on cows and heifers. The correlation of SNP's for individual chromosomes differ amongst every individual cow and heifer, but having the ability of predicting how chromosomes will match up is why genomic evaluations will be a productive tool for advancing genetics. Its ability to remove environmental bias is why genomic evaluations will continue to be a revolutionized new technology that advances the dairy cattle industry. In the end there was a genetically superior sire within the Cal Poly herd among both Holstein and Jersey cows that was most superior and desirable. The possibilities of superior cows and heifers in the Cal Poly herd will catalyze the genetic advancement of its herd if the herd may choose to breed for genetic improved cows and heifers. The overall reliability and creditability of genomic evaluations has held up to its expectations.

Method \mathcal{R} Variance Components

To covariance of the genomic GTPI/GJTPI to the Traditional TPI was equal to 20,007.95 for the Holsteins, and the variance of the Traditional TPI was 39,158.21. Then the slope or covariance equaled .51095, and therefore the variance component for the Holsteins is overstated because it is less than the predicted 1 to 1 ratio (Reverter, 1994). The Jersey's covariance was calculated in the same fashion as the Holsteins and equaled 1557.58. The variance of the traditional was 2,133.1, and therefore the calculated slope was .7301. There was an improvement from the Holsteins variance component, but it is still understated and both values do not agree with the Method \mathcal{R} theory.

POLY GOLDWYN CHERI-ET

USA000064258173 06/09/2008 FEMALE

Cal Poly Corporation, Dairy Science Dept, San Luis Obispo CA 93407-0257

Haplotypes (C=Carrier, T=Tested-free):

GFI: 6.8

HEALTH TRAITS				
	Genomic PTA	Official PA/PTA	Genomic REL %	Official REL %
Net Merit(\$)	446	196	69	45
Daughter Pregnancy Rate (%)	0.5	0.0	62	35
Productive Life (months)	3.7	2.2	66	41
Somatic Cell Score	2.65	2.82	69	41
YIELD TRAITS				
	Genomic PTA	Official PA/PTA	Genomic REL %	Official REL %
Milk	-275	-423	74	51
Fat (lbs)	50	9	74	51
Fat (%)	0.23	0.10	74	
Pro (lbs)	10	-6	74	51
Pro (%)	0.07	0.03	74	
CALVING TRAITS				
	Genomic PTA	Official PA/PTA	Genomic REL %	Official REL %
Daughter Calving Ease	8	8	58	31
Daughter Stillbirth	7.1	6.9	53	31
TYPE TRAITS				
	Genomic PTA	Official PA/PTA	Genomic REL %	Official REL %
Final Score (PTAT)	3.04	2.67	73	54
Feet/Legs Composite	2.29	2.37	NA	NA
Udder Composite	2.38	2.46	NA	NA
Stature	2.83	2.93		
Strength	1.57	1.51		
Body Depth	2.21	2.01		
Dairy Form	2.89	2.20		
Rump Angle	1.42	0.70		
Thurl Width	1.29	1.14		
Rear Legs Side View	0.38	-0.22		
Rear Legs Rear View	2.40	2.32		
Foot Angle	2.36	2.41		
Feet & Leg Score	2.61	2.70		
Fore Attachment	3.19	3.08		
Rear Udder Height	3.22	2.69		
Udder Cleft	2.53	2.76		
Udder Depth	2.13	2.71	77	61
Front Teat Placement	2.02	1.58		
Rear Teat Placement	2.07	1.77		
Teat Length	-0.20	-0.16		
Total Performance Index (TPI)	2005	1716	NA	NA

Genomic PTA calculated using 3K test, November 2011

Haplotypes affecting fertility are reported for 50K and HD reports only.

For more on interpreting this report, visit www.holsteinusa.com**HOLSTEIN ASSOCIATION USA, INC.**1 Holstein Place, PO Box 808, Brattleboro, VT 05302-0808 www.holsteinusa.com • 800.952.5200**Figure 6.** Holstein Association USA Genomic Evaluation

Conclusion

The genomic evaluation project of the Cal Poly dairy generated a lot of support by faculty, industry leaders, and leading genomic companies. Testing nearly 55% of the Cal Poly dairy allowed the Cal Poly dairy staff to reanalyze their genetic progress and set up new benchmarks for their breeding program. Cal Poly seen increased popularity of cows in their herd including a second calf Holstein Goldwyn daughter- POLY GOLDWYN CHERI-ET at 2013 GTPI- and a young jersey heifer- POLY VALENTINO ADREA at 169 JGPI. Both of these cows are among the top 100 cows and heifers for their respected breeds in California, thus generating more possible income for the Cal Poly dairy.

Once the genomic evaluations were received for all of the genomic tests with the exception of the Pfizer genomics that weren't computed because of unclear problems in the system, a set of averages for each breed were computed based on index traits such as REL%, CM\$, NM\$, PL, and GTPI/GJPI. the 59 Jersey's that were tested with a combination of 3K, 6K and 50K SNP markers received an average REL% of 70%, a 200 CM\$ value, 183 NM\$ value, a 1.9 PL value, and a 69 for GJPI. The 51 Holsteins that were tested received an average REL% of 74%, no cheese merit was derived in their indexes, a 134 NM\$ value, .8 PL, and a 1575 GTPI value.

With a value of .51095 variance component for the Holsteins and .7301 for the Jersey's concluded that as reliability increases advancing from non genomic or PA's to genomic evaluations does not agree with the Method R correlation. There has been additional research to provide evidence that there may be a flaw in the generated genomic or PA systems (Wiggans, 2011). It is believed that the traditional PTA's for yield traits for genomic tested cows are higher

than their generated genomic values (Wiggans, 2011). Further research to uncover potential problems with the genomic and traditional TPI systems should be addressed to generate a direct correlation of the values.

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