Calling all breeding enthusiasts!

HERD 15
STRONGER TOGETHER
COLLABORATION IN HERD IMPROVEMENT

PROGRAM & PROCEEDINGS

A wonderful line up of visiting experts across all disciplines of the Herd Improvement industry is in store.

MARCH 11 & 12
BENDIGO ALL SEASONS RESORT
MCIVOR HIGHWAY, BENDIGO

Proudly brought to you by:

Holstein Australia

Dairy Australia
Your Levy at Work

National Herd Improvement Association of Australia Inc. (NHIA)

Australian Dairy Herd Improvement Scheme

ALL INQUIRIES:
EPP Events Pty Ltd
PO Box 341,
Mundijong WA 6123
Tel: 08 9525 9222
Fax 08 9525 5008
donna@eppevents.com.au

HERD 15
STRONGER TOGETHER
COLLABORATION IN HERD IMPROVEMENT

ALL SEASONS RESORT
BENDIGO, VICTORIA
MARCH 11 & 12, 2015

ALL INQUIRIES IN RELATION TO THE MANAGEMENT OF THE HERD '15 SHOULD BE DIRECTED TO:

EPP Events
PO Box 341, Mundijong WA 6123
Tel: 08 9525 9222; Fax 08 9525 5008
donna@eppevents.com.au

On-site inquiries:
Donna Sykes 0412 778 849
Carol Millar 0430 211 216

TABLE OF CONTENTS

WELCOME TO HERD15

Herd '15 is a proud, joint initiative of the NHIA, ADHIS and Holstein Australia that features a tailored and innovative program that is aimed at Herd Improvement industry personnel (from field and technical staff through to management) and dairy farmers with a specific interest in using genetics to achieve the next paradigm of farm business productivity gains.

Significant investment in this event from the four hosting entities has kept registration fees to a minimum, on the back of a policy of encouraging as many people as possible to attend – enabling you to invest in your own and your staff's education and professional development.

We trust that you enjoy the program of events.

CONFERENCE CONTACTS:

Event Managers
EPP Events Pty Ltd
Tel: +61 8 9525 9222
Fax: +61 8 9525 5008
E: donna@eppevents.com.au
Site Contact: Donna Sykes 0412 778 849

CONFERENCE CONVENERS:

Dairy Australia
Level 5, IBM Centre, 60 City Road
Southbank, Victoria 3006
Contact: Chris Murphy
Email: cmurphy@dairyaustralia.com.au
Website: www.dairyaustralia.com.au
Tel: 03 9694 3777 | Fax: 03 9694 3733

National Herd Improvement Association
Unit 1/112 Synnot Street
Werribee VIC 3030
Contact: Carol Millar, General Manager
Email: carol@nhia.org.au
Website: www.nhia.org.au
Tel: 03 9742 7244 | Fax: 03 9742 7696
M: 0430 211 216

Australian Dairy Herd Improvement Scheme
Level 2, Swann House
22 William St, Melbourne VIC 3000
Contact: Daniel Abernethy, General Manager
Email: dabernethy@adhis.com.au
Website: www.adhis.com.au
Tel: 03 8621 4240 | Fax: 03 8621 4280
M: 0417 514 898

Holstein Australia
24-36 Camberwell Road
Hawthorn East, VIC 3122
Contact: Graeme Gillan, Chief Executive Officer
Email: ggillan@holstein.com.au
Website: www.holstein.com.au
Tel: 03 9835 7600 | Fax: 03 9835 7699

HERD15 SPONSORS

The convenors of HERD '15 would like to acknowledge the following companies for their support

PROGRAM

PROGRAM DAY 1

	SESSION CHAIR: DANIEL ABERNETHY, General Manager, ADHIS
9:30	Arrival and registration
10:30 - 10:40	**Opening.** ADHIS Chair and NSW dairy farmer Adrian Drury provides the opening address to welcome delegates from the Australian dairy community to Bendigo.
10:40 - 11:10	**Irish Collaboration.** The Irish Cattle Breeding Federation's Director of Innovation and Geneticist Andrew Cromie will share tales of a decade-long story about partnership, leadership and commitment to produce a better breeding service for Irish farmers.
11:10 - 11:55	**Impact of genomics.** Paul Van Raden, USDA, has worked at the heart of genomic technology development since its invention. Paul will talk about the impact of collaborationand how genomics is producing results that may surprise us.
11:55 - 12:15	**Ten years ahead.** As Dairy Futures CRC CEO, David Nation has his finger firmly on the pulse of global, cutting-edge, animal and forage breeding research. So what does the Australian dairy landscape look like in 2025?
12:15 - 1:15	Lunch
	SESSION CHAIR:CHRIS MURPHY, Group Manager Farm Productivity & Delivery Dairy Australia
1:15 - 1:45	**Where we need to be.** The cows we breed produce the milk that fills processing plants so what does the dairy industry need to be successful and globally competitive and where does herd improvement fit? Industry leader and Fonterra Director, Bruce Donnison joins the conference to discuss.
1:45 - 2:15	**Where are we heading.** Since joining Dairy Australia, Matthew Shaffer has driven the development of a national herd improvement strategy. He will explain how the dairy industry plans to improve dairy herd productivity by 2020.
2:15 - 2:45	**From woe to go.** AgSource Cooperative Services is one of the largest full-service Dairy Herd Improvement organisations in the United States. It's Chief Operating Officer, Patrick Baier will share the organisation's story of how business leadership and direction can make a difference.
2:45 - 3:15	**Using data to tackle difficult on-farm challenges.** Maria Thielen will describe German milk quality initiatives such as milchQplus to get more out of data on farm.
3:15 - 3:45	Afternoon tea
	SESSION CHAIR: CAROL MILLAR, General Manager, NHIA
3:45 - 4:05	**Does AI synchronization really save money?** Andrew Parkinson, Wellbred Genetics analyses case study data to profile the economic impact of synchronisation.
4:05 - 4:20	**The Genetic Progress Report in action.** Peter Williams (ADHIS) and Paul Quinlan (ABS) team up to demonstrate how Genetic Progress Reports impact breeding decisions.
4:20 - 4:40	**New genetic reports.** Zoetis has been a key driver of genomic testing in the USA. Jason Osterstock will talk about how genomic testing is used by American dairy farmers and new reporting services.
4:40 - 5:00	**Sexed semen is changing the face of breeding programs but new tools are now available to make the most of this technology.** Warrnambool Vet Clinic's Jon Kelly is actively involved in developing evidence-based approaches to selecting animals for sexed semen and will share his experiences.
5:00 - 5:20	**Herd testing – Canadian style.** HICO's Joanne De Moel has had the time of her life studying the herd test system in Canada and has some maple-flavoured stories to tell.
7:00	Dinner, Chaired by Graeme Gillan, CEO Holstein Australia. Dinner speaker, Geoff Akers, Dairy Australia

PROGRAM DAY 2

8:00	Arrival and registration
	SESSION CHAIR: MATTHEW SHAFFER, Program Manager – Genetics & Data Management - Farm Profit and Innovation, Dairy Australia
8:30 - 8:35	Chair's welcome and opening address – David Johnston, Federal President, Holstein Australia
8:35 - 8:50	**Continuous improvement** as a philosophy and a practice is fundamental to all that we do. Paul Van Raden returns to the stage to explain why genetic progress requires continually improving methods.
8:50 - 9:40	**New Australian breeding indices** set an exciting path for genetic improvement in Australia. Geoff Akers will open by introducing why Dairy Australia supported a review of the National Breeding Objective Review. Michelle Axford will describe the review process and how farmer preferences and industry feedback has made a difference. Jennie Pryce will explain what we can expect from using the new indices and how to maximize progress.
9:40 - 10:00	**New directions for Type ABVs.** In partnership with industry and researchers, ADHIS is changing the expression of Type ABVs and has plans for further developments as presented by Daniel Abernethy.
10:00 - 10:20	**Q&A panel about Australia's new indices.** Featuring this session's speakers alongside National Breeding Objective Review Task Force Members Patrick Glass and Jo Dickson. Moderated by Ian Halliday, Dairy Australia
10:20 - 10:40	Morning tea
	SESSION CHAIR: MICHELLE AXFORD, Extension and Education Manager, ADHIS
10:40 - 11:15	**What's Next:** Scientists at the Dairy Futures CRC continue to push the boundaries in the world of genomics. As head of the animal improvement research program, Ben Hayes will take us through highlights such as the 1000 bull genome project.
11:15 - 11:45	**Dairy Futures CRC students:** Ben Hayes will join us back on stage to introduce us to some next-gen scientists who will explain the potential impact of their research.
11:45 - 12:00	**Perfect data.** Paul Douglas works with some of Australia's best herd data recorders through Ginfo and the Healthy Cow Project. He will provide some insights on how we can make the most of perfect data.
12:00 - 1:00	Lunch
	SESSION CHAIR: GRAEME GILLAN, General Manager, Holstein Australia
1:00 - 1:20	**Turning data into collaborative decision making.** Patrick Baier returns to centre stage to explain the value of herd recording information and its delivery to farmers as well as their advisors and allied industry partners.
1:20 - 1:40	**Industry panel – industry collaboration and managing change in the business environment.** Panels have been long considered one of the highlights of the HERD conferences. In this edition, the heads of three of Australia's largest semen suppliers examine how they view the value of collaboration in a changing environment. Jayne Senior, Genetics Australia James Smallwood, ABS Australia Mike Huth, CRV Australia Moderated by NHIA Chairman and Holstein Australia General Manager, Graeme Gillan
1:40 - 2:00	**The Australian dairy data** story has evolved since Herd '11 but Tony Francis will provide his perspective on where we need to get to.
2:00 - 2:30	**When 1+1 is more than 2**. The Irish have demonstrated rewards from close connections between herd test and genetics. Andrew Cromie will describe the keys to the Irish success.
2:30 - 2:50	CLARIFIDE Launch by Zoetis
2:50	Closing remarks by Graeme Gillan followed by afternoon tea

Impact of genomic collaboration and the need to continually improve methods

Paul M. VanRaden
USDA Animal Genomics and Improvement Laboratory
Beltsville, MD USA

Continuous improvement

Dairy cattle improve each generation as breeders apply new tools and additional data in genetic selection. Traits included in selection indexes have increased steadily and will further expand because genotypes multiply the value of data collection. An animal can be genotyped once to predict an unlimited number of traits. Producers desire flexible and inexpensive data collection methods, but uniformity is also a major goal. Dairy Herd Improvement organizations in the past had rigid rules to enforce centering dates and monthly testing plans, but then switched to more flexible statistical methods such as test interval method, best prediction, or test day models to include a wider variety of data. Similarly, genomic predictions began in 2008 with a standard chip containing 50,000 markers, but new data sources and computational methods have rapidly emerged, increasing flexibility and reducing costs to obtain genotypes.

Collaboration

Foreign selection of breeding stock has and will continue to greatly impact the domestic populations of most countries. Methods to rank foreign bulls progressed from simple conversion formulas to more advanced multitrait across country evaluation (MACE) and then to genotype exchanges and genomic MACE. All major AI companies in North America collaborated to provide a reference population large enough to estimate even small genetic effects. This collaboration began in 1992 with a common DNA repository for US and Canadian bulls. Some breeders in Europe asked if having so many companies work together was fair, but very quickly, several countries in Europe also merged their reference populations (Lund et al., 2011).

The North American collaboration was extended to include Holstein genotypes from Italy and the United Kingdom, Jersey genotypes from Denmark, and global Brown Swiss genotypes exchanged by Interbull (Intergenomics). Most national genomic evaluations treat domestic and foreign data as the same trait, but can be more accurate by treating MACE as a correlated trait if genetic correlations are < 1 (VanRaden et al., 2012). With the exception of New Zealand where genetic correlations to other countries are low, nearly all researchers found that accuracy of predictions improved when foreign reference bull genotypes were added.

Past surprises

Genotype quality was an immediate and pleasant surprise of genomics, with most markers having error rates < 0.1%. In 2009 when a more complete map of the bovine genome became available, new computer methods called imputation could accurately predict the missing markers from other chips containing subsets of markers. This led to a proliferation of new chips of both lower and higher density that gave nearly the same accuracy for less than half price, or genotyped 15 times more markers for only twice the price. After most ancestor bulls had been genotyped, the ease of correcting pedigrees and ability to discover unknown parents, grandparents, or even great grandparents were also pleasant surprises.

Discovery of many new lethal recessive genes was a pleasant surprise to researchers but perhaps not so pleasant to the owners of many popular bulls and cows now known to carry defects that cause embryo loss. Such defects were easy to detect by searching for haplotypes that never become homozygous in live animals or by using bioinformatics to search directly for damaged genes in DNA sequences. In the case of Holstein haplotype 1 (HH1), the defect in gene APAF1 was easy to detect as a cause of embryo loss in cattle, and deficiency of this same gene was already known to cause embryo loss in mice (Adams et al, 2012). Thus, bioinformatics has become a powerful tool to discover and confirm genetic effects across species. Total worldwide economic loss from the HH1 defect has been nearly a half billion US dollars since HH1 became prevalent around 1970.

Genomic selection is now widely practiced with fairly low cost in part because the basic concepts are free of intellectual property. This makes friendly collaboration possible even among competing organizations and countries. Much of this collaboration involves simply collecting and exchanging large data files or improving the data analysis methods. The U.S.

Supreme Court (2013) decided that DNA tests could not be patented, but courts in some other countries still enforce gene test patents. Because of potential legal disputes, most genomic selection programs do not yet use direct tests for the QTLs with the largest effects such as DGAT1 and instead use tens of thousands of indirect markers. Most chips now contain QTLs and individual gene tests, and including those in selection is simple if legal.

The need for rapid processing (monthly and weekly genomic predictions) was a surprise. Breeding decisions can wait until 1 year of age, whereas DNA samples can be obtained at birth, so the urgency was not obvious. However, marketing and transfer of ownership happens quickly for top animals. Many herd owners now also use genomics as a culling tool, selling calves with low genomic predictions early in life instead of raising them for replacements. High labor costs for calves during their first month created a demand for weekly evaluations (Wiggans et al., 2015). Breeders can also use genotypes as a mating tool to reduce genomic inbreeding (Sun et al., 2013). Genomic relationships of genotyped females with marketed males are provided monthly to breeding organizations and owners.

Future surprises

Rapid growth of genomic databases can quickly cause previously tested statistical methods and validations to become outdated. Computer programs also must be constantly revised to keep up with database sizes that have doubled each year for the past 6 years to nearly 1 million genotyped animals today. When data sets were small, addition of genotypes from all bulls including very old bulls increased reliability. More recent research found that the oldest bulls could be dropped with little loss of accuracy because genotypes for many more recent bulls are available that contain the same DNA. In fact, for the more heritable traits, dropping all of the 26,759 proven bull genotypes causes little loss because the reference population now also includes >100,000 genotyped cows with records. Early tests showed that adding highly selected females did not improve accuracy, but most females now are genotyped while heifers before their phenotypes arrive, reducing any selection bias.

Current statistical methods do not fully account for genomic pre-selection of progeny, genomic merit of mates and herdmates, lack of random sampling, embryo transfer, and extreme prices. In the past, use of highly selected foreign bulls sometimes caused similar biases, but with little effect on bulls tested in domestic sampling programs. Some new genomic biases might be reduced by using single-step instead of multi-step equations, but single-step algorithms cannot yet process very large datasets, and other biases are more difficult to estimate or solve.

Prediction accuracy is usually tested by predicting the latest 4 years of proven bulls from data with the last 4 years truncated (Mäntysaari et al., 2010). This tests the ability of genomic equations to predict 1 generation ahead, but many calves (or embryos) are now 2 or 3 generations away from the proven bulls used to compute the predictions. Also, only those bulls with the highest predicted merit now obtain daughters. This can greatly reduce the variance of true genetic merit and the correlations of predicted with true merit needed to estimate the reliability of the prediction system. The success of genomics has reduced our ability to test how well it works.

DNA sequence data will gradually allow the actual QTLs that cause genetic effects to replace the genetic markers now used in genomic selection (Daetwyler et al., 2014). Genotyping chips at first contained only evenly spaced, unselected genetic markers. Some recent chips also include selected markers from a higher density (777K) chip chosen from those with largest effects. Similarly, sequence variants predicted by bioinformatics or estimated from phenotypes to have large effects are being added to chips. Alternatively, sequencing could be used directly instead of chips if the technology continues to improve rapidly. Use of low density markers to impute the QTLs and sequence variants may continue to be a good option because for genotyping whole herds, costs per animal must be very low. Also, the QTLs must be imputed for all animals previously genotyped with chips that contained only markers.

Long term progress may be difficult to predict because genetic correlations can change across time and because economic functions are nonlinear, whereas selection indexes usually assume linear values. As selection proceeds or management systems and environmental conditions change, different factors can become limiting. The genetic correlation between milk yield and longevity was very positive at about 0.7 in the 1960s but declined quickly to near 0.1 currently (Powell and VanRaden, 2003) along with large genetic increases in milk yield and decreases in fertility. Phenotypic changes in culling decisions were less dramatic, but producers now put less emphasis on yield and more emphasis on all other traits (Norman et al., 2007). Somatic cell score is a good indicator of clinical mastitis, but mastitis researchers were worried when genetic selection on SCS began that eventually cows would simply stop fighting their infections and let the disease win in order to maintain low cell counts. The correlation between SCS and clinical mastitis has not declined yet, but could with intense selection for low SCS.

Genomic evaluations can counteract previous unintended declines in traits that were unfavorably correlated to the selection goal, but only if data are available and breeders act. Long ago, researchers at USDA were surprised when their experimental Guernsey line went extinct after several generations of intense inbreeding (Woodward and Graves, 1933). Researchers at Iowa State were surprised when their line of Tribolium castaneum (flour beetles) went extinct after 16 generations of selecting for a trait correlated by -0.43 with fertility (Berger, 1976). Breeders learned from this early research that they should always monitor trends in fertility, health, conformation, and management traits and invest in collecting new traits. Fortunately, new genomic tools allow faster positive progress that may pleasantly surprise us with how quickly the previous losses can be reversed. Dairy cattle will not become extinct and instead will improve rapidly, contributing more toward feeding the growing human population with each generation.

References

Adams, H.A., Sonstegard, T., VanRaden, P.M., Null, D.J., Van Tassell, C.P., and Lewin, H. Identification of a nonsense mutation in APAF1 that is causal for a decrease in reproductive efficiency in dairy cattle. Proc. Plant Anim. Genome XX Conf., San Diego, CA, Jan. 14–18, P0555. 2012.

Berger, P.J. 1976. Multiple-trait selection experiments: Current status, problem areas and experimental approaches. In: Proc. International Conf. Quantitative Genetics. Ames, IA.

Daetwyler, H D, et al. 2014. Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle. Nature Genetics 46:858–865.

Lund, M.S., de Roos, A.P.W., de Vries, A.G., Druet, T., Ducrocq, V., Fritz, S., Guillaume, F., Guldbrandtsen, B., Liu, Z., Reents, R., Schrooten, C., Seefried, F. & Su, G. 2011. A common reference population from four European Holstein populations increases reliability of genomic predictions. *Genet. Sel. Evol.* 43, 43.

Mäntysaari, E., Z. Liu, and P. VanRaden. 2010. Interbull validation test for genomic evaluations. Interbull Bull. 41:5 pages.

Norman, H.D., Hutchison, J.L., Wright, J.R., Kuhn, M.T., and Lawlor, T.J. 2007. Selection on yield and fitness traits when culling Holsteins during the first three lactations. J. Dairy Sci. 90(2):1008–1020.

Powell, R.L., and VanRaden, P.M. 2003. Correlation of longevity evaluation with other trait evaluations from 14 countries. Interbull Bull. 30:15–19.

Sun, C., VanRaden, P.M., O'Connell, J.R., Weigel, K.A., and Gianola, D. 2013. Mating programs including genomic relationships and dominance effects. J. Dairy Sci. 96(12):8014–8023.

Supreme Court of the United States. 2013. Association for Molecular Pathology v. Myriad Genetics, Inc.

VanRaden, P.M., Olson, K.M., Null, D.J., Sargolzaei, M., Winters, M., and van Kaam, J.B.C.H.M. 2012. Reliability increases from combining 50,000- and 777,000- marker genotypes from four countries. Interbull Bull. 46:75–79.

Wiggans, G.R., VanRaden, P.M., and Cooper, T.A. *Technical note:* Rapid calculation of genomic evaluations for new animals. J. Dairy Sci. 98:(in press; published online Dec. 31, 2014)

Woodward, T.E. and R.R. Graves. 1933. Some results of inbreeding grade Guernsey and grade Holstein-Friesian cattle. USDA Tech. Bulletin No. 339. Summary

2025 – Ten years ahead

David Nation
Dairy Futures CRC

Ten years from now there will seismic shifts in the workforce, technology and global connectedness. Luckily some things will be consistent and retain the social fabric that we now have in the herd improvement industry. I reckon that AI will continue to be the best way to breed cows, and that a local service that includes technicians and high quality advice will still be valued by farmers.

People

As someone from Generation X, I have been well used to having a career surrounded by baby boomers. Many have now retired, but what has not been so clear is the speed that the Millennial generation will replace baby boomers and become the predominant age group. In the USA it is expected that 70% of the workforce will be Millennial in 2025. This generation doesn't recall a time without mobile phones and the internet and is impatient when information flow isn't seamless. They are the best educated and highly innovative; a great combination for driving improvements in herd management (see www.deloitte.com/MillennialSurvey for more information)

Cows

We are now entering an era where genetic improvement will run at double the pace. So one way to get a feel for how much can be achieved is to look back 20 years (to 1995) and consider how much has changed and then project the same amount of improvement when looking forward 10 years. There will be further gains in milk production as well as an ongoing focus on fertility, type and survival. New traits will enable farmers to further diversify their list of desired improvements for their herds.

Pastures

I'll only mention pastures briefly, because the breeding that has happening now will drive most of the new varieties in 2025 (because pasture breeding is a 12 year process). The big change will be new and faster means to produce varieties. These "short-circuit" innovations will lead to increased energy yield and quantity of pasture grown. Low-cost pasture will continue to the basis of a profitable dairy industry.

The period after 2025 is the most exciting as there are game-changing approaches to pasture breeding and new means to edit the plant's DNA sequence that will result in vastly improved varieties in the 2025 to 2030 period.

Herd improvement technology

The first and most important point is that genomics is here to stay. It will only get better as it taps into larger datasets of daughter performance and reveals the mysteries held within entire DNA sequences. The big leap over the next 10 years is to move from routine genotyping of sires to routine genotyping of entire herds. This challenge has been given to geneticists – how do we create a service where the benefits of cow testing are three times the cost?

Another obvious trend is to look at where engineers are focussing their attention in milk machinery companies. Robotics and electronics are heavily used in new machine designs and there will be a proliferation of cow observations. Near real-time knowledge of a cow's production, health, and fertility will give farmers a deeper understanding of each cows' performance. It should be routine to know a cow's pregnancy status and know if she is on heat. Cows with health issues, particularly around calving, will be closely monitored.

One of the areas of disconnect that will be fixed by 2025 is that type traits will be completely aligned with each breed society's view of an ideal cow. The current method of presenting type information does not do this. Farmers might also be able to dial up their own ideal cow, and re-tune all the type results to rank each bull based on their own definition of ideal.

Milk sampling will increase in value. New ways of keeping the integrity of milk samples will be needed so that new tests can look for components that have very low concentrations (often at parts per million or less). There will be a need to tactically choose which cows to sample and new infrastructure to test any cow at any milking will be required.

Hot topics in 2025

Two areas that will be hot topics are how to ensure that cow data is best used to make good decisions and consideration of new technology called genome editing.

Data collection is only useful when it is analysed in a way that farmers can make better decisions. There is scope for constant improvement of how data is analysed and presented, especially as the needs of herd managers evolve.

One of the next frontiers is to directly edit the DNA sequence of cattle (known as genome editing). Multiple new approaches have been proven, and by 2025 the ability to edit will be routine. Science will move much faster than the dialogue with the market and the broader community. I reckon that these discussions will peak in about 10 years time, and the first sires with an edited genome will start to appear on bull lists.

The Value of Herd Testing Information and Delivery in Today's U.S. Dairy Industry

Pat Baier

Summary

In 2004, AgSource recognized the need to adjust our milk recording business model. At that time, we began shifting from a service provider relationship to a partnering relationship with membership. We sought to extend beyond the traditional relationship between a cooperative and its members. We needed to be valued by the entire management team associated with our members. This team includes a combination of consultants, nutritionists, veterinarians, loan officers and A.I. organizations. Our future relied on our ability to define an important role in the new team-based farm management systems forming within our industry.

AgSource's internal database, along with its value-added reporting capability, places the organization in a positive position to support the management of production, reproductive, genetic and now diagnostic data points being created. By demonstrating our strength in developing tools to measure management decisions, we have found our place in the new industry structure and have became an allied business partner. AgSource helps dairy herd consultation teams provide better management support to a shared customer base. The end goal is long-range success for all three entities in this business relationship.

Keywords: dairy herd consultant teams, management decisions, partnering relationship

Introduction

Today's dairy herd consultant is working in an extremely competitive arena and has greater need than ever to demonstrate expertise in order to differentiate from competition. This need has given rise to the development of individualized proprietary data reports and delivery methods. In many cases, these reports include data collected as part of milk recording and testing service. The end goal is to gain the confidence of a customer base by providing sound management guidance that is hard for others to replicate. It is important to avoid operating in a commodity environment. An added piece of this business model is the information is usually being delivered at no additional cost to the dairy farm. The main goal of this activity is to maintain or increase sales of semen, feed additives or other products or services.

This activity has the potential for two negative outcomes: the first being a reduced appreciation and perceived value of milk recording information and resulting data points. The second is the resulting confusion when several different databases are utilized to create benchmarking information.

Our typical herd owner employs the services of two to three different consultants. One consultant may specialize in semen and reproductive services, while another specializes in nutrition services. If each of these service providers is working from a separate database, the herd owner or manager can become confused by the varying data results combined with varying management guidance.

Networking

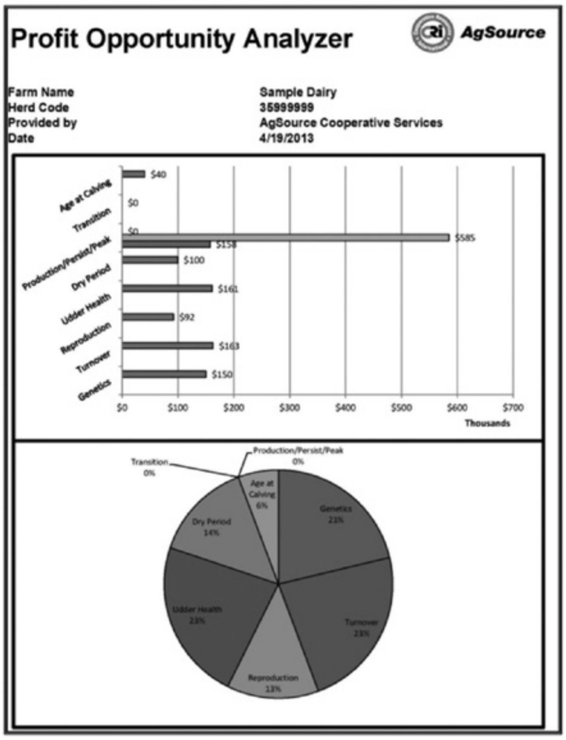
AgSource has identified three key areas where it can support the consulting industry and provide improved service to customers held in common.

First: AgSource works in a third party position. We are able to organize the differing data points through a herd test. We are then able to create management information, benchmarking data by breed, herd size, production levels or other criteria to support each dairy's current need. We can then provide the exact information received at the farm level to the entire herd consulting team through access to MyAgSource. This is a web-based report delivery tool. This allows the consultant to study the herd's information prior to the consultation visit. Consultants and dairy herd managers/owners are busy individuals. Previewing this information allows for meeting time to be devoted to setting direction and making management decisions instead of reviewing data. Reduced meeting time and faster decision making improves efficiencies for both the consultant and herd managers. The consultant's time is better spent evaluating results and formulating recommendations rather than entering data and creating spreadsheets.

Second: AgSource products and benchmarks verify the results of the consultant's efforts by quickly and appropriately identifying the direction a herd is moving in several key management areas. This again allows consultant and herd managers to spend their valuable time evaluating the success or failure of previous management decisions by way of a third party report. Without AgSource, the consultant would have to spend time developing the management evaluation tool along with their other responsibilities. The end effect is more efficient use of billable consulting time. The end effect at the farm level is more time spent evaluating the results of past decisions and defining new direction for the operation. We do realize there is still the consultant or farm manager that enjoys creating and dissecting spreadsheets. For those so inclined, MyAgSource reports can be downloaded into personalized spreadsheets. This gives the individual freedom to work through data points of information to develop individualized lists and sorts. However, the data points of information used are still those from the AgSource delivery system. This holds the information created to the same third party integrity mentioned earlier in this paper.

Third: AgSource has developed reporting and benchmarking product called The Profit Opportunity Analyzer® (POA). Figure 1 is an example of this report. POA is an in-depth analysis tool, designed for use in team meetings with consultants. This tool allows the entire team to cooperatively develop and evaluate the course of action for each herd owner or manager. Once again, each consultant is using shared, consistent management information delivered by AgSource in order to create a team plan all can agree to. If the report is ordered directly, an AgSource representative makes an appointment with and presents the report to the dairy farm's entire management team. Involving all decision-makers and influencers is critical for successful application of the information. The program improves teamwork between all service providers as they consider facts, discuss ways to improve performance and agree on a course of action. Delivering the report allows AgSource to play a valuable role on the team.

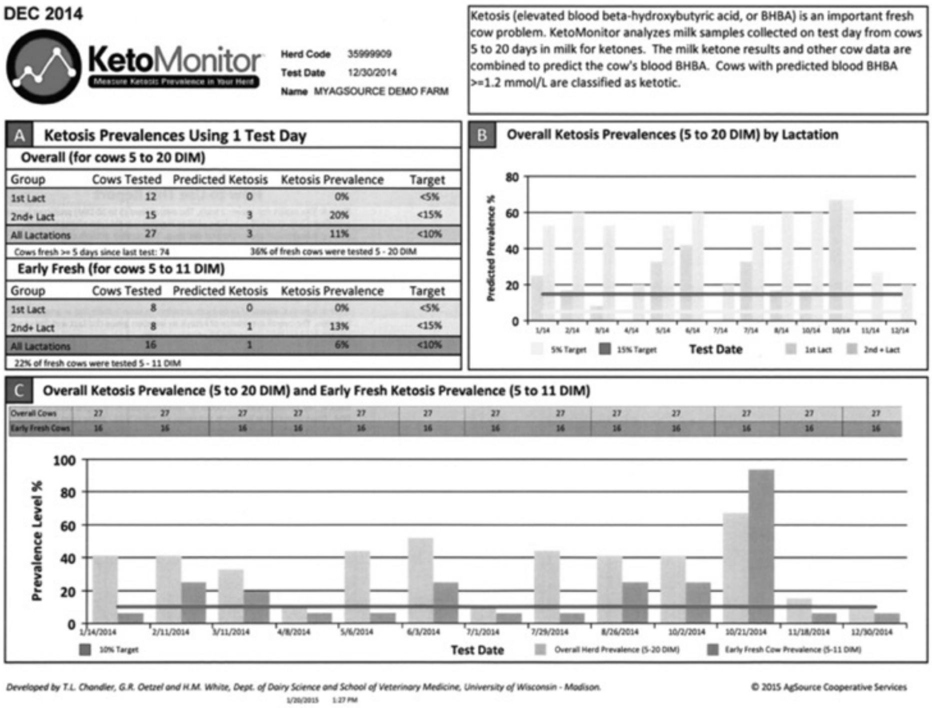
Figure 1 (page one of the 15-page Profit Opportunity Analyzer)



Consultants who purchase and deliver the Profit Opportunity Analyzer on their own are required to attend an AgSource training program. During the training and subsequent refresher programs, AgSource is able to demonstrate value as an allied partner while networking and developing a long-term relationship with an allied industry partner.

Staying current with producers' herd management needs and technology employed is a very important aspect of the AgSource purpose. Research and development are key investments to meet future needs of our clients. One example is the recent development of the AgSource KetoMonitor report. Figure 2 is an example of this new report. The KetoMonitor report combines milk component data from a DHI sample with other information about each cow and establishes a herd prevalence level of Ketosis in cows fresh 5 to 20 days. Ketosis is a manageable but costly disease that can be seasonal and easily impacted by nutritional and herd management changes. A cow with sub-clinical or clinical ketosis creates on average a loss of $289 per lactation in terms of increased health problems, lower reproductive performance and lower production. This new report allows producers to monitor prevalence levels from month to month and take action as soon as prevalence levels of ketosis increase above 10%. The KetoMonitor report was developed by the University of Wisconsin-Madison Department of Dairy Science and School of Veterinary Medicine in cooperation with AgSource.

Figure 2 (page one of the two-page KetoMonitor report)



DEC 2014

KetoMonitor — Measure Ketosis Prevalence in Your Herd

Herd Code 35999909
Test Date 12/30/2014
Name MYAGSOURCE DEMO FARM

Ketosis (elevated blood beta-hydroxybutyric acid, or BHBA) is an important fresh cow problem. KetoMonitor analyzes milk samples collected on test day from cows 5 to 20 days in milk for ketones. The milk ketone results and other cow data are combined to predict the cow's blood BHBA. Cows with predicted blood BHBA >=1.2 mmol/L are classified as ketotic.

A Ketosis Prevalences Using 1 Test Day

Overall (for cows 5 to 20 DIM)

Group	Cows Tested	Predicted Ketosis	Ketosis Prevalence	Target
1st Lact	12	0	0%	<5%
2nd+ Lact	15	3	20%	<15%
All Lactations	27	3	11%	<10%

Cows fresh >= 5 days since last test: 74 36% of fresh cows were tested 5 - 20 DIM

Early Fresh (for cows 5 to 11 DIM)

Group	Cows Tested	Predicted Ketosis	Ketosis Prevalence	Target
1st Lact	8	0	0%	<5%
2nd+ Lact	8	1	13%	<15%
All Lactations	16	1	6%	<10%

22% of fresh cows were tested 5 - 11 DIM

Developed by T.L. Chandler, G.R. Oetzel and H.M. White, Dept. of Dairy Science and School of Veterinary Medicine, University of Wisconsin - Madison. © 2015 AgSource Cooperative Services

In addition to research with educational institutions, AgSource also directly engages dairy herd consultants in the development of new management tools and updates to existing offerings. This not only improves the quality of AgSource products, but also increases buy-in from those who influence the dairy farms AgSource serves. The 2012 introduction of polymerase chain reaction (PCR) testing to identify mastitis pathogens in preserved milk samples is the most recent example of such collaboration. Udder health management professionals have various opinions regarding the application of this relatively new technology. Because of this, a team of university researchers and veterinarians was assembled to assist AgSource with the development of the program and to train other veterinarians and consultants. While taking this team approach did extend the development time for this new product, it has proven to be worthwhile, netting greater support and understanding of the test's value.

Another good example of AgSource networking to produce a useful reporting tool is The Genetic Selection Guide. This tool, jointly developed with Genex Cooperative, breaks down dairy cow and heifer herds into genetic quartiles based on net merit dollars (a single US index for measuring the genetic value of the cow). The Genetic Selection Guide assists herd managers with decisions pertaining to selecting animals of high or low genetic merit and improving their overall genetic make-up of the herd by applying new technologies such as sexed semen and genomics to targeted animals.

Other collaborative efforts have yielded the creation of management guidance tools owned by our networking partners. Our participation is behind the scenes, but once again the data used to create the management tools are data points collected, cleaned and delivered by AgSource routine test day procedures. This again creates consistency among information tools, with results delivered through traditional AgSource reports. It reduces redundancy of activity in the industry and, more importantly, reduces the confusion of varying interpretations of the same data points at the farm level.

Conclusion

Networking with dairy herd consultants is a natural in AgSource's value-added business model. It supports improved management decisions and increases efficient use of consultant and dairy herd owner/manager time. This program also gives consultants the ability to measure and benchmark their customer's results against a large database of raw data points. AgSource's large database allows herds to be compared by breed and size of dairy farm. This single database provides consistent points of reference, which is particularly important if two or more consultants are working with the same dairy farm.

This marketing system encourages direct networking opportunities for AgSource. Coordinating activities with allied industry partners allows AgSource to better serve its members and customers while gaining the support and endorsement of key influencers. The entire program supports and enhances the continued use and reliance on AgSource management information.

Using data to tackle difficult on-farm challenges

Dr. Maria Thielen
German Association for Performance and Quality Testing (DLQ), Bonn, Germany

Introduction

More than 3.6 million cows are herd tested in Germany and more than 70% of these are registered in the herd book. This makes Germany having the largest active cow population in the European Union and even one of the largest worldwide. In Germany approximately 53,000 dairy farmers out of the total 80,000 are currently joined to one of the 12 regional dairy herd improvement (DHI) organisations. These farms are keeping on average 69 cows producing about 8,221 kg milk with 620 kg milk solids per head per year (ADR, 2013).

A highly heterogeneous agricultural structure stands behind these figures. Herd sizes vary from 43 cows in the South over 84 cows in the North-West to 274 animals in Eastern Germany (ADR, 2013). Despite the structural differences the overall developments in the German dairy industry in the last decades have been similar. On the one hand many farms, mainly smaller ones, shut down, e.g. 35,000 farms since 2003; on the other hand the remaining farms increased their herd size rapidly, resulting in the total number of dairy cows in Germany staying relatively constant over the years. These structural changes were accompanied by improvements in herd management tools, animal husbandry facilities, milking technologies, and feeding systems. This led also to an increase in the annual milk yield per cow, which increased for example from 7,355 kg (559 kg milk solids) in 2003 to 8,221 kg (620 kg milk solids) in 2013 in the herd tested herds (ADR, 2003, ADR, 2013).

In contrast to the upward development of the milk yield the udder health has not gone the same direction. German dairy cows have on average a productive life span of just over three years (ADR, 2013), while the fourth lactation is considered to be the most productive one. Udder diseases represented the second most common reason for cows being culled in Germany in 2013 with a proportion of 14.3% (ADR, 2013). Moreover, analysis of random samples in North Germany revealed that every second cow is affected once by clinical mastitis per lactation (Krömker, 2007). And the average somatic cell count (SCC) in Germany even exhibited a slight upwards trend over the last years (ADR, 2002, until ADR, 2013), sitting at an average of 193,000 cells/ml in 2013.

If a more sustainable milk production is to be achieved the optimisation of udder health needs to be prioritised. This in turn will lead to improved animal welfare *per se*, a longer productive life span at an improved health status, i.e. a higher production efficiency, reduction in usage of antibiotics and less milk losses. Obviously, this optimisation of udder health requires comprehensive management skills and technical knowledge by the dairy farmer. However, often the focus has been laid on the health status of individual cows, while the udder health status at herd level and management routines affecting the whole herd have been neglected. A strategic approach is required.

It is well known that communication between the stakeholders plays a vital role in improving udder health. Consulting is a complex process. The reasons for its failure can be manifold. One option of improving udder health more sustainably is if, in general, consultants pursue a more preventative approach and if the farmer's personal needs for communication as well as technical knowledge are taken into account.

MilchQplus project background

The project milchQplus is running from May 2012 until December 2015. Partners of the project are the German Association for Performance and Quality Testing (DLQ) and the microbiology group at the University of Applied Sciences and Arts Hannover. The DLQ is the umbrella organisation of 12 milk recording organisations, two associations for raw milk testing, and one organisation providing IT solutions for animal production. Through its member organisations the DLQ has direct contact to the 53,000 German dairy farmers participating in herd testing. This unique network enables easy and fast transfer of scientific and technical knowledge resulting from this project into the dairy practice.

The project is focussing on three main areas:

1. Improving the herd test report by implementing new key figures for udder health
2. Improving communication between stakeholders
3. Cell differentiation

1. Key figures for udder health

Mastitis is a multifactorial disease. Therefore, the complexity of udder health can only be encountered and solved successfully by a strategic approach. MilchQplus developed new key figures which allow an assessment of the health status of the bovine mammary gland at herd level (Figure 1). While they are based on the SCC results of the individual cows standardly available from the monthly herd testing, these key figures give a picture of existing udder infections, the duration of udder infections as well as new udder infections of the whole herd.

Figure 1. Overview of milchQplus key figures describing the udder health status of the herd. Values for the key figures are from random samples of average and top farms in North Germany (Volling, 2011).

milchQplus Key Figures	Description	Period	Average /Top Farms
(1) Proportion of cows with healthy udders	Proportion of animals with ≤ 100,000 somatic cells/ml of all lactating animals at the current herd test.	Current milk recording	50% / 76%
Categories of somatic cells	Proportion of animals with SCC ≤ 100,000 (= key figure 1) SCC > 100,000 and ≤ 200,000 SCC > 200,000 and < 400,000 SCC ≥ 400,000	Current milk recording	
(2) Proportion of chronically diseased animals with poor cure prospects	Proportion of animals with > 700,000 somatic cells/ml each in the last three herd tests of all currently lactating animals.	Current milk recording	5% / < 1%
(3) New infection rate during lactation	Proportion of animals with > 100,000 somatic cells/ml in the current herd test of all those animals with ≤ 100,000 somatic cells/ml in the previous herd test.	Current milk recording	21% / 9%
(4) New infection rate in the dry period	Proportion of animals with > 100,000 somatic cells/ml in the first herd test after calving of all those animals with ≤ 100,000 somatic cells/ml in the last herd test before drying off.	Moving annual average	28% / 16%
(5) Cure rate in the dry period	Proportion of animals with ≤ 100,000 somatic cells/ml in the first herd test after calving of all those animals with > 100,000 somatic cells/ml in the last herd test before drying off.	Moving annual average	50% / 77%
(6) Rate of heifer mastitis	Proportion of heifers with > 100,000 somatic cells/ml in the first herd test after calving out of all heifers calved in one year.	Moving annual average	41% / 18%

The SCC is commonly used to assess the health status of the udder. MilchQplus uses a SCC of 100,000 cells/ml as an orientation value to distinguish between cows with a healthy udder and cows exhibiting a disturbed mammary gland health. This orientation value is in line with the recommendations of the German Veterinary Medical Society (DVG, 2012) to differentiate between healthy and diseased mammary glands. Also scientific studies show the concentration of other inflammation parameters in milk changes significantly at or below a SCC of 100,000 cells/ml. (Hamann, 2001; Schwarz *et al.*, 2011).

A SCC greater than 100,000 cells/ml does not immediately imply a necessity to treat or even to cull this animal. Instead, this orientation value is applied such that the key figures function as an early warning system for udder health problems in the herd. Only if such problems are recognised early appropriate measures can be taken also at an early stage in order to reduce incidence and prevalence of mastitis.

In detail these key figures are:

1. **The proportion of cows with healthy udders** as defined by a composite milk somatic cell count ≤ 100.000 cells/ml on the current herd test day. If the proportion of cows with healthy udders is too low or has been declining over the past months measures are required to reduce the chance of new infections during lactation. This may include amendments in the animal husbandry, milking routine, milking equipment, and feeding as well as the search for chronically diseased animals in the herd as they can act as a source for new infections.
2. **The rate of chronically diseased cows with poor cure prospects.** This comprises cows which repeatedly exhibited a SCC > 700,000 cells/ml. A high rate provides indication of the spread of cow associated microorganisms in the herd and a possibly inadequate cure rate in the dry period. After consultation with the farm veterinarian these affected cows might be dried off earlier with the appropriate therapy or might be worth considering culling. A change in the general dry cow therapy regime might also be advisable.
3. **The rate of newly diseased animals during lactation.** A high rate of new infections in the lactation period since the last herd test, i.e. cows shifting from SCC ≤ 100,000 cells/ml to > 100,000 cells/ml, reflects current management problems or seasonality effects. If this issue is counteracted successfully this key figure will respond quickly. Besides the calendar date, these new infections can also be depicted according to days in milk pointing to stages of lactation of concern. Many new infections within the first 100 days in milk point to metabolic disorders such as (subclinical) ketosis, whereas many new infections in mid lactation are often caused by inadequate teat condition.

4. **The new infection rate in the dry period** reflects the proportion of cows that encountered a new infection during the dry period demonstrated by a SCC ≤ 100,000 cells/ml before and a SCC > 100,000 cells/ml after the dry period. Mainly environmental mastitis occurs during the dry period. A rise of the new infection rate during that time is favoured by
   - Deficient barn hygiene, especially close to calving time
   - No use of antibiotic dry cow therapy or teat sealer
   - Inadequate udder health status at drying-off, since damaged udder quarters are more susceptible to new infections
   - A milk production of ≥ 15 kg/day at drying off
   - Proportion of cows suffering of milk fever > 5%
5. If a cow can improve its SCC at drying off from below to above the orientation value of 100,000 cells/ml at calving then it is counted by **the cure rate during the dry period.** The dry period enables to cure mastitis in animals over the period of several weeks without milking. The main reasons for failing to achieve a high cure rate are:
   - No use of appropriate antibiotic dry cow therapy.
   - Too many incurably diseased animals in the herd
   - Overcrowding in the barn

   Low cure rates despite the application of antibiotics at drying off reveals a high number of reinfections, so that actions to counteract new infections are required.
6. **The rate of heifer mastitis** covers all new heifers entering the milking herd within the last 12 months showing a first herd test result of > 100,000 cells/ml. Too many heifers with an elevated SCC at the first herd test also indicate a problem within this special animal group. Long term costs occur. Multiparous cows, in contrast to primiparous cows still in the growing process, can compensate milk losses from damaged udder quarters in the remaining quarters in the long term to a certain degree. The main infection pathways are spontaneous infections with environmental pathogens, suckling by other animals or transmission of Staph. aureus by flies. In Germany, spontaneous infections are the main cause of heifer mastitis favoured by stress and hormonal changes around calving, by inadequate closure of the teat tip, a too wide teat canal, a too short teat canal, or by pronounced udder oedema.

   MilchQplus is currently in the process of implementing these key figures into the monthly herd reports across Germany via the DLQ member organisations. Key figures are available either in printed or digital form for a better monitoring system.

   Furthermore, **benchmarking figures** will be provided for each key figure on these herd test reports allowing a comparison with top farms. For this purpose currently the top 25% of farms ranked according to their average herd SCC at the last milk recording are selected within a region. From these farms an average value for each key figure is calculated and presented. These benchmarking figures are to be updated at least on a monthly basis. A comparison with figures from their own region instead of figures sourced from the literature (Volling, 2011) was considered as a stronger motivator for farmers to change operations.

2. Communication between stakeholders

One further goal of milchQplus is to improve the communication between the stakeholders involved in the farm.

Workshops

Starting in 2013 workshops have been carried out for consultants and milk recording personnel within the DLQ member organisations. Content of the first part of the workshop was to raise awareness for the importance of a strategic approach combined with an early warning system to tackle mastitis problems, and how these milchQplus key figures can contribute to such a strategic approach. This technical knowledge was followed by a communication session in the second part. This communication session supported the participants to identify their own personally preferred role in the consulting process. Different kinds of attitudes by farmers to cooperate and to accept new knowledge were presented which are helpful to consider when establishing a trusting relationship. Finally, this session was completed by some basic rules on successful communication.

Interviews with farmers, veterinarians, and consultants

Secondly, in 2013 and 2014 milchQplus team members interviewed dairy farmers, veterinarians and farm consultants across Germany. Nineteen dairy farmers were selected by two criteria: a continuously low SCC in their herds accompanied by an above average milk yield per animal per year. The differing agricultural structures in Germany were reflected in farms selected. The main aims of the interviews with farmers were to investigate what motivates them, how they perceive mastitis on their farm and how they view the risk factors for mastitis. Veterinarians were chosen for interview if they practised veterinary herd health management on dairy farms. Farm consultants were selected if they had long term experience on dairy farms. The interviews with veterinarians and consultants served to verify the results from the interviews with the farmers. They were asked on their own views on risk factors and on their opinion how farmers might judge these risk factors. Similarly, their thoughts on how to motivate a farmer were enquired.

From the interviews the following results were concluded. The perception of mammary gland infections on the farm was reasonably homogenous amongst farmers. After palpation diagnosis and alterations to the milk texture the SCC herd test results were mentioned as the third most important indicator for a diseased mammary gland. However, the point in time when farmers start to take action varied. The SCC threshold when a farmer feels warned of an udder health problem with an individual cow ranged from 150,000 to 600,000 cells/ml in the interviewed group (yellow traffic lights). The SCC threshold when a farmer feels alarmed of an udder health problem with an individual cow ranged from 200,000 to 900,000 cells/ml in the interviewed group (red traffic lights). Interestingly, some farmers did not require a warning step at all, but were directly alerted if a threshold of 200,000 cells/ml was exceeded. The average herd SCC on these farms was < 100,000 cells/ml. The variation for such warning or alert values was not as large amongst veterinarians and consultants.

Farmers listed as the three main risk factors for mastitis the hygiene of the cubicles in free stalls, the feed, and stress. Veterinarians and consultants had similar views on the first two risk factors, but brought the milking process as a third risk factor forward.

In contrast to the risk factors perceived by the farmers, they apply prevention measures firstly to the milking process: teat dipping after milking and the usage of a single cloth per cow for teat cleaning prior to milking, followed by cubicle hygiene, and antibiotic dry cow therapy. Veterinarians considered the hygiene at the milking process and the milking shed itself, the milking routine, the order of cows to be milked, and cubicle hygiene as the most important prevention measures. Consultants believed in cubicle hygiene, disinfections of the clusters between the milking of two cows, and the feed and feeding management as important points to focus on.

The majority of farmers were motivated in their behaviour by happy and healthy cows. This applied also to their udder health management. Interestingly, possible economic losses plaid a minor role. In contrast, veterinarians and consultants tried to motivate farmers by pointing out the costs of mastitis. They see themselves in charge to motivate farmers, however experience that also as a hard task. Furthermore, they also highlighted the often experienced discrepancy between recommendations expressed and recommendations put into practice. Professional honour as well as personal satisfaction with the job also influenced farmers' commitment to achieving a higher udder health status.

The following recipe for success was derived from the interviews:

1. Perception and sensitivity: A diseased mammary gland needs to be detected early. A defined SCC threshold is required to function as an early warning system to judge udder health. This threshold needs to be sufficiently low to allow an early reaction.
2. Action-oriented approach and consistent implementation: A well defined concept of measures specifically adapted to the own farm situation needs to be in place. The concept must be implemented consistently by every single staff member on that farm.
3. "Cow knowledge": It was not quantifiable, but appeared helpful if farmers had a genuine sense and intuition for their cows, cow's health, and potential risk factors for udder health.

Hands-on information material

Thirdly, a bunch of hands-on information material has been made available. Two short films are explaining the above mentioned key figures further. An additional third film was shot on a farm elucidating how to optimise the milking process. This is accompanied by fact sheets on the milking process, mastitis, treatment, animal husbandry etc. as well as check lists to examine the milking process on farm. This material is all easily available via the project website.

3. Cell differentiation

As mentioned above the composition of the somatic cells varies with stage of mammary gland infection. A flow-cytometry method for differentiation of somatic cells in raw milk as an innovative diagnostic tool for the identification of cases of chronically incurable mastitis is developed within the scope of the milchQplus project. The results may help to estimate the prognosis and may give information about the potential prospect of an antibiotic therapy for mastitis. In a second step, a high-throughput method will be developed for cell differentiation in herd test samples. Cell differentiation data implemented in herd test reports will support dairy farmers, veterinarians and consultants to make evidence-based therapy or culling decisions. This feature completes the objectives of the project.

Conclusion

In order to achieve an improved udder health, the complexity of udder health needs to be solved by a strategic approach. The key figures introduced by milchQplus form a valuable tool for this management challenge on a dairy farm. The key figures are both indicators and measurable parameters directly related to udder health. They function as an early warning system for mastitis problems at herd level by revealing the current udder health status, the duration of existing udder infections and the time of new infections in the herd. Benchmarking figures derived from top farms in the region help farmers to assess their own herd situation as well as act as motivator. Thus, these key figures can also be used to set realistic goals for the development of the udder health in the herd as well as to control the effectiveness of improvement and treatment measures taken.

Communication is a crucial part if udder health is to become a success story. Farm consultants and veterinarians are in charge of establishing a trusting relationship with the farmer and of bringing forward the idea of preventing rather than treating mastitis. Risk factors need to be analysed and communicated appropriately. Similarly, a catalogue of measures will only be accepted and implemented if it is tailored and communicated according to the needs of the farmer and his willingness for change.

The unique network backing milchQplus which reaches from a university institute over the DLQ umbrella organisation to all German milk recording organisations allows an immediate contact to the majority of German dairy farmers. Hence, the scientific and technical knowledge gained in milchQplus can directly find its way into the dairy practise.

Funding

The project is supported by funds of the Federal Ministry of Food and Agriculture (BMEL) based on a decision of the Parliament of the Federal Republic of Germany via the Federal Office for Agriculture and Food (BLE) under the innovation support programme. Further funding originates from the DLQ member organisations.

List of References

ADR, 2003 - ADR, 2013. Rinderproduktion in Deutschland. Annual Reports. Edition 2003 to 2013. Arbeitsgemeinschaft Deutscher Rinderzüchter e.V. (German Cattle Breeders' Association), Bonn, Germany.

German Veterinary Medical Society, 2012. Bekämpfungsrelevante Aspekte der Mastitis des Rindes als Bestandsproblem. In: Leitlinien Bekämpfung der Mastitis des Rindes als Bestandsproblem. German Veterinary Medical Society (editor), DVG Service, Gießen, Germany, p 21-27.

Hamann, J., 2001. Relationship between somatic cell count and milk composition. Proceedings of the Animal Health Conference, IDF World Dairy Summit 2001, Bulletin of the IDF No. 372: 56-59.

Krömker, V., 2007. Euterkrankheiten. In: Kurzes Lehrbuch Milchkunde und Milchhygiene, V. Krömker (editor), Parey in MVS Medizinverlage, Stuttgart, Germany, p 47-74.

Schwarz D., U.S. Diesterbeck, S. König, K. Brügemann, K. Schlez, M. Zschöck, W. Wolter & C.P. Czerny, 2011. Microscopic differential cell counts in milk for the evaluation of inflammatory reactions in clinically healthy and subclinically infected bovine mammary glands. J. Dairy Sci. 78: 448–455.

Volling O., 2011. Eutergesundheitsmanagement in Milchviehherden mit sehr niedrigem Herdensammelmilchzellgehalt in Niedersachsen. PhD Thesis, Göttingen University, Germany.

www.milchQplus.de

Genetic Progress Reports: A new way to evaluate progress

Peter Williams
Extension Officer, ADHIS

Paul Quinlan
National Sales Manager, ABS Australia

Introduction

Bull selection choices are permanent and their impact compounds over generations. To help farmers quantify and see the effectiveness of their breeding choices, ADHIS developed the Genetic Progress Report in 2012. The Report is a within-breed analysis of a herd over a ten year period and illustrates genetic gain for profit, production, type, longevity, fertility and mastitis resistance.

The Genetic Progress Report offers a farmer their own herd's genetic picture with little extra effort. Herd information which is collected through regular herd recording is routinely used to produce the cow Australian Breeding Values (ABVs) upon which this Report is based. As is the case for all ABVs, the Report is independent and backed by strong science.

The Genetic Progress Report offers herd improvement service providers a value-adding opportunity to their existing range of services. Herd test centres are able to provide their clients with this new analysis tool using existing data sources. The Report builds on their many years of commitment to data capture. It provides another point of engagement to help their clients build stronger herds for the future.

The purpose of this paper is to explore the current use of Genetic Progress Reports by farmers and their advisors.

The Genetic Progress Report – on farm

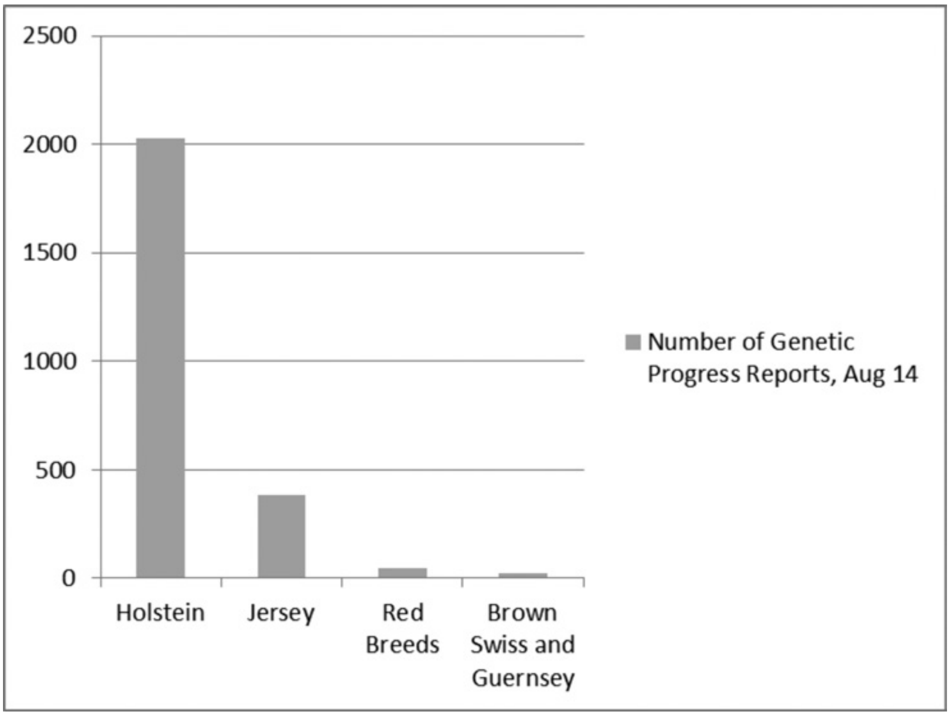
Since Genetic Progress Reports were first released to farmers Australia wide, they have proved to be a very simple but powerful tool to summarise the genetic progress that has been achieved over the past ten years.

The Genetic Progress Reports are produced in line with the routine ABV calculations and released to farmers in April and August each year. To receive a report, the herd must be herd recording so that their herd data is supplied to ADHIS.

All cows in the herd will be included in a Genetic Progress Report as long as the cow qualifies to receive a cow Australian Breeding Value (ABV). This includes having valid production data, at least 50 cows of the same breed and a known sire. A known sire is either an AI sire or a herdbull that has been recorded at a Herd Recording Centre. Calves and heifers are also included in a Genetic Progress Report if they are recorded at a Herd Recording Centre.

In 2014, Australia had 6,314 total dairy herds with 3,023 (48%) herd recording. Of those, 2,481 herds had sufficient data to receive Genetic Progress Reports in August 2014.

Figure 1: Herds with Genetic Progress Reports by breed, August 2014



Case Study – Chris and Diana Place

Finding out his herd ranked in the top 100 in Australia for genetic merit was a welcome surprise to Chris Place, but he was more interested to see opportunities to improve fertility and mastitis resistance through breeding. These are just some of the results from the herd's Genetic Progress Report.

Chris dairies with his wife, Diana and his brother Peter, near Camperdown in Western Victoria. Their 420 cow Holstein herd averages more than 7000L, 285kg fat and 235kg protein from a predominantly grass-based feeding system (including 1.3t pellets/cow).

Breeding decisions have always focused on high production cows that are low maintenance. For many years Chris has selected bulls from the top of the list for Australian Profit Ranking – APR – and within that list, bulls that are positive for udders, feet and legs.

Their Genetic Progress Report, as shown in Figures 2 and 3, shows how much has been achieved with this consistent approach. Since 2013 the herd has been in the top 2% in Australia for APR.

The Genetic Progress Report graphs show the herd's genetic progress (blue line) against the National Breed Average (dotted line) for animals of the same breed. Each year represents a year-of-birth of the animals, so the average of all the animals born in 2003 is represented by a dot. These dots are joined to represent the genetic progress the herd has made over time.

While it's reassuring to see how much can be achieved through breeding, Chris was more interested in the sections of the Genetic Progress Report that showed opportunities for improvement. The report showed that genetic progress for fertility is declining so Chris immediately gave higher priority in his selection decisions.

Figure 2: Genetic Progress Report for Chris and Diana Place's herd (Protein and Fat kg)

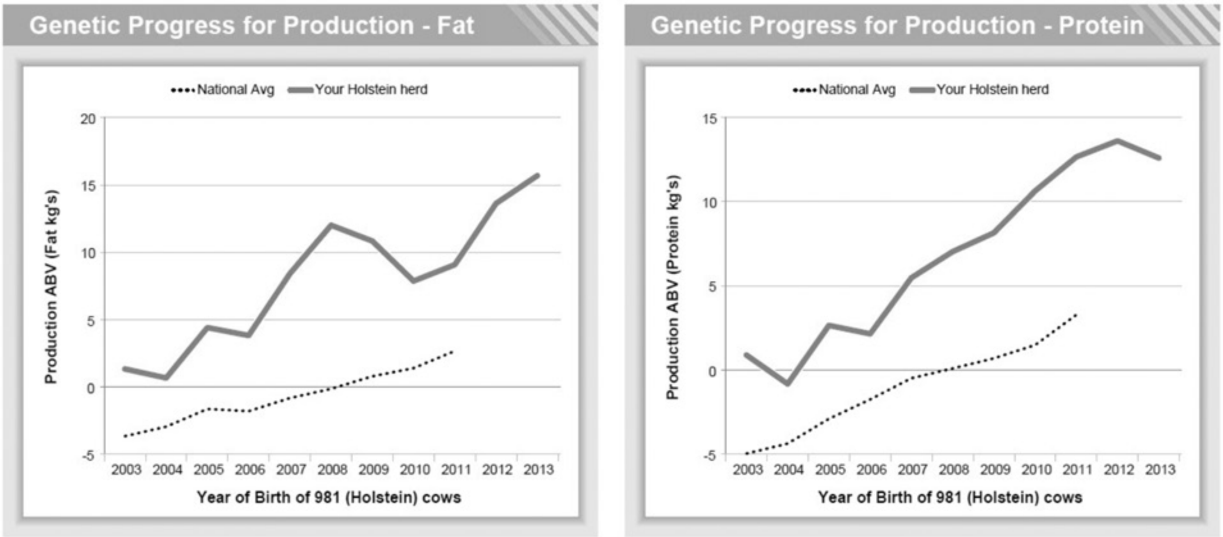
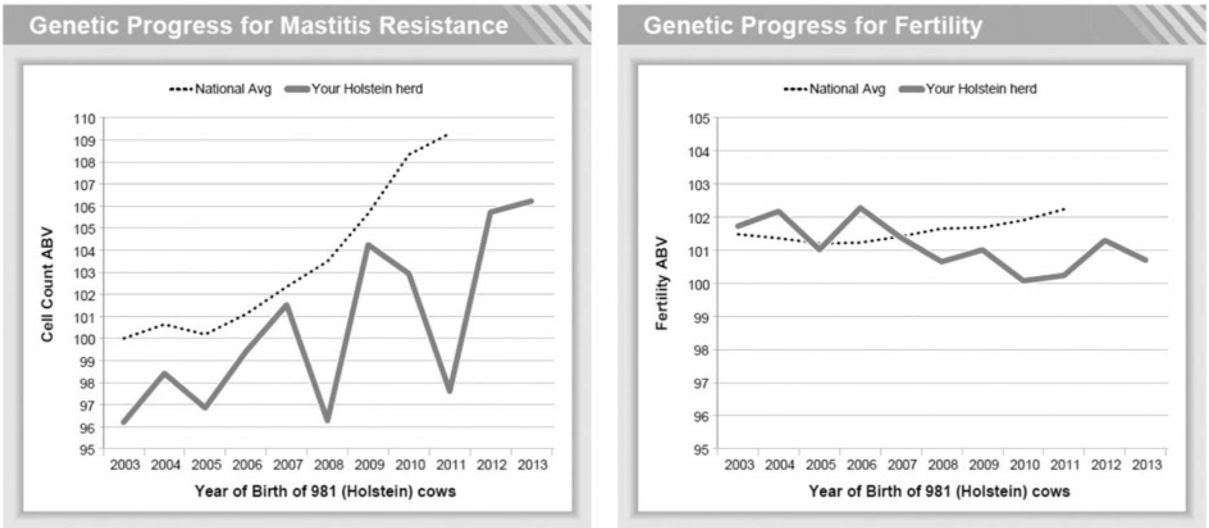


Figure 3: Genetic Progress Report for Chris and Diana Place's herd (Mastitis Resistance and Fertility)



When it comes to selecting sires for the season, Chris normally uses the Good Bulls Guide. His strategy is to go straight to the top four or five APR bulls in the Guide and then check them for the individual traits that are important for his herd. So from now on, he plans to look at fertility and mastitis resistance as well udders, feet and legs.

Chris says making decisions about the herd is made easier thanks to Diana's 'fanatical approach' to record keeping. 'Diana's records allow us to make decisions based on actual herd data rather than gut feel. And the Genetic Progress Report presents our herd data in a very useful format. It's a great tool to help us with our breeding decisions.'

The Genetic Progress Report – supporting advisors

The value of the Genetic Progress Report extends beyond the dairy to enrich the advice provided by a range of professionals. Professionals include herd improvement advisors, farm consultants, milk supply field officers, veterinarians and financiers. Members of this group of professionals vary in their relationship with farmers and with genetics. However, the independent and profit-focused nature of the Genetic Progress Report enables its use across profession.

Herd improvement advisors play an important role in providing advice on bull selection. The Genetic Progress Report provides an independent view of the strengths and potential weaknesses of the herd. With the release of Australia's new breeding indices, an understanding of the characteristics of the herd helps to identify which index should be the focus during bull selections, for example

- Balanced Performance Index (BPI) – achieving overall profit through a blend of production, type and health traits
- Health Weighted Index (HWI) – fast tracking fertility, mastitis resistance and feed saved
- Type Weighted Index (TWI) – fast tracking type

Furthermore, specific traits that should be prioritised can be easily identified to fine-tune the bull list. When breeding the next generation of replacements, every joining decision counts. The Genetic Progress Report enhances bull selection decisions.

The role of farm consultants, milk supply field officers and veterinarians is broader than herd improvement. In a survey of 189 Australian advisors in 2011, respondents were positive about genetics and the use of high ranking bulls (64%) and believed there is a large economic gain in improving the genetic merit within herds (73%). Only 6% were regularly asked to provide advice on semen choices but 66% were interested in learning more about genetics. Interestingly the areas of genetics that were most appealing to this group were the opportunities to make a difference on farm (62%), science based nature (34%), new innovations such as genomics (41%), (ADHIS Good Bulls Guide Advisor Survey, 2011).

As an independent, profit focused tool, the Genetic Progress Report is appealing to this group of professionals. It provides a snapshot of the type of cow that has been bred on a particular farm and opens a discussion on whether it is best suited to the particular farming system. The Report checks that all key traits are moving in the right direction and supports the development of action plans to lift production, fertility and /or mastitis resistance.

For financiers and off farm investors, the Genetic Progress Report identifies the underlying ability of the herd to generate profit. The difference between a herd with an average BPI of $100 and a BPI of $0 is $100 profit/cow/year which is about 10% of Victorian Average Earnings Before Interest & Tax (Dairy Farm Monitor Project 2013/2014). When multiplied over a herd of 300 cows, a difference in annual profit of $30,000 is meaningful. The herds that receive the greatest acknowledgement are those where high genetic merit bulls have been carefully and consistently selected over time. These are also the herds with the greatest ability to generate profit for investors.

For all advisors, accessing good quality data boosts the ability to provide good advice. The Genetic Progress Report includes a quick audit of cow numbers with good data. Herds that practice sound data collection are rewarded with the most complete picture of their herd's genetic potential.

Conclusion

The Genetic Progress Report is a practical output of ADHIS and Dairy Australia's investment in genetic evaluation, genomic technology and genetics extension.

Its value in identifying success and opportunities for improvement is shared amongst farmers and their professional advisors.

For more information about Genetic Progress Reports, go to www.adhis.com.au or speak to your Herd Recording Centre.

The Future Is Now – Application Of Genomic Technologies In Commercial Dairy Production

Jason B. Osterstock, DVM, PhD
Zoetis Genetics, Kalamazoo, MI, USA

Dairy producers globally are being asked to accomplish an amazing feat – produce enough milk to meet skyrocketing demand… and do so with sustainability, efficiency, and affordability top of mind. The challenge is perhaps even greater considering what a commercial dairy really is. It has nothing to do with whether animals are registered with a breed society or not. Commercial dairy production is about producing safe food products in a profitable manner so as to support the relevant stakeholders – families, partners, or shareholders. To that end, the modern dairy producer must be resourceful , ambitious, and willing to consider how new things might help them achieve these lofty goals.

Recent technological advances in genomic technologies have introduced yet another tool for the dairy producer to consider as a complement to existing production practices. With the sequencing of the bovine genome (1) and the subsequent development of commercial translations of the underlying science, cattle producers have been able to achieve unparalleled genetic improvement in a very short period of time. In the US, the generation interval for Holstein bulls has been cut in half (2). Importantly, the technology has proven to have broad applicability in all facets of dairy production from the most elite of family run seedstock operations to the largest corporate dairies.

Basics of Genomic Selection

The principal benefit of genetic testing in dairy cattle is increased reliability of resulting predictions of genetic merit relative to traditional methods of evaluation. This is derived through genomic verification of pedigree and knowledge of the effects of individual genetic markers on predicted performance. Most of the major genetic evaluations around the world have been adapted to accommodate genomic data, the largest of which is the US dairy genetic evaluation managed by the Council on Dairy Cattle Breeding (CDCB) with more than 700,000 genotypes recorded in Holsteins, 95,000 genotypes recorded in Jerseys, and almost 18,000 genotypes recorded in Brown Swiss (3).

Dairy genetic evaluations that incorporate genomic information do so in a way that complements other sources of information including pedigree, performance, and progeny data. In this way, genomic technologies do not replace traditional evaluation methods, but instead apply another layer of data to our understanding of the genetic potential of animals in the herd, or about to enter the herd. This additional information allows us to make more effective decisions about how best to manage genetic potential, resulting in accelerated genetic progress, improved performance, and improved profitability.

In Australia, genetic evaluations of dairy cattle are managed by the Australian Dairy Herd Improvement Scheme (ADHIS) in collaboration with the breed societies and herd improvement companies. For those animals with genotypes available for consideration in the evaluation, genomic data is submitted to ADHIS by the genetic testing laboratory. In early 2015, Zoetis will introduce a genetic test designed to support genomic evaluations of Holstein and Jersey cattle in Australia.

The process by which genomic predictions are derived is quite complex, in large part because we are seeking to understand something that is inherently complex. For the purposes of this discussion, we will keep it relatively simple. There are four potential sources of information that may contribute to our ability to predict the genetic merit of an individual animal; pedigree, performance, progeny performance, and genomic information.

Pedigree data allows one to estimate genetic potential based on available estimates of genetic merit in the sire and dam. There are four potential weaknesses to relying on pedigree data alone. First, it assumes we have pedigree information which is not always the case, particularly in herds with cattle that have not been registered with a breed society, those that use natural service sires, and large operations where many calves can be born in a short time frame. Second, it assumes we know the genetic merit of the sire and dam. We often encounter missing data here as well, particularly on the dam side of the pedigree and in herds using natural service sires that have not been registered.

The third challenge is that in order for pedigree information to be useful, it needs to be correct. In 2013, more than 50,000 of the animals submitted to the United States Department of Agriculture (USDA) – Council on Dairy Cattle Breeding (CDCB) dairy genetic evaluation with genomic data were determined to have an incorrect or missing sire (4). If the pedigree is recorded incorrectly, then pedigree estimates are quite limited. Finally, we know that even though we may have a good idea of the genetic merit of parents, sometimes offspring over-perform or underperform relative to expectation. On average and with sufficient numbers of progeny, the progeny of a given sire and dam will perform at or near the average of the parents. However, some animals get more or less than their fair share of the available gene pool. This is a significant part of the limitations of using estimates of genetic potential derived from pedigree data alone.

Performance data of animals and their progeny are very important contributors to estimates of genetic merit and really reflect the gold standard for establishing the genetic potential of cattle. Historically, this is what has driven the proofs that we have used in AI sires and bull dams. By quantifying the actual performance levels for traits evaluated, we can gain a much better appreciation for the genetic potential an individual animal possesses or has transmitted to their progeny. The downside to this data, particularly in females, is really the time required to obtain it. By the time we have sufficient progeny data in a typical dairy cow, for example, she is likely long gone, if she had enough progeny to do so at all. Effectively, this data doesn't become available until it is too late to make any meaningful selection decisions.

Genomic information is well suited to help complement these other sources of information by filling the gaps noted. We can use genetic markers to verify assigned parentage or even discover missing parents. We can also use genomic data to more accurately predict genetic potential in animals that lack performance or progeny data thus enabling selection decisions much earlier in life. The effects of individual genetic markers are estimated from a reference population and then used to estimate a genomic breeding value using complex, but well established, statistical methods. The resulting genomic estimate is then blended with available pedigree, performance, and progeny data, where available, to derive a final summary estimate of genetic merit. Genotypes provide insight into the genetic material that was inherited and from whom, providing very specific information about the genetic potential of an individual animal.

As there are several, very different sources of information contributing to our estimates of genetic potential, we need some way of quantifying how much we actually know based on all the available data. In dairy cattle, we use the term reliability to describe how much we know and therefore how confident we are in the information. Reliability is actually a statistical parameter estimated from the correlation between the prediction and the animal's true, but unknown, genetic merit. It varies from 0 to 1 with higher values reflecting animals for which we have a lot of information, generally only achieved in AI sires with thousands of progeny.

The important thing to understand about reliability is the practical implications. When making genetic selection decisions, we have to rank or group animals for an outcome we can't see using our best available predictions of that outcome. If we have no information, we can't rank or group the animals for the desired outcome. That's like having a reliability of 0. As we acquire additional sources of information, we can begin to rank or group the animals. If we rank or group the animals in a way that closely matches that outcome of interest (which we still can't see) then our strategies and decisions will be quite effective. Predictions with greater reliability rank animals more closely to that outcome of interest, resulting in more effective selection decisions and accelerated genetic progress.

Despite all of the complexities around how genetic predictions are derived and how the accuracy of the respective types of predictions might be estimated, the application can be quite simple. In fact, there are only 3 possible decisions that can be made that impact genetic improvement.

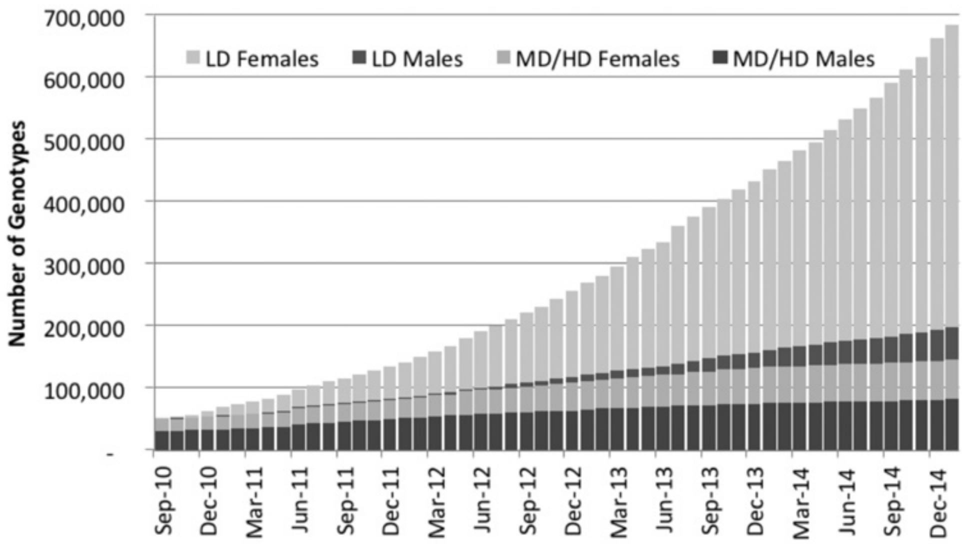
- *Do I want this animal?* – This applies to selection of home-raised replacements, purchase of animals from other herds, or the purchase of semen from a particular bull. The question here is whether we want that individual animal's genetics to contribute in any way to herd performance and profitability.
- *How many progeny do I want from this animal?* – This question can have many answers, but simply put, they are many, some, or none. The answer to this question influences whether we might consider a female as a donor in an MOET or IVF program, how we might allocate sexed semen, or perhaps how we might allocate beef semen should that be part of the herd's management strategy.
- *Who should I mate this animal to?* – This question is really about planning for the next generation. Each animal has strengths and weaknesses relative to the specific breeding objectives of the dairy. Preferentially choosing mates that accentuate strengths and help correct weaknesses is an important component of the use of genomic data. In addition, mating strategies can help producers breed around deleterious recessive conditions (e.g., fertility haplotypes), prioritize unique genetic composition (e.g., horned/polled), and proactively manage inbreeding.

Given these choices, we next need to consider the basic strategy. At the risk of stating the obvious, we want more of the best, more progeny from the best, and we want everyone mated up correctly. Being able to execute this now depends upon our ability to define who the best are which is a ranking / grouping exercise. As described previously, reliability has a significant impact on our ability to rank animals correctly and the use of higher reliability predictions, such as genomic Australian Breeding Values (ABV(g)), provides significant benefit. When done correctly, the result of this genomically-enabled decision making is accelerated genetic progress. The animals destined for production, in this generation and the next, possess greater average genetic merit than would have been achieved otherwise using traditional methods.

Observations from Unites States

Zoetis has been working with dairy producers in the US to implement genomic technologies since 2010. During this period, there has been a significant increase in the number of genotyped animals in the USDA-CDCB dairy genetic evaluation (5). The majority of that increase has been in low density genotyping of Holstein females (Figure 1). This is in large part due to the economic value of genetic testing to the commercial dairy producer through improved inventory management and accelerated genetic progress.

Figure 1: Cumulative number of genotyped Holstein animals in the USDA-CDCB dairy genetic evaluation by sex and genotype density (5). Genotype densities – LD represents all genotypes with <50,000 markers; MD/HD represents all genotypes with >= 50,000 markers.



One of the benefits of the number of dairy producers Zoetis has worked with, and the length of time we have been supporting genetic testing services, is that we have been able to document the genetic progress and see the financial impacts to the dairy. This data is quite powerful in helping producers appreciate the real impact that genetic improvement has on their dairies. For example, one dairy in the Northeast US began testing in 2011 with the primary strategy of selecting heifers as replacements (6). They had more heifers available than needed and, given the cost to raise heifers which is currently over $2,000 USD, they decided that they were going to cull the excess using Net Merit (NM$), an economic selection index developed by USDA (7), as the selection criteria. Over the course of the next 3 years, this dairy continued to test heifers, culling with the same selection intensity – approximately 20% of available heifers were not retained as replacements – and tracking their progress.

Several trends emerged. First, this dairy made significant gains in the average genetic merit of the female progeny they selected as replacements. In 2011, the average NM$ GPTA of retained and culled heifers were 357 and 291, respectively.[1] In 2013, the averages of retained and culled were 476 and 366, respectively. They were now culling heifers that just 2 years prior would have been above the average of those that they retained. Further, their rate of genetic progress was now more than 2 times greater than the breed average.

This herd was also able to clearly demonstrate how accurately the predictions reflect future performance. Daughter pregnancy rate (DPR) is the primary fertility metric in the USDA-CDCB dairy genetic evaluation and is based upon days open. The heritability of this trait is quite low (4%), which has negative impacts on the expected reliability of traditional and genomic predictions, as well as the expected genetic gains over time. However, this trait is extremely important economically to the dairy industry and should be considered in genetic improvement plans. Using production data from this herd, we compared the 21-day pregnancy rate (PR) after a 21 day voluntary waiting period (VWP) observed from June 2013 through April 2014 between females with a DPR value <1 (n=732) and those with a DPR >=1 (n=527). The PR was 21% and 33% in the groups predicted to have low and high fertility respectively. It is remarkable to think that there are groups with reproductive performance that differs by more than 10 percentage points in PR, and that they can be effectively identified as calves. Demonstrating the accuracy of genomic data for traits as impactful as fertility has been extremely valuable in helping dairy producers appreciate the potential benefits of this technology.

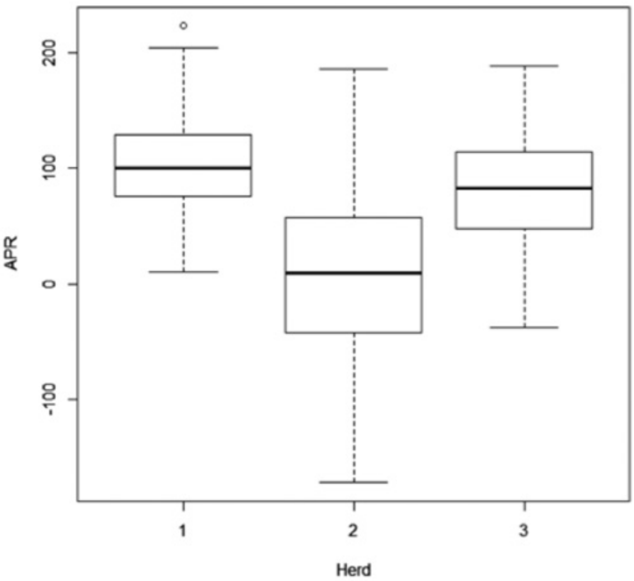
1 *These values are based on the 2010 base and do not reflect changes implemented in December 2014.*

Observations from Australia

Zoetis has worked with ADHIS, Holstein Australia, and dairy producers to test selected populations of young females to better characterize the benefits of genomic technologies in commercial settings. This data can be very useful in understanding the genetic variation within and among herds, as well as the potential impacts of selection decisions executed on the basis of genomic data.

For example, consider Australian Breeding Values (ABV) for the Australian Profit Ranking (APR) derived from genomic data. Evaluation of differences in APR, a selection index designed to describe differences in profitability between animals (8), helps to characterize the economic impacts of selection. Zoetis worked with 3 dairy producers to conduct genetic testing on Holstein heifers in 2014 (6). The distribution of ABV for APR are illustrated in Figure 2. The degree of variation within herd will depend upon each herd's selection objectives, and the diversity of genetic merit in parents within the herd.

Figure 2: Distribution of ABV for APR among heifers tested within 3 commercial herds. Plots illustrate the mean (horizontal line), 1.5 times the inter-quartile range (box), and range (whiskers) observed.

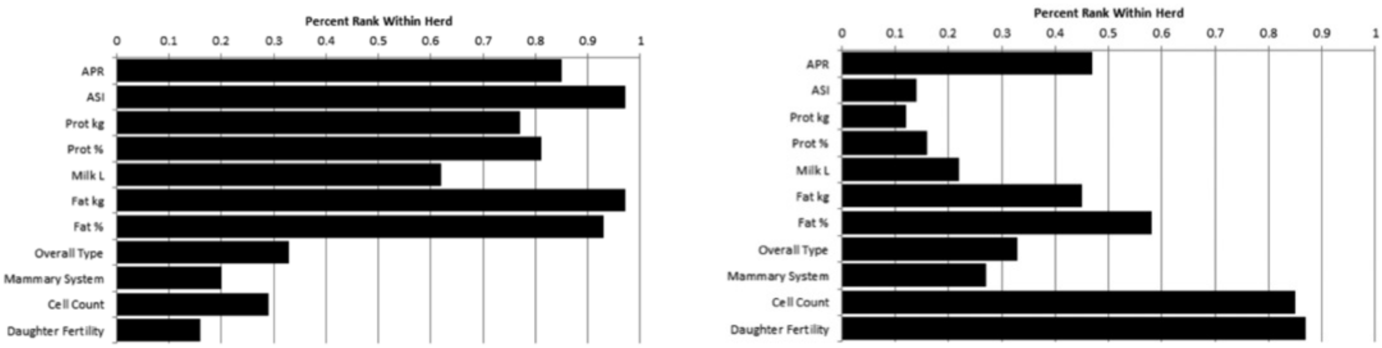


In this example, we can see that Herd 2 has a comparatively large range of APR values within this group of tested heifers. The range observed here (-172 to 186) indicates that there is more than $350 difference in predicted profit between the best and worst animals in this cohort attributed to genetic effects. Consider also how these observed differences might be exploited in a genetic improvement plan. If perhaps the producer has the flexibility to keep just the top 80% of heifers as replacements, by virtue of selecting based on APR, the average of the selected population would increase from an APR of 7 to an APR of 30. Given that the industry rate of genetic progress for APR is estimated to be $8.55 per year (9), this is a meaningful change.

The genomic results can also be quite useful in informing mating decisions as evidenced in Figures 3a and 3b. These two females are from the same birth cohort within Herd 1 and have been characterized relative to their within-herd rank for selected traits. These graphs help to visualize where their respective genetic strengths and weaknesses are compared to the rest of the herd. In this instance, both heifers would have respectable APR values that would likely support their selection as replacement females using that selection objective. However, there is clearly a difference between the two heifers – one demonstrating considerable strength in production with weakness in type and fertility, whereas the other has much higher within herd ranks for cell count and fertility but clear weakness in production traits. When considering the decisions that now influence the next generation, there are clear opportunities to preferentially mate these females to bulls that complement their strengths while addressing the weaknesses revealed by the genetic evaluation.

Importantly, the predictions used to characterize the differences within and among herds, and to inform the selection decisions hypothesized here, benefit from the increase in reliability associated with the use of genomic data within the evaluation. The average APR reliability across these herds was 58.7 (range 45 to 64). Effectively, the reliability of these predictions have doubled over what would have been achieved using traditional pedigree estimates. The result is that any decision made on the basis of this information would yield more effective results, greater genetic progress, and increased profitability.

Figure 3: Within-herd ranks for selected traits in 2 Holstein females from the same birth cohort in Herd 1 demonstrating differences in genetic merit that may inform strategic mating decisions (6).



Conclusions

The use of genomic technologies in the dairy industry continues to expand globally. Importantly, the use of these technologies extend beyond AI sires and bull dams, and we are seeing rapid adoption of these tests in commercial dairies as part of routine heifer development. That shift is driven by the economic benefits associated with the more informed selection decisions afforded by the higher reliability genomic predictions.

In our experience, the key to successful implementation has been to rely on the sophistication of the technology while not allowing that complexity to impact application. By focusing on really just a handful of basic decisions that influence genetic progress, relying on the available selection indexes to drive balanced selection, and avoiding complicated schemes that cannot be integrated into routine production practices, dairy producers can ensure they capitalize on the benefits of genomic technologies.

Literature Cited

Bovine Genome Sequencing and Analysis Consortium. 2009. The genome sequence of taurine cattle: a window to ruminant biology and evolution. Science, pp. 324(5926):522-8.

Wiggans, G. 2013. Current status of genomic evaluation for US dairy cattle. In: China Emerging Markets Program Seminar, Washington, DC, USA. http://aipl.arsusda.gov/publish/presentations/MISC13/China_2013_Wiggans.ppt Accessed: January 15, 2015.

Council on Dairy Cattle Breeding. 2015. Genotype counts by chip type, breed code, and sex code. https://www.cdcb.us/Genotype/cur_freq.html Accessed: January 15, 2015.

VanRaden, P. 2014. Impacts of genomics on genetic improvement. In: Advancing Dairy Cattle Genetics: Genomics and Beyond, Phoenix, AZ, USA, February 2014. http://aipl.arsusda.gov/publish/presentations/MISC14/Genomics_Workshop_vanraden.pptx Accessed: January 15, 2015.

Council on Dairy Cattle Breeding. Genotypes included in evaluations by breed, chip density, presence of phenotypes (old vs. young), and evaluation year-month (cumulative). https://www.cdcb.us/Genotype/cur_density.html Accessed: January 15, 2015.

Zoetis Genetics. 2015. Data on File. Zoetis, Kalamazoo, MI, USA.

VanRaden, P.M. and Cole, J.B. Net merit as a measure of lifetime profit: 2014 revision. http://aipl.arsusda.gov/reference/nmcalc-2014.htm Accessed: January 15, 2015.

Australian Dairy Herd Improvement Scheme. 2010. Technote No. 13 - Australian Profit Ranking (APR): Updated Formula. http://www.adhis.com.au/v2/sitev2.nsf/(ContentByKey)/ExtensionTechnotesandfactsheets?open Accessed: January 23, 2015.

Australian Dairy Herd Improvement Scheme. 2013. Australian Dairy Herd Improvement Report 2013. http://www.adhis.com.au/v2/downv2.nsf/0/0af545034ac09bf7ca2576aa001bb67a?open Accessed: January 23, 2015.

Development of the WVC high fertility cow selector

Dr Jon Kelly
Director and senior veterinarian, Warrnambool Veterinary Clinic

The decline in dairy cow reproductive performance in Australia over the last 20 years has been well documented, with significant falls in conception and submission rates across all breeds.

However, herd reproductive results are reported as averages across the whole herd, a mathematical mean of all cows and their relative prevalence's.

By recording and analysing the key factors that affect dairy cow reproductive performance, things like age, calving dates, insemination history and disease events, the high reproductively performing cows are able to be identified from the previous mating period. Using these identified groups for a particular herd, not industry averages, allows more accurate estimation of high fertility cows prior to the next joining. By selecting the cows most likely to conceive, an extra level of selection can be applied other than for breeding purposes (e.g type, inbreeding etc). An example of this would be high value semen, where an outcome needs to be cost effective, or sexed semen, where fertility is reduced compared to conventional semen.

Warrnambool Veterinary Clinic (WVC) has developed a tool within Dairy Data (a herd management computer program) that allows selection of cows based on criteria that can be manipulated for individual farms. The tool relies on accurate age, calving dates, insemination records and pregnancy test results. Reproductive events that affect fertility, for example difficult calving, metritis, retained membranes can also be included in the selection tool. The tool "rewards" farmers for recording health events that occur, as the more details are entered, the more accurate the tool is when selecting for high fertile cows.

Age

The age of a cow at joining is one of the key criteria for selection. Dairy Data is able to analyse each age group's reproductive performance up to 8 years old. Retrospective analysis of herd data will show which age groups where most fertile in the previous mating period.

In most herds, providing the heifers have achieved industry targets at first calving for body weight, the younger cows are the most fertile, declining rapidly when cows reach 7 year old, or 5th calvers.

Reproductive Indices

Age	Cows	21 day Submission Rate	Calving to 1st service	Calving to Conception	1st Serv. AI Conc. Rate	Overall AI Conc. Rate	6 Week In Calf Rate	21 Week Empty Rate
Targets:		> 90%	~ 75 days	83 days	> 55%	> 60%	> 75%	< 10%
Y	205	51%			36%	37%	91%	3%
2	142	86%	79	94	54%	50%	69%	11%
3	66	95%	67	85	57%	52%	69%	6%
4	85	89%	66	85	47%	50%	69%	10%
5	80	91%	71	94	43%	44%	63%	11%
6	45	95%	60	84	31%	35%	57%	20%
7	33	90%	64	97	37%	36%	48%	15%
8+	29	79%	66	91	40%	39%	51%	20%
Total	480	89%	70	90	47%	46%	65%	12%

* Y = Yearling (any animal that has never calved). Totals do not include Yearlings.

Increasing age

decreasing conception rate

Calving date relative to joining (Days In Milk)

In seasonal calving herds, the days in milk (DIM) relative to mating start date is the most significant predictor of fertility. The longer a cow is calved prior to joining, the more fertile she will be. This rule does not necessarily follow in split calving herds and needs a more detailed analysis.

Dairy data is able to analyse the cows by age group and DIM, broken up into months prior to joining.

Conception Rates & 6 Week In Calf Rates

Most fertile cows

Age	Cows	First Service Conception Rates for cows calved ... < 30 days	30-60 days	61+ Days	6 Week In Calf Rates for cows that calved ... < 30 days	30-60 days	61+ Days
Targets:							
2	142	30%	41%	56%	60%	51%	75%
3	66	50%	42%	66%	50%	57%	79%
4	85	25%	50%	51%	66%	62%	75%
5	80	28%	50%	40%	28%	65%	68%
6	45	20%	27%	41%	60%	55%	58%
7	33	0%	41%	41%	0%	47%	66%
8+	29	25%	26%	60%	50%	40%	70%
Total	480	26%	41%	52%	50%	55%	73%

**rates are for cows calved more than the given number of days at Mating Start Date.

Increasing age

Increasing DIM

Previous Insemination history

The insemination history of a cow can also be used to identify those cows that "get in calf to the first straw". Obviously, the older and more joining periods a cow has, the more accurate this will be, however young cows can be analysed.

Dairy Data displays a successful insemination in green font and an unsuccessful insemination in black font. The selector tool is able to select these cows automatically.

Example of a high fertility 4th calver insemination history:

[F4] - Events | [F5] - Heats / Matings | [F6] - Calvings | [F7] - Herd Tests | Annual Figures | ABVs | Production Graph | Cell Count Graph |

Cow	Date	Sire	Technician	Sexed	Split	Result	Due
1286	24/06/13	DODGE				P	3/04/14
1286	20/06/12	MCCORMICK				P	30/03/13
1286	1/07/11	BLUESKY	noel			P	9/04/12
1286	16/06/10	FOCUS				P	26/03/11

Example of a low fertility 4th calver insemination history:

[F4] - Events | [F5] - Heats / Matings | [F6] - Calvings | [F7] - Herd Tests | Annual Figures | ABVs | Production Graph | Cell Count Graph |

Cow	Date	Sire	Technician	Sexed	Split	Result	Due
1128	7/10/13	ZUMA					
1128	15/09/13	CASUAL					
1128	25/08/13	FRIDAY					
1128	11/07/13	GANGSTER					
1128	18/08/12	SENTINAL				P	28/05/13
1128	27/07/12	BLUESKY					
1128	18/07/12	BLUESKY					
1128	7/07/12	BOSSMORES					
1128	21/06/12	BOSSMORES					
1128	22/07/11	JETTIE	noel				

Health events

Health events and disease, their timing relative to joining and their impact on subsequent fertility has been widely studied. The major causes of decreased fertility have been accurately identified and include

- events related to the reproductive tract (e.g retained membranes, metritis, endometritis) (dirty cows))
- difficult calving
- twins
- Mastitis
- metabolic disease at calving (milk fever or pregnancy toxaemia)
- concurrent illness at joining.

These events, if entered and recorded in Dairy Data, can all be used as selection criteria.

Using the WVC high fertility cow selector on farm

All herds, no matter where they rank in the dairy industry for reproductive performance, have individuals within that particular herd that out perform their herd mates.

When a list of potential high fertility cows is compiled using the selector, the next most important step for cow selection occurs at the time of AI, **and is the most crucial for success. The cow must be on heat!** As Fixed Time Artificial Insemination(FTAI) programs have become more widely used, if 2 identical cows for all the above mentioned criteria are presented, the cow inseminated on heat is more likely to have a successful conception compared to the cow inseminated in a FTAI program.

The following reproductive report is an example of the results that can be achieved using the WVC high fertility cow selector. This herd used the selector to maximise the results achieved using sexed frozen semen in the cow herd. Sexed frozen semen is recognised as having decreased fertility compared to conventional non sexed frozen semen. The herd totalled 480 cows, with 84 cows on heat, in the first round of mating, that were selected as high fertility cows. From the report it can be seen that more younger cows than older were selected. An average conception rate result of 42%, in milking cows for frozen semen, is a very satisfactory result.

Reproductive Indices

Age	Cows	21 day Submission Rate	Calving to 1st service	Calving to Conception	1st Serv. AI Conc. Rate	Overall AI Conc. Rate	6 Week In Calf Rate	21 Week Empty Rate
Targets:		*> 90%*	*~ 75 days*	*83 days*	*> 55%*	*> 60%*	*> 75%*	*< 10%*
Y	20	100%			40%	60%	90%	10%
2	41	100%	81	110	43%	46%	63%	4%
3	27	100%	75	107	37%	43%	55%	11%
4	12	100%	79	117	50%	47%	58%	8%
5	3	100%	77	122	33%	42%	66%	
6	0							
7	1	100%	60	60	100%	100%	100%	
8+	0							
Total	84	100%	79	110	42%	46%	60%	7%

Conception rates achieved to frozen sexed semen in milking cows “selected” from a herd of 480 cows.

Australia's New Dairy Breeding Indices

Dr Jennie Pryce (EcoDev)
Senior Research Scientist EcoDev and Principal Research Fellow La Trobe University
Agribio, Centre for Agribioscience, 5 Ring Road, La Trobe University,
Bundoora, Victoria 3083

Michelle Axford (ADHIS)
Extension and Education Manager, ADHIS, Melbourne

Introduction

The National Breeding Objective (NBO) aims to deliver herds that the Australian dairy industry needs for the future. While Australian Breeding Values (ABVs) express a bull or cow's genetic potential for a single trait such as fertility or protein kilograms, most farmers want to improve more than one trait in their herd. From an Australia-wide perspective, the NBO aims to support genetic selection pressure for an agreed group of desirable traits, providing direction for both bull and cow breeding across the country. Australia's national breeding objective is to increase net farm profit. Over time, the NBO must evolve in response to new knowledge and the demands of dairy businesses. To translate a National Breeding Objective into a practical breeding tool, an index is developed that applies weights to individual ABVs which best match the Objective. The index is used to rank bulls, cows and herds so that superior genetics can be identified and used in breeding programs. As the Objective evolves, so does the index.

Selection experiments

Most, if not all, traits are heritable to some degree. Some traits, such as health and fertility traits have relatively low heritability estimates (<5%) (Egger-Danner et al., 2014), while others, such as milk production, stature and liveweight have higher heritabilities. However, the coefficient of genetic variation appears to be reasonably consistent between traits (Berry et al., 2014). Meaning that even for traits with low heritability there is sufficient genetic variation to make selection feasible.

Demonstrating genetic improvement is important in improving understanding. There are numerous divergent selection lines ranging from maize to mice that show this. In dairy cattle, there have been a few notable experiments that have demonstrated the effect of genetic selection.

One example is Scotland's Rural University College long-running experiment (established in 1973) and currently located in Dumfries, Scotland. Here a genetic selection and control line have been compared at various time-points on two different diets. The control line is UK average for genetic merit of fat plus protein, while the selection line are sired by bulls with the highest breeding values for fat plus protein. The selection criterion has remained the same throughout the experiment.

Table 1. Comparison of animals selected for high fat and protein yield versus control group of UK average genetic merit (Pryce et al., 1999).

Trait	Selection	Control	P<
Oestrus not observed	0.16	0.11	0.001
Conception to 1st service	0.39	0.45	0.05
Days to first heat	53	42	0.01
Calving interval	395	384	0.001
Days Open	124	107	0.001
Days to first service	77	72	0.001

The difference between the 2 lines for measures of fertility is shown in Table 1 (Pryce et al., 1999). The selection line has increased by +3.34kg/year in genetic merit for yield of fat plus protein, while the control line has remained almost flat (Pollott and Coffey, 2010). So, the results clearly show that although single trait selection has been spectacularly successful for milk production traits, there has been a trade-off in fertility, which has deteriorated and is significantly poorer in the selection line compared to the control line. Of course, this is because the selection criterion for the herd is narrow, and does not include traits other than production, and because there is a negative correlation between fertility and yield (Berry et al., 2014). Improving fertility is more difficult to achieve, however, there is ample evidence that selection is possible. For example, in Australia, (Morton, 2011) showed that cows with higher breeding values for fertility also, as expected, had higher 6 week in-calf-rates.

In countries where pasture is a key component of the diet, and there is doubt about the merit of using bulls that were performance tested in a total mixed ration environment, strain trials have been used to demonstrate both the importance of environment interactions with genetic merit, and the economic value of high genetic merit cows (high genetic merit for a profit metric that takes into account the pasture based system). In the New Zealand strain trials, production and fertility of three strains of Holstein-Friesian cattle were compared. The strains were New Zealand 1970s genetics, New Zealand 1990s genetics, (that is twenty years of genetic improvement), and 1990s North American ancestry genetics (Macdonald et al., 2008). Between 45 and 60 cows were bred from bulls of each strain, and then their lactation yields, fertility and body condition scores were compared over three years (total length of experiment including breeding: 6 years). The study concluded that under grazing conditions typical for the New Zealand dairy industry, the New Zealand 1990s strain gave the highest yields and highest fertility.

At a similar time to the NZ trial, a Holstein-Friesian (HF) strain trial was conducted at the Moorepark research station in Ireland (Horan et al., 2005). Three strains of HF were compared on 3 pasture-based feed systems over 3 consecutive years. The three strains of HF were: high production North American, high durability North American, and New Zealand. There were three feeding systems, an abundant pasture system, a high level of concentrate system, and a high stocking rate pasture based system (Horan et al., 2005). The results showed that the high production North American strain had the highest production, while the New Zealand strain had the lowest body weight and highest body condition score. There was a strain x feeding system interaction for yield of milk, fat, and protein. There was a considerable difference in reproductive performance between the strains - the high durability strain (62%) and NZ (57%) strains had a higher conception rate to first AI than the high production North American strain (40%), ($P < 0.05$) (Horan et al. 2005). An economic comparison of the divergent strains in the different feeding systems was also conducted (McCarthy et al., 2007). The analysis showed that, across arrange of milk price systems, the NZ strain in the pasture based and high stocking rate feed systems returned the highest profitability. Interestingly, the results demonstrated that that exclusive genetic selection for increased milk production results in reduced farm profitability because the productivity gains achieved are outweighed by associated increases in reproductive wastage costs in a pasture-based system (McCarthy et al. 2007). The authors concluded their results "reinforced the economic value of genetic improvement based on a selection index encompassing traits of economic significance pertinent to the production environment" (McCarthy et al. 2007).

Australia's National Breeding Objective

Although, these experiments are useful in describing the consequences of single-trait selection, there are clearly more traits that affect profitability. The aim of a selection index is to combine all the traits that affect profit in an economically optimal way. In Australia, the National Breeding Objective (NBO) has been the Australian Profit Ranking (APR) index which included Australian breeding values (ABVs) for milk, fat, protein, somatic cell count, fertility, longevity, liveweight, temperament and milking speed each weighted by their respective economic values.

As time goes on, we continue to develop breeding values for more traits that contribute to net farm profit. It makes good financial sense to ensure that selection for all of these traits is carried out concurrently and in an objective way. Balancing selection on each trait in such a way that maximises profit is the aim of a selection index. Selection index theory (Hazel, 1943) was developed to combine vectors of economic values with matrices of genetic (co)variances to derive an optimal vector of index weights which can be applied to estimated breeding values to produce a single index value for each animal evaluated.

One common misconception is that by adding more and more traits to an index, selection is somehow diluted. This is true if the traits do not contribute anything economically, however if each trait has monetary value, then the net result of multi-trait selection is reduced gain in each component trait, but greater gain in the overall breeding objective. In fact, many countries now have more than 6 trait categories (milk production, type, longevity, udder health, fertility, other) in their national selection objectives (Egger-Danner et al., 2014).

Review process

The Australian Dairy Herd Improvement Scheme (ADHIS) has a policy to review the NBO and the index formulated to meet this objective (currently the Australian Profit Ranking - APR) on a regular basis. The last NBO review took place in 2010. Key outcomes from this review were to increase the emphasis on survival (longevity), fertility and mastitis. ADHIS commenced the current review in late 2013. The purpose of the review that took place in 2014 was: a) to ensure the NBO which is aimed at driving on-farm profit still remains relevant, and b) to develop an index (or indices) based on strong scientific principles which are in line with farmer preferences and meet the agreed NBO. In planning for the current review, greater focus was placed on obtaining direct input from farmers and the wider herd improvement industry to support the standard scientific review of economic inputs and genetic parameters used in the construction of an updated index.

A National Breeding Objective task force was set up to review outputs during the review process, to provide direction and to ensure wider input from farmers and industry was maintained throughout the review. The National Breeding Objective review is on target to deliver an updated set of new indices in April 2015. This paper describes:

1. The farmer engagement and survey process – what do farmers want to select for,
2. The research process in calculating economic values and deriving selection indices
3. Details of the endorsed index.

In 2014, dairy farmers and industry have been asked to think about which traits are needed for the next generation of our herd. Dairy farmers in all regions have been talking about breeding preferences and having a direct say in answering the question 'which cows best meet the needs of Australian 'dairyfarmers into the future'. the NBO task force has carefully listened to farmers' breeding preferences to develop different indices, and to then assess the impact from use of these indices over the next 10-15 years of breeding cows.

Direct Farmer Feedback

There have been two large scale activities to hear directly from farmers. The information was gathered from Australia's longest farmwalk and the National Breeding Objective survey. Both have had a direct impact on developing potential future indices by better understanding the priority farmers place on traits and the breeding preferences of groups of farmers.

Australia's Longest Farmwalk

Australia's longest farmwalk was a series of 26 events on 46 farms in every dairy region. In total, the process involved around 600 participants. It provided an opportunity to share observations about cows and generate ideas about how herds could be improved to meet our future needs. Farmwalk discussions varied widely depending on the region and the views of participants but here are some of the main points:

- Profit remains the main focus for genetic improvement.
- Fertility is a high priority.
- Farmers want a robust functional cow that can survive and thrive in the herd under a variety of conditions.
- Cows that are resilient and flexible to respond to changing dairying environments are desirable (at least in pasture based systems).
- Some traits have an 'ideal' zone. too much milk or too little milk are undesirable. Teats that were too short or too long are undesirable. Extreme overall type and poor overall type are undesirable.
- Our breeding priorities can be different – even between neighbours. For example some aim to maximise milksolids per kilogram of cow liveweight or breeding an easy-care animal while others focus on structural soundness through type.
- Farmers are keenly interested in better understanding the Australian index.

National Breeding Objective survey

On behalf of the NBO task force, ADHIS conducted a large scale on-line survey of breeding trait preferences through March and April 2014. The survey collected information about farm demographics, attitudes and behaviours about genetic decisions from 551 farmers and 15 service providers. a novel survey technique known as 1000minds^{tm} was used to determine trait preferences.

The results provided meaningful insights into trait preferences as well as attitudes and behaviours related to genetic choices. Participants were broadly representative of the Australian industry in terms of region, breed, calving pattern, feed system and herd size.

Trait Preferences

The survey revealed some very interesting results that provide a solid foundation from which to evolve the national Breeding objective. Highlights from the survey include:

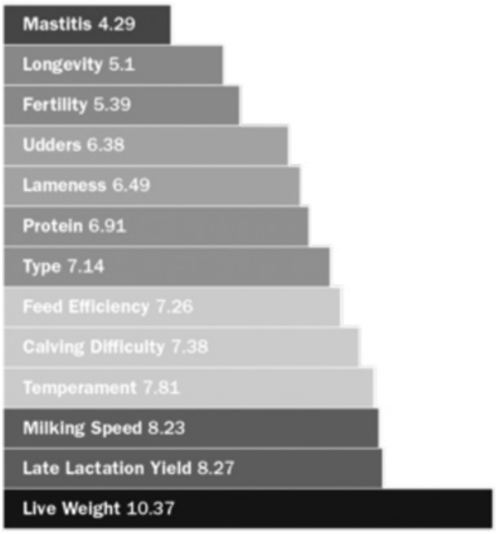
- There is a continuum of breeding preferences rather than distinct and separate groups of farmers.
- Differences in preferences are only moderately linked to production system drivers such as calving pattern and feeding system. Stronger differences in preferences are observed between farmers that register cows with a breed society and those that don't.
- Improved udders and type were important to a broad section of farmers, regardless of the proportion of the herd registered with a breed society.

Farmers had stronger preferences for mastitis, longevity and fertility over and above their purely economic value as illustrated in Figure 1. These results are similar to the general feedback collected through Australia's longest farmwalk. Interestingly, they are the same traits that received additional emphasis in the last NBO review of 2010 following industry consultation.

Mammary system is the highest ranked trait that is not directly included in the current index. Better udders are important to reduce mastitis and improve longevity and can also save time during the milking routine by having less cluster slippage. this feedback clearly indicated that poor udders are a real cost to farmers and that increased farm profits could be realized through improved udders.

Lameness followed closely behind udders. Currently, lameness does not have an ABV so it can't immediately be included in an index. However, lameness warrants further investigation based on the survey results and industry projects to address health traits, including lameness, have recently commenced with the aim of including lameness in a future index.

Figure 1: The order of breeding trait preferences over and above their purely economic value and average trait ranks



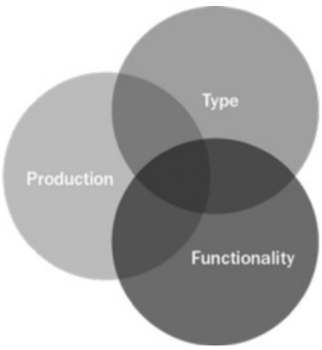
Cluster analysis

The purpose of cluster analysis is to look for similarities in breeding trait preferences. in general, there is a continuum of trait preferences rather than farmers forming distinct and different groupings. However, based on the top 7 traits of each respondent, researchers found three reasonably distinct clusters that can be loosely described as production focused, type focused and functionality focused. a similar number of farmers fall into each cluster. the clusters are not aligned to calving pattern or feeding system. for example, a farmer that calves seasonally could be found in any of the three cluster groups.

It is important to note that some trait preferences were similar across all clusters. for example, all clusters listed mastitis and fertility in their top four traits. Some of the differences in traits and attributes between clusters were:

- Production group – stronger preference for production and longevity. this group has proportionately more Jerseys, are less likely to register cows and are younger in age.
- Functionality group – stronger preference for mastitis and fertility. this group has proportionately more Holsteins, are more likely to register cows and have more full time staff.
- Type group – stronger preference for longevity, mastitis and udders. this group have more Holsteins, even more staff than the functionality group and bigger herds. This group gave higher scores to daughter appearance.

Figure 2: Three broad clusters of trait preferences were observed with mastitis and fertility being common top traits in each



Due to the level of similarity in trait rankings across all farmers and the uniform desire to increase fertility, survival and conformation (particularly mammary system) an updated index can be developed focused on achieving these outcomes. this index would for the most part meet the needs of the majority of farmers.

However the cluster analysis also shows differences in groups of farmers. these differences align to those seeking greater focus on type and those seeking greater focus on fertility/functionality. these philosophies were considered in the specific development of customised indices presented later in the paper.

Development of Economic values

Australia's National Breeding Objective has focused on profit for many years but the balance between generating increased returns from more production and lowering the cost of production has shifted over time. Feedback from the farmwalk suggests that profit is still the dominant focus and direction for breeding cows in Australia.

However, the range of traits and the relative importance of these traits differ from those applied in the Australian Profit Ranking. This suggests there is a need to reassess the economic values for traits.

To analyse the profit from each unit of genetic improvement, a bio-economic model was developed from which the values of each trait are generated. The model repeatedly answers the same question 'all things being equal, how much additional profit will this herd generate by increasing one unit of a particular trait?'. Clearly, a good understanding of economics, management practices and biology of the cow are all required for this model. the model used information collected from farmers, a range of industry, government and herd recording sources, scientific literature, farmers, milk processors, professionals working in the areas of statistics, genetics, nutrition, fertility, mastitis, stock sales and farm performance analysis.

From this analysis and Task Force discussion, new economic values for each trait were agreed.

New traits

New traits have been added and some traits have been re-arranged to ensure the final indices are in line with farmer preferences and that research outcomes are adopted. A new feed saved ABV will be introduced from April 2015 for Holsteins based on research in Australia and globally (Gonzalez-Recio et al., 2014, Pryce et al., 2014).

Given the same level of performance, some cows use feed more efficiently than others. This efficiency has a genetic component that can be selected for using a feed saved ABV. Feed saved is expressed as kilograms of feed saved per cow per year. Selecting animals with higher feed saved has a positive contribution towards profit and is included in all three indices.

For a number of years, several type ABVs have been used to predict survival – particularly in young animals. To better reflect the influence of type ABVs throughout an animal's life, overall type, pin set and udder depth have been separated from survival and will be included as stand-alone traits in the indices.

In addition, the trait of fore udder attachment is included in the TWI to add further weight to type to achieve specific and desired gains in this index.

The last of the new traits is residual survival. The trait of survival has been replaced with residual survival in all indices to ensure that the traits that contribute to survival are treated fairly and are not 'double counted'. Residual survival includes all the reasons why cows leave the herd that are not related to production, fertility, cell count or other traits that have their own economic values in the indices.

Over time, the traits that comprise an index have changed and will continue to change to meet the needs of farmers.

Australia's new selection indices

Direct farmer input and a review of economic trends of different farming systems were used to develop several profit-focused and desired gains indices. Compared to the APR, the indices:

- Increase the rate of improvement for cell count
- Increase the rate of improvement for fertility
- Increase the rate of improvement for survival
- Slow the rate of improvement for production
- Show more progress in type traits, including overall type, mammary system, udder depth
- Increase the rate of improvement for milking speed, likeability and temperament.

In addition to these changes, custom indices have been developed which change emphasis on either type or health traits.

Correlations are high between indices, although significant re-ranking of top bulls, cows and herds is expected.

In total 13 indices with multiple variations have been evaluated by the NBO industry task force. The task force reviewed the assumptions, economic values, impact on production, management and type traits and expected industry acceptance of each index. From the initial field, three indices have been agreed to that are in line with farmer preferences, recognise different breeding philosophies and are backed by science.

Table 2: Descriptions of three new breeding indices

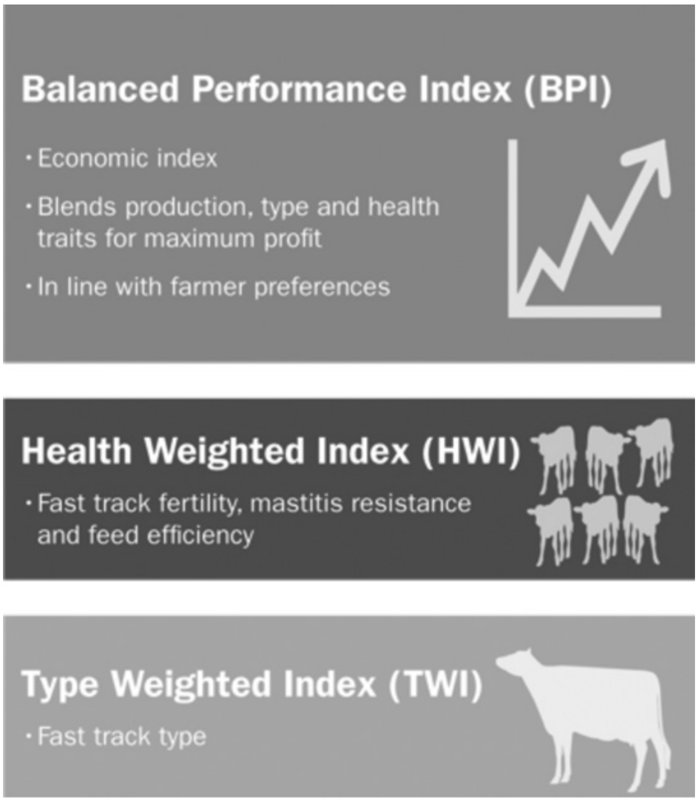
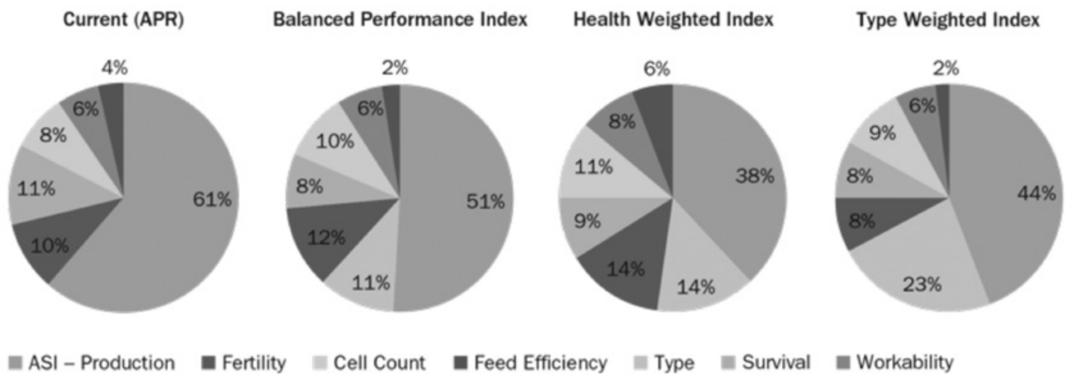


Figure 3: Percent emphasis on trait groups in 3 indices compared to current APR



The Impact of New Breeding Indices

The most important consideration when comparing indices is the outcome that is expected based on the Australian population of cows and the AI bulls used to produce the herd's next generation. The change in traits that is expected based on genetic selection for each index over ten years is illustrated in Figure 4.

Figure 4: Response to selection over 10 years for new breeding indices in trait standard deviation units (Holstein)

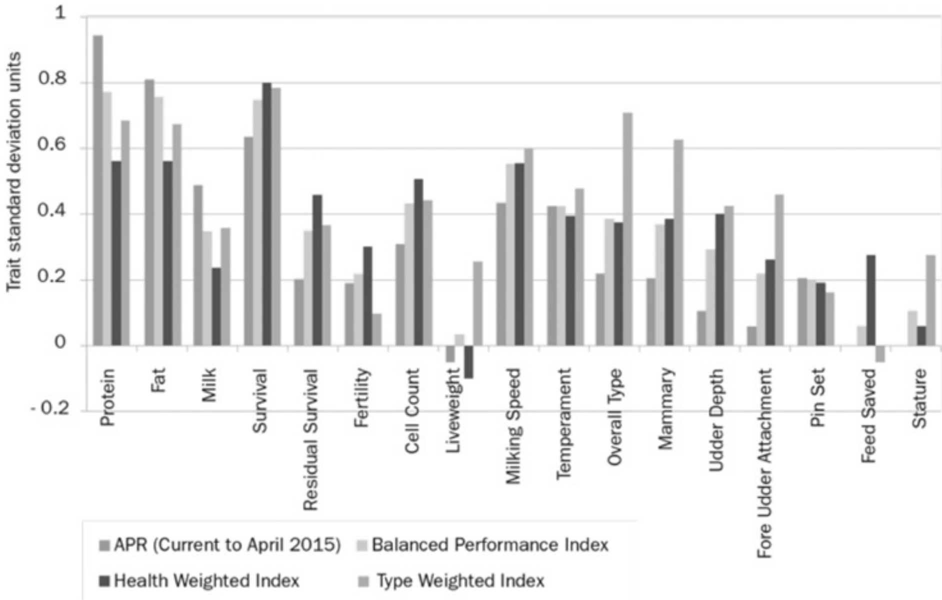


Figure 4 is useful to compare the amount and direction of progress when used to breed cows. Traits could improve, remain stable or decline.

Conclusion

The Balanced Performance Index (BPI) is Australia's new economic index and achieves profit through a balance of efficient production, health and type traits. It is in line with farmer preferences and backed by strong science. to support farmers with a desire to fast-track progress for health traits or type traits, two additional desired gains indices will also be released from April 2015.

The industry task force values the input from whole of industry to the National Breeding Objective review which has guided the development of new indices. The information collected through surveys, farmwalks and meetings has had a direct impact on how cows will be bred in Australia.

References

Berry, D., E. Wall, and J. Pryce. 2014. Genetics and genomics of reproductive performance in dairy and beef cattle. Animal : an international journal of animal bioscience:1-17.

Egger-Danner, C., J. Cole, J. Pryce, N. Gengler, B. Heringstad, A. Bradley, and K. Stock. 2014. Invited review: overview of new traits and phenotyping strategies in dairy cattle with a focus on functional traits. Animal : an international journal of animal bioscience:1-17.

Gonzalez-Recio, O., J. E. Pryce, M. Haile-Mariam, and B. J. Hayes. 2014. Incorporating heifer feed efficiency in the Australian selection index using genomic selection. J Dairy Sci.

Hazel, L. N. 1943. The genetic basis for constructing selection indexes. Genetics 28(6):476-490.

Horan, B., P. Dillon, P. Faverdin, L. Delaby, F. Buckley, and M. Rath. 2005. The interaction of strain of Holstein-Friesian cows and pasture-based feed systems on milk yield, body weight, and body condition score. Journal of dairy science 88(3):1231-1243.

Macdonald, K. A., G. A. Verkerk, B. S. Thorrold, J. E. Pryce, J. W. Penno, L. R. McNaughton, L. J. Burton, J. A. Lancaster, J. H. Williamson, and C. W. Holmes. 2008. A comparison of three strains of holstein-friesian grazed on pasture and managed under different feed allowances. J Dairy Sci 91(4):1693-1707.

McCarthy, S., B. Horan, P. Dillon, P. O'Connor, M. Rath, and L. Shalloo. 2007. Economic comparison of divergent strains of Holstein-Friesian cows in various pasture-based production systems. Journal of dairy science 90(3):1493-1505.

Morton, J. 2011. InCalf fertility data project 2011. Dairy Australia.

Pollott, G. and M. Coffey. 2010. Genetic And Phenotypic Responses To Selection For Dairy Traits In A Single Herd. World Congress Applied to Livestock Production, Leipzig.

Pryce, J. E., O. Gonzalez-Recio, J. B. Thornhill, L. C. Marett, W. J. Wales, M. P. Coffey, Y. de Haas, R. F. Veerkamp, and B. J. Hayes. 2014. Short communication: Validation of genomic breeding value predictions for feed intake and feed efficiency traits. J Dairy Sci 97(1):537-542.

Pryce, J. E., B. L. Nielsen, R. F. Veerkamp, and G. Simm. 1999. Genotype and feeding system effects and interactions for health and fertility traits in dairy cattle. Livestock Production Science 57(3):193-201.

New Directions for Type ABVs

Daniel Abernethy
General Manager ADHIS

Michelle Axford
Extension & Education Manager, ADHIS

Overview

Industry feedback has indicated that there is some confusion in the understanding and interpretation of the confirmation (Type) Australian Breeding Values (ABVs). The range in genetic merit for each type trait varies significantly and this makes it difficult to decide if an animal is superior (or not). For example the range in the type trait 'stature' seen in dairy cattle is quite large. Some cattle are very tall while others are very short. However for other traits, like Rear Leg Set, the difference between cattle with very straight leg compared to very curved (sickle) leg is much smaller.

Without knowing the range in the population it is challenging to determine where a bull or cow sits relative to the population. An update to the expression of Type ABVs in April 2015 aims to enable farmers and industry to readily decide where an individual fits in the population.

Current Expression of Type ABVs

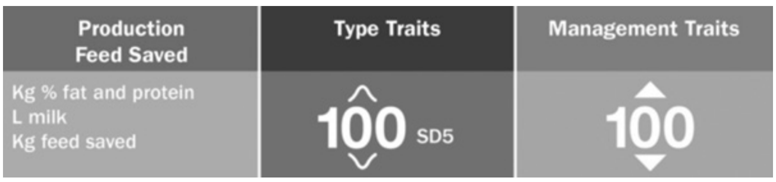
In 2007 ADHIS updated the expression of all non-production traits. Until 2014, Type ABVs were expressed as a relative measure compared to an average of 100. A bull with an Overall Type ABV of 110 was 10% greater than average for Overall Type, or approximately 2 standard deviations above average. A bull with a Pin Set ABV of 110 was 10% greater than the average for Pin Set, or approximately 1 standard deviation above average. Each trait has a different range and standard deviation leaving users unclear about the meaning of the ABV.

New expression of Type ABVs

From April 2015, the expression of Type ABVs and the definition of 'average' are changing to be more consistent with the way in which breeding values are expressed in other countries. This change involves moving from the current definition of type traits to the following new expression

- Type ABVs are standardised and expressed on a common scale where one standard deviation is set to 5 and the average is 100.

Figure 1: Summary of the expression of Australian Breeding Values from April 2015



The purpose of this paper is to summarise the definition of the average, standard deviations and finally why standardisation of type ABVs will assist in interpretation.

Comparing ABVs

Australian Breeding Values (ABVs) as with all estimated breeding values are a relative measure of an animal's genetic merit. A single ABV figure doesn't mean much unless it's compared to another animal or an average.

We can use the analogy of a car where:

- The size of the fuel tank is an absolute measure. For example 60L tank.
- But safety rating is measured in stars and you don't know if a '3 star rating' is good or bad until you compare it to either; the average star rating of all vehicles, to another car, or to the highest star rated vehicle. A star rating is a relative measure.

ABVs, like car safety ratings are relative measures. To make sense of a relative measure, it is useful to understand the average of each ABV and how the ABVs are expressed.

Definition of 'Average'

The 'average' (also known as the 'base') is a clearly defined group of animals to which all others are compared. Around the world, countries will use different groups of animals as their 'average'.

In Australia, the average is defined as cows of the same breed that are 6 years +/- 2 years of age. For example, in 2015, the average includes cows born between 2007 and 2011.

For ease of understanding the average of this group is set to 100 and provides a reference point for comparisons between ABVs for both cows and bulls. In doing so animals with an ABV of above 100 will be above average for the traits and animals with an ABV below 100 will be below average for that trait.

The average is updated each year so that it stays current and is a reflection of the cows that are milking around Australia, today.

Standard Deviations

Before introducing standardised traits, it's useful to explain 'standard deviation'. A standard deviation is a statistical term that is describes how much spread there is in a set of numbers.

- The size of a standard deviation is small if there isn't much variation in the numbers.
- The size is larger if there is greater difference in the spread of the information from best to worst.

In the case of animal performance, there are usually lots of animals that are about average and fewer animals that are extreme (either extremely bad or extremely good). This is a normal distribution pattern of data which is illustrated in Figure 2.

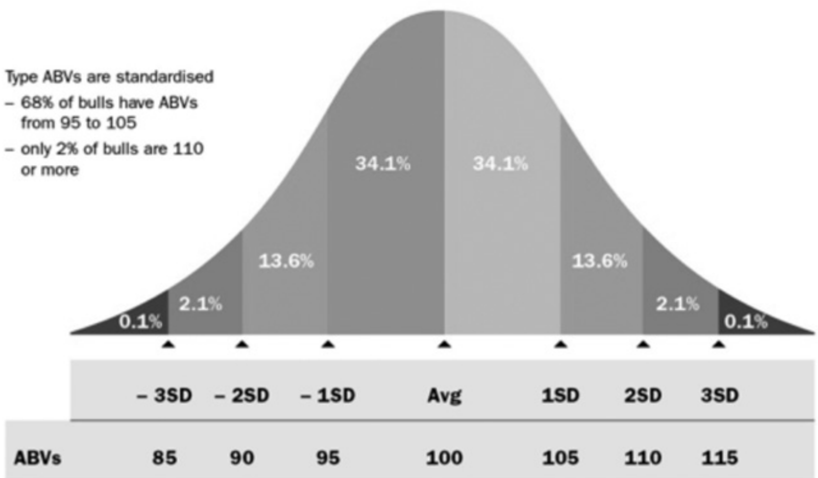
In a normal distribution;

- One third of animals will be within 1 standard deviation above average and another third below average.
- A smaller number (27%) will be between 1 and 2 standard deviations,
- A very small number (4%) will be between 2 and 3 standard deviations, and
- A rare group (0.2%) will be greater than 3 standard deviations.

The size of the standard deviation depends on how much difference exists between the best and worst groups of animals. To apply this to dairy cattle breeding, the trait of Rear Leg Set is a good example. There isn't much difference between best and worst. In fact, the standard deviation is about 5 whereas Stature has more than double the size of a standard deviation (12 for Holsteins).

If you know the size of the standard deviation, it's easy to figure out if an animal is average, a bit above average or extreme for a trait. But how do you know what the standard deviation is for each trait?

Figure 2: Normal distribution curve showing the proportion of a population expected in each standard deviation and related Type ABV from April 2015



Standardising ABVs – The change to Type Expression

The standard deviations have always been available for all traits but you had to dig to find them and then it was difficult to remember them all. This means it wasn't always easy to figure out how good a bull was for a trait relative to the breed overall.

From April 2015, the expression of Type ABVs will be 'standardised'. "Standardising" breeding values is a term used to describe an expression where ABVs reference where the bull sits in the population for their genetic merit for a given trait. By using the same standard deviation (SD) for every trait, it is easier to determine if a bull is 1, 2 or 3 standard deviations above/below the average without having to know what the range might be in the trait.

As shown in Figure 2, the size of the SD for all type traits is set to 5 units. In doing so one SD is 5 units, two SD's is 10 units and so on.

So what does this mean?

- A bull with an Stature ABV of 100 will be average for the trait
- A bull with an Stature ABV of 105 will be 1 SD taller than average
  - (in the top ~16% for the breed)
- A bull with an Stature ABV of 95 will be 1 SD shorter than average
  - (in the lower ~16% for the breed)
- A bull with an Stature ABV of 110 will be 2 SD taller than average
  - (in the top ~2% for the breed)
- A bull with a Rear Leg ABV of 110 will be 2 SD more sickled than average
  - (in the top ~2% for the breed)

By using a standardised expression you do not need to know the range in ABVs for each individual trait, all you need to remember is the number 5.

How does this compare to what I have seen in the past?

When compared to ABVs published in August 2014 the range in ABVs for some traits will go up whilst others will go down. Standardisation changes the minimum and maximum ABV for a trait. For a trait with a large difference between animals, like stature, the range in ABVs will be reduced so the minimum ABV will be about 80 and the maximum about 120. This is simply 4 SD's multiplied by 5 (size of the SD) above or below 100. Only the absolute extreme animals will have ABVs close to these figures. A comparison example for the trait Overall Type is outlined in table 1. This table indicates that for Overall Type ABVs for the Holstein breed will not change very much whereas they will be slightly higher in the Jersey breed (where a bull 1 SD above the average in the old expression was 109, this will drop to 105 in the new expression).

Table 1. Comparison of Old and New Expression of Overall Type for Holstein and Jersey

	Holstein		Jersey	
Trait: Overall Type	Old Expression	New Expression	Old Expression	New Expression
Average Sire/Cow	100	100	100	100
ABV 1 SD above the average	106	105	109	105

Is above 100 always better?

Outside of the expression of type ABVs confusion also exists around the perception of what defines 'good type'. Users of ABVs may assume that a bull that is extreme for all type traits (ie. >110 for all traits) is the ideal or 'best' bull for them. However, this may not be the case.

For example a bull with a very high Stature ABV (say >110) will sire daughters who are, on average, taller than the population. Furthermore a bull with a very high Bone Quality ABV (say >110) will sire daughters that have flatter bone than average.

During the review of the national breeding objective ADHIS held Australia's Longest Farmwalk. This was a series of on-farm discussions around the traits and priorities farmers deem important. During these events many farmers indicated that they no longer seek to increase the stature or 'sharpness' of their cows with a preference for a more medium sized robust cow. For such farmers selecting sires with high Stature and/or Bone Quality ABVs does not suit their breeding objective.

There are also a number of 'intermediate' traits where the extreme at either end is undesirable. Based on the current Holstein Australia classification system the following traits are scored as intermediate optimal traits (ie. An extreme in either direction is undesirable);

- Rump angle
- Udder depth
- Rear leg set
- Front Teat Placement
- Rear Teat Placement
- Teat Length
- Rear Leg Side View

While other traits, extreme values (classification scores 8-9) are marked down. For example foot angle, bone quality, chest width and body depth.

In reviewing the type traits for sires under consideration make sure that you select sires that are of 'good type' for your herd and are aligned with your own breeding objectives. In other words the ideal type ABV for a given trait for you may be 100 or even 95!

A word on comparing breeding values between countries

ABVs are 'tuned' to the performance of cows in Australia. ABVs (including ABV(i)s, ABV(g)s and ABV(ig)s) are available for almost any bull sold in Australia as well as herd recorded or genotyped cows and heifers.

Conclusion

The expression of Type ABVs is changing to improve understanding and interpretation. The new standardised expression utilises a SD range of + / - 5 units. This change is for all type traits. A bull with an ABV of 105 is one SD above the average, 95 is one SD below the average. Farmers and advisors and encouraged to review the ABVs of all type traits of interest and to understand that for some intermediate traits the ABV of 100 may be most suited to their breeding objective.

Illustrations for sample type traits
(Adapted from World Holstein Friesian Federation type harmonisation programme)

Central Ligament

Convex to flat | Slight definition | Deep definition

Lower ABV | Higher ABV

Fore Udder Attachment

Weak and Loose 4-6 | Intermediate acceptable 7-9 | Extremely strong and tight

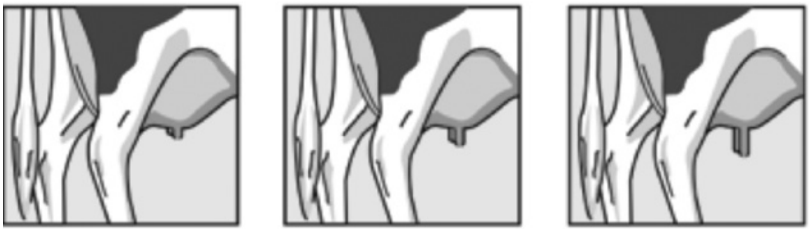
Lower ABV | Higher ABV

Udder Depth

Below hock | Intermediate | Shallow

Lower ABV | Higher ABV

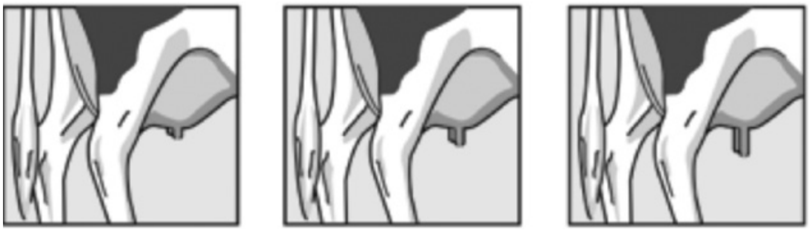
Teat Length



Short | Intermediate | Long

Lower ABV | Higher ABV

Teat Length



Short | Intermediate | Long

Lower ABV | Higher ABV

Front Teat Position

Outside of quarter | Middle of quarter | Inside of quarter

Lower ABV | Higher ABV

Angularity

Lacks angularity | Intermediate angle | Very angular

Lower ABV | Higher ABV

Rump Angle

Level | Intermediate slope | Extreme slope

Lower ABV | Higher ABV

Chest Width

Narrow | Intermediate | Wide

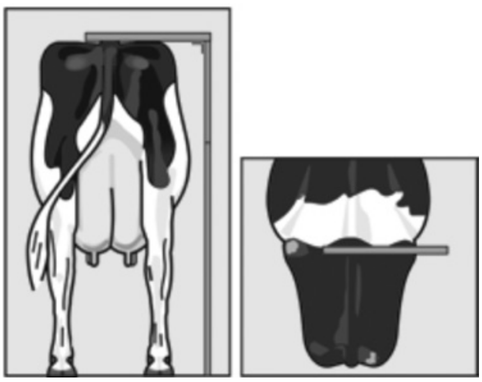
Lower ABV | Higher ABV

Rear Leg Sets

Straight | Intermediate | Sickle

Lower ABV | Higher ABV

Stature



Lower ABV | Higher ABV

The “Modern” Importance of Dairy Cow Data for Future Australian Genetic Improvement

Paul Douglas
Ginfo Project Manager
pdouglas@holstein.com.au

Animal Genetic Improvement in the dairy industry over the last 50 plus years has utilised data and associated genetic correlations to achieve industry wide genetic improvement. From an applied perspective, the base foundation of our genetic improvement systems still prevails. This being that while we are presented with the bulls with high genetic merit, as screened through traditional progeny test systems, what we have effectively done is remove a larger number of potential candidates that would have had a deleterious effect on the population. These bulls, that have some weakness within their genotype, are removed from potential use and consequently the dairy genetic population avoids their inferior genes.

The mechanics of this process has been achieved through herd test and on farm data collection systems that evaluate phenotypes against pedigrees within Australian herds. It is this data on traits that we measure, collect and communicate for genetic evaluation purposes, combined with pedigree, age group and the analysis against other animals within a herd, which supports our system.

And while genetic evaluation systems around the world are not absolute prediction systems, large amounts of good data reduces any impact of data error and further protects us from the poorer genotypes identified through this process.

But we must be reminded. This has only been applied to the phenotype traits that we measure!

If we don’t measure a trait, and measure it effectively and accurately, and communicate this data for genetic appraisal and potential evaluation, then we are vulnerable. That is, we can’t protect the population from any potential poor gene associations if we do not measure and communicate the data.

This is exemplified with the reduction of genetic based fertility whereby data in the past was not analysed to protect the population from the influence of poor genotypes for fertility.

Now, in analysing high value data sets, we have the genetic selection mechanism to reduce the rate of genetic decline for fertility, and implement genetic criteria to improve the genotypes for fertility.

It is important to also remember that gene interactions and associations are not simple but in fact are extremely complex, which further reinforces the need for large quantities of good data to assist with genetic predictions for specific traits.

To reinforce these complexities, I will provide an example of one aspect of gene interactions. There are gene interactions within the Holstein genome that have an unfavourable effect on milk yield and an unfavourable effect on fertility.

There are other gene interactions that that have a favourable effect on milk yield and a favourable effect on fertility – a desired outcome. And then there are gene interactions that have a favourable effect on milk production and an unfavourable effect on fertility – with this last scenario certainly antagonistic to a genetic improvement objective for both production and fertility.

With the possibility of some gene interactions protecting our dairy genetic population from poor production and not protecting from poor fertility, and other gene interactions protecting our dairy genetic population from both poor production and poor fertility, the need for excellent data sets for both of these traits is required to correctly protect the Australian dairy genotype.

In this scenario, if we focus only on production, then the genetic population is potentially vulnerable to both the positive or negative fertility outcomes, and what we have achieved by not measuring and genetically evaluating for fertility, is the stronger influence of poor fertility gene associations within our dairy genetic population.

Therefore – large quantities of high quality phenotype data provides the mechanism to genetically evaluate traits and detect the influences of poor gene interactions.

But now there is more to this story of protecting the population from poor gene interactions.

Genomics is providing a mechanism to further protect the population from poor gene interactions and associated influences.

It provides a more advanced analysis mechanism to comprehend what is actually happening at a gene interaction level.

Genomics provides us with an "earlier warning system" for poor gene interactions. It presents an opportunity to analyse new and potentially more complex traits and to comprehend how they interact with the performance of an Australian dairy cow, and how this can further influence profitably through improvements in production, or reduction of health incidences requiring management and intervention.

As a consequence of the potential of genomic technologies, there is an opportunity to additionally analyse current data sources, as well as investigate new phenotype data collection mechanisms, to further evaluate genetic interactions and prevent poor traits from our dairy genetic population.

With the availability of this technology, the requirements to obtain excellent phenotype data – milk production, fertility, health so we can correlate with Genomic DNA sequence analysis becomes even more important.

Also, genomics in itself is the next step in the improvement of data quality as the correct parents can be verified through the DNA analysis process.

The improved correlation of phenotype data with genomic evaluation systems is what both the Ginfo – Genomic Information, and the HDHC - Health Data for Healthy Cows projects are all about.

The Ginfo project has identified excellent data recording herds from around the country (this can be identified by analysing record numbers and record associations from the data itself), and obtained DNA samples from individual cows associated with individual data sets so that the genomic correlations with milk production performance, and in particularly, fertility traits, can be further strengthened.

The achievement to date is the collection of over 30,000 DNA samples from over 100 herds around Australia from cows that have excellent data sets to further improve genetic correlations.

With the HDHC project, the impetus is to further examine on farm health data resources – especially for mastitis treatments and lameness, and to associate these health occurrences with the DNA captured from respective animals within the Ginfo project. The objective is to further examine potential gene interactions for mastitis or lameness prevalence, and to utilise this information to identify potential gene interactions and genomic predictions for these traits.

With these projects in place, the methodology of phenotype trait data correlated with genome analysis techniques becomes a standard genetic analysis process.

For the future, this means that new or novel phenotypes that increase dairy farm profitability or operating efficiency can be genetically analysed through this genome – data correlation process in order to further protect the Australia dairy herd genotype.

Value-Added Business Planning Improves Financial Performance of Milk Recording Cooperative

Summary

Over the last twenty years, much of the milk recording industry has been evolving from a structure based on a defined market with geographical boundaries and exclusive service rights to a structure which is based on competition and open markets. This process is in various stages in different areas, but moving from monopolies to open markets is an evolutionary process. Because milk recording service providers have frequently been non-profit, government-based or government supported organizations, the price of services offered to farmers has generally been kept low. While this can be viewed as positive for the customer, it becomes a limitation if insufficient profits are generated due to low prices. Lower profit in turn means less investment in product and service improvements. Recognizing this, AgSource Board and management developed a strategic plan to create adequate bottom line performance to generate margin levels necessary to afford investment in technologies for future growth. The first need is investment capital for research and development in technologies including diagnostic testing, web delivery tools and new herd management products. It is important to note that the core member business of AgSource is milk recording. Therefore, the end goal is the delivery of management products and services that will drive improved efficiencies and net farm earnings of the dairy farmer/member of this cooperative. The low-margin environment described above does not create the necessary cash for reinvestment. AgSource leadership needed to create long-term investment capital from other sources. For this reason, AgSource began the process of strategic growth through acquisition. The result of this plan has taken a small cooperative with revenue of just over 9 million in 1999, to one yielding just over 23 million dollars of revenue in 2014.

Introduction

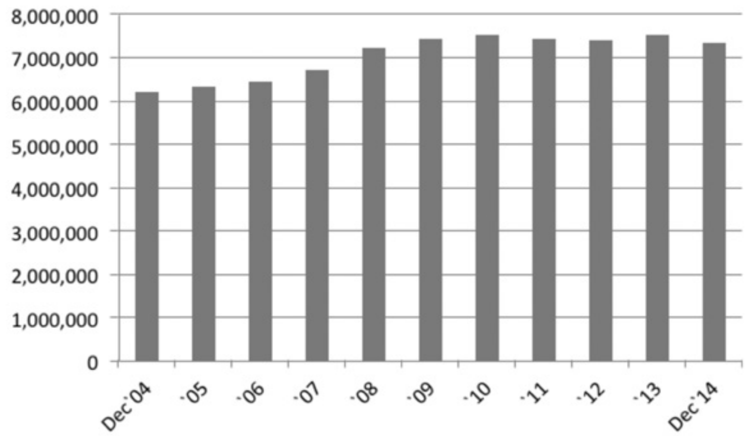
In 1993, AgSource and then 21st Century Genetics (now Genex) formed Cooperative Resources International (CRI). CRI is a holding cooperative which has ownership of both member cooperatives. This form of ownership has several positive points. One of the benefits of this structure resulted in AgSource and Genex sharing expenses related to non-revenue generating areas. Examples of these areas include human resources, finance and fleet management. Another important factor was the power of a combined balance sheet. In 1999, AgSource owned one agronomy laboratory. This operation created higher margins than our milk recording programs. During a strategic planning session it was decided to grow revenue in the agronomy area in order to create appropriate margins to provide needed investment dollars for research and development of new technologies and programs in our milk recording operations. Over a ten year span, starting in the year 2000, AgSource was able to leverage the borrowing power of the CRI balance sheet and acquire four more agronomy laboratories and one food and environmental laboratory. Today, this laboratory business model produces 55% of AgSource total revenue and the margin in operation produces net margins more than twice that of our milk recording operations. On average, in the last four years AgSource has invested nearly $500,000 per year in research and development and technology in our milk recording operation. This would obviously not have been possible without the ownership of the laboratory operations.

Value-Added Selling

In 2004, another strategic decision was made based on one simple fact. When competing on a least cost or commodity basis in the milk recording industry, AgSource would always struggle to create margins necessary to invest in our members' future management information needs. We could not rely solely on higher margins created by the laboratory divisions to create investment capital. So, AgSource made significant investments in converting to a value-added business philosophy. That philosophy can be described as proactively looking for ways to enhance, augment, or enlarge our bundled package for the customer. It is about always seeking ways to create meaningful value and to exceed customer expectations. It is about making our products and services so important to our customers that they cannot afford to replace us, without price being an issue. Our strategy utilizes the "value added" approach as a business philosophy that embraces the objective of developing and delivering higher-valued services to the customer, and selling those services to the customer on that basis.

In the past ten years, AgSource and CRI have adopted a value-added marketing approach which has placed equal value on products and the people necessary to deliver them. It has resulted in a significant improvement in results. In the twelve months ending in May 2004, AgSource had over 360,000 fewer individual cow recordings than in the previous twelve months. Our twelve month total cow tests processed in that year was 6.2 million. In 2014, we processed over 7.3 million cow tests. Comparing 2014 to 2004 shows AgSource grew by more than 1.3 million cow tests.

Figure 1 – Total AgSource Cows Processed by Year
December 2004 – December 2014



The Three-Dimensional Bundle of Value

The value-added selling program has three important principle points all salespeople must hold high. The company, the product, and the sales team must have meaningful value to our member/customer. This system is referred to as the three dimensional bundle of value. It has been the experience of AgSource that adherence to this system, combined with patience and time to allow employees and members to make the paradigm shift to this new marketing approach, will yield success.

Company

It is easy to underestimate the fundamental impact the image of an organization or brand can have on marketplace success. In reality, little success can be expected from improvement in products and services without the foundation provided by a strong organization and positive brand image. By strong we mean reliable, trustworthy and with a history of commitment to quality service. We believe our structure as a member-owned and directed cooperative is positive in the marketplace, and our references here to members and customers is largely interchangeable. We were fortunate to have a positive reputation at AgSource and CRI before engaging in our conversion to a value-added organization. Without this, our challenge would have been much more difficult.

Even with a firm foundation to build on, there was employee training needed at all levels to develop the value of the AgSource/CRI brand. This was necessary because we found that many of our customers had a relationship with and strong loyalty to their local field technician. Loyalty was directed toward the individual rather than the organization that employed them. While this was positive in member retention when we faced competitive challenges, it posed a major limitation in transitioning to a new field technician when we experienced employee turnover. We needed to create a customer relationship bond to our organization without decreasing loyalty to the individual serving the herd. This challenge is ongoing, but we feel we have made progress by involving more and different personnel in providing service, particularly to larger herds. We have employed a more focused brand strategy, and we have broadened our product and service offerings.

This concept also extends to increased reliance on the organization for superior herd management tools. We cannot rely on herdbook programs or the dairy cattle breeding (AI) industry driving demand for our milk recording services. While useful, they do very little to increase recognition of the value of the outstanding management information we provide. If we sell our programs to a new herd primarily on the basis of qualifying for herdbook program recognition or local awards banquets, we have made ourselves reliant on those programs, and potentially victims of them if changes outside our control are made. The evolution of genomic evaluations and the subsequent reduction of progeny testing is a perfect example. It is our responsibility to create recognition of value in what we do. To deliver real value means absolutely nothing in the marketplace if it is not recognized by the customer.

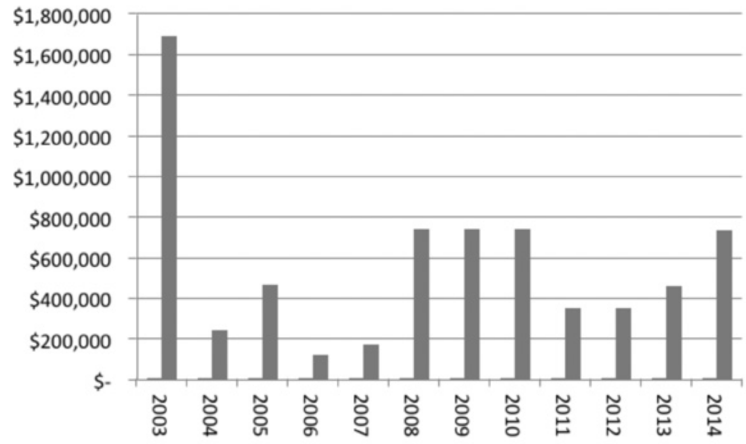
Product

The marketplace does an excellent job in the long run of sifting products and services that are not worth the price. In our organization, we were fortunate again to have a strong foundation. However, we needed to apply more effort to differentiate ourselves from the competition, and to better coordinate market release of new products and services.

An important piece of value-added marketing is the need to create differentiation within the industry. We cannot differentiate ourselves by offering the exact same products with the exact same look. There may be similarities and some parts of delivered product may overlap, but the entire package cannot be the same. Identical services and products result in a commodity-based industry where price is the primary driver of a buying decision.

For this reason, heavy emphasis was placed on development of superior quality herd level management tools mixed with a value-added marketing plan. Once again, I direct your attention to the acquisition of non milk recording industries that would create higher margins. A portion of these new margin dollars created would then be used to invest back into our milk recording programs.

Figure 2 – Capital Investments in AgSource Milk Recording Divisions 2004 – 2014



At AgSource we have adopted a stronger commitment to new product development and enhancement. It is our goal to introduce at least one major new product or enhancement each year. Product releases are coordinated with field training, advertising, industry and member education, and marketing incentives.

To this end, our largest single investment was made in 2003. The mainframe computer that AgSource was using prior to 2003 was originally developed by the Unisys Corporation in 1986. The database architecture was very complex compared to today's relational databases. Making changes to how data was stored in the database was complicated and time consuming. All business logic was written in Cobol programming language and new products generally took from eight to 12 months to program and deliver. Actual processing of DHI records was lower in part because the data access was slower. A cryptic coding language for the highlight color laser printers slowed down product development. Disk technologies improved and more data could be stored in a smaller footprint over time, but it was very difficult to scale the system based on changes in business needs.

Transitioning to a client server system, based on Microsoft's Windows Server operating system and Microsoft SQL server database, presented more possibilities to process records faster and design products in full color. Graphing tools made designing visual presentations of data much easier. The latest database server was designed to run on a virtual machine host (large server that can be divided and used as several individual servers). The relational database makes database design and modification much easier and as a result, database structures for a new product can be developed in days rather than weeks. All data calculations are performed in the database. Both paper reports and report PDFs are generated for each herd by the same application allowing reports to easily be mailed or distributed by email. Most recently a similar architecture has allowed AgSource to provide delivery of report data through an internet based web browser. All these changes provide the platform from which new products can be developed rapidly and delivered in whatever format the customer desires.

Another area of product differentiation that adds value is our increased offering of supply products in conjunction with our regular field service. While most of these products – milking gloves, ID tags, calf coats, etc. – are available from other suppliers, we make it more convenient for our members to order them from us as part of their regular service. This becomes one more reason for them to stay with AgSource when offered competitive options, and adds value to our regular herd test. Our average annual growth in sale of farm supplies by our field staff has been 38 percent in the past three years. The total revenue from this program was over $330,000 in 2014.

People

If there is a "most critical" component to our three dimensional bundle of value it would have to be people. Changing attitudes, performance and perceptions of our own people has been our greatest challenge, but also our most rewarding achievement. Clearly, the most effective way to create recognized value is for us to sell our real value through a well trained field staff that believes in and understands the value and can explain it to our members. Making the necessary progress in this area has required a three-pronged approach – information, motivation, and separation.

Information means training, expertise, and the confidence that it creates. It requires organizational and employee commitment. It is not enough to introduce new or improved products. An educated and effective field staff is required to ensure these products increase the value of our services to our members. To this end, AgSource created an Outreach and Training Department. This staff of six, highly motivated employees spends every working day training employees, members and consultants how to properly use AgSource programs and products. This group directly addresses the value-added principles of creating differentiation, real and perceived value. Giving the member and their consulting team the conclusive impression that AgSource brings extra value to a competitive environment and, for this reason, does not need to compete on a price-only basis.

This team has significantly increased the required training and resources applied to field staff education. We have expanded training on product knowledge and implemented required programs on selling and the importance of the value-added approach. We also developed several new tools in the form of video and on-line programs to deliver this information. Time spent in small groups sharing experiences and information adds to the knowledge base of the local team. We have significantly upgraded the expectations of our field staff to be more than good service technicians.

Motivation is a combination of rewards and recognition that inspires achievement and performance. We all understand the pride of being part of a successful organization committed to meeting the needs of its members. But personal rewards and recognition are also important.

Compensation for on-farm milk recording services is a challenge, and our observations suggest there is tremendous variability in how field service personnel are paid by various organizations. We claim no special insights, and acknowledge the challenges associated with field compensation and changing the methods within it. We do believe that "what gets rewarded and recognized is what gets done." We have made ongoing adjustments in how, and how much, we compensate our field staff. This was a transition from partial commission to a program today that utilizes places employees on full commission. When introducing new products and services we have simultaneously implemented incentives tied to the successful sale of those specific items.

Recognition may be as important as compensation as a motivating tool. We have increased the opportunities to recognize our field staff for sales and service at the organizational and regional level. Monthly newsletters identify top performers in several key areas of sales and service. Regional managers are encouraged to more frequently recognize their staff in front of their peers.

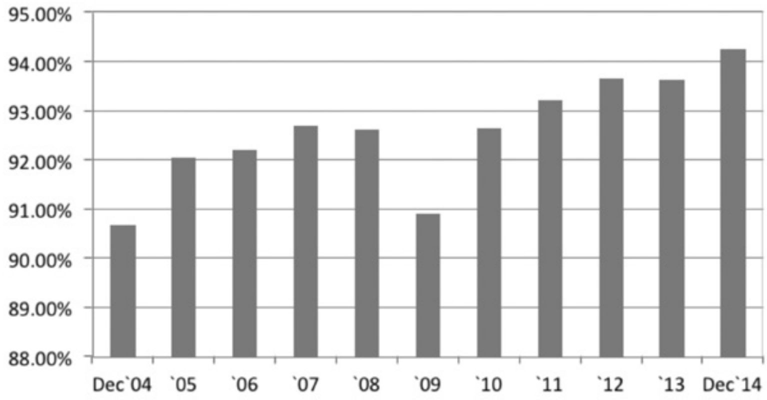
Separation has been used sparingly, but is important. We have found employees who fail to adopt an attitude conducive to delivering and selling added-value, or who fundamentally do not believe in the importance of the products and services we offer, are happier and frequently more successful in another profession. Separation may be voluntary or involuntary and we are fortunate that most employees from whom we have separated have recognized themselves that they would not be able to meet our expectations and made the decision to resign or retire. These separations have the added benefit of sending the message to other employees that we do expect more. We highly value our people, and commit tremendous resources to training and personal development, but the time required to develop a person who may not wish to grow can be very counterproductive.

Conclusion

Benchmarking tools are important management tools we provide to our members. Benchmarking tools likewise are great tools to measure individual and corporate level performance at AgSource. Figure 3 below represents the average percent processed percentage of AgSource employees. This is an average of each year from 2004 through 2014.

Since committing to the philosophy of value-added marketing, AgSource and CRI have experienced positive and measurable results. We recognize dairy prices do factor into the benchmarking tool below. However, we could not have achieved the success of total cow growth and improved percent processing numbers without the steps described in this presentation.

Figure 3 – AgSource Employee Yearly Average Percent Processed December 2004 – December 2014



Milk recording organizations must continue to evolve to remain relevant and meet the needs of dairy producers. AgSource has found this recipe to work best in our set of circumstances. First was the decision to join CRI to split the expenses of certain management overhead divisions. Step two, increase available investment capital through acquisitions of non milk recording businesses and invest the available capital in technologies that will keep AgSource relevant in the changing environment of our dairy industry. Finally, the use of value-added selling principles ensures our membership takes full advantage of the programs and products made available to them to increase on farm profits.

Reference

Reilly, Thomas P., *Value-Added Selling: how to sell more profitably, confidently, and professionally by competing on value, not price.* McGraw Hill, 2003.

HERD
15