



Newsletter Number 6

December 2021

Dear Red Breed Enthusiasts,

Having lots of accurate data is a good thing- right? It can help us make sound decisions without personal bias, which is essential to improve herd efficiency. However, data only tells us what has already happened, and predictive assessments like genomic proofs, rely on the historical performance of relatives to estimate how an immature animal might perform.

While there is no doubt that genomics is the handiest technological advance that has become available in decades, this degree of reliability assumes that the programming itself does not have any inbuilt unintended “personal preferences”. Indeed, many commentators have discussed how the system does not reward worthy performance from less popular strains of genetics within breeds.

The reliability of genomic estimations do vary considerably between national data sets and between trait groups, while some countries only have production traits available. Production reliability varies between 65% to 85%, health traits can be about 85% and conformation roughly 65%. Whereas proven bulls have earned reliabilities well above 90%. So are there ways which breeders can use the latest genetics from genomic sires and improve the performance reliability of their heifer groups?

Is there still a place for wise stock husbandry and good old “gut feel”? Can they add an extra dimension to lower reliability bulls and traits? Conformation traits have been used to predict performance and durability for much longer than herd recording information, but modern milk recording systems have enabled performance data to become the accurate production predictor. The system also records health events and herd life span, which are both valuable herd life predictors. But herd life also depends on cow structure and we seldom record structural failures which cause cows to depart our herds. Classification measures structural traits, rewarding strengths and penalising weaknesses which contribute to early herd departures.

Genomic conformation traits have much lower reliabilities simply because there is less data to support them, often due to farmer reluctance to participate in classification. A worthy piece of advice I received was: “classify first lactation cows for the benefit of the breed and classify later lactation cows for herd promotion”. There is one proviso in this saying, breeders must regularly classify **all** their first lactation cows, not just the best ones or the data base will become biased.

Classification is a tool which can be used to increase the effectiveness of other information to predict cow durability and is the only source of information which supports conformation proofs.

There are costs associated with classifying, including setting aside a day to go through the females with the classifier, time to draft and prepare the group (Australian breeders are not permitted to prepare the animals in any way, they must be assessed in their working clothes), finally the classifiers need to be paid (in some countries there are schemes which assist with this cost). So, what are the gains? Having a personable classifier who clearly explains their assessments can be a reliable source of information for an aspiring breeder, but more importantly there is a breakdown of every individual animal and a summary of group strengths and weaknesses.

But there is no gain unless the breeder utilises the information to determine semen purchases and plans corrective matings. Even if the breeder has a minimal input policy, purchasing genetics which avoid the three group weaknesses highlighted in the summary pages will lead to herd progress.

Many semen company representatives prefer to understand the farm's breeding goals rather than guessing for themselves. If the information is not used constructively then all the effort and cost has been spent for nothing!

Because Red Breed genomics are not as developed as some other breeds, many breeders look forward in anticipation to a time when reliable conformation will be available. In the meantime, using classification information directly to plan corrective matings has the ability to improve the consistency of replacements entering the herd.

Classification days are rarely days of great personal reward with extremely high scores, more often than not they are days of intense learning and re-evaluation. The long term gain from regular classification is more reliable bull conformation proofs (genomic and daughter proven), through a more robust conformation data set.

Another question to consider is: What is the long term effect of the heavy influence of first lactations of bull daughters in developing bull breeding values? Will it lead to high heifer performance followed by lack lustre successive lactations and early herd departures? How important is long herd life and lifetime production?

Many cows which amass high lifetime totals achieve it through above average but not extreme lactations, combined with good fertility and structural strength, enabling them to perform consistently for many years – “invisible cows”. Measuring lifetime production is slow and generation intervals become quite long, but is this a problem? Many believe that if they use a sound breeding programme, their herd replacements will be more worthy individuals. Genomic predictions use recorded pedigree and performance data to predict which calves will become cows with long productive lives. But the data on which these predictions are based must be very sound and that is a challenge for our diverse Red breeds, so perhaps the era of breeding from old cows is not gone yet. Very few will dispute the great value in long herd life because it minimises heifer rearing costs and the effort required to assimilate young cows in to the herd.

Then why would we consider a proposal to implement a breed improvement strategy using extremely short generation intervals? Relying totally on genomic and first lactation performance could move us away from long herd life genetics. Some breeders already fear that using conventional breeding systems the generation intervals are becoming too short and they are asking if their modern herd replacements truly are that much superior.

Well, while we were at the 2019 IRDBF conference dinner watching our New Zealand friends perform their national Haka and singing along to songs made famous by Johnny Cash, there was a small group huddled around a table discussing how short generational breeding might be used to advantage. The conversation was prompted by two considerations:

1. What if inbreeding became too high in the Red breed?
2. What if we discover that Red cows have, or do not have, dominant attributes which are preventing the commercial growth of our breed?

A very, very short generation interval strategy would involve identifying a base group of elite animals, which possess targeted attributes. Place them in an intensive short generation Embryo Transfer programme for perhaps 10 generations in as many years. Genomic assessment would be the major selection tool, as the genetic donors would not be old enough to contribute performance data before the next generation is being bred.

The selection pressure would be intense, and a majority would be removed from the programme as it progresses, while the genetic makeup of the continuing group would become isolated from the general population. Proponents concede the elite group would probably become a little inbred among themselves, but they could offer a degree of outcross genetics to many other herds. The value of this aspect would vary according to local perspectives but having a variety of strains and

traits coexisting within a breed is always healthy. When the desired improvements become firmly stable, general dissemination could begin.

Finance will be a big consideration to get programmes like this started and that raises a number of questions: Who pays for such investments? How do they achieve a return on their investment? Who owns the breed? Should farmer cooperatives be the controlling decision maker? Can we guarantee that cooperatives will remain the property of farmers, or will financial constraints eventually force the cooperatives to sell? In poultry, pork, crop seeds and many other areas, genetic control is dominated by large corporations and even large cooperatives sometimes behave like multinational companies. Are we comfortable to transfer genetic oversight responsibilities to bureaucrats? What is best for our Red cows?

These questions may seem philosophical and far-fetched, so perhaps they could be included in the agenda of the next IRDBF meeting in Estonia? Because there are presently no widely held conclusive answers, I would like to start the discussion now by hearing other points of view. Whether we tackle these questions now or delay them, they will need to be answered at some point in the future.



Craig Hamilton and Graeme Hamilton of OB Flat, Australia look to the future working together.

Our guest contributor is Doug Savage, an expatriate Australian who lives in Canada. Doug is part of the Savage family who continue to breed Illawarras just south of Toowoomba in Queensland and did for a time conduct the Venvale herd, as well as being quite involved in breed politics during the 1980s. During a visit to his farm at the time, he remarked that he hated driving tractors and would much rather be working with cows. After leaving Australia, his love for cows has not waned and he has become a recognized writer for dairy cow magazines. He has kindly gathered his opinions into the following words which combine his cowmanship and observations from the international stage over the last 30 years or so. Read on!

Future Opportunities for Red Breeds by Doug Savage

The move from numerous nationally based red dairy breeds to more of a global red breed with significant interchange of genetics has been a progressive trend over the last 35 years. For the Holstein and Jersey breeds that trend has been even more pronounced and started 20 years earlier. While diversified use of the best red genetics has resulted in production gains that are very competitive with other breeds, the issue of individual red breeds trying to retain their own breed identity only impedes this process of globalization.

The future of red breeds lies in their strengths in areas such as fertility, calving-ease, and health traits – being a problem-free breed with good resiliency and longevity – and yet production must continue to improve to remain competitive. And keeping up with the production advances being made by the Holsteins in this genomic era is no mean feat. From around 1960-2000, selection emphasis in Holsteins was heavily on milk. As fertility and health are inversely correlated with milk, these traits progressively became the Holstein's Achilles heel. That opened a role for the red breeds in cross-breeding to alleviate the problem. While the cross-breeding practice has been adopted by a number of herds in various countries, that window of opportunity may be closing again. Selection for fertility and health traits was added to most national indexes around 2000 (or in the Nordic countries, 15-30 years earlier). The downward trend for these traits for Holsteins leveled out, and then started climbing from 2010 onwards. Indeed, genomic selection has doubled the rate of genetic progress for all traits, with the health and management traits benefitting in particular.

SEXED SEMEN

So, what opportunities exist for red breeds? The first one is to place a much higher emphasis on the use of sexed semen. Producing all herd replacements from only the top cows and heifers in a breeding program really boosts genetic progress. A heifer calf every year from your top cow really makes a big difference. Breeding the lower half of the herd to beef semen results in a more valuable calf to sell, and that should more than cover the extra expense of sexed semen which is usually double that of conventional. Asking bull studs to have sexed semen available on all or most red bulls is a good starting point, and then ensuring enough gets used to justify it. The second step would be to ensure genomic evaluations are available on all red breed animals. There have been enough genetic linkages created over the past 35 years that it should be feasible, as long as enough genomic profiles from different countries are added to the reference set. The reliabilities will not be as high as the 70% we are accustomed to with Holsteins because the data set will be much smaller, but that is not the most important detail. It is how genomic selection is implemented that is more important than the reliability of the evaluation.

GENOMIC SELECTION

A good example comes from Holsteins where in 2009 North America and Europe established separate genomic data bases. Over time there has been nothing to show that one is more accurate or better than the other. However, at that time, given the extensive use of much the same bloodlines, it would have been reasonable to expect that by now there would be just as many influential bulls coming out of Europe as there is from North America. However, in the last 10 years we have again seen North America take the lead in supplying many of the most successful sires of sons worldwide. How did that happen? The big four North American bull studs have been much more aggressive in implementing genomic selection, setting up their own female programs to produce 50-60% of their own bulls. The rest they get from 12-15 private herd programs across North America. Unlike the small, elite breeder herds that bred most of the bulls prior to genomics, these are large scale operations with hundreds if not thousands of recipients and they operate extensive IVF flush programs. Of course, all this does not appeal to the average breeder, who has essentially

been put out of the business of breeding bulls, but the results speak for themselves – genetic progress has doubled; for all traits, health, type, and production. In Europe where studs tended to try and continue working with individual breeders to produce their bulls, they have responded in the last year or two with national or international stud mergers producing much larger stud programs. The history of genomic selection over the next 10 years is not likely to be the same as the last 10 years.

THE ODDS

These programs work based on getting enough eggs for IVF from an 8-month-old heifer to produce a top male as well as a female to be the next donor-dam: The shorter the generation interval, the greater the genetic gains. As a rule of thumb, the offspring can generally be shown to follow a standard bell curve – 6 or 7 out of 10 will fall within a standard deviation either side of parent average, and if lucky, you get one that exceeds parent-average by 2 standard deviations (and one that is 2 standard deviations below). You need to produce 10 daughters to get the lucky one that gets the best genes of both parents. And it's the genomic test that tells you which one that is. Bull studs are not likely to make the same massive investment in such bull-breeding programs for breeds other than Holstein because the potential revenue from semen sales is not as great. However, with creative use of genomic selection and widespread use of sexed semen it will give red breeds a fighting chance.

FEED EFFICIENCY

The only major dairy population where cross-breeding has become a standard practice is in New Zealand, and there the red breed did not get to play a role. The Holstein x Jersey (Kiwi Cross) now makes up around 60% of the national herd. Its popularity was driven by the inclusion of a body-weight adjustment in their Breeding Worth total index more than 30 years ago which is aimed at feed efficiency. Many other countries are now moving to add feed efficiency to their indexes – now based on actual feed intakes rather than body weight predictors – and this may disrupt the dominance of the highest milk producing breed, the Holstein. For the red breeds, positioning themselves to take advantage of feed efficiency proofs that may well reveal them to be highly efficient, problem-free milk producers could prove critical to their long-term future.



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