



Final report

Northern Genomics commercialisation scoping study

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Abstract

Cow fertility is a key driver of profitability in Northern Australian beef enterprises. While substantial genetic variation exists for this trait, it has been difficult to improve. The Northern Genomics Project (P.PSH.0833) successfully developed genomic breeding values (GBV) and Herd Profiles for purebred, composite & crossbred cattle for fertility, as well as for growth and adaptation traits including tick resistance and buffalo fly lesion score. The GBVs were based on a very large cohort of records from commercial cattle (26k females) representing most breeds, crossbreds and composites found in Northern Australia. Herd Profiles were demonstrated in that project to be a useful tool for benchmarking herds in Northern Australia for genetic levels for key traits, especially fertility.

The aim of this project was to commercialise these GBVs and Herd Profiles, to enable accelerated genetic gain for key traits in purebred, composite & crossbred Northern Australian beef herds. Potential commercial production of low cost GBV, along with herd profiles was explored via an Expression of interest. After evaluating five expressions of interest from companies and consortiums thoroughly against the criteria in the EOI, Black Box Co was selected for further consideration. A series of tests, where Black Box Co produced GBVs and herd profiles from raw genotypes, were compared to those produced by the UQ pipeline. This demonstrated that Black Box Co had the capacity to offer the service on a commercial basis.

At Beef 2024, the RePRO BI service, to deliver GBVs for eight traits, along with breed composition, including Bos indicus proportion, horned polled status, and parentage, was launched (<https://www.blackboxco.com.au/blog-posts/reprobi-launch>).

Since the Northern Genomics project concluded, more than 6,000 animals from 20 herds have been added to the reference set to improve accuracy of the GBVs. Many of the genotypes for these animals were contributed by producers.

Several case studies have been used to make the case for widespread adoption of GBVs and Herd Profiles to accelerate genetic improvement for key traits including fertility in Northern Australia. Some herds are already demonstrating improvements in fertility because of selection on GBVs.

Executive summary

Background

The Northern Genomics Project (P.PSH.0833) successfully developed genomic breeding values (GBV) and Herd Profiles for purebred, composite & crossbred cattle for fertility, growth and adaptation traits including tick resistance and buffalo fly lesion score. The GBVs were based on a very large cohort of records from commercial cattle (now more than 40k females) representing most breeds, crossbreds and composites found in Northern Australia. Herd Profiles were demonstrated in that project to be a useful tool for benchmarking herds in Northern Australia for genetic levels for key traits, especially fertility.

In this project, the commercial production of low cost GBV, along with herd profiles was explored and commercialisation pipelines were scoped out with commercial companies via an Expression of interest. After evaluating five expressions of interest from companies and consortiums thoroughly against the criteria in the EOI, Black Box Co was selected for further consideration. A series of tests, where Black Box Co produced GBVs and herd profiles from raw genotypes, were compared to those produced by the UQ pipeline. This demonstrated that Black Box Co had the capacity to offer the service on a commercial basis. At Beef 2024, the RePRO BI service, to deliver GBVs for eight traits, along with breed composition, including *Bos indicus* proportion, horned polled status, and parentage, was launched (<https://www.blackboxco.com.au/blog-posts/reprobi-launch>).

Several case studies have been used to make the case for widespread adoption of GBVs and Herd Profiles to accelerate genetic improvement for key traits including fertility in Northern Australia.

Objectives

The objectives of the project, and key outcomes were:

1. GBVs for fertility, growth and adaptation traits commercially available at low cost for Northern beef producers.

This objective has been achieved. GBVs are now commercially available for Northern beef producers (<https://www.blackboxco.com.au/what-is-repro-bi>)

2. Herd Profile product initially based on SNP arrays available for Northern beef producers, so that genetic level for the above traits can be benchmarked, and areas for improvement identified.

This objective has been achieved. Herd Profiles are now commercially available for Northern beef producers (<https://www.blackboxco.com.au/what-is-repro-bi>). In this project, it was demonstrated that at least 50 animals must be randomly sampled from the herd to get an accurate herd profile.

3. A lower cost herd profiling product developed based on DNA pooling.

A low-cost approach was developed for deriving Herd Profiles based on sequencing pooled DNA. The project was able to demonstrate that this approach gave a similar herd profile to that derived from SNP arrays.

4. Expression of interest released targeting commercial companies and agencies to train and educate staff on the products and explore commercial partnerships for full commercial delivery. Selection of one company to test the pipeline.

An expression of interest for commercialising the GBVs and Herd Profile product was developed. Five organisations or consortiums submitted expressions of interest. After evaluating five expressions of interest from companies and consortiums thoroughly against the criteria in the EOI, Black Box Co was selected for further consideration. Black Box Co demonstrated they had the capacity to offer the service on a commercial basis in a series of tests starting with raw genotypes. The commercial service has been launched as “RePRO BI” (<https://www.blackboxco.com.au/blog-posts/reprobi-launch>).

5. Five case studies documenting how the technology is being used by commercial producers, to demonstrate value on farm, including capturing how GBVs and herd profiles fit into an overall farming system, where genetics, nutrition, pasture management etc must all be integrated.

Case studies demonstrating the value of the technology have been developed by both MLA and Black Box Co. These case studies have been widely profiled in the media. Some herds are already demonstrating improvements in fertility because of selection on GBVs.

Benefits to industry

GBVs for eight traits, including two fertility traits, are now commercially available for purebred, composite & crossbred cattle in Northern Australia. This will enable selection for these traits, in some herds for the first time. Several herds, with GBVs for cohorts over up to five years, have demonstrated improvement in fertility traits because of selection on these GBVs. Herd Profiles are also commercially available, which will enable Northern Australian herds to benchmark their genetic levels for the eight traits. This will guide bull selection decisions and lead to further genetic improvement in large commercial herds. The GBVs and Herd Profiles have been bundled together with horned/pollled tests, parentage, and some genetic disease tests to maximise value from taking a sample from an animal for DNA extraction. Low-cost Herd Profiles are possible using DNA pooling.

Future research and recommendations

During the Northern Genomics Project, traits including udder and teat scores were recorded in some herds. GBVs have not been developed for these traits yet. Given the importance of these traits for calf survival, provided genetic variation was sufficiently high, GBVs for these traits could enable selection for improved calf survival.

Now that the commercial pipeline for GBVs has been established, GBVs can be calculated for any animal using their genotype and SNP effects for a trait. Projects recording traits like methane and consumer eating quality, could develop GBVs for these traits, provided the reference population used to calculate SNP effects is relevant for Northern Australia. This approach should be considered to enable Northern Australian producers with purebred, composite and crossbred cattle to select for these traits.

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1. Background

Cow fertility is a key driver of productivity and profitability for Northern Australian beef enterprises (Taylor and Rudder 1986, Fordyce 2012, Johnstone et al. 2014, Harburg et al. 2018). Genomic estimated breeding values (GBVs) for cow fertility would enable more rapid genetic gains for these traits, through accurate and early selection of animals with high genetic merit. The Northern Genomics Project (P.PSH.0833) successfully developed GBVs for fertility, growth and adaptation traits including tick resistance and buffalo fly lesion score, for purebred, composite and crossbred cattle herds. The GBVs were based on a very large cohort of records from commercial cattle (more than 26k females) of most breeds, crossbreds and composites found in Northern Australia. Close collaboration with the 54 contributing herds has resulted in a cohort of producers already using a research version of the technology. The GBVs models and data are fully described in Hayes et al. (2023).

In this project (P.PSH.1422), the commercial production of low cost GBV, along with other products including herd profiles will be explored and commercialisation pipelines will be scoped out with commercial companies via an Expression of interest. A DNA pooling approach will be evaluated to determine if the cost of providing Herd Profiles can be further reduced.

Case studies with producers will be used to make the case for widespread adoption.

2. Objectives

The objectives of this project were to:

1. Make GBVs for fertility, growth and adaptation traits commercially available at low cost for Northern beef producers.
2. Develop a herd profile product initially based on SNP arrays available for Northern beef producers, so that genetic level for the above traits can be benchmarked, and areas for improvement identified.
3. Develop a lower cost herd profiling product developed based on DNA pooling.
4. Put out an expression of interest released targeting commercial companies and agencies to train and educate staff on the products and explore commercial partnerships for full commercial delivery. Selection of one company to test the pipeline.
5. Develop five case studies documenting how the technology is being used by commercial producers, to demonstrate value on farm, including capturing how GBVs and herd profiles fit into an overall farming system, where genetics, nutrition, pasture management etc must all be integrated.

3. Methodology

3.1 Make GBVs for fertility, growth and adaptation traits commercially available at low cost for Northern beef producers

While the pricing of GBVs is ultimately a decision for the company commercialising the technology, to make genotyping animals as attractive as possible, we took the approach that if a sample from an animal was taken and genotyped, as much information should be delivered back to the producer as possible. Accordingly, a methodology was developed (in the Northern Genomics project), to deliver back GBVs, breed composition (including *Bos indicus* content) and horned polled status, from a single test. Parentage and some disease diagnostics can also be delivered from the same test. The traits for which GBVs have been developed (in Project P.PSH.0833) are:

- Heifer Puberty - Heifer is cycling (1) or not cycling (0) at approximately 600 days, diagnosed by ultrasound.
- Weight (kg) - Measured at approximately 600 days.
- Hip Height (cm) - Measured at approximately 600 days.
- Body condition score - Scored on a scale of 1 to 5, following BREEDPLAN guidelines.
- P4M - Pregnant or not four months after calving.
- Temperament - Scored on a 1 to 5 scale following docility trait guidelines.
- Tick resistance - Scored on a 1 to 5 scale following BREEDPLAN guidelines.
- Buffalo fly lesion score - Scored on a 1 to 5 scale following BREEDPLAN guidelines.

3.2 Herd profile product initially based on SNP arrays available for Northern beef producers

Perhaps the most important question for the herd profile tool is how many animals must be sampled from a herd to get an accurate herd profile? To answer this question, firstly the Northern Genomics GBV results (for 54 herds) was narrowed down to the 44 herds that had >200 animals genotyped. The herd profile (average GBVs and quintile rankings) for these herds was used as a baseline.

Then for each herd, sampled at random were 100, 50, 25 or 10 animals. For the random sample within each herd, the herd profile was again calculated for each herd. Across the 44 herds, a two tailed Students t test was used to determine if the average GBVs from the random sample (100, 50, 25 or 10 animals) was significantly different to the average GBVs for the whole herd (200 animals).

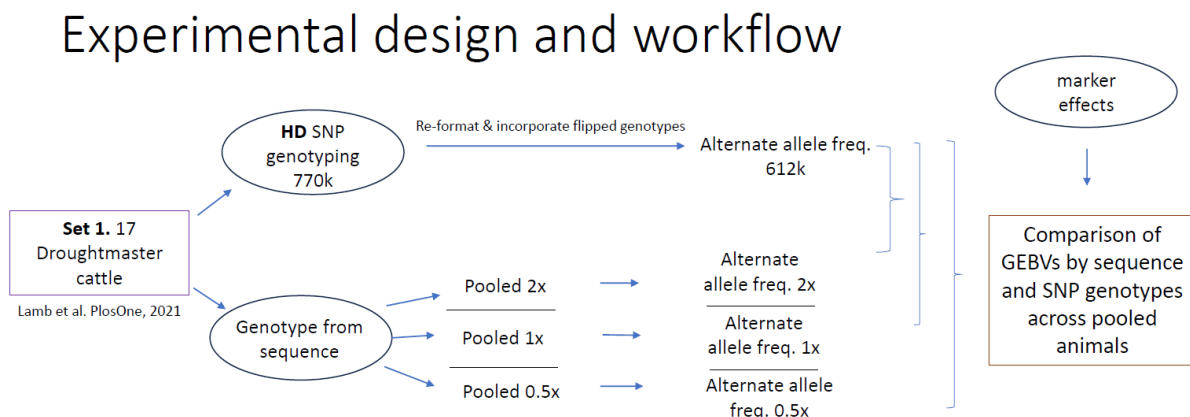
As the purpose of the herd profile is to benchmark each herd for genetic level for each trait, the rank (1-44) for each herd for each trait was calculated, for all animals genotyped, 100 random animals genotyped, 50 random animals genotyped, 25 animals genotyped, and 10 animals genotyped. The correlation of the rank of the herds, for all animals sampled, compared to the level of sub-sampling, demonstrated how much the benchmarking of the herds would change with each size of sampling.

3.3 A lower cost herd profiling product developed based on DNA pooling

An experiment was run to assess if DNA pooling could be used to derive low cost, accurate herd profiles. The approach here was to pool DNA from a cohort of animals, sequence this DNA (using Nanopore sequencing), call allele frequencies from this data, then compare the GBVs and Herd Profiles that are derived from the pooled sequence data to GBVs and Herd Profiles derived from SNP array genotyping, Figure 1.

The key question the experiment was attempting to answer was, what is the coverage of the animals required to get accurate allele frequencies of the SNP markers in the pool, and therefore accurate GBVs and herd profiles for the pool?

Figure 1. Experimental design and workflow for DNA pooling experiment. Seventeen Droughtmaster animals were sequenced at 0.5x, 1x or 2 x coverage. The pooled sequences were used to derive the frequency of the alternate (to the reference sequence) allele, and this information was used to derive GBVs for the pool. These GBVs were compared to GBVs from array genotyping to determine the accuracy of pooled genotyping.



3.4 Expressions of interest released targeting commercial companies and agencies to train and educate staff on the products and explore commercial partnerships for full commercial delivery.

An expression of interest to commercialise the GBVs and herd profile was developed in collaboration with MLA. The key criteria for selecting the commercialisation partner were:

- Demonstrated ability to deliver useful (actionable) information to Northern beef producers from analysis of large data sets.
- An existing extensive network of contacts with Northern beef producers, to ensure maximum penetration of the technology.
- A good understanding of the economic value of key traits like fertility for Northern Beef Producers.
- An understanding of the potential value of genetic improvement to the Northern beef industry, and a capacity to spend time with producers to explain GBV results and Herd Profile results.
- Capacity to deliver GBVs and Herd Profiles, and interpretation of results for many properties.
- Demonstrated ability to collect phenotypic records suitable for updating GBVs reference population over time, demonstrated capacity to store and analyse this data, with an existing client base in Northern Australia.

The EOI that was distributed is presented in Appendix 1. The EOI was advertised on the MLA website, and in addition was sent to multiple parties that could potentially provide the service.

Meetings were held with key applicants for further discussion following receiving written EOI responses.

Once a company was selected from the EOIs, based on their responses against the criteria, a round of capacity testing began, to determine if the company was able to produce GBVs and Herd Profiles given test genotype files.

3.5 Five case studies documenting how the technology is being used by commercial producers

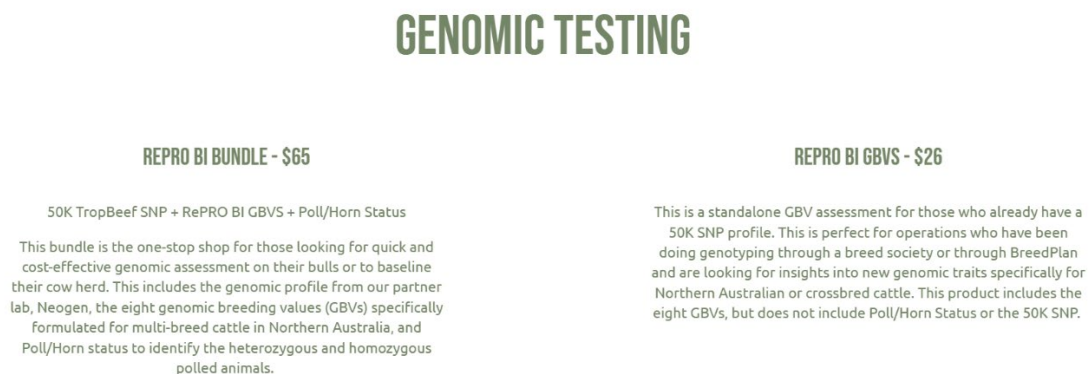
Case studies of producers using GBVs and herd profiles to improve their herds are presented in this report in section 4.5 The case studies attempt to demonstrate the herd improvements that are possible when heifers and bulls are selected on GBVs over a period.

4. Results

4.1 Make GBVs for fertility, growth and adaptation traits commercially available at low cost for Northern beef producers

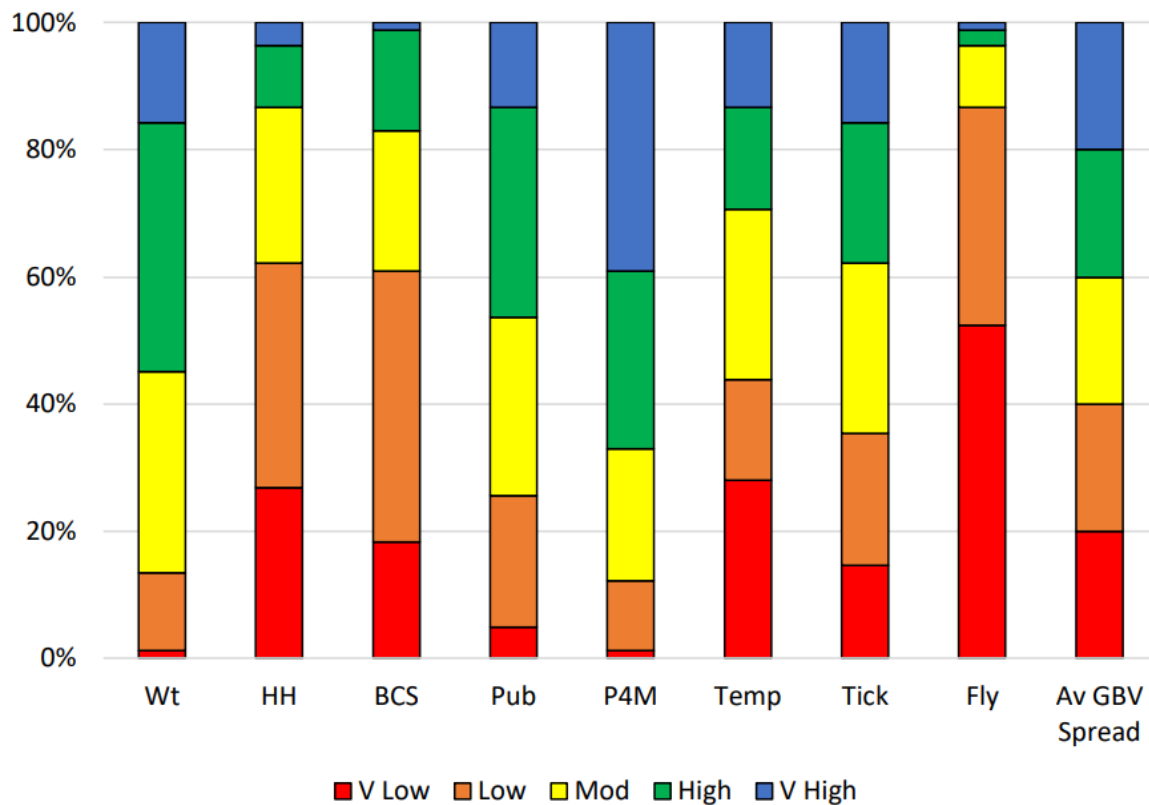
The GBVs and herd profile technology has been commercialised by Black Box Co as the “RePRO BI” product. The product bundles GBV, horned polled status, diagnostics for some genetic diseases, breed composition including *Bos indicus* proportion, and parentage, Figure 2.

Figure 2. Current pricing and package inclusions for RePRO BI GBVs from Black Box Co (<https://www.blackboxco.com.au/genomic-tests>)



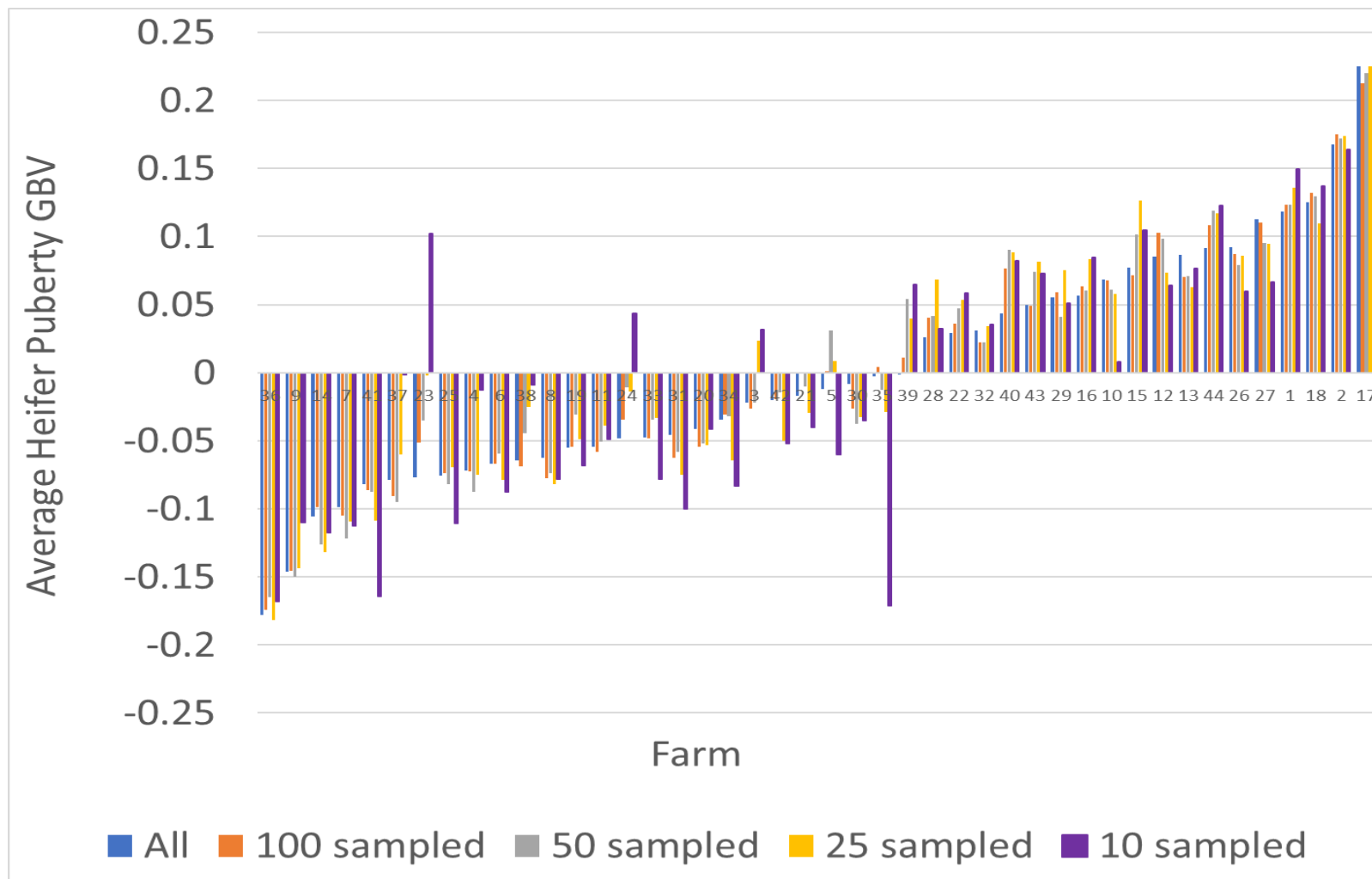
4.2 Herd profile product initially based on SNP arrays available for Northern beef producers

Herd profiles are produced for each herd with a reasonable number of animals genotyped (>100), by determining for each trait what proportion of animals in the herd have GBVs in each quintile of performance, where the quintile of performance is from a comparison across all 60 herds in the Northern Genomics Project, Figure 3.

Figure 3. Herd Profile for an example herd.

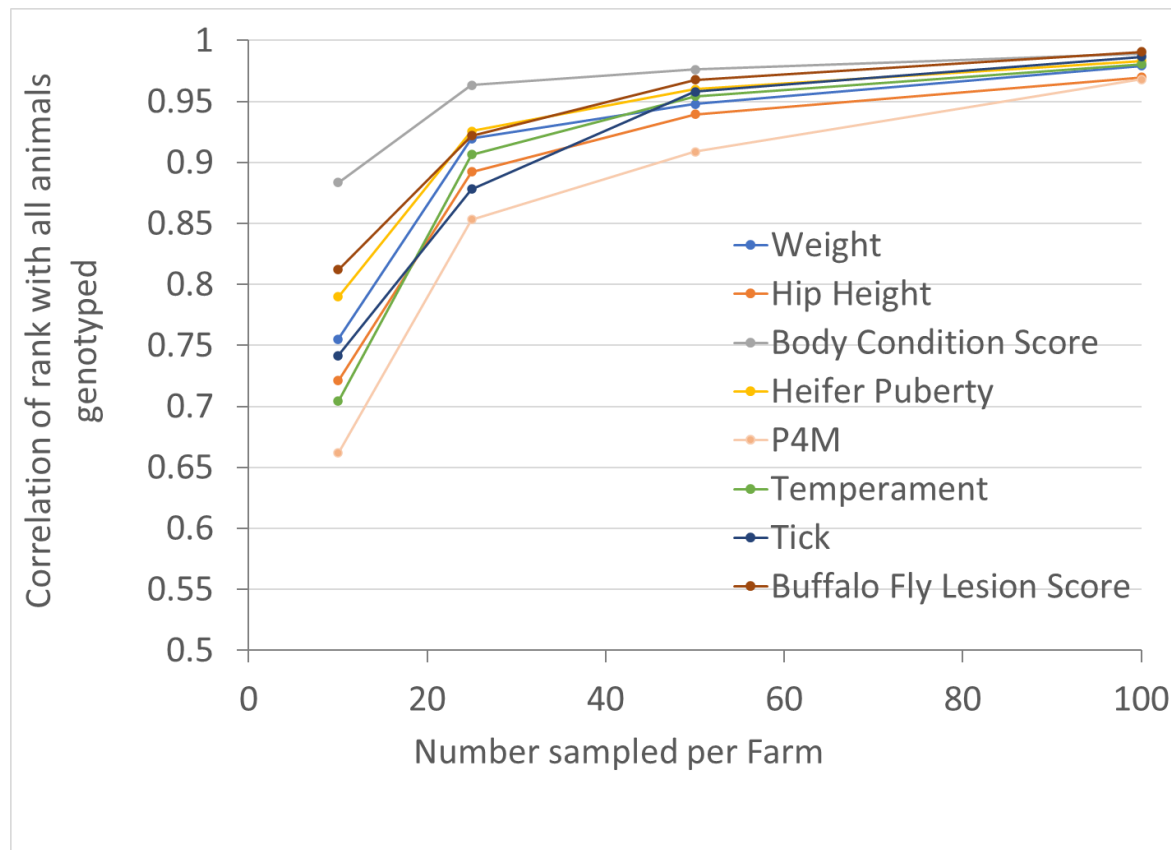
The research component of this objective was to determine the minimum number of animals that had to be sampled in a herd to get an accurate herd profile. To show the difference in average GBVs for heifer puberty across herds for the full data for each herd, compared to 100 animals sampled, 50 animals sampled, 25 animals sampled and 10 animals sampled (e.g. the herd profile for this trait with each number sampled). Figure 4 plots per farm, ranked from lowest to highest on average GBVs for heifer puberty for the whole herd, the average GBVs for each sub sample. The figure shows the differences between average GBVs for the whole herd genotyped and the sub-samples are quite small, until only 10 animals are sampled per herd, at which point the differences can be quite large.

Figure 4. Average GBVs for heifer puberty for 44 herds with greater than 200 animals genotyped, for all animals, 100 animals randomly sampled, 50 animals randomly sampled, 25 animals randomly sampled, and 10 animals randomly sampled. Herds are ranked on average GBVs for all animals



Next, to determine how the herds would perform when benchmarked based on the random sub-samples compared to the full herds, the ranking of the herds with all animals genotyped was correlated, compared to each sub-sample. The results (Figure 5) showed that the correlation when 10 animals were sampled from each herd was quite poor, while when 25 animals were sampled from each herd, the correlations were quite close to 1 (>0.85 for all traits and >0.90 for most traits). When 50 animals were sampled, correlations were >0.90 for all traits.

Figure 5. Correlation of herd rank (1-44) for 44 herds for average GBVs for all animals genotyped and average GBVs for a sub sample of animals, for eight Northern Genomics traits. P4M is pregnant or not four months after calving.



These results demonstrate if 50 animals are sampled per herd, there will be little difference between the herd profile based on all animals in the herd genotyped and the herd profile based on 50 animals genotyped, provided these 50 animals are chosen at random from the herd.

There was no significant difference at this level of sampling as shown in Table 1. In fact, there was no significant difference, as measured by a t-test between any of the levels of sampling and the full herd sampled, although with only 10 animals sampled the differences were closer to significance, especially for P4M (pregnant or not 4 months after calving).

Table 1. Value of Students t-test comparing herd average GBVs for all animals versus 100, 50, 25 or 10 animals sampled per herd. A value of less than 0.05 would indicate a significant difference at $P < 0.05$ for a two-tailed, heteroskedastic test.

Trait	Number sampled			
	100	50	25	10
Weight	0.88	0.88	0.86	0.68
Hip Height	0.90	0.65	0.53	0.89
Body Condition Score	0.92	0.96	0.91	0.81
Heifer Puberty	0.93	0.79	0.75	0.88
P4M	1.00	0.70	0.66	0.35
Temperament	0.95	0.98	0.84	0.70
Tick	0.90	0.92	0.85	0.90
Buffalo Fly Lesion Score	0.92	0.87	0.81	0.66

4.3 A lower cost herd profiling product developed based on DNA pooling.

In the experiment with 17 Droughtmaster animals, allele frequencies from the pooled DNA were very similar to allele frequencies from the high-density SNP array, when the coverage per animal was approximately 2-fold, with a correlation of 0.9 across 709768 SNP. This correlation dropped to 0.8 when the coverage per animal was approximately 1x, and 0.65 when the coverage was 0.5x. This suggests that at least approximately 2-fold coverage per animal, is required for accurate allele frequency, and therefore GBVs estimation, is required.

This conclusion was supported when we calculated average GBVs for the animals from the pooled DNA and compared them to the GBVs from the SNP array, Table 2.

Table 2. Average GBVs from high density SNP array genotyping (HD genotyping), and pooled DNA with approximately 2-fold coverage of each animal, 1-fold coverage of each animal, or 0.5-fold coverage of each animal. Traits are body condition score (BC), body weight at approximately 600 days (BW, kg), heifer puberty (CL) and hip height (HH, cm).

Trait	HD Genotyping	2x coverage	1x coverage	0.5x coverage
X1 (BC)	-3.21	-2.44	-1.82	-2.17
X2 (BW)	-13.9	-12.9	-12.09	-13.40
X3 (CL)	-0.15	-0.12	-.11	-0.09
X4 (HH)	0.14	0.1	0.07	0.04

At approximately 2-fold coverage, the average GBVs in the pool are closest to the average GBVs from the SNP array (HD) genotyping, while at lower fold coverage, the average GBVs increasingly diverges from the average SNP array results.

Some companies are now offering sequencing at a cost as low as \$1/gigabase of sequence. Given the bovine genome is 3 Gigabases, this means 2-fold coverage per animal is approximately \$6/animal. If

we take the above result that at least 50 animals must be sampled for an accurate herd profile, this implies a sequencing cost of \$300 for a herd profile. DNA extraction currently costs approximately \$5 per animal (\$250 per herd profile), so the total cost would be \$550 for a herd profile using the DNA pooling technology. This is currently much cheaper than obtaining a herd profile from SNP arrays on each animal (say \$60 per animal for 50 animals = \$3000). However, it would have to be assessed if there is market for the herd profile product in isolation from individual GBVs (to be assessed by Black Box Co).

4.4 Expression of interest released targeting commercial companies and agencies to train and educate staff on the products and explore commercial partnerships for full commercial delivery.

Expressions of interest were returned from five companies or consortiums. These EOIs were carefully screened against all criteria in the EOI. Black Box Co was selected as a potential provider at this point.

A rigorous assessment was then made of Black Box Co's capability to deliver GBVs and Herd Profiles.

In the first test, a set of 50k genotypes from one of the genotyping labs for 500 animals and dummy DNA marker effects (SNP effects) for 709,768 markers for 8 traits was utilised, in order to assess the ability of the Black Box Co team to run the GBVs pipeline and produce GBVs.

Briefly, the steps in this pipeline are:

- Quality control filtering of the 50k genotypes for animals in the run.
- Imputation of the 50k genotypes for the 500 animals to 709,768 SNP genotypes using a reference panel of key bulls, of breed relevant to Northern Australia, genotyped with high density markers.
- Calculation of GBVs for eight traits for each animal with the imputed set of markers and the SNP effects for the 709,768 markers.

Black Box Co confirmed that they were successfully able to run the pipeline on their virtual servers. In fact, they greatly reduced the run time for producing the GBVs from 4 hours to 1.5 hours by recoding parts of the pipeline to use multiple compute cores to run the imputation program.

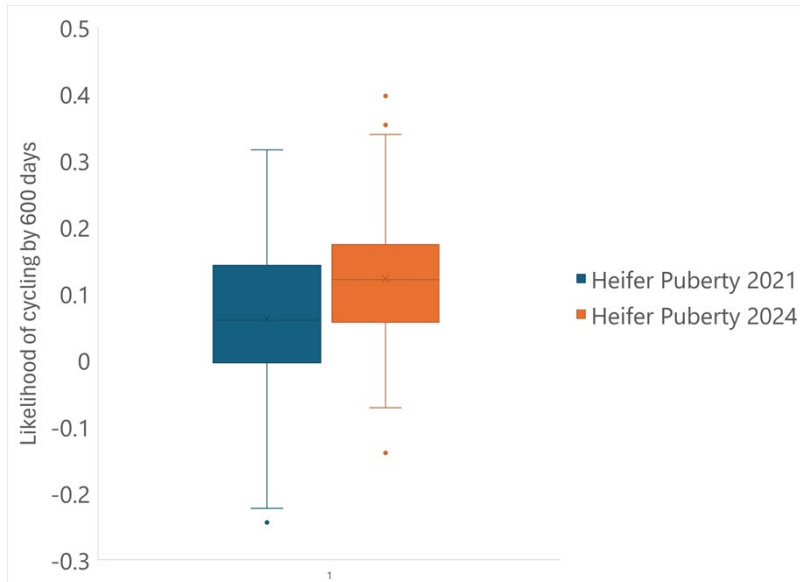
Given this successful run, MLA and Black Box Co then entered a commercial license. Following the signing of this license, a further two tests were conducted to demonstrate that the Black Box Co pipeline and the UQ pipeline were giving the same GBVs and Herd Profile for a set of genotypes from several herds. In both cases, this was confirmed. Strategies to maintain the reference population, to maintain or ideally increase the accuracy of GBVs, have begun to be put in place by BlackBoxCo and are reported on.

4.5 Five case studies documenting how the technology is being used by commercial producers

Quite a few northern beef herds have GBVs of animal cohorts and herd profiles for these cohorts over five years or more. Some of these herds have been using the GBVs for selection, both of bulls and heifers. One example is the Copley's, Brahman breeders near Crows Nest in Queensland. The Copley's use GBVs for heifer puberty to select heifers that will cycle earlier, aiming for a higher

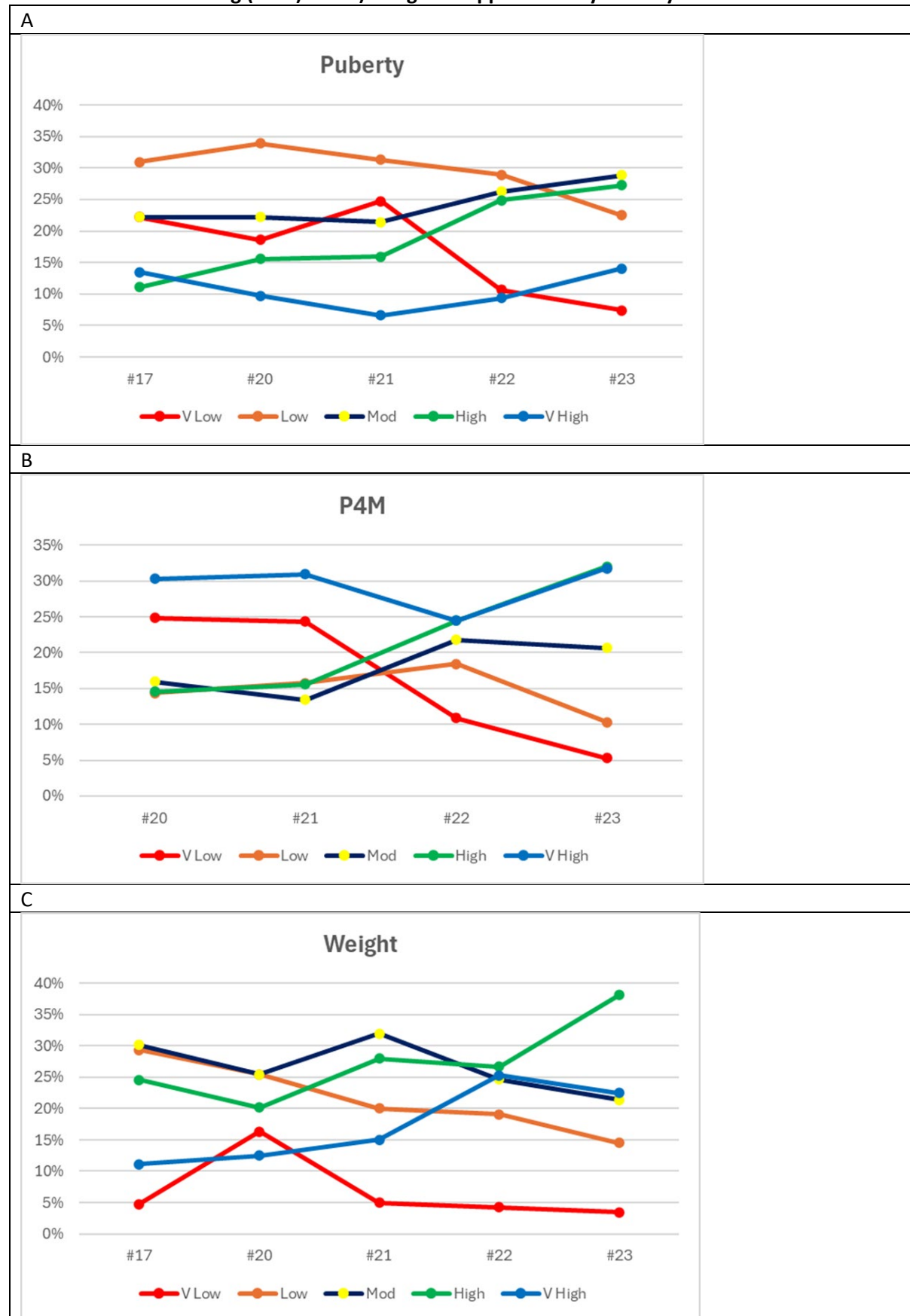
success rate with yearly mating. The Copley's have shifted heifer puberty GBVs substantially over this period, Figure 6, and a greater proportion of heifers are cycling early.

Figure 6. Distribution of heifer puberty GBVs in the 2021 and 2024 heifer cohorts in the Copley herd. A higher value for heifer puberty GBVs indicates the heifer is more likely to be cycling at 600 days.



Another example of GBVs enabling genetic progress for fertility comes from Andrew Mactaggart and families herd. Andrew and his family run a multi-generational beef enterprise north-east of Duaringa, in central Queensland. They have 2,500 open composite breeders, with 40–60% *Bos indicus* content and a balance of British and European genetics, capturing the benefits of hybrid vigour. They have genotyped heifer cohorts in the Northern Genomics project going back to 2017, Figure 7. With strong selection for P4M and heifer puberty, the proportion of each cohort in the high and very high quintile (top 20% and 40% respectively) compared to the Northern beef herd has increased substantially, Figure 7. At the same time 600-day weight has also improved.

Figure 7. Mactaggart herd profiles across 5 heifer cohorts for A) Heifer Puberty, B) Pregnant or not four months after calving (P4M) and C) Weight at approximately 600 days



Case studies based on these results, as well as for other herds, have been described in the media. A feature on the Copley's describing their use of both EBVs and GBVs to improve their herd was developed by MLA (<https://www.genetics.mla.com.au/case-studies/tom-and-marie-copley/>). The Copley's are now the leading herd on Brahman BREEDPLAN.

Andrew Mactaggart and families' herd, along with Michael Flynn's herd was featured in case studies, again from MLA. Michael Flynn has a Droughtmaster bull breeding operation south of Augathella, Queensland. Each year the Flynn's join 3000 females and produce 500 Valeravale Droughtmaster bulls. The two case studies were picked up by Beef Central:

<https://www.beefcentral.com/genetics/genomic-breeding-values-herd-profiling-to-turbocharge-genetic-gain/#:~:text=Genomic%20breeding%20values%2C%20herd%20profiling%20to%20turbocharge%20genetic%20gain,-Beef%20Central%2016>

A case study of the use of GBVs was recently produced by Black Box Co. This case study featured Chris Simpson from CAP genomics in the Brisbane Valley, and described how CAP genomics (composite cattle) were using GBVs and Herd Profiles to develop an internal genetics program to complement their Northern commercial beef strategy.

<https://www.theland.com.au/story/8732032/repro-bi-is-boosting-the-productivity-of-northern-beef-herds/>

The CAP genomics herd was also included as a case study in the Spring 2024 edition of FEEDBACK MAGAZINE, Figure 8. The CAP herd has demonstrated an improvement in heifer puberty over three years of genotyping, Figure 9.

Figure 8. CAP Genomics case study featured in the Spring 2024 edition of MLA's FEEDBACK magazine

Genetics set the baseline for improved production

Five years into developing an internal genetics program to complement their northern commercial beef production goals, CAP Genomics Pty Ltd has found good genetics to be the baseline for creating a cohesive and efficient supply chain through to market.

CAP Genomics was a collaborating herd in MLA's Northern Genomics Project, serving an integral role in the trailing and initial development of a genomic tool, known as RePRO BI. The tool is now commercially available to northern beef producers through Black Box Co – learn more on page 10.

CAP Genomics Managing Director Chris Simpson said leveraging advanced genomic and genetic tools enabled the company to effectively set, target and improve their herd's Genomic Breeding Values (GBVs) and Estimated Breeding Values (EBVs) to better their overall production.

Putting genetics first

According to Chris, CAP Genomics' genetic program aims to enhance the productivity of tropical composite breeds, with a specific emphasis on integrating African-derived *Bos taurus* cattle.

"We currently run just under 2,000 animals, but over the years we've genetically profiled more than 3,000," Chris said.

"While our genetic strategy is still in the development stage, we've found through our involvement in the Northern Genomics Project that developing a strong genetic base through data collection, integrity and science is fundamental in optimising other facets of the beef production process."

Chris said the project enforced the necessity of a strong selective breeding program.

"During the formative years of our internal genetics program, we applied stringent processes to our production system,

such as providing minimal nutritional support and implementing an agnostic natural joining program," Chris said.

"This approach was designed to 'stress-test' our system, allowing us to identify the most resilient and high-performing genetics, as well as poorest performing genetics under challenging conditions.

"By enacting these tests early on, we were able to not only see how our benchmarked traits identified through genomic profiling held up in practice, but also how important genetics are to continued herd productivity despite poor seasonal conditions."

He said, as a result, they determined:

- production levels above 75% were significantly influenced by good nutrition
- good genetics were crucial to optimise calf survival and productivity when environmental conditions and nutritional supply were less than ideal.

"We've discovered that through improving fertility and adaptability to harsher climates, our herd's genetics can set a strong foundation for us to establish a robust production system which supports long-term sustainability and profitability."

Analysing the data

Chris has seen a clear value from integrating advanced genomic tools into their breeding program as a result of their involvement in the Northern Genomics Project.

The RePRO BI tool provided information which they could use to immediately identify sire lines with

sub-par performance – critical for an enterprise which breeds its own bulls.

"Sires have the biggest genetic impact on the herd and this early identification of weaknesses enabled us to make informed decisions about which sires to retain or cull, thereby improving the overall quality of the herd," he said.

SNAPSHOT

CHRIS SIMPSON, CAP GENOMICS – Somerset region, Queensland

AREA
4,500ha

ENTERPRISE
2,000 cattle

PASTURES
Variable native pastures

SOILS
Variable soils

RAINFALL
1,200mm

In the longer term, the continuous genetic profiling with the RePRO BI genomic tool has enabled them to record GBV increases and analyse them alongside sire EBV and dam production data.

"With the tools' aid, we have been able to identify and report the uplifts we saw on the GBV results of our sires and their respective progeny cohorts," Chris said.

"Our success in analysing a sire's average GBV quotient has been reflected through one of our sire selections, acquired off the Maynard Cattle Company, who has produced an average GBV increase of more than 25% on 100% of his progeny.

"These GBV increases reflected the benefits of targeted breeding, demonstrating the effectiveness of our strategy to cull underperforming cattle and focus on enhancing key traits such as fertility and growth."

To better analyse and record herd performance, they overlaid EBVs and dam production data with GBV outputs.

"Combining and analysing GBV outputs, EBVs on sires and dam production data helped us clearly identify top contributors for our embryo donor program – which is aimed at expediting genetic gains from the original GBV benchmarks," he said.

"The outcome of integrating genetic data with a traditional

phenotypic analysis is enhanced decision making.

"Both data sources provide a comprehensive understanding of an animal, to make better informed breeding and culling decisions – ultimately leading to a more productive and more resilient herd."

Opening the doors to collaboration

As CAP Genomics continues to adapt and develop their internal genetics program, Chris said the next step will be to open the doors for collaboration and contributions from other producers.

"We are currently in the process of building an open-source platform (available within 12 months) which outlines our breeding and genetic systems," he said.

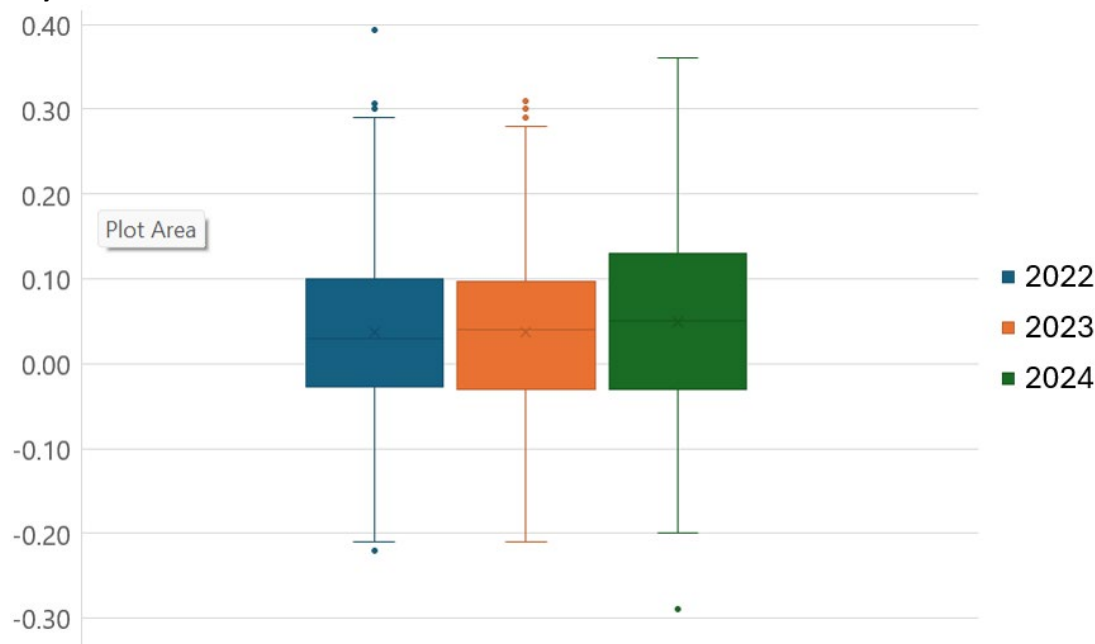
"Through this initiative, we hope to foster connections, innovation and continuous improvement to northern beef herds – as we are all in this together."

LESSONS LEARNT

- Data collection is the key to informed decision making.
- A good genetic foundation will aid long-term productivity when there are periods of nutritional deficiency.

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Figure 9. Distribution of heifer puberty GBVs in the 2022, 2023 and 2024 heifer cohorts in the CAP herd. A higher value for heifer puberty GBVs indicates the heifer is more likely to be cycling at 600 days.



5. Conclusion

This project has successfully commercialised two products, GBVs and Herd Profiles, that will enable Northern Australian beef enterprises with purebred, crossbred and composite breeds to improve fertility and other key traits. Six thousand additional records for heifer puberty, P4M (pregnant or not four months after calving), weight and body condition score have been collected from a range of herds to update the reference population used to calculate SNP effects which predict GBV, to improve their accuracy. For the Herd Profile tool, it was demonstrated that at least 50 animals must be randomly sampled for the tool to accurately represent the genetic level of the herd. In the future, the Herd Profile could be derived from DNA pooling of low cost genome sequence data, if there was a separate market for this tool in addition to the market for GBVs on individual animals. Finally, case studies of herds that have had access to GBVs for up to five years demonstrate that genetic gains for both heifer puberty and P4M can be achieved in Northern Australian herds using the tools.

5.1 Key findings

GBVs for eight traits including fertility and Herd Profiles from the Northern Genomics Project have been successfully commercialised, as “RePRO BI” by Black Box Co.

The GBVs and Herd Profiles have been bundled with horn/polled tests, parentage and disease diagnostics to improve the value that producers get back from taking a TSU or tail hair sample from their animals.

It has been demonstrated that 50 animals should be randomly sampled from the youngest cohort of animals to get an accurate Herd Profile to benchmark a herd, for fertility, parasite resistance, body condition score and other traits.

DNA pooling, followed by low fold sequencing, could be used to substantially reduce the cost of the Herd Profile, if the market for this product, independent of individual animal GBV, exists.

Case studies have demonstrated that selection on GBVs can improve herd fertility, including heifer puberty and P4M.

Strategies to maintain the accuracy of the GBV have begun to be implemented by Black Box Co.

5.2 Benefits to industry

GBVs for eight traits, including two fertility traits, are now commercially available for purebred, composite and crossbred cattle in Northern Australia. This will enable selection for these traits, in some herds for the first time. Several herds, with GBVs for cohorts over up to five years, have demonstrated improvement in fertility traits because of selection on these GBVs. Herd Profiles are also commercially available, which will enable Northern Australian herds to benchmark their genetic levels for the eight traits. This will guide bull selection decisions and lead to further genetic improvement. The GBVs and Herd Profiles have been bundled together with horned/polled tests, parentage, and some genetic disease tests to maximise value from taking a sample from an animal for DNA extraction. Low-cost Herd Profiles are possible using DNA pooling, if there is a market for this product as a standalone from individual GBVs.

6. Future research and recommendations

During the Northern Genomics Project, traits including udder and teat scores were recorded in some herds. GBVs have not yet been developed for these traits. Given the importance of these traits for calf survival (Frisch, 1982), provided genetic variation was sufficiently high, GBVs could enable selection for improved calf survival.

Now that the commercial pipeline for GBVs has been established, GBVs can be calculated for any animal using their genotype and SNP effects for a trait. Projects recording traits like methane and consumer eating quality, could develop GBVs for these traits, provided the reference population used to calculate SNP effects is relevant for Northern Australia. This approach should be considered to enable Northern Australian cattle producers to select for these traits.

7. References

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Hayes, B.J., Copley, J., Dodd, E. et al. Multi-breed genomic evaluation for tropical beef cattle when no pedigree information is available. *Genet Sel Evol* 55, 71 (2023). <https://doi.org/10.1186/s12711-023-00847-6>.

8. Appendix 1. Expression of interest: Northern Genomics commercialisation

The “Northern Genomics Project” has collected fertility, weight, body condition score, tick score and buffalo fly lesion score data on up to 36,000 heifers on 54 properties across Northern Australia. The heifers, representing many breeds, crossbreds, and composites, have been genotyped with a 35k or 50k SNP array. The data have been used to derive prediction equations for GBVs for the traits described above. Validation in independent herds demonstrated the GBVs had useful accuracy across the breeds, crossbreds and composites used in Northern Australia. As well as GBVs for individual animals, the project has also produced Herd Profiles, which benchmark herds for performance in Northern Australian environments. The herd profiles can be used to guide bull selection and culling decisions.

We are seeking a company to commercialise the GBVs and Herd Profiles so they are available to Northern Beef producers, with the aim of accelerating genetic gain in Northern beef herds. This entails working with producers to collect tail hairs or ear punches, for extraction of DNA, submission of these samples to a genotyping company, then calculation of GBVs and Herd Profiles based on these genotypes (and using prediction equation for each trait derived by University of Queensland) for delivery back to the producers.

In 2022, the GBVs were offered as “research breeding values”, calculated by University of Queensland, and interest was strong, with GBVs calculated for more than 15,000 cattle, despite very limited advertising.

Key criteria that will be used to select the company for commercialisation are

- Demonstrated ability to deliver useful (actionable) information to Northern beef producers from analysis of large data sets.
- A existing extensive network of contacts with northern beef producers, to ensure maximum penetration of the technology
- A good understanding of the economic value of key traits like fertility for Northern Beef Producers
- An understanding of the potential value of genetic improvement to the northern beef industry, and a capacity to spend time with producers to explain GBVs results and Herd Profile results.
- Capacity to deliver GBVs and Herd Profiles, and interpretation of results for many properties.
- Demonstrated ability to collect phenotypic records suitable for updating GBVs over time, demonstrated capacity to store and analyse this data, with an existing client base in Northern Australia.

We will provide support for interpretation of results with a cost benefit analysis for using the technology, and case studies from producers who have been involved in the project and so have GBVs for their project heifers.