Report of the Industry Working Group

Chaired by Colin Glass.

Nicola Shadbolt, Steve Allen,

John Penno, John Roche

Report of the Industry Working Group (IWG)

Introduction

Genetic improvement has been a key driver of the success of the New Zealand dairy industry and results from efforts and investment by successive generations of dairy farmers directly and through the ecosystem that they have helped to create and fund.

The IWG has taken an approach that looks to the future and asks how to create the most value for the industry and protect what has been built over generations, taking into account the complex commercial interests, investments and relationships that are fundamental to the system, and recognises that these will continue to evolve. Having two well established players is an advantage to make the changes that are required to maximise genetic gain in the New Zealand herd. In the New Zealand system, LIC has a unique and privileged position, being custodian of inter-generational investments by New Zealand farmers. The IWG believes LIC's scale and resources will benefit New Zealand in the era of genomic technologies, but their position also comes with responsibilities to the whole sector.

The IWG recommendations reflect this view of the New Zealand genetics landscape, and goes a step further to say that there must also be provision for new and serious competitors, able to invest in data and capability for genomic evaluation, to enter the market and offer competitive products to New Zealand farmers. In the IWG view this is an appropriate approach for the dynamic, market-oriented, innovative and globally competitive dairy industry that we have in New Zealand.

The IWG fully appreciates that the issues raised in this report are difficult and complex, and that in the current environment there is frustration, confusion, duplication and siloed ways of working across the system. However the IWG is also encouraged by signs of growing openness to making change that will unlock value for the industry as a whole. The recommendations in this report are a call for change based on a shared, collective responsibility owed by all parties to New Zealand dairy farmers, and for all parties to find solutions through leadership and commitment to work together.

Executive Summary

In answer to the key questions in this Review, the IWG believes the current system for genetic gain in New Zealand is not fit-for-purpose and that the genetic progress of the New Zealand dairy herd has lagged relative to other advanced dairy industries. This is because, for multiple and complex reasons, over the last decade we have not been as successful in adopting genomic technologies to speed up rates of genetic gain. There is broad agreement on this.

The IWG is absolutely confident that New Zealand will catch up and will fully harness the benefits of genomics for faster genetic gain. While there have been bad luck and false starts there have also been a combination of ongoing challenges for using genomic technologies, some of which are unique to New Zealand. The IWG has drawn on expert advice from Professor Ben Hayes to identify and understand these, and his report is being made available to offer others the same opportunity.

The first challenge is our significantly cross-bred dairy herd, requiring a far larger reference population for genomic evaluation (estimated to be at least 400,000 animals) than single-breed herds, particularly for lower heritability traits such as fertility, and requiring high quality genotypic, phenotypic and parentage data. There is not currently a reference population meeting these requirements in New Zealand and it will take significant investment and effort to establish and keep such a population current.

The second factor is the significant decline in the quality and accuracy of New Zealand's phenotypic data. In the genomics era high quality phenotypic data is of even greater importance to be able to make reliable, unbiased genomic estimates, but around 50% of our current data is poor quality. One estimate is that quality data is available for only around 40,000 cows or 10% of the target reference population size.

The third challenge is the lack of confidence of breeding companies and farmers in the use of genomically-evaluated young sires and sons of sires. A range of factors stemming from lower reliability of genomic estimates are causing this, including movement in breeding worth, breeding value figures and rankings for individual animals, as well as potential for multiple and different figures for the same animal (genomic and/or daughter proven) depending on the source of the data and herd recording platform.

These factors are indicative of a genomics-based system that is still reaching maturity, and will continue until the size and quality of the reference populations being used achieves a higher level of reliability for genomic estimates and uptake of young genomic sires increases.

On the other side of the breeding equation, low selection pressure, due to the rapid growth of the national herd in recent decades and declining reproductive performance, has slowed improvement of the average genetic merit of the national herd. Constraints on herd growth and use of technologies like sexed-semen will start to see more selection pressure and farmers will increasingly need good information and support in making management decisions to improve the genetic merit of their herd.

The IWG has made recommendations it believes are the most efficient and effective options for starting to develop a system that enables faster genetic gain in the interests of dairy farmers in New Zealand, leveraging the strengths we have as a small country facing unique challenges.

The recommendations aim to strengthen and reinforce the importance and relevance of the National Breeding Objective, improve phenotypic data quality collected from commercial herds and to create an environment where breeding companies and others can use genomic technologies to make genetic gain as fast as possible.

They focus on providing clear roles and responsibilities for the different aspects of the system aligned to where data, resources and capabilities lie; achieving greater reliability of genomic estimates through fit-for-purpose reference populations with high quality data; increasing transparency of the system and mechanisms for independent audit and validation to build trust and confidence; providing better support to farmers to enable them to improve the genetic merit of their herds and removing sources of confusion; and building New Zealand's technical knowledge and capabilities for multi-breed genomic evaluations.

The IWG has not tried to solve 100% of the issues that parties and stakeholders have raised, but to identify first and fundamental steps toward a better system. The IWG does not have the mandate or capability to develop all the solutions that will be needed. This must be the responsibility of all the key parties in the system using their combined experience and expertise. It is clear that change is required, but to be enduring the key stakeholders must agree and work together. The IWG do not believe regulation is the solution.

These recommendations will not work without all parties committing to working together and showing leadership to overcome the many barriers that are causing frustration and preventing New Zealand from being as successful in genetic improvement as it has in the past, and can be in the future. The IWG aims to reconvene in three months to assess progress against these recommendations.

Terms of Reference for this Review

The Industry Working Group (IWG) was convened by the DairyNZ Board for the purpose of "*providing an objective evaluation of the current state of genetic improvement in the NZ dairy sector relative to other advanced dairy industries, whether this can be substantially improved, and if so to recommend how this can best be done to protect and enhance our competitive position in the global market.*"

The IWG was tasked to "*deliver a Review of the NZ Dairy Genetics Sector that states:*

- *whether or not the current New Zealand system for genetic gain is fit-for-purpose, including whether New Zealand's rates of genetic gain in important production, functional and environmental traits are similar to other advanced dairy industries around the world (and, if not, why not);*
- *the extent of the productive and environmental sustainability losses associated with any difference between NZ rates of genetic gain and those of comparable industries;*
- *the reasons for this state of the sector including demographics (e.g. farming systems, herd size and breed composition), the industry's history and evolution, structure, conduct, contractual arrangements and precedents, IP ownership, investment, supporting regulations or other factors; and*
- *feasible and pragmatic recommendations to sustain optimal genetic gain in the NZ dairy sector (including a path to implementation).*"

The IWG was asked to engage key stakeholders such that they are party to the process and its conclusions.

In the course of developing this report and recommendations, the IWG has engaged with representatives of:

- NZAEL and the NZAEL Farmer Advisory Panel (FAP)
- Breeding/Herd Testing companies LIC and CRV
- Ministry for Primary Industries
- Breed societies JerseyNZ, NZHFA
- Federated Farmers Dairy Industry Group
- Farmers and bull breeders

IWG has also engaged with technical genetics experts Dorian Garrick, Private Consultant, and Peter Amer of Abacus Bio.

The IWG was supported by independent technical advice from Professor Ben Hayes of the University of Queensland.

Professor Hayes has extensive research experience in genetic improvement of livestock, crop, pasture and aquaculture species, with a focus on integration of genomic information into breeding programs, including leading many large scale projects which have successfully implemented genomic technologies in livestock and cropping industries.

He is the author of more than 300 journal papers, including in Nature Genetics, Nature Reviews Genetics, and Science, contributing to statistical methodology for genomic, microbiome and metagenomic profile predictions, quantitative genetics including knowledge of genetic mechanisms underlying complex traits, and development of bioinformatics pipelines for sequence analysis.

The relevance of Professor Hayes' expertise to provide advice to the IWG was confirmed by the key parties, particularly with respect to genomic prediction (of which he was a co-inventor). The IWG is grateful for the support and advice they have received from Professor Hayes. His report is provided as an Appendix to this report.

In undertaking this Review the IWG has maintained an open approach to considering the issues and potential solutions, listened to the views of the parties and stakeholders and focussed on the needs and interests of New Zealand dairy farmers. The IWG would like to acknowledge and express their deep appreciation to all those who gave their time to meet with the IWG and contribute to this Review.

New Zealand's genetic gain performance relative to other comparable industries

The IWG was asked to report on "whether or not the current New Zealand system for genetic gain is fit-for-purpose, including whether New Zealand's rates of genetic gain in important production, functional and environmental traits are similar to other advanced dairy industries around the world (and, if not, why not)."

The IWG has reached the opinion that the current New Zealand system for genetic gain is not fit-for-purpose due to a combination of structural, behavioural and other factors that will be identified in this report.

Making international comparisons of genetic gain requires some caution not to assume genomic estimates align with validated daughter proven performance data, as there are known risks of over-inflation of genomic estimates when reliability is low, and countries have different approaches to collecting phenotypic data enabling actual genetic gain to be assessed.

Data comparing New Zealand's rates of genetic gain with those of other advanced dairy industries around the world suggest that progress has lagged in New Zealand and this is particularly evident during the decade 2010-2020, when the comparison nations made use of the significant advantages offered by genomic selection.

While the specific figures or metrics used to compare our relative performance may be debated, there is no disputing that New Zealand has not seen the uplift in genetic gain that could be expected from genomics since the technology has become commonly used around the world. In fact, the IWG notes that if the analysis of Holstein genetic gain rates only is correct[1], New Zealand's genetic gain lagged other comparable countries even in the pre-genomics era for this single breed. There are no comparisons available for crossbred populations and this, the IWG understands, is a source of complexity for the New Zealand herd.

---

[1] See figure 1A in Professor Hayes' report.

There seems to be alignment among industry and geneticists as to why New Zealand has not had the same success. The differences in performance from 2010-2020 reflect other countries' more successful adoption of genomic technologies to speed up rates of genetic gain. By using young genomic bulls, and, in particular, using the technology to select sons of sires, other dairy producing countries have greatly shortened generation intervals (and achieved other related benefits for breeding), and accelerated genetic progress of the specific breeds in their dairy herd. As noted in Professor Hayes' report, reluctance by the industry to use young genomic bulls and sons of sires "is the main factor limiting genetic gain in NZ".

The reasons for New Zealand's historically lower use of young genomic bulls and sons of sires are complex and are explored further in the next section of the report. In summary the IWG view is that genetic progress in New Zealand has not kept pace with international dairy industries due, at a high level, to a combination of:

- the greater genetic heterogeneity associated with New Zealand's crossbred dairy herd (now 60% of the national herd)[2],
- poor quality and insufficient volume of phenotypic data compromising accuracy and reliability of genomics, and
- a lack of confidence in the use of genomics by both breeding companies and farmers.

In terms of the 'Breeder's Equation', these factors have been a barrier to leveraging genomic technologies to shorten the generation interval and progressing the genetics of elite bulls in New Zealand.

On the cow side of the equation there has also been a slowing of genetic improvement arising from low selection pressure over the last few decades due to the substantial growth of the New Zealand dairy herd from 3.5 million to 4.9 million cows (from 2000-2020)[3], and the significant increase in overseas genetics in the national herd with generally lower fertility, combined with increased herd size and challenges with on-farm capability. Even as growth in the national herd has slowed, genetic gain has continued to be low due in part to declining reproductive performance and slow uptake of sexed semen.

The IWG was also asked to report on the "extent of the productive and environmental sustainability losses associated with any difference between NZ rates of genetic gain and those of comparable industries". Having concluded that New Zealand has not made comparable rates of genetic gain from the use of genomics as other countries, it follows that potential benefits from genetic gain will, also, not have been realised to the same extent. However, it would be very difficult to compare or quantify these accurately, considering there have also been very significant changes in the New Zealand dairy farming system during the same period, relative to international comparisons, and these variables are likely to have a greater impact on profitability, and N-surplus and greenhouse gas emissions (indicators of environmental sustainability), than changes in cow genetics. There is also the need to consider potential benefits for New Zealand being slower to fully adopt genomics, in that we can learn from the experience of others around unintended consequences from rapid uptake of this new technology, such as increased rates of in-breeding.

---

[2] 3 Regional dairy statistics | Dairy_Statistics_2022-23_book.knit (dairynz.co.nz)

[3] https://connect.dairynz.co.nz/2022-23_Dairy_Statistics/national-dairy-statistics.html#herd-production-statistics

To answer the Board's question as to whether the current situation can be substantially improved, the IWG has no doubt that it can be. New Zealand has had a slow start in uptake of genomic technologies for genetic improvement, but there is every opportunity to catch up and fully realise the benefits of genomics for achieving genetic gain. As well as the technical and structural recommendations outlined in this report, success also requires a meaningful behavioural shift from all players toward better cooperation and increased collaboration, in their own interests as well as those of the dairy industry.

Genetics will have an increasingly important role to play in optimising the New Zealand dairy herd in a growth-constrained environment, to increase productive efficiency with the lowest possible greenhouse gas emissions intensity and to meet New Zealand's international commitments, so that every cow is the very best cow for New Zealand's unique farming environment.

The reasons for the current state of the sector with respect to genetic gain

The IWG was asked to report on "the reasons for this state of the sector including demographics (e.g. farming systems, herd size and breed composition), the industry's history and evolution, structure, conduct, contractual arrangements and precedents, IP ownership, investment, supporting regulations or other factors."

In the IWG's view, the key question is why New Zealand's use of young genomic bulls and sons of sires has been lower than other countries. All the mentioned reasons in the Terms of Reference have played a role and the causes are complex. They do not rest with any one party or area of the system but cut across all aspects. As noted above the IWG believes a combination of three factors has been key: New Zealand's mixed-breed dairy herd, declining phenotypic data quality and lack of confidence in genomics.

The IWG agrees with the view that the genomics era has different requirements than the preceding progeny-test era and that, in several key areas, we have been slow to adapt to this fundamental shift and equip dairy farmers to do the same.

1 New Zealand's mixed-breed dairy herd

As outlined in Professor Hayes' report, New Zealand is unique in that a large proportion of cows in the population are crossbred (60% and growing) and crossbred (HFrxJ) bulls are also used. The multi-breed composition of the New Zealand dairy herd makes achieving high reliabilities of genomically-estimated breeding values (gBVs) much more challenging and, importantly, this was not understood when use of genomic technologies became widespread toward the end of the first decade of the 2000s. As highlighted by Professor Hayes in Table 1, this derives from the higher number of ancestors for mixed bred animals as opposed to a single breed (estimated to be around 5x higher for our mixed breed herd including crossbreds). A further factor is the low heritability of some traits of interest for New Zealand.

As a result of the very 'New Zealand' mixed breed profile, the reference populations providing the data on the traits of interest to New Zealand (as reflected in the National Breeding Objective (NBO)) must be significantly larger than in a more genetically homogenous, single breed population or for more heritable traits. The extent of this greater requirement was not understood in the early stages of employing genomic selection globally.

As presented by Professor Hayes, a reference population (with high quality phenotypic, parentage and genomic data) of around 400,000 cows would be appropriate for New Zealand to make genetic progress in selecting for low heritability traits. Neither LIC, CRV or NZAEL have a reference population of this size (although the IWG understands the breeding companies are continuing efforts to enlarge their reference populations).

New Zealand breeding companies have been conducting genomic evaluations over the last decade with suboptimal reference population sizes for a mixed breed herd. The reliability of the genomic proofs has therefore been low and, as a result, there has been low trust and confidence in use of the technology.

Table 1

		Trait heritability	
Scenario	Effective population size	0.3	0.1
Single breed	100	45,933	136,906
Multi breed	500	131,592	392,425

Source: Analysis of Prof Hayes, Table 1: Size of reference population (cows genotyped and recorded for the trait) required to achieve a reliability of 0.7 for genomic estimated breeding values for young genomic bulls (with no daughters), for trait heritabilities of 0.3 (e.g., production) and 0.1 (e.g., fertility), for single breed and multi-breed populations. Based on the formula of Goddard and Hayes (2009).

Appropriate methodologies for genomic evaluation in multi-breed populations are still evolving. As well as the requirement for larger reference populations, multi-breed populations also require more complex genetic evaluation models, to take account of breed effects, heterosis, and to avoid bias. Professor Hayes' report provides analysis of published reports by LIC and CRV on the reliability of their genomic evaluation models.

2 Insufficient phenotypic data in terms of volume, quality and accuracy

Experts have advised the IWG that around 50% of data from herds is of a poor quality. Data quality is of critical importance for genomics as reference populations based on poor data will lead to increased bias and lower reliability.

Genomics requires sufficient numbers of genotyped cows with good trait records, however New Zealand does not have enough cows with both high quality ancestry and phenotypic data covering both production traits from herd testing and Traits other than Production (TOP). As noted above, TOPs of interest like fertility generally have lower heritability requiring a larger reference population size and robust data. To achieve this for a reference population of at least 400,000 cows is a significant increase from where we are today (IWG understands there may only be around 40,000 cows with sufficient quality of phenotypic data or 10% of this target). To close this gap it is suggested to take a targeted approach, as the wider the data set to be collected is, the harder it will be to get good quality data.

Currently data from herd testing supplies DIGAD with 46 fields required by the regulations to be provided by certified Herd Testers. Around 110 other (unregulated) fields are currently provided for animal evaluation purposes as a result of commercial negotiation between NZAEL and the breeding companies/Herd Record Providers i.e. LIC and CRV. The breed associations also play a key role in collecting TOP data. However data from cross-bred herds on commercial farms may not be adequately represented given that they make up the majority of the national herd.

The factors that have led to the declining quality of phenotypic data include:

- The changing demographics of the New Zealand dairy farming system where both cow numbers and farm size increased significantly over the last 20-30 years, creating challenges for accurate record keeping of calving dates and parentage, and farm systems became more diverse (e.g. milking regimes other than the historic standard of milking twice per day)
- New Zealand has a less frequent level of testing than is standard in other parts of the world and this is becoming worse. New Zealand had four tests per year, whereas the standard internationally is for monthly pm/am herd testing - about ten herd testing events for each cow across a lactation. In response to cost pressure, many farmers may be only testing once per year (either an am or pm test).
- Even if there is an accurate measurement of pm/am milk volume, fat and protein percentage, data such as breed, dams and sires and date of calving is less accurate. For example many herds have inaccurate calving data, evident from fewer calving days being recorded than mating days (more reliably recorded by technicians) or more calvings recorded on the same date. It is also not possible to see where poorer cows have been temporarily withdrawn and preferentially fed or where hormonal interventions might have been used. There is also a lack of correct parentage information on the female side for many cows in New Zealand.

3 A lack of confidence to use genomics

Considering New Zealand farmers' uptake of breeding technologies from the 1960s onwards would have rivalled most nations, low confidence and trust in genomic technologies is probably the primary reason why there hasn't been the same uptake of young genomic sires in New Zealand during the last decade. Instead, farmers have shown a continued preference by many for daughter proven bulls, and the use of 'team approaches' by breeding companies, to mitigate the risks of less reliable estimates of Breeding Worth (BW) and Breeding Value (BV).

As outlined in Professor Hayes' report, New Zealand has had false starts in the use of genomic technologies for animal improvement and this has undermined confidence in the use of genomic young sires. This experience gave breeding companies good cause to be cautious in promoting animal insemination (AI) products based on genomics alone to their customers, and farmers good reason to be cautious in using young genomically-evaluated sires.

As well as the false starts, confidence in the use of genomics by farmers and breeders has been undermined by the movement in BW and individual BVs that occurs when reliability is low and as actual daughter performance data become available and the early genomic evaluations are replaced by values based on actual daughter performance.

This is a feature of genomics and a marked shift from the progeny-test era. It is analogous to changes in financial reports from forecasts to actual figures, a phenomenon farmers will be very familiar with. While farmers and breeders have understandably expressed concern at the level of movement in BW and BV figures for individual animals, it is a feature of genomics that will abate over time as reference populations used for genomic evaluations increase (to at least 400,000 cows) and parentage accuracy and the quality of phenotypic data improve. Professor Hayes highlights Australia's experience where, once reliability of around 70% had been achieved, there was an improvement in farmer confidence to use young genomic sires.

Reference populations are critical for genomics. Reliability should increase with a larger reference population, resulting in smaller differences between genomically estimated BW (gBW) and a daughter proven BW. The trend from such a comparison is a key indicator of the successful adoption of genomics and that breeding companies are doing the right things, and it should be regularly and transparently monitored and reported on.

An issue that is further confusing farmers and undermining trust more broadly in the information they receive about BW and BV is that they may have multiple numbers for the same animal from different trusted sources (potentially up to three BW figures for the same bull and based on the same NBO if they are CRV customers (i.e. an NZAEL figure, an LIC figure and a CRV figure)). There are gBWs based on the inclusion of genomic data and BWs based purely on daughter proven data. The gBW numbers will differ from entity to entity, as they are based on different and smaller than desirable reference populations for calculating gBW which can result in quite a different gBW for the same bull. Overall, the differences observed by farmers and drawn to the attention of the IWG can be significant.

In addition, as noted in Professor Hayes' report, because the accuracies of gBV from each evaluation are modest (e.g., 0.5-0.74), the gBV calculated by the different organisations will have a low to modest correlation and this will be reflected in major re-ranking of young bulls on gBV between organisations.

These variations in bull gBW have a consequential impact on Cow BW which can have a direct financial impact on farmers. This is of particular concern for share milkers as the genetic merit of their herds has implications for herd financial value and their ability to secure sharemilking positions. Of serious concern from a genetic gain perspective is that farmers may not have the best information to base their breeding and other management decisions on. The variability also risks undermining the value of having a NBO to guide the industry toward the optimal genetic make-up of a cow for New Zealand conditions. Some breeders and farmers have lost confidence and trust in the New Zealand BW system (including to start looking internationally for their genetics with the risk of suboptimal outcomes in the New Zealand context).

NZAEL has indicated it will soon include genotypes in their animal evaluations based on a reference population that they are developing, but this will not resolve the confusion. There is a risk that farmers and breeders may give NZAEL figures credence given their industry-good, independent position. Perversely, NZAEL may generate the least reliable genomic estimate in the market, given their considerably smaller reference population.

Some industry practices have also been highlighted that add to mistrust of the animal breeding companies and impact on the information available to support farmer decision making. These include:

> <u>Restrictions on the use of Cow BW</u>: The IWG understands that there are IP protection arrangements applying to Cow indices and animal evaluation outputs for cows, including Cow BW that is evaluated against the NBO, such that only LIC is able to provide or publish Cow BW in New Zealand. LIC does so to its MINDA clients and other parties under commercial terms.
>
> The implication for CRV or any other breeding company is that they must enter into commercial arrangements with LIC to gain access to Cow BW information or to publish Cow BW information to their own customers, even if they were to have the technical capability to produce their own cow genomic evaluations using their own data.
>
> The possible implications for genetic gain are that it restricts identification of dams of young genomic bulls and the use of genomic information by dairy farmers to select heifers for breeding.

This is potentially less relevant currently, but would be more important if sexed semen use increases in New Zealand, for example, and for use in dairy beef.

Restrictions on information to farmers: It has been reported that breeding companies may not provide genomic test results of bull SNPs to the bull breeder unless they decide to purchase the bull and then only after the purchase is made. The IWG understands this practice may be changing.

On many occasions the IWG has heard the view that the genotype should belong to the farmer who owns the animal from which the genotype has been collected. The IWG view is that the value is not in the genotype itself but in the evaluation of an individual genotype against the wider reference population dataset. Its value, therefore, is dependent on the animal breeding company's infrastructure and capabilities for genomic evaluation (their IP).Without this a genotype has little value to a farmer.

However, that does not mean that companies should withhold data that unfairly disadvantages farmers from being able to understand the potential or market value of their bull, particularly when they are negotiating the sale of that bull with the breeding company concerned. The IWG understands that contractual terms between breeding companies and farmers place restrictions on the use of the first generation of progeny for artificial insemination. However the IWG has heard and agrees that, subject to these restrictions, the information still has value to a bull breeder for their own breeding requirements.

Sustaining optimal genetic gain in the New Zealand dairy sector

The IWG was asked to make "feasible and pragmatic recommendations to sustain optimal genetic gain in the NZ dairy sector (including a path to implementation)". In the next section the IWG sets out its view on the most feasible and pragmatic options for improvement to ensure New Zealand can capture the opportunities of genomics for sustaining optimal genetic gain aligned to current and future NBOs.

The recommendations are based on conclusions and judgements made through the course of this review. These are set out here to provide context for the IWG's recommendations.

Data quality:

Addressing the decline in data quality is an urgent priority. Expert advice suggests rather than seeking to lift the quality of all herds recorded (which would create additional costs for farmers and is unlikely to be adopted) there should be a more targeted focus on elite commercial herds to provide high quality phenotypic data for a reference population of at least 400,000 cows. High quality phenotypic data on daughters is also needed to assess how well the system is working and should be available for all the traits in the NBO. Farmers who are providing high quality data should be rewarded to recognise that they are doing the heavy lifting for other farmers who benefit from the data without the cost of collecting it.

The IWG does not recommend making any changes to NZAEL's role with respect to maintaining and managing DIGAD.

Industry structure:

New Zealand's genetics industry is, for all intents and purposes, a duopoly, with two main players in LIC and CRV, and a few other smaller companies. It is characterised by being a relatively small market with power and resource imbalances. LIC is by far the dominant player with a market share for herd testing and animal breeding above 80%, near universal coverage of its farmer facing platform MINDA, and a history in the sector that provide it with many competitive advantages.

These are also advantages for New Zealand dairy farmers in the genomics era where large data sets and increasingly sophisticated methodologies are required. LIC has the necessary scale, capabilities and ability to invest in developing their reference population and their expertise in genomic evaluation, while CRV has global reach and access to leading global technology, expertise and capability.

Other competitors should be welcome if they bring similar levels of investment to the market, but not at the expense of a commercially sustainable animal breeding industry that can continue to invest in new technologies and bring them to market in New Zealand, including operating breeding programmes to produce the animals best suited to our unique dairy conditions.

At the same time, LIC has a dominant and privileged position in the New Zealand market. The IWG acknowledges that LIC has fiduciary duties to its shareholders. However as custodians of inter-generational investment by New Zealand dairy farmers, LIC also has wider responsibility for the overall interests of the industry and what is good for the sector. The IWG respects the commercial IP interest in genotypical data as essential to incentivising sustained investment. However the IWG believes there is an opportunity for LIC to take a more open approach that would enhance their business by building confidence in genomics and therefore increasing farmer demand for young sires and potentially other AI technologies.

Areas that would be material for increasing genetic gain are:

- as a first-best option, reducing confusion for farmers by cooperating to ideally achieve one BW figure for every cow and bull;
- if this can’t be achieved, then LIC could make Cow BW more easily usable by others, to enable any animal to be evaluated against the National Breeding Objective.

In addition, LIC could work more effectively with bull breeders to explore ways of providing genomic evaluations of bulls in a fair and reasonable way, that rewards their IP but recognises the generations of farmers who have contributed data over many years. While there is a global trend toward creating nucleus herds, some experts have warned this could lead to genetic silos and having a vibrant bull breeding sector helps to mitigate this risk.

As a farmer cooperative these interests should be well aligned to those of LIC’s shareholders and customers, and, if LIC is confident in the products it has to offer, it should not be threatened by more information being in the market place.

The IWG does not believe NZAEL is in a position to provide an equivalent level of resources and expertise to that of LIC or CRV, nor that farmers should pay through their levy to duplicate data and services they already pay for from their breeding companies. New Zealand is too small to try and maintain multiple substantial reference populations, infrastructure and teams of experts working in isolation.

The NBO:

The NBO plays a critical role in establishing the breeding goal or ‘target’ animal best suited to New Zealand dairy systems and conditions. The aim of the current NBO is to produce animals that are “most efficient converters of feed into farmer profit” and is based on historical data to determine the economic value of different traits.

Genetics is by nature a long game, while the dairy sector globally is dynamic and expectations of customers and consumers change. Ensuring New Zealand is able to anticipate the industry's future needs requires broad input and agreement from industry participants in establishing the NBO and robust input from scientific experts. It should also have a forward-looking approach to identify potential traits that will be important for the future and the data that should be collected to support their possible inclusion in the NBO when the time is right.

There is strong support across the board that establishing and operating the NBO should continue to be an industry good, independent function of NZAEL.

A single database/reference population:

Genetics experts have stressed the benefits of having a single combined reference population with high quality phenotypic data to run multi-breed evaluations in New Zealand, and the IWG agrees that this would be the best outcome.

Professor Hayes has recommended a possible model for doing this that would combine available data and expertise in New Zealand under a new joint venture, while maintaining independence and the ability for other companies to also obtain genomic evaluations. NZAEL has proposed a model, whereby they would operate a single database for the New Zealand reference population and produce cow and bull genomic estimated BW and BVs based on the NBO.

However the inability of the key players to agree on such an approach after years of discussion demonstrates these are unlikely to be achievable, although if any prospect of 'free-rider' risk could be addressed it is possible there could be stronger cooperation on data sharing. The IWG has heard there is a greater openness from LIC to improving data inter-operability with MINDA in areas that will create value for farmers.

The IWG is aware that there are alternate models to produce one BW per cow or bull that might enable genotypical information to be shared without requiring genotypes, and therefore IP, to be shared. One example is the model used in the Netherlands under CRV's leadership (often referred to as 'the Dutch model'). However technical experts advised that such a model would not be a good fit for the multi-party model in New Zealand or meet our needs for high quality animal evaluation information. Other models based on reciprocal data sharing models are also not a good fit for New Zealand where the benefits would be asymmetrical given the dominant position of LIC.

Both LIC and CRV have expressed interest in developing a 'Dutch model' for New Zealand and they should work together to explore this further and see whether a model that would be fit-for-purpose for New Zealand can be developed.

However, effort spent on trying to achieve a comprehensive single national database of phenotypic, genomic and parentage information has so far has made no ground, and, in the IWG's opinion, has instead contributed to division in the industry and less cooperation rather than more as the three main parties appear to operate in silos. It may also have prevented them from focussing and working together to stem the critical decline in phenotypic data quality that has occurred.

The IWG believes improvements within the current structure (of two well-established breeding companies in LIC and CRV), that leverage the strengths of the key players, are likely to have lower costs and still be beneficial for genetic gain, particularly bearing in mind that reference populations are not static but must be continually refreshed, and that this is an area where technology will continue to evolve so that investment must be ongoing and sustainable.

Core Data and the regulatory framework:

The *Dairy Industry (Herd Testing and NZ Dairy Core Database) Regulations 2001* cover herd testing and the provision of information from certified herd testers to the manager of the core database. Other aspects of animal evaluation are not regulated. Core data required cover only 46 fields of phenotypic data and adding any other data would require changes to the legislation following the normal government processes for regulatory change.

In 2018 the Ministry for Primary Industries (MPI) consulted on how to ensure that the regulated ('core') dataset remains well aligned with the dairy industry's current and future animal evaluation needs. MPI's consultation document acknowledged that the current prescriptive approach that specifies a list of data to be provided by herd testers "does not accommodate changing needs or farming practice and is not readily updated. Any prescribed list is likely to become outdated in a relatively short time, and the process of amending regulations can take some time."[4] MPI also noted that "ideally the regulatory regime pertaining to core data should be made sufficiently flexible to accommodate the contribution of genomic data for the future."

The IWG view is that there is not a case to compel the provision of genotypes, as has been advocated for by some parties. There is a risk such a step would face fierce opposition and, if it was successful, could disincentivise future investment in genomic data collection and technologies by the breeding companies to the disadvantage of New Zealand dairy farmers.

The limited scope of the regulations currently means that the sector is free to determine for itself what systems and structures for animal evaluation will work best for New Zealand and, with good will, establish its own arrangements in the interests of New Zealand dairy farmers.

Multiple BW

In the genomics era and without a single reference population for New Zealand, we are unlikely to return to simpler times when there was only one BW per animal unless parties are able to cooperate on a system to achieve this as recommended by this report. It is also likely that the trend of breeding companies developing their own indices of emerging traits beyond the NBO to differentiate themselves in the market is likely to continue.

In the absence of a system to generate one BW for each cow and bull, it is important to limit confusion for farmers from seeing multiple or changing BW or BV figures or other indices. Farmers should be readily able to understand, through extension, the source of the data and the extent to which they reflect genomic estimates or daughter proofs. They can then chose what information they wish to rely on. NZAEL can and should assist them through independent monitoring and analysis of breeding company performance.

---

[4] https://www.mpi.govt.nz/dmsdocument/30906-Dairy-Herd-Improvement-Industry-Review-of-Regulation page 6

Reliability of genomic estimates

LIC is building its reference population to a level that will achieve increased reliability of its gBW. Given the dominance of LIC in the market this will go a long way to enabling New Zealand to catch up with other countries and their success in using genomics to expedite herd improvement.

However, additional transparency mechanisms would build confidence in the animal evaluation information provided by LIC, CRV or any other breeding company. NZAEL or DairyNZ's independence and industry-good purpose are well suited to auditing the methodologies being used for genomic evaluation and to providing regular and transparent monitoring of the breeding companies and their success in using genomics to achieve genetic gain as measured through daughter proven assessments and in line with the NBO. In this respect it is important to maintain a database of phenotypic data alone to provide a benchmark for assessing progress in improving the reliability of individual genomic predictions and analysis of how genetic gain is tracking at a national herd level.

Increased genotyping of heifers

A further proposal to increase the reference population is to incentivise genotyping of heifers. This can support farmer selections for breeding, with some benefit for genetic gain (although not as significant as sire selection), through contributing more genotypes to the reference population, as has been the case in the USA and Australia. Genotyping heifers also has the benefit of improving the accuracy of parentage phenotypic data. LIC has initiatives underway to increase genotyping of heifers, but the IWG understands their restriction on use of Cow BW and third-party data on MINDA are a barrier to other breed companies increasing cow genotyping.

Screening international genetics

If other countries are ahead in genetic gain, it makes sense that New Zealand could benefit from their progress where there could be overseas genetics aligned to the NBO. However there is also a risk of international genetics being imported into the New Zealand herd that run counter to the NBO unless there is an ability to gain accurate genomic evaluations for bulls not bred in New Zealand – especially for reproductive and longevity (TOP) traits. Some stakeholders have advocated for a system where anyone should be able to screen international bulls against the New Zealand dataset. However, this risks undermining investment by breeding companies in developing New Zealand reference populations and breeding programmes specifically to meet New Zealand's unique needs. It is not clear to the IWG why there should be open access for anyone to core assets that New Zealand dairy farmers have invested in over many decades.

It is a difficult problem to solve and must continue to fall largely to LIC and CRV to incorporate appropriate international genetics in their breeding programmes as the least-risk pathway for these to come into New Zealand and to consider how they might offer some kind of screening service on a commercial basis to others in the interests of the dairy industry. The steps to increase confidence in the New Zealand NBO and BW system outlined in this report could also encourage farmers and breeders to return to the domestic market for genetics bred specifically for New Zealand conditions.

Recommendations for increasing use of genomics in order to drive faster genetic gain in the New Zealand dairy herd[5]

1. Strengthen the role and impact of the National Breeding Objective (NBO) for achieving genetic gain in the New Zealand dairy herd

1.1. **NZAEL** should continue to be responsible for stewardship of the NBO on behalf of the dairy industry.

1.2. **NZAEL** should establish a process for broad industry engagement in setting the NBO, with critical importance placed on agreement from the animal breeding (AB) companies and input from dairy processors, so that there is good alignment between the NBO, breeding programmes and industry trends. This process should include identifying the long-term needs of the industry and agreeing objectives for traits that are likely to be important in the future, and NZAEL, in collaboration with the industry, should take responsibility for trait definitions and incorporation of any new traits into the NBO. Examples include saturated fat vs less saturated fats, environmental sustainability (traits that lead to less N loss – urination frequency, GHG yield and intensity), labour (an expanded Traits Other than Production (TOP)).

1.3. **NZAEL** should provide regular analysis that shows the rate of progress toward the NBO based on actual genetic progress at the national herd level relative to both individual traits and as measured by NBO based BW. They should also provide a regular analysis of the relationship between BW improvement and increases in farm profitability.

2. Improve phenotypic data quality collected from commercial dairy herds

2.1. A more targeted approach to herd recording should be established by **NZAEL**, **LIC** and **CRV** that differentiates elite herds based on the quality of the genotypic and phenotypic data collected and maintained (and the owners should be rewarded for doing so) from farms that achieve lower standards of herd recording. The approaches developed need to be commercially self-sustaining.

2.2. **NZAEL**, **LIC** and **CRV** should work collaboratively to establish a system whereby farmers receive a herd recording quality ranking (such as 1-5 stars) and other incentives to record good data. The IWG is aware companies may already have initiatives that incentivise good data collection, however there is a need for a step change to address current deficiencies in phenotypic data quality and to build a high quality reference population of at least 400,000.

2.3. This quality ranking system must include parentage/genomic testing, whether reproduction information is accurately recorded, how many times per lactation herds are recorded for milk and component production, the variation in these records, what percentage of the herd is well recorded, and inclusion of other traits deemed important in the NBO such as live weight and other TOP.

2.4. High quality phenotypic data sets must be built to enable daughter proofs for progress toward the NBO to be regularly and transparently evaluated as set out in 1.3. This data will also be

---

[5] The IWG recognise our recommendations are focused on the current major players within the system, and that over time the system and the key players will evolve. It should be taken as read that as significant players emerge, they should be expected to adopt the principles being promoted in this report as they develop their commercial models and relationships within the industry.

important in accurately evaluating the reliability of the initially published genomically derived BW against the proven BW of sires (see section 3.1.1 below).

3. Create an environment that encourages and supports breeding companies and others to use genomic technologies to make genetic gain (aligned to the NBO) as fast as possible

3.1. Increase farmer trust in and, therefore, demand for, use of younger genomic sires:

3.1.1. **NZAEL** should have the data and means to monitor and audit the methodologies being used for genomic evaluation and reliability of genomic predictions of the breeding companies to help farmers make sound decisions about sire selection, build farmer confidence in genomics and create a strong incentive for breeding companies to make accurate genomic predictions. This should include publishing an annual validation report comparing daughter-proven performance with the genomically estimated breeding values for young genomically selected bulls to show the trends in reliability of those estimates over time. These genomically selected bulls would be part of the RAS list which is discussed in 3.1.2. below. These validation reports should be referenced in extension activities anticipated under 3.1.7 below. The initial report should be published in 2025 evaluating recent sires against currently available daughter proofs.

3.1.2. Animal evaluation roles should reflect where data and capabilities best lie. Genomic evaluations of bulls should continue to be the role of the breeding companies. Retrospective evaluation of bulls using daughter proven phenotypic data should be the role of NZAEL as outlined in 3.1.1 above, however publication of RAS lists which farmers use for sire selection needs to also include genomic information where its available and has met agreed standards as audited and verified by NZAEL. The NZAEL RAS list should be based on gBWs provided by breeding companies and presented alongside NZAEL's assessments as set out in 3.1.1 and 3.1.3.

3.1.3. **LIC** and **CRV** should work together to develop a system that integrates CRV and LIC individual genomic breeding values to achieve one 'national' gBW figure for bulls and cows, regardless of which breeding company has evaluated them or which farm management software is used (MINDA or myHERD). It is recognised that this will be complex and require commitment from both parties to finding technical solutions that enable this in a way that protects their respective IP, however it is very important that this is achieved. The system also needs to provide access on reasonable commercial terms to third parties wishing to have their animals genomically evaluated, without undermining investment by LIC or CRV in developing their reference populations and related IP. NZAEL's role is to audit and verify the integrity of the system that is developed and implemented.

3.1.4. **Breeding companies** presenting any animal evaluation figures to farmers should provide accessible and easily understood information that enables farmers to understand how a figure has been derived, such as whether it is genomically estimated or includes daughter proven data, and distinguishes BW or BV based on the NBO from evaluations using any other index or novel traits.

3.1.5. Any commercial practices by **breeding companies** (where they have agreed to genomically test a young bull) that lead to withholding or delaying provision of genomic test results to farmers, regardless of whether they wish to purchase the young bull, should be strongly discouraged.

3.1.6. **NZAEL** should immediately discontinue developing its own reference population.

3.1.7. **NZAEL, LIC and CRV** should work together to coordinate extension activities that educate and support farmers on the importance of the NBO, genetic gain and accurate data collection, and provide information and tools that enable farmers to improve the genetics of their own herds.

3.2. Strengthen industry cooperation on reference populations to improve the reliability of genomic prediction by breeding companies

3.2.1. **LIC and CRV** should agree on a process for one-to-one genomic data swaps for mutually beneficial development of each of their reference herds.

3.2.2. **NZAEL, LIC and CRV** should encourage genotyping of heifers to increase the reference population and support farmer decisions on selection of heifers to mate with top dairy bulls to breed replacements.

3.3. Establish world's best practice genomic evaluations for multi-breed populations and encourage adoption in New Zealand.

3.3.1. **DairyNZ** should convene an international workshop of leading scientists in multi-breed genomic evaluation to devise the best approach for multi-breed genomic evaluations, including New Zealand scientists from CRV, LIC and NZAEL. Specifically the workshop needs to agree on the optimal size of a reference population for New Zealand, the quality of our current phenotypic dataset and how it can be improved, and the application of future techniques and models for New Zealand's multi-breed system.

3.3.2. **Breeding companies** should publish their models for genomic evaluation regularly and at least every 2 years.

Pathway to implementation

The IWG has engaged openly with the main parties at a senior management and Board level in the development of its recommendations and received constructive feedback. Encouragingly, the main parties have also indicated a willingness to work together. The IWG has developed its final recommendations taking this feedback into account and note the strong alignment to address the identified challenges.

Several recommendations require the parties themselves to come together and create a workable solution, and the IWG proposes to reconvene after three months (October 2024) to review progress and make further recommendations as required. The IWG acknowledges that when industry actors come together for the purpose of addressing sector-wide challenges, it is important that they are alert to competition law issues and adopt appropriate measures to safely navigate potential Commerce Act 1986 risks. The parties must also ensure that all of their proposed activities in connection with implementing the recommendations in this report are compliant with the Act. This should be a focus of the parties as they work through the recommendations and should be reported on to the IWG at the three-month review mark.

The IWG recommends that workstreams should be developed by the Parties across the main areas. These include:

1) the process for establishing the NBO,

2) improving phenotypic data quality,

3) developing a system to achieve one gBW, and

4) cooperating on communication, education and extension services for farmers regarding the importance of genetic gain.

The IWG considers priority needs to be given to holding the workshop recommended in 3.3.1. While challenging, it is also important to secure commitment of the parties to the exploratory work outlined in 3.1.3 to identify a workable system for establishing one gBW.

It is not possible to find solutions for 100% of situations that will arise or all of the issues that have been raised in the course of this Review. The recommendations above are a starting point. It is leadership from the key parties and a commitment to cooperation that will bring about the necessary change to ensure New Zealand has the best possible future dairy herd for a productive, sustainable and globally competitive dairy industry.

APPENDIX

Report on “Objective evaluation of the current state of genetic improvement in the NZ dairy sector relative to other advanced dairy industries”, Professor Ben Hayes, University of Queensland

Final Report: Objective evaluation of the current state of genetic improvement in the NZ dairy sector relative to other advanced dairy industries

Aim.

This project aims to evaluate the current state of genetic improvement in New Zealand dairy cattle, post the introduction of genomic selection, and compare the rate of improvement to other countries. The project will recommend pathways to improving genetic gain, including in light of what has been achieved in other countries, ultimately to ensure NZ maintains or ideally improves it position in a competitive global market place.

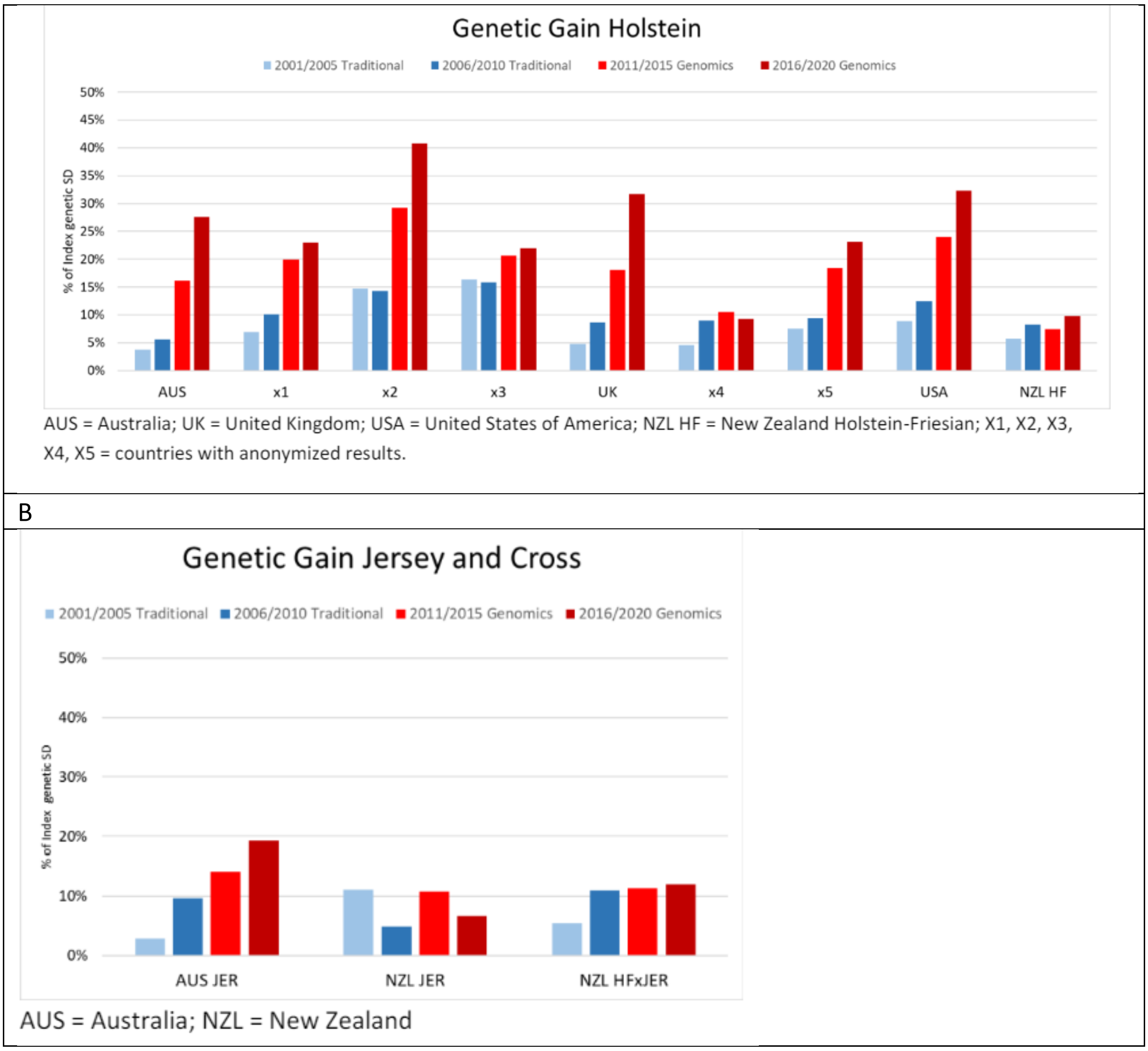
Approach.

A series of interviews (20 people) were conducted with key stakeholders in genetic improvement in New Zealand, and key players in genetic improvement in other countries used to benchmark genetic improvement in New Zealand. Questions asked depended on the role of the interviewee, but included questions like “Can you describe the main barrier to increasing genetic gains in NZ”, “In your opinion why is the use of young genomic bulls by NZ dairy farmers lower than in other countries”, “why do AI companies in NZ use young genomic bulls as sire of sons less aggressively than other AI companies”, and “what is the main structural barrier to improving genetic gain in NZ”? Any relevant publications and reports were also reviewed, and these are cited where appropriate.

Benchmarking rates of gain in the New Zealand dairy industry against rates of gain in other countries following the introduction of genomic selection

Prior to the introduction of genomic selection, NZ was among the world leaders in genetic gain, with gains very close to the maximum possible under progeny testing (Garrick 2021). However, fifteen years after the introduction of genomic selection, the rate of gain in New Zealand lags behind other countries, Figure 1. Note that the Figure expresses genetic gain as a percentage of the genetic standard deviation in the index – this is a good metric for genetic gain, as expressing the gain in this way takes account of differences in traits in the index, and the different genetic diversity in herds around the world. The gain in New Zealand during this period is less than a third that achieved in other countries.

A



AUS = Australia; UK = United Kingdom; USA = United States of America; NZL HF = New Zealand Holstein-Friesian; X1, X2, X3, X4, X5 = countries with anonymized results.

AUS = Australia; NZL = New Zealand

Figure 1. A. Holstein yearly genetic gain expressed as a percentage of the genetic standard deviation of the index for New Zealand and other countries, B. Jersey and crossbred yearly genetic gain expressed as a percentage of the genetic standard deviation of the index for New Zealand and other countries. Figures from BENCHMARKING GENETIC PROGRESS ACROSS DAIRY INDUSTRIES IN THE ERA'S BEFORE AND DURING GENOMICS (S. Savoia, K. Stachowicz and P. Amer, Abacusbio, 2022).

Further dissection of the rate of gain identifies the reason New Zealand lags behind other countries – a low rate of using "young genomic bulls" (bulls 1-3 years of age with a estimated breeding value from pedigree and genomic information only, no daughter information) as both sires of the next generation of sires and sires of cows. In many countries useage of young genomic bulls approaches 100% in both pathways. This had led to a considerable reduction in generation interval (from 7 years to 3 years) which has resulted in at least a doubling of the rate of genetic gain (eg. Guinan et al. 2023). Another way of saying this is that genomics means that very high genetic merit bulls can be identified much earlier than with progeny testing, which has led to accelerated genetic gains.

In New Zealand usage of young genomic bulls is much more limited

- " the proportion of cows in each birth year that were sired by 2 and 3 year old bulls has declined from a peak of 36% cows achieved in 2011 and 2012 birth years to 13% in the years 2013-2018, increasing to 18% in 2019" (Garrick 2022).

- "The average age of CRV sires of sires is consistent with many of these animals having been progeny tested before their use as the sire of sons. The data from LIC bred cows shows a sizeable reduction in the 2009 birth year – reflecting release of LIC's first team of 2 and 3year old GS bulls. Further reductions in unweighted average age of sires of sires were apparent in 2010 and 2011, and these reductions flowed through in the weighted average in 2012. However, ages increased again for the next 3 birth years. Only the 2017 bull birth year demonstrates a reduction in age based on cows with LIC ancestry" (Garrick 2022).

Discussions with LIC do suggest that in recent years there is increasing use of young genomic bulls to breed sires, and that the generation interval is falling as a consequence, however this will take some time to show up in genetic trends.

A brief history of genomic selection in New Zealand

It is important to understand why the use of young genomic sires is lower than in other countries. There are two reasons for this. The multibreed nature of the NZ herd means that much larger reference populations are required to achieve high reliabilities of genomic estimated breeding value than for the single breeds (eg Holstein or Jersey) used in other countries. This issue will be discussed in more detail below.

Additionally, the introduction of genomics in NZ was very early (Harris and Johnston 2010), and suffered from two major incidents:

- The first crop of genomic young bulls (bulls that are not yet progeny tested and are marketed on their genomic breeding values only) did not perform as expected, and performed no better than the best progeny tested bulls. This was the result of genomic prediction methodology issues.
- One of the first young genomic bulls carried a genetic defect (in the prolactin receptor, "hot and hairy"). This was just very unlucky.
- This severely undermined confidence in NZ of young genomic sires.
- The fallout from these incidents are that there has been a low uptake of semen from young genomic sires (21%), compared to other countries where uptake is now very high (close to 100% in many cases).
- Breeding companies have also been reluctant to use young genomic bulls and sons of sires. This is the main factor limiting genetic gain in NZ, compared to what other countries have achieved. The lack of gain following the introduction of genomics in NZ has been documented by NZAEL and others.
- There is also a lack of confidence in data used to build reference populations (genotyped cows with good trait records). This stems from problems such as errors in parentage error assignments, and reduction in the frequency of herd recording over time. There is also a lack of pedigree information on the female side for many cows in NZ. Note that genomics could solve this.

The NZ multi-breed challenge

New Zealand is unique in that a large proportion of cows in the population are crossbred, and crossbred (HxJ) bulls are also used. This multi-breed composition makes achieving high reliabilities of genomic estimated breed values much more challenging – reference populations must be large enough such that all chromosome segments, whether derived from Holstein or Jersey, are captured and evaluated. Table 1 compares the size of reference population (cows genotyped and with phenotypes) required in a multi-breed population to a single breed population, for traits with heritabilities of 0.3 (eg production) and 0.1 (fertility).

Table 1. Size of reference population (cows genotyped and recorded for the trait) required to achieve a reliability of 0.7 for genomic estimated breeding values for young genomic bulls (with no daughters), for trait heritabilities of 0.3 (eg production) and 0.1 (eg. fertility), for single breed and multi-breed populations. Based on the formula of Goddard and Hayes (2009).

		Trait heritability	
Scenario	Effective population size	0.3	0.1
Single breed	100	45,933	136,906
Multi breed	500	131,592	392,425

As well as larger reference populations, multi-breed populations also require more complex genetic evaluation models, to take account of breed effects, heterosis, and to avoid bias (see Hayes et al. 2023 for a recent review).

The LIC genomic evaluations have recently been described by Harris (2022). These evaluations do account for heterosis and breed effects, and follow the methodology described by Fernando et al. 2016. There were 200,000 cows with genotypes and phenotypes in the reference set used to derive genomic estimated breeding values (GEBV). The LIC genomic evaluations were evaluated is three cohorts of young sires that recently received progeny tests, Table 2. The table makes clear that for example 40,000 genotypes are likely to result in fairly low reliability estimate breeding values.

Table 2. Bias and accuracy of genomic estimated breeding values (GEBV) for the 3-yr cohorts of test sires from the validation regression model for breeding worth (BRW) index (from Harris 2022).

	Genomic BRW		Pedigree BRW	
	Bias	Accuracy	Bias	Accuracy
Holstein-Friesian (HF)	0.90	0.73	1.08	0.42
HF × Jersey cross	0.96	0.61	0.79	0.27
Jersey	1.0	0.74	0.91	0.33

The validation tests showed the GEBV were close to unbiased (a bias of 1 would indicate no bias, bias <1 indicates the GEBV over predict performance and bias >1 indicates GEBV under-predict performance.

The accuracies of GEBV were considerably higher than estimated breeding values from pedigree, Table 2. The accuracies of GEBV were also very much in line with expected accuracies given reference set size (if the heritability of Breeding worth is taken as 0.1, which is reasonable give the contribution of fertility and other low heritability traits to breeding worth, and effective population is 500 and the reference set size is 200,000, then the expected accuracy from Goddard and Hayes (2009) is 0.75, which is close to the 0.73 in Table 2).

Reliabilities of GEBV using the CRV reference population, and reference populations shared across countries, have also been evaluated in validation populations, Haile-Mariam et al. (2020). These reliabilities were 0.5 or above for production traits (eg accuracies of 0.7 or greater).

Note that reliability is accuracy squared. So the reliability achieved for HF and Jersey with 200,000 cows in the reference population by Harris (2022) is 0.73*0.73 = 0.53. In Australia, it was observed that use of young genomic sires by dairy farmers really accelerated when reliabilities of GEBV exceeded 0.7, as this value there was considerably less movement (re-ranking) of the GEBV when the sires received their first daughter information (another way of saying this is that farmers' confidence in the GEBV was greatly increased when reliabilities exceeded 0.7). The extension message to encourage use of young genomic sires is also simplified when reliabilites of GEBV are high – when reliabilities of GEBV are low, a "teams" approach is usually recommended, where selection of a team of young genomic sires for use on a farmers' cows is encouraged, to mitigate the risk of individual bulls EBV moving down overt time. This can be a complex message to get across, and can reduce confidence in the use of young genomic sires.

Table 1 indicates that 400,000 cows are likely required in the reference population for reliability to achieve >0.7 reliability for BRW.

Structural barriers to achieving reliable genomic evaluations in NZ identified by interviewees

Three organisations in New Zealand either are, or are proposing to, calculate genomic estimated breeding values (GEBV) for breeding worth (CRV, LIC and NZAEL). This causes considerable confusion in the market place, and is very likely to undermine farmers confidence in GEBV. This is because the three organisations have different, and in most cases sub-optimal, reference populations for calculating GEBV, which can result in quite different GEBV for the same bull. In addition, because the accuracies of GEBV from each evaluation are modest (eg 0.5-0.74), the GEBV calculated by the different organisations will have a low to modest correlation. The maximum correlation that can be achieved is the accuracy of GEBV from one organisation multiplied by the accuracy of GEBV from another organisation, for example 0.7 accuracy from one organisation and 0.7 accuracy from another organisation results in a correlation 0.49, which will be reflected in major re-ranking of young bulls on GEBV between organisations.

Another barrier to improving genetic gains reported by interviewees include monopoly ownership of cow genomic BRW, which restricts identification of dams of young genomic bulls, and use of genomic information by dairy farmers to select heifers for breeding. Bull breeders were also reportedly unable to get back their GEBV on young bulls in a timely fashion, which limited what they could do with these bulls.

Relative to other countries, the limited use of sex semen in NZ also means there is limited potential to select replacement heifers on genomic information. Genotyping of heifers has been a major driver of uptake of genomics in other countries, if not genetic gain (this is discussed in more detail below).

According to some interviewees, methods for genomic evaluation are opaque, which makes it hard to know if these methods are world leading, which is important particularly given the crossbred/multi-breed nature of the NZ dairy population, which is unique globally and proposes a particular challenge that other countries do not have to deal with. It is not known if these interviewees were aware of the recent publication by Harris (2022), which does describe the method used by LIC at least in some detail, and the publication of Haile-Mariam (2020) which describes the situation for CRV.

Given this multi-breed challenge, it is worth pointing out the appropriate benchmarks for NZ dairy cattle genetic gain may in fact be multi-breed beef and sheep populations, rather than pure-bred dairy populations. Nevertheless, substantial gains have been made (particularly in sheep) in other multi-breed populations.

According to interviewees that hold important positions in dairy cattle genetic improvement overseas, the lack of systematic and transparent validation of genomic estimated breeding values limits farmer confidence and therefore uptake of semen from young genomic bulls.

One interviewee noted the importance of keeping a balance between the openness of genetic evaluation and incentive for breeding companies to make genetic gains. According to them if the system is completely open to competition this could discourage investment from NZ companies in breeding. This is a valid point.

Potential pathways to improving reliability of genomic evaluations in NZ

The ideal genomic evaluation for bulls and heifers in NZ would use a reference population that includes all cows that have been genotyped and trait recorded to date, regardless of breed composition or organisation. If all organisations were to pool their reference populations, high reliabilities of GEBV would be achieved, farmers would have more confidence in using young genomic sires, generation intervals would decrease, and rates of gain should increase as observed in other countries. The most straightforward way to do this is to have a single organisation have access to all reference population data, and calculate GEBV with this reference population. Other compromises are possible, but are typically sub-optimal, in that biases or reduction in accuracy can be introduced.

After considering all the discussions with the people interviewed, and the current limitations to genetic gains in NZ, a way forward can be envisioned, with multiple components. The following recommendations together represent the recommended way forward.

Establish a data quality index.

It is critical for the integrity of the genomic reference population that only cows in herds with high quality data recording are used (that is genotyped, and their trait records enter the genomic evaluations). *It is recommended that a herd data quality index be set up for NZ.* Such an index would include whether fertility information is recorded, how many times per lactation herds are recorded for milk and component production, the variation in these records, what percentage of the herd is well recorded, and consideration of other traits such weight and conformation. All cows to be added to the reference population should have parentage allocated by genotypes, to avoid pedigree errors. A data quality ranking (eg 5 stars to one star) could be awarded to herds for recording good data. Herds could also be incentivised to record good data by offering free or subsidised genotyping to these herds, this would enable selection of heifers for breeding, or possible identification of bulls dams.

Encourage genotyping of heifers for selection

In other countries, genotyping of heifers by dairy farmers for selection of which heifers to keep in the herd is common practise, with millions of heifers genotyped worldwide each year. While this has a relatively small impact of genetic gains relative to selection of young genomic bulls with very high genetic merit, it does have the benefit that these genotypes are incorporated into the reference population almost automatically when the heifers are performance recorded. This is how countries such as the USA and Australia have managed to assemble such large reference populations. The promotion of the value of genotyping heifers, for parentage as well as selection (using a 50k panel that can be used for genomic evaluations) should be promoted. Note that heifer selection with GEBV becomes particularly attractive as the use of sexed semen becomes more widespread, as there are more heifers to select from. In dairy-beef schemes, GEBV can be used to identify the heifers with high genetic merit to be mated to top dairy bulls to breed replacements, and the low genetic merit (low GEBV) heifers can be mated to beef bulls to produce cross-bred steers for beef production.

Initiate world's best practise for multi-breed genomic evaluation.

Genomic evaluations for multi-breed populations are much more challenging than for purebred populations, see Hayes et al. (2023) for a recent review on this topic. Unfortunately, consensus on the best approach for multi-breed evaluation has not been reached by the scientists working in this area. Nevertheless, considerable advancements have been made in this area recently. A suggestion would be to have an international workshop, where the leading scientists in this area are invited to devise the best approach for multi-breed genomic evaluations, with NZ Dairy as interesting test case. This workshop should include NZ scientists from the two AI companies.

Develop a transparent multi-breed genomic evaluation open to all AI companies.

One possible way to improve transparency, and availability of multi-breed evaluations, once the best model has been determined using the approach above, would be to have a new entity run these evaluations. One way of doing this that would take advantage of the considerable expertise and capacity within NZs AI companies in genomic evaluation, would be to have this entity as a subsidiary of one or both of the AI companies, perhaps as well as NZAEL,but with completely independent governance (eg an independent board). A good governance structure is absolutely critical for this approach, to build trust that the new entity does not favour one AI company over the other. The cost per bull evaluation could reflect the contributions of the different organisations (eg. CRV, LIC, NZAEL) to the reference population. The methodology used for the multi-breed evaluations, and results in terms of accuracy and bias, should be published in an international journal at least every two years, or whenever significant updates are made.

One proposal would be, once this entity is in place, to open genomic evaluations to other companies as well. However entry into this system would have to recognise the very considerable investment in reference populations to drive genomic evaluations by the two AI companies. A good model would be that any new entrant would have to contribute at least 50,000 genotyped cows, with the cows identified with the data quality index above. It should be noted that it could be quite difficult for companies not selecting for BW to find bulls that rank highly for BW, given the difference in BW and breeding objectives overseas, as well as differences in production system (eg performance on total mixed ration versus performance on pasture only have a correlation of about 0.7).

Validation.

Absolutely key to building farmer (and AI company!) trust in genomic evaluations, the first step in increasing demand and use of young genomic sires, is regular and transparent validation of genomic estimated breeding values (eg from the genomic evaluations described above). This would seem to be clear role for NZAEL. As daughters of genomic bulls received their first lactation and fertility records, the GEBV for the young genomic bulls could be compared to these records and "validated" (or otherwise). In other countries, sizable extension campaigns to increase the use of young genomic sires have been run off these validation results, and this could happen in NZ as well. Note that the design of the validation experiment, for example the spread of herds used for validation, is important to achieve unbiased results. This validation would also allow different methods for multi-breed genomic evaluations to be compared and benchmarked, such that the best method could be used for ongoing evaluations.

Avoiding the inbreeding trap

Many countries have observed a substantial rise in inbreeding, in some cases a doubling, following the introduction of genomic selection (Scott et al 2021, Makanjuola 2020, Tenhunen et al. 2024). Inbreeding is associated with decreased trait performance, particularly for traits such as fertility, and a rise in the prevalence of recessive defects. The rise of inbreeding with genomic selection reflects the very intense use of young genomic bulls as sires of sons. It is somewhat surprising this has occurred, given there are well known strategies to avoid inbreeding such as optimum contribution selection and their genomic equivalents (eg Wray and Goddard 1994, Meuwissen 1997 Schierenbeck et al 2011).

New Zealand has a unique opportunity to avoid "the inbreeding trap" that other countries have fallen into, for two reasons 1) the risk of falling into this trap is now very clear, and 2) just two companies supply the majority of AI sires in New Zealand, which means these companies could relatively easily design genomic optimum contributions breeding programs to both maximise gain and manage inbreeding.

References

Scott BA, Haile-Mariam M, Cocks BG, Pryce JE. How genomic selection has increased rates of genetic gain and inbreeding in the Australian national herd, genomic information nucleus, and bulls. J Dairy Sci. 2021 Nov;104(11):11832-11849. doi: 10.3168/jds.2021-20326.

Garrick D. 2022. Characterisation of the rates of Genetic Gain and related matters. Report for NZAEL.

Guinan FL, Wiggans GR, Norman HD, Dürr JW, Cole JB, Van Tassell CP, Misztal I, Lourenco D. Changes in genetic trends in US dairy cattle since the implementation of genomic selection. J Dairy Sci. 2023 Feb;106(2):1110-1129. doi: 10.3168/jds.2022-22205.

Goddard ME, Hayes BJ. Mapping genes for complex traits in domestic animals and their use in breeding programmes. Nat Rev Genet. 2009 Jun;10(6):381-91. doi: 10.1038/nrg2575.

Hayes BJ, Copley J, Dodd E, Ross EM, Speight S, Fordyce G. Multi-breed genomic evaluation for tropical beef cattle when no pedigree information is available. Genet Sel Evol. 2023 Oct 16;55(1):71. doi: 10.1186/s12711-023-00847-6.

Harris BL. Genomic evaluations for crossbred dairy cattle. JDS Commun. 2022 Feb 10;3(2):152-155. doi: 10.3168/jdsc.2021-0176.

Fernando, R. L., H. Cheng, B. L. Golden, and D. J. Garrick. 2016. Computational strategies for alternative single-step Bayesian regression models with large numbers of genotyped and non-genotyped animals. Genet. Sel. Evol. 48:96.

Harris BL, Johnson DL. Genomic predictions for New Zealand dairy bulls and integration with national genetic evaluation. J Dairy Sci. 2010 Mar;93(3):1243-52. doi: 10.3168/jds.2009-2619.

Makanjuola BO, Miglior F, Abdalla EA, Maltecca C, Schenkel FS, Baes CF. Effect of genomic selection on rate of inbreeding and coancestry and effective population size of Holstein and Jersey cattle populations. J Dairy Sci. 2020 Jun;103(6):5183-5199. doi: 10.3168/jds.2019-18013.

Tenhunen S, Thomasen JR, Sørensen LP, Berg P, Kargo M. Genomic Analysis of Inbreeding and Coancestry in Nordic Jersey and Holstein Dairy Cattle Populations. J Dairy Sci. 2024 Apr 10:S0022-0302(24)00740-9. doi: 10.3168/jds.2023-24553.

Wray N, Goddard ME. Increasing long-term response to selection. Genet. Sel. Evol., 26 (1994), pp. 431-451

Meuwissen THE. Maximizing the response of selection with a predifined rate of inbreeding J. Anim. Sci., 75 (1997), pp. 934-940

Schierenbeck S, Pimentel ECG, Tietze M, Körte J, Reents R, Reinhardt F, et al. Controlling inbreeding and maximizing genetic gain using semi-definite programming with pedigree-based and genomic relationships. J Dairy Sci. 2011;94:6143–52.

Haile-Mariam M, MacLeod IM, Bolormaa S, Schrooten C, O'Connor E, de Jong G, Daetwyler HD, Pryce JE. Value of sharing cow reference population between countries on reliability of genomic prediction for milk yield traits. J Dairy Sci. 2020 Feb;103(2):1711-1728. doi: 10.3168/jds.2019-17170.