INFOHERDS, GENOMIC SELECTION FOR DAIRY CATTLE IN NEW ZEALAND

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SUMMARY

The New Zealand (NZ) dairy industry is serviced by two key sources of genetic evaluations; firstly, the national evaluation delivered by DairyNZ via its subsidiary NZAEL, and secondly, the private evaluations delivered via the major breeding companies (LIC and CRV). The genetic evaluation ecosystem is changing, with genomic selection (GS) enhancing the accuracy of predictions across a wider range of traits. Improving rates of genetic progress and pursuing outcomes which assist with the industry's social license to operate, such as animal welfare and environmental impacts, via genetic pathways are some of the potential benefits of genomics for the dairy industry.

This study presents some of the benefits of an industrywide GS strategy underpinned by a modern and independent pipeline that integrates a source of genomic and phenotypic data. This source – known as the Infoherds programme – would act as a genomic reference population, with dairy herds managed under commercial conditions supplying data to improve prediction accuracy and to facilitate the development of novel traits within existing genetic evaluations.

The results demonstrate that GS could unlock between NZ$185 and NZ$245M in additional value of genetic gain per year to the NZ dairy industry – a 60-80% increase in the value of historic rates of improvement. Realising this potential requires a strategy for successfully implementing genomics via an independent information infrastructure co-ordinated by NZAEL.

INTRODUCTION

DairyNZ via its subsidiary NZAEL is investigating a programme to engage industry information herds (Infoherds) as a source of data contributing to the future genomic evaluations of strategically important traits, including those to be incorporated in the national economic selection index, Breeding Worth (BW). To develop a road map for rolling out the programme, we must value the implementation of genomic selection (GS) to the NZ dairy industry, and then identify potential data sources and integration needs.

The successful implementation of GS depends on the existence of a reference population. Information herds can be large and complex projects requiring an overarching strategic vision to ensure they achieve their key objectives. Disparate priorities, such as building farmer confidence in GS by improving accuracy of prediction, the introduction of novel traits, and support of on-farm management decisions, must all fit into an overarching goal of building a platform for industry genetic evaluations and shared data.

In many countries, the integration of genomic information into genetic evaluation systems underpinned by the collection of phenotypic and genotypic data has improved and accelerated genetic trends (García-Ruiz *et al.* 2016). However, this has not been observed in New Zealand, which might reflect the substantial breed admixture in the national herd as well as the pasture-based production, not common in most countries. Until the industry can integrate genomic information into a standard industrywide platform, the potential value of genomics to the broader industry is unlikely to be fully exploited. This potential value comprises a combination of:

1) Increased genetic progress via the adoption of superior young genomic sires instead of older daughter-proven (DP) sires,

2) Increased prediction accuracy through the estimation of genomic variant effects and more reliable parentage information, and

3) Increased industry engagement, introduction of new traits, cost-effective use of novel phenotypes in selection and decision making on-farm, and improved R&D collaboration.

In New Zealand, Infoherds would contribute to the national Dairy Industry Good Animal Database genetic evaluations as well as to the private evaluations delivered via major breeding companies (LIC and CRV). These companies will also benefit from Infoherds, as an additional source of phenotypic and genotypic data to their traditional herd testing programs and sire proving schemes. The information herd project therefore aligns with these breeding programs and creates a platform for better industry integration to support farmers.

This study presents some of the benefits of an industrywide GS strategy underpinned by a modern and independent pipeline that integrates a source of genomic and phenotypic data. This source – known as the Infoherd programme – would act as a genomic reference population, with dairy herds managed under commercial conditions supplying data to improve prediction accuracy and to facilitate the development of novel traits within existing genetic evaluations.

MATERIALS AND METHODS

This paper uses a geneflow modelling framework to analyse the combined effects of increased adoption of young genomic sires (by 5, 10 or 30% per year) in conjunction with an increased selection differential between GS and DP sires (20 and 40 BW units until 90% adoption). These parameters were used because commercial GS sires had an average initial superiority of 30 BW units over DP sires available in the same year (2021). The difference at 20 BW was deliberately chosen to be conservative, given the inflation issues around GS sires that have been experienced in many dairy industry evaluations around the world. The proportional use of GS sires in 2021 was set at 30%, with increments of 5% from 2016 to 2021. The increased adoption of GS sires and increase in the SD of the BW from new trait additions enabled by Infoherds, were assumed to be intertwined.

GS increases prediction accuracy for young sires, enabling farmers to select younger sire teams and avoid the need for progeny testing of prospective sires within sire proving herds. This shortens the generation interval and subsequently accelerates the rate of genetic progress (Lush 1937).

To estimate the economic impact of a higher adoption rate of young GS sires in the dairy industry, we created a model following the principles of recursive geneflow model methodology outlined by Matthews *et al*. (2019) and Fetherstone *et al*. (2021). It assumes that the average merit of calves born in a given year is half the merit of the sires available for use that year and half the merit of the cow herd, where the sire merit is a weighted combination of DP and GS sires, and the cow merit is set as a weighted combination of calf merit from 2 to 9 years prior.

The model was parameterised with the current BW genetic trend in dairy cows and a base status quo scenario where there is a 30% adoption rate of young GS sires. The results are calculated as the net present value (NPV) of the cumulative increase in merit of the cow herd over the base year value. The NPV was calculated using a discount rate *r* of 5%, and 4.9M breeding cows. The annualised NPV of genetic improvement was calculated as the cumulative NPV divided by the sum of the discount factors from year 0 to 20.

RESULTS AND DISCUSSION

The results of the geneflow modelling showed that the current uptake in adoption of young GS sires should lead to an 18% increase in genetic trend and a 39% increase in the annualised benefits after 20 years. However, a more aggressive increase in adoption and higher selection differential between DP and GS sires through improved evaluation systems could result in a 50% increase in genetic trend over historic and annualised benefits of genetic improvement of up to $495M.

Genetic trend in cows increased from 12.5 BW/year in the *status quo* to 13.3 and 15.8 BW/year after 20 years for the two levels of bull selection differential, 20 and 40 BW units/year, respectively.

The higher level of trend was attained earlier with faster adoption leading to increased benefits (Figure 1), resulting in total cumulative benefits for genetic improvement over the 20-year timeframe modelled of over $5.8B (differential of 20 BW/year) and $6.6B (40 BW/year). Relative to the *status quo* base scenario, the increase in total cumulative benefits ranged between $89M and $243M with different rates of adoption of GS bulls at the same 20 BW differential. This resulted in annualised benefits between $423M and $434M. The higher initial selection differential between GS and DP sires (40 BW) led to an increase in cumulative benefits between $658M and $1,065M, and annualised benefits between $465 and $495M (Table 1), depending on the adoption rate.
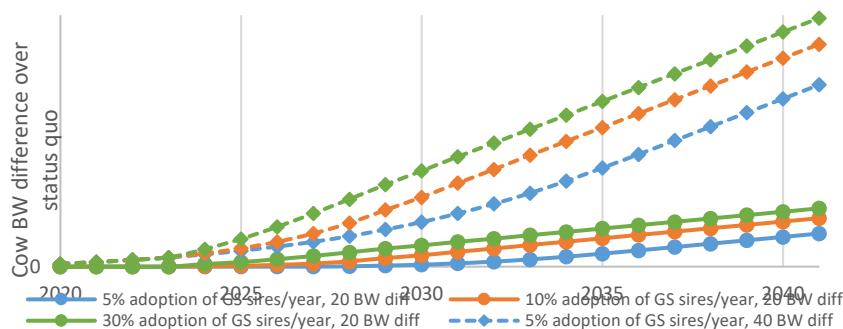

Figure 1. Difference in mean cow BW over the status quo base scenario for each of the increased adoption scenarios, under 20 and 40 BW differential scenarios

Table 1. Value of increased adoption of young sires and higher BW to the NZ dairy industry

Scenario	Genetic trend after 20 years	NPV Benefits after 20 years (NZ$M)	NPV of cumulative benefits (NZ$M)	Annualised benefits (NZ$M)
Historic	10.6	$4,038.66	-$1,569.64	$300.00
Base: max adoption of 50% of GS sires, 20 BW difference	12.5	$5,608.31		$416.60
Adoption of GS sires by 5% per year up to 90%, 20 BW diff	13.3	$5,697.30	$89.00	$423.21
Adoption of GS sires by 10% per year up to 90%, 20 BW diff	13.3	$5,778.74	$170.44	$429.26
Adoption of GS sires by 30% per year up to 90%, 20 BW diff	13.3	$5,851.73	$243.43	$434.68
Adoption of GS sires by 5% per year up to 90%, 40 BW diff	15.8	$6,266.39	$658.09	$465.48
Adoption of GS sires by 10% per year up to 90%, 40 BW diff	15.8	$6,481.26	$872.95	$481.44
Adoption of GS sires by 30% per year up to 90%, 40 BW diff	15.8	$6,673.98	$1,065.67	$495.76

The impact of improving fertility and survival evaluations, as well as adding clinical mastitis and lameness in BW, and recording high-quality phenotypes with the Infoherds structure, were incorporated into the model. The benefits of increased adoption of young GS sires, the addition of

new traits, and enhanced accuracy of existing traits to BW, could unlock $185-$245M in additional value of genetic gain per year, a 60 to 80% increase on the value of genetic improvement.

Berry (2019) identified areas of benefit with the integration of genomics to livestock breeding programs. For the NZ dairy industry, potential areas of benefit from adoption of GS, supported by Infoherds, involve improved rates of genetic gain and industry engagement. These represent key areas of interest for NZAEL alongside prompt development of systems to monitor genetic diversity, inbreeding and recessive gene frequencies across the entire population, and developing strategies to support the sustainable management of the national genetic resource.

Implementation of genomics within NZAEL also provides several intangible benefits. This includes an independent benchmark of sire offerings from each breeding company. It also enables farmers to review breeding value data on their commercial milking cows and heifers. However, in the current absence of a national genomic evaluation platform, the independent benchmark function is severely compromised until young bulls marketed based on genomic information have daughter records included in the conventional pedigree based NZAEL evaluation. Thus, these intangible benefits comprise a) helping NZAEL to fulfil a crucial role as an independent source of genetic improvement information for the dairy industry, which at the moment does not own, control or have access to a genomic data pipeline to support its R&D programmes; b) supporting industry compliance to underpin more robust assessments of individual farm emissions, shifting from generic parameter estimates of emissions to estimates based on the actual genetic profile of individual herds; and c) industry-wide added value from GS, as the broader industry fully benefits from the genomic resource only when the data and information is available for use by all herds and service operators.

CONCLUSIONS

Whilst genomics has been implemented within the NZ dairy industry for approximately 10 years, the potential value of the technology is yet to be fully realised. This might be reflecting the substantial breed admixture in the national herd as well as the pasture-based production which requires a specific reference population to explore the full effectiveness of genomic selection. A concerted collaborative effort at national level to overcome these limitations is now essential to ensure that the full industry benefits are realised. Additional benefits have also been identified from supporting sustainable management of genetic diversity within the national herd.

It is currently uncertain how funding and data flows will be managed, but stakeholders and potential partners must be engaged for the project to succeed. The value proposition for Infoherds has been previously identified. Communicating this clearly to potential stakeholders, as well as the opportunity cost associated with inaction, will be essential for building productive partnerships.

ACKNOWLEGEMENTS

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