Benchmarking genetic progress across dairy industries in the era's before and during genomics

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Background

In 2020 AbacusBio compared the genetic trends from the dairy industries of several countries to assess the impact of genomic selection on the genetic progress of dairy cattle.

The analysis has been updated in 2022 including two more years of available data and extending the group of the considered countries for a better representation of the dairy industry at international level.

This report compares genetic trends from the dairy industries of Europe, North America, and Oceania using data either publicly available or supplied by the breeding organizations of the countries concerned.

Please note that extreme care must be taken when comparing the overall performance of breeding programs in different countries. For this reason, many of the countries that contributed data to this analysis would prefer for their countries results to remain anonymous. The main value of the results provided in the report is to compare how rates of genetic progress have transitioned through the pre-genomics and during genomics time periods while taking a global perspective.

Material and Methods

Data used in the analysis were available for the dairy industries of 9 countries.

Australia, United Kingdom, USA and New Zealand agreed to make their result shared publicly. The other 5 countries providing data, have not granted permission for their results to be made publicly available, and therefore their results were anonymised.

For each dairy industry, the following data has been used in the analysis:

- cows' national total merit index, averaged by cows' year of birth for cows born between 2001 and 2020.
- genetic standard deviation of the national total merit index (either provided by the Organisation running genetic evaluation or estimated using proven bulls' national indexes and reliabilities).

For each dairy industry, the cows' genetic trends have been split into 4 intervals (each 5 years in length):

1) 2001-2005
2) 2006-2010
3) 2011-2015
4) 2016-2020

The intervals "2001-2005" and "2006-2010" were considered as "before-genomics" era; the intervals "2011-2015" and "2016-2020" as "during-genomics" era.

The yearly genetic gain within-interval has been calculated as the slope (regression coefficient) of the genetic trend in the 5 years, obtaining for each dairy industry 4 yearly genetic gains (1 for each interval) in the unit of the industry's national total merit index.

However, each country's selection index is expressed on a different scale due to:

- different currency
- different unit of expression (animals own genetic potential vs what it passes to its progeny)
- different weightings applied to the traits that make up the index
- different contributions of traits contributing to the index
- different degree of genetic variation among animals due to differences in average performance (e.g., intensive feeding systems versus pasture-based systems).

Therefore, the genetic gain trends have then been expressed as percentage of the genetic standard deviation of the country's selection index. Although this is a useful approach for expressing the results of the different industries in the same scale (%), results should be treated with extreme caution due to:

- differences between countries in computation of the genetic standard deviation of the index
- differences across countries in the balance of index emphasis on traits with low versus high heritability, it is harder to make standard deviations of progress in indexes with strong emphasis on low heritability traits with relatively low accuracy of merit prediction
- year of last revision of the selection index, when the index weights change, earlier years gains reflecting selection for an index that is different to the current index are disadvantaged
- it is a highly likely that most recent year average predictions for animals that don't yet have their own performance records are biased upwards, making most recent years genetic trends artificially inflated.

The suggestion is therefore to assess the results within country and breed only, focusing on how much the yearly genetic gain has changed during the 4 considered intervals, moving from the "before-genomics" to the "during-genomics" era.

Results are presented in the current report separately for Holstein (data from all countries), Jersey (data from Australia, and New Zealand) and crossbred (data from New Zealand only) breeds.

Results

Holstein

Table 1 shows the yearly genetic gain (expressed as a percentage of the genetic standard deviation of the national total merit index) of Holstein cows in each dairy industry.

Table 1. Holstein yearly genetic gain expressed as a percentage of the genetic standard deviation of the national total merit index.

Country^	AUS	X1	X2	X3	UK	X4	X5	USA	NZL HF
Index*	BPI	-	-	-	PLI	-	-	NM$	BW
Revision#	2020	-	-	-	2022	-	-	2021	2022
Interval									
2001-2005	4%	7%	15%	16%	5%	5%	8%	9%	6%
2006-2010	6%	10%	14%	16%	9%	9%	9%	12%	8%
2011-2015	16%	20%	29%	21%	18%	10%	18%	24%	7%
2016-2020	28%	23%	41%	22%	32%	9%	23%	32%	10%

^ 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.

* BPI = Balanced Performance Index; PLI = Profitable Lifetime Index; NM$ = Net Merit $; BW = Breeding Worth.

Year of latest revision of the index

In general, most of the countries had a steady genetic gain during the "before-genomics" era, with yearly average values of 8% and 10% of index genetic standard deviation for the 2001-2005 and 2006-2010 intervals, respectively.

The increase in the yearly genetic gain observed in 2011-2015 (from 10% in 2006-2010 to 18% on average) should reflect the impact of genomic selection across the dairy industries.

Genetic trends have further increased in the latest 5 years (2016-2020), with an average yearly gain of 24% (0.24 genetic SD of the index per year across countries).

Such further increase can be explained by larger genomic reference populations available at national level; genomic bulls' daughters becoming an increasing part of dairy herds internationally; replacement heifers genomically selected; as changes in selection intensities.

Genomic inflation could also be causing upward biased estimates of genetic trends in the most recent year cohorts. Because all of the sires of cows born in the 2011-2015 period will have been fully progeny tested in the genetic evaluation runs used for this study, they would be less likely to be influenced by

genomic inflation. We recommend that the international trend predictions for the 2016 to 2020 window be treated with caution.

Moreover, recent revisions to the selection indexes in most of the countries considered in the analyses could contributed to the observed increase in the last interval (2016-2020). Indeed, revisions to indexes that result in a significant shift in trait emphasis artificially penalise earlier trends which were focusing on a different index at the time but are now being measured using the most current form of the index.

Figure 1. Holstein yearly genetic gain expressed as a percentage of the genetic standard deviation of the index.
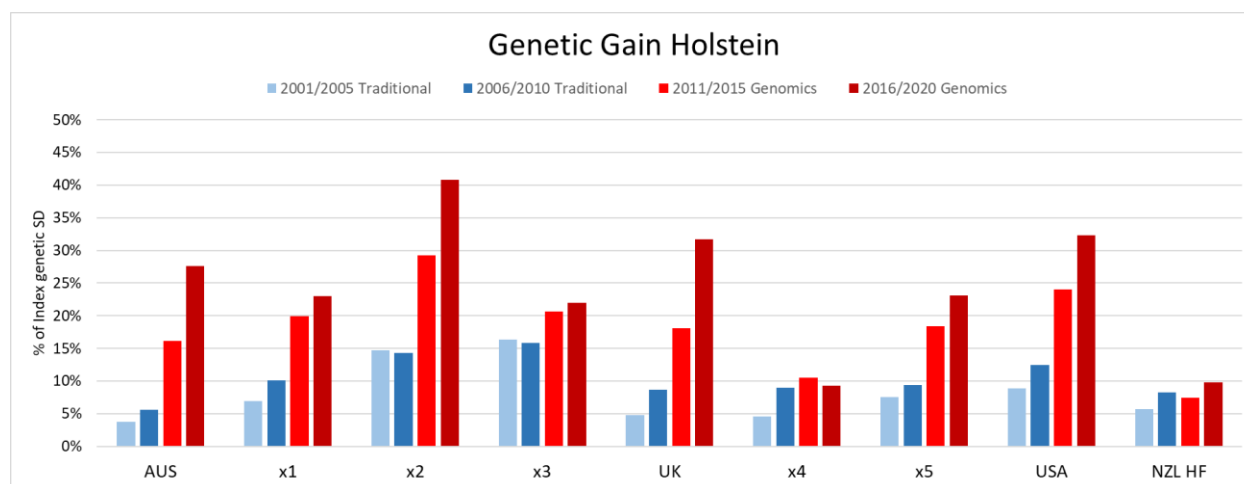
AUS = Australia; UK = United Kingdom; USA = United States of America; NZL HF = New Zealand Holstein-Friesian; X1, X2, X3, X4, X5 = countries with anonymized results.

In terms of differences between countries, it is worth mentioning that the countries considered in this analysis have certainly implemented genomic selection in different ways and at different timing, showing therefore differences in when and in which amount the increase in yearly genetic gain was observed.

If a country has implemented genomic selection early, and no further changes have been introduced after it, the yearly genetic gain in most recent years looks steadier than in countries with a later implementation of genomic selection.

Among the countries with public results, the ones that joined international genotype exchange *consortia* (UK and USA members of *North America Partners*) seemed to have benefitted from the access to a large reference population of bulls.

Although Australia does not benefit from an international reference population, a high proportion of cows in the country are daughters of foreign bulls genomically selected overseas. Moreover, Australia's revision of its national index in 2015 and 2020 has increasing the rate of farmer acceptance of genetic evaluation results when choosing bulls on farm with positive impact on the genetic gain observed in the country.

In New Zealand the yearly genetic gain for Holstein Friesian cows during the "before-genomics" era was aligned with the average one. After the introduction of genomics, New Zealand genetic gain has not followed the same increases observed in the other countries. The focus in New Zealand has been very much on domestic unique germplasm, targeting a unique breeding objective, with less contribution of international sires to domestic genetic progress.

Jersey and Crossbred

As expected, the yearly genetic gains observed in Jersey and Crossbred cows are lower than the ones observed in the Holstein Friesian breed. This reflects the much smaller population pools to work from.

In Australia the genetic gain of Jersey cows showed a constant increase during the considered intervals, with values moving from 3% in 2001-2005 to 19% in 2016-2020.

The genetic gain of Jersey cows in New Zealand has been somewhat inconsistent, with gain values ranging from 5% to 11% in the considered 20 years. Demand by commercial farmers for semen from Jersey bulls with larger liveweight than indicated economically optimal by the national index may be a factor in the genetic trends shown for Jerseys in both NZ and Australia. In 2015, the penalty on liveweight in the Australian Jersey index was removed, while in NZ, it is possible that AB companies have selected for larger Jersey sires desired by farmers, at the expense of some index merit.

The genetic gain of New Zealand crossbred cows has been steady in the transition from the "before-genomics" to the "during-genomics" era. The implementation of genomics doesn't seem to have a remarkable impact on increasing the genetic gain of these animals.

Table 2. Jersey and NZ crossbred (HF*JER) yearly genetic gain expressed as a percentage of the standard deviation of the index.
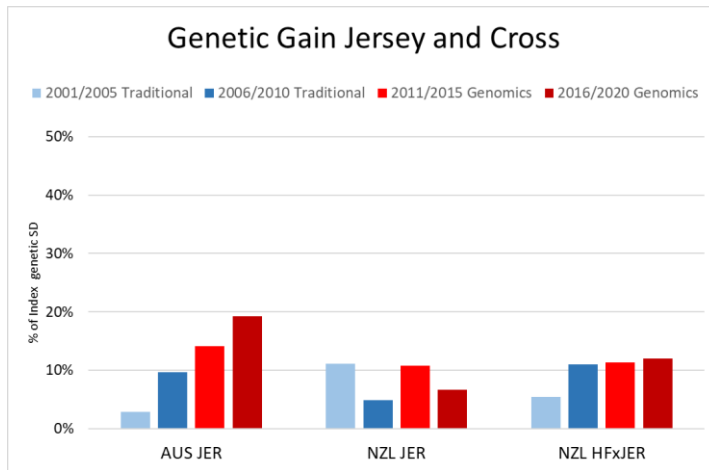
Country^	AUS JER	NZL JER		NZL HF*JER
Index*	BPI	BW		BW
Revision#	2020	2022		2022
Interval				
2001-2005	3%	11%		5%
2006-2010	10%	5%		11%
2011-2015	14%	11%		11%
2016-2020	19%	7%		12%

^ AUS = Australia; NZL = New Zealand

* BPI = Balanced Performance Index; BW = Breeding Worth.

Year of revision of the index

Figure 2. Jersey (JER) and NZ Crossbred (HF*JER) yearly genetic gain expressed as a percentage of the standard deviation of the index.

AUS = Australia; NZL = New Zealand