Cost benefit analysis of a dairy genomic reference population

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Summary

Genomic selection requires a reference population of animals with phenotype and genomic information. However, the costs of setting up a reference population can be prohibitive. Here, we have shown that a reference population of 100 herds (of approximately 300 cows/herd) has a rate of return of 81% or benefit (net present value) to cost ratio of 2.3, when the returns are valued as industry improvements in rates of genetic gain achieved from improved accuracies of selection. The rate of return increases with the size of the reference population (to 152% in the scenarios tested, when 250 herds were included) or a cost-benefit ratio of 4.2. However, the estimated cost of collating phenotypes and genotyping a 250-herd genomic reference population is around $10 million. The cost could be offset by having a model where calves are genotyped and encouraging farmers to contribute to the cost of genotyping where they can use the information for their own management decisions.

Keywords: genomic selection, phenotyping strategy

Introduction

Milk recording, which is the conventional source of production breeding value information, has declined in Australia over the past 15 years, from 7,405 herds in 2000/01 to 2,764 herds in 2015/16 (www.datagene.com.au accessed 26/09/17). Australian farmers still value conformation (Martin-Collado et al., 2015), however, the collection of conformation (type) data has decreased by over 50% since the introduction of genomics. Traditionally, breeding companies paid to collect the data on type and workability traits for young bulls through offering farmers that collected the data lower semen prices. However, in the era of genomic young sires, the incentive to collect information on a bull that may no longer be on the market is reduced. Furthermore, genomic selection for low heritability traits, such as resistance to disease, using data from dedicated reference populations is a promising way to achieve improvements in these traits (Egger-Danner et al, 2015). Finally, the number of bulls being progeny tested has fallen dramatically, as bull companies have moved from progeny testing a few bulls to a wide-scale genomic screening of many bulls. These changes have reduced the ability to accurately assess traits either using traditional or genomic breeding values. The net result, without action, is that reliabilities for all traits reduce over time, particularly for non-production traits which are especially threatened due to the sparsity of data available.

Australia has had a female genomic reference population in place from 2012. In 2016, the decision was made to transition the reference population from a research activity to a commercial activity (funded primarily by Australian dairy farmers). The aim of this study was to provide a cost-benefit analysis for large-scale genotyping of females.
Material and methods

Contribution of selection to profit

The base (starting) scenario was 100 herds with annual genotyping of two-year olds only (this is the current Australian Ginfo model), the average herd-size was assumed to be 300, the average replacement rate was 25%. In year 1 we assumed that 7,500 animals had genotypes for all scenarios. This was compared to two additional scenarios: 1) genotyping all rising two year-olds entering the herd and 2) genotyping all female calves. For both scenarios, increments were 50 herds per year until 250 herds were reached.

The following traits were assessed and their $h^2$ are shown in brackets: type (0.25), health (0.05) and Balanced Performance Index (BPI; 0.2). The BPI is an economic selection index that weights breeding values according to their approximate contribution to profitability (Byrne et al., 2015). The economic benefit of genetic improvement can be assessed by quantifying the impact of increases in reliability on the rate of genetic gain in these trait groups. The equations of Daetwyler et al. (2008) were used to calculate the reliability for genomic reference populations of various sizes and trait groups of varying heritabilities.

$$Rel = \frac{N\sigma^2}{N\sigma^2 + q}$$

Where $N$ was the number of genotyped individuals in the reference population with phenotypes, $h^2$ is the heritability of the trait, $q$ is the number of independent chromosome segments, defined as $q=2 NeL_g$ where $Ne$ is the effective population size (assumed to be 100) and $L_g$ is the length of the genome in Morgans (assumed to be 30). Daetwyler et al. (2008) provided a correction for the prediction of $Rel$ which is to add $(Rel+Relq)/2N$. For health and BPI it was conservatively assumed that 1.75 repeat records ($n$) per animal were available and for these traits, $h^2$ in the equation above was replaced with $\frac{n}{1-h^2} + n$ (Cameron, 1997).

The value of the contribution of genotyped females to increasing reliability was assessed in terms of the value of improvement in the BPI by using the Breeder’s equation, which is a calculation of the expected economic response to selection ($\Delta G$) assuming the predicted reliability from the Daetwyler et al. equation and a uniform selection intensity and generation interval (following Gonzalez-Recio et al., 2015):

$$\Delta G = \frac{Ir\sigma_A}{L}$$

Where $L$ is the average generation interval (assumed to be 4), $I$ is the selection intensity (assumed to be 1.75, which is equivalent to selecting the top 10.1% of the population) and $r$ is the accuracy of genomic selection (and is the square-root of the reliability obtained from the Daetwyler et al. (2008) equation) and $\sigma_A$ is the genetic standard deviation of the BPI, which was assumed to be $88$ and $1$ improvement in BPI was assumed to be equal to $1$ more profit. The total economic benefits per cow were estimated to be from improved reliability of genomic breeding values for health, type and other BPI traits. For simplicity of calculation, it was assumed that the contribution to BPI was 10% for both health traits and type traits with the remaining 80% being attributable to other traits in the BPI. To convert the estimates to a
national equivalent the results were multiplied by 1,600,000 which is the national herd-size of Australia.

**Costs associated with phenotyping and genotyping**

The exact costings of genotyping and phenotyping are commercially sensitive. However, the total amount of genotyping and phenotyping costs per herd of 300 cows was estimated to be $12,585. Overheads (staff salaries) were also included in the calculations. Throughout this paper, the calculations are shown in Australian dollars (at 22/09/17 AUD$1 = USD$0.80 source xe.com).

**Results and discussion**

*Table 1. Predicted reliabilities ($R^2$) and internal rates of return (IRR) after 10 years of selection for health, type and the Balanced Performance Index (BPI), 10-year net present values (NPVs) of economic benefits of selection and costs for 100-250 herds where replacement rising 2 year olds are genotyped each year.*

<table>
<thead>
<tr>
<th>Herds</th>
<th>Type $R^2$</th>
<th>Health $R^2$</th>
<th>BPI</th>
<th>Cost</th>
<th>NPV</th>
<th>IRR</th>
</tr>
</thead>
<tbody>
<tr>
<td>100</td>
<td>0.47</td>
<td>0.31</td>
<td>0.64</td>
<td>$5,195,000</td>
<td>$12,050,144</td>
<td>81%</td>
</tr>
<tr>
<td>150</td>
<td>0.48</td>
<td>0.42</td>
<td>0.72</td>
<td>$6,969,875</td>
<td>$27,443,554</td>
<td>117%</td>
</tr>
<tr>
<td>200</td>
<td>0.53</td>
<td>0.50</td>
<td>0.78</td>
<td>$8,598,875</td>
<td>$37,503,026</td>
<td>148%</td>
</tr>
<tr>
<td>250</td>
<td>0.56</td>
<td>0.55</td>
<td>0.81</td>
<td>$10,080,313</td>
<td>$42,057,399</td>
<td>152%</td>
</tr>
</tbody>
</table>

*Table 2. Predicted reliabilities ($R^2$) and internal rates of return (IRR) after 10 years of selection for health, type and the Balanced Performance Index (BPI), 10 year net present values (NPVs) of economic benefits of selection and costs for 100-250 herds where replacement calves are genotyped each year.*

<table>
<thead>
<tr>
<th>Herds</th>
<th>Type $R^2$</th>
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<td>0.64</td>
<td>$5,195,000</td>
<td>$12,050,144</td>
<td>81%</td>
</tr>
<tr>
<td>150</td>
<td>0.48</td>
<td>0.39</td>
<td>0.70</td>
<td>$6,913,938</td>
<td>$22,141,556</td>
<td>92%</td>
</tr>
<tr>
<td>200</td>
<td>0.53</td>
<td>0.44</td>
<td>0.74</td>
<td>$8,087,000</td>
<td>$30,408,697</td>
<td>119%</td>
</tr>
<tr>
<td>250</td>
<td>0.56</td>
<td>0.48</td>
<td>0.77</td>
<td>$9,312,500</td>
<td>$34,460,648</td>
<td>125%</td>
</tr>
</tbody>
</table>

Increasing the size of the female genomic population from 100 to 250 herds will lead to increased accuracies, especially for health traits, which could increase from 0.31 (100 herds) to 0.55 (250 herds; Table 1) when 2-year olds are genotyped or to 0.48 (250 herds) when calves are genotyped (Table 2). However, the improvement in reliability for all traits is larger when the reference population increases from 100 to 150 herds than from 200 to 250 herds. Similarly, in early years, the contribution of additional phenotypes to the reference population is high and this diminishes in later years (results not shown).

The cost of having a female genomic reference population is substantial, for the schemes considered it ranged between $5 million and $10 million over a 10-year period and may be too costly to run. The highest rates of return are achieved for 250 herds using the 2-year old
genotyping model. However, the rates of return are comparable when cows from 200 herds are genotyped. To put this in context, the cost per unit increase in reliability through increasing the number of herds from 100 to 150 for the calf scenario (Table 2) is $214,867. The equivalent for 150-200 herds is $234,612 per unit of reliability, the amount jumps to $306,375 per unit of reliability going from 200 to 250 herds. The same pattern is reflected by the internal rates of return with the difference per 50 herd change in the reference population reducing as the number of herds increases. The results imply that the incremental benefits are greatest up to 200 herds in the reference population.

Asking farmers to contribute to genotyping costs is one way to improve the affordability of these schemes. Farmers are likely to prefer calf or heifer genotyping schemes as they can use the results to make management decisions, such as selling lower genetic merit calves on the basis of genomic breeding values, instead of incurring rearing costs. The compromise is that not all genotyped heifers will enter the milking herd and therefore have the phenotypes of greatest value.

One of the assumptions was that the average selection intensity across pathways was 1.75 (top 10.1%). Assuming BPI has an SD of $88, a selection intensity of 1.75, an accuracy of 0.8 and generation interval of 4 years, the theoretical genetic gain possible is $30.80/year which is much higher than the actual current rate of genetic gain (approximately $10/year improvement in BPI). Reducing the selection intensity to 1 would result in none of the strategies being profitable. Therefore, there is a challenge to the dairy industry to maximise selection intensity through widespread use of high BPI sires. Another issue is the extent of use of genomic information in selection decisions, which we assumed was the entire national herd. This is justified as most selection decisions are likely to include information from genomic proofs. However, for the 100 herd scenario to break-even genomic selection needs to be in use for around half of the national herd.

The costs of setting up a female genomic reference population are high. However, under the assumptions presented in this paper, the ratio of benefits to cost is high enough to justify this investment, especially if some of the genotyping costs are borne by the participating farmers. The Australian dairy industry has opted for a genomic reference population of 200 herds where calves are genotyped and farmers make a contribution to genotyping costs.

**List of References**


