

European Innovation Partnership Wales

Assessing the potential of genomic testing dairy heifers to increase genetic gains and financial returns

Final report

Trevor Lloyd, Ty Mawr
Aled Morris, Marian Mawr
Aled Jones, Bwthyn Hendy
Rhys Jones, Old Llwyn Onn Farm
Tom Bletcher, Argoed Hall Farm
Dewi Jones, Llysfasi
Huw Jones, Pengwern Farm
Giles Rowland, Bachymbyd Fawr
Ceredig Evans, Erw Fawr
Victoria Hicks, Kite Consulting
Will Jones, Kite Consulting
Neil Blackburn, Kite Consulting

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Project in brief

- *432 heifers genomic tested in 2018*
 - *21 heifers had mis-identified sires on their parentage (4.9%)*
 - *Average cost of heifer rearing for the participating farms was £1,420*
 - *15.4% of heifers tested failed to reach the end of their first lactation*
 - *Average age at first calving was 24.9 months*
 - *Average first lactation performance was 8,216kgs and 100 days to conceive from 2.16 services*
 - *A reduction in average £PLI from traditional to genomic proofs of -£44 was significant*
 - *A hypothetical breeding scenario resulted in 23% of heifers being incorrectly bred, which resulted in lost £PLI potential of £6,914 for the next generation*
 - *Days to conception and number of services were more closely related to genomic fertility index than traditional fertility index (statistically significant $p < .05$)*
 - *Number of high SCC occurrences was more closely linked with genomic SCC index than traditional SCC index (statistically significant $p < .05$) but not cumulative SCC*
 - *No difference in relationship for milk or solids yield against genomic or traditional milk kgs*
 - *Cost benefit of genomic testing was calculated at £19.39 per animal*
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Background

This project set out to investigate the benefits of genomic testing dairy heifers. Historically, estimated breeding values have been the only information available to farmers to base breeding decisions on. These parent averages are only 35% reliable when it comes to predicting future performance. With the introduction of commercially available genomic DNA testing in the UK market several years ago, the opportunity to increase the reliability of breeding values from 35% to between 60 – 70% arose.

However, genomic testing adds an extra £25 to £30 onto rearing costs, which is off-putting considering these animals will not start 'paying back' their rearing costs until their 2nd lactation. Consequently, the cost benefit to genomic testing animals needs to be quantifiable before considerable uptake in this innovative technology is seen.

This project set out to understand what the cost benefit for genomic testing would be based on individual farm heifer rearing cost information, genetic profile and compare the correlation between parent average and genomic testing with future performance.

The project started on 1st December 2017 and finished on 31st October 2020.

Recruitment, Testing & Lactation performance

A total of 9 participating farms in North Wales took part in the project that are all Holstein/Friesian herds. Heifers were selected for testing based on their birth date in order to fit in with the project timeline, which resulted in 432 heifers that were eligible across the 9 farms. Quality of animal records was an issue for several herds. This mainly concerned the correct use of breed codes and sire/dam ID's for the heifers, which is a lesson learnt from the project.

The genomic testing was performed in April 2018 by a farm technician to reduce testing and sampling errors. The results arrived back in June and July 2018. However, AHDB performed a profitable lifetime index (£PLI) rebasing in spring 2020, which subsequently meant that the original genomic £PLIs need to be reduced by £149 in order to match today's £PLI levels.

One of the additional benefits of genomic testing is that it will identify any incorrect sires, of which this project found 21 heifers with mis-identified sires (4.9%). The tests were able to correctly identify 20 out of 21 sires for these heifers and amendments to their parentage were made accordingly. Israel & Weller (2000) found that genetic gain reduced by 4.3% when incorrect sire parentage rate of 10% occurred.

The average heifer rearing cost for the group was calculated at £1,420/head with the lowest farm at £1,199 and highest at £1,570 giving a range in costs of £370 amongst the group. There was almost a 50/50 split in farms using contract rearers at some point during the heifer cycle.

The project then had to wait until these heifers had calved and started their first lactation. As all herds were milk recorded, the project was able to download lactation performance for these animals in September 2020. A total of 30 animals did not reach the start of their first lactation and a further 37 animals did not complete their first lactation (15.4%). Reasons for exits reported by the participating farms included infertility, TB culls and injury.

The project achieved a final dataset consisting of 291 animals that had genomic and traditional PTA results and complete 305d lactation information. Some animals had not fully reached 305 days in their first lactation or had missing fertility information. There were also several animals whose traditional PTA's could not be recalculated because their sire didn't have an official UK proof available.

Table 1. Average and range in first lactation performance.

	Age at first calving (months)	305d milk kgs	305d solids kgs	No. of high SCC events	Cumulative somatic cell count (SCC)	Days to first service	Days to Conception	No. of Services
Min.	18.9	4,667	371	0	10	25	38	0
1st Quartile	23.27	7,136	567	0	26	51	64	1
Median	24.6	8,190	641	0	39	59	84	2
Mean	24.9	8,216	635	0.7835	108.6	64.18	100	2.158
3rd Quartile	26.2	9,220	707	1	84.5	72	131	3
Max.	33.63	13,054	965	9	2111	150	304	7

Genetic Analysis

Until a heifer reaches their second lactation, the only genetic information available is what's known as their Parent Average PTA (Predicted Transmitting Ability). This is a composite of their family pedigree information, mainly their dam and sire's genetic evaluations, which are produced by AHDB every quarter. Once the heifer has enough production information of her own, then this will start to be incorporated into her genetic evaluation. However, PTAs are not an indicator of that animal's future performance; they are an estimate of how much of a certain trait that animal will have, on average, received from its parents. This contrasts with genomic evaluations, which give an indication of that animal's future performance.

This project set out to compare the difference between traditional PTAs and genomic PTAs for the same animals to help farmers understand the cost benefit for having this additional information early on in an animal's life. Tables 2 and 3 below show the summary statistics for the main genetic traits the project was able to look at alongside lactation performance. Please note that these traditional (parent average) PTA's were recalculated in September 2020 using pedigree information from the August 2020 proof run.

Table 2. Traditional PTA results.

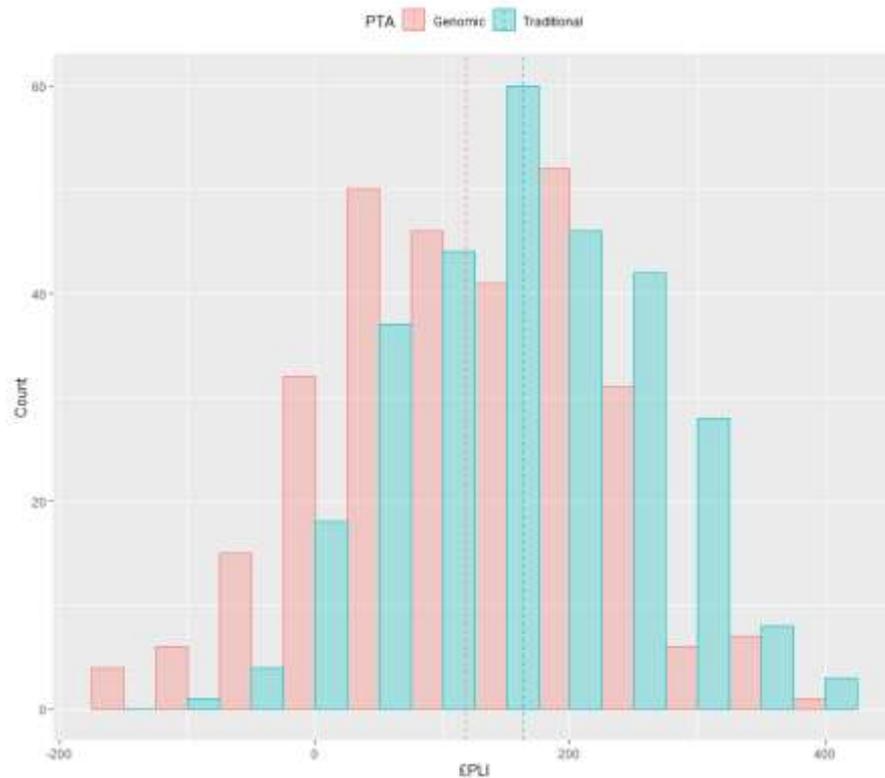
	£PLI	Fertility index	Milk kgs	SCC
Min.	-89	-10	-315	-22
1st Quartile	98	-0.8	36.5	-8.5
Median	155	1.7	159	-5
Mean	162.6	2.277	172.1	-4.601
3rd Quartile	233.5	5.35	308	-1
Max.	394	14.6	766	16

Table 3. Genomic PTA results.

	£PLI	Fertility index	Milk kgs	SCC
Min.	-171	-5.3	-311	-30
1st Quartile	42	2.15	95	-14
Median	121	4.7	259	-9
Mean	118.2	5.114	269.1	-9.213
3rd Quartile	193	8.05	431	-4
Max.	388	16.8	984	11

For Tables 2 and 3, please note that the somatic cell count (SCC) index is a negative trait, therefore a negative value is more desirable than a positive one.

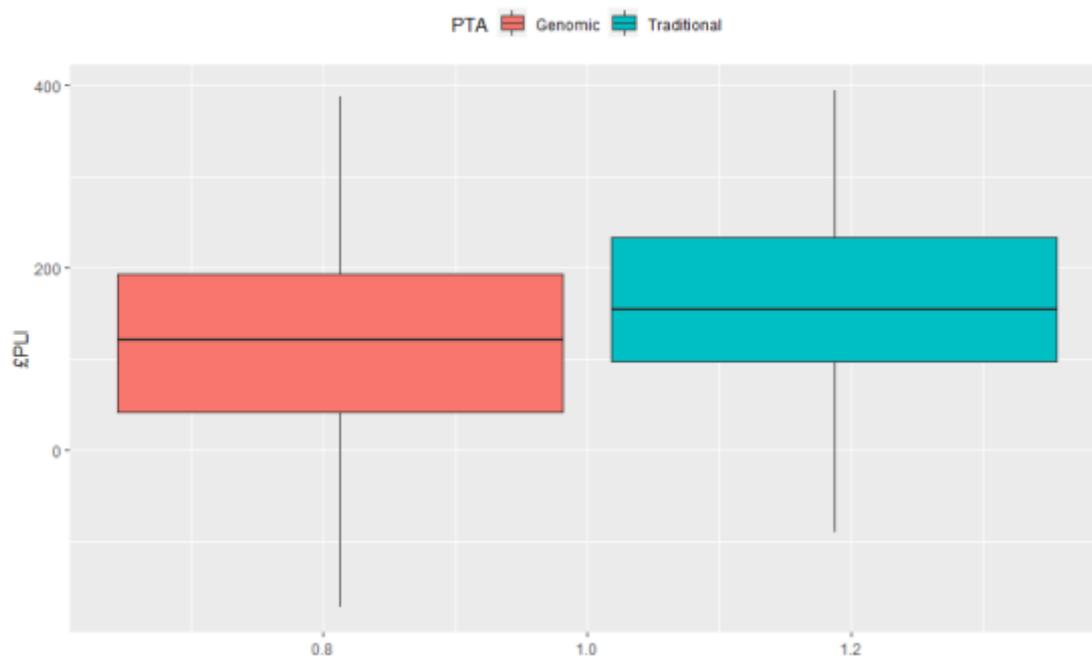
When comparing the selection index £PLI (Profitable Lifetime Index), where a higher £ value is more desirable, the average genomic £PLI was £44.4 lower than the traditional £PLI index. The change in distribution of heifers based on their genomic or traditional £PLI PTA can be seen in Graph 1.



Graph 1. Histogram of £PLI values for genomic and traditional PTAs.

The reduction in mean £PLI for genomic compared to traditional PTA is identified by the two dashed lines. The change in mean is clearly a result in the change in distribution to the left with many heifers receiving lower genomic £PLI values compared to when their traditional PTAs were estimated. A paired t-Test was conducted to compare the mean £PLI of heifers for their traditional and genomic PTAs. The difference between the average genomic £PLI (M= £118.20, SD = £105.42) and traditional £PLI (M= £162.70, SD= £96.38) was significant (conditions; $t(580) = -5.295$, $p = .000$). From this, it was concluded that the reduction in mean £PLI for genomic PTAs was significant, therefore, these results suggest that traditional £PLI values significantly over estimate an animal's true £PLI value. This can be visually demonstrated by viewing the box plot in Graph 2.

Graph 2. Box plot of genomic £PLI and traditional £PLI PTAs.



The change in £PLI from traditional to genomic didn't just shift values however, it also re-ranked animals too. To demonstrate this, a theoretical selection point of £150 PLI was used to decide whether heifers would be bred to a beef or dairy sire and what the differences would be if genomic or traditional £PLI was used. The £PLI selection index is designed to be an initial sort for animals to make breeding decisions on as it is a composite of production, health, fertility and longevity traits. Therefore, this exercise aims to demonstrate the number of animals that would have been incorrectly selected if only traditional £PLI values were known.

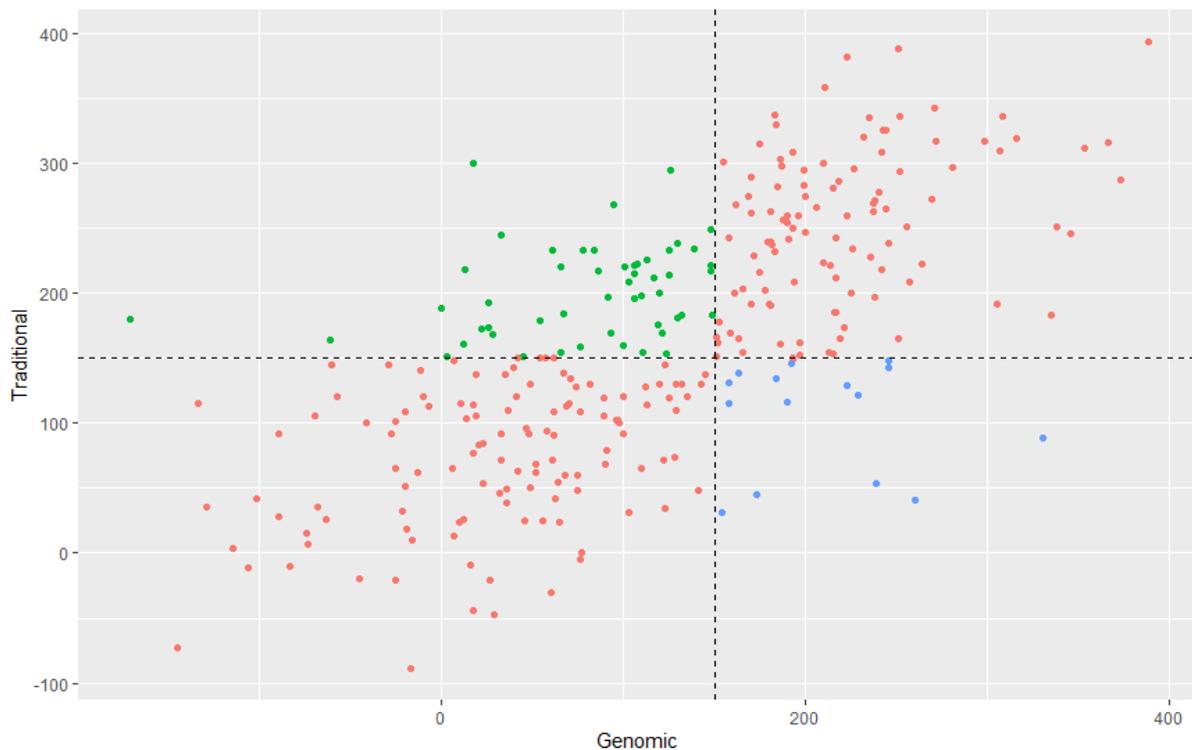
Graph 3 displays the relationship between traditional and genomic £PLI values. The animals in red are those that were correctly identified as being either above £150 or below £150 PLI by both traditional and genomic PTA (224 heifers = 76.9%).

The animals in blue are below £150 based on traditional PTA but were above £150 PLI on genomic. In the hypothetical breeding scenario, if only the traditional £PLI value was known, then these animals would have been bred to a beef sire and their genetics would not have been passed onto future replacements. These blue animals (16 heifers = 5.4%) therefore represent lost opportunities for improving genetic gain within the dairy herd. The average genomic £PLI of the blue animals was £209, meaning a loss of £3,344 in £PLI to be passed onto future generations.

On the other hand, the green dots represent animals that were above £150 PLI on traditional PTA but were actually below £150 once their genomic PLI was known. These heifers (51 heifers = 17.5%) would have been served to dairy in our hypothetical breeding scenario, which means that their overestimated genetics would be passed onto the next generation of dairy replacements. This means that genetic progress is slowed in the herd because of incorrectly determined £PLI values when only traditional PTAs are used. The average genomic PLI for

these heifers was £80, which is £70 lower than the £150 threshold set for selecting heifers to serve to dairy. As a consequence, lost PLI potential equates to £3,570 for this group of animals compared to the minimum genetic equivalent of heifers served to dairy could have been if genomic PLI was known at the time of breeding.

Graph 3. Scatter plot showing the theoretical cut off point at £150 PLI for making breeding decisions using either genomic or traditional PTA's.



Graph 3 therefore shows us the potential breeding mistakes that can be made when solely using traditional PTA values as 22.9% of heifers were mis-identified as being either above or below £150 PLI.

Combining the use of female genotyping alongside sexed semen usage is most advantageous for increasing the rate of genetic gain in the herd (Bérodier et al., 2019). Rate of genetic gain should be an important consideration for all dairy farms as it provides an opportunity to maximise the benefits of 'routine' farm practice such as cow breeding. Cole & VanRaden (2018) demonstrated that US improvements in production from 1957 to 2015 were evenly divided between improvements in genetic potential as well as feeding and management improvements. Although the amount of gain from genetics or improved environmental factors varies by how heritable a trait is, this can help producers decide what needs to be prioritised in their system in order to improve performance based on their desired traits.

Relationship with future performance

1) Heifer rankings vs actual performance

Having reviewed the genetic analysis and differences between traditional and genomic PTAs, the lactation performance added another dimension to help determine the cost benefit to genomic testing. Actual lactation performance can be seen in Table 1.

To compare the relationship between actual performance and both genomic and traditional PTAs, we ranked the heifers into quartiles for each trait and then looked at the average first lactation performance for these quartiles to determine any trends. The questions we were looking to answer were:

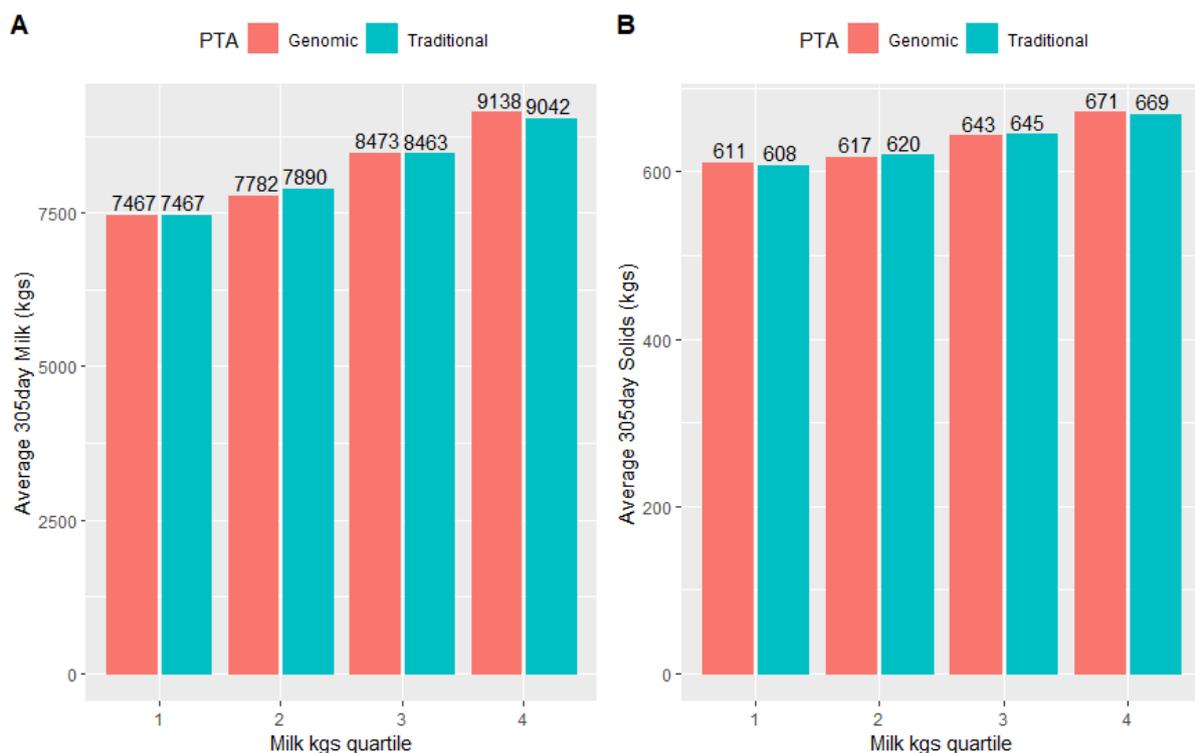
1. Are our best genetic animals, ranked either by their genomic or traditional PTA value, truly our best performers?
2. Are our worst genetic animals, ranked either by their genomic or traditional PTA value, truly our worst performers?

We focussed on three areas: milk production, fertility and SCC. For milk production we looked at 305day milk yield and solids production against their milk kgs trait. For fertility analysis, we used days to conception, days to first service and number of services against their fertility index trait. For SCC, we used the number of high SCC (greater than 250) and their cumulative 305d SCC against their SCC index.

In Graphs 4 to 6, the quartiles represent:

- 1 = Bottom 25%
- 2 = Bottom 25 to 50%
- 3 = Top 25 to 50%
- 4 = Top 25%

Graph 4. First lactation milk production against PTA quartile for milk kgs.



A = 305day milk yield average by milk kgs quartile.

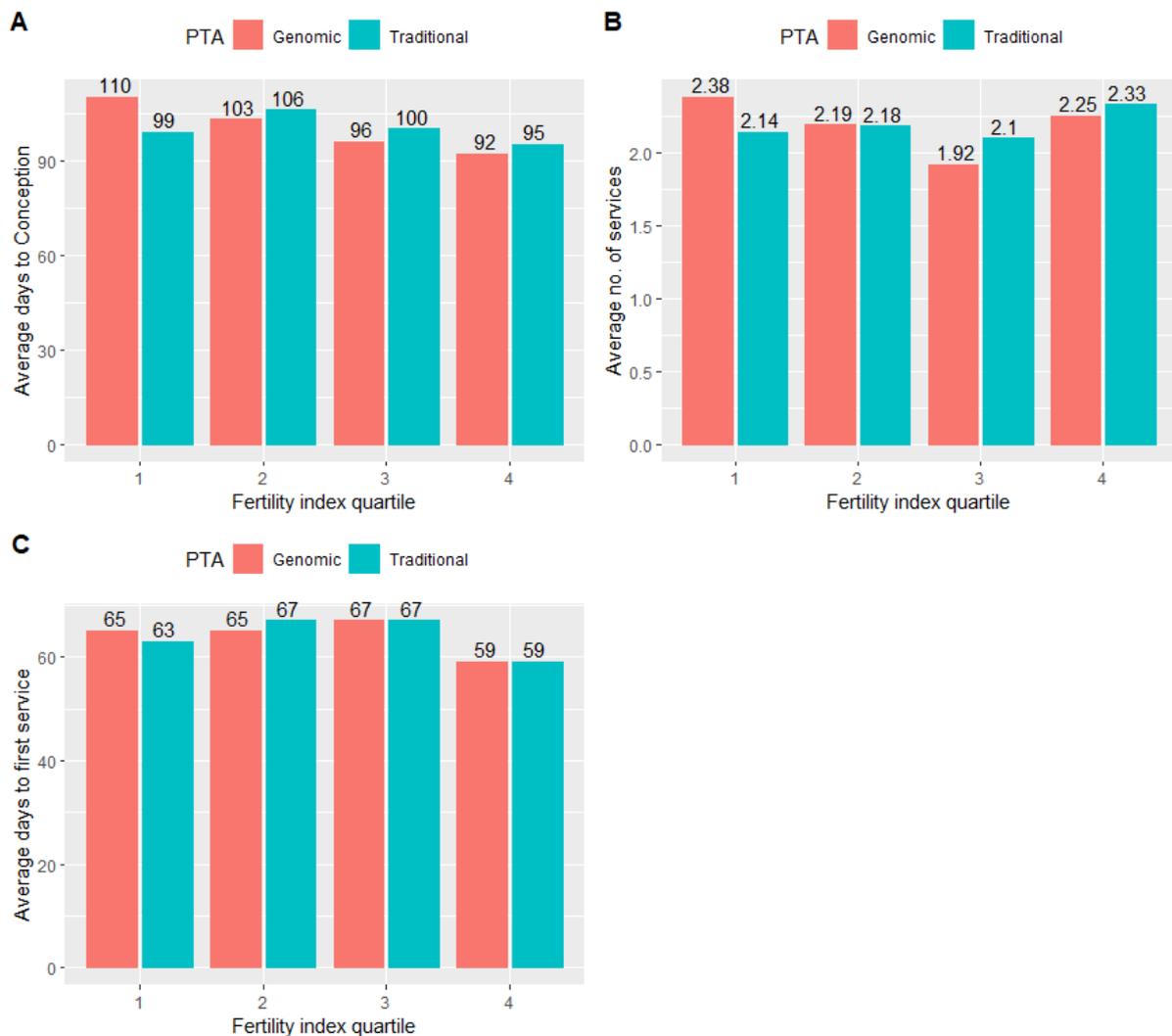
B = 30day solid yield average by milk kgs quartile.

Comparing the milk production performance of heifers against either genomic or traditional PTA for milk kgs did not show any differences. There were small numeric differences but these were not statistically significant (see Table 4). From this graph alone, we can conclude that our best and worst heifers genetically are also our best and worst performers whether they

are ranked by genomic milk kgs or by traditional milk kgs PTA. This may be because milk yield is a highly heritable trait at 0.55.

This is in contrast to experience from University of Wisconsin-Madison dairy herd that found a difference of 4,801 pounds (2117.7 kg) of 305 day mature equivalent milk when cows were sorted by genomic milk PTA, compared to only 2,366 pounds (1073.2 kg) based on sire PTA (Weigel, Mikshovsky, & Cabrera, 2015).

Graph 5. First lactation fertility performance against PTA rank for fertility index.



- A = Average days to conception by fertility index quartile.
- B = Average number of services by fertility index quartile.
- C = Average days to first service by fertility index quartile.

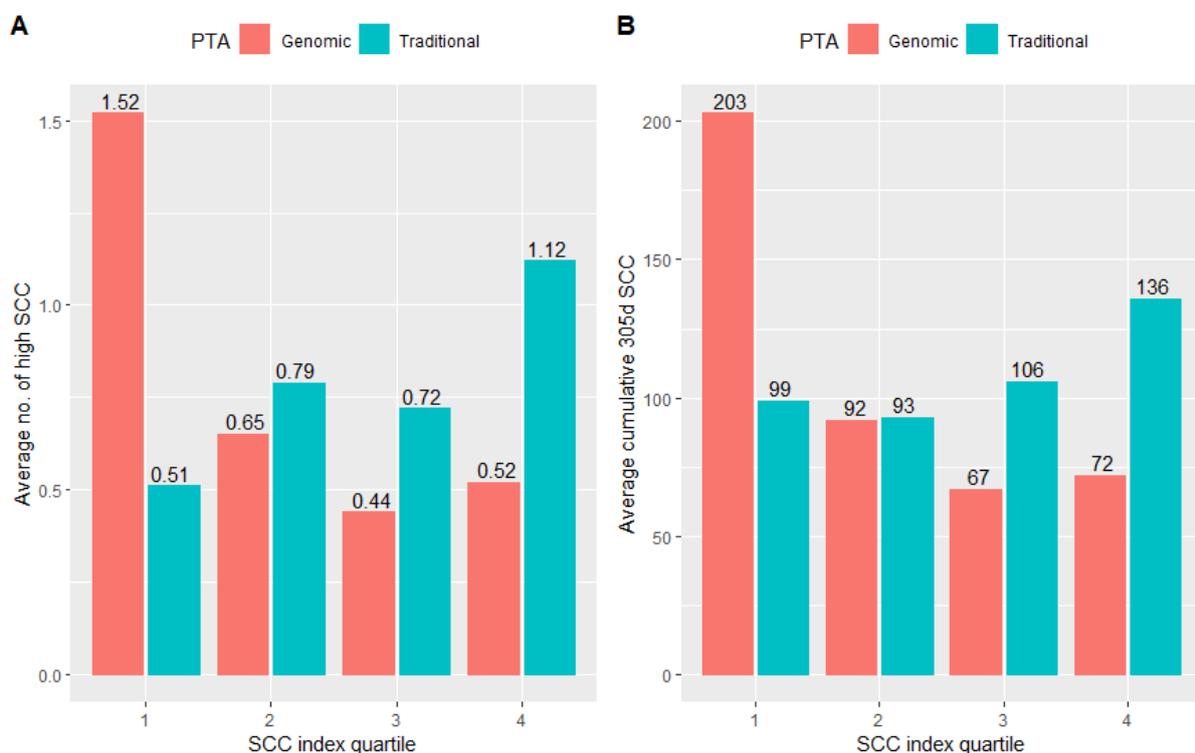
In contrast to milk production, fertility performance shows different patterns based on the type of PTA used to rank heifers on their fertility index. In graph 5A, there is a difference of 18 days to conception when comparing top and bottom 25% based on genomic fertility index. On the other hand, there is only a difference of 4 days between the top and bottom 25% based on traditional fertility index, with average days to conception actually increasing between these two quartiles. Therefore, our best and worst animals genetically were our best and worst animals when ranked by genomic fertility index but not by traditional fertility index. This

difference was statistically significant (Table 4). The average difference for all quartiles on graph 5A works out at 5.25 days, which if you account for the cost of an extended lactation at £5 per day works out at £26.25; this would cover the ex-vat cost of genomic testing.

A differing pattern of performance can also be seen for number of services (Graph 5B), although this isn't as clear as days to conception. Looking at number of services when ranked by genomic fertility index, the bottom 25% did have the highest number of services on average, and although this figure decreases through the quartiles, the top 25% have the second highest average number of services. The picture for traditional fertility index is more mixed with the bottom 25% having the second lowest number of services and the top 25% having the highest number of services. Despite the mixed picture for fertility performance ranked by both genomic and traditional fertility index, the differences were statistically significant (Table 4). There could be a management factor at play here if producers chose to give higher genetic merit animals more chances to conceive and hence would have higher number of services in order to retain these superior genetics in the herd.

Despite finding significant differences between the relationship for days to conception and number of services against fertility index, average days to first service (Graph 5C) did not show any differences in performance. Again, there could be a management factor confounding these results based on a farm's voluntary waiting period (the number of days a farm waits before serving that animal after calving).

Graph 6. First lactation SCC performance by SCC index quartile.



A = Average number of high SCC by SCC index quartile.

B = Average cumulative 305day SCC by SCC index quartile.

The most striking point from looking at graphs 6A and 6B is that the bottom 25% of heifers ranked by genomic SCC index had the highest average number of high SCC occurrences and

also the highest cumulative SCC. This is in stark contrast to the performance of animals when ranked by their traditional SCC index; the poorest SCC performance occurred in the top 25% for both high SCC occurrences and cumulative SCC. However, only number of high SCC were considered to be statistically significant (Table 4) despite the trend seen in cumulative SCC. Therefore, our worst animals for SCC performance were genuinely our worst genetically when ranked by genomic SCC index, however, the opposite was true when ranked by traditional SCC index.

2) Correlations

From the comparison of quartile rankings for first lactation performance against certain genetic traits, it is clear that there were differences for some fertility and SCC parameters between genomic and traditional PTAs. To determine if these relationships were statistically significant or not, we compared the correlation coefficients for each performance parameter against genomic and traditional PTA values.

Table 4. Correlation coefficients for genomic and traditional PTAs against first lactation performance.

	Average	SD +/-	Correlation Coefficients						P Value
			Genomic Fertility index	Traditional Fertility index	Genomic Milk (kgs)	Traditional Milk (kgs)	Genomic SCC index	Traditional SCC index	
Genomic Fertility index	5.11	4.18							
Traditional Fertility index	2.28	4.48	0.7251						
Conception (days)	100	49	-0.1531*	-0.0409*					0.0091
No. serves	2.5	1.33	-0.0543*	0.0501*					0.0159
Days to first service	64	20.5	-0.1052	-0.0653					0.3566
Genomic Milk (kgs)	269	235.38							
Traditional Milk (kgs)	172	206.50			0.7238				
305d milk kgs	8216	1491.3			0.4769	0.4612			0.6773
305d solids kgs	635	106.74			0.2582	0.2790			0.6192
Genomic SCC index	-9.21	7.54							
Traditional SCC index	-4.60	5.83					0.6193		
No. of high SCC	0.78	1.65					0.2352*	0.0779*	0.0017
Cum. SCC 000's	109	235.30					0.2363	0.1525	0.0931

* Denotes statistically significant result at p value <.05 or lower.

The test for significance used to determine if the null hypothesis should be rejected was based on Pearson and Filon's z (Pearson, 1898). The correlation coefficients were calculated in Microsoft Excel and then passed to the cocor R package (Diedenhofen & Musch, 2015) via the web interface at <http://comparingcorrelations.org/> to compute the z statistic and p values.

The tests carried out were based on dependent groups with overlapping variables using a two tailed test.

This analysis confirmed the visual differences from reviewing the animal rankings. The relationships found to be statistically significant were:

- Days to conception and fertility index
- Number of services and fertility index
- Number of high SCC index

From this, we can conclude that the difference between two correlations, such as days to conception and genomic fertility index vs days to conception and traditional fertility index, is significantly different. The relationships that were not found to be statistically different (the null hypothesis was retained) were:

- Days to first service and fertility index
- 305day milk production and milk kgs
- 305day solids production and milk kgs
- Cumulative SCC and SCC index

While traditional PTAs are not designed to be an indicator of an animal's future performance, the relationship between milk kgs PTA and 305d yield showed the strongest positive correlation regardless of genomic or traditional milk kgs. For less heritable traits such as fertility and SCC, it was a mixed picture. The strength of the correlations were a lot lower, and some negative, but despite this, a number of significant differences were found.

Conclusions

The ability for genomic testing to identify inferior or superior heifers at an early age has been proven for health, fertility and production. Specific advantages for improving fertility and SCC performance by selecting animals based on genomic PTAs instead of traditional PTAs has been demonstrated. The economic advantage for reducing days to conception equated to £26.25.

The benefit of genomic testing lies in the increased progression of genetic gain. The hypothetical breeding scenario suggested within this report demonstrate a potential loss of £6,914 of PLI that would not be passed down to future generations. Averaged over the cohort of animals that made it through to the final analysis plus 15.4% to account for losses (290 + 45), this equates to £20.64 PLI lost per animal.

The total economic benefit generated from genomic testing totalled £46.89, minus the cost of genomic testing at £27.50 creates a cost benefit of £19.39. However, this does not account for the additive and compound interest that investing in herd genetics creates, nor the benefits of correcting sire ID.

Increasing the rate of genetic gain should be a priority for all dairy farmers given the increasing environmental concerns and requirements they're continuously faced with. Improving fertility and health with the use of genomic testing will allow herds to increase the productive life of the herd. This in turn will reduce replacement rate and allow the freedom for selection intensity to occur. At an average rearing cost of £1,420, capital tied up in herd replacements is large and reducing this will release cash for other activities, such as genomic testing.

This project did not investigate differing genomic testing scenarios but this should be a consideration for producers looking to start genomic testing. Herds that are expanding and need to maximise heifer numbers are unlikely to gain the full cost benefits witnessed within this project as they will not be able to instigate selection pressure. However, herd expansion may come into question in the future with the implementation of the Clean Air Strategy and integration of the Clean Air Act 1993 within the UK Government's Environmental Bill. Therefore, expansion via improving herd genetics to improve performance in order to maximise output from every cow place will be important.

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