

## A Nuffield Farming Scholarships Trust Report

Award sponsored by

# John Oldacre Foundation

John Oldacre Foundation

How can UK dairy farmers use genomics to breed a better herd?

**Neil Eastham** 

June 2019

## NUFFIELD FARMING SCHOLARSHIPS TRUST (UK)

Awarding life changing Scholarships that unlock individual potential and broaden horizons through study and travel overseas, with a view to developing farming and agricultural industries.

"Leading positive change in agriculture"

"Nuffield Farming" study awards give a unique opportunity to stand back from your day-to-day occupation and to research a subject of interest to you. Academic qualifications are not essential, but you will need to persuade the Selection Committee that you have the qualities to make the best use of an opportunity that is given to only a few – approximately 20 each year.

Scholarships are open to those who work in farming, food, horticulture, rural and associated industries or are in a position to influence these industries. You must be a resident in the UK. Applicants must be aged between 22 and 45 years (the upper age limit is 45 on 31st July in the year of application). There is no requirement for academic qualifications, but applicants will already be well established in their career and demonstrate a passion for the industry they work in and be three years post tertiary education. Scholarships are not awarded to anyone in full-time education or to further research projects.

Full details of the Nuffield Farming Scholarships can be seen on the Trust's website: <u>www.nuffieldscholar.org</u>. Application forms can be downloaded, but only online submission is accepted.

Closing date for completed applications is the 31<sup>st</sup> July each year.

Copyright @ Nuffield Farming Scholarships Trust

ISBN: 978-1-912059-17-1

Published by The Nuffield Farming Scholarships Trust Southill Farm, Staple Fitzpaine, Taunton, TA3 5SH Tel: 01460 234012 Email: director@nuffieldscholar.org www.nuffieldscholar.org





Date of report: June 2019

*"Leading positive change in agriculture.* Inspiring passion and potential in people."

Title	How can UK dairy farmers use genomics to breed a better herd?							
Scholar	Neil Eastham							
Sponsor	John Oldacre Foundation							
Objectives of Study Tour	To explore how UK dairy farmers can benefit from the use of genomics by understanding more about how producers are using genomics and realising a return on their investment.							
	Learn more about the role the vet can play and consider the future application of genomics.							
Countries Visited	Ireland, The Netherlands, Belgium and Italy USA, Canada							
Messages	<ul> <li>Genetic improvement on UK dairy farms is worth the effort</li> <li>Faster genetic progress can be realised with genomics</li> <li>UK dairy farmers can benefit from an increased use of female genomic testing</li> <li>Breeding objectives and strategies must be optimised to realise a return on investment when genomic testing</li> <li>Vets have an opportunity to add value</li> <li>Long term industry success in the field of breeding and genetics will ride on data</li> </ul>							

## **EXECUTIVE SUMMARY**

Good genetics are fundamental when considering the profitability of any dairy enterprise. A structured approach to breeding can be a highly cost-effective way of improving herd performance. Genetics directly influence a number of key areas of management including: production, milk quality, health, fertility and feed efficiency.

Genomic testing has transformed the dairy industry's understanding of genetics. Genomic test results are significantly more reliable than traditional parent average values as they reveal more about the genetic potential an animal actually inherited. Using genomic testing, an animal's genetic potential can be revealed early in life, and genetic progress can be accelerated with confidence.

The rate of genetic gain in the genomic era has doubled. Early on, the major focus of genomic testing was the benefit in identifying high quality young bulls early. Now farmers can use exactly the same power of prediction for females as a cost-effective tool to make more precise management, selection and breeding decisions on-farm.

Whilst the adoption of genomics on the male side is high, the number of UK dairy farmers genomictesting their females is low. I set out to explore why this might be by visiting producers who are benefiting, as well as meeting with other stakeholders. I wanted to understand more about how producers are using genomics in practice, consider the potential returns that can be realised, and learn more about the role the vet can play.

The key finding from my study was that faster genetic progress can be achieved on UK dairy farms with the use of genomics. However, in order to exploit the opportunity, farmers must have clear breeding objectives and optimise their breeding strategy. For most the motivation to test should be to identity the animals with the lowest genetic merit. There must be scope to deselect these animals if a return on investment in genomic testing is to be realised.

The amount of information returned after genomic testing can be overwhelming. As farmers look to realise the maximum return from their investment, they must have confidence in those who are advising them, in a space where independent advice is a rarity.

Genetics alone is not the whole answer: to complement focused-enhanced breeding it is essential good herd management is practised. The combination of genetics and excellent management will yield the best results. Armed with on-farm data and a clear understanding of the breeding objectives the vet can be well placed to identify those herds where an investment in genomic testing is likely to increase productivity and profitability.

The importance of data has never been greater. Existing and new data sources on-farm represent an exciting opportunity for further genetic improvement. Through sensor technology and on-farm recording procedures, farmers should be encouraged to record as much high quality data as possible. In return, stakeholders should be prepared to reward farmers with financial remuneration or access to improved services.

## Contents

EXECUTIVE SUMMARY	ii
1. Personal introduction	1
2. Background to my study subject	2
2.1. The Mendelian sampling phenomena	2
2.2. My Nuffield Farming study – a "Summer" project	3
3. Research and travel undertaken	4
4. The importance of genetic improvement	5
5. The genomic revolution	6
5.1. What is genomics?	6
5.2. The advent of genomic testing	6
5.3. Adoption of genomic testing	8
6. Using genomics to predict the future with confidence	9
6.1. Achieving genetic gain by meeting the needs of the breeder's equation	9
6.1.i. Accuracy	9
6.1.ii. Selection intensity	
6.1.iii. Genetic variation	
6.i.iv. Generation interval	
7. Applications for breeding and beyond	16
8. Practical use of genomics on farm	
8.1. Realising genetic gain through the use of genomic-proven sires	
8.2. Female genomic testing – capitalizing on the same power of prediction.	21
8.3. Ranking reassurance – a race to the top vs. finding value at the bottom	21
8.3.i. Case Study: Breeding success at Bomaz	21
8.3.ii. Case study: Great cows start with healthy cows	22
8.3.iii. Case study: Fertility focus at Rocking-S	23
9. Breeding strategies to maximise genetic progress	24
9.1. Sell	24
9.1.i. Case Study: Canadian dairy farm identifies niche market for surplus stock	24
9.2. AI	25
9.2.i. Sexed semen - Dairy	25
9.2.ii. Beef semen	
9.2.iii. Conventional semen	27
9.3. Embryo Transfer and OPU/IVP	27

10. Realising a return from a long-term investment
10.1. Is female genomic testing the next logical step?28
10.2. Making an investment in genomics pay28
11. A testing solution – A role for the advisor?
11.1. Case study: Breeding advisor31
11.2. Case study: Test provider
11.3. Case study: Vet
12. The role of the evaluation body – when industry collaboration meets big business
13. Future applications of genomic testing
13.1. "In the age of the genotype, phenotype is king"
13.2. New traits represent new opportunities
13.2.i Case study: Feed efficiency
13.2.ii. Case study: Feed efficiency in practice
13.3. Role of big data
13.4. Beyond genomics
14. Conclusions
15. Recommendations
16. After my study tour
18. Glossary
19. References
20. Acknowledgements
21. Appendices
Appendix 1: Comparison of selection indices from 15 different countries
Appendix 247
Appendix 3: Getting to grips with genetics48
Appendix 4 : The process of genomic testing51
Appendix 5 : Available Holstein sires April 201955

#### DISCLAIMER

The opinions expressed in this report are my own and not necessarily those of the Nuffield Farming Scholarships Trust, or of my sponsor, or of any other sponsoring body.

## **CONTACT DETAILS**

Neil Eastham Email: neil.eastham@bishoptonvets.co.uk Twitter:@neileastham Address: Larkspur, South Crescent, Ripon. HG4 1SN.

Nuffield Farming Scholars are available to speak to NFU Branches, Agricultural Discussion Groups and similar organisations

Published by The Nuffield Farming Scholarships Trust Southill Farmhouse, Staple Fitzpaine, Taunton TA3 5SH Tel : 01460 234012 email : <u>director@nuffieldscholar.org</u> www.nuffieldscholar.org



## 1. Personal introduction

I grew up on a Lancashire dairy farm where my family continue to milk 340 pedigree Holsteins cows. I graduated from the University of Liverpool in 2007, realising my lifelong ambition of becoming a vet. Soon after I joined Bishopton Veterinary Group in Ripon, North Yorkshire. In 2014 I completed a Diploma in Bovine Reproduction and in January 2017 I became a partner in the practice.

Bishopton Veterinary Group is an independently owned, multi-discipline practice with five centres across North Yorkshire. As one of fourteen dedicated ruminant vets I am responsible for veterinary care on a large number of livestock farms. A significant amount of my time is spent carrying out preventative herd and flock health work as well as providing traditional ambulatory and emergency care.

Through our sister company RAFT Solutions Ltd I am involved in delivering advanced breeding solutions on-farm including: embryo collection and transfer, ovum pick up and bull fertility testing. A proportion of my time is also spent delivering training to both farmers and vets.

Outside of work I am a council member of Yorkshire Agricultural Society and a committee member of Future Farmers of Yorkshire and North East Holstein club. I have been senior Holstein steward at the Great Yorkshire Show since 2017. My wife Heather is a small animal vet and together with our son Fergus we live in Ripon.



Figure 1: The author, Neil Eastham



## 2. Background to my study subject

The Holstein cow has been an unfailing source of inspiration throughout my life. From a young age I have had a fascination with breeding and genetics. In my early years this was born from a desire to compete at the very top in the showring. In recent years my outlook has changed. I now find myself striving to understand more about the influence that breeding and genetics has on health, productivity and profitability.

As a child I was once told by an aging eminent Holstein breeder that breeding was an 'art'. Over the following years, as I engaged the science part of my brain with increasing vigour, I found myself challenging this statement.

In reality breeding is wholly scientific. In order to make progress, measurements of performance are needed for different traits, and individuals must be compared against their contemporaries before selection decisions are deployed. Whilst matings can be carefully orchestrated, the genetic make-up of any resulting offspring is unpredictable.

Maximal genetic progress doesn't result from avoiding the pitfalls that are inevitably associated with an approach based on 'art'. The fastest rate of progress is realised when acceptance is reached that genetics is the science of heredity.

## 2.1. The Mendelian sampling phenomena

Gregor Mendel is recognised as the founder of the modern science of genetics. His work established many of the rules of heredity, now referred to as the laws of Mendelian inheritance.

Despite having the same parents, the appearance of my brother and myself is different. This difference or variation is at least in part due to us inheriting different genes. Whilst each of our parents has passed on one of their two copies of each gene, which copy we have each received is completely random.

When considering the number of genetically different individuals that could result from a single mating between a cow and a bull there are over one quintillion possibilities. The genetic make-up of a cow is hardwired at conception. Imagine my excitement when I realised that a genomic test could be used to more accurately predict an animal's genetic merit by taking into account the genetic material that was inherited.



Figure 2: The author (right) and his brother Richard



## 2.2. My Nuffield Farming study – a "Summer" project

I must thank Summer for the inspiration behind my project. It's not that the idea came to me whilst lying on a sun lounger on a hot summer's day. It's Summer the cow I must thank. Samlea Mccutchen Summer was born on the 11<sup>th</sup> November 2015 at Walmsley Fold, the family farm. There was much excitement about her arrival as her dam had been shown successfully. Summer didn't disappoint and during 2016 she collected many prizes.

At a similar time, she was amongst the first batch of our heifers to be genomic tested. Unfortunately, her genomic test results were poor, her genetic merit was low and she ranked as the worst heifer born in 2015. A difficult decision ensued. Did I follow my heart and breed her back to Holstein? Or follow my head and breed her to beef (much to the disgust of that eminent breeder!)?



Figure 3: Genomic testing helped shed light on "Summer's" genetic merit. Photo: author's own

After seven services to an Aberdeen Angus she finally conceived, entering milk production some three months later than her contemporaries. Without the genomic test result she would have been bred to Holstein.

Three years after the infamous test, and following a lengthy first lactation, Summer has recently left the herd. She failed to conceive for a second time, failing to cover the costs associated with rearing. A decision to deselect her from contributing genetics to the future of the herd has been vindicated.

Of course, I'm doing something I know I shouldn't do. I'm focussing on one individual when genetic progress should be reviewed at a population level. Perhaps that's the infrequently used 'art' part of my brain trying to surface!



## 3. Research and travel undertaken

During late Autumn 2018 I visited Ireland, the USA, Canada and Italy. In Spring 2019 I toured the Netherlands and Belgium. My travels took 8 weeks in all, to learn more about the application of genomic testing in the dairy sector. These countries were chosen as they were early adopters of the use of genomic technology, but also faced continual challenges in terms of increasing the number of females genomic-tested.

In each country I met with farmers and representatives from breeding companies, evaluation bodies, testing labs, veterinary practices, farm consultants and academia.

\*\*\*\*



(1) A briefing in London.

(2) Joining the week-long Contemporary Scholars' Conference attended by all new Nuffield Farming Scholars worldwide, location varying each year.

(3) A personal study tour of approximately 8 weeks looking in detail at the Scholar's chosen topic.

(4) A Global Focus Tour (optional) where a group of 10 Scholars from a mix of the countries where the scheme operates travel together for 7 weeks acquiring a global perspective of agriculture.

\*\*\*\*\*

The Nuffield Farming Scholarships scheme originated in the UK in 1947 but has since expanded to operate in Australia, New Zealand, Canada, Zimbabwe, France, Ireland, and The Netherlands. Brazil, Chile, South Africa and the USA are in the initial stages of joining the organisation.



## 4. The importance of genetic improvement

By 2067 the world's population will reach 10.4 billion<sup>1</sup>. Over this period worldwide annual consumption of dairy products (fresh milk equivalent) is expected to rise from 87 kg per person to 119 kg per person<sup>1</sup>. To achieve the additional 600 billion kilograms required an average dairy cow on the globe would need to double its annual yield from 2,405 to 4,531 kg<sup>1</sup>.

Continual genetic improvement will play an important role in meeting the above consumer demands.

During the past 50 years advancements in science, such as the introduction of genomic testing, have resulted in rapid genetic gains in the dairy sector. The development, adoption and ongoing refinement of selection indexes has helped farmers to overcome the pitfalls of the single trait selection commonly practised in the 1980's and 90's. During this period, despite significant increases in milk production, selection for the milk trait had the unintended consequence of worsening somatic cell count, lifespan and fertility.

Profitable Lifetime index (£PLI) is an economic selection index published by the Agriculture and Horticulture Development Board (AHDB) as part of its genetic evaluation service. Tailored towards all year-round calving herds, £PLI is weighted intuitively on traits of economic importance. This enables farmers to select for improvement across a range of traits in a single step.



Figure 4: Relative weightings of traits included in £PLI (Source AHDB)

Selection indexes differ around the world (see **Appendix 1**) to reflect differing breeding goals<sup>2</sup>. **Appendix 2** outlines how the Irish selection index is helping farmers to target improved performance. **Appendix 3** provides a synopsis on the origins of the cow, sets out the basic principles of genetics and outlines how estimations of genetic merit are calculated in the genetic evaluation process.



## 5. The genomic revolution

Around the turn of the century research in the field of genetics moved at pace from the study of individual genes to that of the whole genome. The developments that would ensue have changed the field of animal breeding for evermore.

## 5.1. What is genomics?

Genomics is the study of the whole genome of an organism. Whole genome selection, more commonly known as genomic selection, was proposed by Meuwissen in 2001<sup>3</sup>. However, it wasn't until the Bovine Genome Project (BGP) was initiated in 2003 that the DNA tools became available to bring earlier postulations to fruition. In 2009 the BGP group published the first bovine genome for a Hereford cow named L1 Dominette 01449<sup>4</sup>.



Figure 5: Hereford cow L1 Dominette 01449. https://www.nature.com/news/2009/090423/full/news.2009.395.html

## 5.2. The advent of genomic testing

Meuwissen demonstrated that estimated breeding values could be calculated from genetic markers along the genome. A successful marker would be abundant and show variation between individuals. Single Nucleotide Polymorphisms (SNP's) refer to variation between individuals at single nucleotides (A, C, G, and T) along the genome.





Figure 6: An example of a SNP between two individuals. Source: Authors own

The work of the BGP group along with Dominette's sequenced genome provided the framework from which over 2 million SNP markers were identified. After genotyping it would now be possible to examine SNP differences between individuals and associate these differences with traits of interest.

Rather than use whole genome sequencing which would be costly and time consuming, the first commercially available SNP-based genotyping chip was released in December 2007 and provided genotype data for 54,609 SNP markers<sup>5</sup>. At a cost of \$225 this signalled a 1000-fold decrease in the cost of genotyping and paved the way for many bulls (dead and alive) to be genotyped<sup>5</sup>. Their genotypes, together with millions of daughter records, would provide the early reference population and prediction equations needed to incorporate genomics into the traditional genetic evaluation process.

Official genomic predicted transmitting abilities (gPTA's) were first released in 2009 in the US. Initially the number of males tested outnumbered females. The artificial insemination (AI) industry immediately benefited as the cost of testing bulls was subsidised to recognise their early contribution of bull genotypes. The costs associated with genomic testing later decreased as cheaper low density SNP chips were made available.

Genotype imputation is the process whereby SNP sites not covered by a lower density SNP chip can be inferred<sup>6</sup>. Statistical techniques are used to estimate genotypes at loci not directly genotyped by the SNP chip<sup>6</sup>. This can be achieved with high accuracy and, as a result, genotype imputation is *How can UK dairy farmers use genomics to breed a better herd? ... by Neil Eastham* A Nuffield Farming Scholarships Trust report ... generously sponsored by John Oldacre Foundation



celebrated as a breakthrough in the evolution of genomic testing<sup>6</sup>. This has made whole-herd genotyping more common and females now account for over 90% of the genotyped population.

**Appendix 4** provides an overview of how gPTA's are calculated.

## 5.3. Adoption of genomic testing

The number of genotyped dairy animals across the world has risen sharply since the introduction of testing. The table below outlines increases realised between January 2009 and January 2019.

Table 1: Number of animals genotyped between January 2009 and January 2019. Source: CDCB

Countries	Jan 2009 Total count	Jan 2019 Total Count		
United States and Canada	22,344	3,020,000		
France	8,500	550,000		
Netherlands	6,000 combined	465,000		
New Zealand		140,000		
Germany	3,000	785,000		
Ireland (beef and dairy)	4,500	1,500,000		
UK	0	90,000		



## 6. Using genomics to predict the future with confidence

The rate of genetic gain in the genomic era has doubled<sup>5</sup>. Early adopters of genomics have long accepted a genomic proof as an accurate indication of a bull's eventual daughter's proven proof and many are now practising whole herd genomic testing to further expedite genetic gain<sup>5</sup>.

## 6.1. Achieving genetic gain by meeting the needs of the breeder's equation

The "breeder's equation" is central to realising genetic progress. The rate of genetic gain can be measured as per the following equation:

GENETIC PROGRESS		ACCURACY x SELECTION INTENSITY x GENETIC VARIATION
	=	
YEAR		GENERATION INTERVAL

The role of genomic testing on each of the variables included in this equation is now considered:

## 6.1.i. Accuracy

Reliability is used to indicate how accurate an estimate of genetic merit is. The reliability figure for a PTA varies dependent on the amount and source of information used in its calculation.

For example, the reliability of a milk PTA (Predicted Transmitting Ability) for a female calf is low, in the region of 34-39%. This is because the prediction is simply an average of the genetic merit of its sire and dam. This is referred to as the calf's parent average.

Once a cow is aged (6+ lactations) the reliability of the milk PTA will reach 70-75% due to the contribution of lactation performance data. The PTA value is now nearer to the true breeding value and subject to a lot less change than a parent average PTA but the farmer has had to wait a long time to achieve high reliability.

Genomic testing significantly increases the reliability of PTA values. For young bulls and heifers without any performance data the resulting gPTA figures are based on pedigree and genomic information. In the UK the reliability of the gPTA for milk can reach 65-70% in the young tested heifer. This is equivalent to the reliability of the milk PTA for an untested third or fourth lactation cow.

See next page for a table which illustrates the difference in reliability between parent average and gPTA values for £PLI (Profitable Lifetime Index) and production traits across a group of youngstock.

(Pressing the zoom tool on right of screen will much improve legibility)



								Production	1			Fitn	iess		
£PLI	£PLI Rel	Identity	Cow	Inbreeding %	Birth Date	Rel%	Milk (kg)	Bfat (%)	Prot (%)	LS	SCC	FI	Main.	Mastitis	Gen.
			Dam												
			Sire												
$\downarrow$				\$	\$	$\oplus$	$\Diamond$	\$	$\Rightarrow$	\$	(	\$	\$	\$	\$
688	57	182494603142 182494202508 221337302215	SAMLEA TRIX TONI SAMLEA FANTASMIC TONI TOPCROFT PESKY TRIX	7.2	20/04/2018	69	575	0.00	0.11	0.4	-22	11.6	2	-2	G
626	27	182494203215 182494102605 12283318	SAMLEA PERSEUS ICEPOP SAMLEA COLLUDE LOLLYPOP WESTCOAST PERSEUS	6.1	17/11/2018	34	541	0.09	0.07	0.5	-21	8.7	11	-2	
615	28	182494103200 182494502574 3132198315	SAMLEA AGRONAUT REGINA SAMLEA BILL ROBIN MR RUBI-AGRONAUT 73287	6.3	26/10/2018	35	331	0.16	0.08	0.5	-27	8.0	6	-3	
587	56	182494603100 182494602225 3124720459	SAMLEA APPLEJAX DELIA SAMLEA PRIDE DELIA SEAGULL-BAY-MJ APPLEJAX	7.8	09/12/2017	67	467	-0.03	0.00	0.5	-35	14.2	-1	-4	G
577	56	182494703066 182494602183 3124720459	SAMLEA APPLEJAX SIXPENCE SAMLEA WINDSOR FIVEPENCE SEAGULL-BAY-MJ APPLEJAX	6.0	21/10/2017	67	625	-0.08	-0.03	0.6	-29	14.2	2	-3	G
551	56	182494503099 182494302159 3124720390	SAMLEA DANCER DILL SAMLEA CASPIAN TARRAGON SEAGULL-BAY JO DANCER	9.9	09/12/2017	67	1015	-0.02	-0.04	0.2	-20	0.7	7	-2	G

Table 2: illustrates the difference in reliability between parent average and gPTA values for £PLI and production traits across a group of youngstock. The green 'G' symbol denotes that this particular animal has been genomic tested.

Heritability describes the extent of variation for a trait that is attributable to genetics. In the traditional evaluation process a trait with low heritability (e.g. fertility) requires more information (e.g. daughter records) to produce a breeding value with the same reliability as a high heritability trait (e.g. protein yield).

Genomic testing provides more information for low heritability traits. For protein yield the extra information provided after genomic testing equates to 34 additional daughter records: whereas a genotype is worth the equivalent of an additional 131 daughter records for fertility.

## 6.1.i.a. Case study: A role for direct genomic values?

I met with Lynsay Beavers, the Industry Liaison Coordinator at The Canadian Dairy Network (CDN), Guelph. Since the launch of Canadian gPTA's in August 2009 CDN has also published direct genomic values (DGVs). These are based purely on the animal's genotype and, unlike gPTA's, they do not include the contribution of pedigree and performance data.

Whilst the correlation between DGV's and gPTA's is still strong, some breeders perceive that DGV's are a better predictor of future performance. CDN recently carried out a study investigating figures of daughter-proven bulls against their DGV or gPTA figures prior to having daughters. The study concluded that DGV was consistently poorer at predicting subsequent genetic merit.

No extra gains in genetic merit (above using gPTA) could be realised by breeders who preferred to use bulls with the highest DGV values. Based on these results CDN is to stop publishing DGV's from December 2019.

This inclusion of pedigree alongside DGV increases and demonstrates the importance of reliability, thereby giving the farmer greater confidence and accuracy when using the resulting gPTA figures.



## 6.1.ii. Selection intensity

The selection differential is a measure of the difference between the average genetic merit of the animals selected for breeding and the average genetic merit of all animals in the population from which they were selected. The higher the selection differential the greater the selection intensity.

Historically, bringing a bull to market involved progeny testing which was both time consuming and expensive. Increases in reliability have meant that selection decisions can be made with greater confidence in early life. A move from selecting bulls based on parent average PTA's to using gPTA's has helped increase selection intensity.

Research published in 2006 suggested that by avoiding progeny testing, bull breeding companies could save up to 92% of their costs<sup>7</sup>. However, the reinvestment required to maintain competitiveness should be considered.

Newborn calves with high gPTA figures have a much higher value than a calf with a good pedigree only. If breeding is moved in-house by the AI company significant costs are incurred in carrying out the advanced breeding techniques (Embryo Transfer (ET) and Ovum Pick Up (OPU)/In vitro embryo production (IVP)) required to compete in the race to produce the next best animal. Lastly, younger genomic-proven bulls produce fewer marketable straws of semen (approximately 35-50% of that produced by a 5-year old bull), so more bulls are required to stand in stud at any given time<sup>8</sup>.

#### 6.1.ii.a. Case study: Embryos drive selection intensity at CRV

At The Dairy Breeding Centre in Wirdum, The Netherlands, I was given an overview by Thomas van der Gaast of how genomics has affected bull selection at CRV. The Centre is home to 160 high genetic merit heifer donors. OPU/IVP is used to generate 10,000 embryos per year, these are sold for €100 each and along with an additional 1500 embryos purchased by CRV they are implanted on satellite farms across The Netherlands.

The resulting 2500 heifer calves and 2500 bull calves are genomic-tested, and the heifers and bulls with the highest genomic figures are purchased back by CRV. In the future CRV would like to generate 20,000 embryos per year at Wirdum. Thomas commented: *"The more embryos that are available, the higher the selection intensity and the greater the chance of producing a top class bull or heifer"*.

#### 6.1.iii. Genetic variation

Genetic variation plays a vital role in realising genetic gains through selection. Heritability can be used as a measure of genetic variation. Whilst traits with high heritability are thought to be easier to improve through breeding, even traits of low heritability (e.g. fertility) can be improved as sufficient genetic variation exists to apply selection pressure. This is especially important when one considers the significant economic cost of some low heritability traits such as fertility and longevity.



## 6.1.iii.a. Case study: UK Fertility Index trait packs a punch

In the UK a genetic index for daughter fertility (Fertilty Index) was launched after research concluded that a component of fertility performance was controlled by genetics. Figure 7 plots the genetic (predicted calving interval based on genetics) and phenotypic trend (actual calving interval (CI)) for fertility since 1995.



Figure 7: Genetic and phenotypic trends for fertility in the UK since 1995. Source: AHDB.

In the 1990s and early 2000s selection for milk had the unintended consequence of worsening fertility. This was due to the negative genetic correlation that exists between the traits milk and fertility, and an inability during this time to select on the trait fertility.

Following the introduction of the trait fertility index in 2005 and its subsequent use by the industry, this trend has been reversed. The consequence has been a lowering of calving interval. Whilst some of this improvement can be attributed to improved management it is thought 50% of the improvement is due to genetic selection.

Increases in selection intensity and decreases in the generation interval have the potential to increase inbreeding and decrease genetic variation. However, inbreeding is described by many as an inevitable consequence of genetic progress and results from the mating of individuals that are closely related genetically.

The deleterious effects of inbreeding have been explored and attempts at modelling their significance made. Dr Sinéad McParland at Teagasc investigated inbreeding in the Irish cattle herd and found it was the fertility traits that are affected most by inbreeding. Dr McParland's work concluded that the



12.5% inbred animal is expected to have an 8.8 day longer CI, an increase in age at first calving of 2.5 days, and a reduced survival to second lactation of 4%.

Work in the UK by AHDB has demonstrated similar trends with a 1% increase in inbreeding above 5% expected to result in a reduction in PLI of £10. The general advice to farmers has been to avoid matings that resulted in an inbreeding co-efficient of >6.25%, the level of inbreeding that would result from mating first cousins. However, having spoken to several quantitative geneticists during my study it seems that advice around controlling inbreeding needs to focus on monitoring the rate of inbreeding change.

#### **6.i.iv.** Generation interval

Generation interval is defined as the average age of parents when their progeny are born. As the divisor in the breeder's equation a decrease in the generation interval has the effect of increasing the rate of genetic gain. A recent study documented generation intervals for the four paths of selection in US Holsteins<sup>9</sup>. Figure 8 below highlights where decreases have been realised since the introduction of genomic testing.



 Figure 8: Changes in genetic selection differentials and generation intervals in US Holstein dairy cattle as a result of genomic selection.
 Key: SB = sire of bulls, SC = sire of cows, DB = dam of bulls and DC = dam of cows. García-Ruiz A, Cole JB, VanRaden PM, Wiggans GR, Ruiz-López FJ, Van Tassell CP (2016) Proc. Natl, Acad Sci USA 113:E3995-4004.



By far the greatest decrease has been for the SB path; this is due to the move from using progeny testing to the use of genomic testing. The downward trend in generation interval for DB path is because virgin heifers are now the most common bull dams. The ability to collect more frequently from a younger age, use reverse sorted semen, less semen, and collect during the first trimester of pregnancy has meant that OPU/IVP has superseded embryo transfer as the advanced breeding technique of choice in many territories around the world.

#### 6.1.iv.a. Case study: Advanced breeding techniques help lower generation interval

In Canada I visited the Boviteq West facility at Abbotsford, BC. Operated by Westgen (a division of Semex) the facility serves as a residential OPU facility for both Semex-owned heifers and heifers privately owned by farmers. OPU collections are performed by Dr. Lisa McCrea, a local private veterinary practitioner.



Figure 9: Dr. Lisa McCrea performs OPU on a heifer at Boviteq West, Abbotsford, BC. Photo author's own



Collections commence at approximately seven months of age. Heifers are superstimulated with Follicle Stimulating Hormone (FSH), in a process called coasting, to increase the number and quality of recovered oocytes. These are transported to the Boviteq laboratory where they are cultured and fertilised. Any of the Semex-owned embryos making it to day seven are graded; those of freezing quality are biopsied and genomic tested.

In the UK conventional embryo collection and transfer remains the most popular form of advanced breeding. Cost can be a deterring factor of OPU/IVP and FSH is a significant proportion of the cost. For this reason, as well as public perception concerns around use of reproductive hormones, some OPU/IVP teams (e.g CRV) are not coasting, with minimal effects on performance reported.



## 7. Applications for breeding and beyond

Aside of the genomic breeding values, genomic testing provides users with other valuable pieces of information, such as:

## a. Parentage Verification

If a true ancestor is genotyped the accuracy of discovery is very high. Because the accuracy of discovery is high (especially for sires) gaps in the pedigree can be filled and this has the effect of increasing the reliability of the gPTA's.

Reported parentage error rates in females vary according to the country. In Ireland levels were low at 7.5% (ICBF) with higher rates reported in Canada (8-10% CDN) and the US (10-15% Zoetis).

## b. Genetic recessives and Haplotypes

Genomic testing also includes a routine screen for a number of known recessives and haplotypes.

An animal carries two copies of a gene or haplotype (a short section of DNA strand): one inherited from its sire, the other from its dam. An animal is said to be homozygous for a gene or haplotype if they inherited the same copy from both parents. Alternatively, they may be heterozygous, meaning the genes or haplotypes they inherited are different.

For all known haplotypes affecting fertility, as well as Holstein Cholesterol Deficiency (HCD), control is via genes that are recessive rather than dominant. For genetic recessives, only homozygous animals are affected. Heterozygous animals are often referred to as carriers but are unaffected by their carrier status. For the fertility haplotypes, affected animals die from early embryonic loss while HCD results in early calf mortality.

## b.i. Case study: HCD in Canada

Whilst HCD was first discovered in Germany in 2015, it can be traced back to the popular Canadian bull Maughlin Storm. CDN reported that 7% of animals born in Canada in 2018 are carriers of HCD. Unsurprisingly CDN has identified this as the haplotype requiring most attention.

According to CDN's Lynsay Beavers, genomic testing can play a significant role in helping breeders to reduce the incidence of HCD. By genomic-testing females the status of the female can be determined and carrier animals identified. Safe matings with bulls of a known published status can then be practised.

continued on next page



## c. Genetic characteristics

For some breeders ascertaining an animal's status for hair colour and/or horn status (polled versus horned) is considered important.

## d. Genomic Inbreeding

Genomic inbreeding figures provide owners with a more accurate prediction of inbreeding than pedigree inbreeding estimates. This information can then be utilised in precision mating software to control the rate of inbreeding in the next generation.

#### e. Milk protein components

Different milk proteins may offer health benefits or enhance cheese yield. In the US there was growing interest in the milk protein traits A2 beta casein and kappa casein, driven by the emergence of new premium markets for specialist milks and processor interest in improving efficiency.



Figure 10: Front page from the July 2018 edition of Progressive Dairyman (USA).

The B gene for kappa-casein has been associated with an increase in milk, protein and cheese yield. Animals carrying two copies of the A2 gene for beta casein are known to produce milk containing only the beta casein A2 form, and this has been linked to possible health benefits. Genomic testing can be used to provide a profile of the animal's status for these and other milk proteins.

How can UK dairy farmers use genomics to breed a better herd? ... by Neil Eastham A Nuffield Farming Scholarships Trust report ... generously sponsored by John Oldacre Foundation



## e.i. Case study: Targeted use of milk proteins

Brian Fiscalini milks 1500 cows in Modesto, California. Approximately 10% of milk goes into producing artisan cheeses on the farm.

Brian is targeting the use of A2A2 and BB bulls to increase the frequency of these desirable genes within the herd. In the near future, Brian sees a time where he will use his genomic test results to group animals according to their milk protein status. A2 milk or milk from BB cows could then be sold off the farm at a premium or used in the dairy to make cheese.

The A2 milk company operates in the UK. As the milk market evolves due to changing demands of the consumer it seems likely that the potential health benefits of A2 milk will continue to draw attention. The likelihood of processor interest in kappa casein is less clear. However, it seems logical that those farms with an existing understanding of their herd's genetic status through genomic testing have the critical information needed to make selection and breeding decisions that would allow early capitalisation should incentive-based contracts around kappa casein become available in the UK.



## 8. Practical use of genomics on farm

The availability of genomics now spans both males and females across multiple dairy breeds.

## 8.1. Realising genetic gain through the use of genomic-proven sires

Genomic-proven sires now account for 70% of inseminations on UK dairy farms. There has been a marked shift in the UK from using daughter-proven sires to genomic-proven sires since the introduction of UK genomic evaluations in 2012 (see Figure 11).



Figure 11: Percentage use of young genomic proven versus daughter proven sires in the UK. Source: AHDB

Similar trends are recorded in other countries, with genomic-proven sires accounting for 60% of inseminations in The Netherlands, 65% in Canada, 70% in the US and 80% in Ireland.

In the UK the average genetic merit of young genomic bulls outstrips that of daughter-proven bulls, illustrated in Figure 12 using the trait £PLI.

See Figure 12 on next page





Figure 12: Average £PLI of young genomic proven versus daughter proven bulls. Source: AHDB.

Despite the genetic merit gap some farmers are reluctant, or completely against, the use of young genomic bulls, preferring to use higher reliability daughter-proven bulls.

Validation work in the UK has demonstrated strong correlations between early genomic and subsequent daughter-proven evaluations (*see Figure 13 below*).

Predicted Transmitting Ability (PTA)	Aug '18 (average)	Change since 2014	Correlation between Aug '14 and Aug '18
Reliability (milk, fat and protein) %	83	15	
Milk kg	452	30	0.85
Fat kg	15.0	-0.6	0.85
Protein kg	13.7	0.1	0.86
Fat %	-0.03	-0.02	0.90
Protein %	-0.01	-0.01	0.87
Reliability (SCC)	83	14	
SCC	-11	0	0.83
Reliability (Lifespan)	69	9	
Lifespan	0.25	-0.01	0.80
Reliability (Fertility Index)	72	9	
Fertility Index	3.2	0.3	0.85

Figure 13: Correlation between early genomic-proven (2014) and subsequent daughter-proven proofs (2018) for 7,745 bulls in the UK. Source AHDB.



Producers not using genomic-proven bulls are slowing down their potential rate of genetic gain. By the time a bull becomes daughter-proven they could have used him a minimum of 3 years earlier.

Many of the farms visited throughout my study were using 100% genomic-proven bulls. As well as using a team of bulls these farmers managed the risk of re-ranking by using only the genomic-proven bulls with the highest genetic merit. That way, if a drop occurred, then the bull's figures would still be comparable with the available daughter-proven bulls at the time.

## 8.2. Female genomic testing – capitalizing on the same power of prediction.

In the US, 12% of eligible heifers are genomic-tested per year (CDCB). In Canada it is estimated that 7% of eligible heifers are tested (CDN), markedly higher than the 2% currently tested in the UK.

Testing was almost exclusively carried out on young heifers, to capitalise on the largest possible increases in reliability. Animals were then ranked according to their genetic merit and aligned with a breeding strategy.

## 8.3. Ranking reassurance – a race to the top vs. finding value at the bottom

During my study I wanted to understand more about what motivated farmers to genomic-test their females. Broadly speaking farmers seemed to fit into two groups: those looking to accurately identify animals at the top, and those motivated to find the bottom animals.

#### 8.3.i. Case Study: Breeding success at Bomaz

As we took a walk through the cows at Bomaz Farms in Hammond, Wisconsin, it was apparent that owner Bob Zwald was a true cow enthusiast. Bob's breeding objectives are clear: he wants a high producing, healthy, robust cow that could complete a long productive life.

Bob was very open that it is the thrill of finding the animals at the top that motivates him to genomictest. Several bulls in recent years have been sold into AI and, whilst revenue from these had been lucrative, Bob was quick to point out that in order to have something of interest to the AI companies a huge amount of continual investment was needed.

When asked if he was worried that in-house breeding programmes by the AI companies had reduced their need to source bulls from farmers like himself, Bob commented that the AI companies will always need to look elsewhere. He believed it would be impossible for them to maintain the female genetic diversity needed to service the entire industry.

See photo on next page





Figure14: Visit to Bomaz Farms. Photo: author's own

#### 8.3.ii. Case study: Great cows start with healthy cows

"Healthy cows are profitable cows" according to Lloyd Holterman at Rosy-Lane Holsteins in Watertown, Wisconsin. "It's not what you see, it's what you can't see that makes her so special" he says as he points to a picture of his favourite cow RosyLane LLC Delta 10090. Her genomic results are an enviable line up with particularly high genetic merit for components and health traits.



Figure 15: Two high genomic merit females bred at Rosy-Lane. Photos author's own

How can UK dairy farmers use genomics to breed a better herd? ... by Neil Eastham A Nuffield Farming Scholarships Trust report ... generously sponsored by John Oldacre Foundation



Lloyd is a huge believer in the role that genetics plays in terms of herd health. Selection for Net Merit (\$NM) with a focus on fertility and productive life is used when selecting bulls and ranking heifers after genomic testing. This has paid off with the herd currently averaging an impressive 31,000lbs milk/cow/year alongside a 36% pregnancy rate and 58% conception rate.

Similar to Bomaz, it's the sale of high genetic merit animals and genetics that's the biggest motivator for genomic testing. Following genomic testing in January 2018, RosyLane LLC Frazzled 11270-ET ranked as the number one TPI (Total Performance Index) and number two \$NM heifer in the world. Shortly after she was sold for over \$600,000. Frazzled 11270 was the sixth generation to be genomic-tested at Rosy-Lane.

## 8.3.iii. Case study: Fertility focus at Rocking-S

Similar attempts are being made at Rocking S dairy in Modesto, California, to increase longevity and yield by reducing the culling rate. The target is to decrease the percentage of milking heifers in the herd from 45% to 35%. Manager Siebren Jacobi stressed his motivation for testing was to "find the low ones", highlighting that "genomic testing is enabling us to be more accurate in our selection".

Recent analysis demonstrated the value of genetic improvement across this large herd. The 3008 individuals with a DPR (daughter pregnancy rate) gPTA of over two had a first service conception rate (FSCR) of 55%, and 71% of individuals were pregnant by 150 days in milk (DIM). However, those 2174 individuals with a gPTA below one had a lower FSCR at 43% and only 58% were pregnant by 150 DIM.

At Rocking-S the belief was that the most cost-effective way of increasing the herd average was to deselect those at the bottom.

Despite the motivation for testing differing between farms it was clear that all the farms visited had a clear understanding of their breeding objectives. This helped them to determine their selection criteria and pinpoint the traits they would use to rank their heifers once genomic results were received.



## 9. Breeding strategies to maximise genetic progress

For those farmers who were genomic testing, having a clear set of breeding strategies was deemed crucial. These strategies were tailored to the individual farm and often executed with absolute precision. Ruthless decision-making was a repeating theme. These farms were both financially and emotionally invested and had complete confidence in the technology.

The different breeding strategies used on-farm are now considered:

## 9.1. Sell

Several farms sold surplus heifers once they had been genomic-tested. Only a small number were selling elite individuals; most heifers sold were those with the lowest genetic merit and went into the beef sector or as replacements onto another dairy farm. Buyers were not always made aware that they had been genomic-tested, nor did the buyers ask.

Most heifers were sold before breeding, perhaps even pre-weaning. Some were kept longer, bred to beef or used as an embryo recipient and subsequently sold new calved.

## 9.1.i. Case Study: Canadian dairy farm identifies niche market for surplus stock

Milking over 300 cows with robots in Chilliwack, BC, George Dick is a firm believer in the progress that genomic testing can realise. His goal is to hit 2kg of fat solids sold per cow per day against a current figure of 1.68kg. All the calves are genomic-tested before breeding. Rather than sell a surplus immediately, George is looking to capture a different market in the Fraser Valley.



 Figure 16: Calves at Dicklands farm. Photo author's own

 How can UK dairy farmers use genomics to breed a better herd?
 ... by Neil Eastham

 A Nuffield Farming Scholarships Trust report
 ... generously sponsored by John Oldacre Foundation



Describing a beef calf as a *"waste of a uterus"* due to the lack of a market for crossbred beef calves in the area, George uses his lowest genetic-merit animals as embryo recipients. His long term aim is to sell his lowest genetic-merit cows as freshly calved second lactation cows on to a growing number of farms in the Fraser Valley that are installing robotic milking machines.

## 9.2. AI

All the farms visited were exclusively using AI. Bomaz Farms sold homebred bulls that didn't make the grade for the AI companies off the farm as future stock bulls. This provided a premium for Bob over what he would get for them selling them as beef and enabled the purchaser to access genomic-tested bulls just below the grade for AI.

In the UK most stock bulls are sold purely on 'looks' and/or low reliability parent average figures. Farmers should be encouraged to genomic-test prospective bulls before they are used, or target those bulls with existing test results.

#### 9.2.i. Sexed semen - Dairy

The routine use of sexed semen is now common on many dairy farms, as confidence and availability in the product has increased.

With 90% of offspring expected to be female, sexed semen is used widely on maiden heifers to capitalise on higher conception rates and high genetic merit (*c.f.* adult cows). Many herds are also using sexed semen successfully on adult cows, with no reported drop in conception rate after switching from conventional semen.

On some farms there was a perceived lack of choice, with sexed semen not available from some of the best bulls. The sexing process reduces significantly the number of straws that can be produced per ejaculate, and semen from some bulls is unable to withstand the sexing process. Together with market demand concerns, it is likely that these factors play a role in determining which bulls are sexed.

#### 9.2.i.a. Case study: Use of sexed semen in Ireland

Dr Stephen Butler from Teagasc outlined that, in order to be viable, the spring calving herds in Ireland would need to achieve at least a 54% conception rate with sexed semen. A large field trial was conducted in 2018: 8000 straws (4000 conventional and 4000 sexed) were used from 10 bulls across 160 farms. Six of the bulls resided in Ireland and their semen was shipped to the UK for processing; four bulls resided in the UK or The Netherlands.

Relative conception rate for the sexed semen was 76%. Whilst the 90% threshold was achieved by the resident bulls, the performance of bulls stood in Ireland was poor. Given the popularity of fresh semen during the breeding period (which can yield 5x the number of straws from one ejaculate *cf.* conventional) and that all the bulls in the top 75 for EBI are Irish bred, discovering a method of successfully sexing and using shipped semen is important. The study concluded that further research



is required on how the timing of AI, use of synchronisation, and methods of heat detection affected conception rate.

## 9.2.ii. Beef semen

Beef semen was being used on low genetic-merit animals from which a replacement animal was not required. Many farms were using beef and sexed semen exclusively, thereby reducing the number of low value dairy bull calves born. This was particularly popular on the Jersey farms visited. In the US, sales of beef semen onto dairy farms has grown. Published figures from the National Association of Animal Breeders (NAAB) show a 59% increase in domestic beef sales<sup>10</sup>.

#### 9.2.ii.a. Case study: Beef from dairy

In Merced, California, Van der Woude Farms now view their beef calf sales as a crucial revenue stream. Following commencement of genomic testing and the use of sexed semen and ET/OPU-IVP, over 60% of the 3200-head dairy herd are bred to Aberdeen Angus. The resulting calves are sold at 5-6 months at a target weight of 550 lbs.



Figure 17: Beef calves in feedlots at Van der Woude Farms. Photo author's own.



Sexed beef semen is now available to enable farmers to capitalise on the higher value of a male calf. To be cost effective, enough premium must exist to cover the additional cost of the semen and mitigate any costs incurred through reduced fertility.

## 9.2.iii. Conventional semen

Several farms were still using conventional dairy semen, but this was often at reduced levels compared to historic use. According to some breeders, the unavailability of sexed semen from some of the best sires necessitated this practice. On some of the farms visited this was reverse sorted (sex sorted after having been processed as conventional) as part of the IVP process.

## 9.3. Embryo Transfer and OPU/IVP

The popularity of OPU/IVP was increasing in many of the countries visited.

#### 9.3.i Case Study: IVP embryo use overtakes AI

At the 2000-cow herd of Swiss Lane Farms in Michigan, USA, over 100 OPU/IVP-derived pregnancies were being generated per month.

By increasing selection intensity through the widescale use of OPU/IVP, genetic gain per year (\$94 Net Merit/year) was much higher than that realised across the wider industry.

This approach means the farm had an inventory of surplus embryos available for sale. In the future they envisage there will be a growing market for 'off the shelf' embryos.

As well as using genomics to identify elite female donors a few breeders were using genomic data to optimise recipient selection. This involved deselecting the lowest genetic-merit heifers as potential recipients if they had low genetic-merit for fertility. These would be bred to beef semen rather than risk poor conception rates with high value embryos.



## **10.** Realising a return from a long-term investment

I was keen to understand how those farmers who were genomic testing had realised a return on investment (ROI) from the process. It was clear that, in order to extract value from genomic test results, the extra information must be used to improve the quality of decision making on farm.

## **10.1.** Is female genomic testing the next logical step?

Any farmer contemplating genomic testing needs evidence that an investment in genetics on their farm will realise a return. One way of assessing this is to look at the response to selection for a given trait. An assessment of performance (e.g milk yield) against genetic merit (sire PTA for milk) will outline the response that the herd is currently realising from genetics.

On a well managed farm the response for the trait "milk" should be an additional 1kg of milk per lactation for every additional 1 kg of milk from the sire. A failure to achieve this could be due to the environment and management limiting the animal's ability to express their genetic potential. In some cases it may be worth addressing these areas before investing in genomic testing.

Breed also plays a role. Increases in reliability for Holsteins after testing are greatest, although increases across other pure breeds are also significant. Up until recently genomic results have only been available for purebred animals ( $\geq$  87.5% of any one breed). Recently (April 2019) genomic crossbred evaluations have become available in the US based on crosses of the five main breeds (Holstein, Jersey, Brown Swiss, Guernsey or Ayrshire). It is expected that crossbred genomic evaluations will become available in other countries soon, giving those farmers who crossbreed the same opportunity to capitalise on genomic testing.

A clear set of breeding objectives before embarking on genomic testing is also important. To determine these the farms that I have visited had done a full review of their current and future needs based on their farming system, milk contract, herd health challenges, current performance and current genetic base. Following this review they were in a position to identify the traits that they wished to improve through breeding. These selection criteria were then used to carry out bull selection and rank the females once they had been genomic-tested.

## **10.2.** Making an investment in genomics pay

The best combination of breeding strategies to use alongside genomic testing is an important consideration when looking to realise a ROI from genomic testing. Professor Albert De Vries of The University of Florida has carried out a large amount of research in this field and found that a common scenario has been for producers with a surplus of heifers to test in order to help them decide which heifers to keep. According to Albert, when more heifer calves are created, the result is often that cows are unnecessarily culled.

The importance of rightsizing a herd has been a key driver in the marketing campaign of CLARIFIDE<sup>®</sup> by Zoetis. A recent study concluded that net replacement cost was the largest herd production metric



to influence net income<sup>11</sup>. Therefore Zoetis have developed a number of tools to help their customers 'rightsize' their herd.

Whilst I understand that surplus heifer sales serve as a useful cash crop to initiate testing in year one, I was keen to understand what the best policy for heifer generation in successive years was.

Modelling by Albert has demonstrated additional value in generating more dairy heifers than needed<sup>12</sup>. This results in a higher selection intensity as a greater number of heifers to choose replacements from results in an increase in the selection differential and a greater rate of genetic gain. The following graph (Figure 18) illustrates the relationship between the percentage of animals kept and lifetime net benefit.

If nothing is known about all of the calves tested, then culling approximately 10% results in a positive return on investment. When traditional parent average values are known, 15% of the heifers must be culled to cover the cost.



Figure 18: Relationship between percentage of animals retained and net benefit (\$). Source A. De Vries.

In the UK the demand for young dairy heifers varies from region to region and farmers may be reluctant to sell surplus heifers at what they feel is a poor price. However, these surplus heifers are simply a by-product of the attempt to maximise selection intensity. Their value is not realised through their sale price, it is realised by the rate of genetic gain achieved in their counterparts that are retained.

In the UK, herds in high prevalence TB areas are likely to carry a surplus of heifers (as a safety margin in case of losses); however, they are unlikely to be willing to sell these heifers or indeed able to. If choosing to genomic-test, these herds will need to use other strategies to realise value.

Further work by Albert demonstrated it was often worth producers using sexed semen to generate this greater surplus, especially in those herds with a high response to selection. Herds with good fertility further benefit from the addition of beef AI as crossbred calves can represent a valuable



income stream, and they may generate the required surplus from less animals than are actually in the herd. Albert commented that in some cases this can be a more profitable strategy.

The financial viability of utilising OPU/IVP has also been explored. Studies suggest the use of OPU/IVP on the very top heifers, alongside the use of sexed semen on the next best heifers, can result in a positive net return when the worst heifers are used as recipients, or culled<sup>13</sup>.

Whilst the 100% exclusive use of OPU/IVP will provide an unrivalled rate of genetic progress this will be at a significant cost. Sexed semen from top genomic-proven bulls is by comparison an inexpensive and formidable competitor and in many cases will help farmers to harness almost as much benefit at a significantly reduced cost.

In The Netherlands and the USA I witnessed the use of custom indexes, developed in place of standard selection indexes. These focused only on those traits that had been identified as important on the farm in question, and were used for sire selection or the ranking of heifers after genomic testing. A limitation of this approach was that, often, custom indexes included only a small number of traits, overlooking that many traits affect profitability, and also that correlations exist between traits.



## 11. A testing solution – A role for the advisor?

With so much to consider before, during and after genomic testing, I was keen to explore what role the advisor could play. It was apparent that advice in this field was coming mainly from three sectors: breeding advisor, test provider and the vet.

## 11.1. Case study: Breeding advisor

A growing number of AI organisations are offering female genomic tests. Jay Shannon from Semex gave me a valuable insight into their female genomic test offering. Their digital platform Elevate<sup>™</sup> enables producers to manage their genomic test orders, access results and work with their breeding advisor to rank animals, plan matings, correct parentage errors, manage inbreeding and access Immunity+<sup>™</sup> results.

Some farmers thought that working with just one breeding company would limit their sire selection. Others were happy to extract value from a close working relationship, many listing the mating service provided as an important way for them to optimise the use of their genomic results. Very few of the farms visited were buying semen from only one company, choosing to pay a little more per straw but capitalising, they felt, in the long run through greater choice.

In order to cater for the different genetic needs and budgets of UK dairy farmers the AI companies offer a range of bulls with different attributes. **Appendix 5** illustrates the choice that exists across the Holstein breed. The difference in £PLI between the top and bottom available bulls equates to an expected profitability difference of £1151 across the lifetime of their respective daughters. Whilst the very highest genetic merit bulls are more expensive, the relationship between cost and genetic merit is not linear and there are many affordable bulls with high genetic merit.

With no one company offering more than 30% of the available bulls, opening up selection to all companies would appear to be an important strategy in terms of increasing selection pressure: to maximise the rate of genetic gain whilst controlling increases in the rate of inbreeding.

## 11.2. Case study: Test provider

In the USA I spent time with Flavio Silvestre, Paul Fernandez and Ralph Bruno, three of the Dairy Production Specialists (DPS) at Zoetis. In the pre-sale phase, the DPS are responsible for carrying out a genetic audit of the herd exploring the herd's current genetic strengths and weaknesses against a review of phenotype performance and herd health goals.

Tools are also available to report on heifer inventory and potential ROI. They are also on hand to help the farmer rank their animals and optimise the different breeding strategies used. Ongoing monitoring includes reviewing compliance and inventory numbers, as well as measuring the response to selection.





Figure 19: The author with DPSs Ralph Bruno and Paul Fernandez and Zoetis customer Brain Fiscalini. Photo: author's own

The ongoing support from the DPS undoubtedly helped customers bond to both continued testing and other Zoetis brands.

## 11.3. Case study: Vet

Only a small number of farms visited involved their vet in decisions around breeding. In most cases this appeared to be because the vet had chosen not to be involved.

In Abbotsford, BC, I met with Marty Darrow, a practising farm vet for over 35 years. Marty had been the main driving force of a part-government-funded research project exploring the value of genomic testing on 34 dairy farms across three regions of Canada.

Marty listed a desire to help his clients be more profitable as a major factor behind his involvement in the project. He also felt vets were well placed to advise on genomics as they were truly independent.

Strong correlations were realised between genomic predictions and production outcomes from the 3500 female animals tested. Genomic testing proved to be a much more accurate predictor of actual performance than parent average. Having calculated the cost of heifer rearing on each farm, this retrospective analysis demonstrated that genomics could be used successfully to identify heifers at a young age that were unlikely to ever recoup the costs associated with rearing.

Meeting Marty reaffirmed why, as a vet, I feel I should be involved in the breeding decisions made on my clients' farms. When asked what he thought the biggest barrier to more vets getting involved was, Marty cited a lack of training at college on breeding and genetics as the main detractor.

The picture in the UK is similar. Like Marty, the small number of vets who are successfully providing a service to their clients on genetics appear to be those who have championed the cause.



# 12. The role of the evaluation body – when industry collaboration meets big business

The success of the genetic evaluation process relies largely on volume and quality of data collected from appropriate representative populations, which must then be processed accurately through the use of evidenced evaluation procedures.

In many of the countries visited it was clear that the evaluation body had no commercial interest in the animals being evaluated, and these bodies have forged close working relationships within the industry to access and process data into meaningful evaluations for the benefit of all farmers.

Through transparent methods their work looked to promote best practice with regard to: methodology, exploring and correcting for potential errors (e.g. bias), identifying emerging threats (e.g. recessives and haplotypes) and preserving genetic variation whilst realising significant genetic gain.

Figure 20 below illustrates the extension activity undertaken by ICBF in Ireland. Source ICBF.



Figure 20: extension activity undertaken by ICBF in Ireland. Source ICBF.

Improvements to national evaluation processes are constantly being made. Recently CDCB started using an 80k chip to improve the accuracy of their genomic predictions. Other countries are expected to follow.



In the UK, AHDB have continued to partition producer levy and funding towards improvements to the genetic evaluation process. These improvements will benefit all dairy farmers, not just those who can access PTA or gPTA data for females.

The on-line herd genetic report (HGR) is also continually improving. This is used by farmers and approved third parties to access herd genetic PTA and gPTA data. In the UK many farmers are critical of their AHDB levy whilst often being unaware that part of their levy funds the genetic evaluation process. At present only 29% (1790) of eligible herds have established HGR accounts. This service alone represents a significant opportunity to realise a return on their levy investment.

A growing number of companies are now offering proprietary genomic evaluations. These have been developed and marketed for the company behind them to differentiate their genomic test or portfolio of bulls from the competition.

Popular examples include CLARIFIDE PLUS<sup>®</sup> (Zoetis) and Immunity+<sup>™</sup> (Semex). The methodology behind each prediction differs significantly. As part of my study I met the teams behind each of these proprietary predictions and learnt more about their evolution.

Dr Tony McNeil, Zoetis, outlined that CLARIFIDE PLUS<sup>®</sup> utilises on-farm producer-recorded health data to produce genomically-enhanced predictions for cow and calf wellness. Interpretation of CLARIFIDE PLUS<sup>®</sup> results is based on examination of the individual cow and calf wellness gPTA's and/or use of the selection index Dairy Wellness Profit (\$DWP), which includes wellness traits alongside the standard traits published by CDCB. To practically implement the use of CLARIFIDE PLUS<sup>®</sup> results, many producers have elected to use \$DWP as their headline selection index.

When challenged on the likely robustness of the farmer-recorded health data used, Dr McNeel highlighted that millions of records had been included in the evaluation. This had made it possible for reliabilities of >50% for the six cow-, and 39% for the three calf-, wellness traits to be achieved in young genomic-tested females.

Immunity+<sup>™</sup> predictions are based on genomically enhanced direct measures of immune function with associations to health. Females genomic tested through Semex are classified as either High, Medium or Low immune responders. Similar classification of the bulls marketed by Semex is performed but customers are only made aware of high immune responders. These are marketed as Immunity+<sup>™</sup>.

At the University of Guelph, I met with Professor Bonnie Mallard and her team who developed the original cow side-test for Immunity+<sup>™</sup> and performed the genome-wide association study used to determine the genomic regions associated with Immune function. When asked how farmers should use their Immunity+<sup>™</sup> results, Professor Mallard commented that husbandry measures could be tailored towards the animal's status, e.g. the provision of extra colostrum could help calves born from animals classified as low immune responders. The strategic use of Immunity+<sup>™</sup> bulls in matings was also discussed, and this functionality is included in the Elevate<sup>™</sup> programme.

As new traits continue to be released by the evaluation bodies there are a growing number of instances where the farmer will be able to access both a proprietary and standard genomic evaluation for the same trait, e.g. mastitis in the USA through CLARIFIDE PLUS<sup>®</sup> and CDCB. As each mastitis gPTA



will have been calculated differently, it is likely the animal will re-rank between evaluations. This could cast doubt over the validity of one or both figures and ultimately lead to confusion on how to interpret the results.

Another concern is that, in the absence of an overseeing governing body, there is no official validation process in place to approve proprietary predictions. It is largely therefore down to the farmer and/or their advisor to evaluate the credibility of a proprietary evaluation. This should include a review of the methodology used to calculate the prediction. Only once this is performed should a decision be made as to whether the proprietary index is utilised.



## **13. Future applications of genomic testing**

The adoption of genomics has doubled the rate of genetic gain. Despite this we are still very much in the early stages of adopting this technology. Whilst progress for production and conformation have been significant the focus of attention has been to target improvements in health and fitness traits.

Farmers can now select directly for health. In the future it is likely that new novel traits relating to health, reproduction, efficiency and environmental impact will be developed.

## 13.1. "In the age of the genotype, phenotype is king"

This is a frequently quoted phrase from Professor Mike Coffey of the Scottish Rural University College (SRUC) and perfectly illustrates the continual need for high quality phenotype data to improve existing genetic predictions and realise predictions for new traits.

## 13.2. New traits represent new opportunities.

When considering which new traits should be targeted, I learnt that two factors should be considered. Firstly, new traits should have low phenotypic and genetic correlations with existing traits; they should bring new information. Secondly, they should have value to farmers. Where the cost of measuring is high because specialised equipment is required, it is important that the resulting predictions are of high value to the farmer.

## 13.2.i Case study: Feed efficiency

Feed efficiency (FE) has increased significantly over recent years, mainly as the result of selection for increased milk yield. As feed represents the largest variable cost on any dairy farm there is a huge amount of interest in providing an FE index for farmers to directly use for selection.

In the past, genetic indices for FE have been based on the relationship between production and body size, as the costs associated with directly collecting enough feed intake data to produce a genetic index of adequate reliability were prohibitive. Now, with genomics, a small, deeply phenotyped population can be used to predict phenotypes for all animals.

As a result, interest in FE has grown. ST Genetics recently launched their proprietary EcoFeed<sup>™</sup> trait. Elsewhere academia and research institute collaborations like the Global Dry Matter initiative look to combine feed intake data from nine countries to create a large reference population for genomic selection of dry matter intake.

The Efficient Dairy Genome Project is another international project aiming to develop genomic-based methods for selection of dairy cattle with improved FE and lower methane emissions. The reference populations within the project are genotyped and genomic data, alongside detailed performance data, is interrogated to examine phenotypes such as Residual Feed Intake (RFI, defined as the difference in actual intake and intake predicted, based on body size and level of production).

How can UK dairy farmers use genomics to breed a better herd? ... by Neil Eastham A Nuffield Farming Scholarships Trust report ... generously sponsored by John Oldacre Foundation



Dr Filippo Miglior of CDN and The University of Guelph outlined the motivation behind the project, "cows with greater feed efficiency can produce more milk from fewer inputs, whilst also producing less methane and less manure. Selecting for cows with improved FE will lead to more efficient production and reduced feed costs."



Figure 21: Machine used for recording methane emissions at The Elora Research Station – Dairy Facility, Guelph. Photo author's own

Preliminary estimates from the project show that breeding animals with increased FE and reduced methane emissions can reduce feed costs by \$108/cow/year and decrease methane emissions by an estimated 11-26%. Whilst increases in overall genetic merit help reduce methane emissions indirectly, direct selection for reduced methane emissions represents an exciting opportunity to decrease the environmental footprint of the dairy industry.



## 13.2.ii. Case study: Feed efficiency in practice

CRV are working with a number of collaborators including Wageningen University to realise genomic predictions for RFI. Data has been collected from over 5500 genotyped cows on research farms. The aim is to reach over 10,000 genotyped cows over the next two years through collaboration with five additional commercial farms. Further collaboration with other countries is hoped to increase the reliability of RFI predictions from 40% to 60%.

The Alders family at Overloon installed their feed bunkers and weigh scales in 2017 and are already seeing big differences between animals. The top 25% of the herd for feed efficiency are producing 9kg of extra milk per day when compared to those animals in the bottom 25%.



Figure 22: Feed intakes being recorded at Alders Dairy, Overloon, The Netherlands Photo author's own

UK dairy farmers are also set to benefit from predictions for FE. AHDB are currently forging international collaborations to access a reference population of sufficient size to produce accurate breeding values for FE. Working with the SRUC, current research also extends to exploring the use of mid infra-red spectral data from milk as a potential predictor of useful phenotypes, as well as genotyping more animals to improve the accuracy of TB Advantage predictions.

It is also expected that genomic inbreeding figures will be launched in the UK shortly. These will provide producers with more precise measures of inbreeding for genomic-tested animals than the current pedigree-based inbreeding coefficients. Through use of the inbreeding checker on the AHDB HGR, or via computerised mating programmes, farmers will be able to curtail increases in inbreeding and avoid matings between animals that could result in lethal defects.

Within the EU funded project GenTORE, very detailed phenotypes are to be collected from dairy and beef farms using sensors and novel technologies. This precision phenotyping is to be used to develop



proxies for resilience and efficiency, culminating in the development of management tools and genomic predictions for farmers.

Elsewhere work is ongoing to explore how precision phenotyping can improve existing traits. Fertility continues to be a key financial driver and the role of new phenotypes to predict fertility could be a useful way of more accurately predicting the physiological status of the cow, e.g. progesterone level or length of oestrus.

## 13.3. Role of big data

As dairy farmers continue to specialise and invest in mechanisation and sensor technology, the amount of data generated on farm is growing exponentially. Professor Miel Hostens at The University of Ghent used the following analogy to explain this:

For every 1 tanker of milk there are....

2 tankers of muck3 tankers of water4 gigabytes of data

Unsurprisingly a growing number of farmers are beginning to question who owns this data? The farmers I met were often unclear on who can access their data or indeed how it is being used. As a result they run the risk of missing out on a share of the value derived from research discoveries based on data sets that include their data. As farmers withdraw their involvement from services like milk recording, data flows into centralized databases utilised by national genetic evaluation processes are lost, and wider benefit across the industry is lost as well.

Professor Yvette de Haas at Wageningen University outlined how a new initiative called JoinData is helping improve transparency around ownership of data in The Netherlands. Participating farmers retain ownership of their data, most of which originates from sensors and other high-tech tools on the farm. It is up to individual farmers to decide which other parties are given access to their data.

Farmers can make their data available for projects. Collaboration with research centres and institutes (e.g. CRV, Agrifirm, Friesland Campina and Lely) will ensure this data is used in models and products that will return value to dairy farmers.

## 13.4. Beyond genomics......

By providing breeders with access to genetic variation that would otherwise be unavailable, gene editing poses a massive opportunity to create individuals that carry certain desirable traits. Such examples could include the insertion of known polled or heat tolerance genes. These traits have been introduced successfully through natural mating strategies in the past, but this has always been at the expense of genetic merit and, as a result, industry uptake has been poor.

Epigenetic effects are known to modify gene expression rather than alter the genetic code itself. More work is needed to understand these effects and how they are triggered.



## 14. Conclusions

## 1. Genetic improvement on UK dairy farms is worth the effort

Genetic improvement is permanent and cumulative over generations. At a time when dairy farmers must continue to modernise and specialise in order to maintain competitiveness, genetic improvement represents a cost-effective way for farmers to meet the growing demands of their consumer.

## 2. Clear breeding objectives are crucial

Every dairy farm should have a set of breeding objectives to reflect their current and future needs. Only once the breeding objectives are set should the selection criteria be determined. Selection should focus on those traits where an improvement through breeding will help achieve the breeding objectives.

## 3. Faster progress can be realised with genomics

Genomic testing is changing the way dairy producers make management, selection and breeding decisions. Early on, the major focus of genomic testing was to identify high quality young bulls early. However, the same power of prediction can now be used for female youngstock, and female testing now represents a useful management tool available to dairy farmers.

## 4. Optimal use of different breeding strategies to drive value from genomic testing

The adage that data is only as good as what you do with it is wholly relevant to genomic test results. Many breeding strategies can be deployed. An ideal combination would result in increased income and decrease costs whilst maximising the rate of genetic gain.

## 5. A role for the vet

Genetics play a fundamental role in herd health. As vets, it is imperative that we have an understanding of the genetic potential of the herds that we are working with. This is vital when looking to set realistic targets and recognise when failures to harness genetic potential are occurring.

On-farm observations and data analysis provide vets with an appreciation of those challenges that can be, at least in part, addressed through breeding. With an understanding of the statistical nature of breeding and the science behind genomics, vets are well placed to provide advice in a field where independence is a rarity.

## 6. The power of data

Since the advent of genomic testing the focus for many has been the genotype. Focus is now shifting back to the phenotype as we increasingly realise that existing and new data sources from the farm combined, represent great potential for further genetic improvement.



## **15. Recommendations**

## 1. A greater understanding of the role of genetics is needed.

More farmers need to understand and appreciate the value that genetic improvement represents. Industry steps should be taken to educate farmers on how to interpret PTA and gPTA data. Farmers and associated third parties should be encouraged to access herd genetic data to review genetic strengths and weaknesses and determine effective breeding objectives.

## 2. Dairy farmers can benefit from an increased use of genomics

All dairy farmers should look to capitalise on the superior genetic merit of genomic-proven bulls versus their older daughter-proven counterparts.

Female genomic testing should be added to the list of options that dairy farmers should consider when looking to increase the productivity and profitability of their farm. For most, the motivation to test should be to find the bottom end. There must be scope to deselect these animals if a ROI in genomic testing is to be realised.

## 3. Maximal value must be realised from female genomic testing

Female genomic data must be used to drive ruthless decision making. Tested females should be ranked according to their suitability for the farm and its breeding objectives. Along with other breeding females, tested females should then be aligned to a defined breeding strategy. The use of sexed dairy and conventional beef semen, together with the sale of surplus low genetic merit heifers, is likely to yield the greatest short and long term financial returns.

## 4. Vets have an opportunity to add value.

Mindful that an element of health, welfare and productivity is directly related to the breeding decisions made on farm, vets must equip themselves with all the skills necessary to successfully advise their clients on breeding and genetics. More teaching on breeding and genetics should be offered to vets at an undergraduate and postgraduate level.

## 5. Long term industry success in the field of breeding and genetics will ride on data

Transparency around the ownership and use of data must improve. A failure to do so will result in farmers withdrawing willingness to share data, causing widespread impacts on the industry. Through sensor technology and daily recording procedures farmers should record as much high quality data relating to health, production and management as possible. In return, stakeholders should be prepared to reward farmers with financial remuneration or access to improved services.



## 16. After my study tour

I have already started to apply some of the lessons learnt from my Nuffield Farming Scholarship. At a practice level I have a growing number of clients who are genomic testing and I am helping them to maximise their return from this investment. I continue to work with my veterinary colleagues to help our clients understand more about the role that breeding and genetics play within their business.

At an industry level I have run several training courses for vets and farmers on breeding and genetics during my scholarship, and I will continue to use this as a platform to share my findings. I have also written numerous articles and made several public appearances.

On the family farm where it all began, genomic testing continues to be used a selection tool, helping us to maximise genetic gains and optimise returns from our breeding programme.

**Neil Eastham** 

June 2019



## **18. Glossary**

Allele	A different form (or variant) of a gene.
BLUP	Best Linear Unbiased Prediction
DNA	Deoxyribonucleic Acid
EBV	Estimated Breeding Value
Gene	A unit of information which constitutes a region (or locus, pl. loci) of DNA that encodes the instructions for building a protein.
Genetic Merit	How an animal ranks relative to other candidates for selection on its ability to produce superior offspring due to inherited performance.
Genetics	The study of genes, variation and heredity.
Genomics	The study of genomes; the complete set of genetic material within an organism.
Genotype	The genetic constitution of an individual at one or more loci.
Genotyping	Process of determining the genotype of an individual.
gPTA	Genomic Predicted Transmitting Ability
Haplotype	Set of alleles inherited as a unit from a single parent.
Heritability	The additive genetic variation in a trait expressed as a proportion of the total phenotypic variation in the trait.
Phenotype	The set of observable characters (traits) of an individual.
ΡΤΑ	Predicted Transmitting Ability
Reliability	A measure of accuracy or degree of confidence in a genetic index.
SNP	Single Nucleotide Polymorphism



## **19. References**

- Invited review: Learning from the future—A vision for dairy farms and cows in 2067.
   J. H. Britt, R. A. Cushman, C. D. Dechow, H. Dobson, P. Humblot, M. F. Hutjens, G. A. Jones, P. S. Ruegg, I. M. Sheldon and J. S. Stevenson.
   J. Dairy Sci. 101:3722–37412.
- Symposium review: Possibilities in an age of genomics: The future of selection indices.
   J.B Cole & P.M VanRaden.
   J. Dairy Science. 101; 3686-3701.
- **3. Prediction of total genetic value using genome-wide dense marker maps.** Meuwissen TH1, Hayes BJ, Goddard ME Genetics 2001 Apr; 157(4):1819-29.
- 4. **The Genome sequence of Taurine Cattle: A window to ruminant biology and evolution** The Bovine genome sequencing and analysis consortium, Christine G. Elsik, Ross L. Tellam Kim C Worley.

Science 2009 Apr; 324: 522-528

- 5. Genomic selection in dairy cattle: The USDA Experience Wiggans, GR,. Cole, J.B., Hubbard, S.M., Sonstegard, T.S. Annual Review of Animal Biosciences 2017. 5:309-27
- 6. Genomic selection of dairy cattle: A review of methods, strategies, impact. Weigel, K.A.

Journal of Animal Breeding and Genomics. 2017 1(1):1-15

7. Strategy for applying genome wide selection in dairy cattle. Schaeffer LR

J Animal Breeding and Genetics. 2006 123:218-223.

- 8 <u>https://articles.extension.org/pages/74738/genomic-selection-has-changed-dairy-sire-selection</u>
- 9. Changes in genetic selection differentials and generation intervals in US Holstein dairy cattle as a result of genomic selection García-Ruiz A, Cole JB, VanRaden PM, Wiggans GR, Ruiz-López FJ, Van Tassell CP (2016) Proc. Natl. Acad Sci USA 113:E3995-4004.
- **10.** <u>https://www.naab-css.org/news/2018-naab-regular-member-unit-sales-%E2%80%93-record-year</u>
- 11. <u>https://www.dairybusiness.com/better-cows-can-mean-more-profit-how-genetics-paves-</u> <u>the-way/</u>
- 12. <u>https://www.progressivedairy.com/topics/a-i-breeding/looking-for-greater-economic-value-</u> <u>from-genomic-testing</u>
- Economic and genetic performance of various combinations of in vitro-produced embryo transfers and artificial insemination in a dairy herd.
   Kaniyamattam K, Block J, Hansen PJ, De Vries A.
   J Dairy Sci. 2018 Feb; 101(2):1540-1553.
- 14.The cattle genome reveals its secrets.David W Burt. Journal of Biology 2009 8:36

## 15. Unlocking the bovine genome.

Ross L. Tellam, Danielle G Lemay, Curtis P Van Tassell, Harris A Lewin, Christine G. Elsik, Kiim C Worley.

BMC Genomics 2009 10:193



## 20. Acknowledgements

I'd like to extend a massive thank you to the Nuffield Farming Scholarships Trust and my sponsor The John Oldacre Foundation for affording me this incredible opportunity.

I'd like to thank the class of 2018 for their support and friendship. Thank you also to my mentor Jo Speed for providing advice and reassurance over the last 18 months.

A big thank you also to my fellow partners and colleagues at Bishopton and RAFT Solutions for their unrelenting support.

Lastly I'd like to thank my wife Heather for embracing her new found love of cows and genomics! I could not have embarked on this journey without her.

See APPENDICES over page



## **21.** Appendices





Source: *Symposium review*: Possibilities in an age of genomics: The future of selection indices. J.B Cole & P.M VanRaden. J. Dairy Science. 101:3686-3701.

Appendix 2 is overleaf



## **Appendix 2: Irish national herd benefits from use of selection index.**

At Moorepark, the Animal and Grassland Research and Innovation Centre operated by Teagasc, Dr Frank Buckley explained how research is helping to demonstrate the value of higher genetic merit. The national selection index in Ireland is Economic Breeding Index ( $\in$ EBI) and is published by Teagasc and the Irish Cattle Breeding Federation (ICBF).  $\in$ EBI is tailored towards spring calving and manufacturing-based milk contracts (*see Appendix 1*).

In 2012, Teagasc established the Next Generation herd. The herd is made up of two distinct groups of animals based on €EBI: elite (average €EBI = €154 (ICBF 05/17)): and national average (NA) (average €EBI = €51 (ICBF 05/17).

Economic analysis based on data collected was extrapolated to simulate a 40-hectare unit. Profit differences matched the expectation based on €EBI, with a difference of over €200 per cow and €600 per hectare favouring the elite group.

At a national level €EBI has delivered €750m additional profit across the industry over the last 20 years. This figure is expected to exceed €1 billion by 2020. At the individual farm level confidence in EBI was high, with a number of the farms I visited selecting purely on EBI.

For example, Tom Griffon, a Bandon-based producer who milks 175 spring calving cows, continues to use EBI as his primary selection index. Using the Herd Plus online reporting tool from ICBF, Tom regularly monitors the herd's progress with regard to €EBI.



Tom Griffon pictured with one of his favourite cows and another singled out as one of the worst (clue - she is the one exercising her objection to Tom's comment!). Photo: author's own



## **Appendix 3: Getting to grips with genetics**

## - Origins of the Bovine

The cow belongs to the taxonomical superorder Certartiodactyla, an ancient group of mammals that first appeared some 60 million years ago<sup>14</sup>. There are over 800 cattle breeds worldwide and these domesticated cattle (*Bos Taurus and Bos Taurus indicus*) can be traced back to ancestral aurochs (*Bos Taurus primigenius*)<sup>14</sup>. Throughout domestication the cow has been an important economic and social resource to humans as well as in some instances an important religious figure<sup>15</sup>.

As a ruminant the cow is capable through a complex metabolic pathway of converting low quality plant fibre (e.g. cellulose which is undigestible to humans) into an energy-rich foodstuff (milk, muscle and fat). It is estimated that cattle could graze approximately three quarters of the world's farmed land<sup>15</sup>. It is unsurprising therefore that in the face of rapid human population growth the number of cattle reared globally has increased in parallel and now exceeds 1 billion per year.

## - Basic genetic principles

Like humans, cattle are multicellular organisms that are made up of trillions of cells. Almost all these cells contain DNA. It is this DNA that carries the genetic instructions for the development, functioning, growth and reproduction of living organisms.

DNA is made up of a double helix structure comprising of two strands coiled around each other. Each strand in turn is made up of building blocks called bases (or nucleotides). There are four types of base: cytosine [C], guanine [G], adenine [A] or thymine [T]. Base pairing rules exist so that only A can pair with T and C with G. It is this pairing that holds the double helix structure of DNA together. The order of these bases is unique to the individual and serves as the blueprint of life.

The entirety of an organism's DNA can be referred to as its genome. Cattle have over 3 billion base pairs. DNA is packaged into structures called chromosomes. Cattle have 30 pairs of chromosomes (29 Autosomal and 1 sex linked). A copy of each chromosome is received from each parent at conception (sperm and egg cells carry only one copy each) and, as a consequence, approximately half the genetic material is received from each parent.

Genes can be described as regions of DNA that encode the instructions for building a protein. These can be of varying length and are present at defined locations (loci) on a chromosome. Cattle have approximately 22,000 genes, of which 14,000 are common to all mammalian species.

Sources of genetic variation exist due to mutation, recombination and random mating effects. Mutations arise from a change in the sequence of DNA due to external factors or internal errors during DNA replication. Recombination occurs during the process of creating the genetic material carried in sperm and egg cells. During this process pairs of chromosomes align and divide, allowing genetic material to be exchanged. Lastly, random mating refers to population-level variation and relates to the fact that mating is made at random with regard to a particular characteristic.

## - Understanding breeding values

An observable physical property of a cow (e.g. a trait relating to appearance or performance) can be described as a **Phenotype (P)**. This is the product of: **Genetics (G)**, the **Environment (E)** and the way they interact **(GE)**.



The relationship between the three factors is summarized using the following equation:

#### $\mathsf{P} = \mathsf{G} + \mathsf{E} + \mathsf{G}\mathsf{E}$

Most traits of interest in dairy animals show continuous variation. Quantitative genetics is a branch of population genetics that deals with phenotypes that vary continuously (e.g. milk yield); such traits are often controlled by many genes and are influenced by the environment. Qualitative genetics refers to when the phenotype can be assigned into discrete classes (e.g. hair colour). Typically these traits are controlled by single genes and the environment plays no role in their expression.

In order to maximise performance for traits of interest it is important to recognise that the combination of genetics and excellent management will yield the best results. The aim of animal breeding is to select those animals to become parents that will improve the genetic level in the next generation. To identify the individuals with highest genetic merit we need to ascertain their estimated breeding value (EBV) for those traits that are deemed important.

Traditional evaluations (without the use of genomics) are based on the animal's pedigree together with its own performance (if available). It is possible to calculate an estimated breeding value because the genetic component of the above equation can be further subdivided based on the expected action of genes that the animal is predicted to carry. The classification is as follows;

## 1. Additive genetic variation.

This variation results from the fact that animals carry different versions of the same genes (called alleles) and these all contribute towards the phenotype. Some alleles are known to be favourable and contribute to a better phenotype. For a quantitative trait such as milk yield which is affected by many genes, the summation of these allele effects is used calculate the breeding value. It is the additive genetic variation that we try and influence through breeding.

2. Non additive genetic variation encompasses two further types of gene action: Dominance and Epistasis.

These non-additive effects result from the interactions between genes.

The role of calculating breeding values is fulfilled by an evaluation body (AHDB Dairy in the UK). Breeding values are available for those individuals that have a recorded sire and reside in a herd that is engaged in milk recording. Figures are updated and released every four months. The evaluation process relies on access to a huge amount of data including: ancestry (BCMS records and pedigree herd book data), milk production, health and survival records (from milk recording organisations) and type classification data (breed society classification data).

By using statistical models, quantitative geneticists can estimate the proportion of the total variance that is attributable to genetics, versus that due to the environment. Contemporary group effects in genetic evaluations can be accounted for through use of a Best Linear Unbiased Prediction (BLUP) model. When calculating an animal's genetic merit and assigning it a breeding value, BLUP enables the effects of the environment to be removed.

In the UK estimated breeding values for males and females are expressed as Predicted Transmitting Abilities (PTA's). These represent half the breeding value (PTA = EBV  $\times$  0.5) and predict to what extent a trait will be passed on to the next generation. Reliability figures are published for each PTA and predict the likelihood with which the PTA will change with time as more information is added to the evaluation.



Parent average PTA's are available for heifers or bulls that are too young to have recorded performance data (either from themselves or from daughters). These are simply an average of the genetic merit of the dam and sire. As a consequence, the reliability of these figures is low.

see Appendix 4 overleaf



## Appendix 4 : The process of genomic testing

#### **STEP 1 – SAMPLE THE ANIMAL**



Test kits are requested from service provider. In the UK, genomic testing is offered by milk recording organisations, breeding companies, vets and herdbook societies. In Ireland and The Netherlands/Belgium there was only one service provider, ICBF and CRV respectively. However in the US, Canada and Italy greater choice existed.

A hair, ear notch, saliva or blood sample containing the animal's DNA is taken.

In the US CDCB have reported that of the submissions made in 2018 (*see right*) ear notch was the most popular method of sampling.

Source	Samples (No.)	Samples (%)
Tissue (ear)	579,255	81
Hair	102,229	14
Blood	14,656	2
Nasal swab	656	<1
Semen	319	<1
Unknown	17,048	2

#### STEP 2 – EXTRACTION OF DNA



The DNA is extracted at a lab

Case study: Visit to Zoetis genomic testing lab. Kalamazoo, MI, US.

Two floors of the Zoetis building in Kalamazoo are dedicated to the animal genetics division. Dr Jason Osterstock (Executive Director) outlined the rapid growth that the genetic services division of Zoetis

had realised since the commercialisation of genomic testing. They now offer testing solutions for beef and sheep sectors, as well dairy, through their US market leading test, CLARIFIDE<sup>®</sup>. As one of the fastest growing parts of the business, genetic services is described as one of the most important and fits within their continuum of care mantra: PREDICT. PREVENT. DIAGNOSE. TREAT.

Seventeen PhD Geneticists and a large team of scientists and support staff work in the sample processing laboratory, genetics R&D and customer services departments. Success in the domestic market has resulted in Zoetis extending their offering to a growing number of countries outside of North America. Much of this success is described as due to their approach to customer support (*see Chapter 8*) and proprietary predictions available through the CLARIFIDE PLUS test (*see chapter 9*).

## STEP 3 - The DNA is put onto a SNP-chip

The sequence of bases that make up the DNA can then be read at various known locations along its length.

The price of testing was comparable between providers (£23-£33 per test for a standard female test). The commonly used tests were low density, with SNP chip density typically ranging from 6k up to 60k.

#### STEP 4 – The SNP code is sent to the evaluation centre

#### A SNP key is used to produce a set of gPTA's for the animal.

In order to turn the SNP code (see left) returned by the genotyping lab into a meaningful set of breeding values for the farmer the evaluation body must create, maintain and grow a reference population (SNP Key). The first Holstein and Jersey genomic evaluations released in the US in 2009 were based on the genotypes of 15,000 bulls with daughters (daughter proven). It wasn't until 2012 that UK genomic evaluations were released by AHDB for Holstein bulls in the UK. Given the influence of foreign sires in the UK (particularly from North America) a sharing agreement between the UK, US, Canada and Italy was a vital step in establishing a reference population that provided enough relevant genotypes to reliably predict performance in the UK.

The UK reference population for Holsteins has now grown to over 30,000 daughter-proven genotyped bulls. Similar collaboration was vital to establish genomic evaluations for smaller breeds in the UK (Holsteins account for approximately 80% of all dairy inseminations in the UK). The introduction of British Friesian genomics was made in August 2016 and Ayrshire, Jersey and Guernsey genomic evaluations followed in April 2017.









## STEP 5 – Genomic Predicted Transmitting Abilities (gPTA's) are published

Official gPTA's are calculated monthly and released to farmers via their genotyping service provider. These are updated and released alongside official traditional evaluation figures for non-tested individuals in April, August and December. Between releases genomic evaluation figures for marketed bulls are not released, to prevent fluctuations between official evaluations.

In order to ease the workloads of the genotyping labs and speed reporting to farmers, the US, Canada and The Netherlands have introduced weekly preliminary results. These provide farmers with genomic results 2-3 weeks after submission (*c.f.* 6-8 week wait currently experienced by UK farmers). This enables farmers to enact breeding strategies more quickly.

The organisations responsible for genetic evaluations in all of the countries visited participated in Interbull activity. Interbull is a permanent sub-committee of the International Committee for Animal Recording (ICAR) and was established to develop a single system for comparing evaluations across different countries and genetic bases as accurately as possible.

Multiple-trait Across Country Evaluation (MACE) was introduced by Interbull in 1995 to provide a method of calculating international genetic evaluations. This takes into account information from each country using all known relationships between animals, both within and across populations. MACE also accounts for re-ranking between countries due to genotype by environment interactions.

A separate set of results is calculated for every participating country. Interbull does not rank animals in any way and only calculates breeding values on the different country scales. Member countries are responsible for ranking sires using their own breeding objectives and publishing the results. Since the advent of genomic testing, new methodologies (e.g. GBLUP and GMACE) have been put place by evaluation bodies and Interbull to incorporate genomic (DNA) data, alongside pedigree and performance data, into existing genetic evaluation models. On-going collaboration and data exchange between countries as well as continual review, ensure improvements to the validity of modern-day genetic evaluations continue to be made.

See overleaf for a set of gPTA's for a genomic-tested female



## A set of gPTA's for a genomic-tested female

holsteinuk		+ 01182494/03066 (F)				03003124720437			
holstein & britis	h friesian	Date of Birth: 21/10/2017	PLI £	577 (RIb% 56)		ç	SAMLEA WINDSOF	RFIVEPENCE	
		Eartag: UK182494703066	Inbre	eding % 6.0		0118249	4602183 VG86		
Holstein Produ	uction	Young Genomic Pedigr	ee Index 0	alculated 4/19					0
PLI £577		56% RIb							
Production Tra	ait		Value	Managem	ent traits		PTA	Relia	bility %
Production reli	iability %		67	SCC (%)			-29		68
Milk KG			625	Mastitis (9	6)		-3		68
Fat KG			17.6	Lifespan (I	act)		0.6		59
Protein KG			17.5	Fertility In	dex		14.2		02
Protein %			-0.03	Maintenar	-8- 100		2		44
Persistency (%)	)		0	Maincenar			-		
Holstein Type		Young Genomic Pedigr	ee Index 0	alculated 4/19					0
TM 0.98		53% RIb							
Trait		-3 -2	-1	0	+1	+2	+3		Value
Type Merit	Poor							Excellent	0.98
Mammary	Poor							Excellent	1.04
Legs & feet	Poor							Excellent	0.61
Stature	136 cm							160 cm	0.27
Chest width	Narrow			-				Wide	-0.09
Body depth	Shallow							Deep	-0.86
Angularity	Coarse			-				Open Rib	-0.19
Rump angle	High pins							Low pins	0.29
Rump width	Narrow			-				Wide	0.14
Rear leg side	Straight							Sickled	0.94
Foot angle	Low							Steep	-0.48
Fore udd att	Loose							Tight	1.05
Rear udder ht	Very low							Very high	0.71
Udder supp	Broken							Strong	0.61
Udder depth	Below hor	·k						20cm above	1.01
Front teat of	Outside							Close	-0.48
Teat length	Short							Long	0.51
Rear teat of	Apart			-				Close	-0.09
Teat nos side	Close							Anart	0.07
Temperament	Poor			_				Good	0.15
Fase of milk	Slove			_				East	-0.19
Locometion	Poor							Excellent	0.76
Cond Score	Low							Hich	0.70
Cond Score	LOW							Lini Ruj	0.31

See overleaf for Appendix 5



## **Appendix 5 : Available Holstein sires April 2019**

COMPANY	NO. BULLS	NO. OF GENOMIC	NO. OF AVERAGE DAUGHTER £PLI		MIN £PLI	MAX £PLI
		PROVEN	PROVEN			
ALTA	106	88	18	611	304	842
BULL SMN	52	34	18	582	106	785
COGENT	179	134	45	525	-159	819
CATTLE GEN	7	0	7	263	51	454
CRV	31	22	9	570	-21	774
DOR	22	3	19	281	-77	597
DOVEA	8	2	6	350	191	661
FIR	1	0	1	-172	-172	-172
GBB	7	0	7	16	-263	256
GENUS	399	227	172	521	-288	863
GSU	25	1	24	497	315	672
HENIKERS	2	2	0	548	426	669
IRG	1	0	1	369	369	369
MGN	97	53	44	452	61	790
SEMEX	195	78	117	445	-156	804
UKD	29	18	11	526	153	773
VIKING	26	21	5	590	305	846
WWS	136	81	55	534	-59	820
UNSPECIFIED	16	1	15	380	124	614
ALL	1339	765	574	507	-288	863

Table 3: Table to show available Holstein sires April 2019

Source: Holstein UK <u>http://www.holstein-uk.org/animaldata</u>



Published by The Nuffield Farming Scholarships Trust Southill Farm, Staple Fitzpaine, Taunton, TA3 5SH Tel: 01460 234012 | Email: director@nuffieldscholar.org