

Adopting Genomics

Sheep Breeders' Round Table



16th November 2024

Introduction (and an apology)

- Society celebrates its 50th anniversary this year
- An original import of 13 rams and 26 ewe lambs
- Approaching 2M animals in the database
- Leading terminal sire breed
- Significant influence on the national ewe flock
- Society continually evolved over the last 50 years
 - Integrating science and technology into the business
 - Overcoming technological barriers
 - Supporting breeders
 - Increasing genetic gain in Texels
- Use of genomics is the latest example



Adopting genomics



Enjoy the ride!

- This hasn't been a quick or straightforward journey
- Where it all began
- We collected some data, and learnt plenty
- Where are we now?
- What the future holds...



In the beginning...

- Initial discussions 10-15 years ago
- Aligned to external consultancy recommendations to AHDB
- Encouraged the collection of genomic data (genotypes) plus measures (phenotypes)
- Why do we want to do this?
 - Determine an animal's value from birth
 - Increased accuracy of selection
 - Greater selection intensity / genetic gain



- Google AI tells us genomics can help improve livestock productivity in many ways
- Why wouldn't we want to do this? Let's crack on

What does genomics look like?

**MAIN
POPULATION**

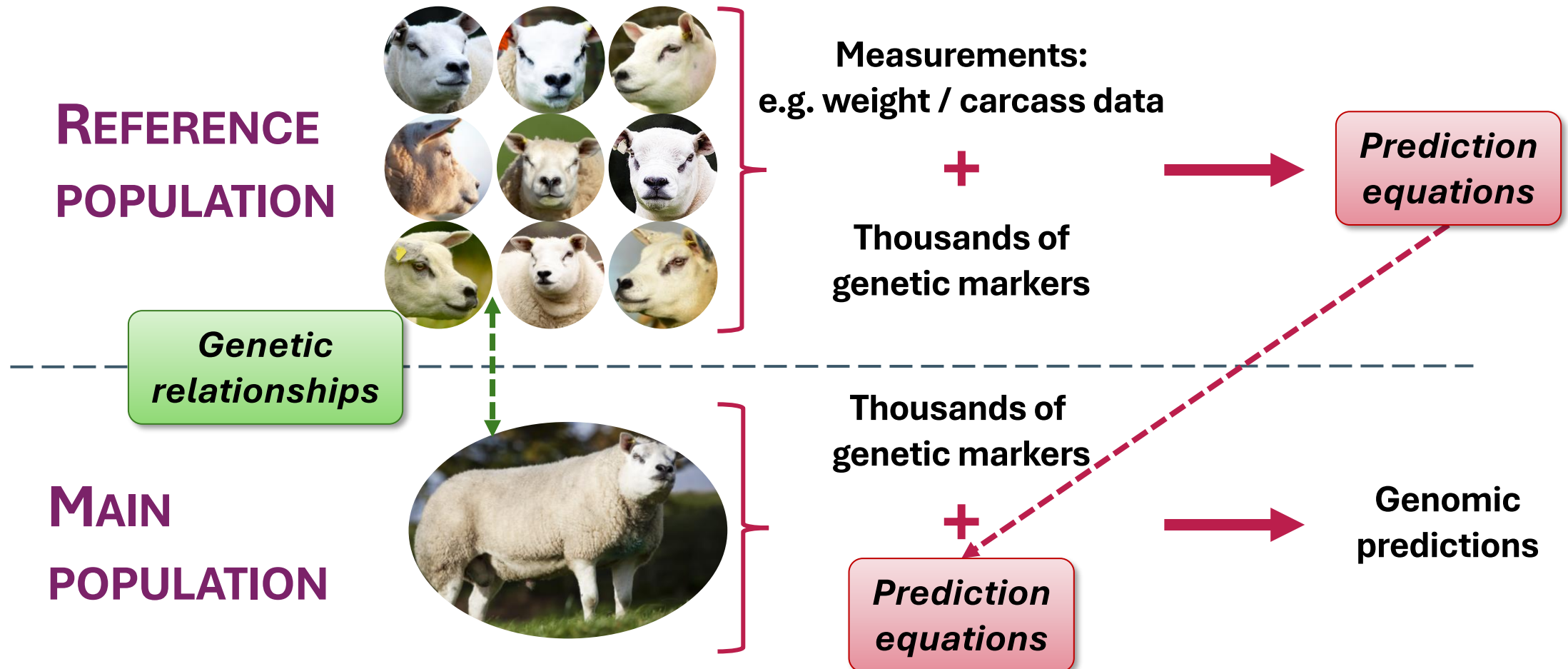


**Thousands of
genetic markers**



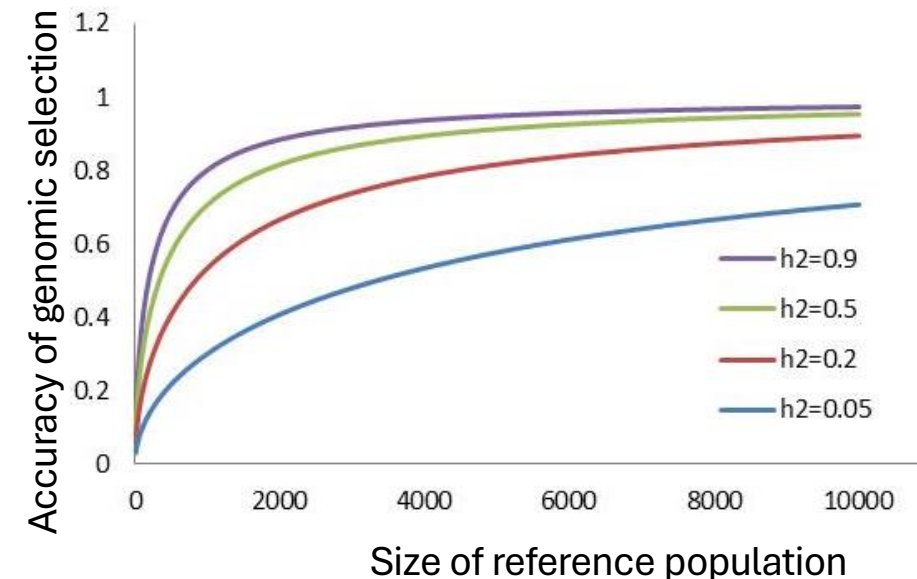
**Genomic
predictions**

If only it was that easy



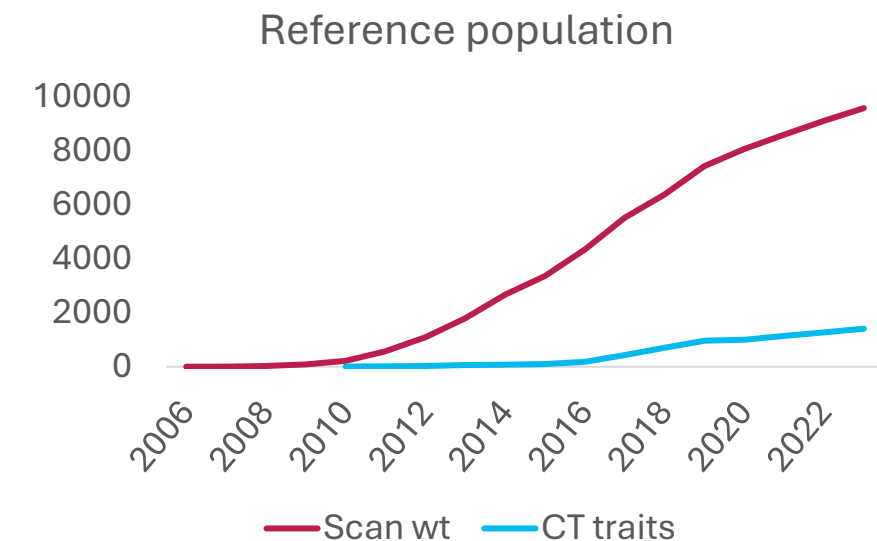
Need to build our reference population

- First, we needed a database that was viable, functional and sustainable
- Major project on its own
 - Foundation to build on
 - Delivers core services (pedigree)
 - Support performance recording with associated data pipelines
- Two main aspects of reference population management
 - Size – how many animals?
 - Relevance – which animals?
- Refresh population every year
- Over time, the reference population is replaced
- Creates an overhead cost for the business



Building our reference population

- *Ad-hoc* and proactive basis
- Genotype all males registered
 - If affordable is a good place to start, provides data on a cross-section
 - Good for pedigree services, but no guaranteed phenotype (trait) data
- Genotyping all CT scanned lambs (gold-standard phenotyping tool)
 - No cost to member (Society-funded)
 - Provides extra CT phenotypes
- Research projects
- Scan weight ref pop >9,000
- CT trait ref pop ~1,500



What do we gain (and lose) from genomics?

- Two-step evaluation
 - Only benefits genotyped animals
 - Two levels of breeding values (genomic vs non-genomic)
- Single-step evaluation
 - All animals benefit (some more than others)
 - Main beneficiaries are young (unproven animals)
 - Major benefit is an increase in accuracy values
- Compared results from NTS / Texel pedigree and Texel ssgblup
 - Single-step is preferred option
 - Increased accuracy and spread of data
 - Texel data remains in NTS to support this evaluation

	TERMINAL INDEX			
	Average	Min	Max	Accuracy
NTS	£2.64	£-4.31	£15.99	44.6%
Texel pedigree	£3.61	£-6.77	£18.85	44.5%
Texel genomic	£3.03	£-4.87	£17.48	45.0%

Is it worth it?

- Some animals appear 'worse'
- Only 0.5% increase in average accuracy
- Estimated 15% re-ranking of animals

The trouble with our times is that
the future is not what it used to be.

Paul Valéry

quote fancy

There are other considerations...

- As a valuable modern breed registry, we *should* use genomics
 - To confirm parentage
 - Provide information on single marker traits, e.g. Scrapie
- Provides added confidence in our pedigrees
- More information for breeders about their animals
- ‘Threat’ of Sheep Ireland
 - Already using genomics extensively
 - Large proportion of Texels exported to Ireland
 - Was possible they’d identify pedigree inconsistencies
- Had to assess level of pedigree inconsistencies
 - Relatively low level of issues



**What's the impact
on traditional
registry services?**



Adopting genomic evaluations

A significant undertaking, and major milestone in Society history

- Two major development aspects run in parallel
 - Development of iTexel to accept and publish the new data
 - Production of the single-step genomic evaluation [with SRUC-Egenes]
- iTexel development
 - Update data tables to accept new data
 - Publishing of parentage-verification data
 - Online
 - Certificates
 - Sale charts
 - Catalogues
- Single-step genomic evaluation
 - Cleaning genotype data and parentage results
 - Correct parentage inconsistencies
 - Retain as much genotype information as possible
 - Analysis of preliminary results

Where are we now?

- Running genomic evaluations since March
 - All animals
 - All traits
- Has led to the development and introduction of new policies
- Single marker information published where available
- Parentage routinely checked (updated if necessary) monthly
- Verified parentage information published on iTexel

DETAILS	
NAME TEXEL SOCIETY DANNY	
FLOCK BOOK NUMBER TXL2000002	BIRTH TYPE 2
DATE OF BIRTH 10/03/2020	SEX ♂ Male
BREED Texel	STATUS Alive
BIRTH NOTIFIED Yes	REGISTERED Yes
INBREEDING COEFFICIENT 1.2	
SCRAPIE GENOTYPE ARR/ARR	
MICROPHTHALMIA GENOTYPE Resistant (G/G)	
PARENTAGE VERIFICATION Sire DNA-verified Dam DNA-verified	

How do genotyped animals benefit?

- Compared accuracy values of the Terminal Index
- Animals with / without scan weight phenotype
- Genotyping an animal without phenotyping gives similar accuracy to phenotyping the animal without genotyping it
- Simplest (hassle-free) approach to improve accuracy is to genotype
- Incurs a cost for members

- **BUT**

- Does this mean members will stop phenotyping?
- If so, how sustainable is the reference population?
- Is there a cost : benefit?

TERMINAL INDEX ACCURACY				
GENOTYPE				
Trait	Phenotype	Yes	No	Overall
Scan weight	Yes (av. acc. %)	81.4	70.5	71.4
	No (av. acc. %)	72.5	40.8	41.4
Overall acc. (%)		75.8	44.1	45.0

For the future

- Continue to innovate
- Define reference population requirements
- Develop a more structured approach to phenotyping and genotyping
- Look 'beyond genomics'



Acknowledgements



Texel Society

- John Yates
- Board and Committee members
- Paul Phillips
- Staff past and present



AbacusBio

- Tim Byrne
- Fiona Hely
- Anouk Schurink



- Karolina Kaseja
- Jo Conington
- Samir Id-Lahoucine
- Mike Coffey



Map of Ag

- Andrew Cooke
- Kim Saunders
- Amanda Anderton
- Daniel Buchanan
- Various developers and designers



A question...

- A change to the usual approach where I answer questions
- An attempt at interaction...
- What does the audience now think...

A question...

- A change to the usual approach where I answer questions
- An attempt at interaction...
- What does this mean?

Should genomic evaluations be adopted for use with all pedigree breeds?

- If yes, what is the main benefit?
- Improved performance figures
 - Improved confidence in pedigree

A question...

- A change to the usual approach where I answer questions
- An attempt at interaction...
- What does this mean?

Should genomic evaluations be adopted for use with all pedigree breeds?

How will individual breeds affordably maintain / increase phenotyping of commercially relevant valuable traits?

- Improved performance
- Improved confidence in pedigree



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