Genomics 101:
Building for the Future

Ron Lewis
Animal Science, University of Nebraska-Lincoln
NSIP Technical Advisor

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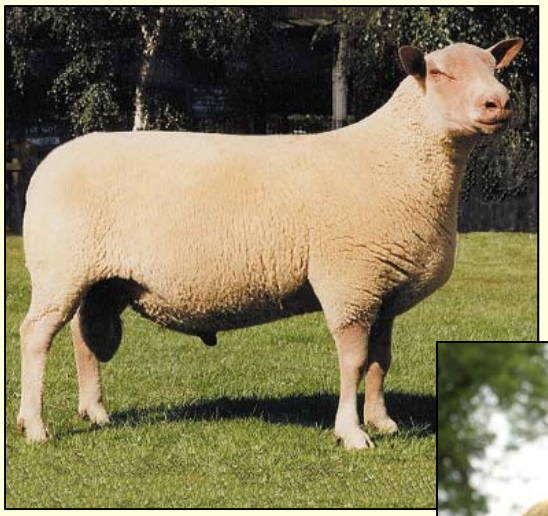
NSIP
National Sheep Improvement PROGRAM

Grateful to sponsors

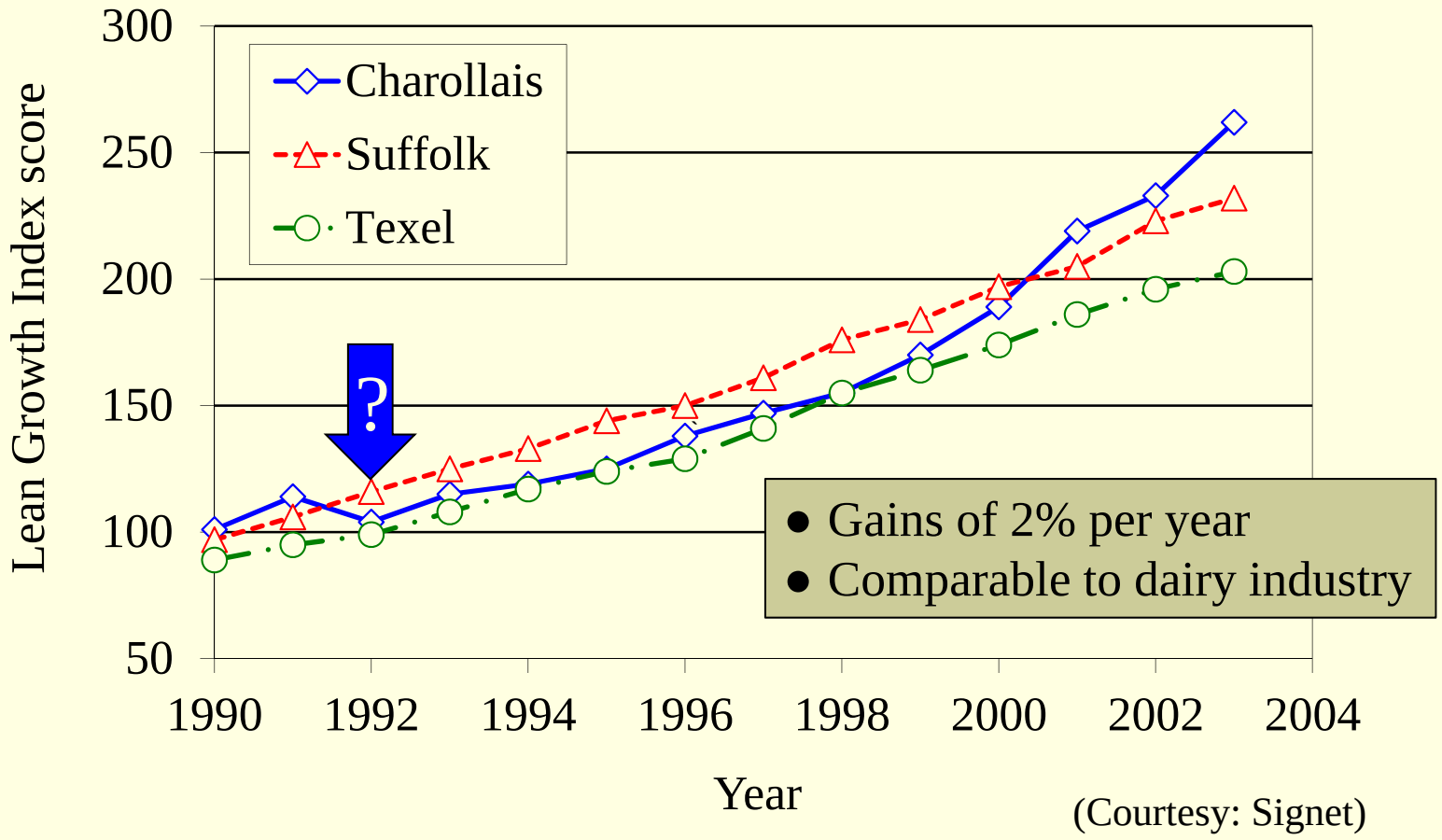
United Kingdom industry example

- Terminal sire breeds



United Kingdom industry example

- Gains in industry schemes



(Courtesy: Signet)

U.S. industry example (Leading Edge)

Category	Weight EPD (lb.)†		Progeny weaning weight (lb.)§
	Weaning‡	Post-weaning‡	
Weight	4.6	9.2	108.6
Muscle	1.9	4.2	104.1
Difference	2.6	5.0	4.5

† EPD from July 2019, weighted by the number of lambs with a wean weight from each ram.

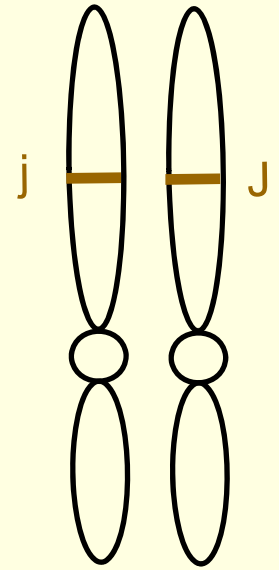
‡ Weaning and post-weaning weights recorded at 45 to 90 and 90 to 150 days, respectively.

§ At, on average, 161 days of age.

Major genes

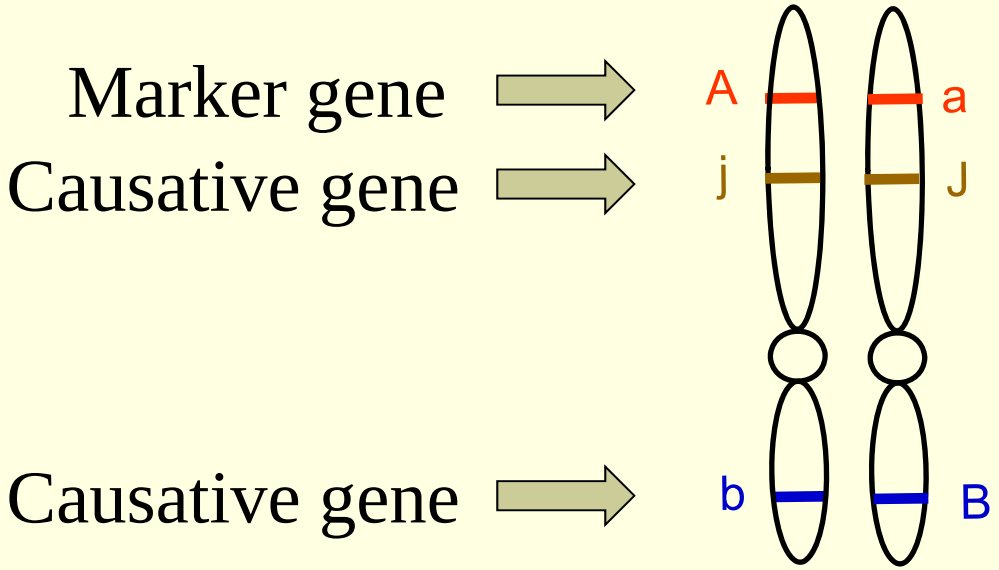
- A genes with a pronounced effect on performance

Causative gene



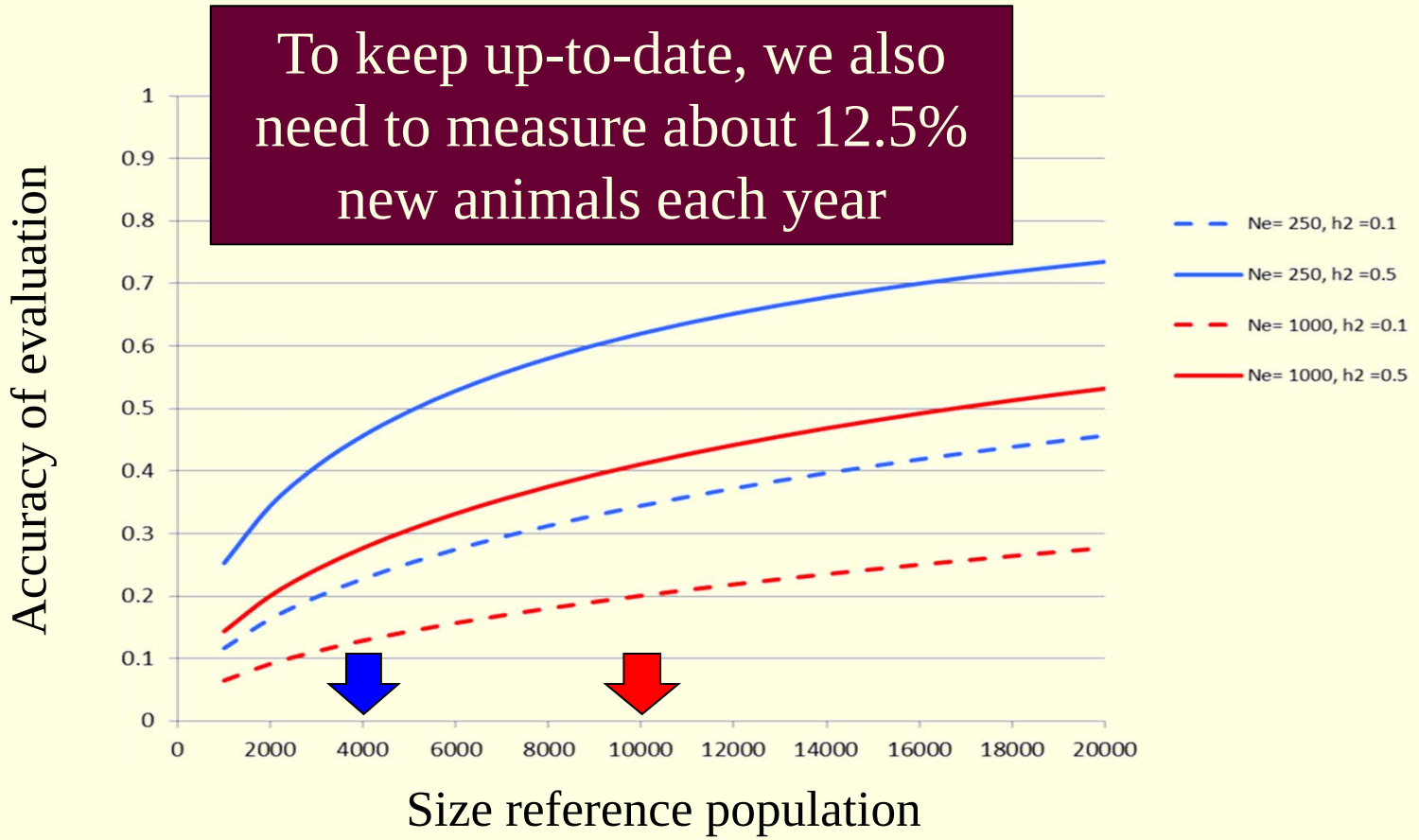
Genetic markers

- A detectable gene at one location on the chromosome used to mark a causative gene at a nearby location



Reference populations

To keep up-to-date, we also need to measure about 12.5% new animals each year



(Goddard, 2009; Hayes et al., 2009; van der Werf et al., 2011)

Applications

- Parentage
- Genetic conditions
- Genomic selection
- Delineating breeds

Parentage

- Challenges in recording pedigree information
  - Particularly in multiple-sire and extensive systems
- Parentage panel
  - With a limited number of markers, can reliably assign parentage (Heaton et al., 2014)

Parentage (sire)

- Typically 163 genetic markers on parentage panel
- Assignments based on exclusion of sires
  - Key that full suite of potential sires are included

Animal	Marker 1	Marker 2	Marker 3
Lamb	AB	AA	BB
Sire 1	BB ✓	AA ✓	AB ✓
Sire 2	AA ✓	AB ✓	~~A~~A ✗

Parentage (Leading Edge)

- Leading Edge Project
  - 42 Suffolk rams mob mated to 1,100 commercial white-faced ewes
- Among 1,457 lambs with a tissue (DNA) sample, 92% aligned with a sire
  - Nearly all losses were lab based

Genetic conditions

- For some traits of economic interest, genes with major causative effects have been identified
- Examples
  - Fecundity (Demars et al., 2013; Martin et al., 2014)
  - Mastitis susceptibility (Rupp et al., 2015)
  - Myostatin (Clop et al., 2006)
  - OPP virus resistance (Heaton et al., 2012)
  - Scrapie resistance (Elsen et al., 1999; Barillet et al., 2009)
  - Spider syndrome (Cockett et al., 1999; Beever et al., 2006)

Genetic conditions

- For some traits of economic interest, genes with major causative effects have been identified
- Still, such major genes are comparatively rare
  - Traits of interest have proven to be more complex than anticipated
  - Most traits are influenced by thousands of genes, each gene having a small effect

Needed a broader approach

(Meuwissen, Hayes and Goddard, 2001)

Genomic selection

- Each marker typically explains a small proportion (< 1%) of genetic variation in a trait
- Genome-Enhanced Breeding Values (GEBV) are predicted from the sum of the effects of all markers across the entire genome
- As an outcome, GEBV can more accurately indicate an animal's true genetic merit

Predictions are based on associations between markers and actual performance for traits of interest

Genomic selection (accuracy)

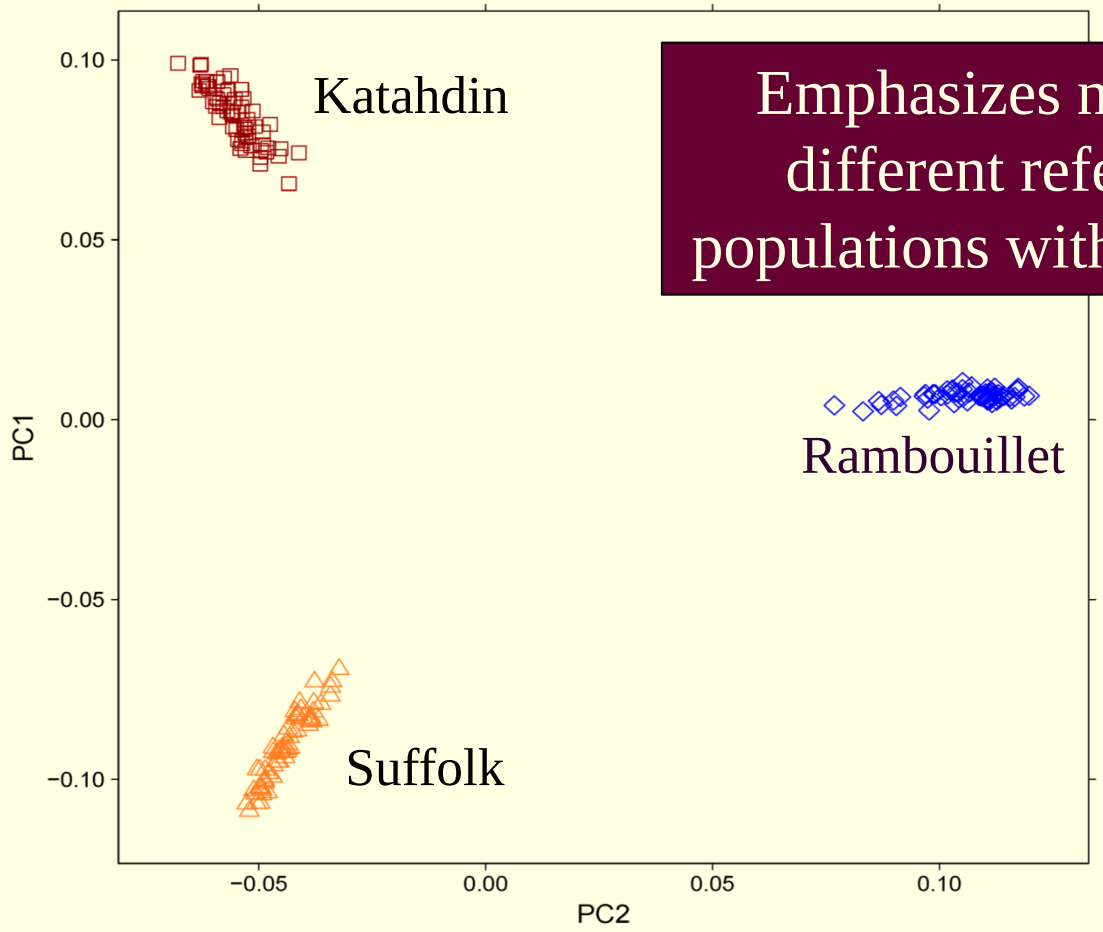
Traits	Gain in accuracy	Location	Reference
Carcass, meat quality	5 – 10%	Australia	Daetwyler et al., 2012
Meat, fleece, litter size	5 – 27%	New Zealand	Auvray et al., 2014
Milk production	10 – 20%	France	Baloche et al., 2014

Gain in accuracy closely tied to the amount of genomic and performance information available

Delineating breeds

- 64 sheep in each of 3 breeds genotyped
  - Katahdin, Rambouillet, Suffolk
- Chosen to reflect the diversity in each breed
  - Primarily rams
  - National Sheep Improvement Program (NSIP) records on themselves and on at least five progeny

Delineating breeds



Emphasizes need for different reference populations within breeds

Products

- Targeted panels
- Arrays
- Whole genome sequence

Products (panels)

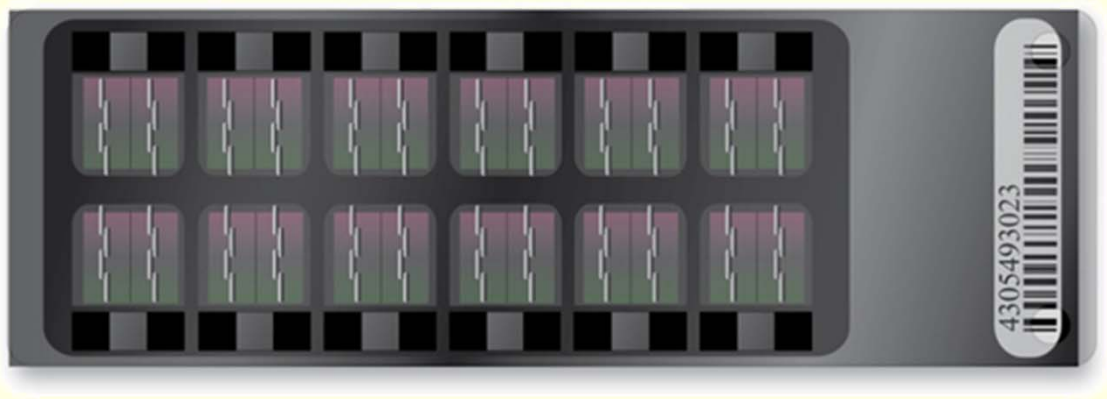
- Targeted panels (<2K markers)
  - Parentage; major genes

Products (low density)

- Targeted panels (<2K markers)
- Low density array (15K markers)
  - Parentage; major genes; towards genomic selection

Products (medium density)

- Targeted panels (<2K markers)
- Low density array (15K markers)
- Medium density array (50K markers)
  - Parentages, major genes; genomic selection; towards causative gene discovery



Products (high density)

- Targeted panels (<2K markers)
- Low density array (15K markers)
- Medium density array (50K markers)
- High density array (600K markers)
  - Parentages, major genes; genomic selection; causative gene discovery

Products (sequence)

- Targeted panels (<2K markers)
- Low density array (15K markers)
- Medium density array (50K markers)
- High density array (600K markers)
- Whole genome sequence
  - The “Full Monty”

Products (used)

Location	Number of markers			
	<2K	15K	50K	600K
AU/NZ	54,657	16,721	584	194
U.S.‡	3,185	387	968	1,100
Europe	131	3,593	687	720

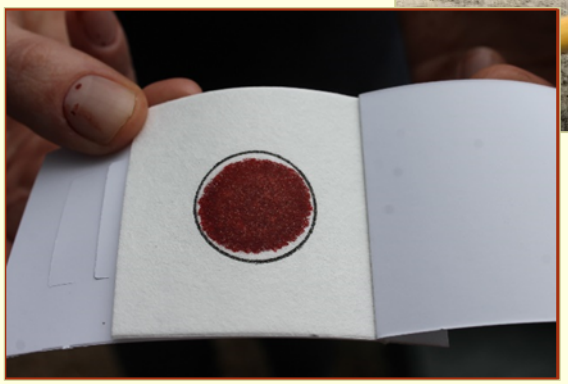
‡Mostly from research groups

Ahead?

- Routine sampling
- Tackling difficult-to-measure traits
- Working together

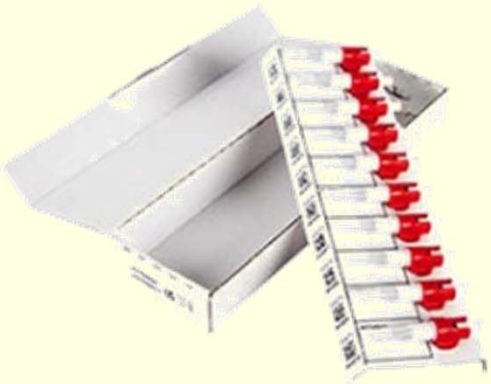
Routine sampling

- Routinely collecting DNA samples



Routine sampling

- Routinely collecting DNA samples



Tackling difficult-to-measure traits

- Greatest opportunity with genomics is in tackling difficult-to-measure traits

Tackling difficult-to-measure traits

- Traits expressed later in an animal's life
  - Longevity
- Traits expressed in only one sex
  - Fertility, litter size, mastitis
- Traits that are expensive and/or challenging to measure
  - Lamb survival, maternal bonding, aseasonality
  - Carcass & eating quality
  - Feed efficiency
  - Methane emissions?

Working together

- Incorporating genomics into the U.S. sheep industry can only be achieved together
- It will entail
  - Widespread performance recording
  - Extensive sample collection and genotyping
  - Integrating that information into a genetic evaluation system to everyone's advantage
- It is a long term commitment

...yet all signs are it is worth it!

Thank you for listening

Questions?