# A journey: opportunities & challenges of melding genomics into U.S. sheep breeding programs

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# My talk

- Genomics road trip
  - Map
  - Major genes
  - Genetic markers
  - Genome-enhanced BV
- Bumps along the road
  - Reference populations
  - Costs
- Reflecting on the trip
  - Key equation
  - A better pedigree
  - Improving hard-to-measure traits
- Starting a new trip
  - Who to visit
  - Sharing the road

# A road map


SOUTH DAKOTA
WYOMING
NEBRASKA
IOWA
COLORADO
KANSAS
MO
Missouri R.
Spencer
Yankton
Vermillion
Chadron
Valentine
Fort Robinson State Park
Niobrara/Missouri National Riverways
Ashfall Fossil Beds St. Hist. Park
Agate Fossil Beds Nat. Mon.
O'Neill
Sioux City
South Sioux City
Wayne
Alliance
Norfolk
Scottsbluff
Gering
Scotts Bluff Nat. Mon.
Chimney Rock Nat. Hist. Site
Columbus
Fremont
Blair
Omaha
Council Bluffs
Boys Town
Papillion
Bellevue
Plattsmouth
Loup R.
Platte R.
L. McConaughy
Sidney
Ogallala
North Platte
Grand Island
Seward
York
Lincoln
Crete
Lexington
Kearney
Fort Kearney St. Hist. Park
Hastings
Minden
Holdrege
Sterling
Nebraska City
Homestead Nat. Mon. of America
Beatrice
McCook
Republican R.
Atchison
0 20 40 60 80
Miles
World Sites Atlas (sitesatlas.com)

# A road map

UNL campuses?

Need a more detailed map

# A road map

Animal Science Complex?

I still have not found my office …

… but I am much closer than I was before!

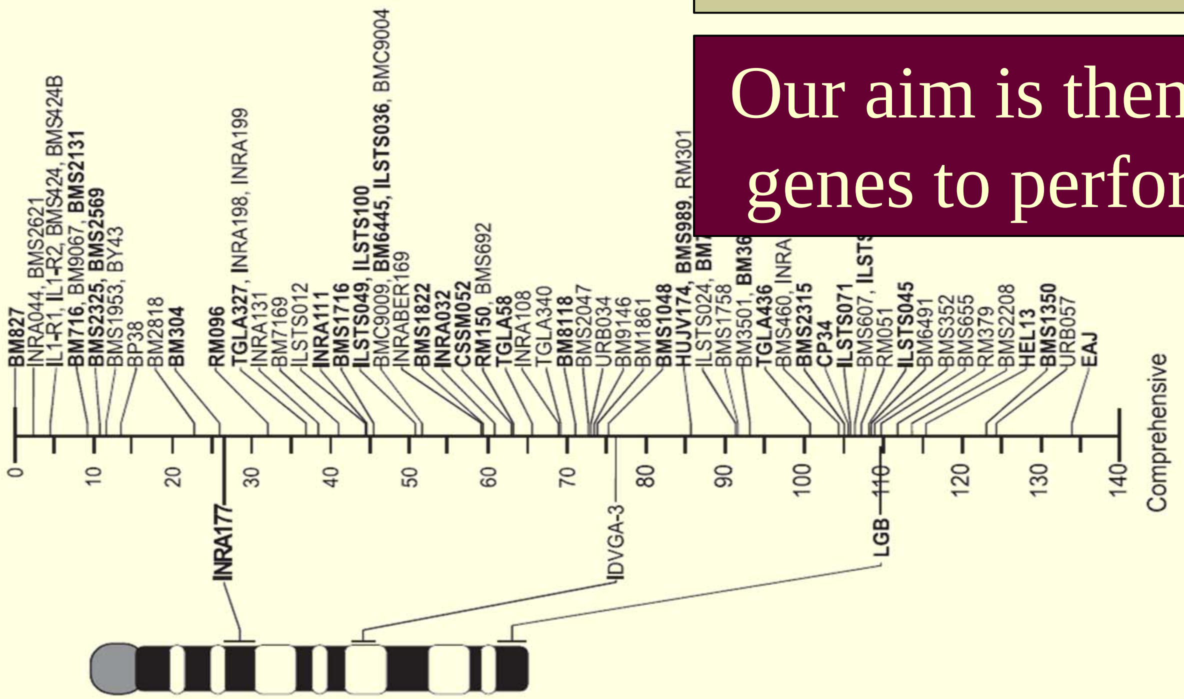
Need an even more detailed map

# A chromosomal road map

- A map locating positions of genes at loci along a chromosome

With a more detailed map, we locate more, although not all, genes

Our aim is then to link genes to performance



# Major genes

- For some traits of economic interest, we have found genes with major causative effects
- Examples
  - Fecundity (Demars et al., 2013; Martin et al., 2014)
  - Mastitis susceptibility (Rupp et al., 2015)
  - Muscling (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)

# Major genes

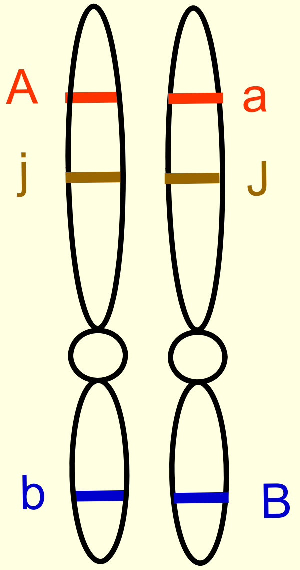
- For some traits of economic interest, we have found genes with major causative effects
- Yet major genes are comparatively rare
  - Traits of interest have proven to be more complex than anticipated
  - Most traits are influenced by thousands of genes, each gene having a small effect

Needed a broader approach

(Meuwissen, Hayes and Goddard, 2001)

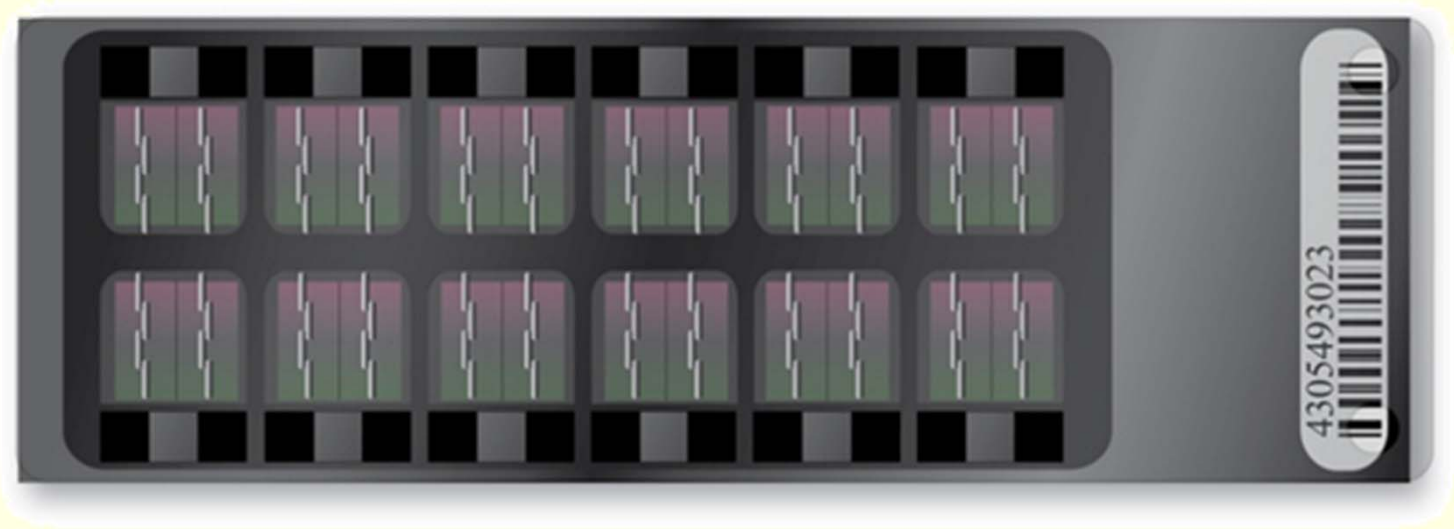
# Genetic markers

- A detectable gene at one location on the chromosome is used to mark a causative gene at a nearby location
- When the locations are physically closer, there is less opportunity for recombination, making markers more informative



# Illumina OvineSNP50 Beadchip

- Provides 54,241 evenly spaced markers across the sheep genome (chromosomes)



# Genome-enhanced breeding values

- 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

# Gain in 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 |

The extent of gain in accuracy is closely tied to the amount of available genomic and performance information

# Reflecting on the trip

- Key equation
- A better pedigree
- Improving hard-to-measure traits

# Key equation

- Key equation

$$\Delta BV_X/_t = \frac{r_{BV_X, P_X^*}(i_X)\sigma_{BV_X}}{L}$$

- Genomic tools allow
  - Increased accuracy (⇧ $r_{BV_X, P_X^*}$)
    - Because of GEBV
  - Decreased generation interval (⇩ $L$)

# Form a better pedigree

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

Increases accuracy

# Improve 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?

Increases accuracy & decreases generation interval

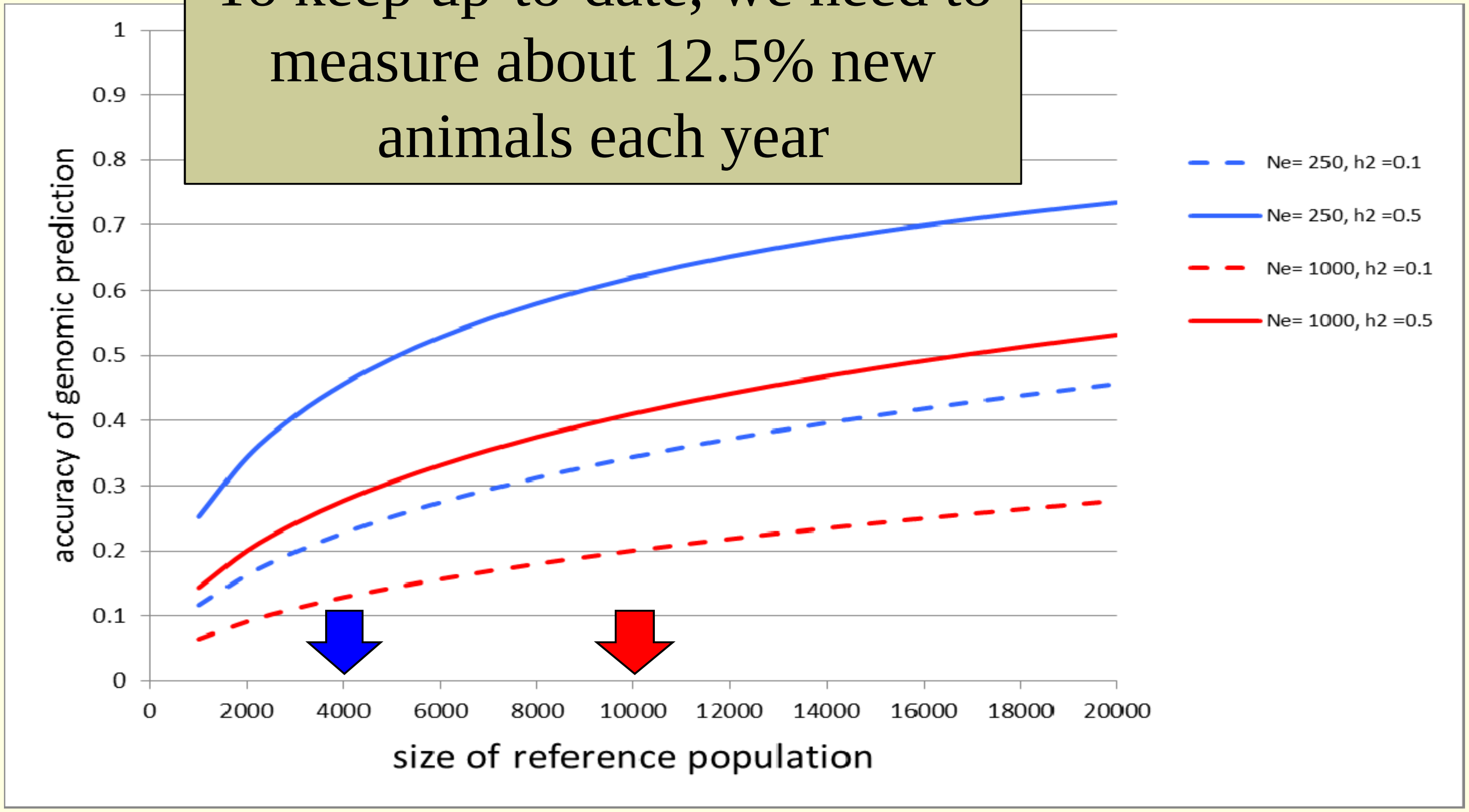
# Bumps along the road

- Reference populations
- Costs

# Reference populations

- Accuracy of GEBV depends on availability of substantial genomic and performance information
- Requires large reference populations in individual breeds
    - “Large” to capture genetic diversity within a breed
    - “Within breeds” because genomic predictions do not extend well across breeds
        - We have lots of breeds
    - Validation (training) must be ongoing
        - Accuracies deteriorate as ancestors used to form genomic predictions become more distant

# Reference populations



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

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

# Costs of genotyping

- Value of an animal is relatively low in sheep
  - Yet, per animal, cost of genotyping is nearly the same across species
  - Hopefully costs will continue to fall

# Costs of genotyping

- Need to consider alternative strategies
  - Higher density (more detailed) genotyping of key sires
  - Lower density genotyping of others with imputation
    - Younger animals
    - Mature ewes with good phenotypic data
  - Parental panel with key major genes

# Starting a new trip

- Who to visit
- Sharing the road

# Who to visit

- Let’s Grow funding
  - “Engaging the New Biology: establishing the foundation for genome-enhanced breeding values in the U.S. sheep industry”
- Objective one
  - Provide producer education on genomic tools
- Objective two
  - Devise efficient strategies to collect genomic data

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# Who to visit

- Sampling strategies
  - Four approaches will be considered, including the closeness of genetic relationships
- Samples collected
  - Blood cards
  - On 1,000 Suffolk & 1,000 Rambouillet NSIP recorded sheep
- Intended outcome
  - A reservoir of genomic samples on performance recorded sheep as the first step toward establishing reference populations

# Sharing the road

- Incorporating genomics into the U.S. sheep industry will necessitate
    - Extensive performance recording
    - Strategic genotyping
    - Substantial costs
        - Both in dollars and in enthusiasm
- It can only be achieved together

# Thanks for listening

- I appreciate the invitation to present this webinar, and support from ASI and the Let's Grow committee

Questions?

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