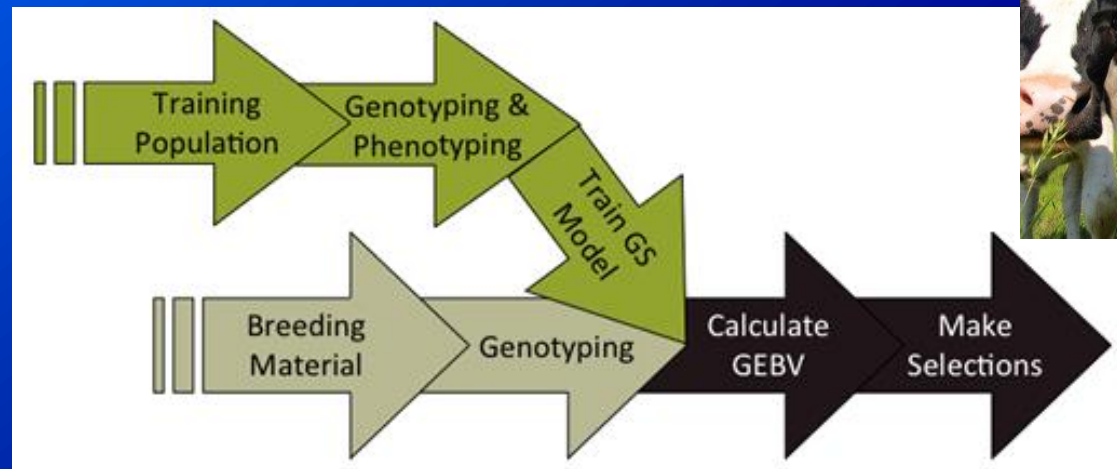


Genomic Selection



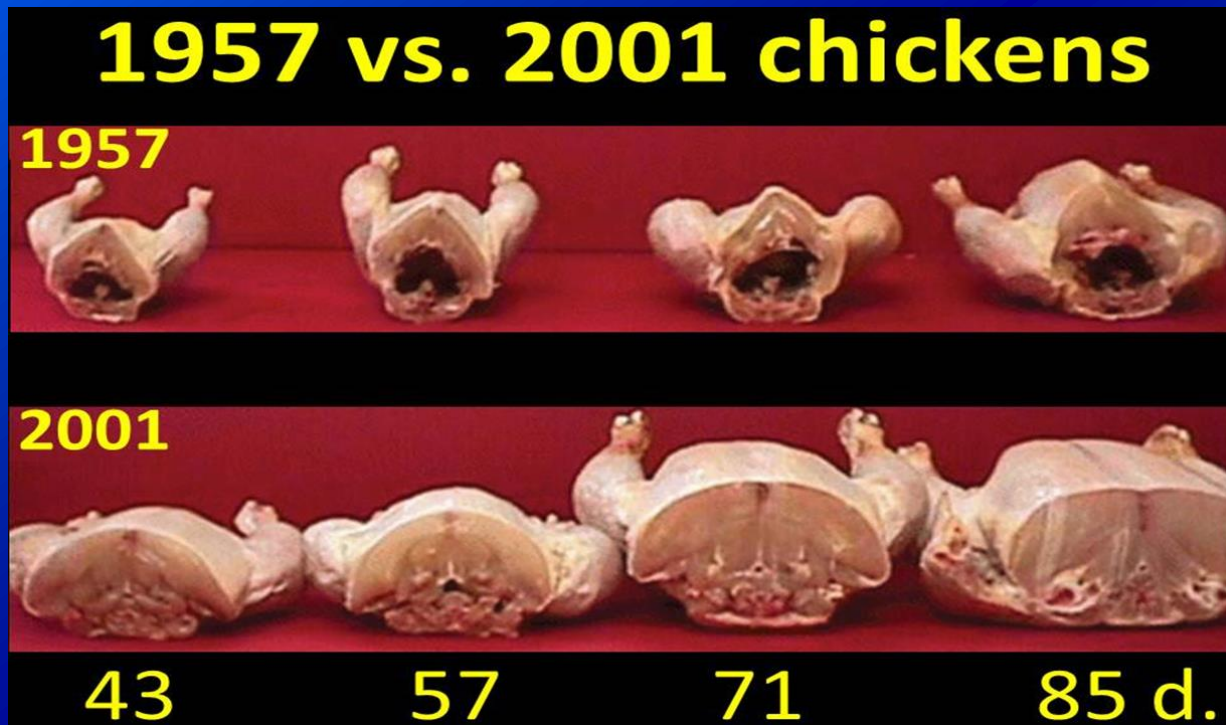
Eric Hallerman
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Virginia Polytechnic Institute and State University
Blacksburg, VA 24061, USA
540-231-3257 ehallerm@vt.edu

Animal breeders have used selection on phenotypes to great effect



Breeding based on objective performance recording has been spectacularly successful.....

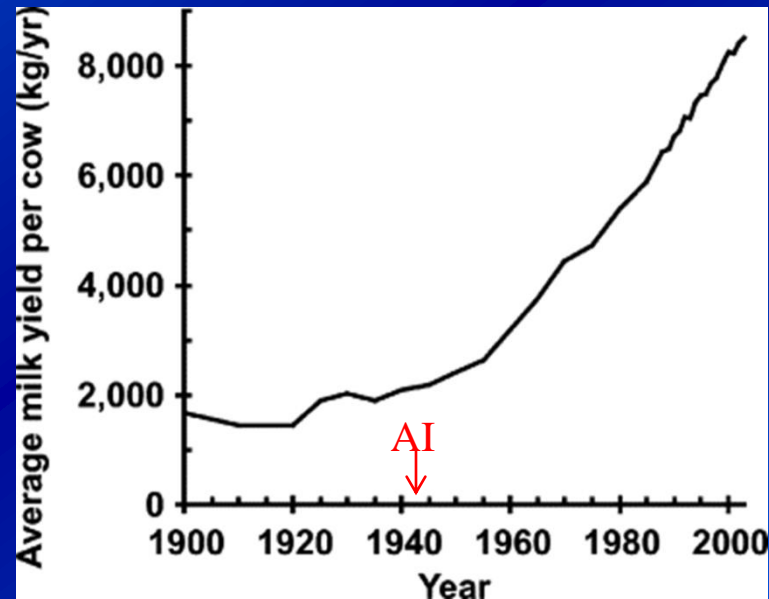
- Havenstein et al. (2003) quantified improvement of growth, livability, and feed conversion of 1957 versus 2001 broilers when fed representative 1957 and 2001 broiler diets (Poultry Science 82:1500-1508).



Chickens reach
market age in
less than half
the time

Improvement
due to diet
about 14%;
due to genetic
improvement
about 428%

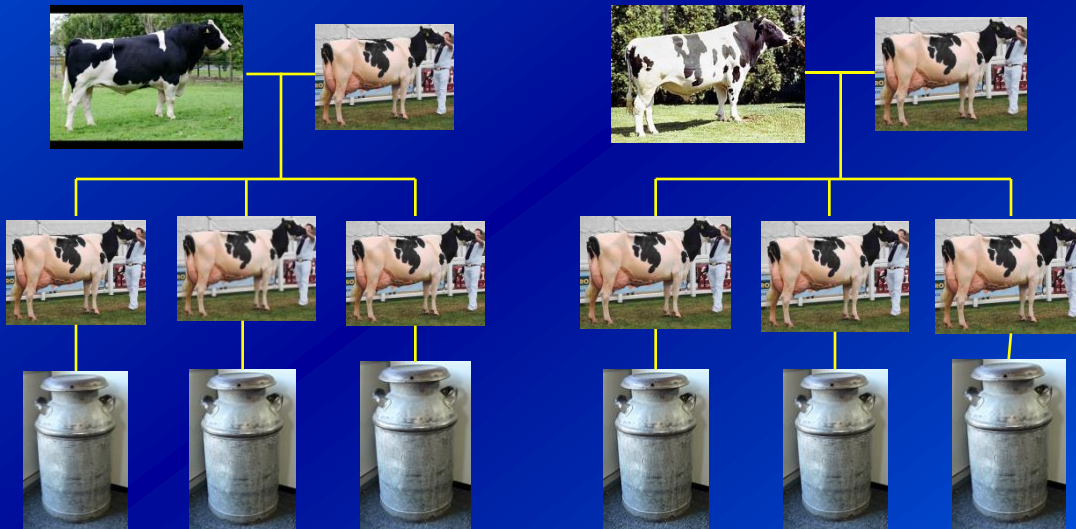
Breeding based on objective performance recording has been spectacularly successful.....



- A 369% increase in production efficiency
- About half is attributable to genetic improvement, dissemination of which is enabled by artificial insemination (AI)
- VandeHaar, M.J. and St-Pierre, N. (2006). Major advances in nutrition: Relevance to the sustainability of the dairy industry. *Journal of Dairy Science* 89, 1280-1291.

Progeny testing in dairy cattle

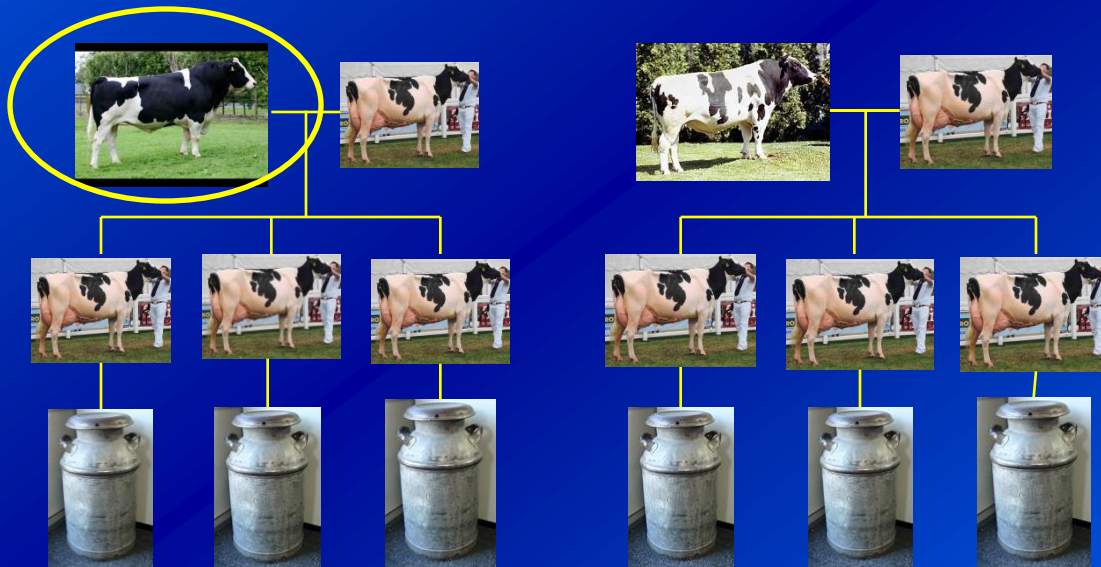
- The success of AI is built upon an *existing* system of genetic improvement. *Let's consider that for dairy cattle...*
- Milk production is a trait expressed by *females*...but we can impose greater selection pressure on *males*
- → Program of *progeny testing* (the “daughter design”)



- Sons of proven sires and elite dams = *candidate bulls*
- *Progeny testing* – each candidate is bred with ~300 heifers, and the milk yield of each daughter is recorded

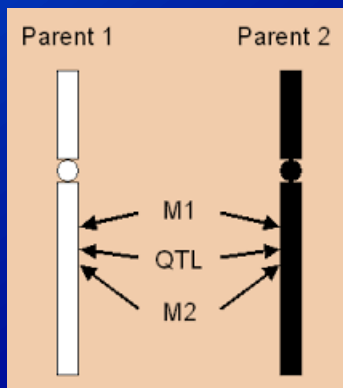
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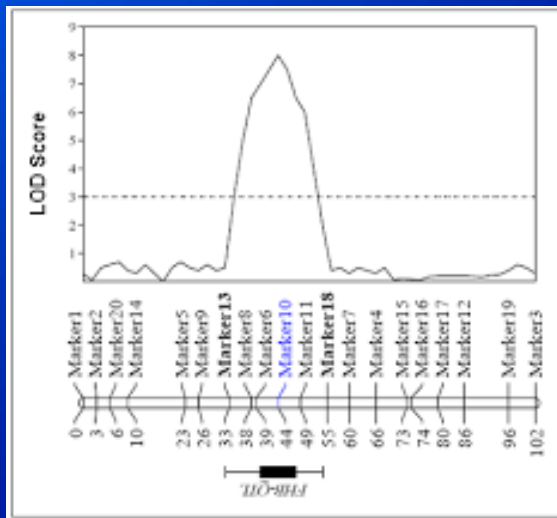
- Sons of proven sires and elite dams = *candidate bulls*
- *Progeny testing* – each candidate is bred with ~300 heifers and the milk yield of each daughter is recorded
- Those bulls producing the highest-yield daughters are selected as *proven bulls*
- *Effective, expensive, time-consuming*

- Progeny testing programs are expensive – *how can we make them most cost-effective?*
- There are *many* potential progeny testing candidates
- **Can we *pre-select* progeny testing candidates and improve rate of gain** (Soller and Beckmann 1984)?
- *Can we use genetic markers for this purpose?*
- First, we'd have to link them to performance-enhancing alleles. *Here's how:*



- Saturate the genome with genetic markers
- With statistics, test the associations of markers with performance
- If you get a significant test result, you conclude that markers (*M1* and *M2*) are *linked* to a quantitative trait locus (QTL)
- You can select for the marker allele(s) → *marker-assisted selection* (MAS)

- 1990s:
- Development of *genetic linkage maps* for agricultural animals
→ more *efficient* QTL interval mapping

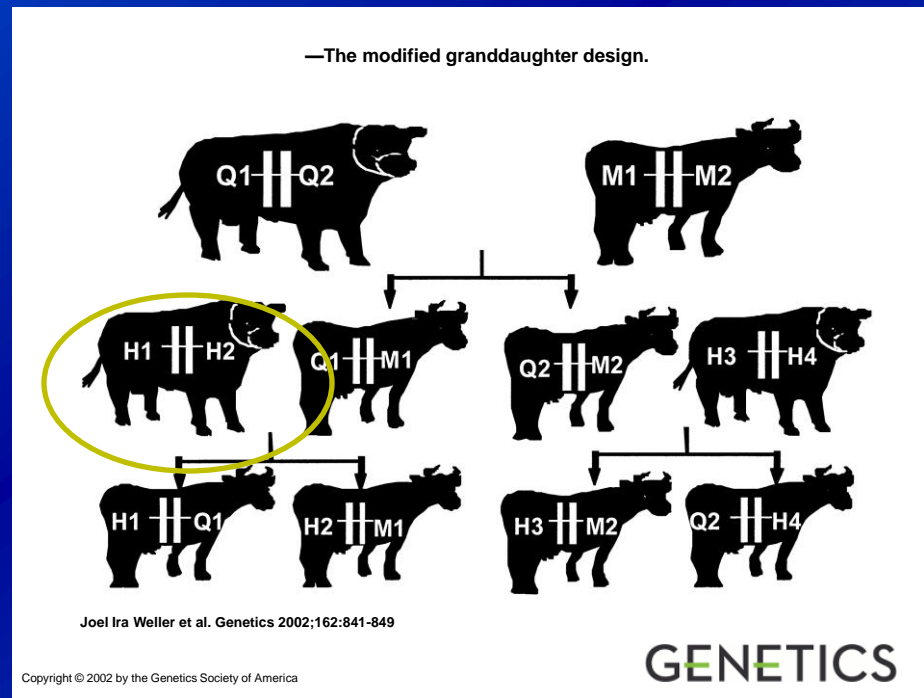


← Significance of linkage of a trait with marker, in this case, using log-odds ratio

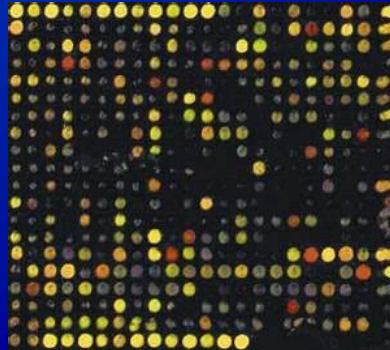
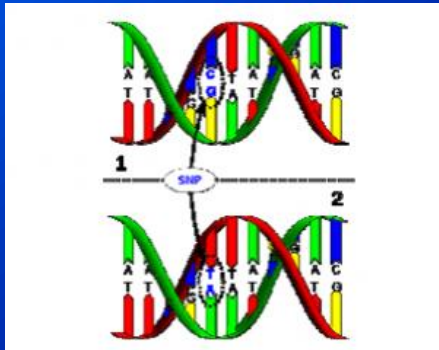
← *Linkage map* for a chromosome, an ordered listing of genetic markers

- Development of conceptual models of how best to *incorporate* MAS into conventional performance-based animal breeding

- Using old-style genetic markers, note that by the time you complete the performance evaluation and genotyping, you actually be evaluating granddaughters and applying the findings to select grandsons of that elite sire!





- **2000s and 2010s** – Development of single nucleotide polymorphisms (SNPs), SNP chips, chip scanning platforms, and whole genome sequences → cost-effective screening of (tens of) thousands of SNPs of known genomic location



Illumina genotyping arrays

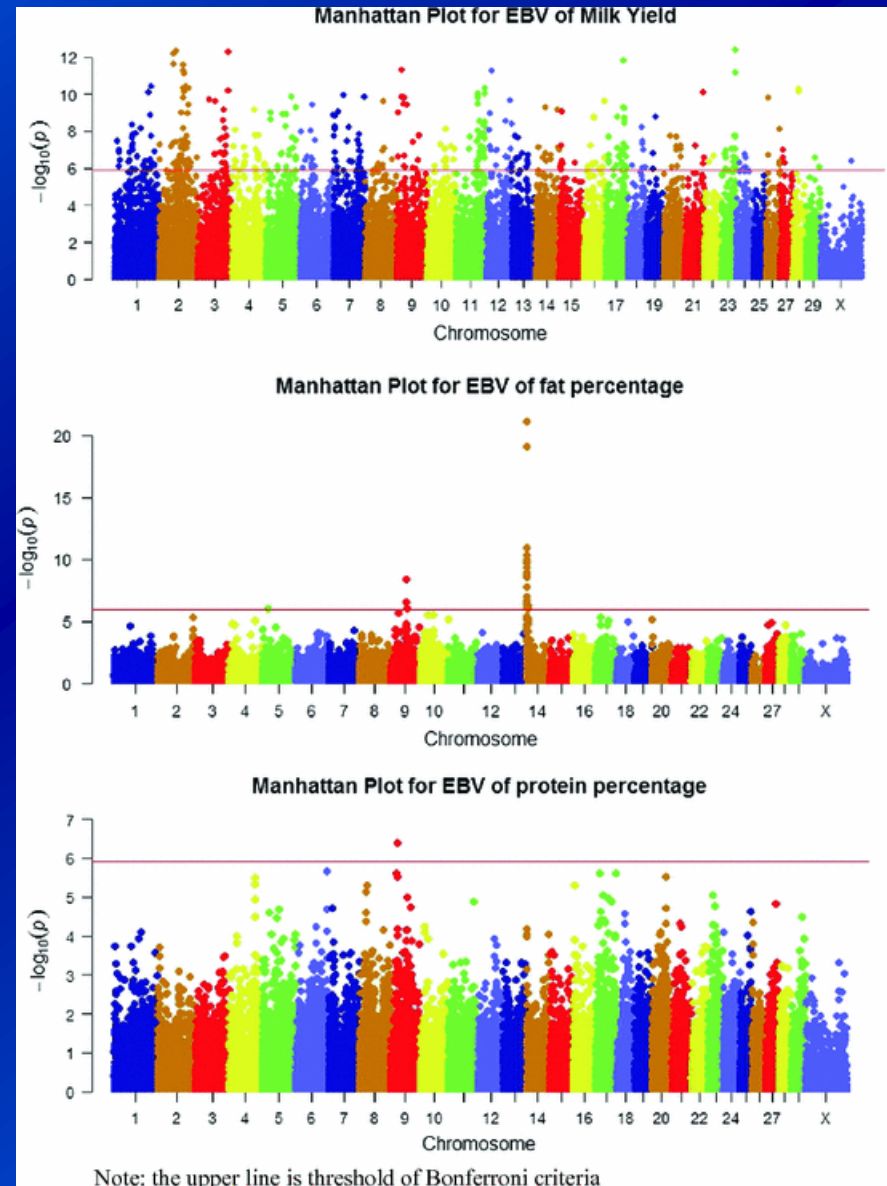
- **BovineSNP50**
 - 54,001 SNPs (version 1)
 - 54,609 SNPs (version 2)
- **BovineHD**
 - 777,962 SNPs
- **BovineLD**
 - 6,909 SNPs
 - Allows for additional SNPs (e.g., GeneSeek Genomic Profiler)

15th NAC-QTL Workshop, Athens, Italy, 31 May 2012 (2)

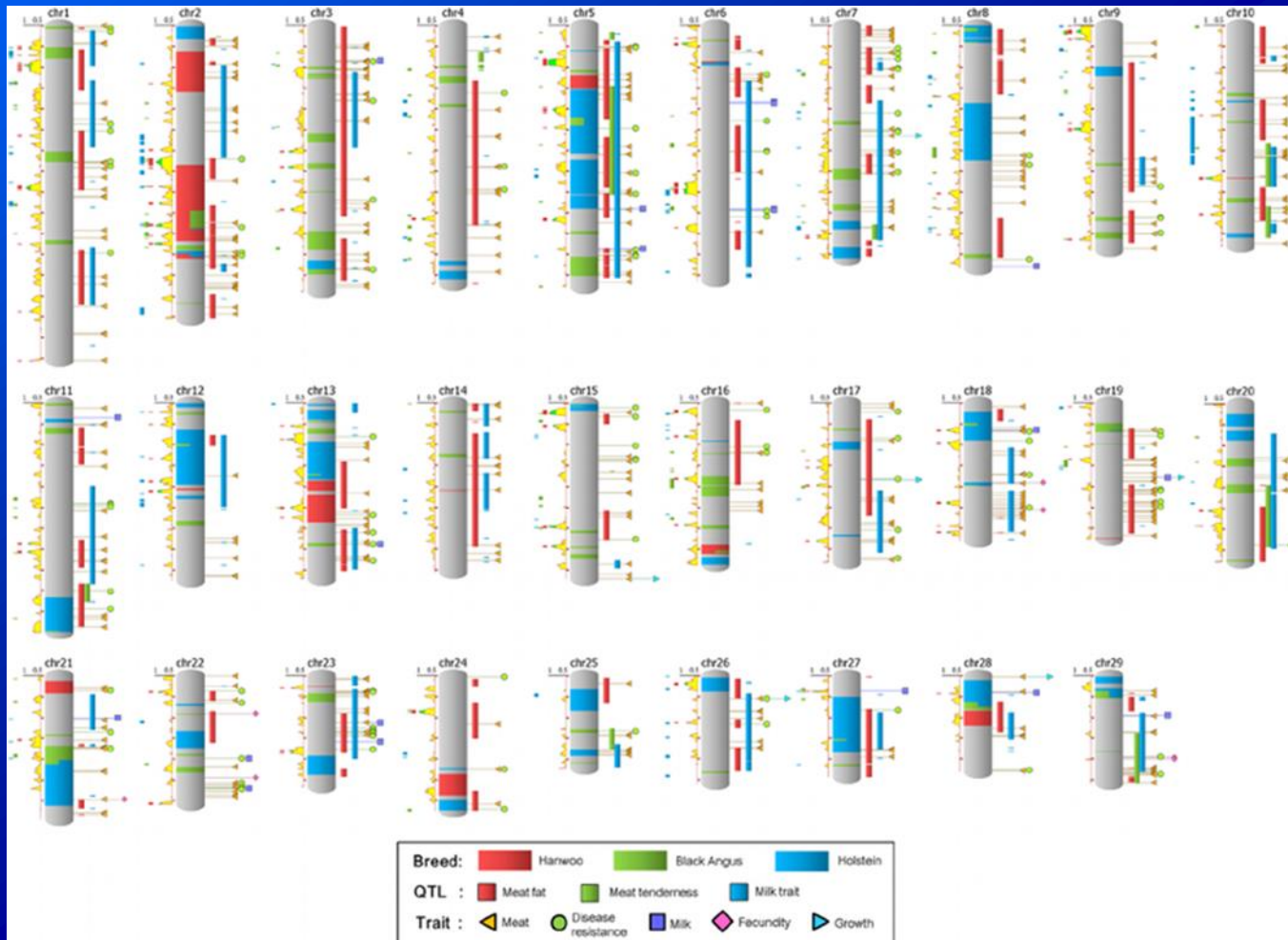


This technology makes screening rapid and cost-effective

- → “Genome scan” for traits of interest
- Note significant associations for milk yield, fat content and protein content for Russian Holstein cattle (Sermiyagin et al. 2017)



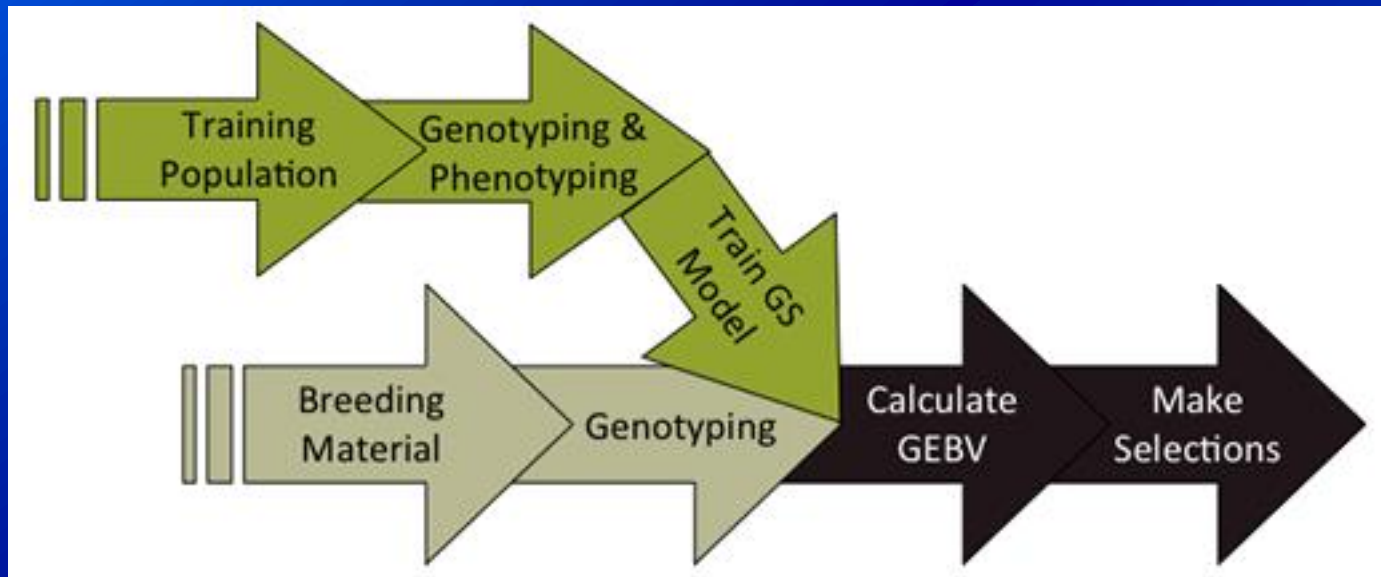
- These analyses can be integrated to show both milk- and meat-related traits, e.g., for Korean Hanwoo cattle (Lee et al. 2013)



→ Breeding value of each chromosome segment

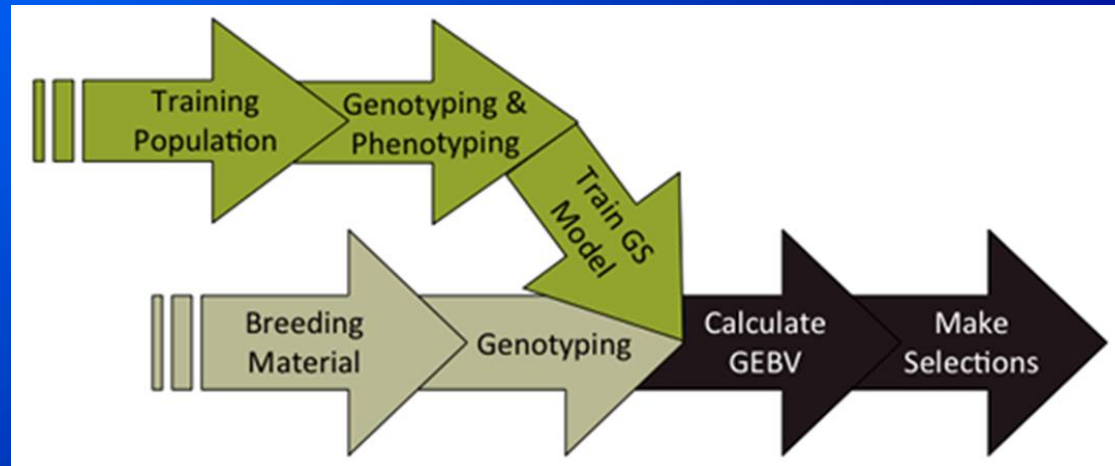
2010s – let's apply this approach for “genomic selection”

- Overview of the process...



- *Let's take this step by step...*

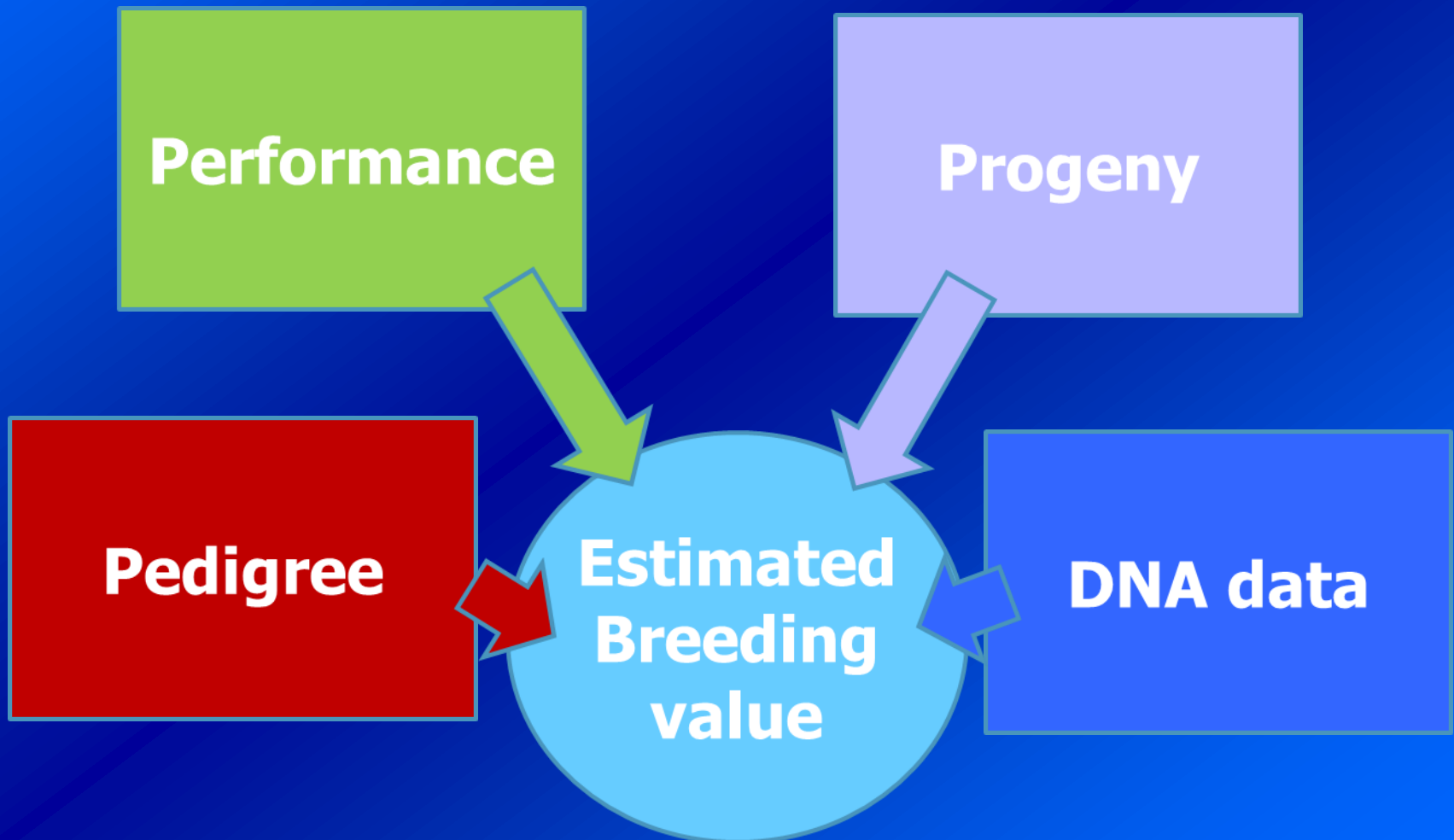
Breeding value prediction in dairy sires



- **Training population** – thousands of animals performance phenotypes and underlying genotypes
- **Training** – estimate the breeding value of every chromosome fragment contributing to performance
- **Prediction** – the results of this training can be used to develop prediction equations to predict the merit – the *genetic breeding value* – of new animals (young candidate bulls)

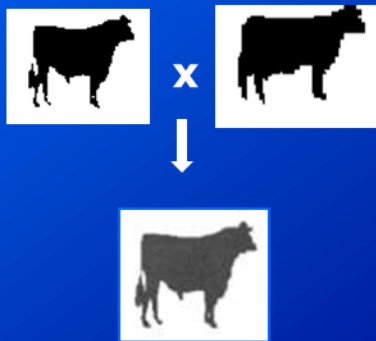
Information sources for estimated breeding value (EBV) genetic merit:

DNA is just *one* source of data

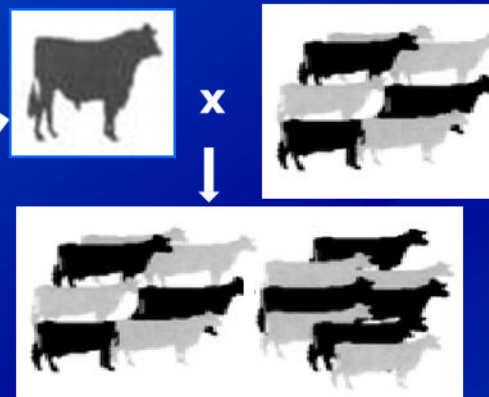


Let's compare methods for breeding value prediction in dairy sires

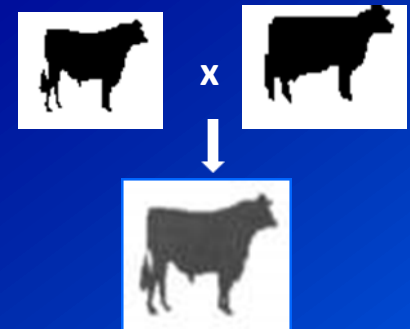
Young sire
Parent Average



Young sire
Progeny Test

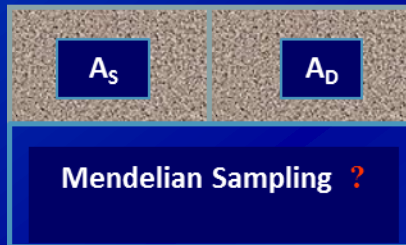


Young sire
Genomic
Selection

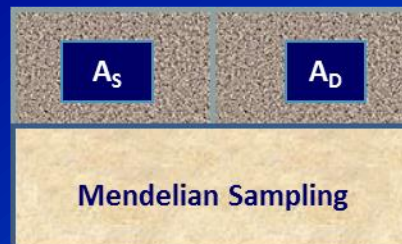


5 years; \$50,000 cost

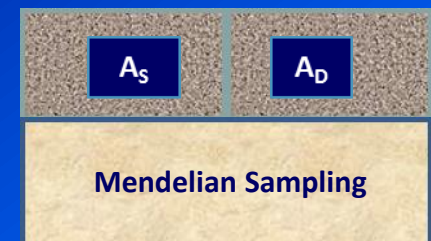
Birth; << \$50,000 cost



RELIABILITY **0.34**

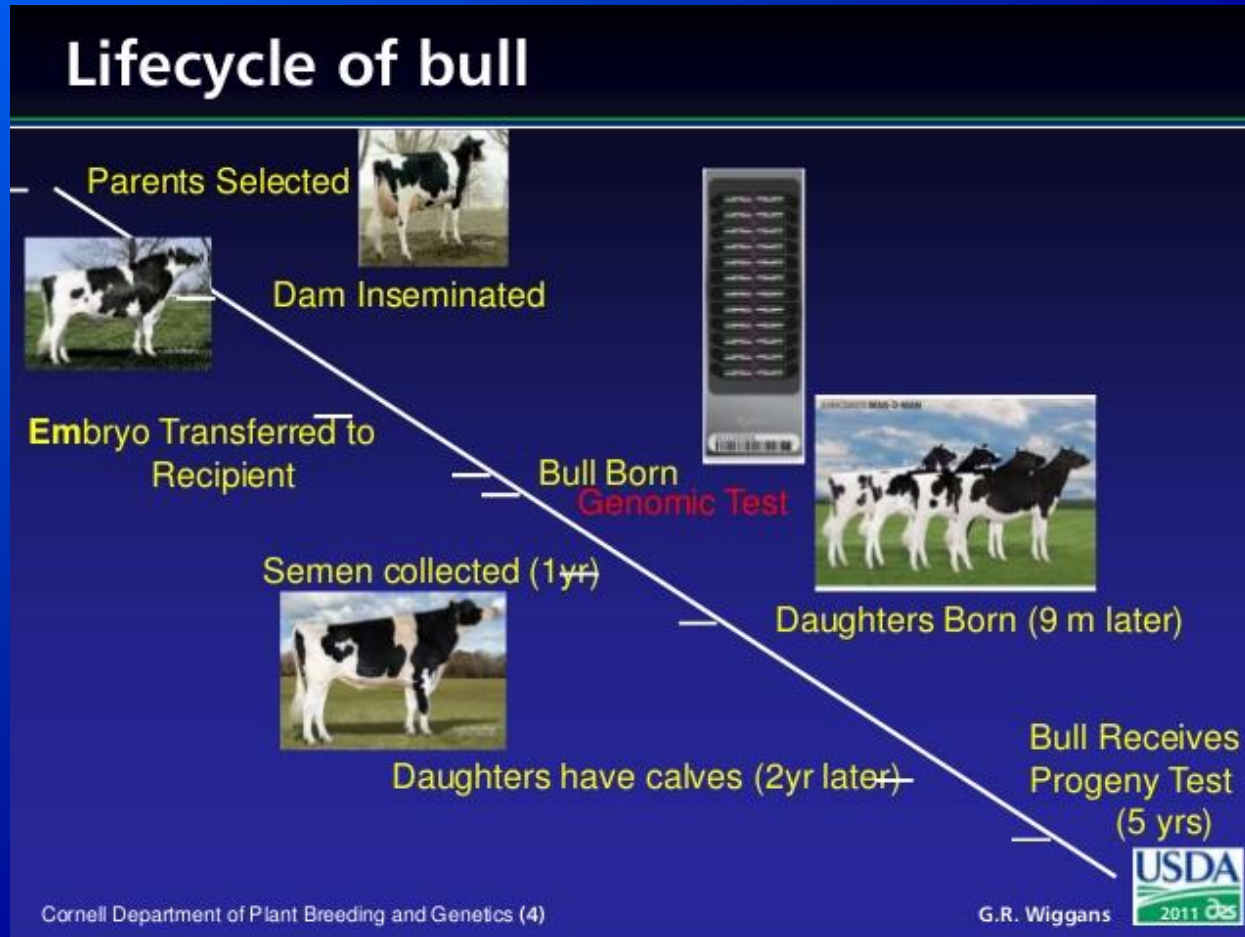


RELIABILITY **0.88**



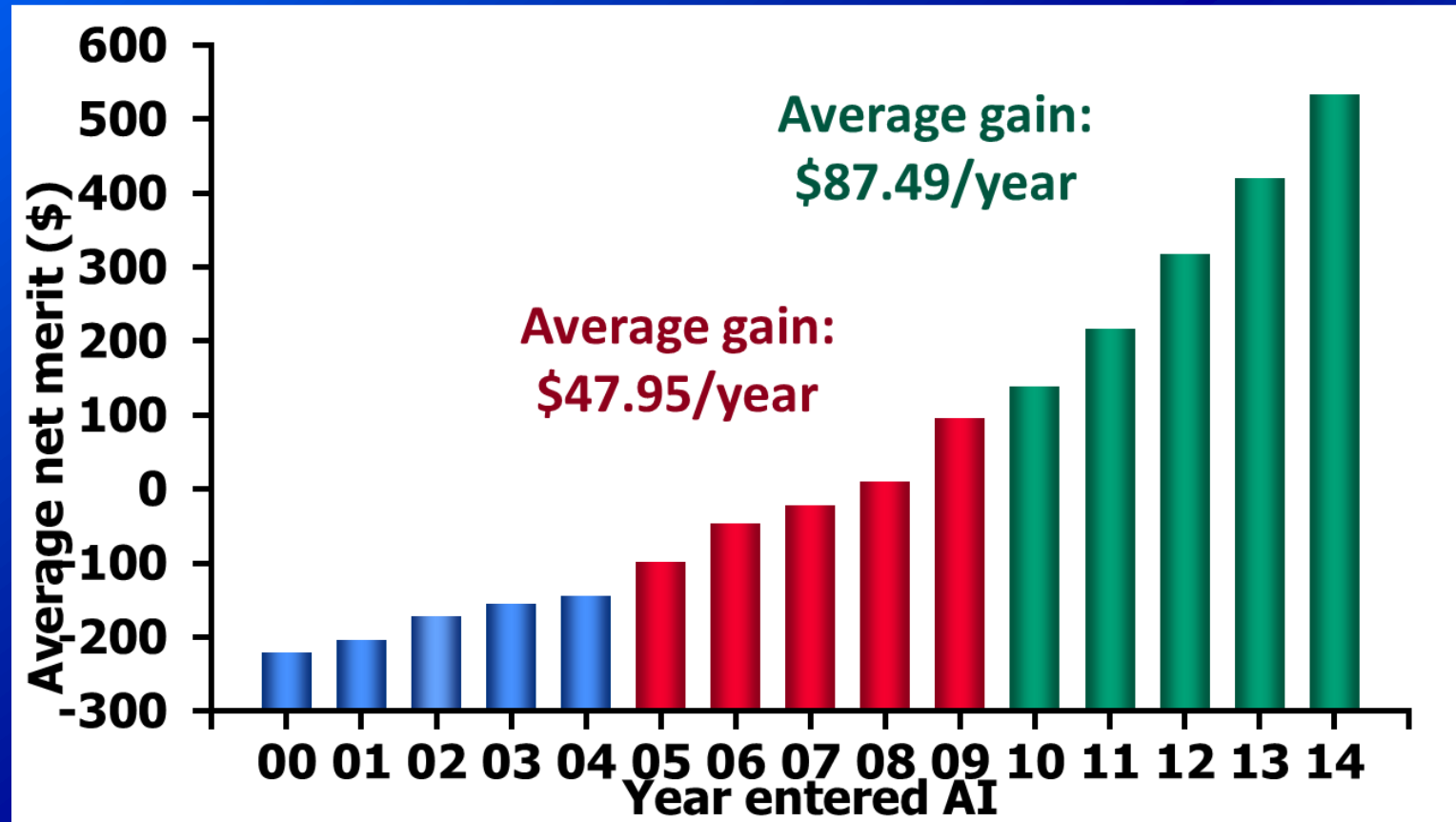
RELIABILITY **0.75**

Note that this approach decreases generation interval...



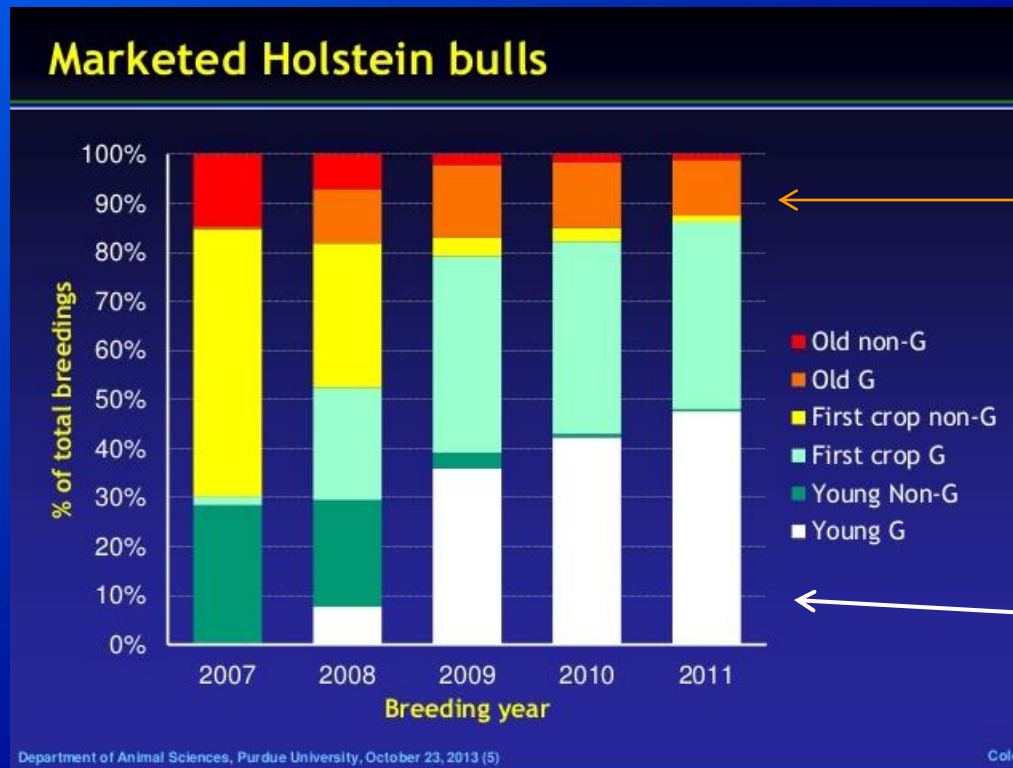
...and can increase rate of genetic gain

The rate of genetic gain in marketed Holstein bulls has *doubled* since introduction of genomic selection in 2009



George Wiggins, USDA-ARS (7/2015)

The rate of adoption of genomic selection has been rapid



Grand-daughter design

New design – drop the progeny testing

The dairy industry is well suited to genomic selection



- High use of artificial insemination
- Only one breed - Holstein
- Clear selection goal (total net merit)
- Large number of high-accuracy AI sires for training dataset
- Extensive, uniform collection of data on traits
- Central evaluation (USDA-Animal Improvement Programs Laboratory) receives genotypes
- Well established analyses and theory for increasing rate of genetic gain
- AI companies fund the genotyping because they realize cost savings in terms of young sire program

Records in U.S. dairy database

■ Pedigree records	71,974,045
■ Animal genotypes	1,035,590
■ Lactation records (<i>since 1960</i>)	132,629,200
■ Daily yield records (<i>since 1990</i>)	641,864,015
■ Reproduction event records	179,559,035
■ Calving difficulty scores	29,528,607
■ Stillbirth scores	19,567,198

The beef cattle industry is *not* well-suited

- Little use of artificial insemination
- Relatively few high-accuracy sires for the training dataset
- Multiple competing selection goals – cow/calf, feedlot, processor – little data-sharing between sectors
- Few/no records on many economically-relevant traits
- Many breeds, and some are small with limited resources
- Crossbreeding is important



We need to achieve some progress to adapt this approach to Africa...

- Regional breeding programs (ILRI, ...)
- Means for distributing improved lines (artificial insemination, whole animals – esp. males)
- System for reporting
- Performance back to breeding nucleus
- Database – performance, genetic linkage of markers to traits
- Need to define roles for NGOs, universities, private sector
- *A large, but do-able challenge... (EH)*

