

**Genomics Approaches
to Improve Economic Traits**

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What is Genomics

Goal: learn about structure, function, and evolution of all genomes, past and present

Genetics: science of inheritance, with clearly defined branches.

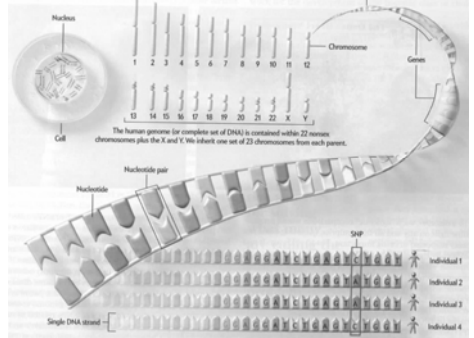
Genomics: combines all branches of genetics:

- Cytogenetics
- Molecular genetics
- Classical (Mendelian, qualitative) genetics
- Quantitative genetics
- Population genetics

Areas of Genomics

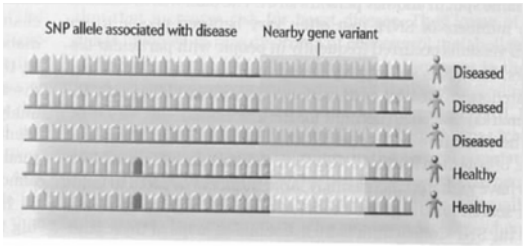
- **Classical Genomics**
Created to manage huge amount of new information resulting from advances in genomics
- **Physical Genomics**
Physical composition of genome
- **Statistical Genomics**
Statistical and computing methods developed for and used in analysis in (ever increasing amount) of genomic data.

Genes & genomes



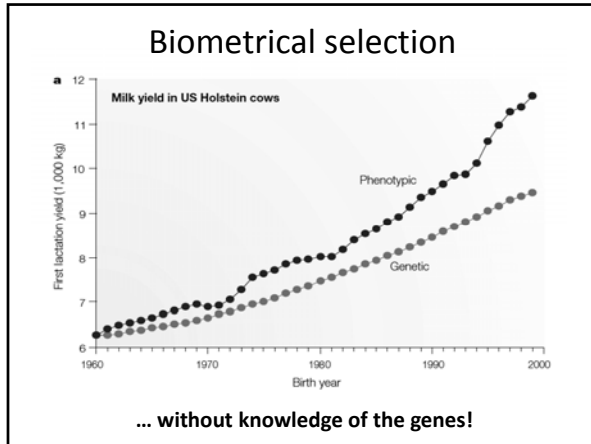
Genetic polymorphism

Association



Traditional selection based on genetic merit

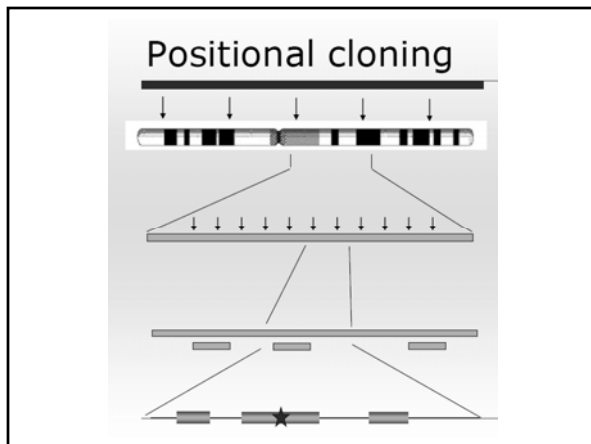
- For more than 40 yr, breeders used genetic evaluations to identify superior animals
- These methods improved phenotypic measures for milk production and milk components



- ### Limitations to selecting on predicted BVs
- Population effects on genetic diversity
 - Selection is optimized for genetic gain (short term response vs. long term response)
 - Ability to improve lowly heritable traits
 - disease resistance, reproduction, duration of productive life

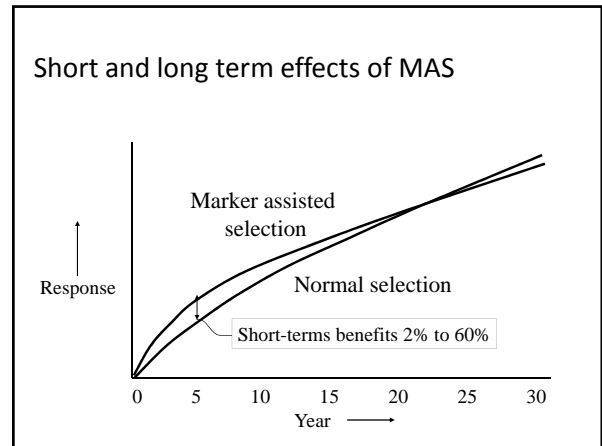
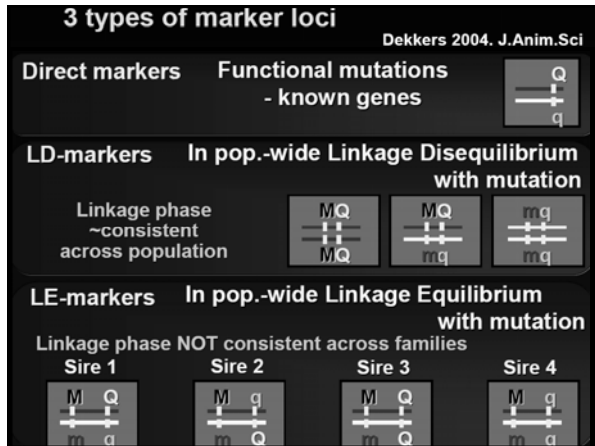
Information from genetic markers to identify desirable alleles plus BVs, resulting in genetic gains

- ### Before genomics
- QTL detection and genome mapping using linked markers
 - Positional cloning
 - Selection against undesirable alleles (fatal recessive)
 - MAS strategies
- Molecular tools were used but they did not revolutionize the breeding programs**



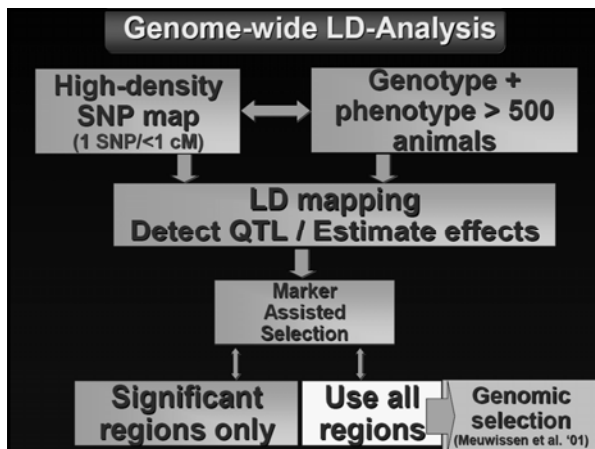
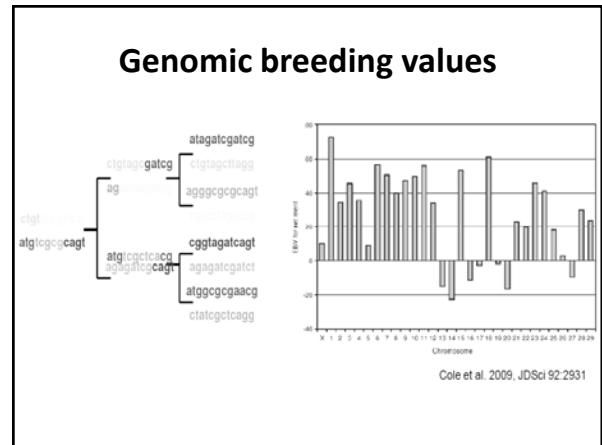
Genetic defects

=> Highly effective gene or marker assisted selection



Genomic selection

- Genomic selection refers to selection decisions based on genomic breeding values
- GEBV are calculated as the sum of the effects of dense genetic markers, or haplotypes of these markers, across the entire genome



Reliabilities of GEBV

- For young bulls without progeny test results in the reference population were between 20 and 67%
- Straightforward BLUP method for estimating the marker effects gave reliabilities of GEBV almost as high as more complex methods

Why Genomic Selection

Quantitative traits:

- a large number of loci are affecting the trait
- with any one locus capturing only a limited proportion of the total genetic variance
- relatively small gains with limited markers available
- cost of genotyping these markers is high

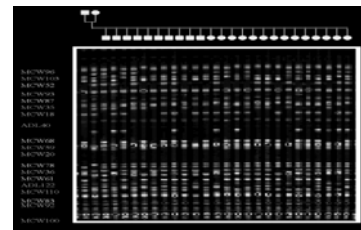
Will this and other developments in the field of genomics have any consequences for dairy cattle breeding?



Genomic Selection Revolution

- First, the recent **sequencing** of the bovine genome, which led to the discovery of **many thousands** of DNA markers, in the form of SNP
 - DNA sequencing technology development
 - reduction in the cost of genotyping
- Second, possible to make **very accurate** selection decisions using predicted-BV by **dense marker data** alone

Technically and practically it is become possible to genotype one animal for 20.000 – 60.000 SNPs at a reasonable price



The GS "revolution" ... without knowing the genes

2009 Premier Sires Holstein-Friesian Team - DNA Proven

Sire	Birth	Death	Age at Death	Height	Weight	Score	Rank	Genetic Value
1.
2.
3.
4.
5.
6.
7.
8.
9.
10.

inSire, markergeselectie, jonge stieren

Accuracy of GEBV

1. Level of linkage disequilibrium (LD) between the markers and the QTL
2. Number of animals with phenotypes and genotypes in the reference population from which the SNP effects are estimated
3. Heritability of the trait in question, or, if deregressed breeding values are used, the reliability of these breeding values
4. Distribution of QTL effects

Genome-wide LD-MAS on all regions

Meuwissen et al. (2001 Genetics: 1819)

Mixed model for prediction of marker effects

$$y = \sum \text{marker haplotype} + e$$

↑
random (Bayesian)

$N_e = 100$

Estimates from 2200 individuals

EBV accuracy	Marker distance
0.85	1 cM
0.81	2 cM
0.75	4 cM

Genomic selection and inbreeding

Use of DNA information reduces inbreeding True vs. pedigree estimated inbreeding:

Estimation of ΔF from genomic information

Balanced selection schemes for the future

- Selection will be intensified through genomic selection
- Management of inbreeding level is needed
- New and more precise tools to estimate ΔF from genomic relationships
- Mating strategies and genomic information?

Cumulated response to selection with the two alternative strategies of selection

Conclusions

- MAS has not been applied much:
 - Lack of explained genetic variation
- GS may be a break through in use of SNPs
 - High accuracy (sometimes)
 - But many problems still unsolved
 - Method for estimation of SNP effects
 - Marker density needed: will get sufficient density
 - Practicalities: missing genotypes
 - Implementation in breeding scheme

Summary

GS will change breeding programs in near future, already happens in dairy

Same reliability for all traits in both sexes

Shorter generation intervals

GS will improve possibilities to select for functional traits (e.g. health, fertility)

Utilization of genomic relationships provide new tools for risk management in breeding programs