

Genetics of Feed Efficiency and Applications for the Dairy Industry

Stephanie McKay
University of Vermont
Department of Animal Science
304 Terrill Hall
570 Main St.
Burlington, VT 05405
Phone: 802-656-2075
Email: stephanie.mckay@uvm.edu
<http://asci.uvm.edu/labs/mckay/>

Question

- Can we increase milk yield while decreasing feed cost?
- If so, how can we accomplish this?

In the last 100 years...

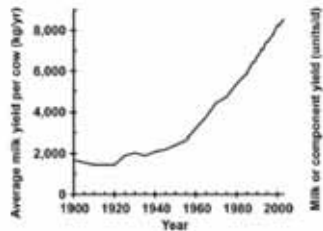


Figure 1. Milk production per cow in the United States over the past 100 yr.

- Milk production has increased because producers have been selectively breeding for high producing animals.
- Now we need to focus on selecting for more feed efficient cattle.

VandeHarr, MJ and N. St-Pierre. 2006. Major advances in nutrition: relevance to the sustainability of the dairy industry. *J. Dairy Sci* 89:1280-1291

What is Feed Efficiency?

- There are multiple definitions
- “The most appropriate for dairy production is still unclear (Berry, 2009)” (Cole *et al.* 2010)
- Essentially, feed efficiency is pounds of milk produced per pound of dry matter consumed

Measures of Feed Efficiency

- Feed conversion efficiency:
 - Gross feed efficiency
 - ECM/DMI
- Residual feed intake (RFI):
 - The difference between the actual feed intake and feed intake predicted from animal performance.

Achieving Greater Feed Efficiency

- We can accomplish this by:
 - Increasing milk yield while maintaining current dry matter intake
 - Decrease dry matter intake and maintain the same milk yield

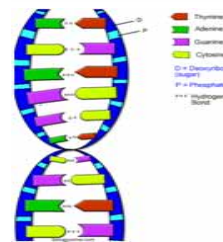
Feed Efficiency, Genetics and Genomics

- Our goal is to identify genetic markers that are associated with feed efficiency to facilitate marker assisted selection or genomic selection

What is genomics?



Human chromosome 1 is 247 million bases long
All chromosomes = 3 billion bases
Humans have ~100 Trillion cells



♦ The study of genomes...

♦ DNA = Deoxyribonucleic acid

- Comes in 4 flavors A,C,G,T (bases or nucleotides)
- Double stranded helical molecule
- Long strings of DNA form chromosomes
- The set of all chromosomes defines the genome
- Humans and cattle are diploid (have two copies of each chromosome)

Qualitative vs. Quantitative Traits

- Qualitative Traits:
 - Phenotype is affected only by a single gene
- Quantitative Traits:
 - Controlled by multiple genes
 - Have continuous variation in phenotypes
 - The more genes involved in the phenotype, the more continuous the distribution of phenotypes.
 - Are a product of environment and genetic factors
 - Nutrition, Climate
 - Some genomic regions associated with a quantitative trait exhibit stronger effects than others
 - these are called major effect and minor effect

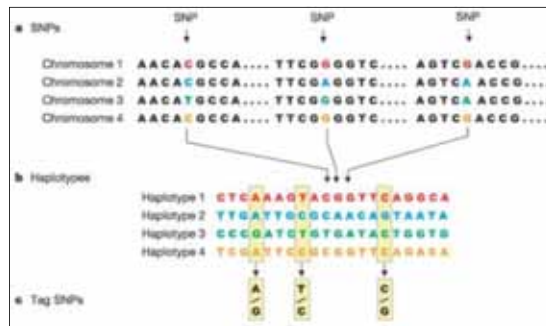


Which Genes are Involved?

- How do we find out which genes are associated with economically important traits?
 - Genotype animals with SNPs located across the genome
 - Analyze data to locate regions of the genome that are associated with changes in the phenotype of interest
- To do this we need:
 - Genetic Markers (SNPs)
 - Locations of Genetic Markers
 - Pedigrees
 - Phenotypes

Genetic Markers & SNPs

- SNP stands for Single Nucleotide Polymorphism
- SNPs are DNA variants that occur as single base changes
- We find SNPs by sequencing the DNA of many animals.

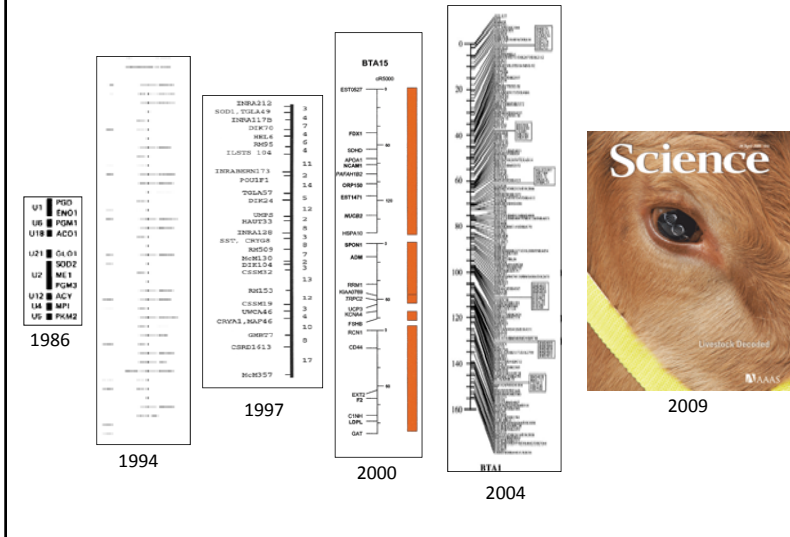


Locations of Genetic Markers

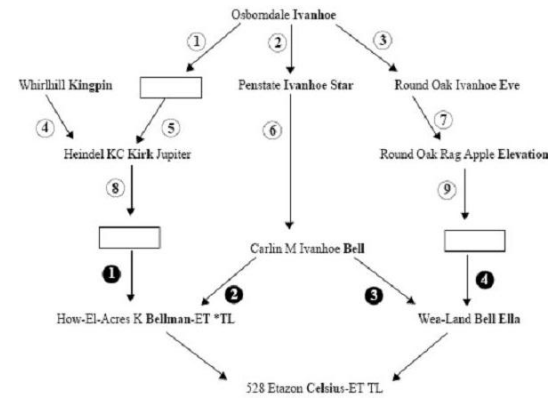
- Why do we need to know their locations?
- *Bos taurus* genome size:
 - 29 autosomes
 - ~3 billion base pairs
 - ~25,000 genes



Maps of the Bovine Genome over Time

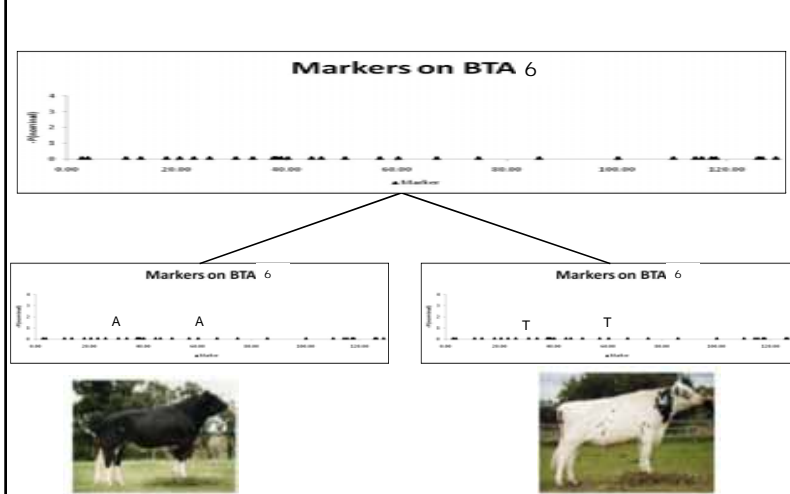


Pedigree



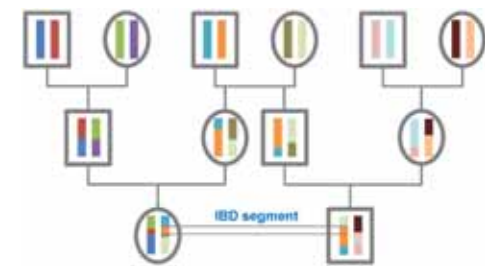
http://www.extension.org/pages/11174/dairy-cattle-inbreeding#Ux4D_E2YaUk

Locating the Genes



Identical By Descent

- An ancestor many generations ago leaves descendants
- Each generation, the ancestor's chromosome is broken down by recombination, until all that remains in the current generation are small conserved segments of the ancestor's chromosome
- The segments that are descended from a common ancestor without intervening recombination are called identical by descent (IBD)



http://en.wikipedia.org/wiki/Identity_by_descent

Feed Efficiency QTL Data

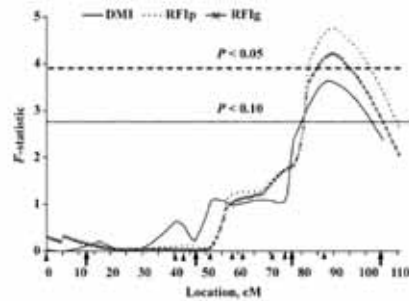
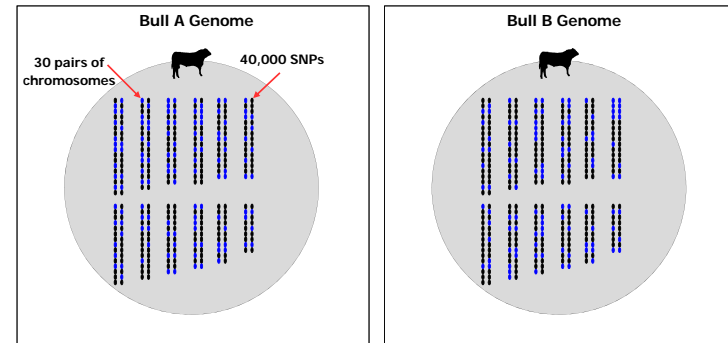


Figure 3. Across-family F -statistic profile for DMI and residual feed intake on chromosome 12. Horizontal lines represent the chromosome-wide threshold values from 2,000 permutations. Relative marker locations are indicated by triangles (SNP) or arrows (microsatellite) on the horizontal axis. RFIg = genomic residual feed intake; RFIp = phenotypic residual feed intake.

Nkrumah J. D., Sherman E. L., Li C., Marques E., Crews D. H., Jr., Bartusiak R., Murdoch B., Wang Z., Basarab J. A., and Moore S. S. (2007). Primary genome scan to identify putative quantitative trait loci for feedlot growth rate, feed intake, and feed efficiency of beef cattle. *J Anim Sci* 85: 3170-81.

Pedigree vs Genomic Relationships



- Pedigree relationships reflect the average number of genes shared identical by descent (IBD) between two individuals
- We can determine the actual number of genes IBD using SNP genotype data

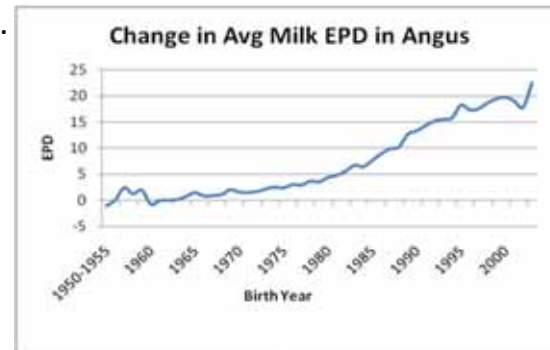
Using Genomics For Selection

Let's chat about selection...



Selection

- Selecting for a trait of interest should result in changes in allele frequency over time.



Morsci N.S., Schnabel R.D. & Taylor J.F. (2006) Association analysis of adiponectin and somatostatin polymorphisms on BTA1 with growth and carcass traits in Angus cattle. *Animal Genetics* 37, 554-62.

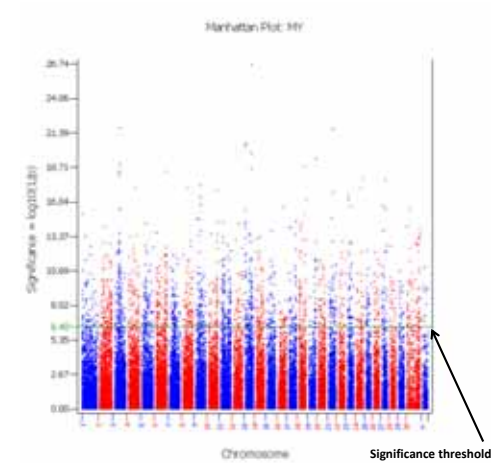
From SNPs to Genotypes

- From 3K to 770K SNPs can be simultaneously assayed on a SNP Chip
 - 2008: BovineSNP50 – 54,000 SNPs
 - 2010: Illumina - 800,000 SNPs in Spring
 - 2010: Affymetrix - 800,000 SNPs in Summer
- Data generation is rapid, cost effective and data are complete (95%) and accurate (99%)



Genome Wide Association Analysis

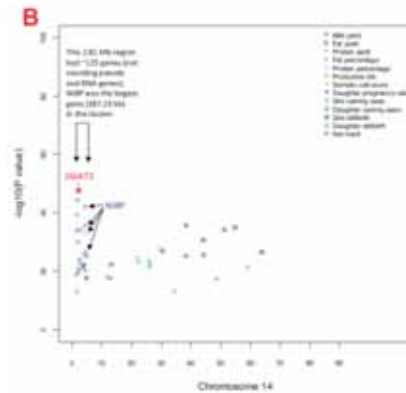
- 1,654 Holstein
 - Including elite and average cows
- 45,878 SNPs
- 31 traits



Cole, J.B., Wiggans, G.R., Ma, L., Sonstegard, T.S., Lawlor, T.H., Crooker, B.A., Van Tassell, C.P., Yang, J., Wang, S., Matukumalli, L.K. and Da, Y. M. Genome-wide association analysis of thirty one production, health, reproduction and body conformation traits in contemporary U.S. Holstein cows. 2011. *BMC Genomics* 12:408

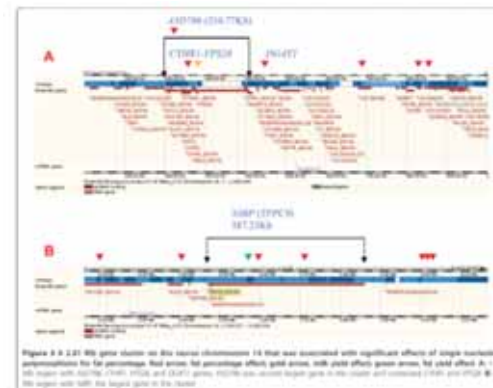
Fine Mapping

- 2.81 Million base pair region of chromosome 14
- Contains 125 genes
- 19 SNPs associated with an economically important trait



Cole, J.B., Wiggans, G.R., Ma, L., Sonstegard, T.S., Lawlor, T.H., Crooker, B.A., Van Tassell, C.P., Yang, J., Wang, S., Matukumalli, L.K. and Da, Y. M. Genome-wide association analysis of thirty one production, health, reproduction and body conformation traits in contemporary U.S. Holstein cows. 2011. *BMC Genomics* 12:408

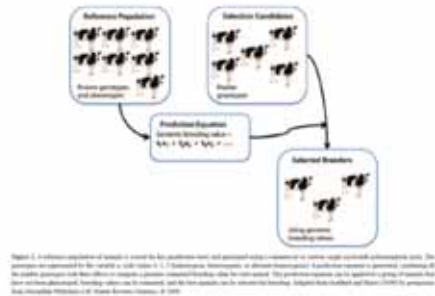
Fine Mapping Continued



Cole, J.B., Wiggans, G.R., Ma, L., Sonstegard, T.S., Lawlor, T.H., Crooker, B.A., Van Tassell, C.P., Yang, J., Wang, S., Matukumalli, L.K. and Da, Y. M. Genome-wide association analysis of thirty one production, health, reproduction and body conformation traits in contemporary U.S. Holstein cows. 2011. *BMC Genomics* 12:408

Genomic Selection

- Reference population of cows is genotyped and phenotyped with a high throughput SNP chip.
- A statistical model is constructed that estimates the effect of each SNP relative to the economically important trait.
- This results in a prediction equation that calculates Genomics Estimated Breeding Values
- This information can be used for selective breeding and management decisions



Eggen, A. The development and application of genomic selection as a new breeding program. *Animal Frontiers* 2:10-15

Use genomics for breeding and management decisions

- Selective mating of animals based on the genes they actually possess
- Manage animals more individually, based on their genetic potential
 - For example, if you have a cow whose GPTA shows her to be higher for Somatic Cell Score than her parent average, you may monitor her more closely for mastitis



- Using genomic technology provides a more accurate insight into their animals' genetic potential at a much earlier age

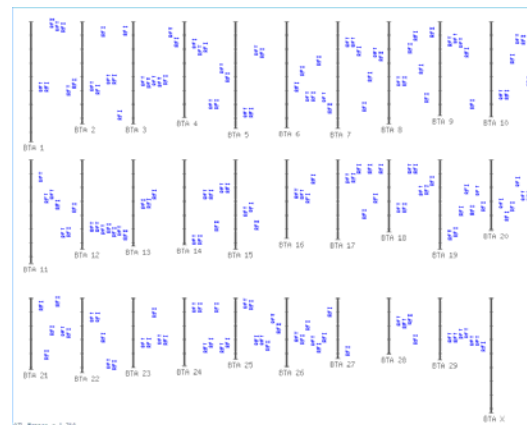
www.holsteinusa.com

So...What Are The Issues?

- Which definition and measure of feed efficiency is most appropriate for dairy cattle?
- Cost of genotyping enough animals to do a study of this kind

Service	U.S. Price	International
Genomic Testing (Breeder)	\$99	\$117
Genomic Testing (Buyer)	\$125	\$157
Genomic Testing (Buyer)	\$250	\$307

In Beef Cattle this is more straight forward...



- Every chromosome in the genome has been shown to harbor a region associated with RFI

QTL Report v.1.760

<http://www.animalgenome.org/cgi-bin/QTLdb/BT/index>

Questions?

