


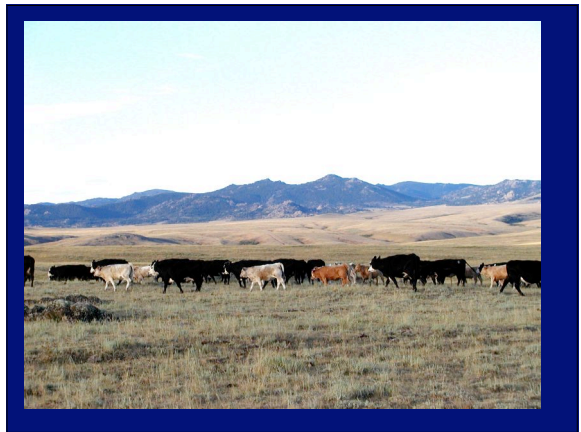
UNITED STATES DEPARTMENT OF AGRICULTURE  
 AGRICULTURAL RESEARCH SERVICE

**ARS NATIONAL PROGRAMS**

**“Today’s Beef Cattle Genetics Research and Education Engine: *Ready and Primed for the Industry’s Future?*”**



Ronnie D. Green  
 National Program Leader  
 Food Animal Production  
 USDA / ARS



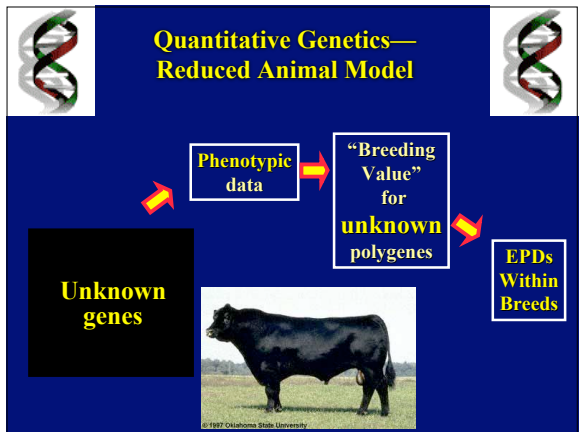
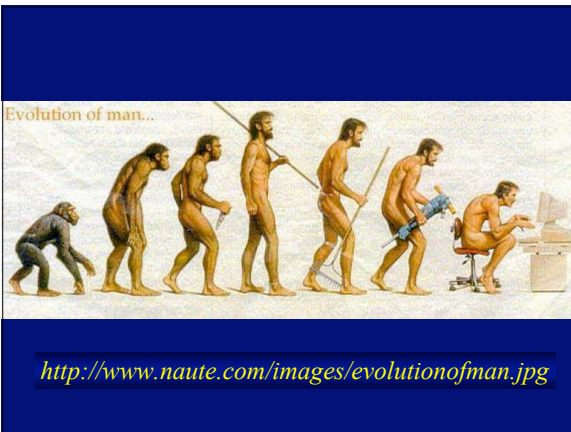

3201 Frederick Avenue • St. Joseph, MO 64508 • (816) 283-5100 • Fax (816) 233-9703 • E-mail: angus@angus.org

**Late 1950s-  
 Early 1960s**





**January 1967  
 Denver, CO**



**AMERICAN ANGUS ASSOCIATION™— THE BUSINESS BREED**

3201 Frederick Avenue • St. Joseph, MO 64506 • (816) 383-5100 • Fax (816) 233-9703 • E-mail: angus@angus.org

**Breed Average EPD and \$Values - Spring 2007**

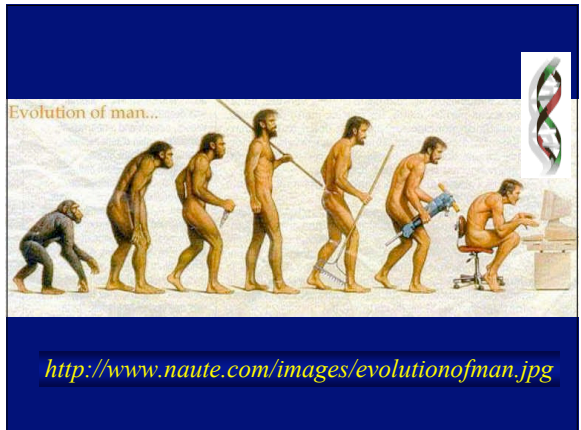
	PRODUCTION					MATERNAL			CARCASS			ULTRASOUND			\$VALUES							
	CE	BW	WW	YW	YH	SC	CEM	Milk	MW	MH	SEN	CW	Marb	RE	Fat	IMF	RE	Fat	\$W	\$F	\$G	\$B
Current Sires <sup>1</sup>	+5	+2.3	+39	+73	+4	+32	+6	+19	+32	+5	+7.94	+5	+14	+14	-.001	+08	+18	+003	+22.54	+17.25	+13.70	+29.15
Main Sires	+5	+2.3	+42	+76	+3	+37	+6	+20	+35	+5	+5.83	+6	+16	+15	+0.00	+08	+17	+004	+23.45	+21.79	+12.83	+30.19
Supplemental Sires	+5	+2.0	+43	+80	+4	+41	+7	+22			+3.50	+7	+23	+21	-.001	+15	+30	+008	+24.59	+29.40	+14.91	+34.54
Current Dams <sup>1</sup>	+3	+2.4	+35	+63	+4	+19	+5	+17	+31	+5	+11.12					+04	+08	+002	+20.77	+9.86	+12.48	+22.73
Non-Parent Bulls	+5	+2.3	+40	+74	+4	+32	+6	+20			+6.01					+13	+22	+005	+23.46	+18.07	+14.61	+32.28
Non-Parent Cows	+5	+2.3	+40	+74	+4	+4	+6	+20			+8.94					+15	+24	+005	+23.99	+18.51	+14.82	+32.43

<sup>1</sup>at least one calf recorded in herd book within the past two years

American Angus Association™ 3201 Frederick Ave. St. Joseph, MO 64506

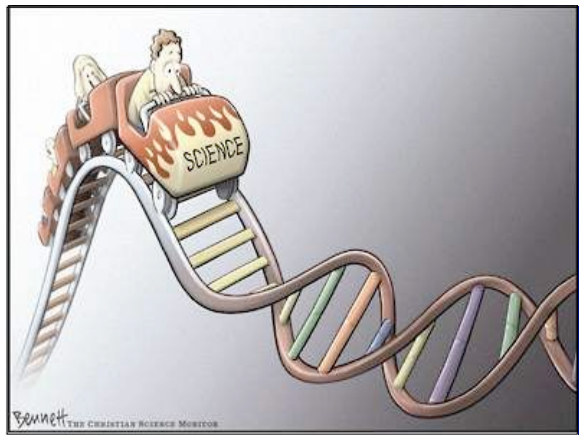
Contact us: phone 816.383.5100 fax 816.233.9703 e-mail

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## From gene to genome

- **Gene**
  - The functional and physical unit of heredity passed from parent to offspring
- **Genome**
  - The DNA comprising the complete genetic complement of an organism
- **Genomics**
  - 1986 -- a new scientific discipline of mapping, sequencing, and analyzing genomes

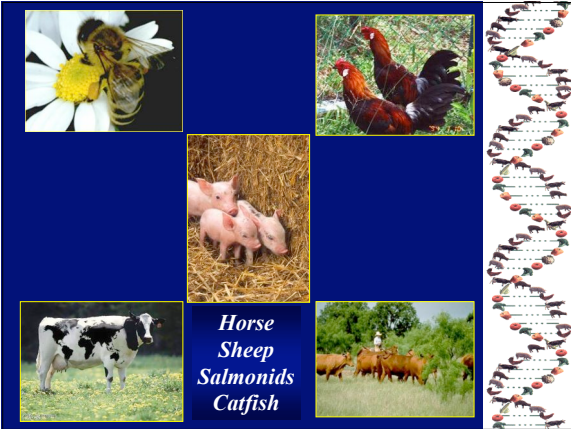


## Important genes affecting production traits -- bovine

- **Leptin** - fat deposition / DMI
- **DGAT** – milk production
- **BGHR** – milk components
- **Thyroglobulin** - marbling
- **Calpastatin** - tenderness
- **Calpain** - tenderness
- **Somatostatin** -- marbling

genome.gov  
National Human Genome Research Institute  
National Institutes of Health

YOU COULD HAVE THE WHOLE HUMAN GENOME  
DO YOU WANT IT?  
IT GOES UNRAVELLED



## International Collaboration


- NIH / NHGRI -- \$25M
- USDA -- \$11M
- State of Texas -- \$6M
- Genome Canada -- \$5M
- U.S. Beef Councils -- \$1.2M
- Australia -- \$1M
- New Zealand -- \$1M




**Project Total ~ \$50M**


## Bovine Genome Sequence – Final Assembly – v. 3.1

- ~7.2-X coverage of the genome
- Total of 27.9M sequence reads
- Avg. trimmed read length - ~700 bp
- Size of the genome 2.87B base pairs
- N50 supercontig size - ~1M bp
- Used the International Integrated Map to order the assembly (Snelling *et al.*, 2007)
- Released to GenBank and available through BCM web-site at: [www.hgsc.bcm.tmc.edu/projects/bovine](http://www.hgsc.bcm.tmc.edu/projects/bovine)




## Bovine SNP Project

- Current Status of Project:
  - Genotyping completed on total of ~500 animals (19 breeds) for total of 40K SNP
  - (Breeds include:
    - Angus, Hereford, Limousin, Charolais, Red Angus, Piedmontese, Romagnola, Brahman, Santa Gertrudis, Beefmaster, Nellore, Gir, N'Dama, Sheko, Holstein, Jersey, Brown Swiss, Norwegian Red, Guernsey)



**Bovine HapMap Consortium**





**BFGL and AIPL – BARC**  
Collaborators: Taylor and Moore

USA Agricultural Research Service

News & Events

**New Techniques to Top Bulls for Breeding**

Genetic testing is helping breeders identify the best bulls for their herds. This is done by analyzing the DNA of the bulls and comparing it to a reference genome. This allows breeders to select the best bulls for their herds, based on their genetic makeup. This is done by analyzing the DNA of the bulls and comparing it to a reference genome. This allows breeders to select the best bulls for their herds, based on their genetic makeup.

GenomeWeb Daily News  
The GenomeWeb Intelligence Network

to 10,000 samples.

Ethiopia to Develop Bovine BeadChip, Plans to Market It in Early 2007

August 24, 2006

By a GenomeWeb Staff Reporter

ADDIS ABABA (GenomeWeb News) - Biogen Technologies Ltd. plans to develop a new multi-allele BeadChip and will be ready next year.

SNP content will be developed with contracts at the US Department of Agriculture's Agricultural Research Service, the University of Missouri-Columbia, and the University of Alberta.

The content will use data from the draft sequence of the cow genome and is expected to be available in the next few months. The partners will use the SNP markers to map quantitative trait loci and to identify breed effects.

Biogen plans to offer the BeadChip as a new product in early 2007 as a standard lab test after it analyzes the data from 10,000 samples.

The project will also include the development of a reference genome for genotyping more than 10,000 cattle samples representing breeds of different levels of genetic diversity.



## ... to genomic selection.

Cost-effective whole genome SNP genotyping

+

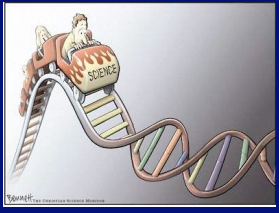
Long-range LD in livestock

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Advanced statistical genetics (e.g. Meuwissen & Goddard)

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**Genomic selection**



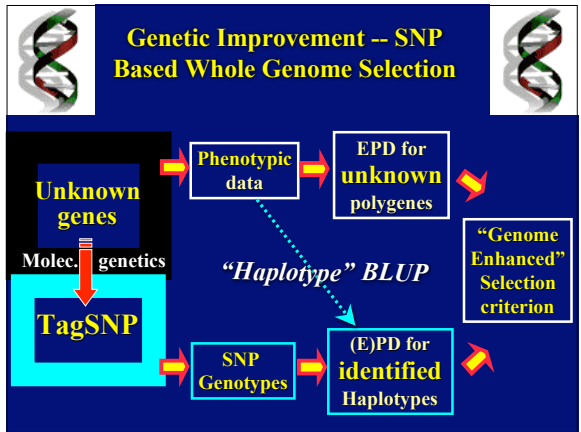
Could have major impact in animal and human genetics !



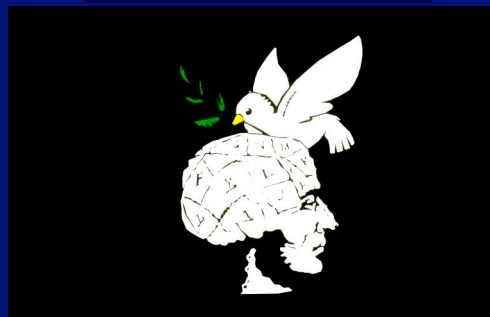
## Cost effective whole genome SNP genotyping ...100K SNP for \$200?

**0.2 cents per genotype**



## PHENOMICS.....




**Adaptability / Functionality???**

- ## Genomics Research
- Production traits
  - Meat quality, healthfulness, and yield
  - *Feed efficiency – expensive to measure*
  - *Reproduction- dissect components*
  - *Genetic resistance to disease*
  - *Stress resistance*
  - Select for multiple traits
  - Management “by genotype” – *precision mgt*

### NEWFOCUS

## Closing the Net on Common Disease Genes

Hope data sets and faster cost analytical methods are speeding up the search for DNA variations that confer an increased risk for diabetes, heart disease, cancer, and other common ailments.



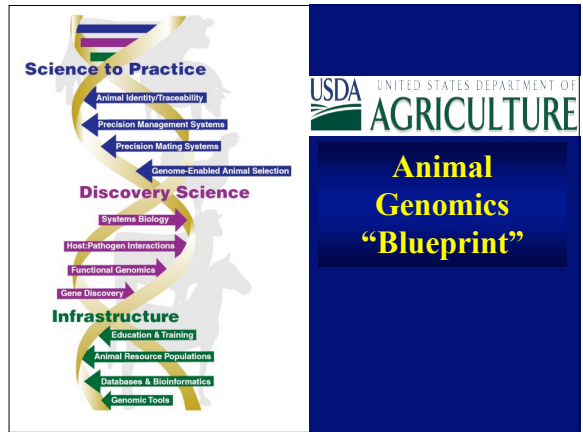
**ARTICLE SUMMARY OF COMMON DISEASE GENES**

Genetic epidemiology studies of large-scale genome-wide association studies (GWAS) have identified thousands of DNA variations associated with common diseases. However, the vast majority of these associations remain unexplained, and the underlying biological mechanisms are often unknown. This article discusses the challenges of identifying common disease genes and the potential of new technologies to accelerate the discovery of these genes.

**Common haplotypes**

Genetic epidemiology studies of large-scale genome-wide association studies (GWAS) have identified thousands of DNA variations associated with common diseases. However, the vast majority of these associations remain unexplained, and the underlying biological mechanisms are often unknown. This article discusses the challenges of identifying common disease genes and the potential of new technologies to accelerate the discovery of these genes.

- ## Genomics Research – Host-Pathogen Interaction
- *FMD, Avian Influenza, BSE/TSEs*
  - *PRRS, BRD, BVD, Johne's*
  - *Parasite resistance*
  - New vaccine development
  - New drug targets / immunomodulators
  - *Gut “Microbiome” / metagenomics??*



- ### Science to Practice Priorities
- 1) Whole-genome enabled animal selection.
  - 2) Prediction of genetic merit of individual animals from genome-based data combined with phenotypes.
  - 3) Integration of genomic data into large-scale genetic evaluation programs and the use of genomic information to design precision mating systems.
  - 4) “Precision management systems” to optimize animal production, health, and well-being.
  - 5) Genomic capabilities that enable parentage and identity verification (traceability).



- ### Industry Dissension
- BSE / food safety / biosecurity.
  - Trade policy.
  - National animal identification.
  - Country-of-origin labeling.
  - Increasing consolidation / integration and impacts on market structure / price discovery.
  - Producer-funded promotion and research.

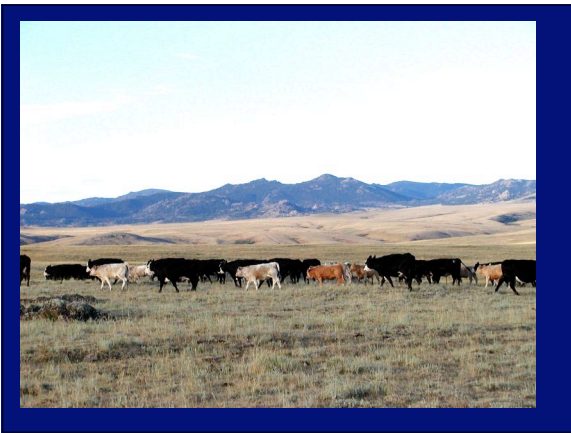
- ### Societal and Industry Shifts – “Macro”
- Increased call for decreasing the “environmental footprint” of production.
  - Competition for energy sources and feedstuffs for alternative energy production.
  - Increased attention to animal well-being and welfare.
  - Increased brand / process/ historical identity of products.
  - Increased purchasing power for “non-traditionally produced” beef products.

## Societal and Industry Shifts – “Micro”

- “Push to narrow the gene pool” – *yet disagreement on abandonment of heterosis in the cow herd.*
- Need for information continues to accelerate – with commercial industry desiring tools for functionality, health and adaptability ERTs.
- Desire to move from a “breed” world to a “gene pool” perspective.
- Mining the genome in the post-genome sequence world is here to stay – but – we are not well structured to handle current and future data.

SAVAGE, Md. and MINNEAPOLIS - June 11, 2002

MetaMorphix signs deal to develop genetic selection tool using cattle genome -- Exclusive agreement with Cargill's Caprock Cattle Feeders and Excel Corporation expected to result in superior beef for consumers



### Financial “Re-Direction”

**National Beef Cattle Evaluation Consortium**

Presenting Paper on the Use of Insulin-Like Growth Factor I (IGF-I) as an Indicator Trait in a Genetic Evaluation for Feed Efficiency

**Members:**

- Colorado State University - M. Eims
- Cornell University - J. Pollak
- University of Georgia - J.K. Bert and

**Affiliates:**

- Iowa State University - D. Garrick
- University of Kentucky - Darrah Bullock

### Beef Cattle Breeding and Genetics

↓


### Renaissance?

**2007**

**BEEF IMPROVEMENT FEDERATION**  
Improving the beef industry through performance evaluation

**Beef Cattle Breeding and Genetics**

**Renaissance**



**Renaissance Questions**

➤ Where are the scientists and educators with the practical knowledge of industry needs going to come from?

**University Trailblazers**

**Guy Lonergan  
Mark Allan  
Darrell Mark  
Duane Wulf  
Dan Moser**




**Renaissance Questions**

➤ How will we fill the huge deficit of quantitatively skilled people needed to be able to make sense of all of these new data? *We need to re-open the textbook on beef cattle quantitative genetics!*

➤ Who is going to educate the public using what kinds of models and platforms?

➤ What is going to be the role of breed associations in the future? Today is eerily reminiscent of the LMA discussion of the past decade relative to sale barns?


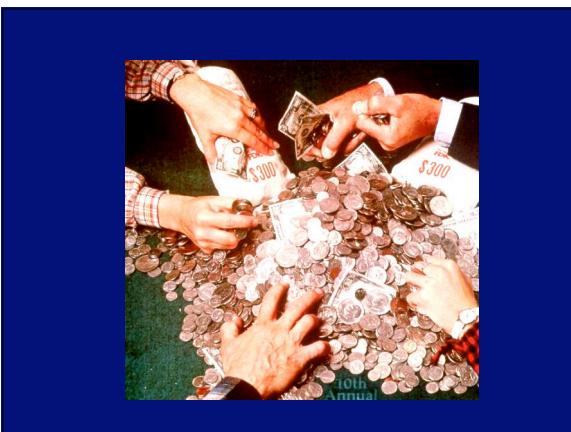


**Renaissance Questions**

➤ Are we looking closely enough at what is evolving in this arena in other regions of the world – principally Australia / New Zealand and Brazil? What about in competing industries?

➤ *Is it possible that animal agriculture in the U.S. could be shipped off shore? Careful study of the real agenda of various “social conscience” groups is warranted.*

➤ Is there adequate funding available in today’s research, higher education, and outreach system to address these challenges?

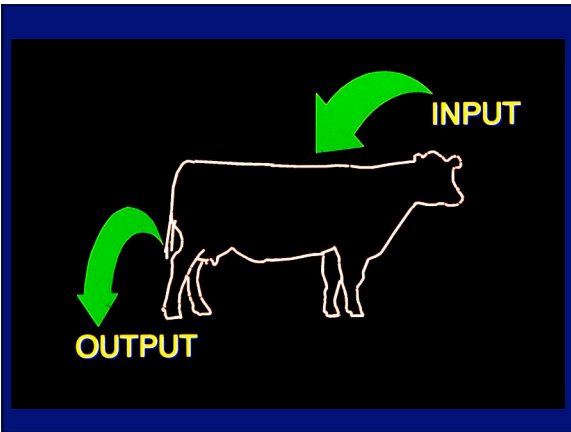



**Agricultural Research, Education and Outreach**

**USDA** **ARS** **CSREES**

- National Institute of Food and Agriculture (NIFA)** – New \$1B agency to be built over next 7 years to provide competitive grants for basic agricultural research – would be outside of USDA REE?
- CREATE-21** – Reformation of current USDA REE agencies plus Forest Service research in to new structure – would abolish ARS, CSREES, ERS, and NASS. Requires doubling of current REE budget to retain capacity now in ARS. Seeks to increase competitive grants funding.



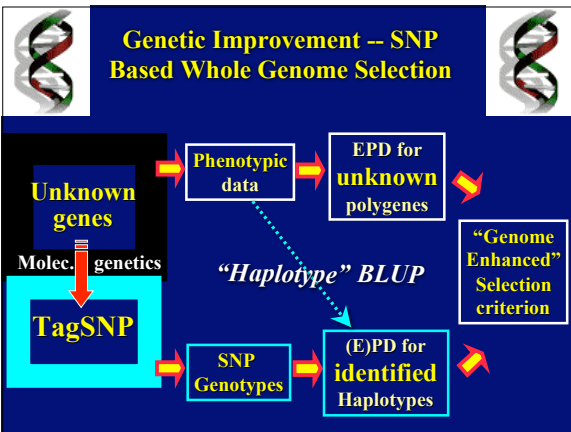


*Leadership for 2047?*

**BEEF IMPROVEMENT FEDERATION**  
Improving the beef industry through performance evaluation

**Sal Forbes**  
**Frank Baker**  
**Ferry Carpenter**

**Jim Brinks**  
**Bob DeBaca**  
**H.H. Stonaker**







*“Carpe diem.....”*