ANGUS

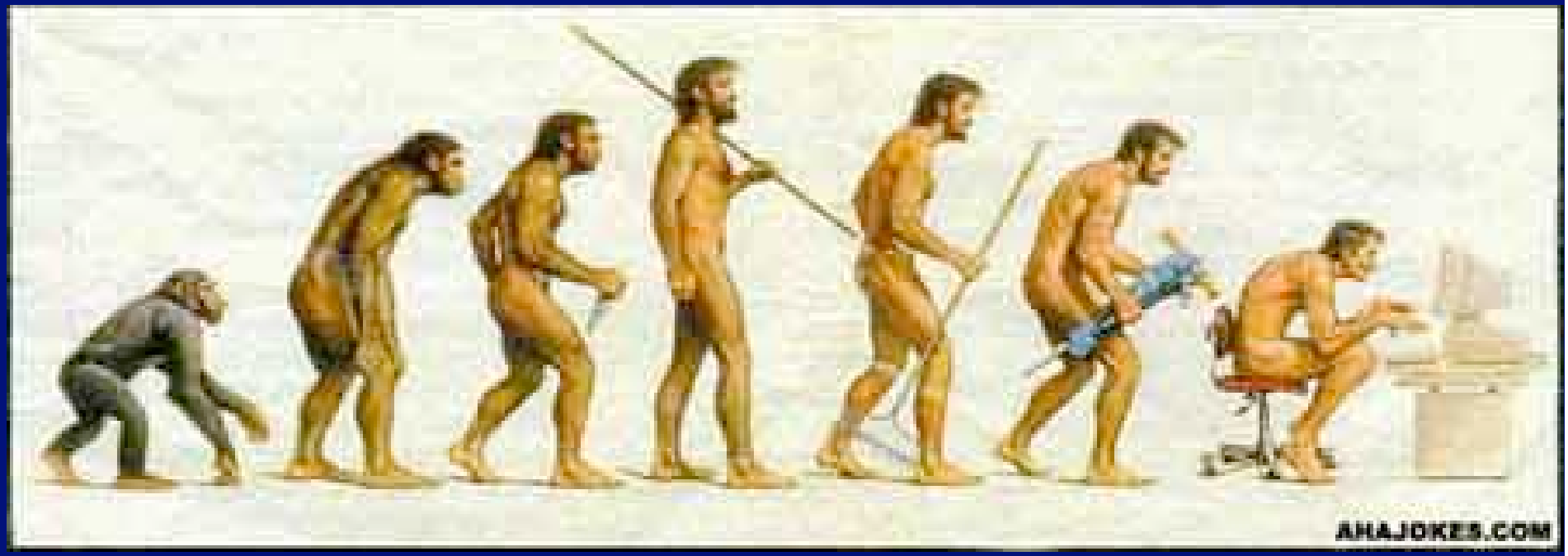
THE BUSINESS BREED

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

American Angus Heritage

Evolving in to the Era of the Genome

Ronnie D. Green
National Program Leader
Food Animal Production
USDA / ARS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Late 1950s-
Early 1960s

American
HEREFORD
ASSOCIATION

Whole Herd

Quantitative Genetics—Reduced Animal Model

Unknown genes

Phenotypic data

"Breeding Value" for **unknown** polygenes

EPDs Within Breeds

1985

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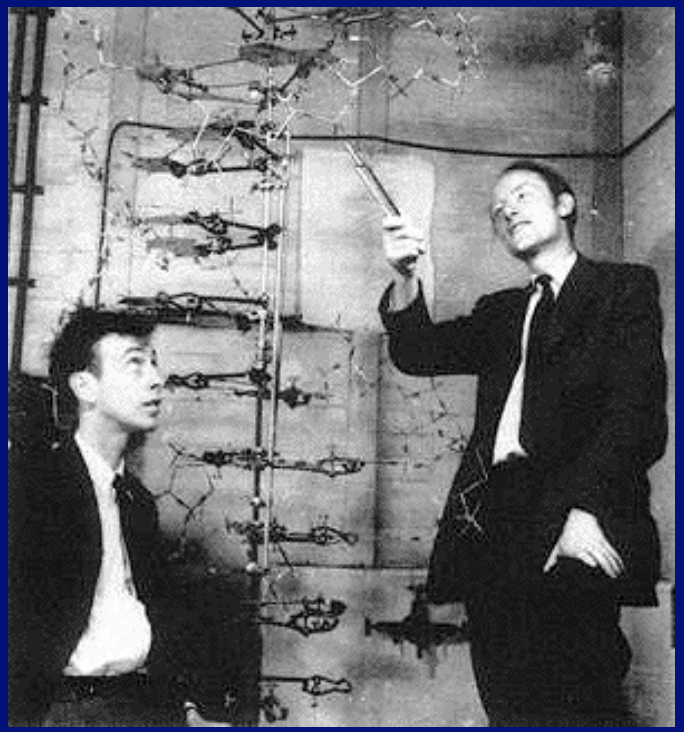
Fall 2004

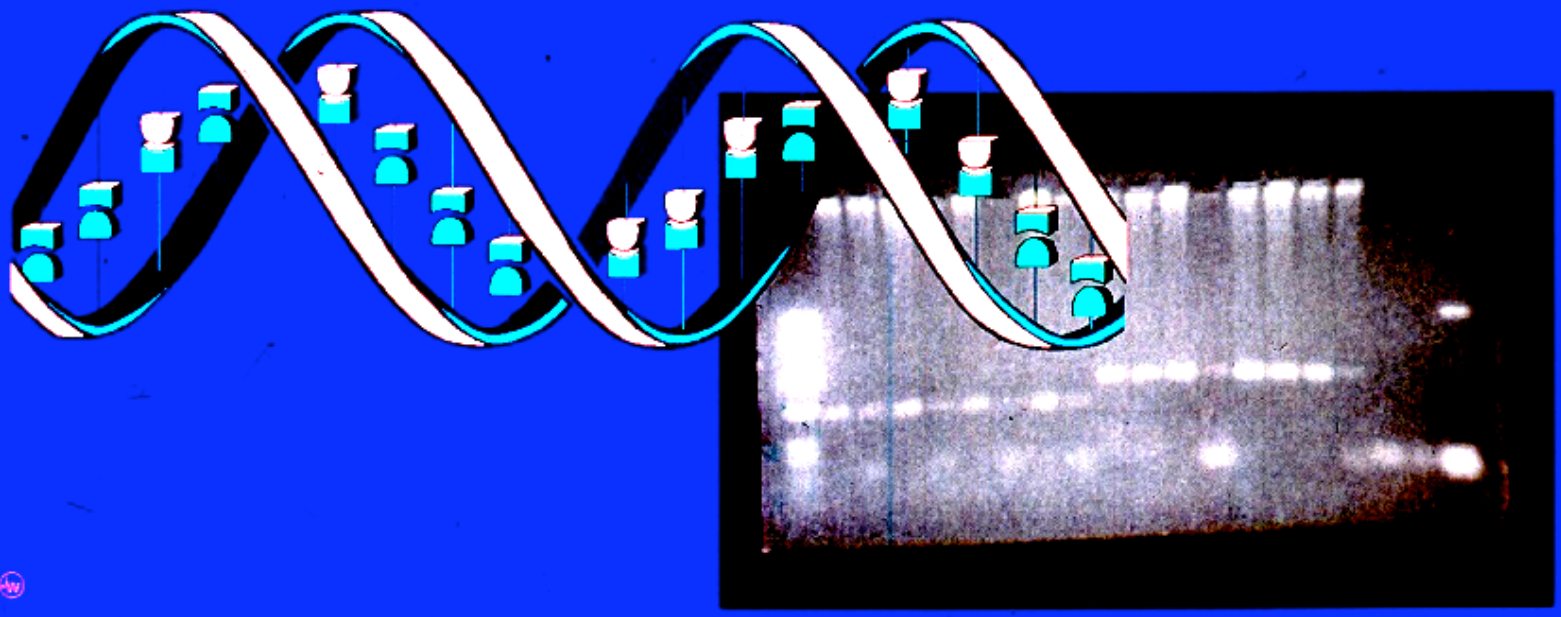
Expected progeny difference (EPD) and $Value averages, standard deviations (SD) and minimum/maximum.

Trait	No. EPD	No. records	Avg.	SD	Min	Max
Birth weight, lb.	4,501,628	3,604,414	1.9	2.1	-10.2	13.7
Weaning direct, lb.	5,208,022	4,245,870	17	17	-60	80
Weaning maternal(milk), lb.	5,208,022		8	9	-38	44
Yearling weight, lb.	5,208,022	2,107,425	31	31	-80	138
Yearling height, in.	631,736	344,082	.3	.4	-1.9	2.5
Mature weight, lb.	2,477	21,165	4	29	-120	154
Mature height, in.	2,477	21,165	.7	.7	-2.3	3.9
Scrotal circumference, cm	574,081	282,021	.10	.43	-3.69	3.18
Carcass weight, lb.	5,767	76,109	2	9	-43	53
Marbling score	5,767	76,109	.07	.16	-.65	.99
Ribeye area, sq. in.	5,767	76,109	.07	.17	-.75	.87
12th-rib fat thickness, in.	5,767	76,109	.000	.019	-.111	.096
% retail product	5,767	76,109	.05	.31	-1.25	1.47
Ultrasound intramuscular fat, %	730,617	381,882	.00	.13	-.70	1.08
Ultrasound ribeye area, sq. in.	730,617	387,311	.03	.20	-1.05	1.29
Ultrasound fat thickness, in.	730,617	389,251	.000	.014	-.097	.112
Ultrasound % retail product	730,617	389,251	.03	.24	-1.43	1.40
Current Sires[1]	**No. Indexes**					
Feedlot Value ($F), $ per head	21,041		12.79	11.98	-56.36	74.50
Grid Value ($G), $ per head	18,162		12.21	6.14	-25.85	42.58
Beef Value ($B), $ per head	18,162		24.39	10.70	-49.48	62.75

50th anniversary of DNA structure



DNA Technology for Livestock



DNA Genetic Code Dictates Amino Acid Identity and Order

DNA Sequence Is the Genetic Code.

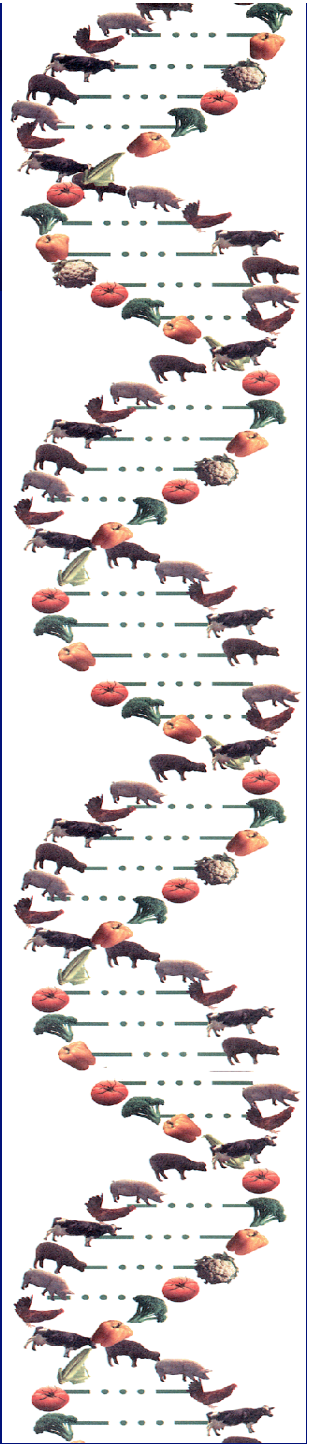
GCA AGA GAT AAT TGT . . .

. . . *Growing Protein Chain*

Y-GA 98-648

A Mammalian Genome

- 3 billion base pairs (A, G, C, and T)
- Every cell has two copies (alleles) of each chromosome
- Estimated 30,000 to 40,000 genes (two copies or alleles of each gene)
- Maybe 400,000 proteins produced



Genomics

- Structural
  - The construction of high-resolution genetic, physical, and transcript maps of an organism
  - Highest resolution physical map of an organism is its complete DNA sequence

- Functional
  - Global (genome-wide) approaches to analyze gene function and expression

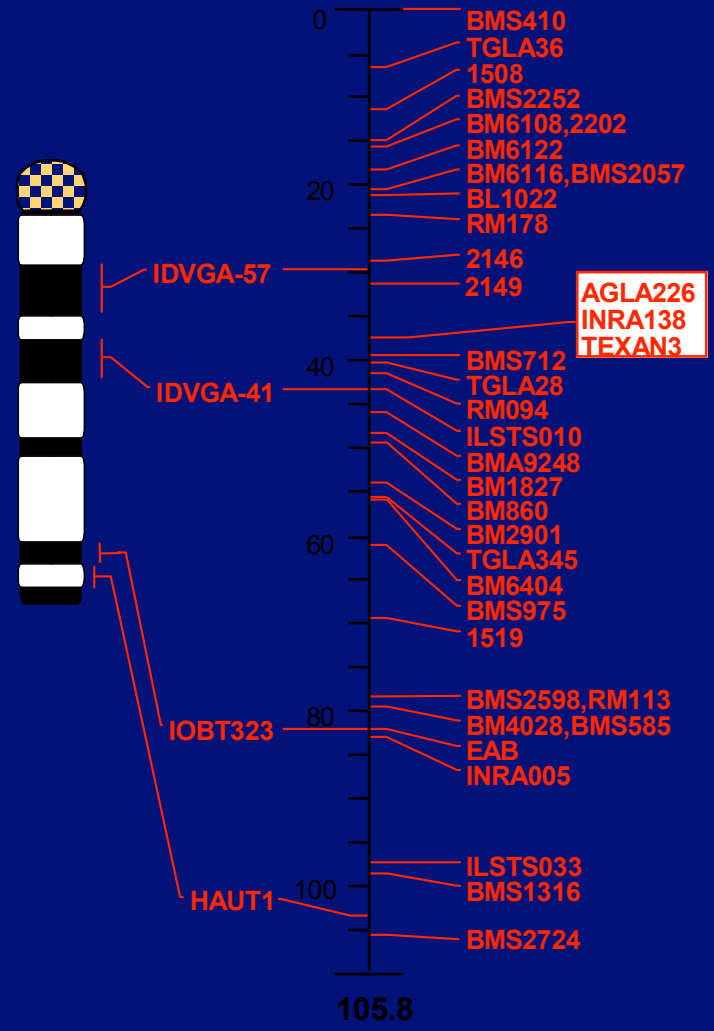
Genomics Research

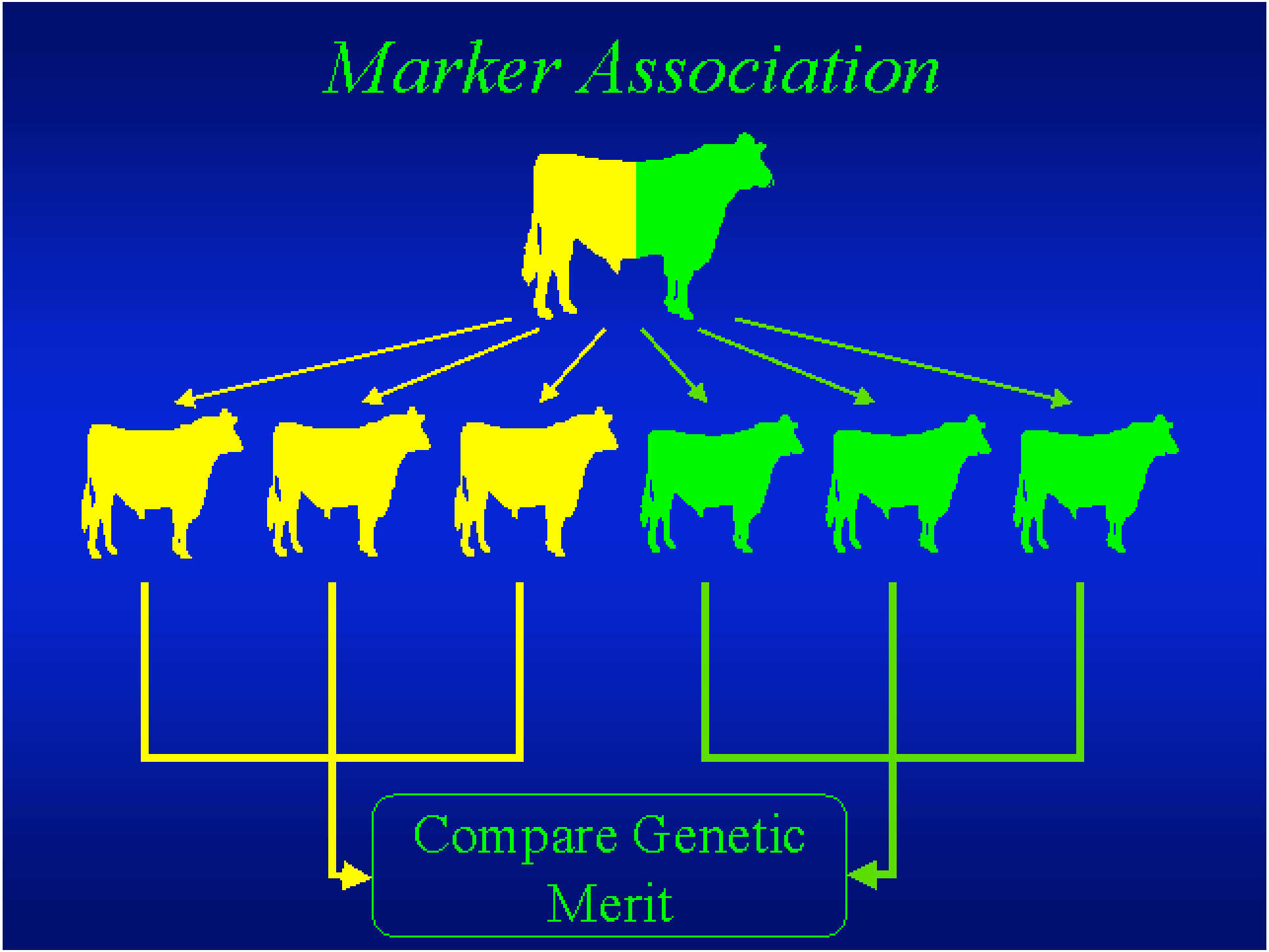
- Develop road maps of each chromosome (genetic linkage maps)
- Utilize linkage maps to identify chromosomal regions
- ‘Fine map’ the region to identify the gene

Genomics Research

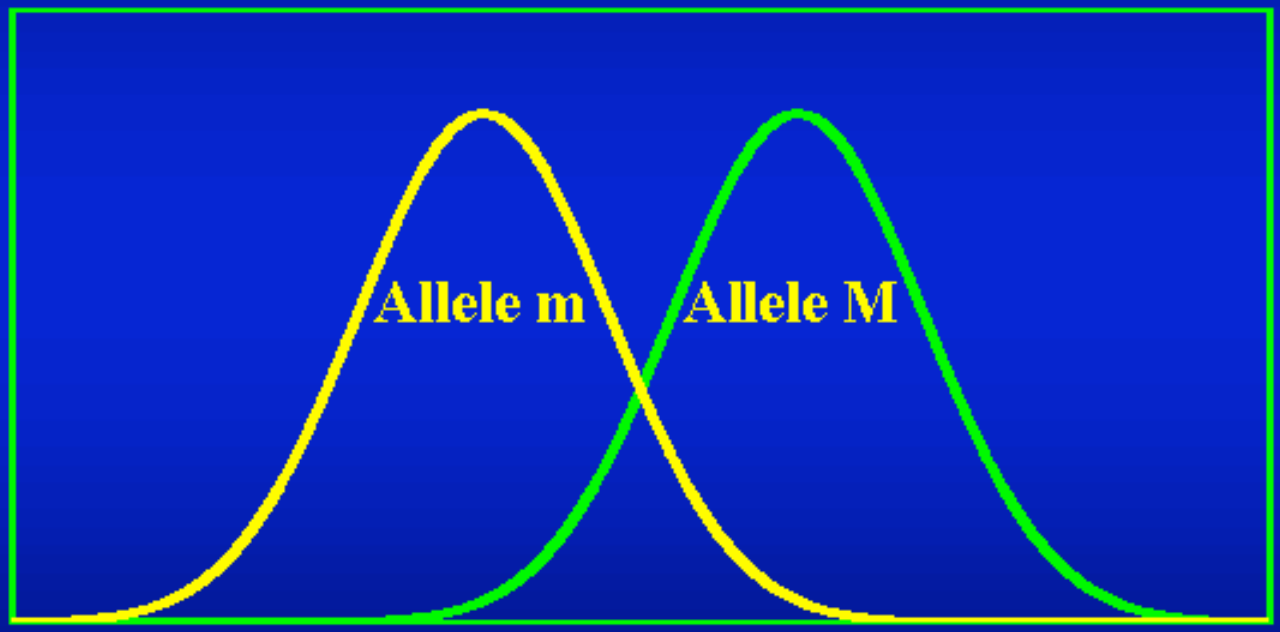
- Cattle linkage map
  - First goal 300 markers
  - Today > 9000 markers
- Pig linkage map
  - >5000 markers
- Sheep linkage map
  - > 1200 markers, ~50% bovine markers work

Cattle Chromosome 12




Marker Association
Compare Genetic Merit

Marker Association



Genetic Merit

Family from sire 921690 (PA)

X

PA

X

n= 209

Traits Measured

Growth traits:

- Birth weight (kg)
- Weaning weight (kg)
- Yearling weight (kg)
- Postweaning average daily gain (kg/d)

Predicted carcass traits:

-Retail product yield (%)
- Fat yield (%)
- Bone yield (%)
- Dressing percent (%)

Measured carcass traits:

- Hot carcass weight (kg)
- Fat depth (cm)
- Marbling score
- Longissimus muscle area (cm^2)
- USDA yield grade
-Est. kidney, pelvic, & heart fat (%)
-Rib bone
-Ribfat
- Ribmus
- Warner-Bratzler shear force 2 or 3 d postmortem (kg)
- Warner-Bratzler shear force 14 d postmortem (kg)

GENOME SCAN RESULTS IN ALL RESOURCE FAMILIES

BTA1

RPYD
FATYD

BTA2

MSTN

MARB, RPYD
MARB

BTA3

WBS14

MARB, RPYD
Fat yield

BTA4

RPYD, FATYD

HCW, ADG

BTA5

FAT, YG, RPYD, WBS14
RIBBONE, DP, RIBFAT, BWT

BTA6

BTA8

FAT

BTA15

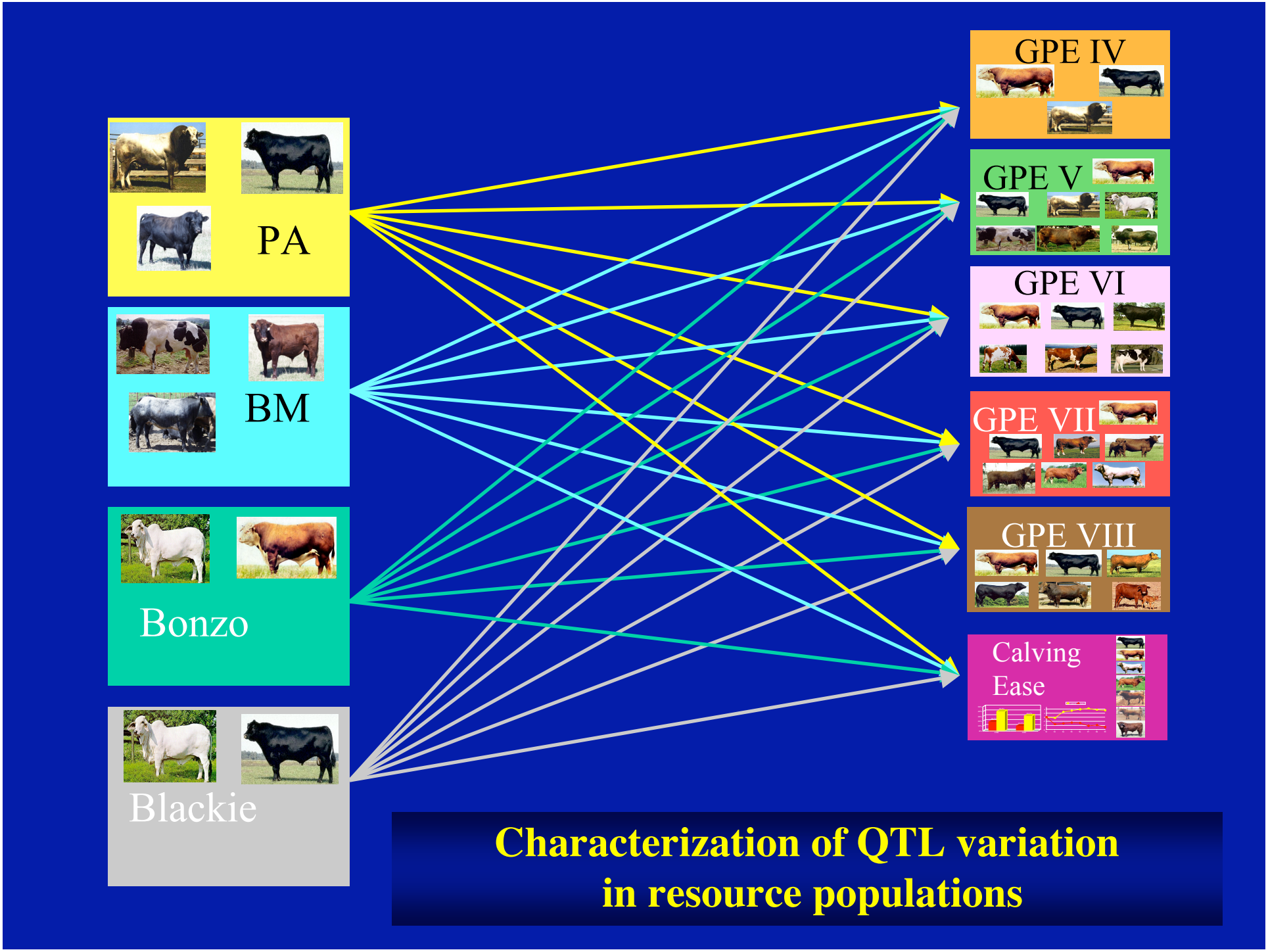
WBS14

BTA27

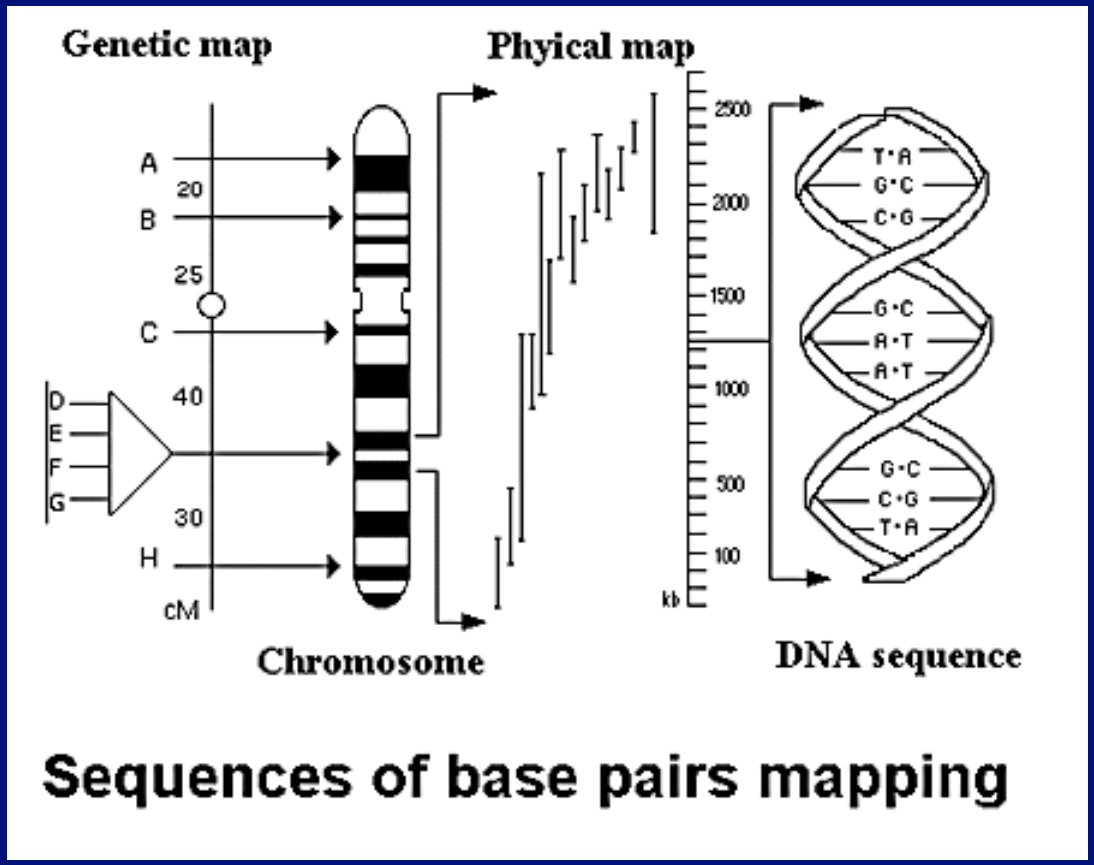
Dairy Form

BTA29

WBS3, WBS14, Calpain

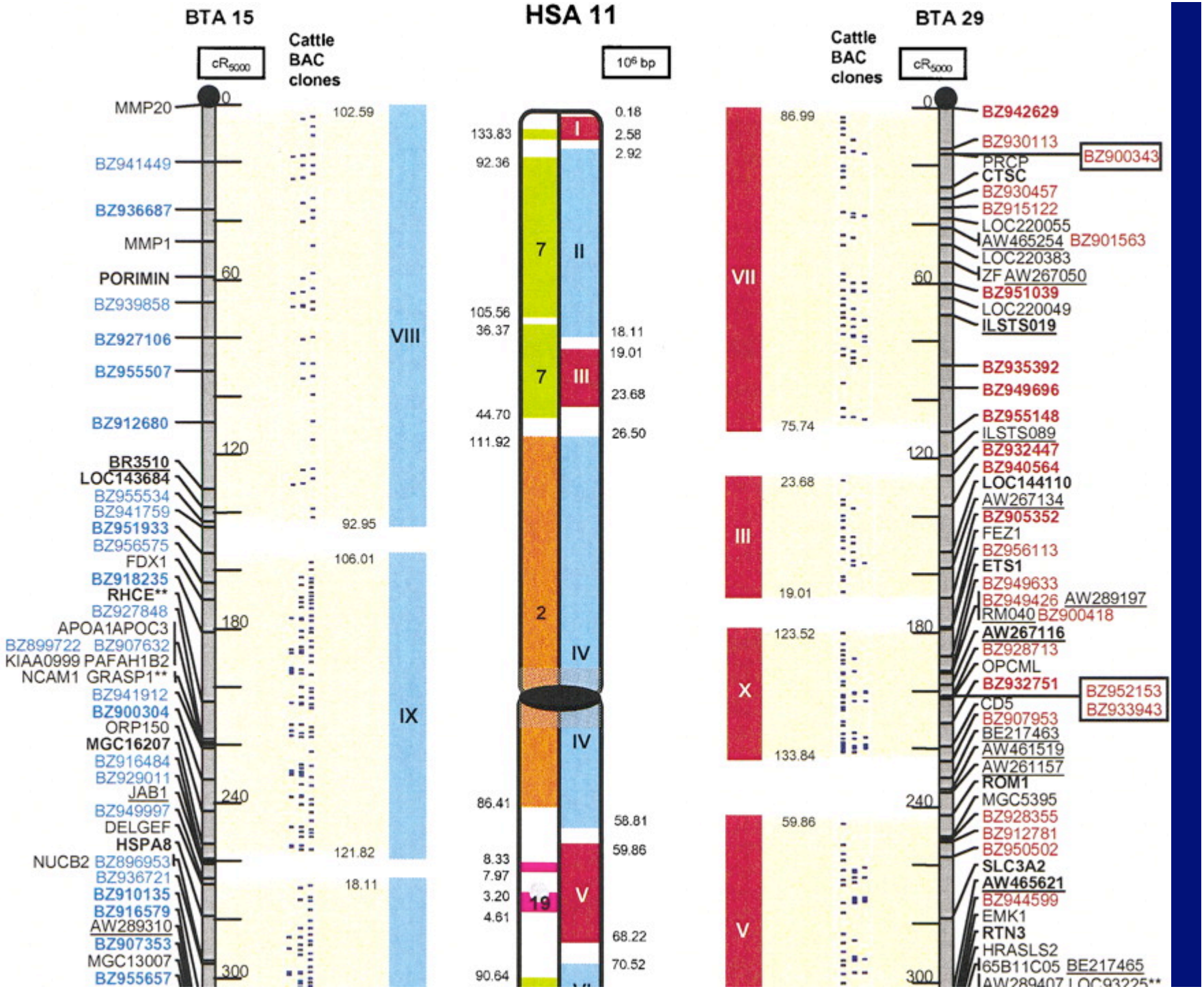

PA
BM
Bonzo
Blackie
GPE IV
GPE V
GPE VI
GPE VII
GPE VIII
Calving Ease
Characterization of QTL variation in resource populations

Mapping a trait to a gene

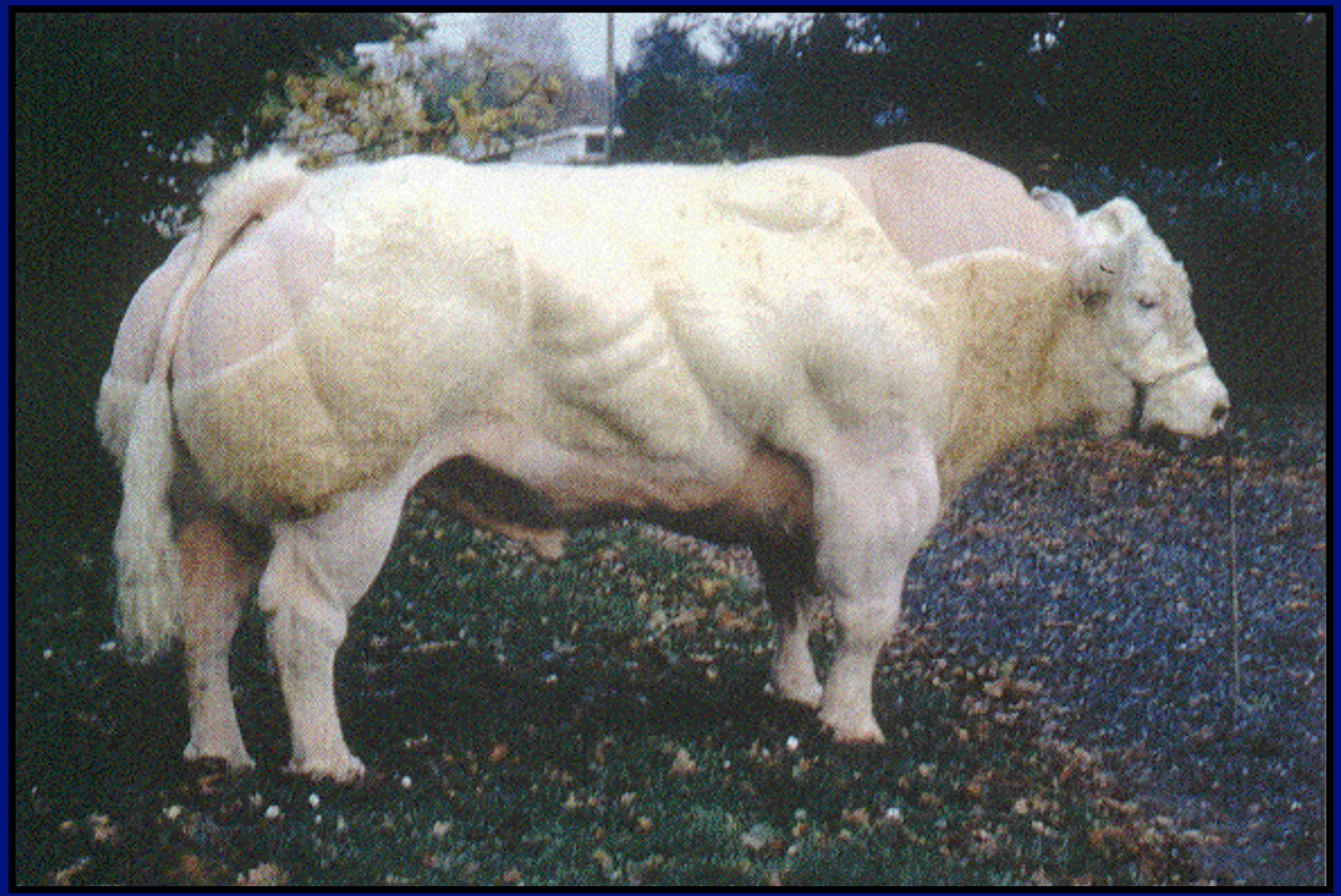


Fine Mapping

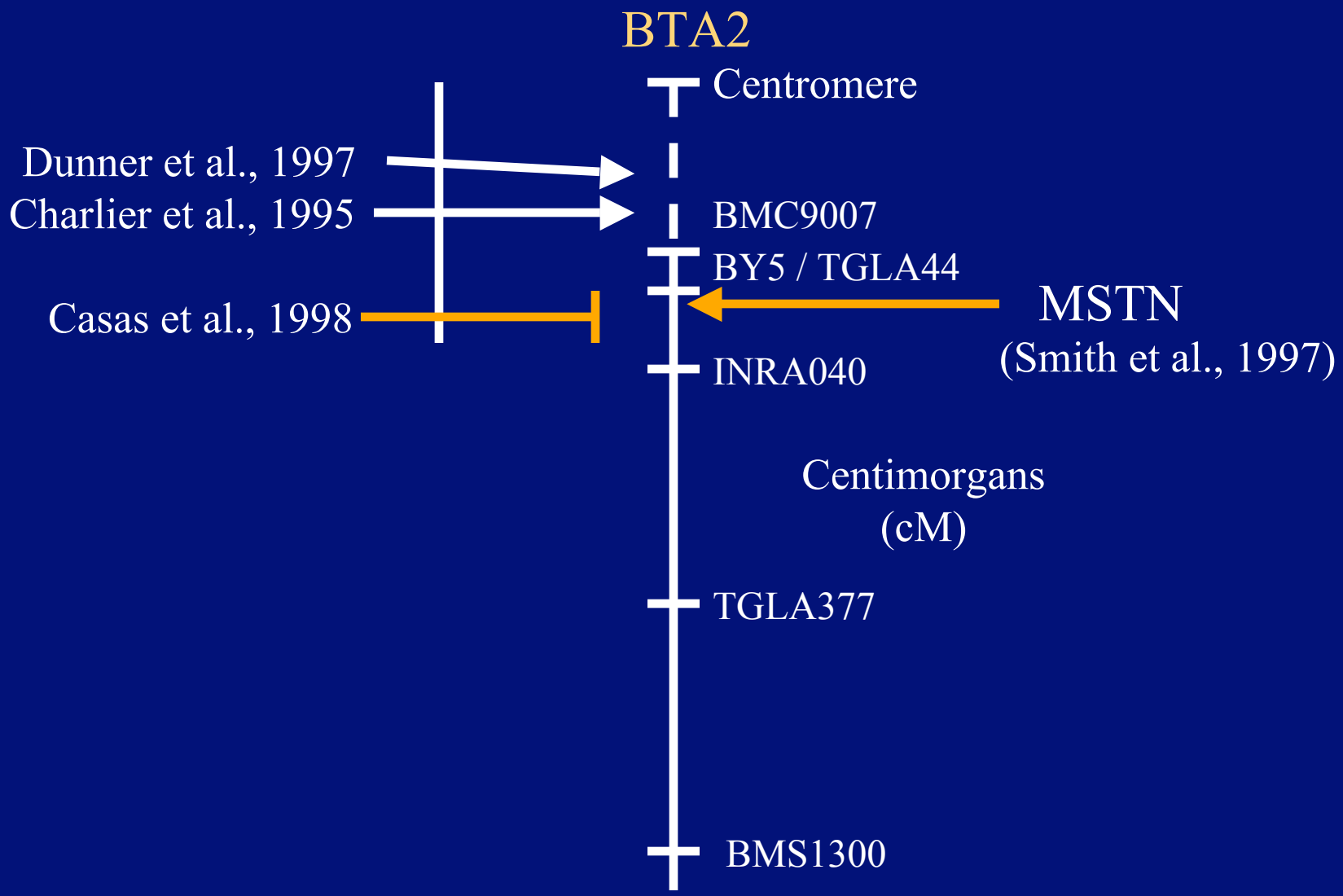
- Use additional DNA markers and animals to refine the location of the QTL (gene)
- Use human and mouse mapping information (Comparative Mapping)


BTA 15
cR5000
Cattle BAC clones
MMP20
BZ941449
BZ936687
MMP1
PORIMIN
BZ939858
BZ927106
BZ955507
BZ912680
BR3510
LOC143684
BZ955534
BZ941759
BZ951933
BZ956575
FDX1
BZ918235
RHCE**
BZ927848
APOA1APOC3
BZ899722 BZ907632
KIAA0999 PAFAH1B2
NCAM1 GRASP1**
BZ941912
BZ900304
ORP150
MGC16207
BZ916484
BZ929011
JAB1
BZ949997
DELGEF
HSPA8
NUCB2 BZ896953
BZ936721
BZ910135
BZ916579
AW289310
BZ907353
MGC13007
BZ955657
0
60
120
180
240
300
102.59
92.95
106.01
121.82
18.11
VIII
IX
HSA 11
10^6 bp
133.83
92.36
105.56
36.37
44.70
111.92
86.41
8.33
7.97
3.20
4.61
90.64
0.18
2.58
2.92
18.11
19.01
23.68
26.50
56.81
59.86
68.22
70.52
I
II
III
IV
IV
V
7
7
2
19
BTA 29
Cattle BAC clones
cR5000
BZ942629
BZ930113
PRCP
CTSC
BZ930457
BZ915122
LOC220055
AW465254 BZ901563
LOC220383
ZF AW267050
BZ951039
LOC220049
ILSTS019
BZ935392
BZ949696
BZ955148
ILSTS089
BZ932447
BZ940564
LOC144110
AW267134
BZ905352
FEZ1
BZ956113
ETS1
BZ949633
BZ949426 AW289197
RM040 BZ900418
AW267116
BZ928713
OPCML
BZ932751
CD5
BZ907953
BE217463
AW461519
AW261157
ROM1
MGC5395
BZ928355
BZ912781
BZ950502
SLC3A2
AW465621
BZ944599
EMK1
RTN3
HRASLS2
65B11C05 BE217465
BZ900343
BZ952153
BZ933943
0
60
120
180
240
300
86.99
75.74
23.68
19.01
123.52
133.84
59.86
VII
III
X
V

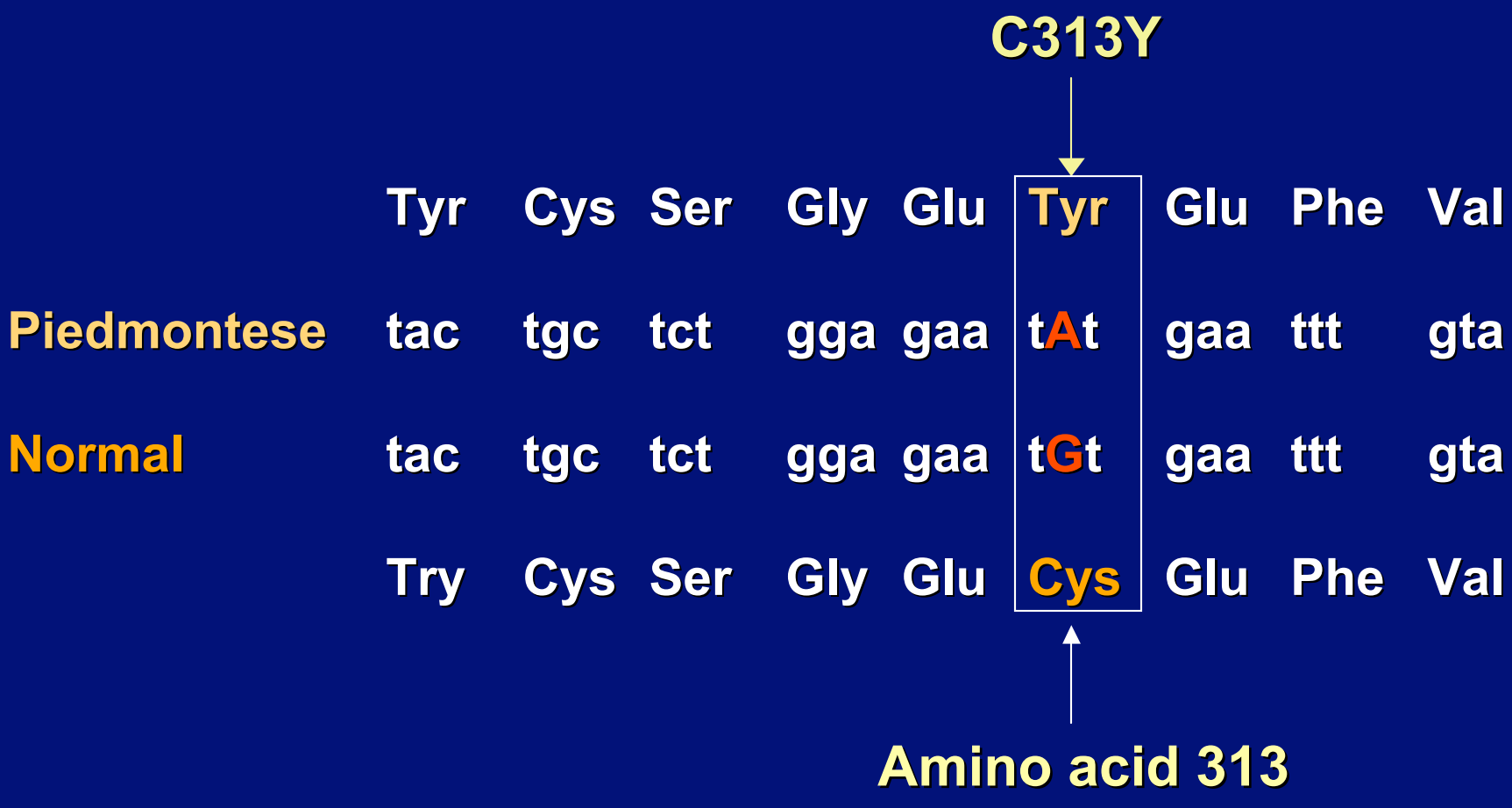
Fine Mapping Double Muscling



Myostatin (MSTN) location on BTA2



Piedmontese Myostatin Allele

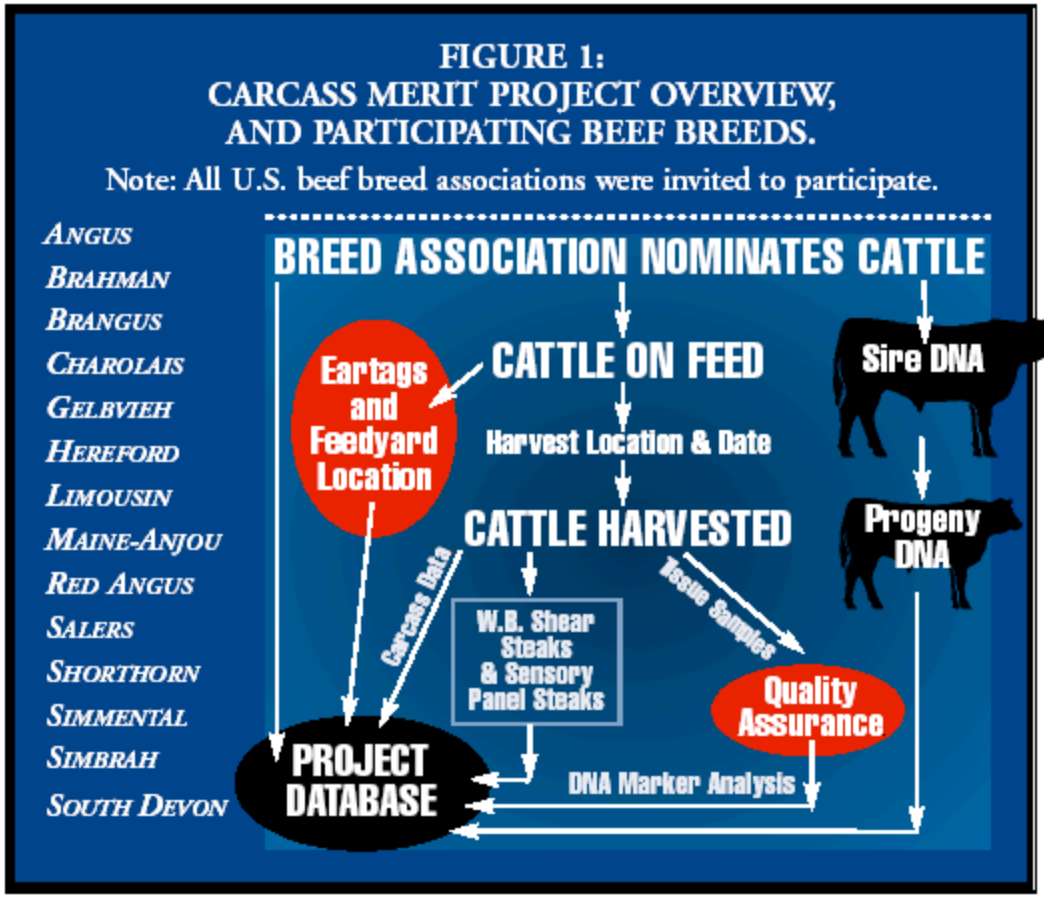


Materials and Methods

Selection and testing of progeny

Thirteen breed associations (representing 14 breeds) provided over 8,500 progeny of the most widely used sires within their respective breeds, primarily from commercial cowherds, for this research. The final analysis excluded data from 883 progeny because of incorrect animal or carcass identification. One or more reference sires of each breed were used in each test herd to tie contemporary groups together within breeds. The number of progeny included in the study from each breed was dependent on registration numbers, where breeds with larger numbers of animals registered had a greater number of progeny. Each breed association coordinated the following aspects of the study for its respective breed:

1. *Sire selection*
2. *Progeny testing*



segregation, project guidelines specified first, that each breed designate 10 bulls as DNA sires and secondly, that each DNA sire have 50 progeny

discovers additional carcass merit QTL. Project managers advised breed associations to collect additional blood samples to keep on file for their

TABLE 2

SIGNIFICANCE LEVELS OF QTL EFFECTS FROM MULTIPLE TRAIT HYPOTHESIS TESTS.[a]

Trait	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Q11
Shear Force	0.5	0.5	0.5	0.32	0.25	**0.008**	0.5	**0.040**	0.16	0.49	0.5
Overall Tnd	0.5	0.5	0.5	0.37	0.44	**0.001**	0.5	**0.030**	0.49	**0.004**	0.5
Fat Thickness	0.1	0.5	0.48	**0.043**	**0.030**	0.12	0.2	0.5	0.1	0.34	0.33
Marbling	0.15	0.4	0.44	0.31	0.32	0.11	0.12	0.5	0.06	0.37	**0.002**
Ribeye Area	0.5	0.5	0.18	0.44	0.32	**0.011**	**0.008**	**0.037**	0.5	0.5	0.5
Hot Carc Wt	0.5	0.5	0.19	0.47	0.5	0.47	**0.006**	**0.002**	0.5	0.5	0.49
Flavor	0.5	0.45	0.5	0.5	0.28	0.3	0.34	**0.022**	0.32	0.11	0.33
Overall Tnd	0.5	0.29	0.5	0.5	0.45	**0.01**	0.35	**0.015**	0.5	0.24	0.5
Juiciness	0.5	0.33	0.46	0.11	0.5	0.107	**0.024**	0.49	0.5	**0.050**	0.41
Overall Tnd	0.5	0.37	0.49	0.31	0.5	**0.021**	0.45	0.09	0.5	0.14	0.46

[a]Significance levels expressed to one or two decimal places are textbook values, those expressed to three decimal places are from permutation tests.

TABLE 3

PERCENTAGE OF PHENOTYPIC VARIANCE ACCOUNTED FOR BY EACH QTL.

Trait Name	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Q11
Shear Force	1	0	1	3	3	**12**	0	**6**	3	1	0
Overall Tnd	0	1	1	1	0	**10**	2	**8**	0	4	0
Myofib Tnd	1	2	0	1	0	**9**	2	**8**	0	4	0
Cn Tiss Tnd	3	1	0	0	0	**12**	4	**8**	0	2	0
Cooking Loss	4	2	**5**	0	3	1	0	**0**	2	2	1
Flavor	1	1	0	3	2	1	3	3	2	**5**	3
Juiciness	0	4	1	**6**	0	**6**	**7**	0	0	**5**	3
Marbling	1	2	2	2	1	4	4	1	4	1	**8**
Fat Thick	3	1	3	**5**	**6**	4	3	2	2	2	2
Internal Fat	0	**7**	0	3	**5**	2	0	1	2	1	1
Hot Carc Wt	1	0	2	0	0	2	**6**	**10**	0	1	3
Ribeye Area	0	0	4	2	3	**7**	**7**	3	0	1	1

TABLE 4

CORRELATIONS AMONG EFFECTS OF QTL 6
(PROPORTION OF PHENOTYPIC VARIANCE ACCOUNTED FOR BY QTL 6 ON THE DIAGONALS).

Trait Name	Trt	WBSF	OT	MT	CT	CL	FL	JC	MB	FT	KPH	HCW	REA
Shear Force	WBSF	**0.12**											
Overall Tnd	OT	-0.96	**0.10**										
Myofib Tnd	MT	-0.99	1.00	**0.09**									
Cn Tiss Tnd	CT	-0.89	0.95	0.96	**0.12**								
Cooking Loss	CL	0.67	-0.86	-0.84	-0.76	**0.01**							
Flavor	FL	0.31	0.62	0.32	0.57	-0.57	**0.01**						
Juiciness	JC	0.11	0.04	0.04	0.27	-0.74	0.79	**0.06**					
Marbling	MB	0.23	-0.57	-0.41	-0.62	0.90	-0.85	-0.24	**0.04**				
Fat Thick	FT	-0.40	0.43	0.28	0.03	0.18	0.85	0.70	0.84	**0.04**			
Internal Fat	KPH	-0.79	0.93	0.99	0.70	-0.90	-0.43	-0.66	-0.19	0.41	**0.02**		
Hot Carc Wt	HCW	-0.23	0.18	0.02	-0.16	-0.51	-0.35	-0.45	0.87	0.54	1.00	**0.02**	
Ribeye Area	REA	0.17	0.09	0.14	0.06	0.47	-0.57	-0.77	0.35	0.91	0.21	-0.02	**0.07**

Important genes affecting beef production traits

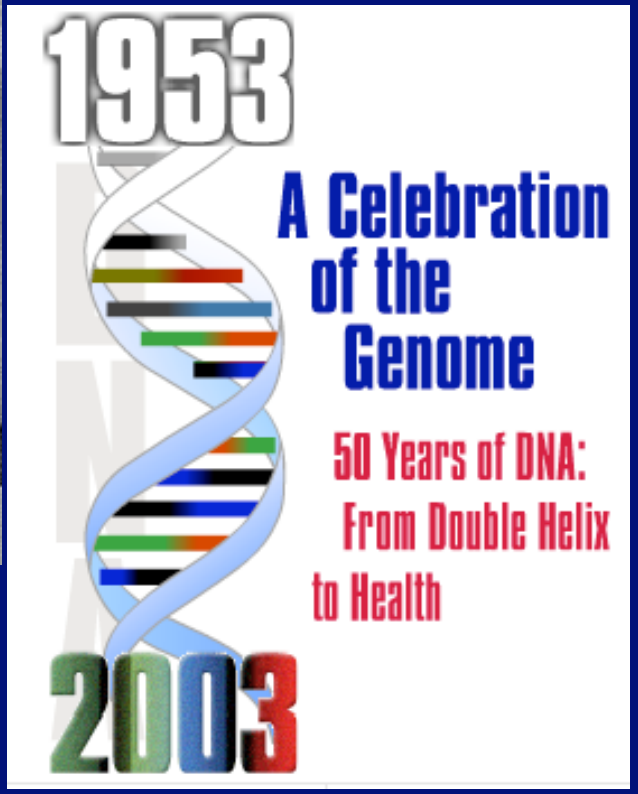
- Thyroglobulin- marbling (GS Marbling)
- Calpastatin- tenderness (GS Tenderness)
- Calpain- tenderness (two SNP)
- Leptin- fat deposition (SNP)
- DGAT - fat deposition in milk
- Somatostatin -- marbling
- ROCR (Marbling) – Australia CSIRO??

We are at a Critical Juncture.

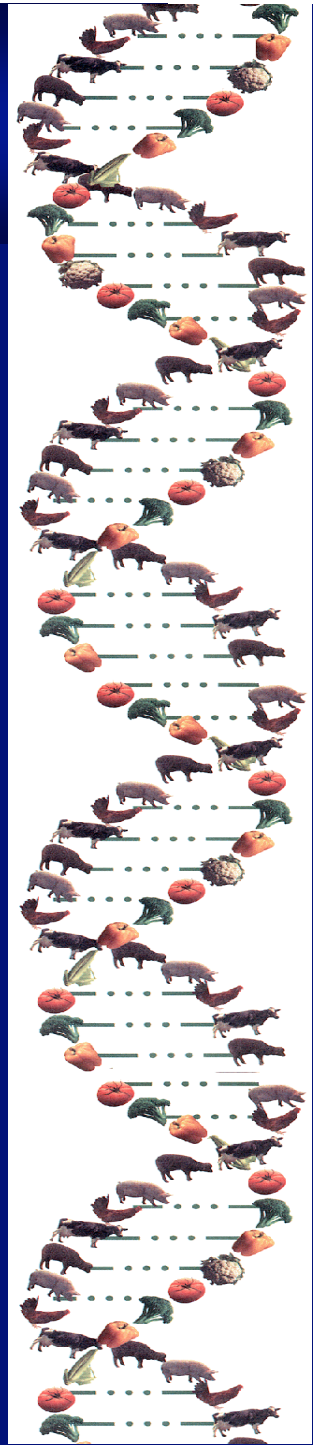
Current limitations in genomics research

- **The few genes that we have been identified only explain a small part of genetic variation**
- **Time and expense to identify the majority of genes that affect a single trait**
- **Need for more genomics-enabling infrastructure**

50th Anniversary of DNA Structure – THE FINISHED HUMAN GENOME



Genomic Sequencing?



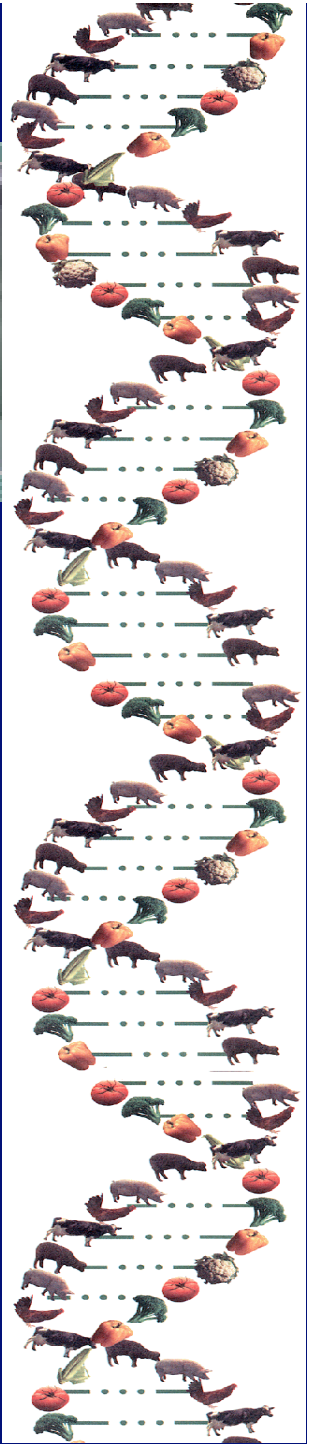
Interagency Coordination Essential….

- ***Interagency Working Group on Domestic Animal Genomics***
  - Executive Office of the President
    - Office of Science & Technology Policy (OSTP)
    - National Science & Technology Council (NSTC)
    - Committee on Science (co-Chairs NIH, NSF, OSTP)
- Established in winter 2002
- Charter members
  - DOE, FDA, NIH, NSF, OMB, OSTP, USDA
- Chairperson -- Joseph Jen, USDA/REE
  Executive Director – Ronnie Green, USDA/ARS

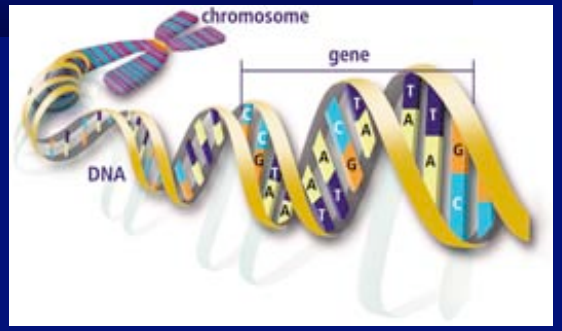
genome.gov

National Human Genome Research Institute

National Institutes of Health



International Collaboration



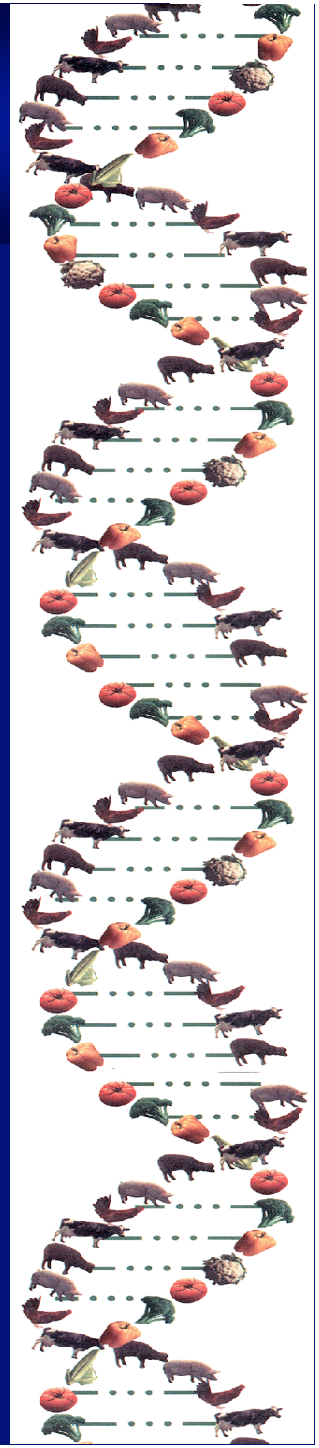
- *Australia -- $1M*
- *Genome Canada -- $5M*
- *New Zealand -- $1M*

Domestic US Collaboration

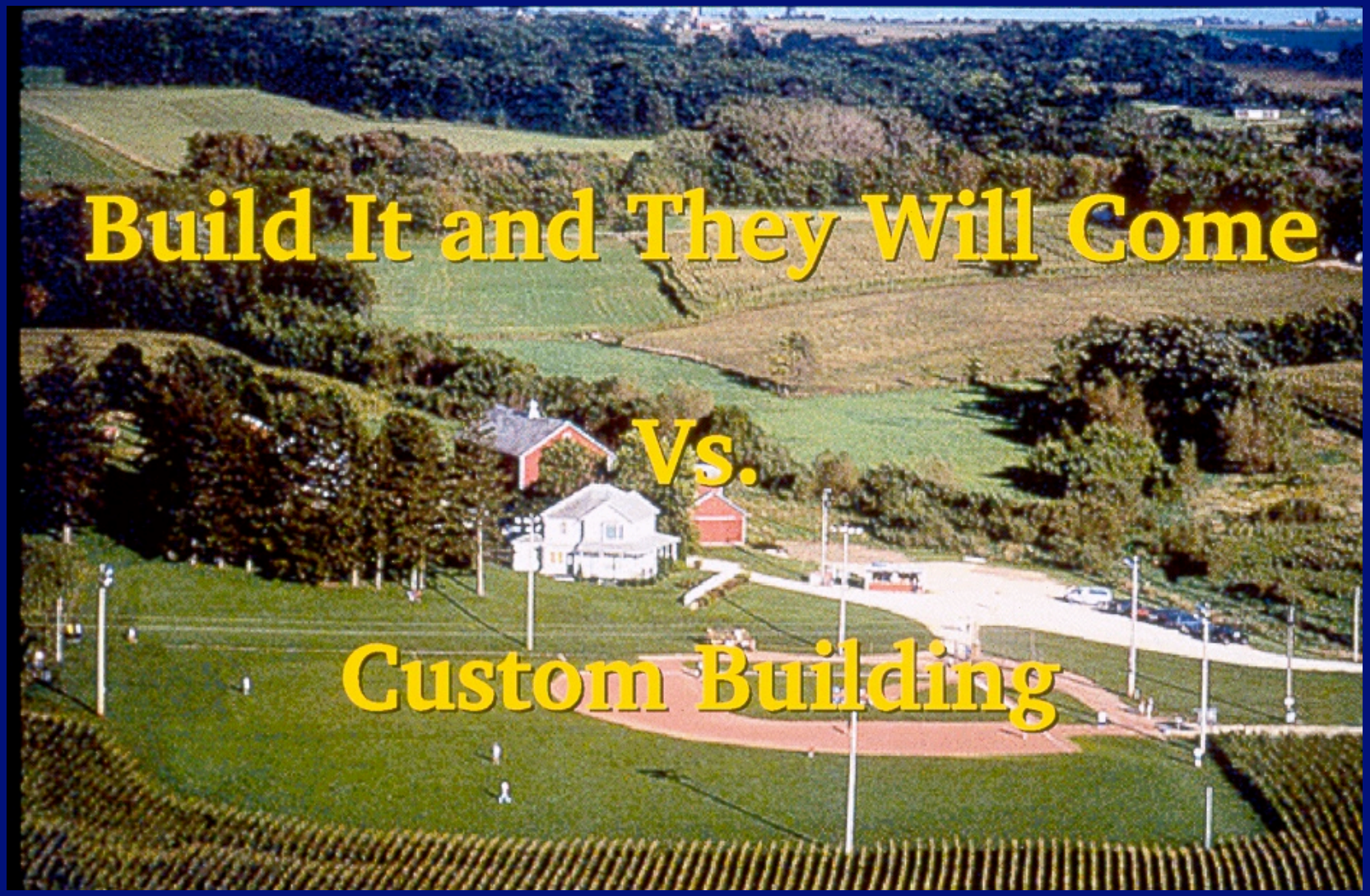
- *NIH / NHGRI -- $25M*
- *State of Texas – $10M*
- *USDA -- $11M*
- *Beef Councils (Natl., TX, SD) – $0.8M*

Project Total = $53M

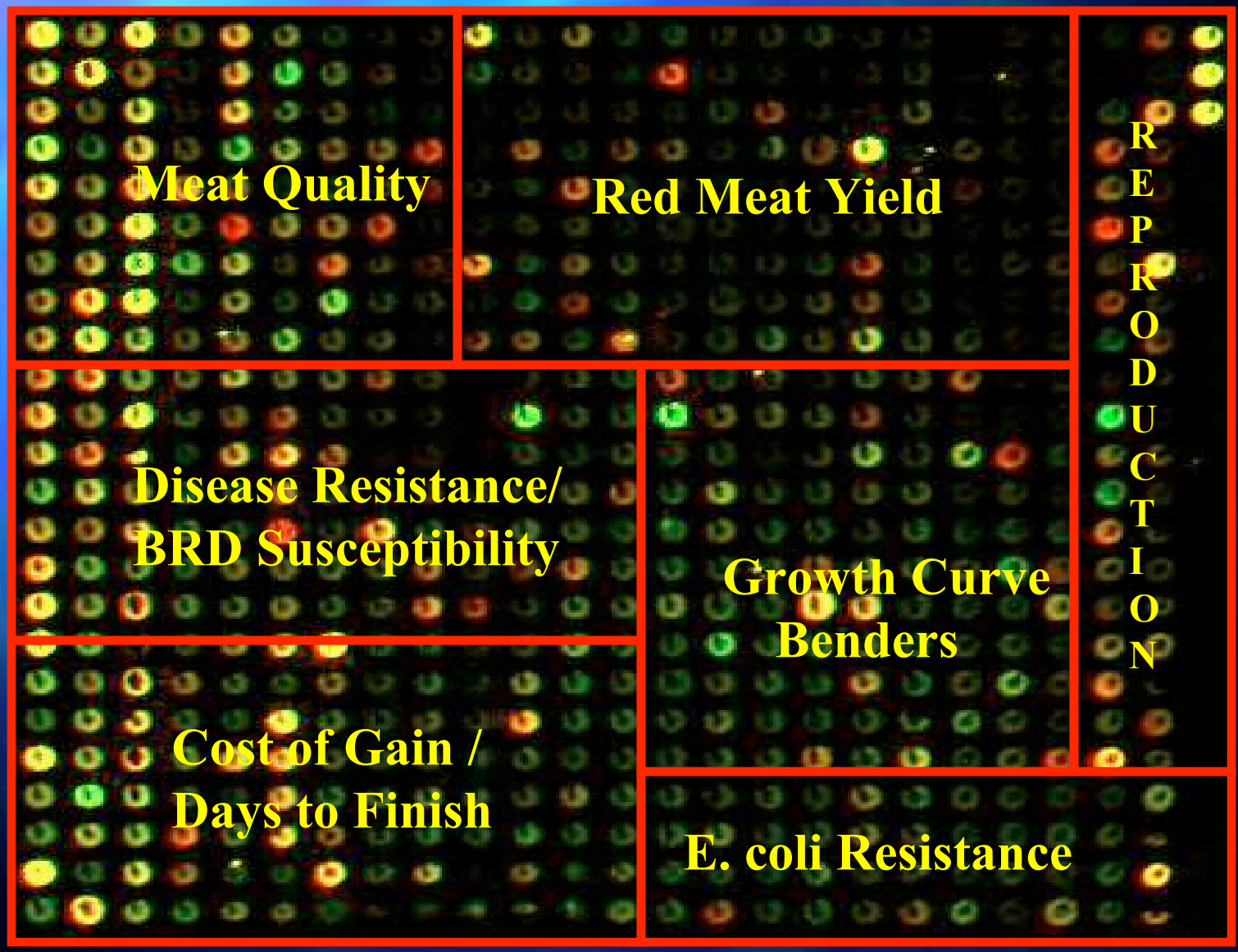
Genomic Sequencing?



Launch: Dec. 2003
Expected Finish: early 2005


Build It and They Will Come
Vs.
Custom Building

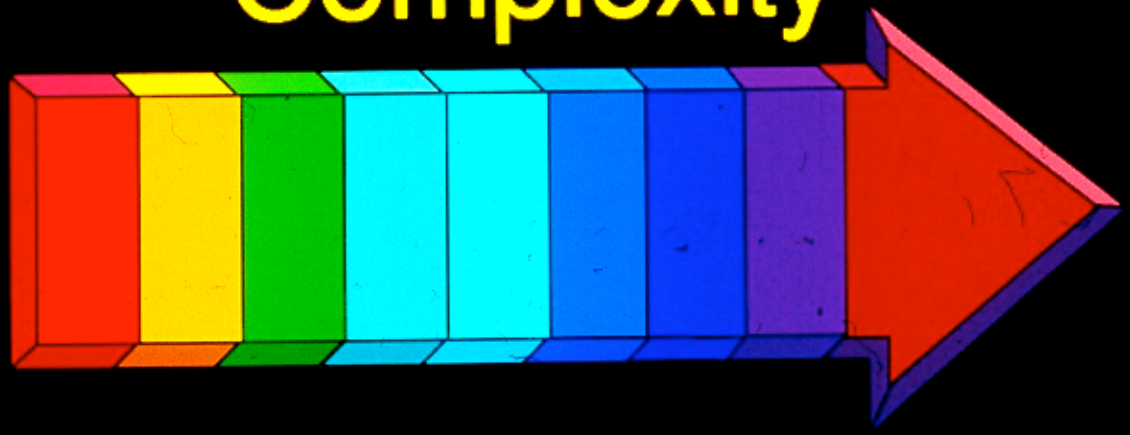
Breeding on a Chip



Simplicity

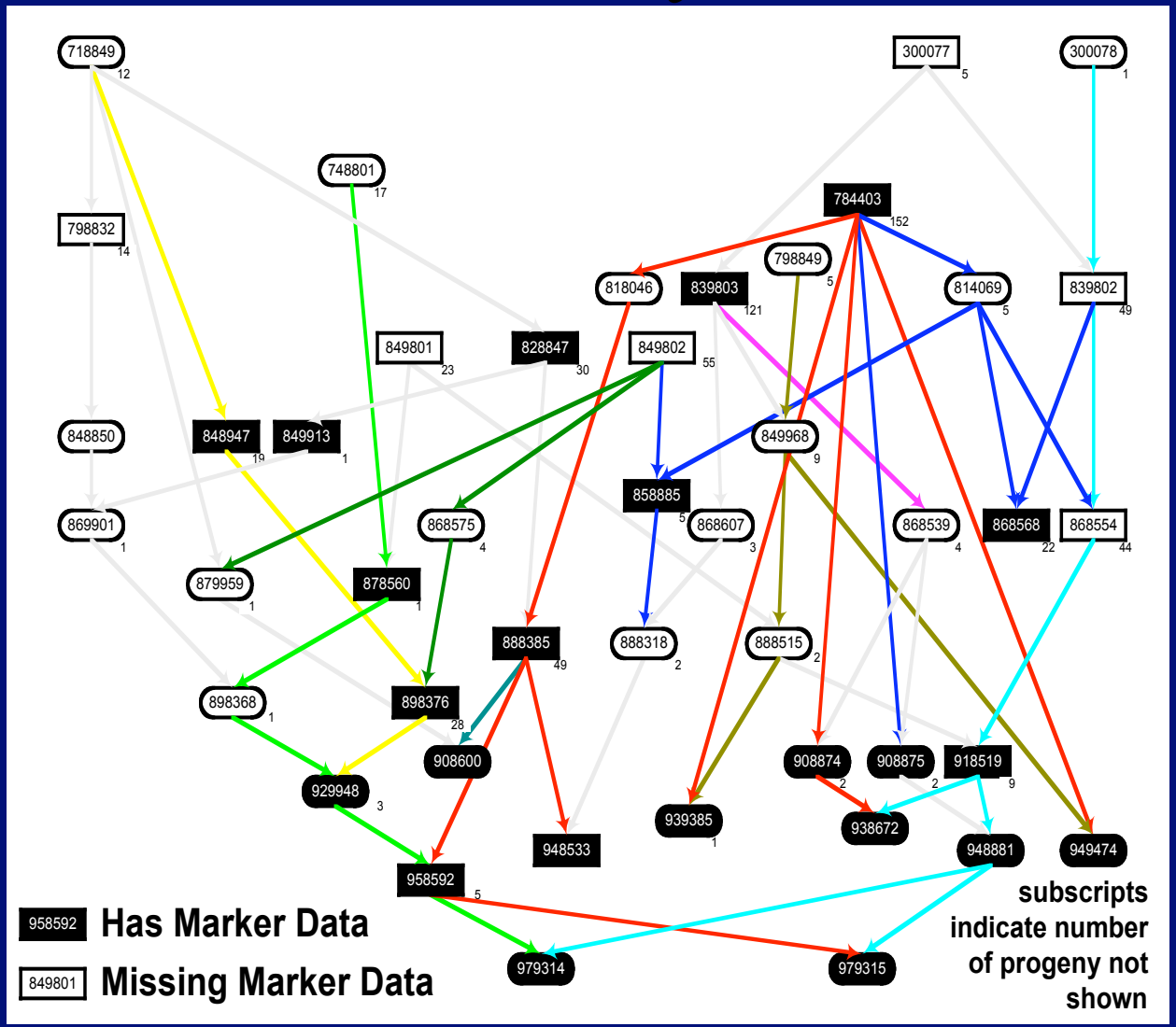
vs.

Complexity



Challenges in Applying MAS in the Beef Industry:

- Complex Pedigree
- Many Small Families
- Missing Marker Data
- Censored Data



Marker Assisted Selection in the Twinning Population

Animal	Residual EPD	Chr. 5:40	Chr. 7:60	Chr. 7:125	Marker Adjusted EPD
979447	22	+6	+5	+3	36
979405	27	+3	+5	-2	33
979413	20	+6	+3	+2	31
979328	19	+4	+3	+1	27

Genetic Improvement -- DNA Based Gene Selection

Unknown genes

Molec. genetics

Identified QTL

Phenotypic data

EPD for unknown polygenes

QTL-BLUP

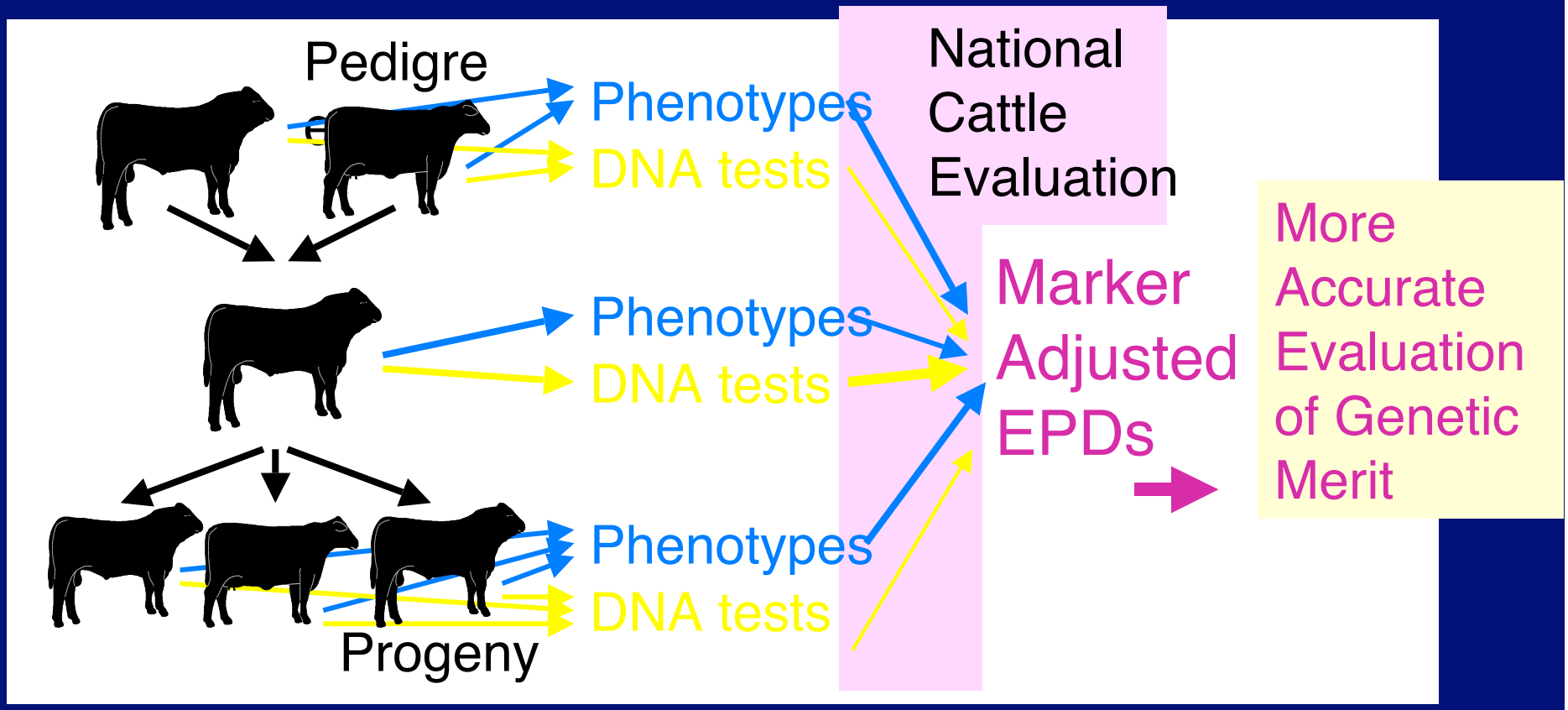
?

Selection criterion

Genotypic data

(E)PD for identified QTL

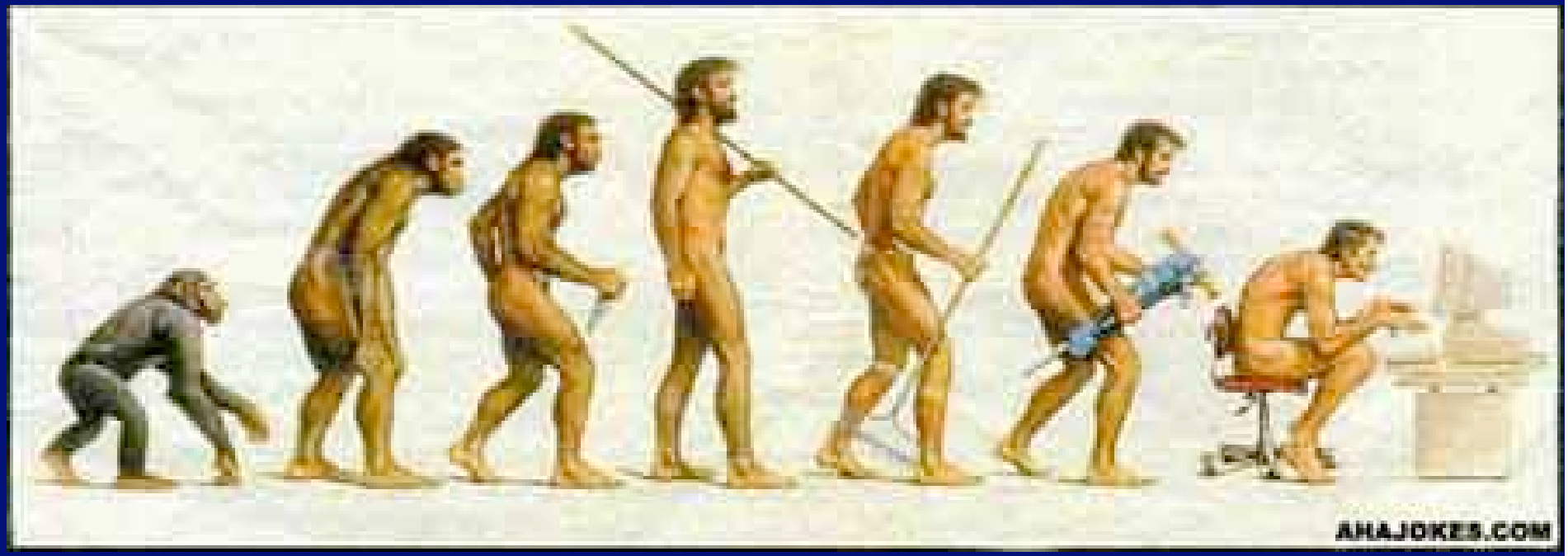
National Beef Cattle Evaluation Consortium (NBCEC) QTL Team



- Incorporation of DNA test results into National Cattle Evaluations

National Beef Cattle Evaluation Consortium
Colorado State University-Cornell University-University of Georgia-Iowa State University


México


AHAJOKES.COM

Genomics Research

- Carcass traits- marbling , tenderness
- Growth – bend growth curve
- ***Feed efficiency – expensive to measure***
- ***Reproduction- dissect components***
  - ***Twinning – heritability from 7 to 35%***
- ***Animal health- difficult to measure***
- Select for multiple traits
- Management “by genotype”

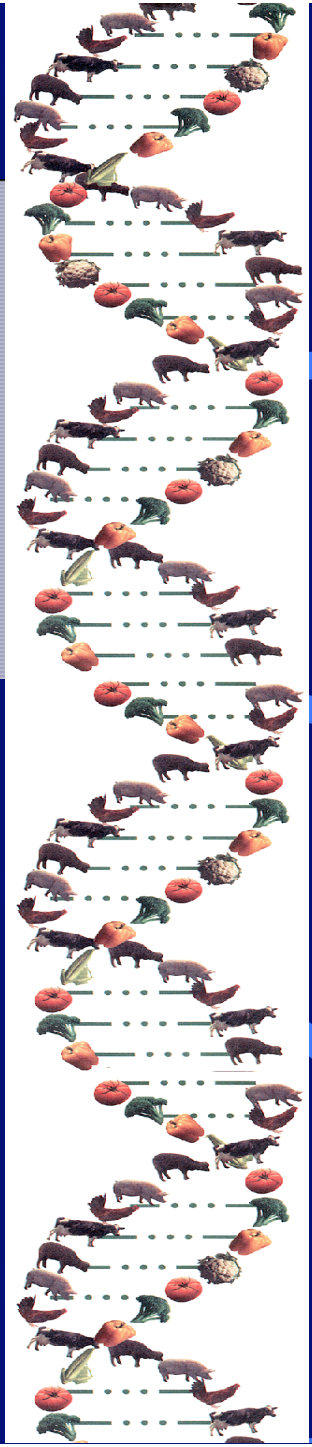

G
N
M
K
F
L
H
J

Genomics Research -- Health

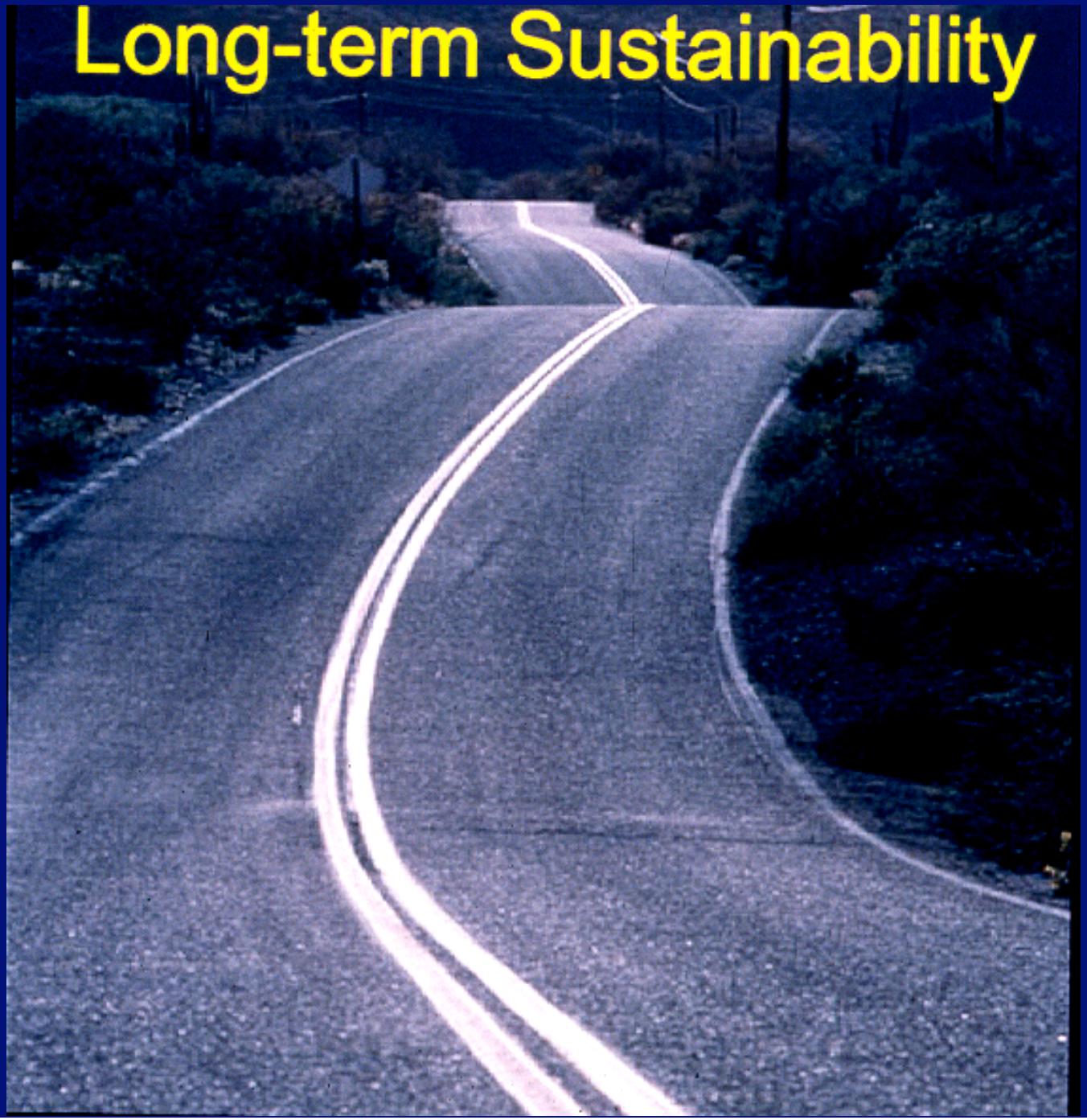
- PrP Gene – Scrapie, CWD, BSE?
- HEXA – UK identified for BSE?
- ***FMD***
- ***Fescue Toxicosis***
- New vaccine development
- New drug targets


Animal Identification Plan
United States
USAIP
"Protecting American Animal Agriculture"
United States Animal Identification Plan
(USAIP) Information Site
Click on animal to view proposed USAIP Plan under development.
USAIP Home
Resources
Questions?
Work Plan
Send Comments

??????????????????



Long-term Sustainability



Business Models???

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*

Enter site in:

GeneSTAR Pricing - International

- Online Ordering - International
- GeneSTAR Pricing - International

GeneSTAR Marbling

No. of Samples	Price per sample US $
25 samples or less	US$85.00
26 to 100 samples	US$65.00
101 to 500 samples	US$55.00
Over 500 samples	US$45.00

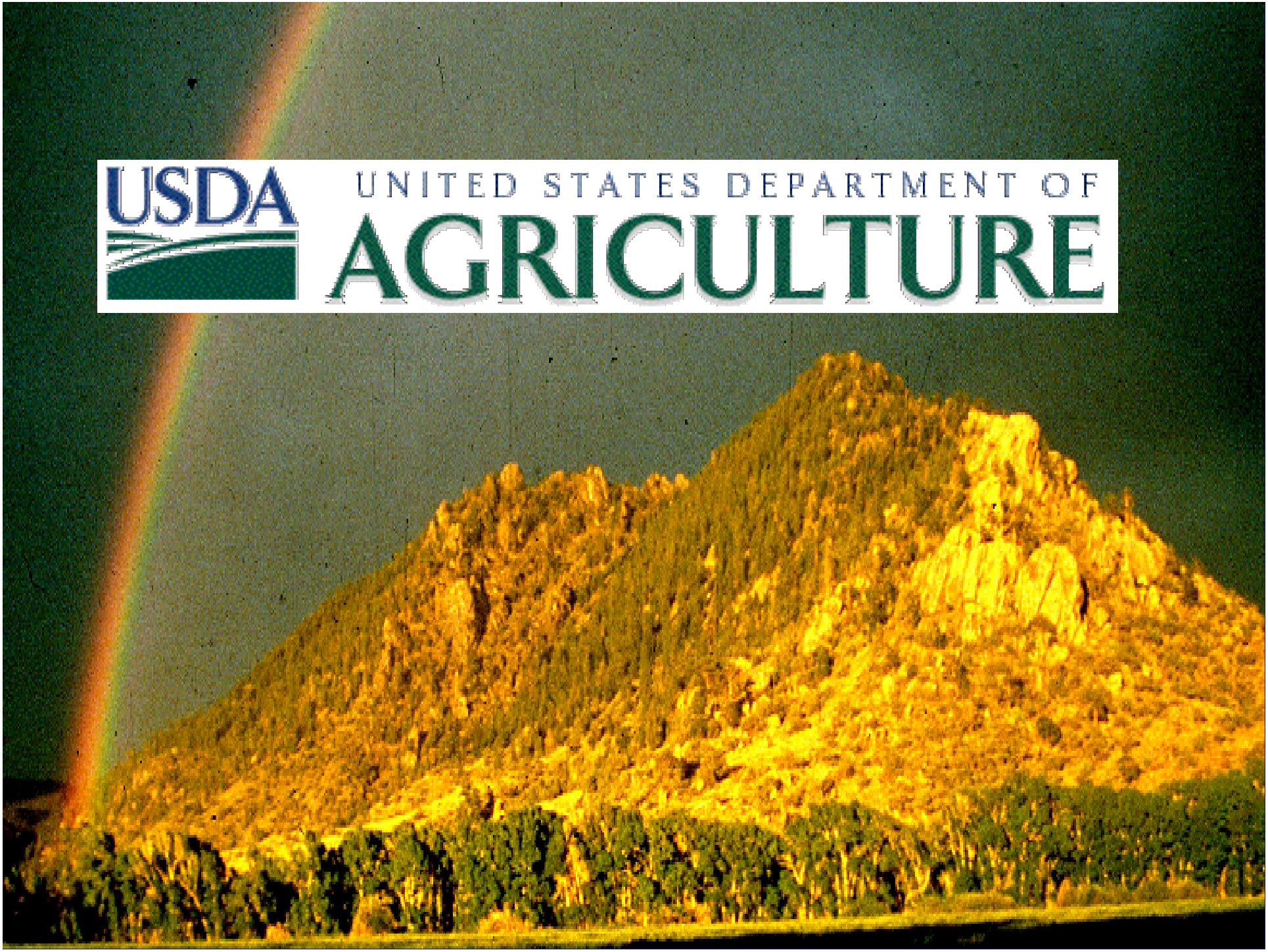
GeneSTAR Tenderness 2

No. of Samples	Price per sample US$
25 samples or less	US$100.00
26 to 100 samples	US$80.00
101 to 500 samples	US$70.00
Over 500 samples	US$60.00

GeneSTAR Marbling and GeneSTAR Tenderness 2

Price for tests submitted as a single sample

No. of Samples	Price per sample US$
25 samples or less	US$160.00
26 to 100 samples	US$120.00
101 to 500 samples	US$95.00
Over 500 samples	US$80.00


USDA
UNITED STATES DEPARTMENT OF
AGRICULTURE


GeneSTAR®
SureTRAK®
SireTRACE™

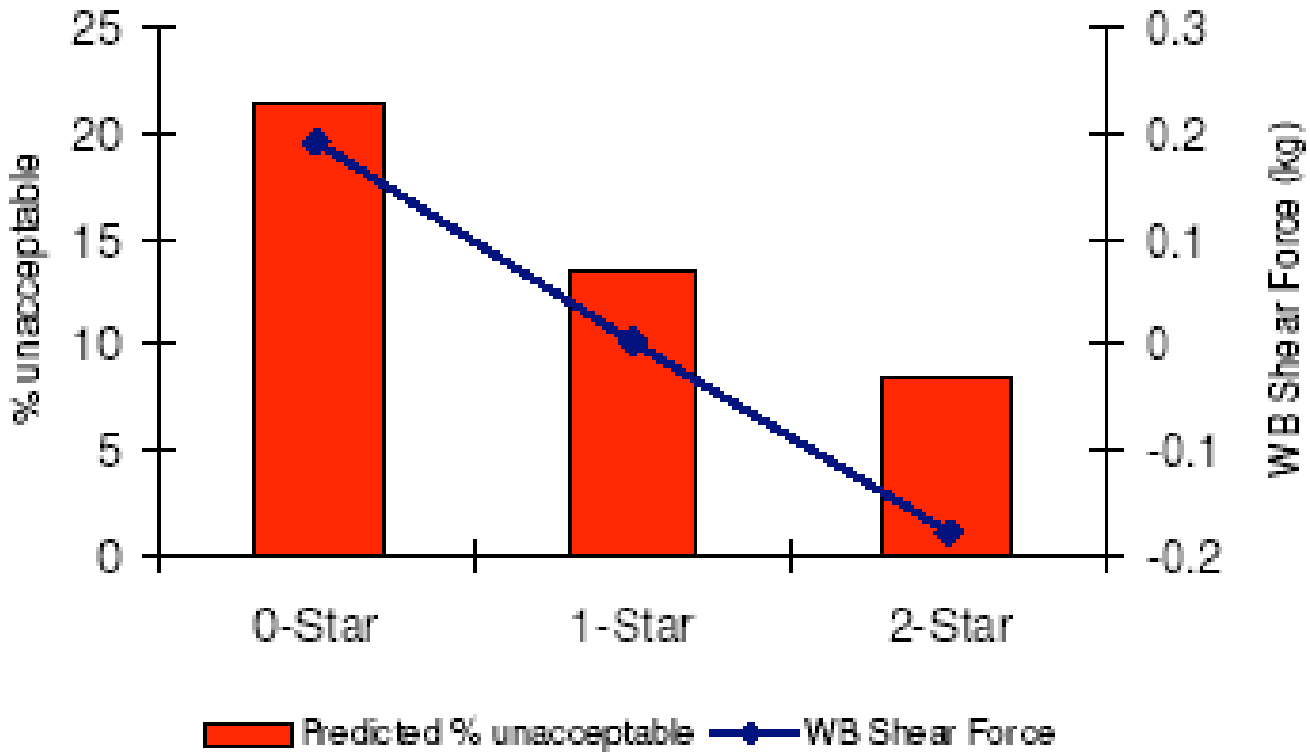


Figure 2. Relationship between % unacceptable carcases as judged by consumers and Warner Bratzler (WB) Shear Force values (deviation from mean) for 0, 1 and 2-STAR animals