

Dairy Cattle Breeding in the United States

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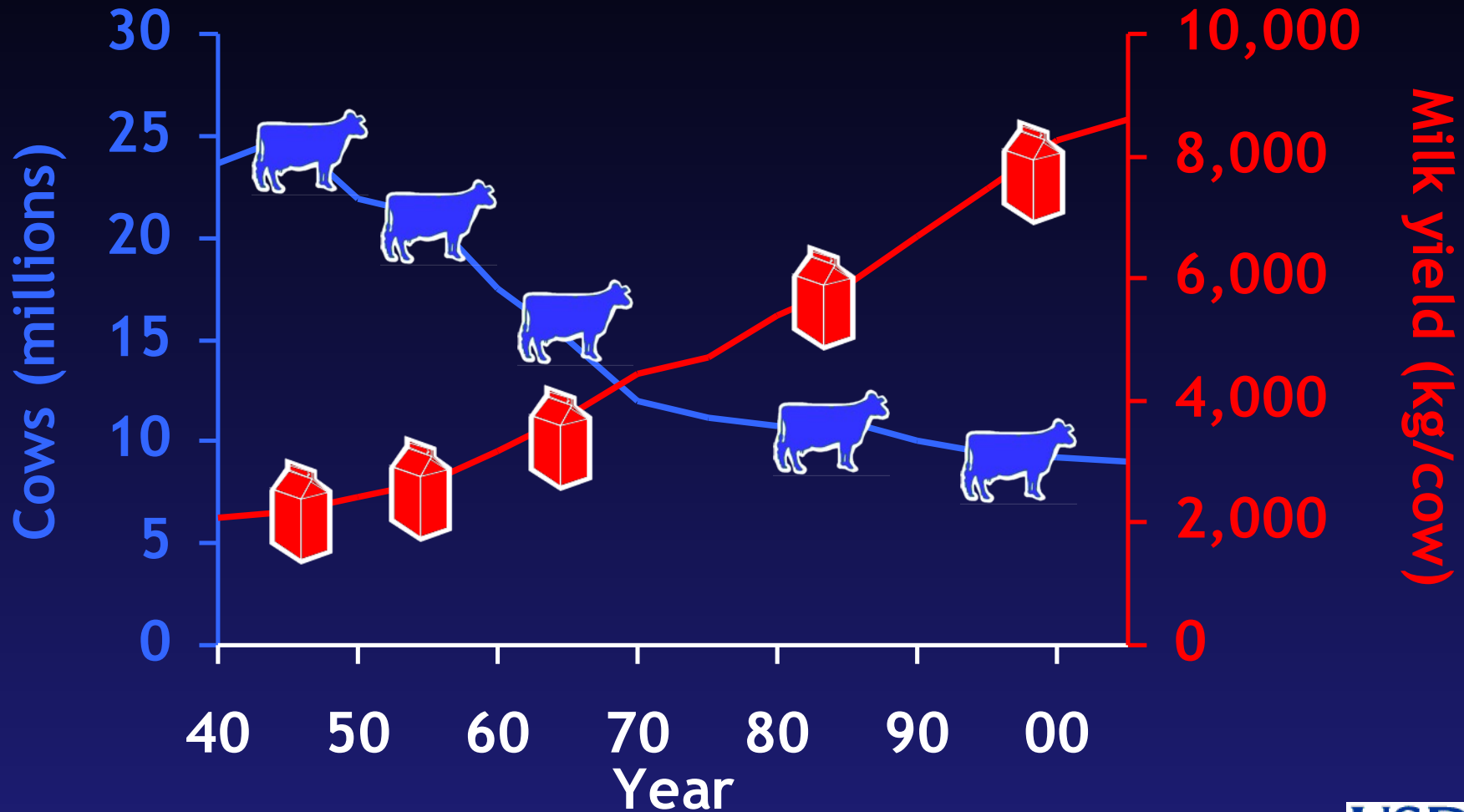
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U.S. dairy statistics (2004)

- ◆ 9.0 million cows
- ◆ 67,000 herds
- ◆ 135 cows/herd
- ◆ 19,000 lb (8600 kg)/cow
- ◆ ~93% Holsteins, ~5% Jerseys
- ◆ ~75% bred AI
- ◆ 46% milk recorded through Dairy Herd Improvement (DHI)

U.S. dairy population and yield



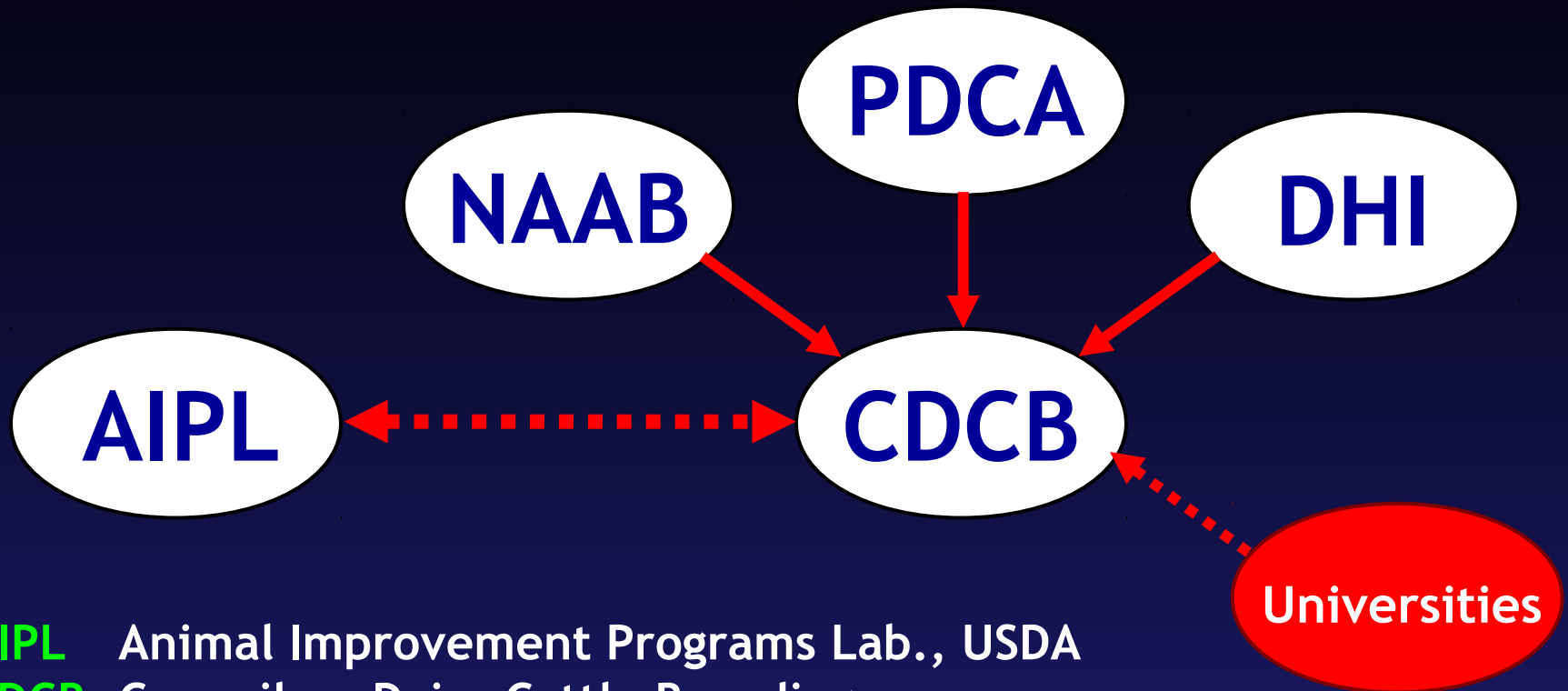
DHI statistics (2004)

- ◆ 4.1 million cows
 - ◆ 97% fat recorded
 - ◆ 93% protein recorded
 - ◆ 93% SCC recorded
- ◆ 25,000 herds
- ◆ 164 cows/herd
- ◆ 21,250 lb (9640 kg)/cow
 - ◆ 3.69% fat
 - ◆ 3.09% (true) protein

U.S. progeny-test bulls (2000)

- ◆ Major and marketing-only AI organizations plus breeder-proven
- ◆ Breeds
 - ◆ Ayrshire 10 bulls
 - ◆ Brown Swiss 53 bulls
 - ◆ Guernsey 15 bulls
 - ◆ Holstein 1436 bulls
 - ◆ Jersey 116 bulls
 - ◆ Milking Shorthorn 1 bull

National Dairy Genetic Evaluation Program



AIPL Animal Improvement Programs Lab., USDA

CDCB Council on Dairy Cattle Breeding

DHI Dairy Herd Improvement (milk recording organizations)

NAAB National Association of Animal Breeders (AI)

PDCA Purebred Dairy Cattle Association (breed registries)

A IPL mission

- ◆ Conduct research to discover, test, and implement improved genetic evaluation techniques for economically important traits of dairy cattle and goats
- ◆ Genetically improve efficiency of dairy animals for yield and fitness

A IPL research objectives

- ◆ Maintain a **national database** with animal identification, production, fitness, reproduction, and health traits to support research on dairy genetics and management
- ◆ Provide data to others researchers submitting proposals compatible with industry needs

AIPL research objectives (*cont.*)

- ◆ Increase **accuracy of genetic evaluations** for traits through improved methodology and through inclusion and appropriate weighting of deviant data
- ◆ Develop **bioinformatic tools** to automate data processing in support of **quantitative trait locus detection**, marker testing, and mapping methods

AIPL research objectives (*cont.*)

- ◆ Improve genetic rankings for **overall economic merit** by evaluating appropriate traits and by determining economic values of those traits in the index
- ◆ Improved profit functions are derived from reviewing incomes and expenses associated with each trait available for selection

A IPL research objectives (*cont.*)

- ♦ Characterize **dairy industry practices** in milk recording, breed registry, and artificial-insemination to **document status and changes** in data collection and use and in observed and genetic trends in the population

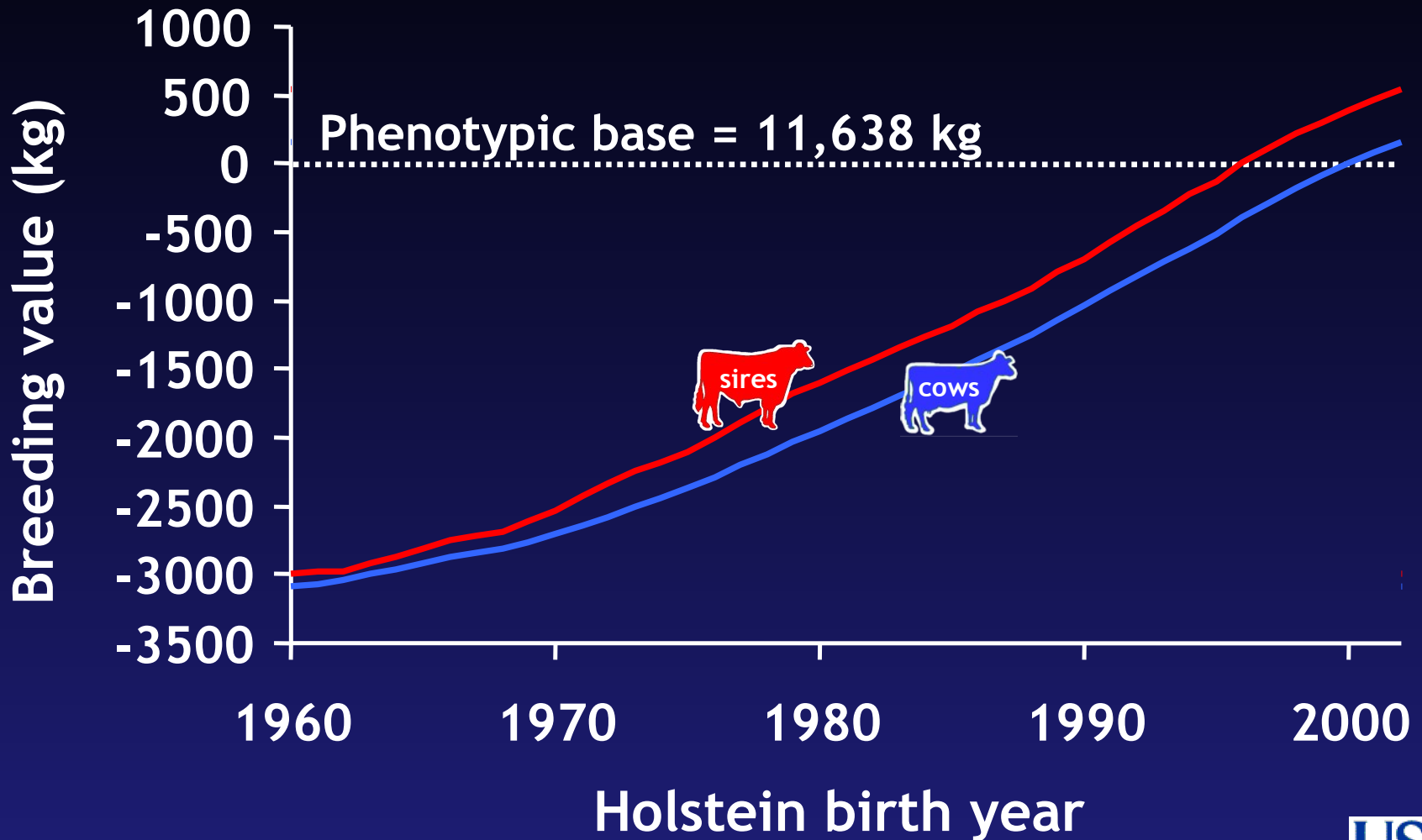
Traits evaluated

- ◆ Yield (milk, fat, protein volume; component percentages)
- ◆ Type/conformation
- ◆ Productive life/longevity
- ◆ Somatic cell score/mastitis resistance
- ◆ Fertility
 - ◆ Daughter pregnancy rate (cow)
 - ◆ Estimated relative conception rate (bull)
- ◆ Dystocia and stillbirth (service sire, daughter)

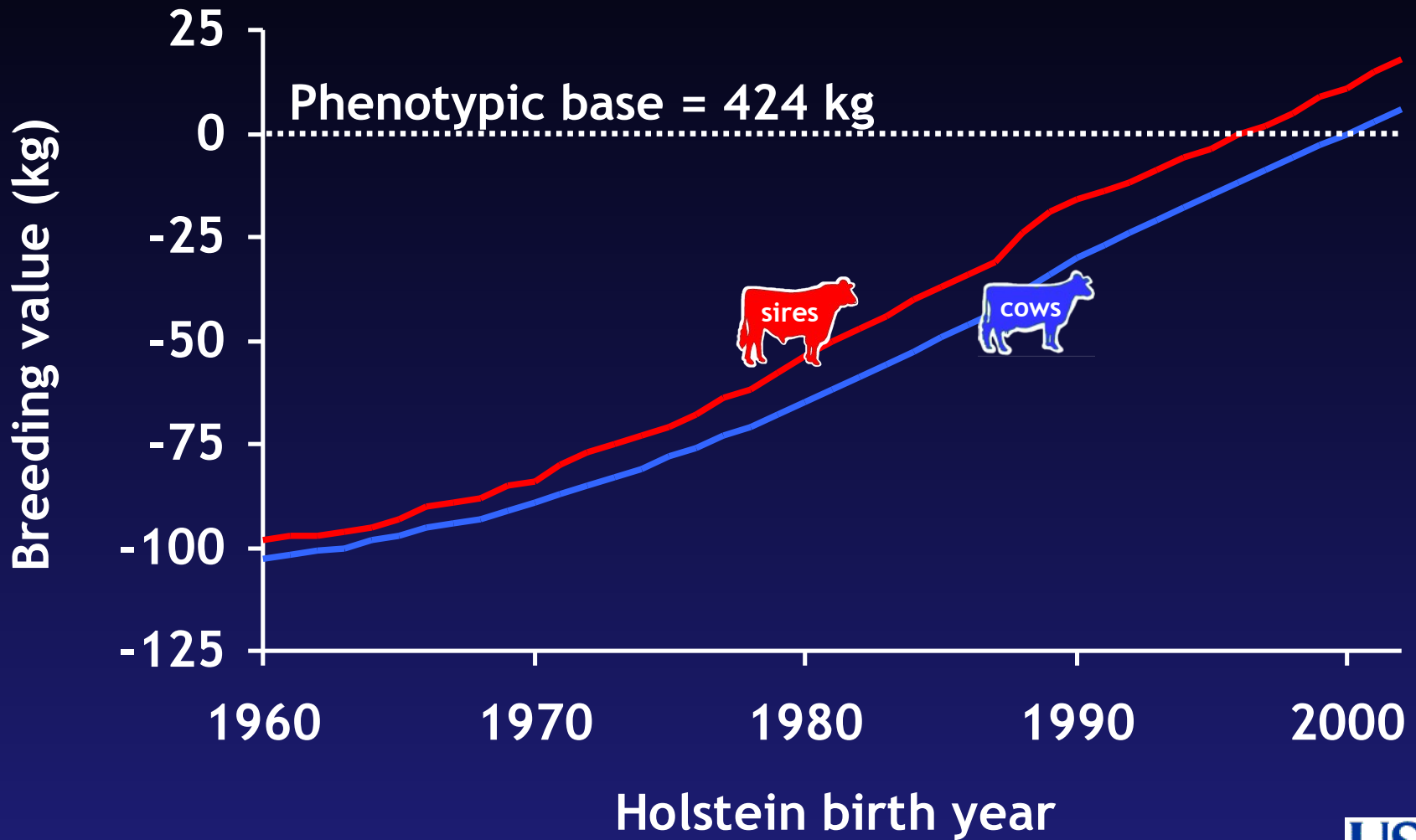
Evaluation methods

	Heritability
◆ Animal model (linear)	
◆ Yield (milk, fat, protein)	25 - 40%
◆ Type (Ayrshire, Brown Swiss, Guernsey, Jersey)	7 - 54%
◆ Productive life	8.5%
◆ SCS	12%
◆ Daughter pregnancy rate	4%
◆ Sire - maternal grandsire model (threshold)	
◆ Service sire calving ease	8.6%
◆ Daughter calving ease	3.6%
◆ Service sire stillbirth	3.0%
◆ Daughter stillbirth	6.5%

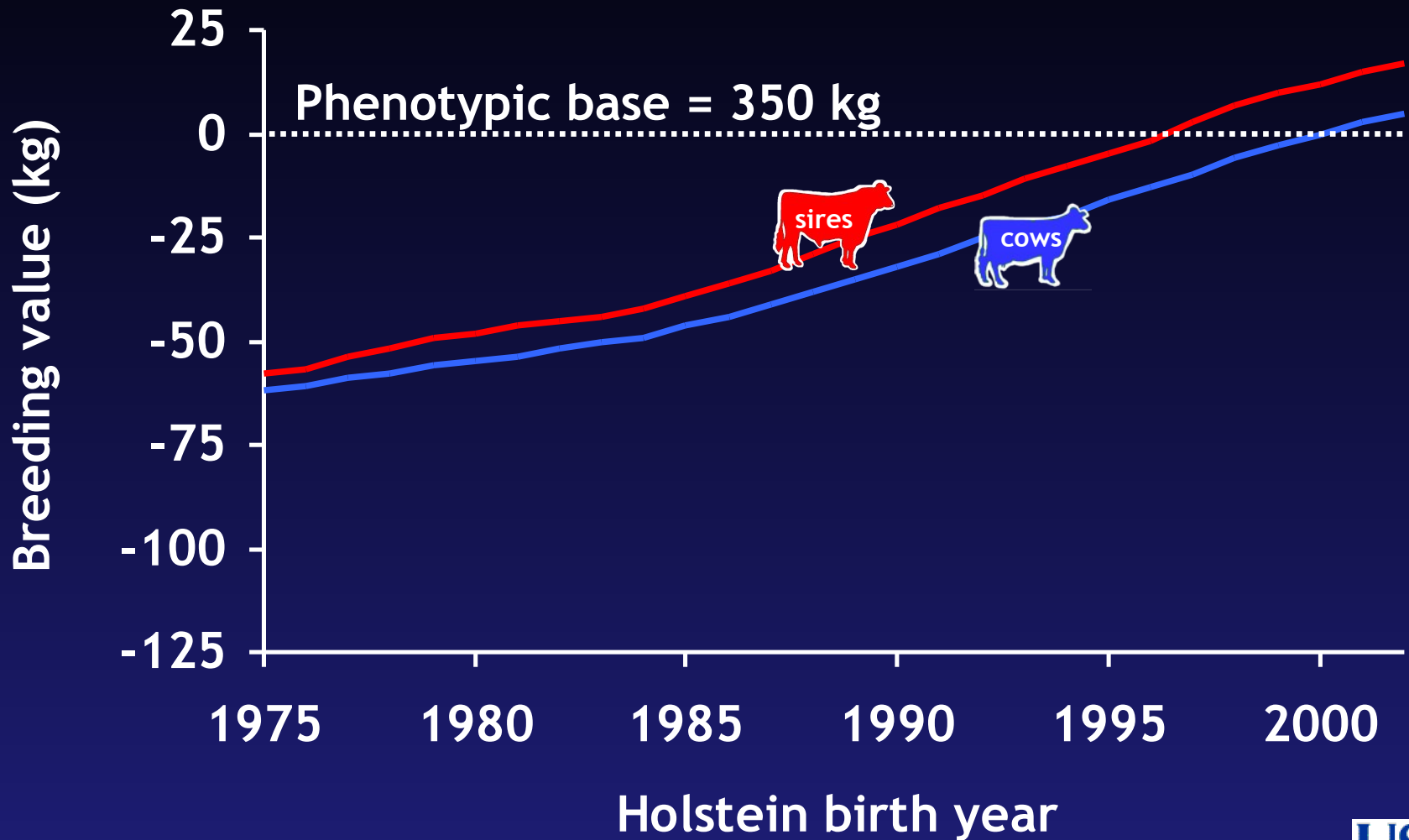
Genetic trend - Milk



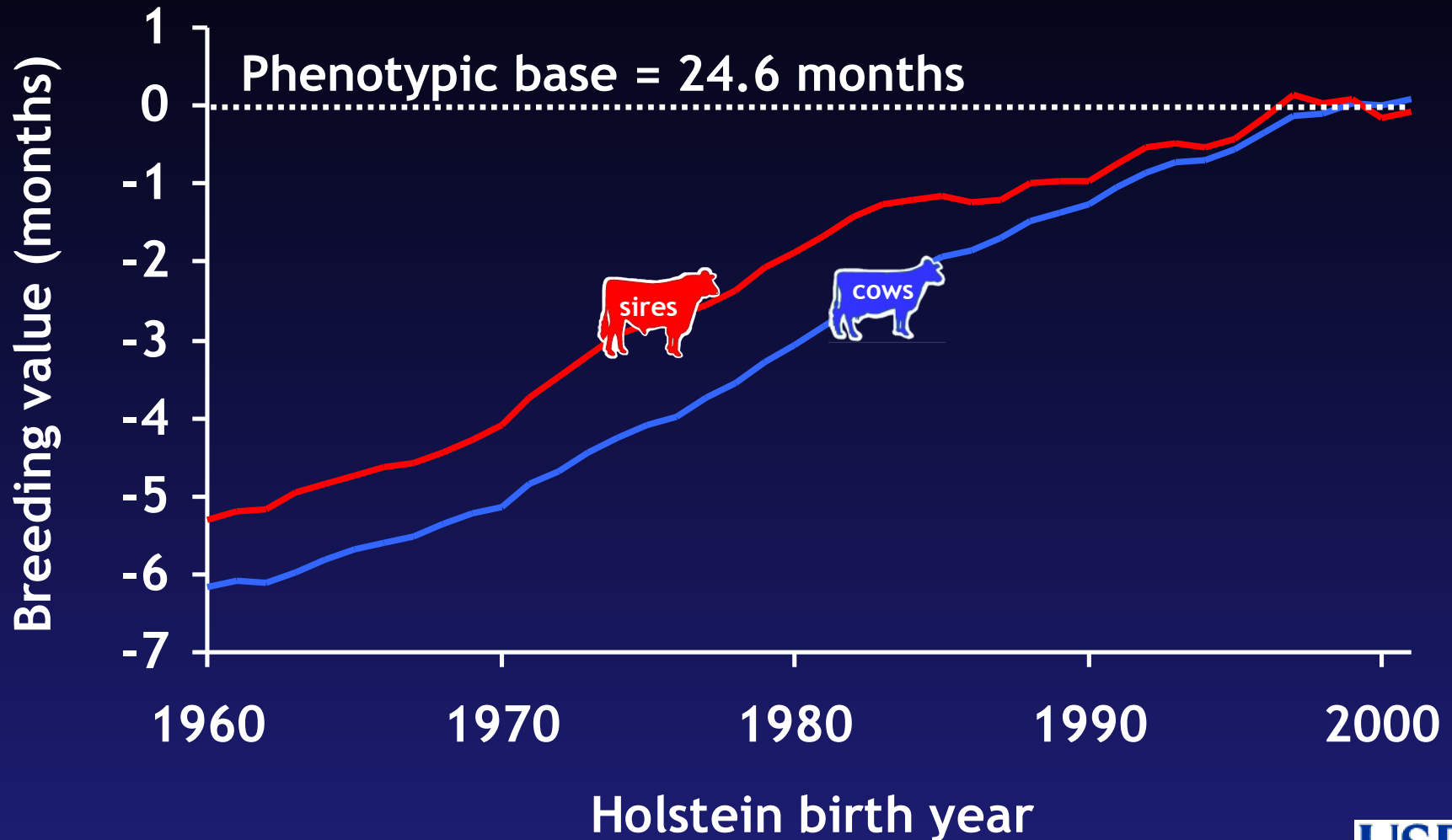
Genetic trend - Fat



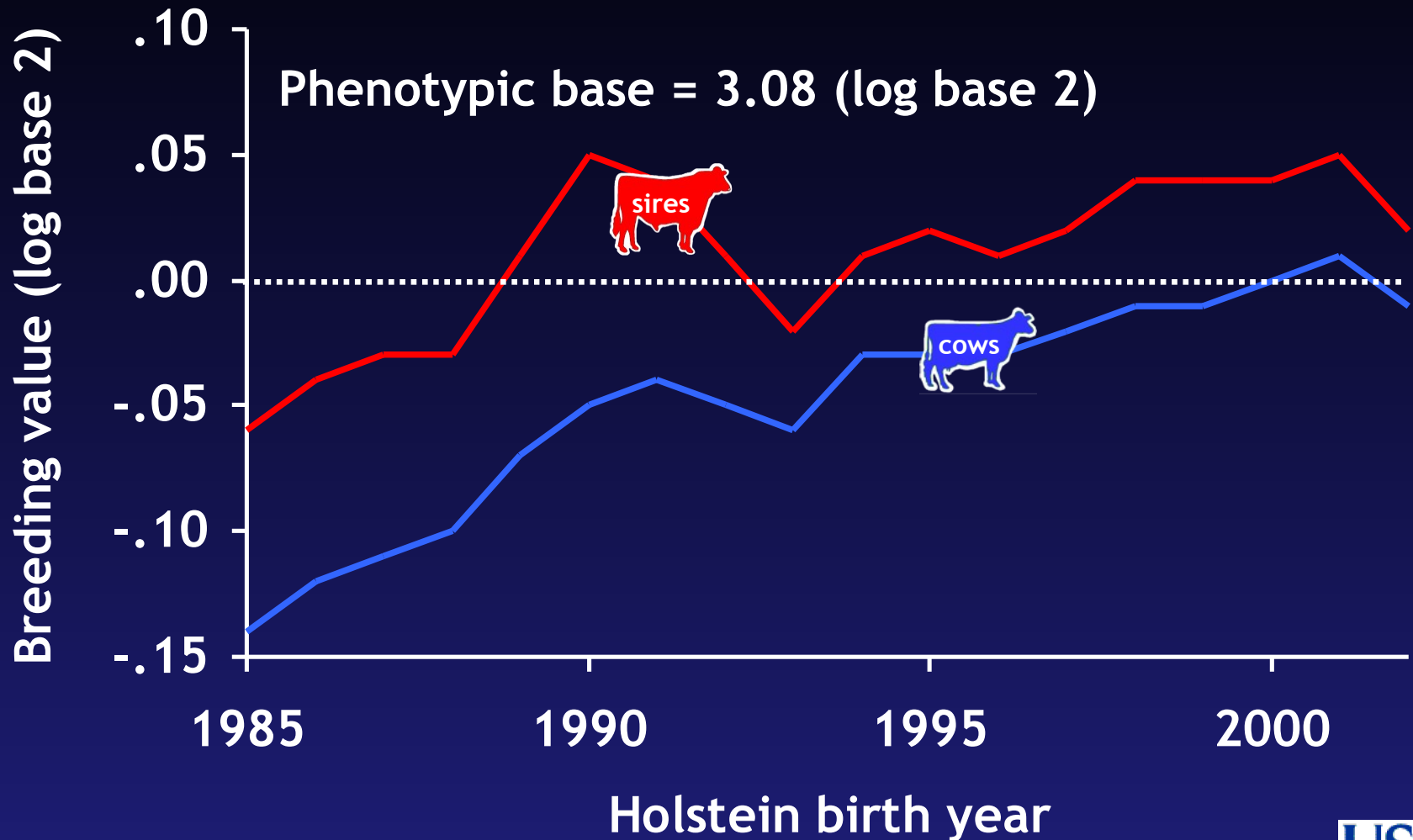
Genetic trend - Protein



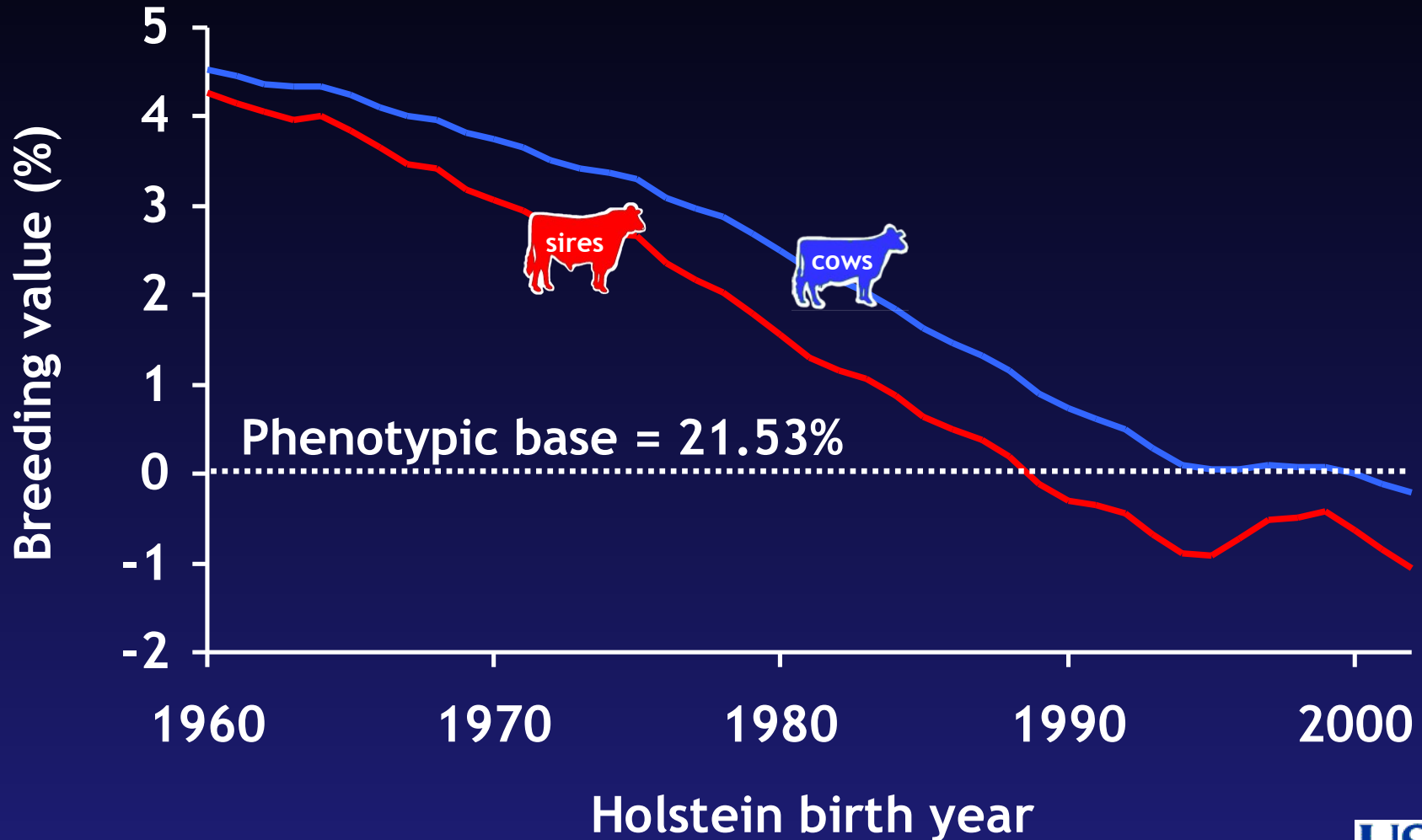
Genetic trend - Productive life (mo)



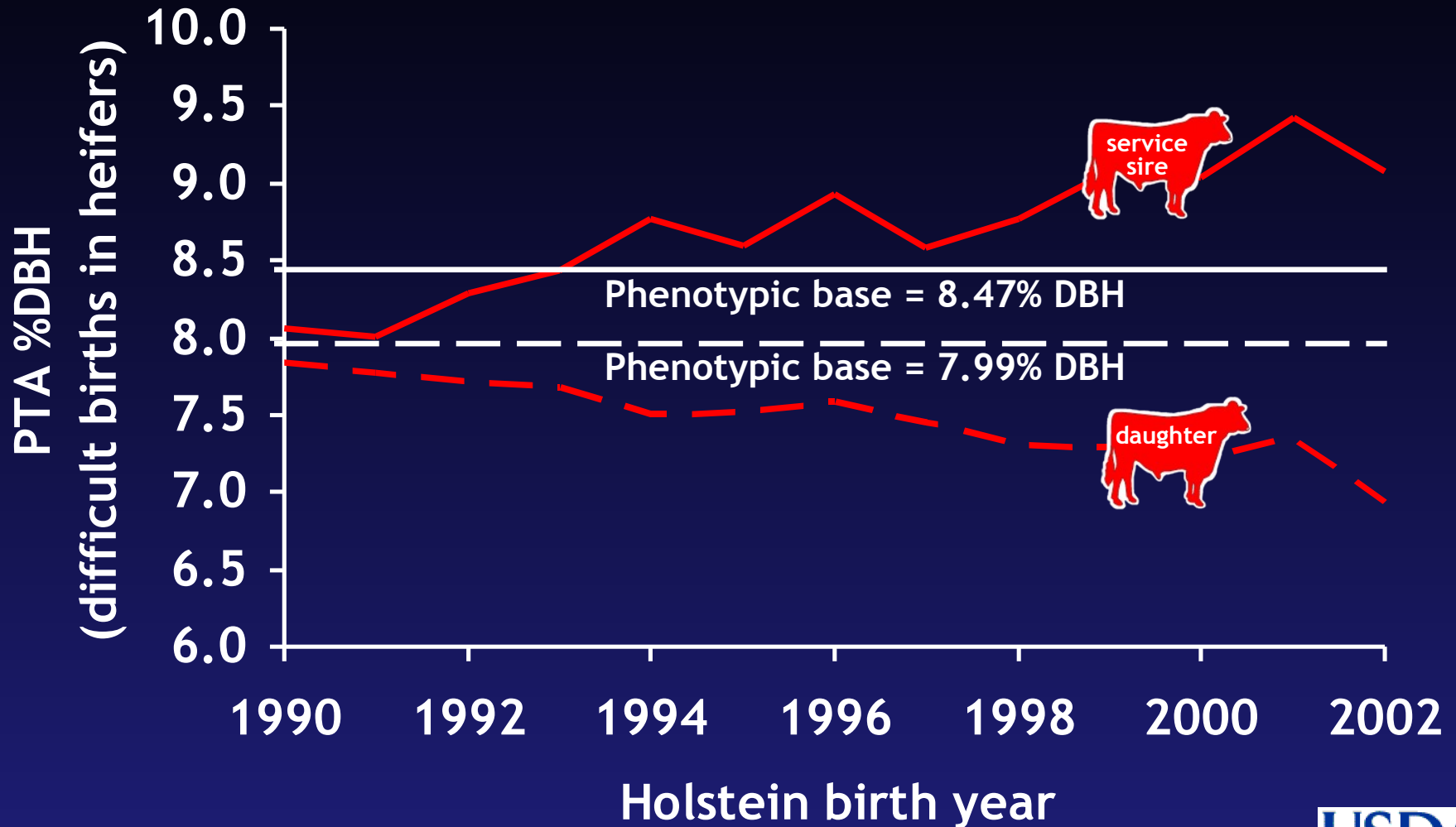
Genetic trend - Somatic cell score



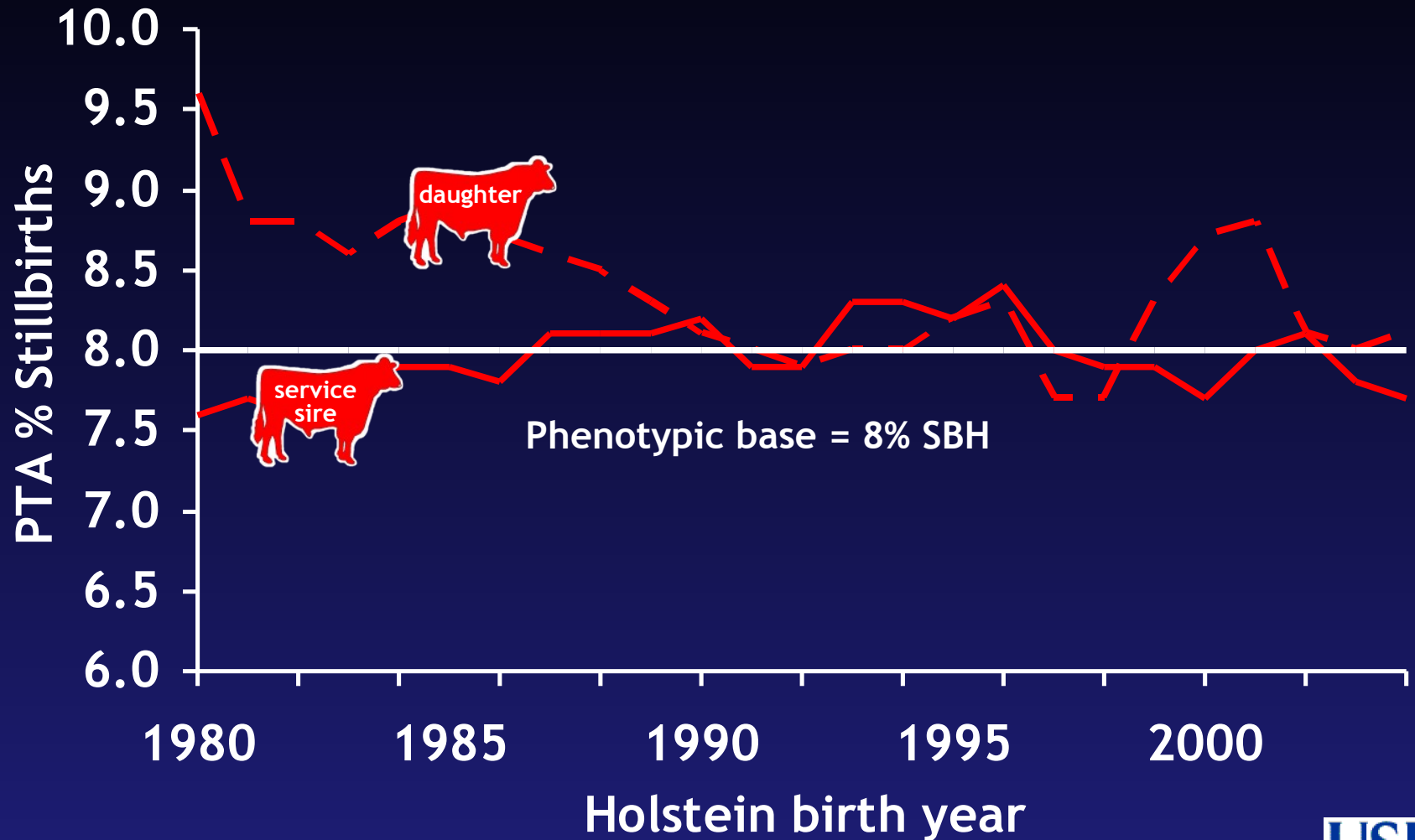
Genetic trend - Daughter pregnancy rate (%)



Genetic trend - calving ease



Genetic trend - stillbirth



Genetic-economic indices

Trait	Relative value (%)		
	Net merit	Cheese merit	Fluid merit
Milk (lb)	0	-12	24
Fat (lb)	23	18	23
Protein (lb)	23	28	0
Productive life (mo) (PL)	17	13	17
Somatic cell score (\log_2) (SCS)	-9	-7	-9
Udder composite (UDC)	6	5	6
Feet/legs composite (FLC)	3	3	3
Body size composite (BSC)	-4	-3	-4
Daughter pregnancy rate (%) (DPR)	9	7	8
Calving ability (\$) (CA\$)	6	4	6

Index changes

Trait	Relative emphasis on traits in index (%)						
	PD\$ (1971)	MFP\$ (1976)	CY\$ (1984)	NM\$ (1994)	NM\$ (2000)	NM\$ (2003)	NM\$ (2006)
Milk	52	27	-2	6	5	0	0
Fat	48	46	45	25	21	22	23
Protein	...	27	53	43	36	33	23
PL	20	14	11	17
SCS	-6	-9	-9	-9
UDC	7	7	6
FLC	4	4	3
BDC	-4	-3	-4
DPR	7	9
SCE	-2	...
DCE	-2	...
CA\$	6

Persistency

Introduction

- ◆ **At the same level of production** cows with high persistency milk more at the end than the beginning of lactation
- ◆ Best prediction of persistency is calculated as a function of trait-specific standard lactation curves and the linear regression of a cow's test day deviations on days in milk

Best Prediction

◆ Selection Index

- ◆ Predict missing yields from measured yields
- ◆ Condense daily into lactation yield and persistency
- ◆ Only phenotypic covariances are needed
- ◆ Mean and variance of herd assumed known

◆ Reverse prediction

- ◆ Daily yield predicted from lactation yield and persistency

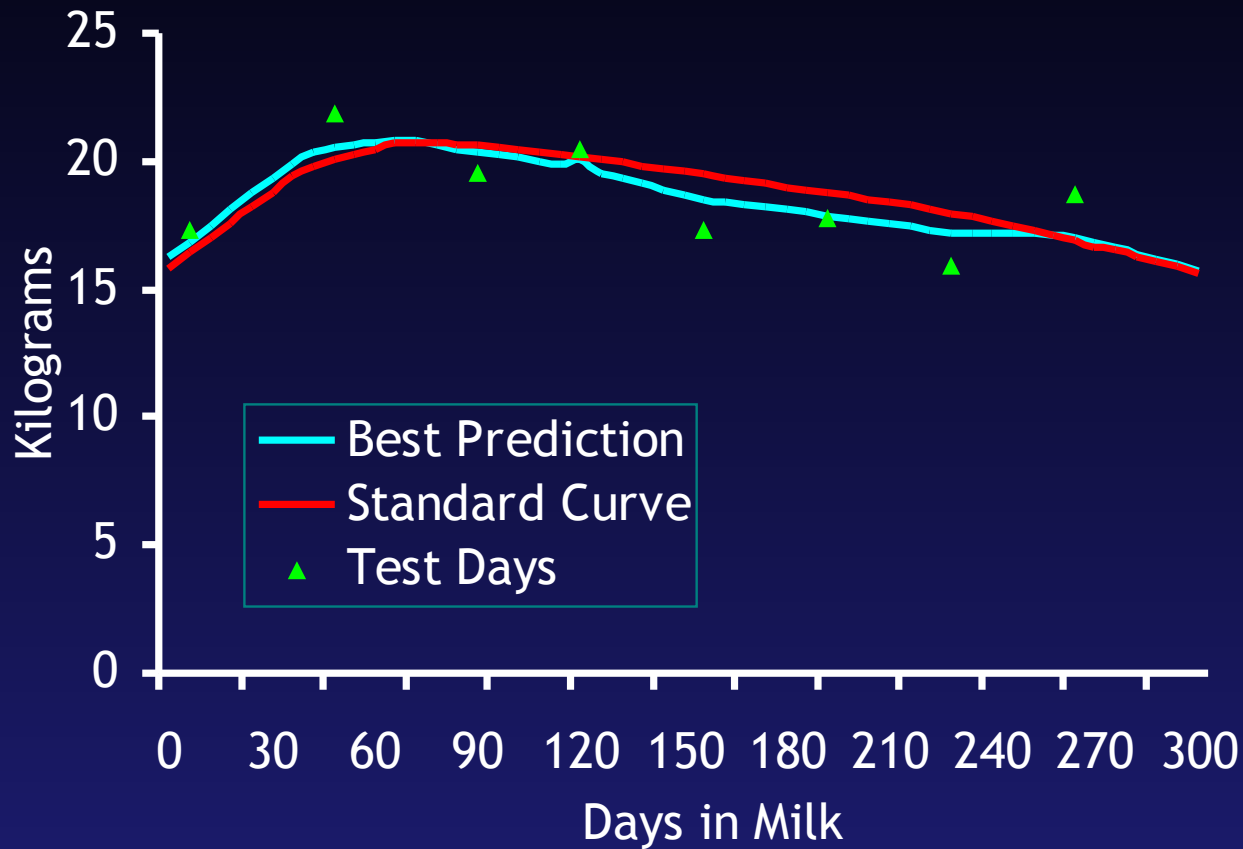
Persistency

Cole and VanRaden 2006 JDS 89:2722-2728

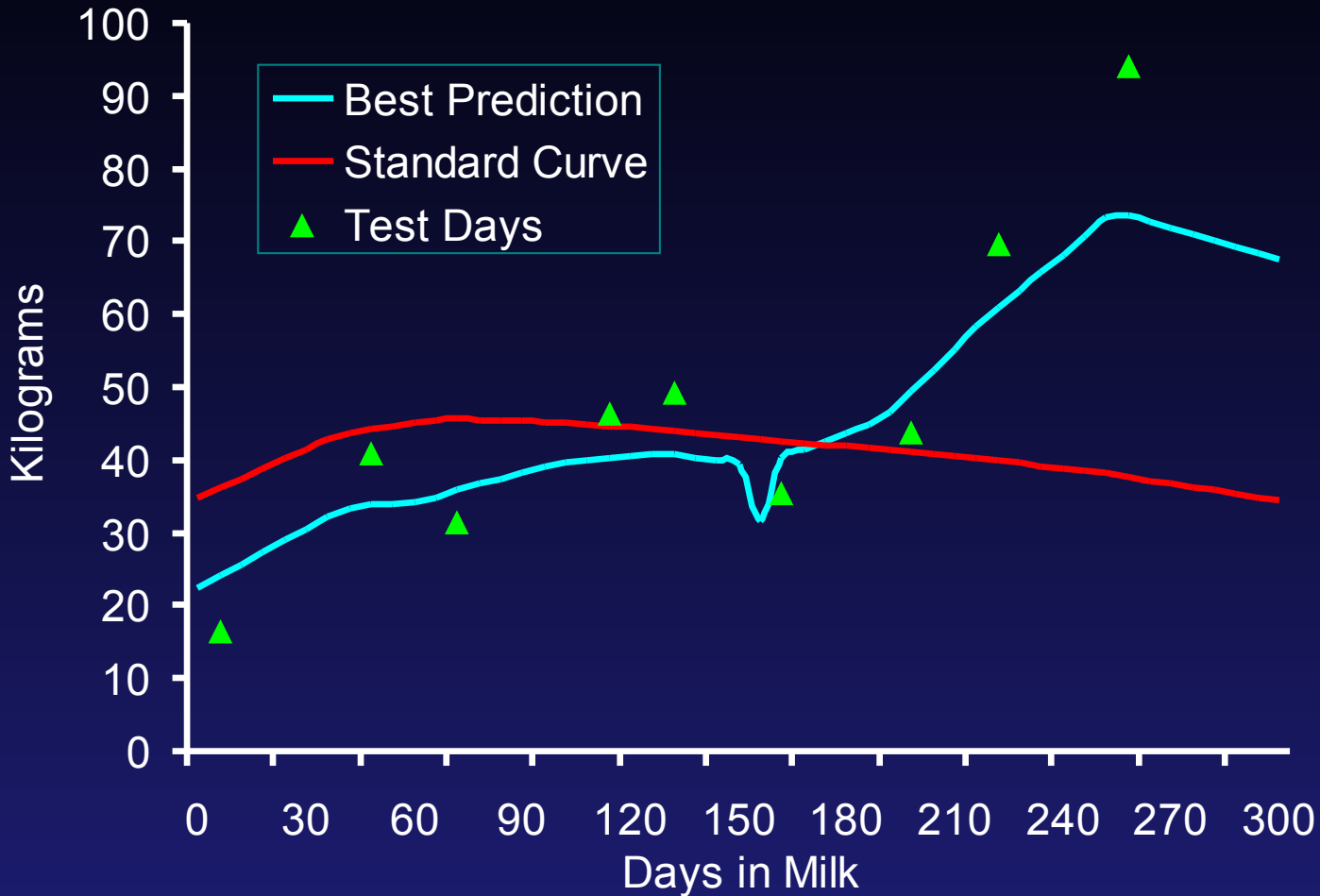
◆ Definition

- ◆ 305 daily yield deviations ($DIM - DIM_0$)
- ◆ Uncorrelated with yield by choosing DIM_0
- ◆ DIM_0 were 161, 159, 166, and 155 for M, F, P, and SCS
 - DIM_0 have increased over time
- ◆ Standardized estimate

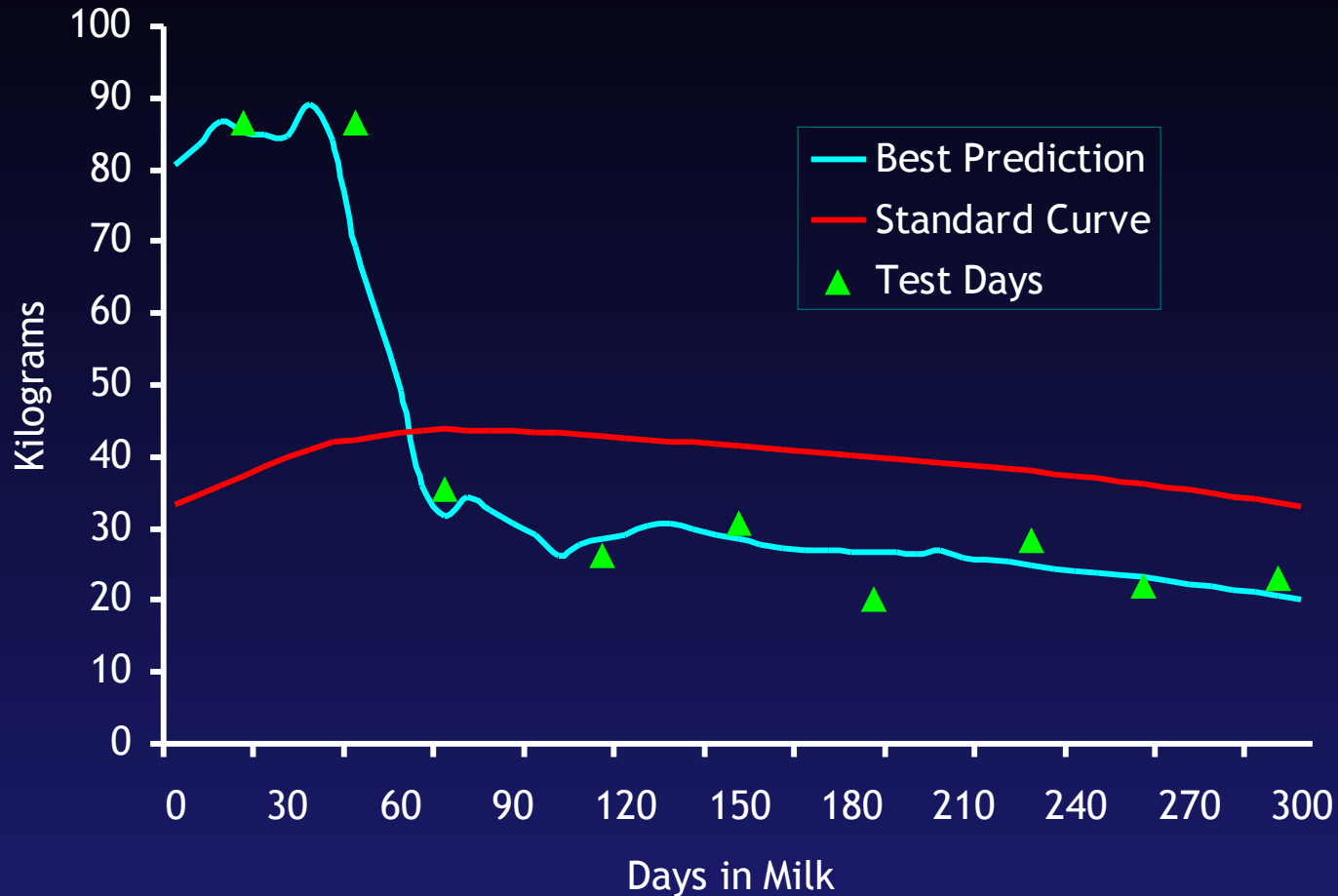
Cow with Average Persistency



Highest Cow Persistency



Lowest Cow Persistency



Model

Repeatability animal model:

$$y_{ijkl} = hys_i + lac_j + a_k + pe_k + \beta(do_{jk}) + e_{ijkl}$$

y_{ijkl} = persistency of milk, fat, protein, or SCS

hys_i = fixed effect of herd-year-season of calving i

lac_j = fixed effect of lactation j

a_k = random additive genetic effect of animal k

pe_k = random permanent environmental effect of animal k

do_{jk} = days open for lactation j of animal k

e_{ijkl} = random residual error

(Co)variance Components

	σ_a^2	σ_{pe}^2	σ_e^2	h^2	rept
PM	0.10	0.09	0.85	0.10	0.18
PF	0.07	0.08	0.79	0.07	0.15
PP	0.08	0.07	0.70	0.09	0.17
PSCS	0.02	0.03	0.64	0.03	0.07

Correlations Among Persistency Traits

	PM	PF	PP	PSCS
PM		0.83	0.87	-0.48
PF	0.72		0.82	-0.41
PP	0.91	0.72		-0.58
PSCS	-0.19	-0.11	-0.14	

¹Genetic correlations above diagonal, residual correlations below diagonal.

Genetic Correlations Among Persistency and Yield

	M	F	P	SCS
PM	0.05	0.10	0.03	-0.04
PF	0.12	0.12	0.00	0.00
PP	-0.02	0.08	-0.09	-0.11
PSCS	-0.23	-0.28	-0.20	0.41

Factors Affecting Persistency

- ◆ **Parity:** 1st lactation cows tend to have flatter lactation curves than later lactation cows
- ◆ **Nutrition:** underfeeding energy will reduce peak yield, leading to higher persistency
- ◆ **Stress:** low persistency in cows under handling or heat stress
- ◆ **Diseases?**
- ◆ **Breed differences?**

Summary

- ◆ Heritabilities and repeatabilities are low to moderate
- ◆ Routine genetic evaluations for persistency are feasible
- ◆ The shape of the lactation curve may be altered without affecting production

Diseases and Persistency

Appuhamy, Cassell, and Cole 2006

- ◆ Other measures may improve disease resistance through indirect selection, e.g. productive life (PL), body condition scores, and persistency
- ◆ Studies of the effect of diseases on milk yield is abundant in literature
- ◆ Investigations of relationships between diseases and other traits are lacking (Muir et al., 2004)

Objectives

- ◆ Investigate the effect of common health disorders on persistency
- ◆ Estimate phenotypic correlations among diseases and persistency
- ◆ Measure breed effects (Holstein and Jersey) on these relationships

Materials and Methods

Daily milk yield records of **Holstein** and **Jersey** cows at the Virginia Tech Dairy Complex from 07/18/2004 to 06/07/2006

	Holstein	Jersey
First lactation (L1)	41	10
Second lactation (L2)	34	08
Third and later (L3+)	40	15
Total Lactations	115	33
Total cows	93	33

Definition of Disease Variables

Mastitis (MAST) : All causes of udder infections

MAST1 : in first 100 days (stage1)

MAST2 : after 100th DIM (stage2)

Post Partum Metabolic Diseases (METAB): Milk fever and/or ketosis

Other diseases: LAME, DA, MET, PNEU, DIARR

Statistical Analysis

$$P_{ijklm} = L_i + Y_j + D_k + O_l + e_{ijklm}$$

where:

Y_{ijklm} = Lactation **persistence** of cow m

L_i = Effect of i^{th} **lactation** ($i = 1, 2, \& 3$)

YS_j = Effect of j^{th} **calving year-season** ($j=1, 2, 3, 4, 5 \& 6$)

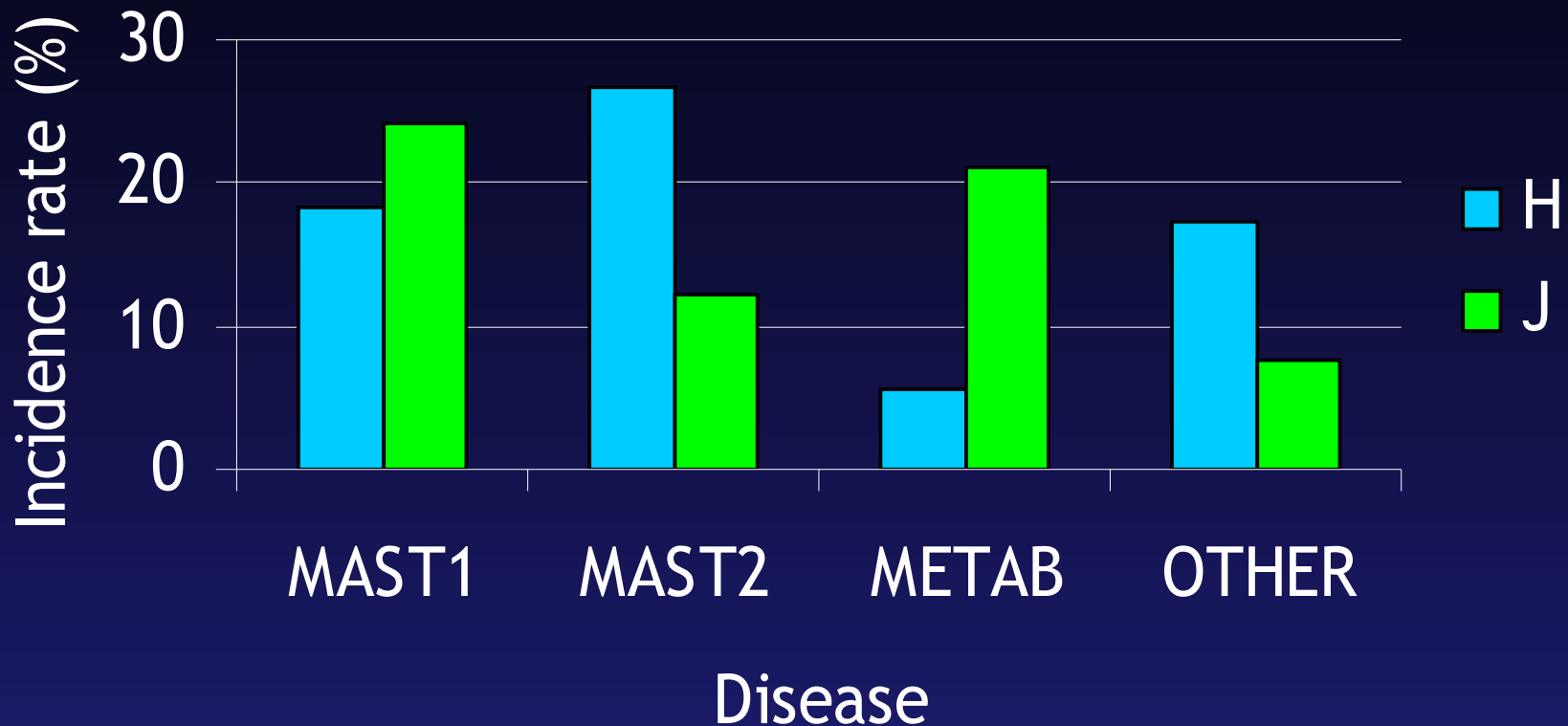
D_k = Effect of k^{th} status of **the disease** ($k = 1$ or 0)

O_l = Effect of l^{th} status of **other diseases** ($l=1$ or 0)

e_{ijklm} = **residual** effect

(**Other diseases** includes all diseases beside the disease of interest.)

Disease incidence rates in Holstein (H) & Jersey (J) cows



Diseases and Breed on Persistency

Factor	Levels	LS Mean	Correlation
	0	-0.18	
MAST1**	1	-0.76	-0.24
	0	-0.3	
MAST2	1	-0.55	-0.09
	0	-0.35	
METAB	1	0.37	-0.08
	H	-0.11	
BREED**	J	-0.74	

** Significant ($p < 0.05$)

Conclusions

- ◆ Mastitis in early lactation has a significant, negative effect on persistency
- ◆ Mastitis in late lactation and post partum metabolic diseases have non-significant, but negative, effects on persistency
- ◆ Persistency differs significantly between Holstein and Jersey cows

All-Breeds Evaluation



Goals

- ◆ Evaluate crossbred animals without biasing purebred evaluations
- ◆ Accurately estimate breed differences
- ◆ Compute national evaluations and examine changes
 - ◆ PTA of purebreds and crossbreds
 - ◆ Changes in reliability
- ◆ Display results without confusion

Methods

- ◆ All-breed animal model
 - ◆ Purebreds and crossbreds together
 - ◆ Unknown parents grouped by breed
 - ◆ Variance adjustments by breed
 - ◆ Age adjust to 36 months, not mature
 - ◆ 1988 software, good convergence
- ◆ Within-breed-of-sire model examined but not used

Unknown Parent Groups

- ◆ Groups formed based on
 - ◆ Birth year (flexible)
 - ◆ Breed (must have >10,000 cows)
 - ◆ Path (dams of cows, sires of cows, parents of bulls)
 - ◆ Origin (domestic vs other countries)
- ◆ Paths have >1000 in last 15 years
- ◆ Groups each have >500 animals

Data

- ◆ Numbers of cows of all breeds
 - ◆ 22.6 million for milk and fat
 - ◆ 16.1 million for protein
 - ◆ 22.5 million for productive life
 - ◆ 19.9 million for daughter pregnancy rate
 - ◆ 10.5 million for somatic cell score
- ◆ Type evaluated in separate breed files
- ◆ Calving ease joint HO, BS, and HO x BS
- ◆ Goats in all-breed model since 1988

Crossbred Cows

with 1st parity records

Year	F1 (%)	F1 cows	Back-cross	Het > 0	XX cows
2005	1.3	8647	2495	12621	4465
2004	1.2	7863	1983	11191	3947
2003	.9	6248	1492	9051	3111
2002	.7	4689	1467	7338	2564
2001	.5	3491	1330	5878	2081

Reliability

- ◆ **Crossbred cows**
 - ◆ Will have PTA, most did not before
 - ◆ Accurate PTA from both parents
- ◆ **Purebred animals**
 - ◆ Information from crossbred relatives
 - ◆ More contemporaries

All- vs Within-Breed Evaluations

Correlations of PTA Milk

Breed	99% REL bulls	Recent bulls	Recent cows
Holstein	>.999	.994	.989
Jersey	.997	.988	.972
Brown Swiss	.990	.960	.942
Guernsey	.991	.988	.969
Ayrshire	.990	.963	.943
Milking Shorthorn	.997	.986	.947

Display of PTAs

- ◆ Genetic base

- ◆ Convert all-breed base back to within-breed-of-sire bases
- ◆ Each animal gets just one PTA
- ◆ $PTA_{brd} = (PTA_{all} - mean_{brd}) SD_{brd} / SD_{all}$

- ◆ Heterosis and inbreeding

- ◆ Both effects removed in the animal model
- ◆ Heterosis added to crossbred animal PTA
- ◆ Expected Future Inbreeding (EFI) and merit differ with mate breed

Schedule

- ◆ Interbull test run Feb. 1, 2006
 - ◆ Trend validation
 - ◆ Convert all-breed PTA back to within-breed bases
- ◆ Scientific publication (JDS)
- ◆ Implementation
 - ◆ Expected May 2007

Conclusions

- ◆ All breed model accounts for:
 - ◆ General heterosis
 - ◆ Unknown parent groups by breed
 - ◆ Heterogeneous variance by breed
- ◆ PTA converted back to within breed bases, crossbreds to breed of sire
- ◆ PTA changes more in breeds with fewer animals

Genomics

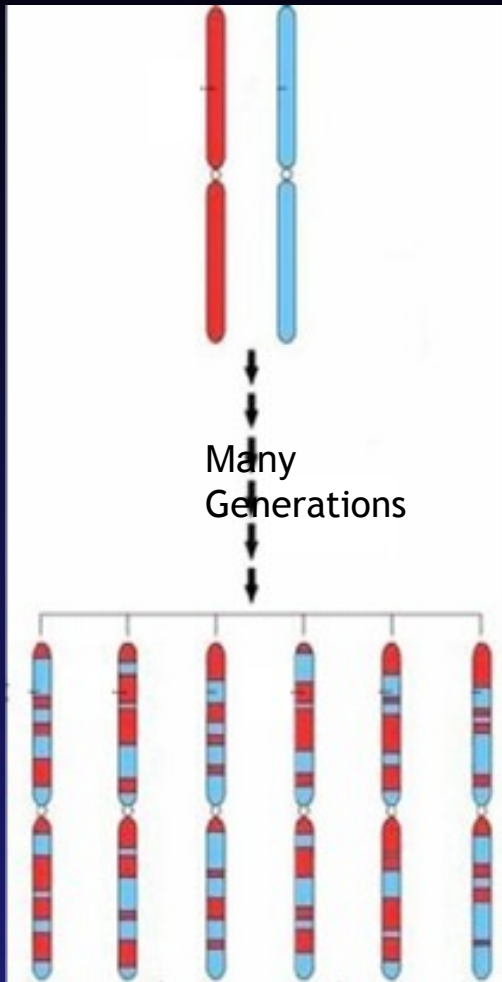
SNP Project Outcomes

- ◆ **Genome-wide selection**
- ◆ **Parentage verification & traceability panels**
- ◆ **Enhanced QTL mapping & gene discovery**

Linkage disequilibrium (LD)

- ◆ Non-random association of alleles at two or more loci, not necessarily on the same chromosome
- ◆ Not the same as linkage, which describes the association of two or more loci on a chromosome with limited recombination between them

Concept of a HapMap



The population is young enough that large segments of the genome are not disrupted by recombination (LD)

Genome Selection

- ◆ **Animals are genotyped at birth**
- ◆ **Genomic EBV calculated for many traits**
 - ◆ **Even those not typically recorded (e.g. semen quality)**
- ◆ **Accuracy is predicted to be similar to progeny test evaluation**

Advantages of Genome Selection

- ◆ Generation intervals can be reduced
- ◆ Costs of progeny testing can be decreased
- ◆ More accurate selection among full sibs
 - ◆ Decreased risk in selection program

Low-cost parentage verification

- ◆ SNP tests may make parentage validation cheap enough for widespread adoption
- ◆ Develop a database and software to check parentage and suggest alternatives for invalid IDs
- ◆ Determine rate of parentage errors in a sample of herds

In Conclusion

Ongoing Work

- ◆ **New traits**
 - ◆ Stillbirth (HOL)
 - ◆ Milking speed (BSW)
 - ◆ Rear legs/rear view (BSW, GUE)
 - ◆ Bull fertility (transferred from DRMS)
- ◆ **Improved online tools**
 - ◆ Fully buzzword-compliant
 - ◆ Web services for data delivery
- ◆ **Choice of scales**

Senior research staff

