

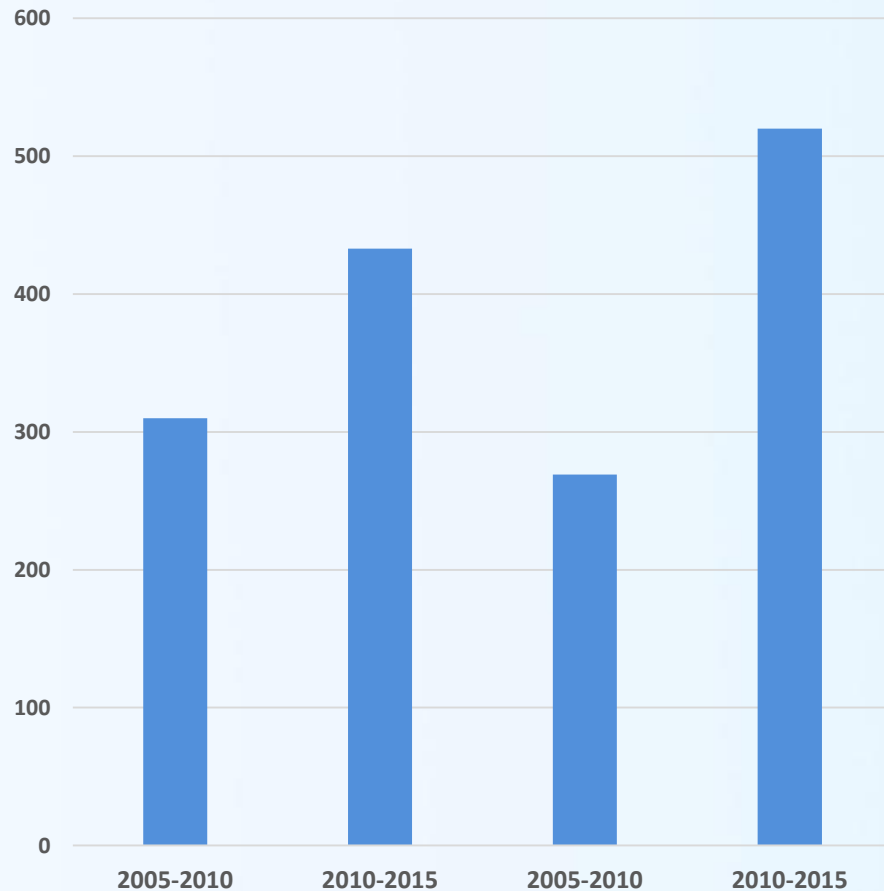
# Genetic Gain, Inbreeding and Mating Programs In the age of Genomics



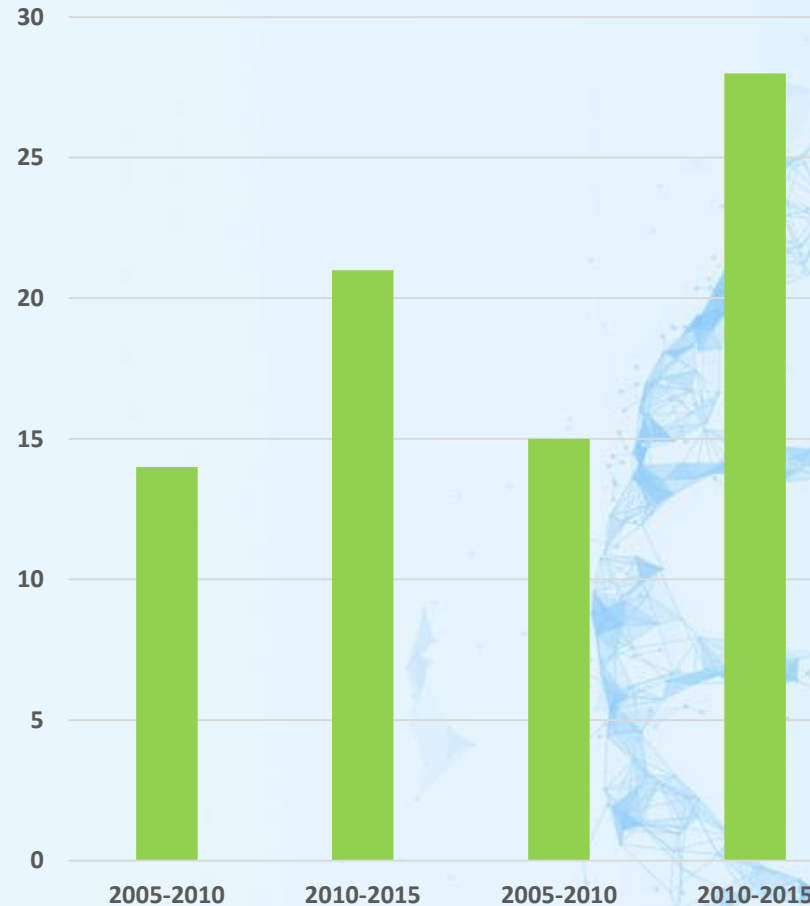
**Additive Genetics –  
Inbreeding Depression =  
Economic Gain**

# Comparison Last Five Years Before and First Five Years After Introduction of Genomics Production Traits

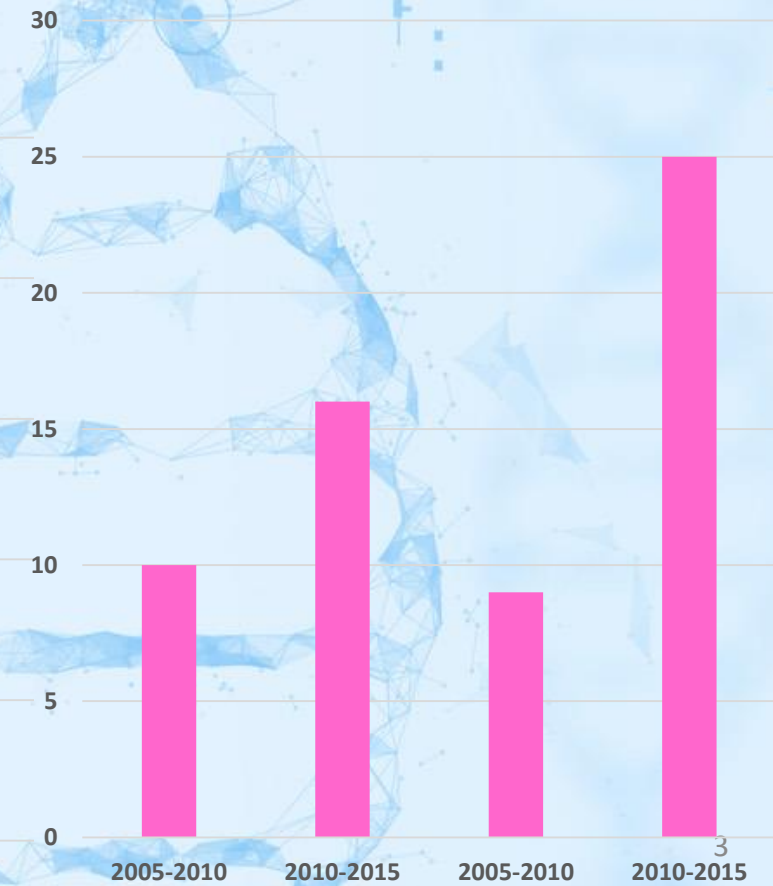
**COW MILK BULL**



**COW FAT BULL**



**COW PRT BULL**



# Comparison National Holstein DHI Averages

Test Plan	Number of Herds	Number of Cows	Average Number of Cow	Milk	Fat%	Fat	Protein %	Protein
All plans 2017	13,321	3,586,789	269	11,508 L	3.76	433 kg	3.11	358 kg
All plans 2015	14,662	3,642,037	248	11,343 L	3.68	417 kg	3.08	350 kg
All plans 2010	17,578	3,776,761	215	10,539 L	3.61	381 kg	3.06	323 kg

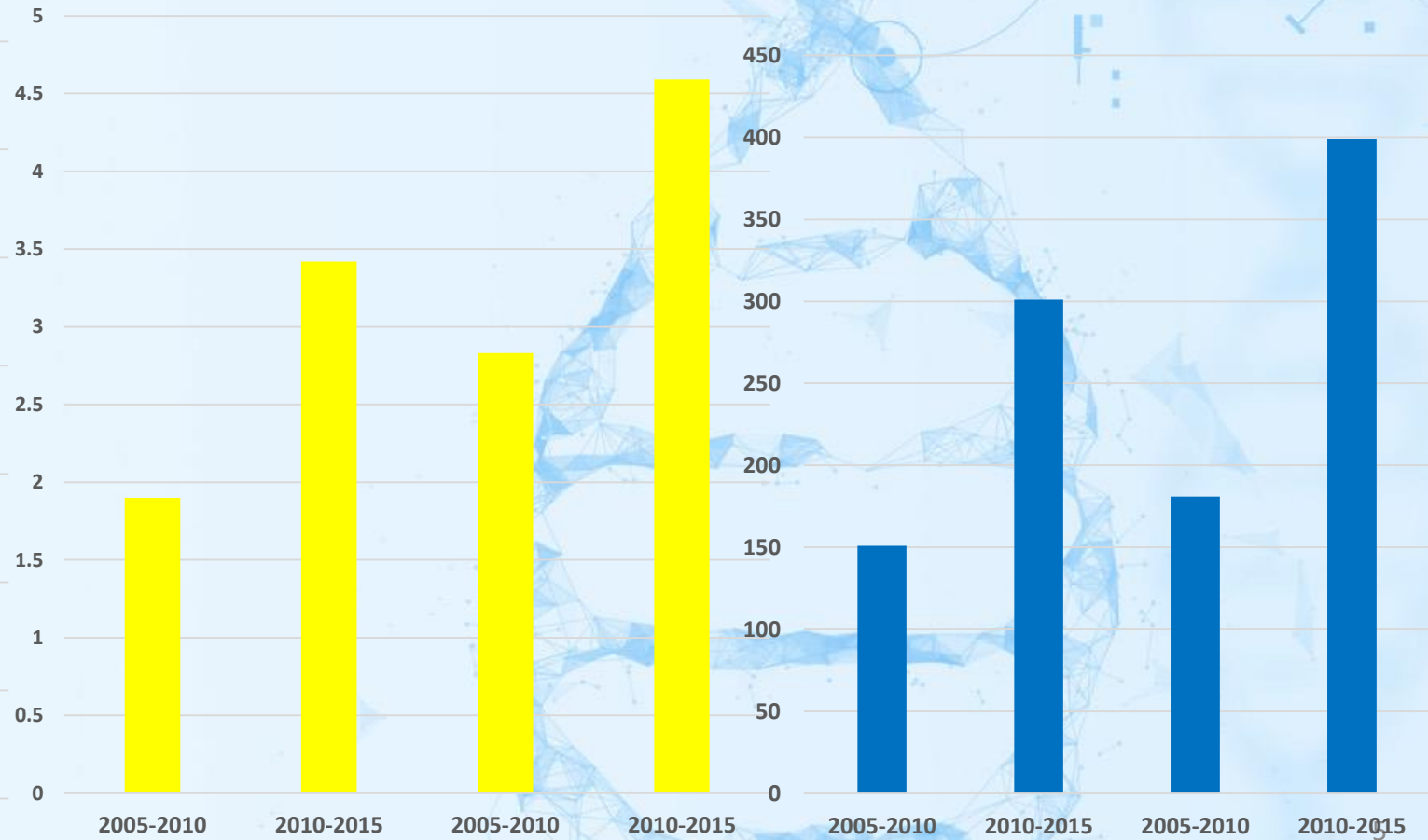
## 47% of US Dairy Cow Population is on DHI Test



# Comparison Last Five Years Before and First Five Years After Introduction of Genomics Fertility, Productive Life and Net Merit

**COW DPR BULL**

**COW PL BULL COW NM\$ BULL**



# Change in Pregnancy Traits Over Time in DHI Herds

## Inseminations Per Pregnancy

2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016
2.6	2.6	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.4	2.4	2.3

## Average Days from Calving to First Breeding

2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016
87	86	85	83	81	81	79	78	78	78	78	78

## Average Days from Calving to Last Breeding

2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016
146	145	141	136	133	132	130	126	126	124	122	120

## Average Calving Interval

2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
423	423	418	417	412	409	408	404	403	401	399

# Improvement in Somatic Cell

Birth Year	Cows	SCS	BV	Rel	Sire BV
2015	834165	2.32	-0.18	0.36	-0.31
2010	854539	2.37	0.00	0.41	-0.05
2005	720088	2.74	0.09	0.41	0.12

# Comparison of Somatic Cell in DHI Herds Overtime

Year	Milk Per Day	Somatic Cell
2005	32.3 L	296
2006	32.3 L	288
2007	32.4 L	276
2008	32.6 L	262
2009	32.8 L	233
2010	33.0 L	228
2011	33.2 L	217
2012	33.7 L	200
2013	34.2 L	199
2014	34.6 L	200
2015	35.1 L	204
2016	35.5 L	203
2017	35.5 L	197
Annual trend	0.24 L	-7.61



# Reasons Cows Leave herds DHI 2010 compared 2015

Termination code 2015	Parity 1	Parity 2	Parity 3	Parity 4	Parity 5	Parity 6+	All
Lactation ended normally	74.3	66.8	57.9	50.1	43.7	37.8	64
Lactation ended with abortion	0.3	0.3	0.3	0.2	0.2	0.2	0.3
Sold For Dairy	4.5	2.8	2.4	2.4	2.5	2.7	3.3
Locomotion problems	0.7	1.2	2	2.9	3.5	4	1.5
Low production	5	6.3	6.6	7.1	7.8	8.9	6.1
Reproduction problems	3.7	5	5.4	5.7	6.1	6.3	4.8
Unspecified reasons	6.4	8.8	12	14.7	16.8	19	9.9
Mastitis or high SCS	2	4.2	6.3	7.9	9	9.6	4.6
Died	3	4.6	7	8.9	10.5	11.5	5.5
Termination code 2010	Parity 1	Parity 2	Parity 3	Parity 4	Parity 5	Parity 6+	All
Lactation ended normally	76.8	69.6	61.1	53.1	46.9	40.8	66.3
Lactation ended with abortion	0.4	0.4	0.3	0.3	0.3	0.2	0.4
Sold For Dairy	4.4	3	2.6	2.5	2.4	2.6	3.3
Locomotion problems	0.7	1.3	2.2	3.1	3.8	4.1	1.7
Low production	3.7	4.7	5.3	5.7	6.2	7.1	4.7
Reproduction problems	3.6	5	5.3	5.6	5.9	6.6	4.8
Unspecified reasons	5.6	8	11	13.9	16	18.3	9.2
Mastitis or high SCS	1.7	3.3	5.1	6.5	7.7	8.5	3.9
Died	3.1	4.8	7.2	9.3	10.7	11.7	5.7

# Improvement in Livability

Birth Year	Cows	BV	Rel	Sire BV
2014	560028	1.19	0.24	1.64
2010	898760	0.00	0.28	0.31
2006	779028	-1.26	0.28	-1.77

# Comparison of Gain Between Registered Cows and Commercial Cows

peutics, veterinary care, and replacement animals (34).  
SD. From 1985 to 2000, there was no clear trend in any of the four paths for SD of SCS (Fig. 2). In fact, the SD for the three more influential paths were all positive (worsening, because a lower value for the SCS is preferred) until 2005. The DC had slightly positive until 2005. The introduction of genomic selection produced a rapid and substantial increase in SD in the SB, SC, and DB paths. Most notably, the SD in the SB path increased by a factor of 10 between 2001–2005 and 2011–2015, from 0.26 to 4.07. This increase is due largely to the influence of a single bull, O-Bee

**Table 1. Estimates of genetic change per year from segmented regressions of PBV on birth year for all cows (All Cows) or the subset of cows registered in the national herdbook (Registered cows) for six traits: milk, fat, and protein yields; SCS; PL; and DPR**

Group	Trait	1981–1985	1986–1990	1991–1995	1996–2000	2001–2005	2006–2010	2011–2015
All cows	Milk	74	79	85	74	64	55	67
	Fat	2.8	3.2	2.2	2.2	2.1	2.6	3.8
	Protein	1.8	2.6	2.6	2.6	2.1	1.8	2.6
	SCS	0.014	0.016	0.005	0.014	−0.002	−0.024	−0.035
	PL	0.25	0.14	0.17	0.03	0.16	0.45	0.88
	DPR	−0.46	−0.54	−0.52	−0.42	−0.20	0.06	0.28
Registered cows	Milk	66	74	66	61	54	50	109
	Fat	2.6	3.1	1.1	1.7	1.8	2.2	6.0
	Protein	1.7	2.8	1.9	1.8	1.8	1.6	4.1
	SCS	0.011	0.006	0.012	0.010	−0.001	−0.021	−0.044
	PL	0.01	−0.02	−0.01	0.00	0.07	0.41	1.17
	DPR	−0.46	−0.48	−0.39	−0.30	−0.27	0.02	0.26

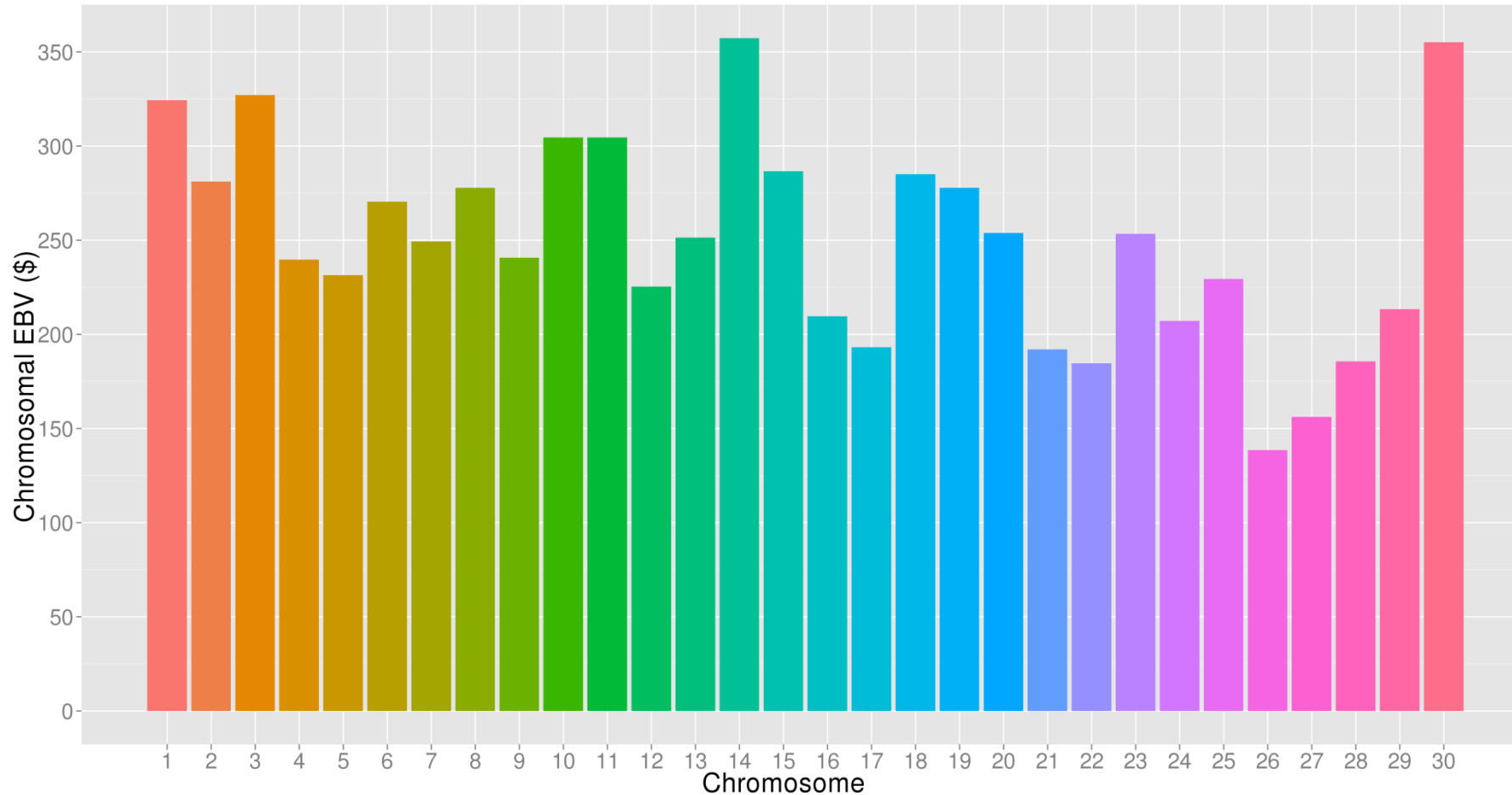
# Index changes over time

## Relative emphasis in USDA index (%)

Trait	PD\$ 1971	MFP\$ 1976	NM\$ 1994	NM\$ 2000	NM\$ 2003	NM\$ 2014	NM\$ 2016	NM\$ 2018
Milk	52	27	6	5	0	-1	-1	-1
Fat	48	46	25	21	22	22	22	27
Protein	...	27	43	36	33	20	20	17
Longevity	...	...	20	14	11	19	14	12
SCS (mastitis)	...	...	-6	-9	-9	-7	-7	-4
Udder	...	...	...	7	7	8	8	7
Feet/legs	...	...	...	4	4	3	3	3
Body size	...	...	...	-4	-3	-5	-4	-4
Pregnancy rate	...	...	...	...	7	7	7	7
Calving	...	...	...	...	4	5	5	5
Heifer Conception	...	...	...	...	...	1	1	1
Conception rate	...	...	...	...	...	3	3	2
Health Trait Index	...	...	...	...	...	...	...	2
Livability	...	...	...	...	...	...	7	7



# What's the best cow we can make?

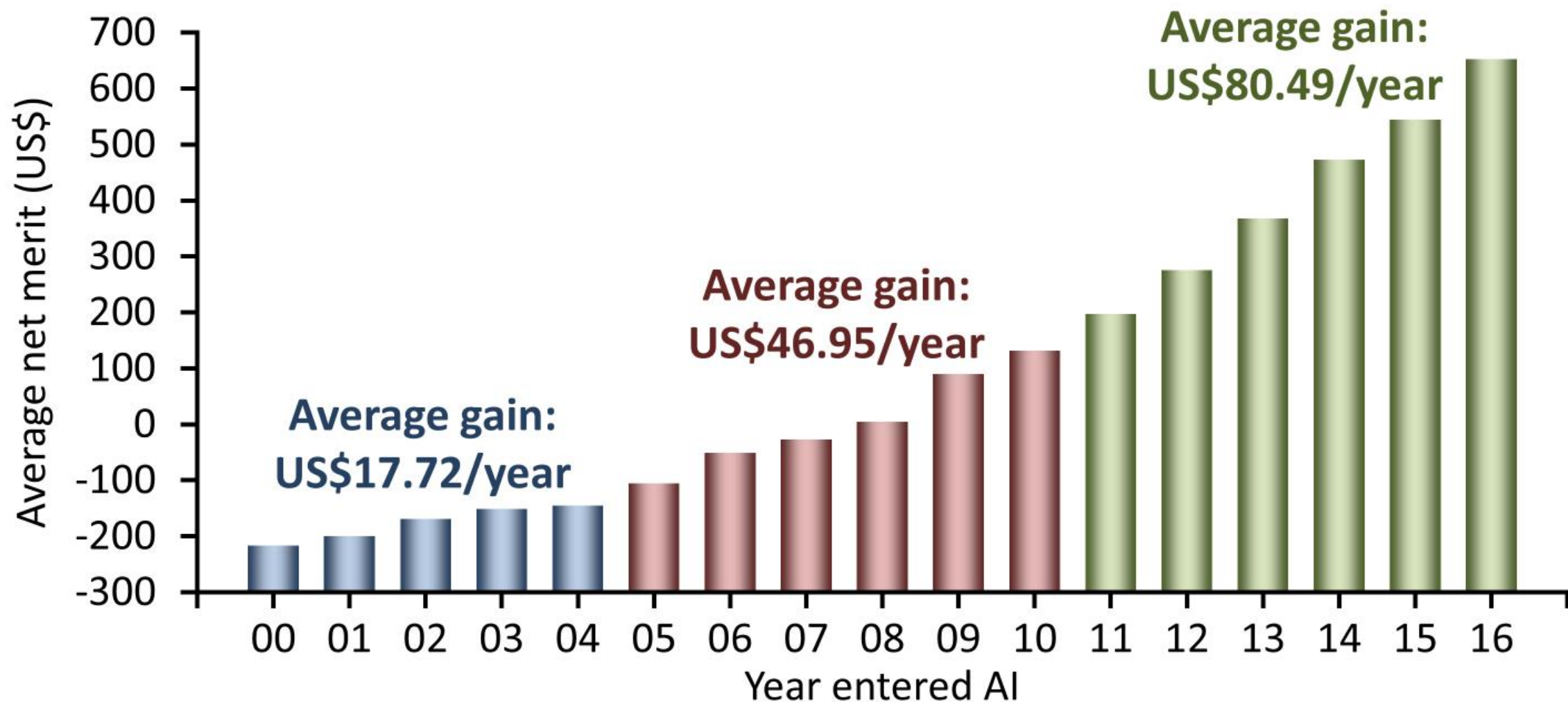


**A “supercow” constructed from the best haplotypes in the Holstein population would have an EBV for NM\$ of **+\$7,515 !****

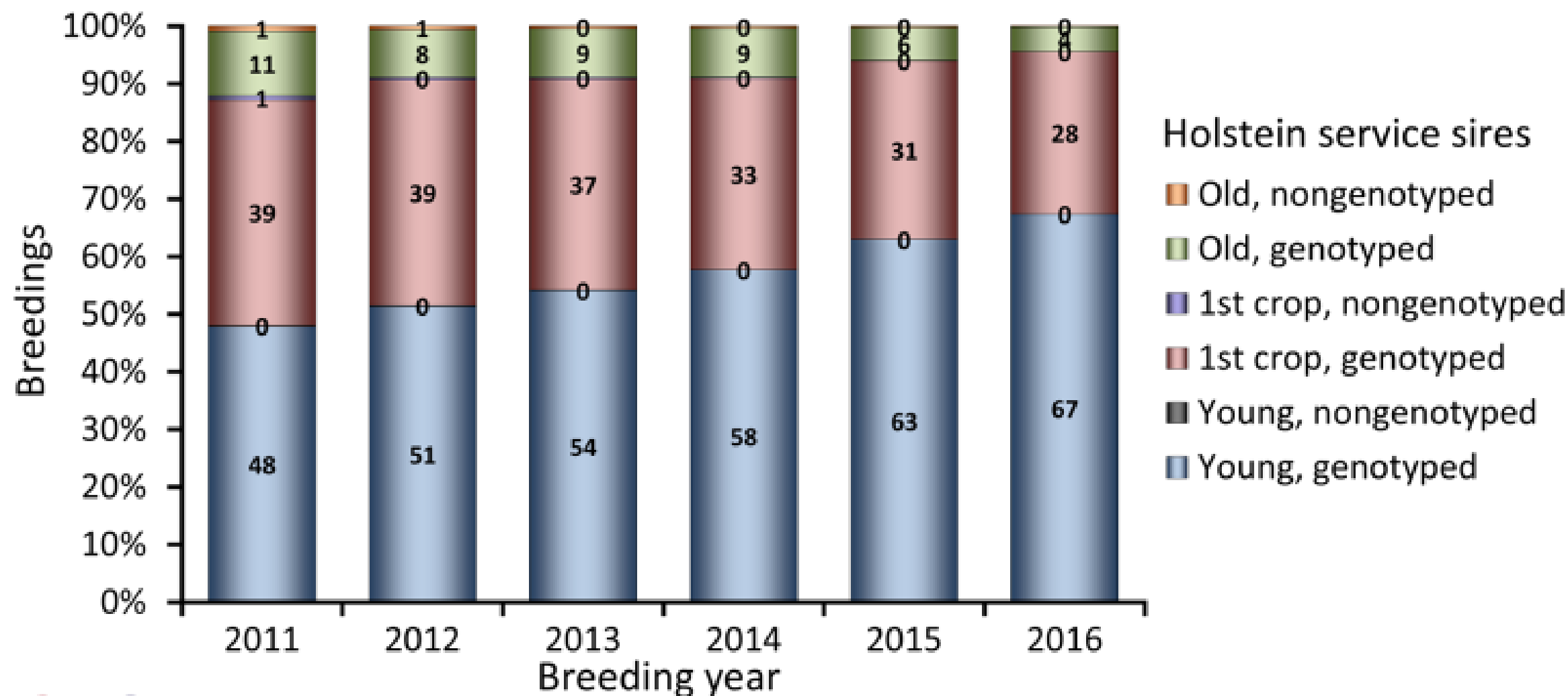


**Additive Genetics –  
Inbreeding Depression =  
Economic Gain**

# Marketed Holstein bulls



# AI breedings to genomic bulls





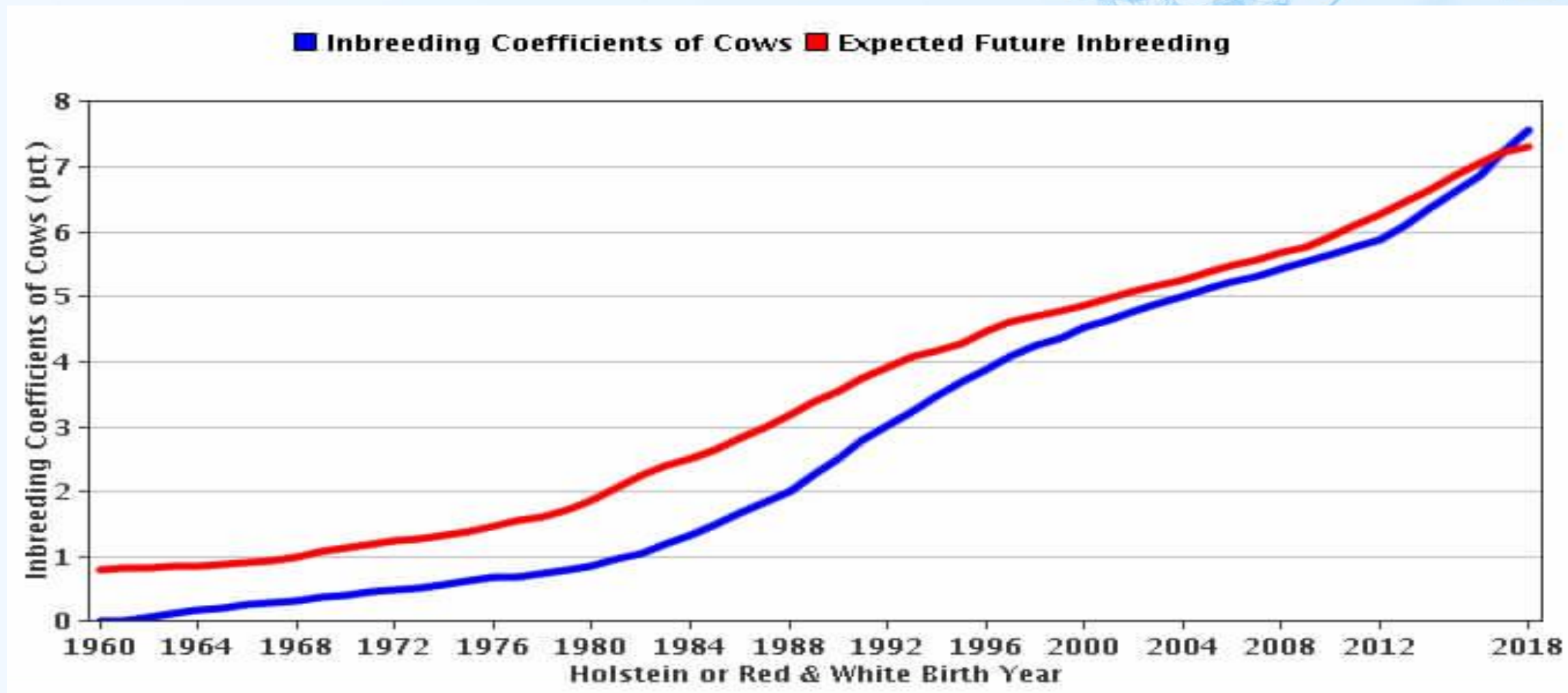
# Some Terms

- Expected Future Inbreeding-Based on pedigree the expected future inbreeding level of an animal's offspring when bred to the general population. If a cow has a EFI of 7.5% her offspring will be 7.5% inbred when bred to the average bull.
- Genomic Future Inbreeding-Based on the genomic relationship between an animal and other animals that have been genomically tested.
- Inbreeding-Based on pedigree the inbreeding level of an individual animal.
- Genomic Inbreeding-The actual inbreeding derived from their genomic evaluation.

# Change in Inbreeding Cows

Birth Year	Cows	Percent Inbreeding	Expected Future Inbreeding
2018	1156042	7.60	7.36
2015	1861463	6.56	6.72
2010	1927372	5.67	5.93
2005	1659733	5.13	5.37

# Inbreeding Cows

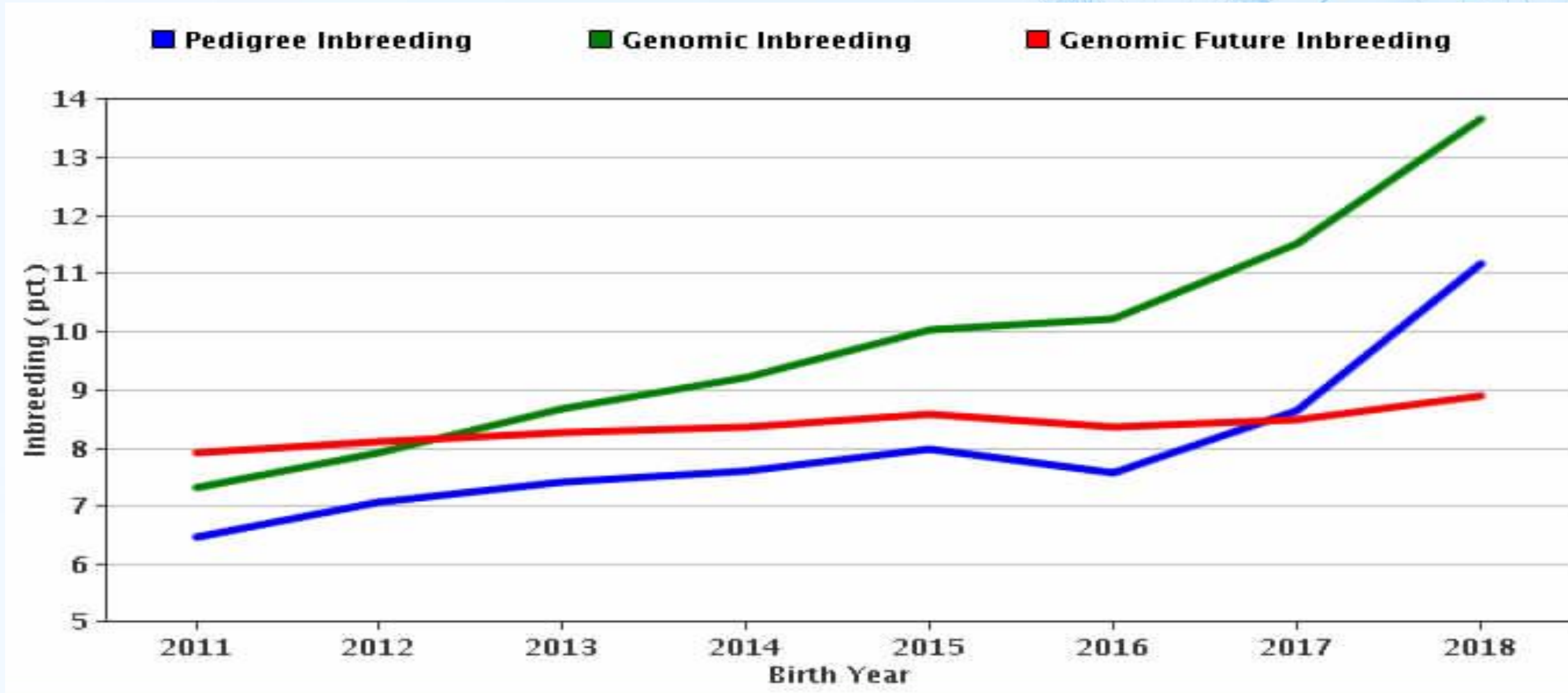


# Change Inbreeding Genomic Tested Young Sires

Birth Year	Bulls	Pedigree Inbreeding	Genomic Inbreeding	Genomic Future Inbreeding
2018	14679	11.17	13.66	8.90
2017	24431	8.65	11.52	8.48
2016	23103	7.56	10.21	8.37
2015	20834	7.98	10.03	8.59
2014	18470	7.61	9.22	8.36
2013	15246	7.40	8.69	8.26
2012	17287	7.06	7.93	8.10
2011	11847	6.48	7.31	7.92



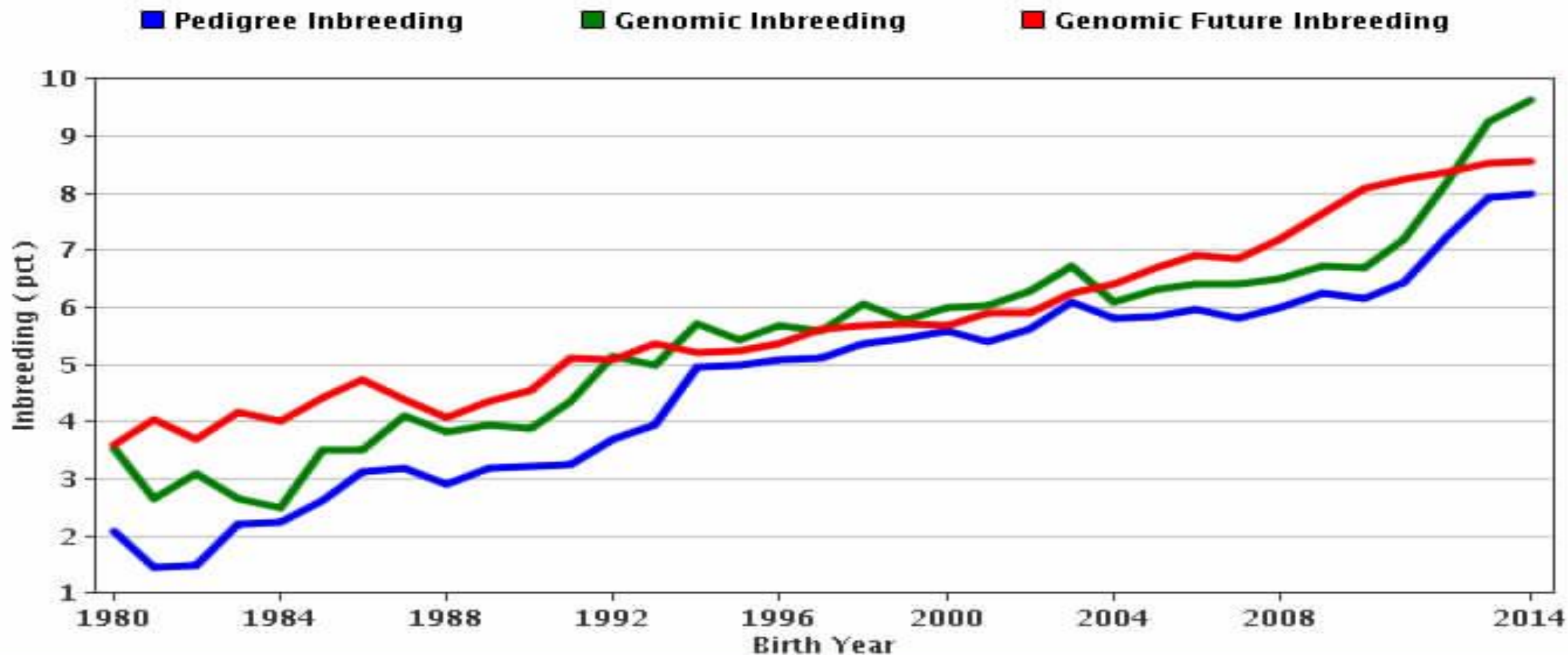
# Genomic Future Inbreeding Young Sires



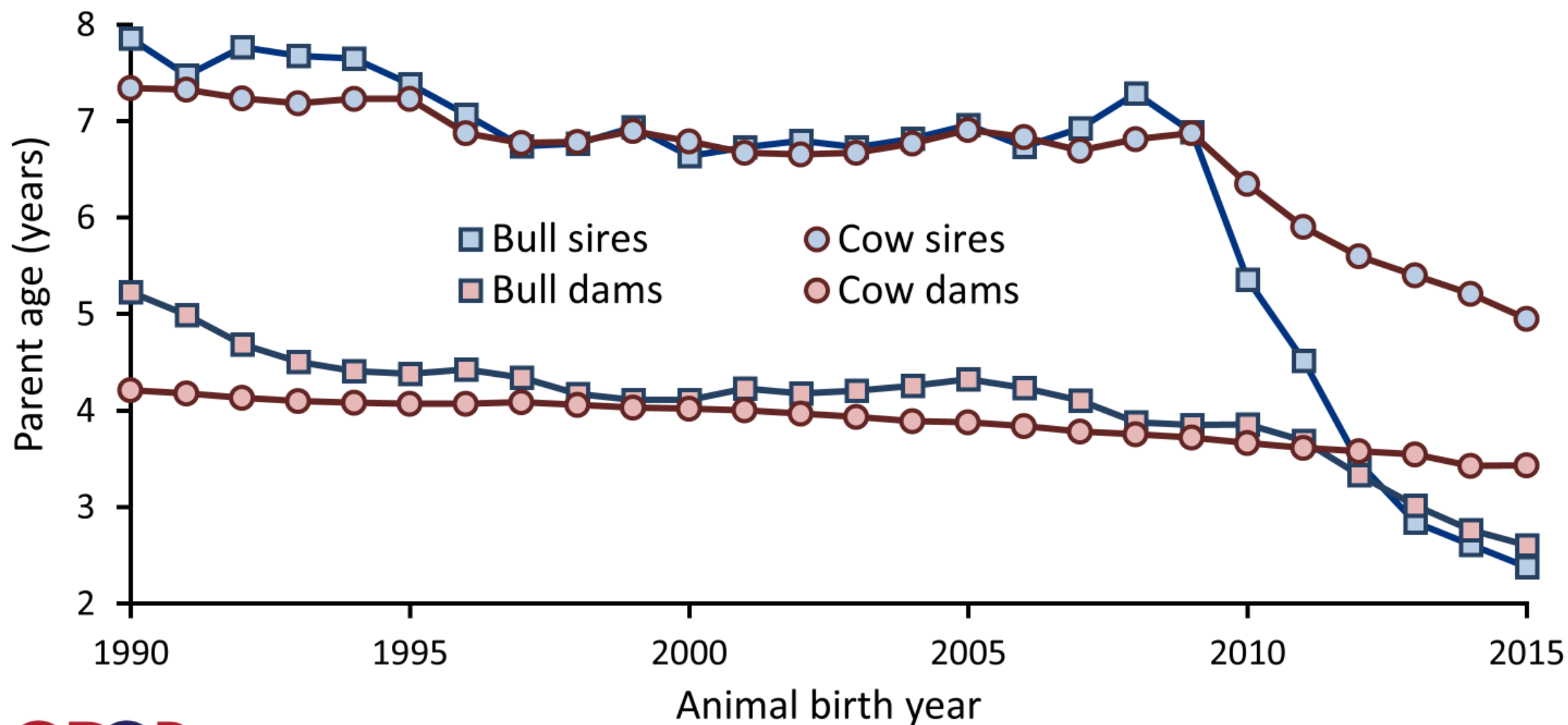
# Change Genomic Inbreeding Proven Bulls

Birth Year	Bulls	Pedigree Inbreeding	Genomic Inbreeding	Genomic Future Inbreeding
2014	1168	8.17	10.13	8.73
2013	2020	7.96	9.51	8.63
2012	2700	7.24	9.27	8.55
2011	2234	6.49	7.34	8.00
2010	2392	6.14	6.76	7.88
2009	2056	6.27	6.85	7.50
2008	2040	6.02	6.64	7.16
2007	2290	5.80	6.51	6.92
2006	2332	5.98	6.49	6.91
2005	2124	5.86	6.42	6.69
2004	2000	5.82	6.21	6.40
2003	1369	6.09	6.83	6.27
2002	1351	5.63	6.39	5.95

# Proven Sires



# Generation interval – Holstein





# Before Genomics six generations in 33 years

- 023HO00206 TRADITION DOB: 08/18/1974 NM\$ -349 gEFI 4.5%
- 001HO01464 CLEITUS DOB: 10/26/1981 NM\$ -214 gEFI 4.1%
- 011HO03073 LUKE DOB: 05/07/1988 NM\$ -573 gEFI 5.7%
- 011HO04623 HERSHEL DOB: 07/30/1995 NM\$ -203 gEFI 6.9%
- 029HO11111 BOLTON DOB: 09/11/2001 NM\$ +205 gEFI 6.8%
- 029HO14142 DORCY DOB: 09/17/2007 NM\$ +437 gEFI 7.1%
- NM\$ +786 gEFI +2.6%

## With Genomics Six generations in 12 years

- 029HO14142 DORCY      DOB: 09/17/2007      NM\$ +437      gEFI 7.1%
- 007HO11314 MOGUL      DOB: 06/22/2010      NM\$ +624      gEFI 8.1%
- 151HO00681 RUBICON      DOB: 12/20/2012      NM\$ +953      gEFI 8.2%
- 551HO03418 DYNASTY      DOB: 09/10/2015      NM\$ +980      gEFI 8.1%
- 551HO03600 NASHVILLE      DOB: 07/04/2017      NM\$ +1056      gEFI 8.6%
- HOUSA00023ETZ0353      DUE: 05/04/2019      NM\$ +1094      gEFI 9.0%
- NM\$ +657      gEFI +1.9%

Last three generations in 34 months

- ART will further reduce the generation interval

# Additive Genetics – Inbreeding Depression = Economic Gain

# U.S. PTAs are Adjusted for Inbreeding

Trait	Inbreeding depression/1%	Trait value in NM\$	\$ Value /1% F
Milk	-63.9	-0.004	-0.3
Fat	-2.37	3.56	-8.4
Protein	-1.89	3.81	-7.2
Productive life	-0.26	21	-5.5
Somatic cell score	0.004	-117	-0.5
Daughter pregnancy rate	-0.13	11	-1.4
Cow conception rate	-0.16	2.2	-0.4
Heifer conception rate	-0.08	2.2	-0.2
Cow livability	-0.08	12	-1.0
Net merit \$	-25	1	-25

# An Example With Four Bulls

Unadjusted NM\$	Percentage EFI	Adjusted NM\$
1000 NM\$	7%	825 NM\$
1000 NM\$	8%	800 NM\$
1000 NM\$	9%	775 NM\$
1000 NM\$	10%	750NM\$



# UK estimates of inbreeding depression

- Inbreeding depression per % inbreeding
- Starting from 5% inbreeding upwards
- Expressed as PTA
- Similar to estimates from other countries
- £PLI impact per % inbreeding
- Approx. -10 £PLI

	1%
Milk kg	-8
Fat kg	-0.3
Protein kg	-0.3
SCC	0.1
Calving Interval	0.1
NR56	-0.04
Fertility Index	-0.2
Life Span	-0.01
Calf Survival	-0.2

AHDB 2019

Genetics Selection Evolution 2014, 46:71

# Identification of genomic regions associated with Inbreeding Depression in Holstein and Jersey Dairy Cattle

Jennie E. Pryce, Mekonnen Haile-Maram, Michael E Goddard, Ben J Hays

Terms you will begin to hear a lot

**Runs of Homozygosity**

**Genomic Inbreeding Matrix**

**Percent of Homozygosity**

# Additive Genetics – Inbreeding Depression = Economic Gain





CHROMOSOMAL<sup>™</sup>  
**MATINO** ♀

**Creating  
the Most  
Profitable  
Herd**





# Mating Program Goals

What is the goal of a breeding a program?

Do develop a more profitable dairy farm

What improves profitability?

Increased production

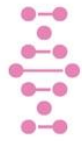
Improved health traits

Longer Productive Life

Improved Fertility

How to achieve

Most important part of any mating program:



CHROMOSOMAL<sup>™</sup>  
**MATING** 

# A well established science in a modern, efficient, flexible new suite!

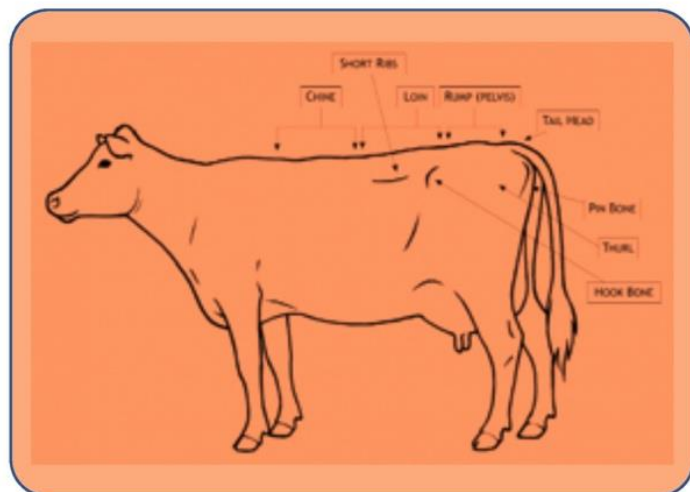


## The first mating programs were very basic:

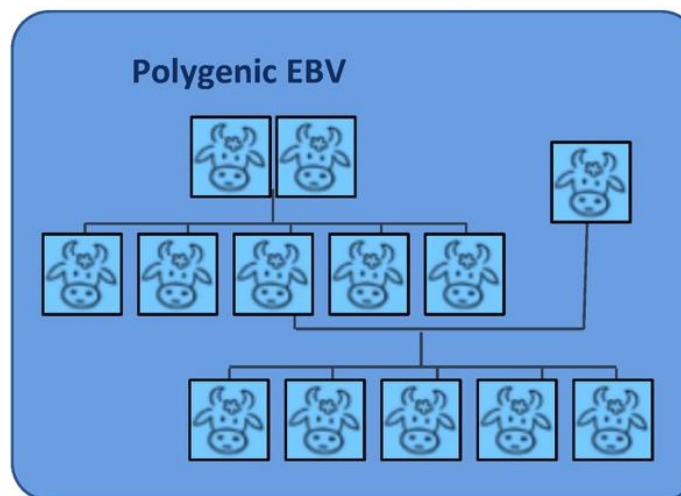
- 1** Focused on breeding wide bulls to thin cows and average strength bulls to average strength cows
- 2** The next generation of mating programs included more traits
- 3** Shallow uddered bulls were bred to deep udder cows
- 4** Straight leg bulls bred to cows with too much set
- 5** The problem with corrective mating programs was they did not consider genetics of the cow
- 6** Phenotype does NOT equal genotype
- 7** Pedigree matings became popular as they accounted better for genetics
- 8** This does not mean that animal evaluations are not needed
- 9** Cows must be scored to provide information for the genetic evaluations
- 10** Today genomic mating programs are rapidly growing in popularity as they provide the most accurate information



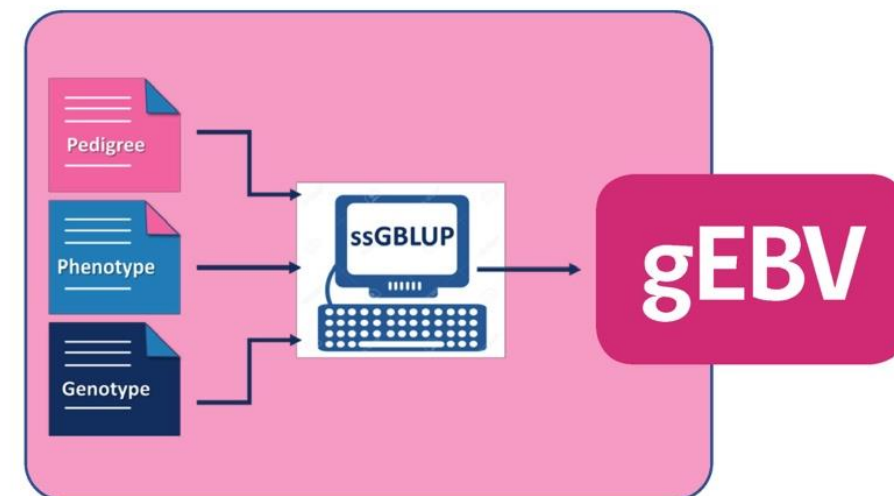
## Phenotypic-based (Linear Scoring)



## Pedigree-based (Parents' Averages)



## Genomics-based



- One size doesn't fit all .
- A multi-functional program to meet the needs of markets in different countries and regions.
- Maximize herd GEBV.

- Optimize Whole Herd Profitability.
- Manage recessive disorders in a herd.
- Maximize the frequencies of beneficial haplotypes or genomic regions.

**Accounts for the economic impact of inbreeding**

# SELECT THE CORRECT BULL TEAM

J. Dairy Sci. 96 :8014–8023 [http://dx.doi.org/ 10.3168/jds.2013-6969](http://dx.doi.org/10.3168/jds.2013-6969)

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## **Mating programs including genomic relationships and dominance effects**

**1 C. Sun ,\*2 P. M. VanRaden ,† J. R. O’Connell ,‡ K. A. Weigel ,§ and D. Gianola §**

**\* National Association of Animal Breeders, Columbia, MO 65205 † Animal Improvement Programs Laboratory, Agricultural Research Service, US Department of Agriculture, Beltsville, MD 20705-2350 ‡ School of Medicine, University of Maryland, Baltimore 21201 § Department of Dairy Science, University of Wisconsin–Madison, Madison 53706**



# Chromosomal Mating Provides the Predicted Producing Value of the Offspring or PPV

**For most traits PPV is what is used for the first step in CMP**

**The equation is:**

$$\text{CowPTA} + \text{BullPTA} + B * (\text{cowEFI} + \text{bullEFI}) - B * \text{inbreeding of calf} = \text{PPV}$$

**Where B = inbreeding depression of selected Trait**

**Cow NM\$ = 643 EFI 8.2**

**Bull NM\$ = 818 EFI 7.8**

**B = Net Merit 1% = \$25**

$$(643 + 818) + 25(8.2 + 7.8) - 200 = 1661 \text{ NM\$ PPV}$$

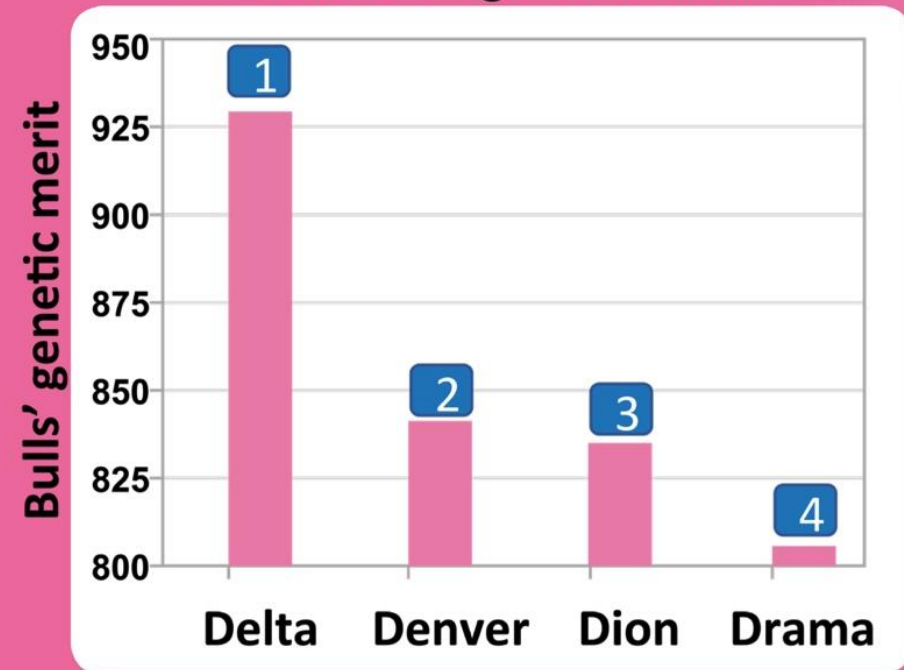
# Additive Genetics – Inbreeding Depression = Economic Gain



# Comparing Mating One Cow with Four Full Brothers



Mating priorities based on  
bulls' own genetic merit



# Comparing Mating One Cow with Four Full Brothers

## 523H01468 Delta

Own +928NM\$

Progeny's performance

Pedigree +1,888NM\$ IB **12.68%**

Genomic +1,755NM\$ IB **18%**

## 551H000690 Denver

Own +840NM\$

Progeny's performance

Pedigree +1,806NM\$ IB **12.68%**

Genomic +1,773NM\$ IB **14%**

## 551H000695 Drama

Own +804NM\$

Progeny's performance

Pedigree +1,762NM\$ IB **12.68%**

Genomic +1,634NM\$ IB **17.5%**

## 523H001470 Dion

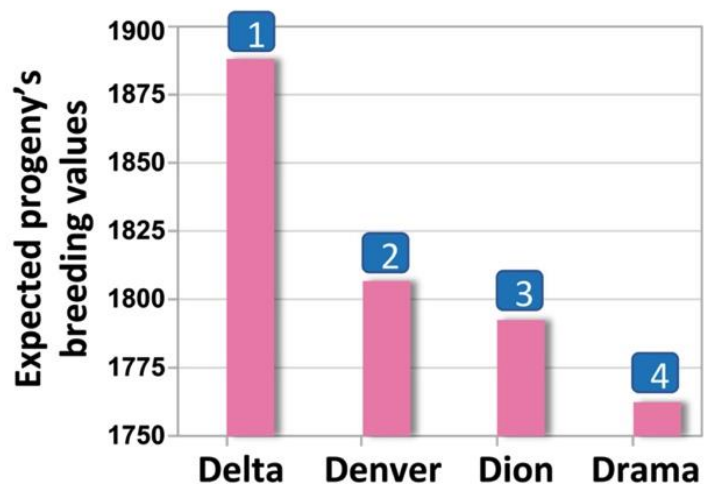
Own +834NM\$

Progeny's performance

Pedigree +1,792NM\$ IB **12.68%**

Genomic +1,781 NM\$ IB **13.1%**

Mating priorities using PEDIGREE BASED matings



Mating priorities using GENOMIC BASED matings





# Genomic mating programs



- Reduce inbreeding using genomic instead of pedigree relationships
  - Genomic relationship of each live female to each marketed bull
  - File contains 1 million females × 5,000 males
- Genomic mating increases heifer calf value by
  - **+\$84** compared with pedigree mating (1.3% lower inbreeding)
  - **+\$214** compared with random mating (2.9% lower inbreeding)
- Also improves conception rates by avoiding recessive carrier matings
- Also reduces inbreeding of bull calves, promoting faster growth

# What can genomics do on commercial farms?

- Traditionally, commercial farms create very little genetic progress on the female side
- This is due to selection restriction imposed by replacement rates
- Most genetic progress comes in through the male side (AI sires)
- So we have very small selection intensities and very low accuracies of selection

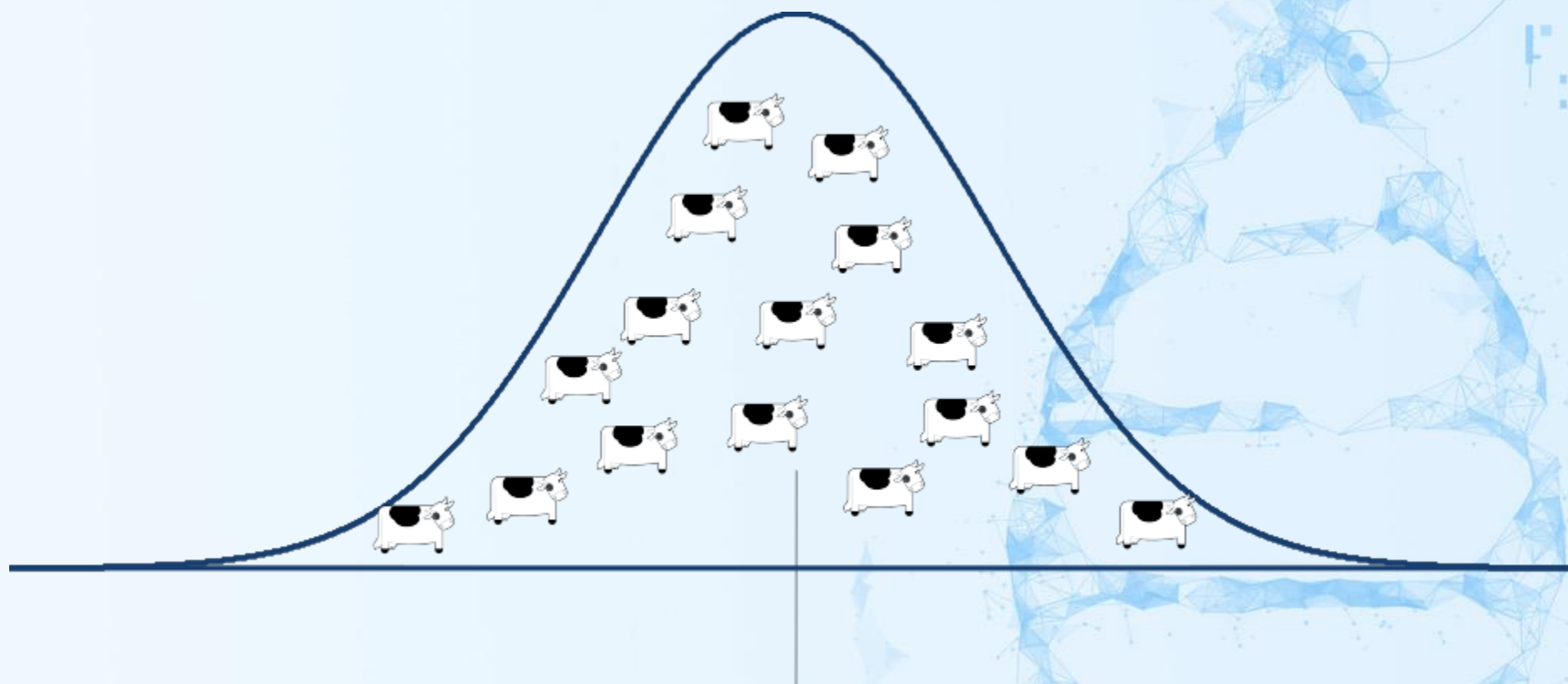
# Example of introducing genomic selection bundled with sexed semen

*„Breeders Equation“*

$$\Delta G = \frac{i * r * \sigma}{GI}$$

- **$\Delta G$**  = Genetic progress per year
  - **$i$**  = selection intensity
  - **$r$**  = accuracy of selection
  - **$\sigma$**  = additive genetic standard deviation
  - **$GI$**  = generation interval
- Sexed semen leverages selection intensity ( $i$ )
  - Genomic prediction increases accuracy of selection ( $r$ )

# The cow population on a dairy farm

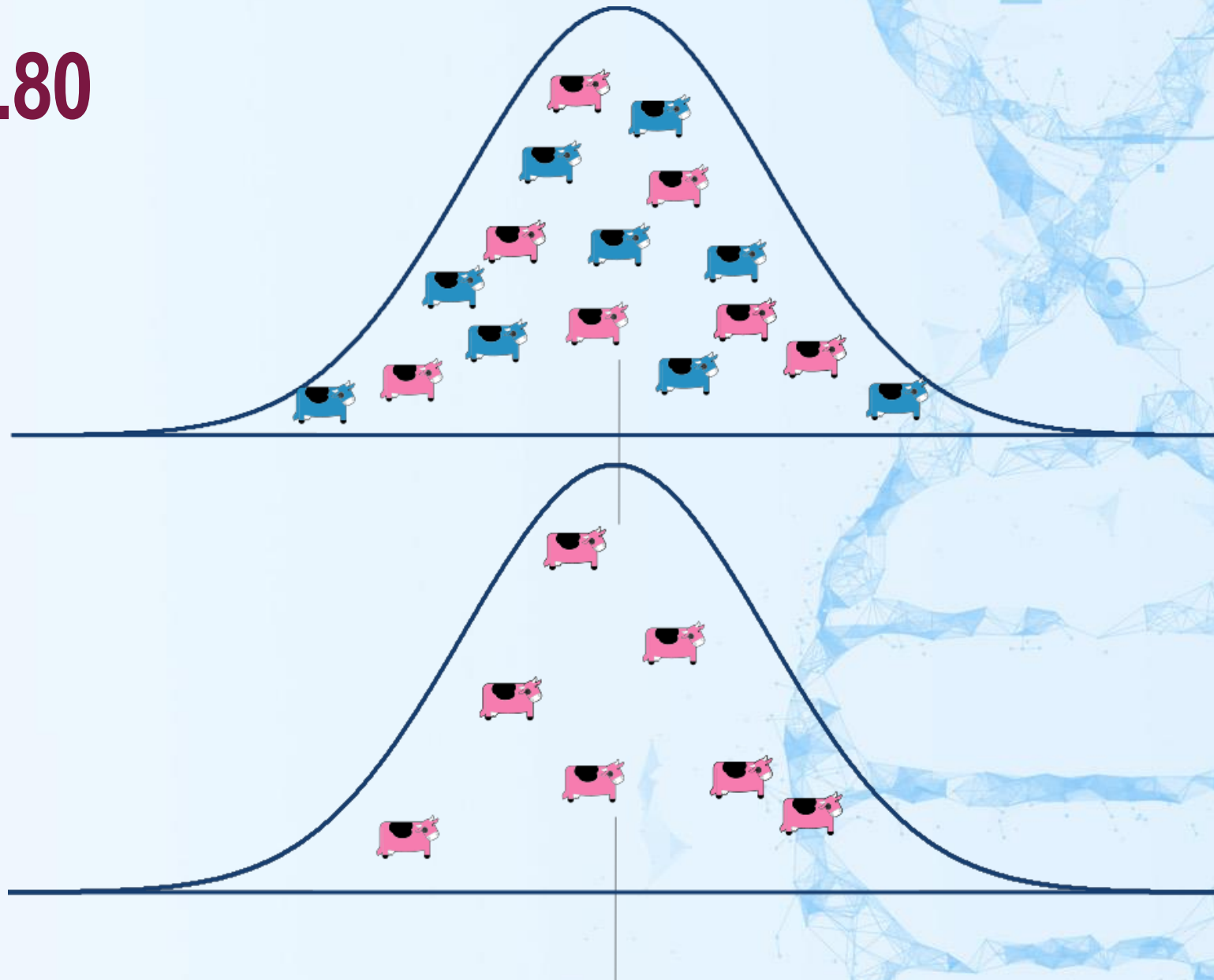




# Example

Traditional	
$\sigma$	NM\$197
i	0.35
r	0.40
GI	3.5
$\Delta G$	NM\$7.88

$\Delta G \approx \$7.80$



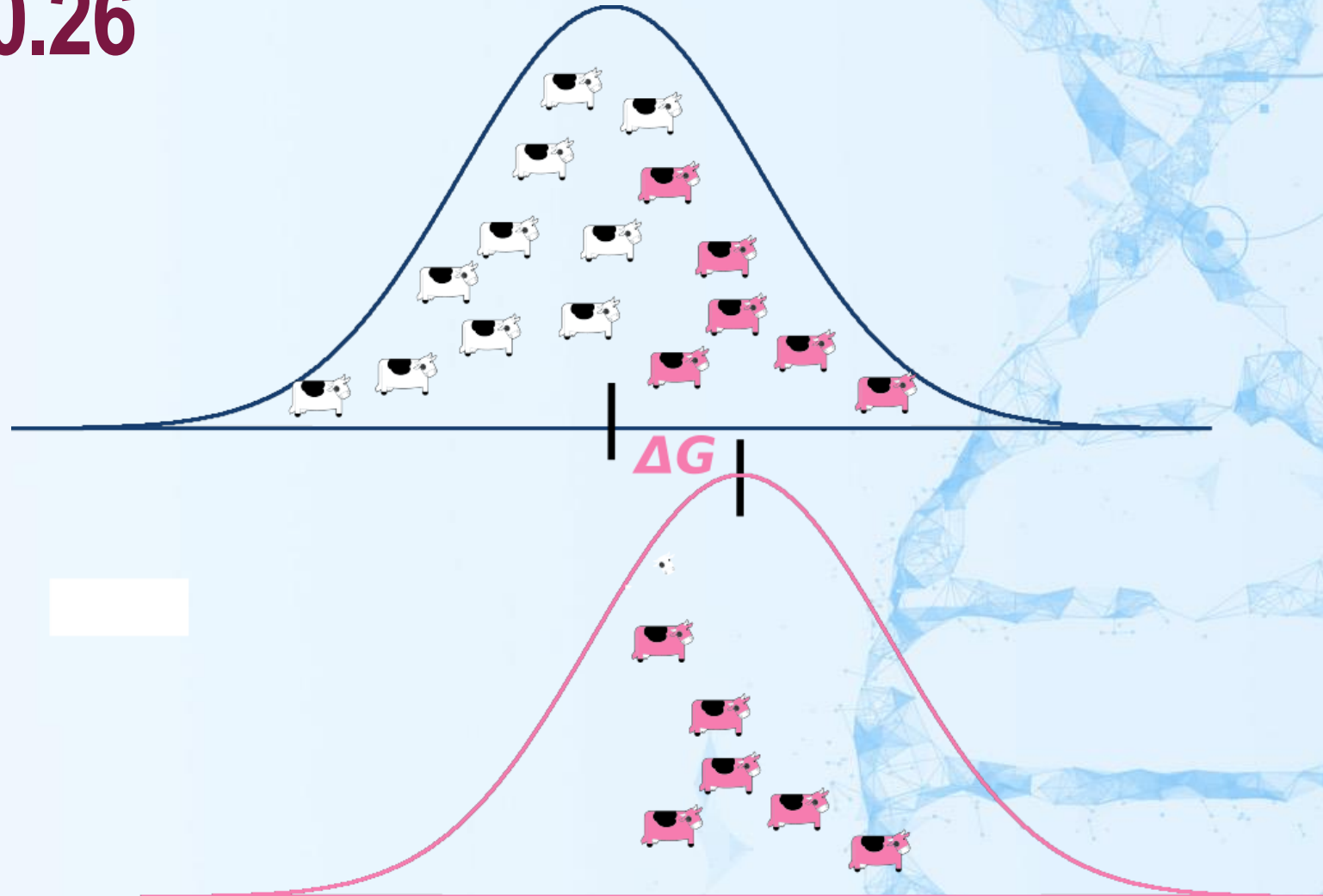
# Example

- 1) Sexed semen – Select from more females and shorter generation interval.

Traditional	
$\sigma$	NM\$197
i	0.35
r	0.40
GI	3.5
$\Delta G$	NM\$7.88

Sexed Semen	
$\sigma$	NM\$197
i	0.96
r	0.40
GI	2.5
$\Delta G$	NM\$30.26

$$\Delta G = \$30.26$$





# Example

1) Sexed semen – Select from more females and shorter generation interval.

2) Genomics – Select more accurately

Traditional	
$\sigma$	NM\$197
i	0.35
r	0.40
GI	3.5
$\Delta G$	NM\$7.88

Sexed Semen	
$\sigma$	NM\$197
i	0.96
r	0.40
GI	2.5
$\Delta G$	NM\$30.26

Sexed Semen + Genomics	
$\sigma$	NM\$197
i	0.96
r	0.70
GI	2.5
$\Delta G$	NM\$52.95



THE BEST WAY TO PREDICT  
THE FUTURE IS TO

*Create it*

**ST**♂**enetics**®  
♀