# Pros and cons of hitchhiking: The truth about inbreeding in dairy cattle

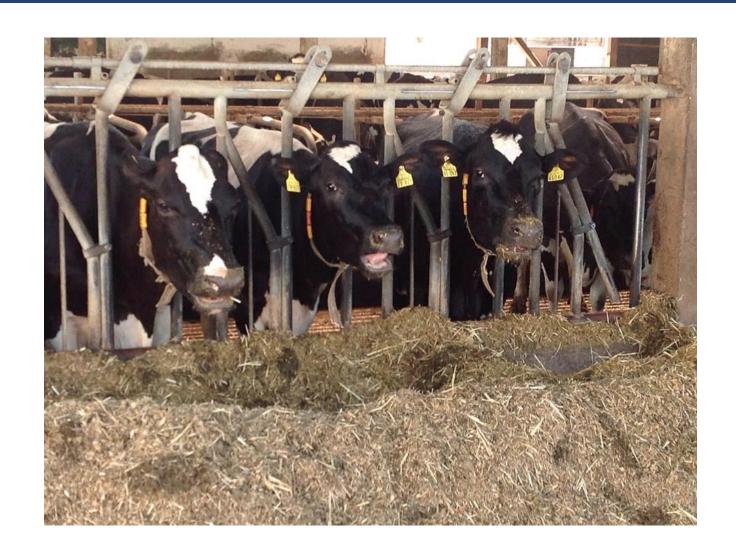
## John B. Cole

USDA, Agricultural Research Service
Henry A. Wallace Beltsville Agricultural Research Center
Animal Genomics and Improvement Laboratory
Beltsville, MD 20705-2350



## **Topics for discussion**

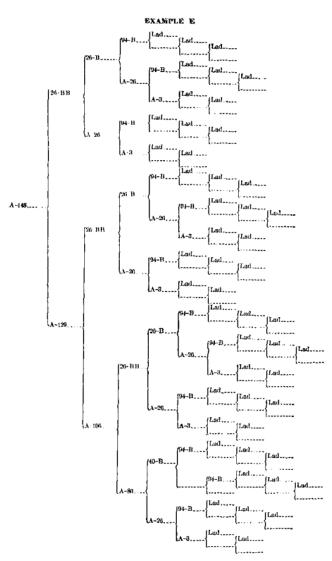
- What is inbreeding, and what causes it?
- (Why) is it bad?
- How do we measure it?
- Is it changing in the Holstein breed?
- Can we do anything about it?
- Take-home messages



# What is inbreeding, and what causes it?

## Inbreeding results from the mating of related animals

- It's the proportion of the genome that is identical because it came from the same ancestor
- Inbreeding results when related animals are mated to one another
- Inbreeding is inevitable in a finite population
  - It can be managed, but not stopped



Source: Swett et al. (1949)

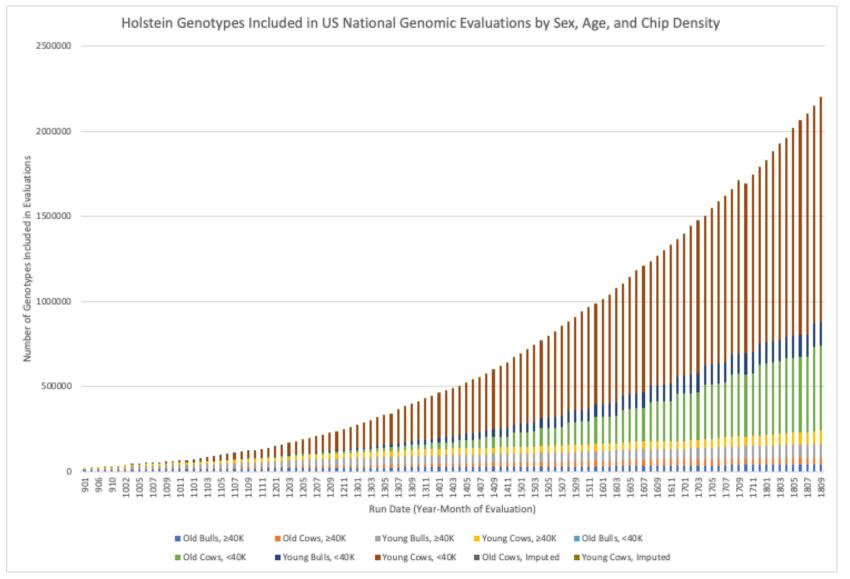
## More efficient selection, more inbreeding

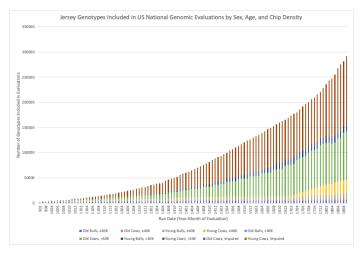
Theory	Author	Year	Species
Single-gene inheritance	Mendel	1865	Peas
Multiple-gene inheritance	Fisher	1918	Humans
Pedigree relationship matrix	Wright	1922	Cattle
Selection index	Hazel & Lush	1943	Plants, cattle
Mixed linear models	Henderson	1963	Cattle
Genomic prediction	Meuwissen	2001	Animals
Genomic relationship matrix	VanRaden	2008	Cattle
_ •			

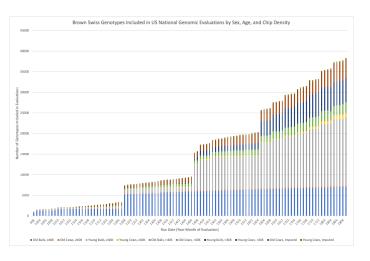
**Also application** 

First database with 1 million genotyped individuals was USDA/Council on Dairy Cattle Breeding in July 2015

## Genotypes are plentiful



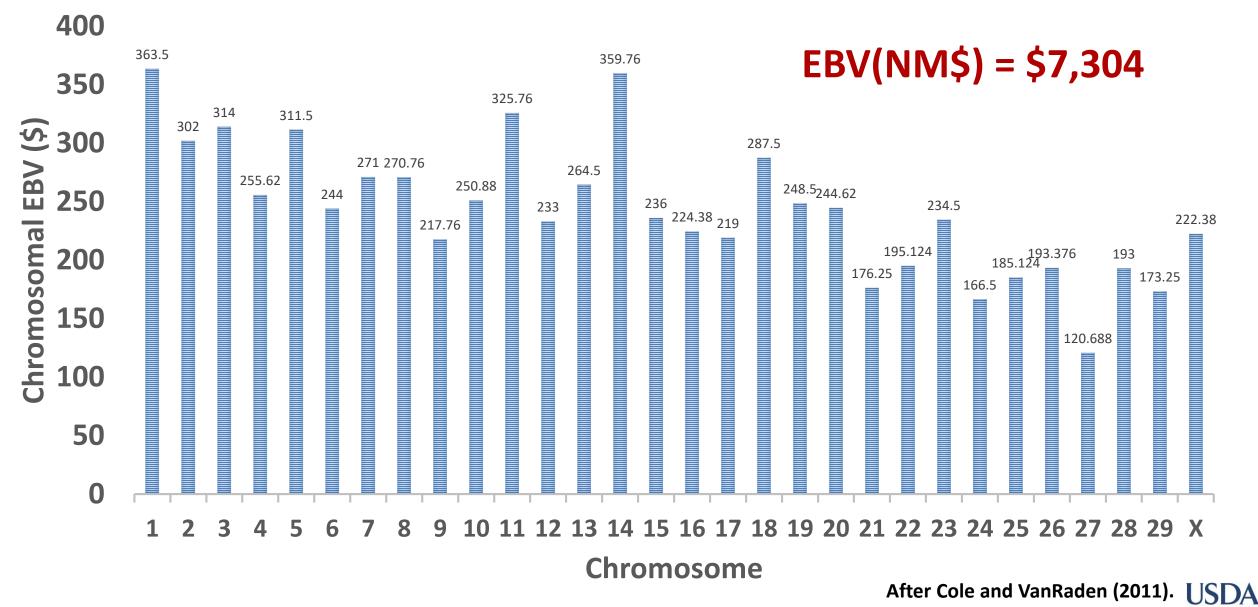




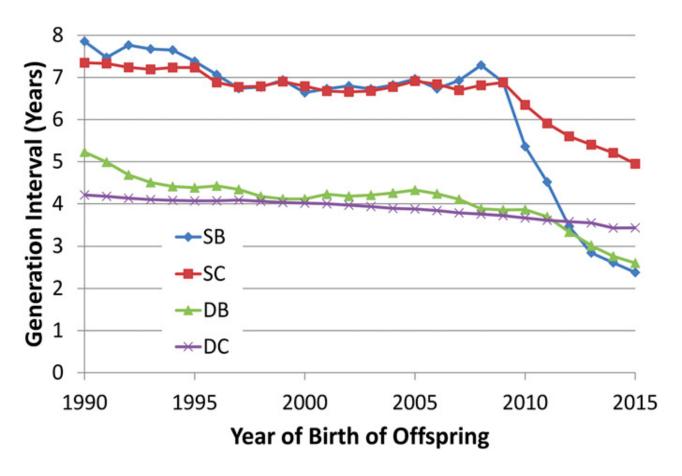
**Source:** Council on Dairy Cattle Breeding (2019).

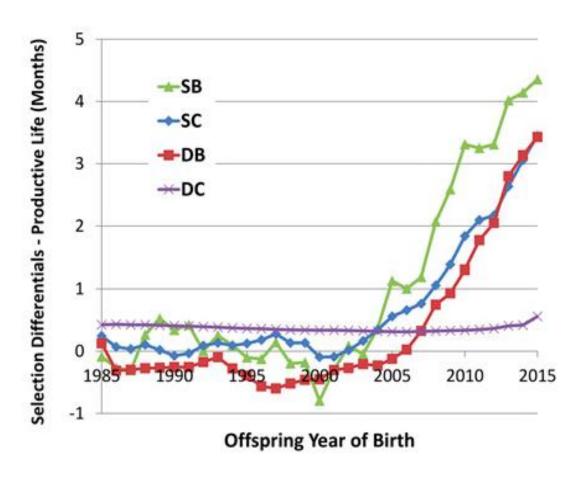


## We want to get the best DNA together in one animal



## Genomic selection lets us go really fast





**Source:** García-Ruiz et al. (2016).



## We're in an endless race to find the highest index bull

- Al breeds bulls to meet market demands
- High genetic merit bulls have high marketability
- Lower inbreeding rates result in slower genetic gains
- Who is willing to go slower to better manage inbreeding?



Source: Wikimedia Commons.

# (Why) is it bad?

## Inbreeding often has undesirable effects

- Harmful loci increase in frequency and are more likely to be paired-up
  - e.g., Haplotypes such as HH1
  - This is thought to account for most inbreeding depression
- Slow inbreeding more effective at selecting against harmful loci
- Undesirable loci travel along with desirable loci if they're close together ("hitchhiking")



Trait	Effect/1% gain
Milk yield	-50 lb
Fat yield	-1.5 lb
Birth weight	-0.24 lb
Yearling weight	-1.5 lb
Weight at 4 years	-5.0 lb
Height	Slight decrease
Survival to 1st calf	-2 %
Services to conception	+0.05
Days to first service	+3.0
Age at puberty	Delayed

Source: Schmidt et al. (1988).

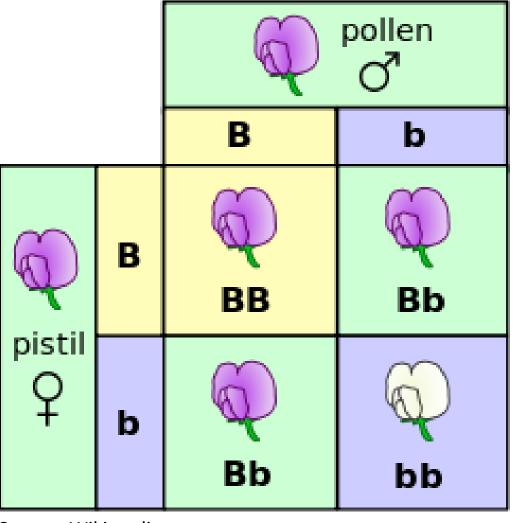


# Mendelian recessives are exposed by inbreeding

- Classical model of inheritance
- One locus, typically with two alleles
- Often exhibit complete dominance

• e.g

**Source:** The Far Side.



Source: Wikimedia.

# Mendel's garden: a pilgrimage



## There are many known recessives in U.S. Holsteins

Haplotype	Functional/ <i>Gene</i> name	Chromosome	Location (Mbp)	Haplotype frequency (%)	Timing <sup>1</sup>
HBR	Black/red coat color/MC1R (MSHR)	18	14.71	0.75	_
HCD	Cholesterol deficiency/APOB	11	77.87	2.28	W
HDR	Dominant red color/MC1R (MSHR)	3	9.36	0.03	_
HH0	Brachyspina/FANCI	21	20.77	1.65	E,B
HH1	APAF1	5	62.81	1.28	E
HH2	<del>_</del>	1	93.50-95.58	1.21	Ε
HH3	SMC2	8	93.75	2.64	Ε
HH4	GART	1	1.99	0.23	E
HH5	TFB1M	9	91.85-91.94	2.39	Ε
HH6	SDE2	16	29.01-29.05	0.44	Old age
ННВ	BLAD/ITGB2	1	144.77	0.21	W
HHC	CVM/SLC35A3	3	43.26	1.10	E,B
HHD	DUMPS/UMPS	1	69.15	0.01	Ε
HHM	Mulefoot/LRP4	15	76.81	0.05	В
HHP	Polledness (dominant)/POLLED	1	2.57	0.88	_
HHR	Red coat color/MC1R (MSHR)	18	14.71	3.29	_

<sup>&</sup>lt;sup>1</sup>Timing of embryonic loss/calf death for homozygous animals: B = calf death at/shortly after birth, E = embryonic loss/abortion, W = calf death weeks/months after birth (Cole et al., 2016; Cole et al., 2018).



## Is the number of defects increasing?

- MacArthur et al. (2012) estimated that human genomes contain ~100 loss-of-function mutations, and ~20 completely inactivated genes
- The mutations are there even if we have not identified them yet
  - Example: HH6, mutation in SDE2 (Fritz et al., 2018)
- Our detection methods are improving as our technology improves
- New mutations do occur, but they are very rare

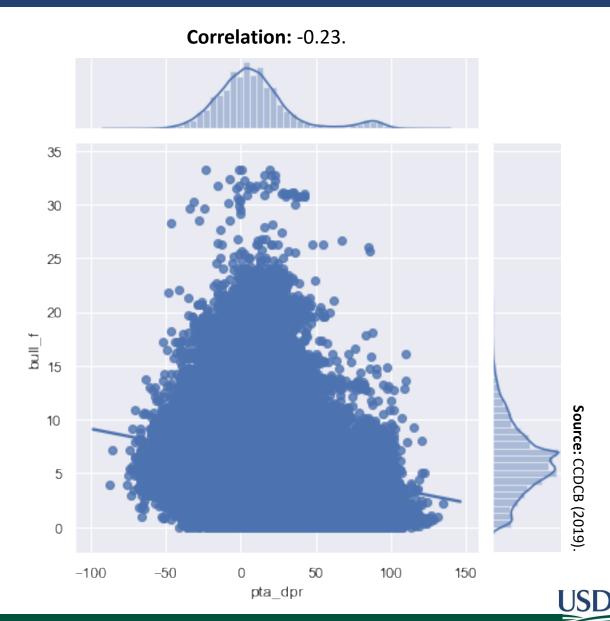
## Estimated cost of genetic load

- Cole et al. (2016) estimated annual losses of at least \$10.7 million due to known recessives.
- Average losses were \$5.77, \$3.65, \$0.94, and \$2.96 in Ayrshire,
   Brown Swiss, Holstein, and Jersey, respectively.
- This is the economic impact of genetic load as it affects fertility and perinatal mortality.
- Actual losses are likely to be higher.

## We don't really know how much is too much

- Selection is now on indices that include health and fitness data
- This avoids past mistakes from focusing on only one or a few traits
- Will we see genetic merit gradually fade away, or will we cross a threshold and suddenly crash?
- *Interviewer:* "How did you go bankrupt?"

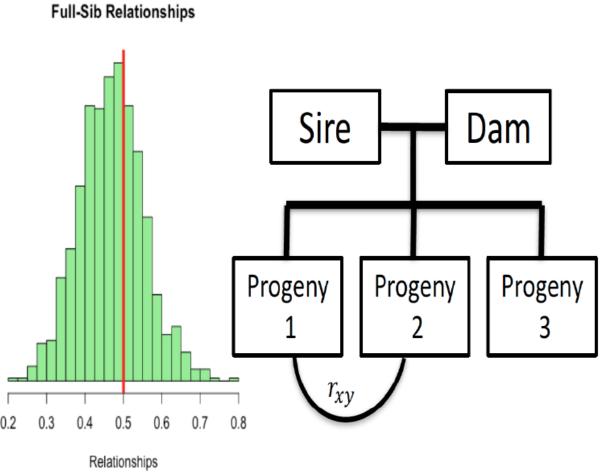
**Ernest Hemingway:** "Two ways. Gradually, then suddenly."



### How do we measure it?

## Pedigree and genomic inbreeding

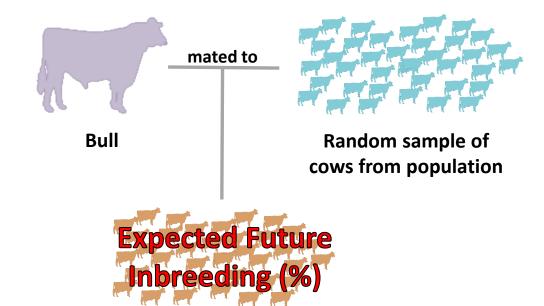
- Pedigree inbreeding is based on the passing of chromosomes from parents to offspring over many generations
- Genomic inbreeding is based on the actual pieces of chromosomes passed from parents to offspring over many generations
- Inbreeding increases as pedigrees get deeper
- However, the age of inbreeding may matter, too



Source: Christian Maltecca (2019).

## **Expected future inbreeding (EFI)**

- Inbreeding is a property of an individual animal
- Expected future inbreeding is the average inbreeding expected when a bull is mated to a random sample of cows from the population
- The more related a bull is to the population, the higher the EFI
- Genomic future inbreeding (GFI) is based on the same concept



#### 7HO6417 O MAN \*

O-BEE MANFRED JUSTICE-ET (EX-94-GM)

HOUSA122358313 100% RHA-NA

TR TV TL TD Born: 03/08/1998

aAa: 435216 DMS: 345,456

Breeder: Gary, Gaylon & Steve Obert, Dakota, IL

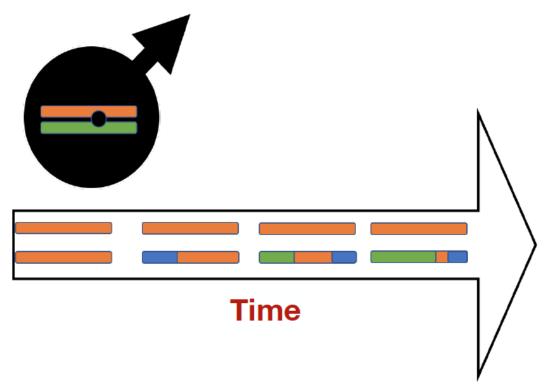
Beta-Casein: A1A2 GFI: 10.49

Kappa-Casein: BB Beta-Lactoglobulin: AB Haplotypes HH3C HH1T HH2T HH4T HH5T HH6T

Source: Select Sires.

## Runs of homozygosity (ROH)

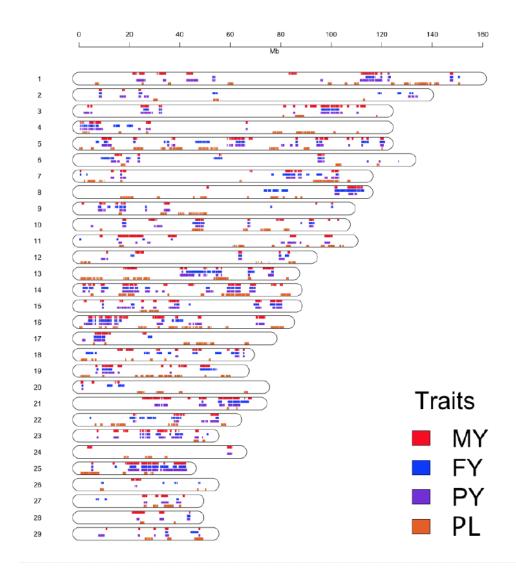
- Recent inbreeding produces long stretches of DNA shared in common
- Old inbreeding is represented by much shorter pieces of shared DNA
- ROH provide information about specific places in the genome
- Old stretches of inbreeding may have been purged of harmful loci



**Source:** Christian Maltecca (2019).

## ROH used to find undesirable, but not lethal, regions

- Some mutations in the population are sub-lethal: they harm performance but don't kill animals
- They are more difficult to find than lethal haplotypes
- May appear in ROH

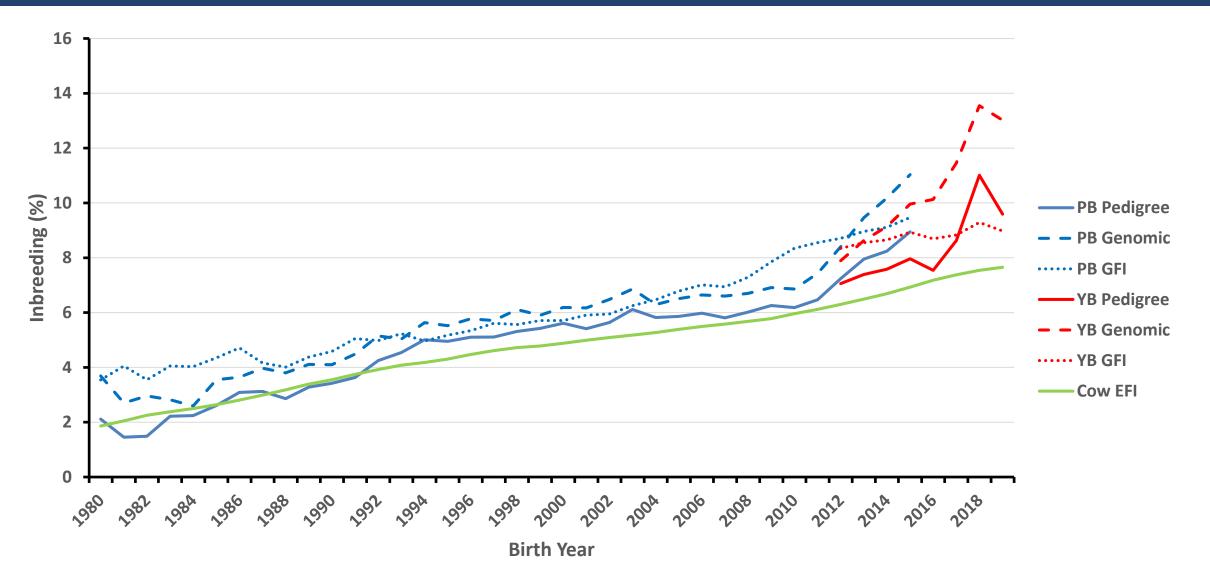


Source: Christian Maltecca (2019).



## Is it changing in the Holstein breed?

## Pedigree and genomic inbreeding of Holsteins



# **ROUND OAK RAG APPLE ELEVATION (007H000058)**

f <sub>p</sub>	0.0		 HOUSA000000933122	1944-03-28	WIS IDEAL		
f <sub>G</sub>	-3.3	HOUSA000001013415		1947-03-28	Wis Burke		
NM\$	NM\$ -567		1944-03-28				
TPI	843	HOUSA000001271810	HOUSA00000933122	1955-03-23 1944-03-28	TIDY BURKE ELEVATION WIS IDEAL	1	58k
		HOUSA0000	HOUSA000001013415 HOUSA000002454577 03348181	1947-03-28 1944-03-28 1950-09-18	Wis Burke  CARINE MERCEDES BURKE IDEAL		
			HOUSA000002948518	1947-09-19			
HOUSA00001491007			1965-08-30	ROUND OAK RAG APPLE ELEVATION	4	778k	
			HOUSA000000848777	1947-01-04	OSBORNDALE TY VIC		
		HOUSA0000	)1189870	1952-04-26	OSBORNDALE IVANHOE	1	58k
			HOUSA000002471271	1947-11-29			
HOUSA000005749758		HOUSA000005749758	HOCAN00000239301 HOUSA000001294924 HO	1962-07-14 1951-11-30 1954-02-15	ROSAFE CENTURION		
		HOUSA0000	HOUSA00001064446 HOUSA000003757944	1959-01-07 1947-09-23 1953-11-16 1949-02-17	ROUND OAK MONTVIC P F GENERAL		

# MARA-THON BW MARSHALL-ET (007H005375)

f <sub>P</sub>	5.8			OUSA000001556373	1968-11-19	GLENDELL ARLINDA CHIEF		-
•Р	5.0		HOUSA00000169		1975-11-20	ARLINDA ROTATE	4	778k
$f_G$	8.9			OUSA000007370146	1969-08-14			
·G	0.5	HOUSA00000			1982-03-06	ARLINDA MELWOOD-ET	4	778k
NM\$	-78		НС	OUSA000001531866	1968-01-27	PACLAMAR COMBINATION		
•			HOUSA00000931	11697	1976-12-10	ARLINDA COMBI MELODY		
TPI	1548		HC	OUSA000008155956	1972-05-04	ARLINDA CARLIN MELODY		
		HOUSA000002103297			1989-05-19	MAIZEFIELD BELLWOOD-ET	1	58k
				OUSA000001441440	1963-01-20	PENSTATE IVANHOE STAR	1	58k
			HOUSA00000166	67366	1974-05-16	CARLIN-M IVANHOE BELL	4	778k
			НС	OUSA000007832117	1970-10-18	B & W HEILO CREAMELLE		
		HOUSA00001	2052401		1984-10-13	BREN-WAY BELL BETSY		
			HC	OUSA000001626813	1972-08-06	MARSHFIELD ELEVATION TONY	1	58k
			HOUSA00001130	02033	1982-09-15	BREN-WAY TONY BESSIE		
			HC	OUSA000010533152	1980-07-01			
HO	OUSA000002	2290977			1995-03-24	MARA-THON BW MARSHALL-ET	4	778k
				OUSA000001441440	1963-01-20	PENSTATE IVANHOE STAR	1	58k
			HOUSA00000166	67366	1974-05-16	CARLIN-M IVANHOE BELL	4	778k
			НС	OUSA000007832117	1970-10-18	B & W HEILO CREAMELLE		
		HOUSA00000	1912270		1983-01-25	EMPRISE BELL ELTON	4	778k
				OUSA000001556373	1968-11-19	GLENDELL ARLINDA CHIEF	4	778k
			HOUSA00001024	18397	1979-06-02	MONARCHIAL GLENDELL EFFIE		
			HC	OUSA000008786528	1974-07-23			
		HOUSA000014840387			1990-05-02	MORGAN-VALLEY ELTON MARA		
			НС	OUSA000001650414	1973-06-28	S-W-D VALIANT	4	778k
			HOUSA00000181	18972	1980-02-02	MEL-EST VALIANT IROS MELVIN	1	58k
				OUSA000008560247	1973-11-02	MEL-EST ELEVATION IROSE ROSITA		
		HOUSA00001			1986-05-26	MORGAN-VALLEY MARCIS MARY		
			HC	OUSA000001682467	1975-01-22	WAGNERSCREST IVANHOE ASTRONAUT	1	58k
			HOUSA00001102		1982-03-01			
			НС	OUSA000008510667	1973-08-09			

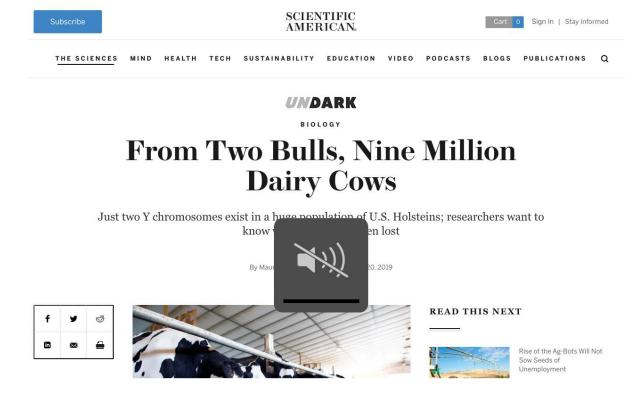
# PINE-TREE ACURA-ET (029H018960)

;	12.8		HOUSA000139005002	2007-09-17	COYNE-FARMS DORCY-ET	1	58k
Р	12.0		НО840003006972816	2010-06-22	MOUNTFIELD SSI DCY MOGUL-ET	1	58k
F_	17.1		HOUSA000062784081	2006-04-23	MOUNTFIELD MARSH MAXINE-ET	1	58k
G	17.1	HOUSA00007	2254526	2013-01-05	WOODCREST MOGUL YODER-ET	8	77k
VM\$	1,065		HOUSA000060597003	2003-03-03	ENSENADA TABOO PLANET-ET	4	778k
	_,		НО840003008363689	2011-03-21	WOODCREST PLANET YAKARA-ET	3	3k
ГРІ	2,895		HOUSA000066893887	2009-05-18	COYNE-FARMS BKEYE YVONNE-ET	1	58k
	-	Н0840003128557482		2015-11-15	ABS ACHIEVER-ET	17	140k
			HOUSA000060996956	2004-10-31	BADGER-BLUFF FANNY FREDDIE	1	58k
			HONLD000543756297	2011-06-16	APINA ALTAEMBASSY-ET	2	58k
			HOUSA000064969166	2008-12-01	STRAUSSDALE PLANET ELLA	1	58k
		НО84000301		2013-09-30	COMPASS-TRT AMRC AE J925-ET	8	77k
			HOUSA000064966739	2008-12-23	ROYLANE SOCRA ROBUST-ET	1	58k
			HOUSA000070640281	2011-07-26	SEAGULL-BAY MISS AMERICA-ET	2	58k
			HOUSA000066228178	2009-04-16	AMMON-PEACHEY SHAUNA-ET	1	58k
]	H084000314	2332520		2017-11-25	PINE-TREE ACURA-ET	17	140k
			HOUSA000069398748	2010-06-30	MOUNTFIELD MSY MAURICE-ET	2	58k
			НО840003009554583	2012-05-22	S-S-I MAURICE PARTYROCK-ET	2	58k
			НО840003006972817	2010-06-22	JK-GOLD SSI DORCYPIE7042-ET	1	58k
		НО84000301		2014-01-01	S-S-I PARTYROCK PROFIT-ET	8	77k
			HO840003006972816	2010-06-22	MOUNTFIELD SSI DCY MOGUL-ET	1	58k
			НО840003009554577	2012-05-17	S-S-I MOGUL MAHO 8054-ET	7	9 k
			HO840003004672693	2010-08-26	S-S-I ROBUST MAHO 7083-ET	2	58k
		НО840003132116871		2016-03-13	PINE-TREE 9882 PROF 7019-ET	20	19k
			HOUSA000064966739	2008-12-23	ROYLANE SOCRA ROBUST-ET	1	58k
			HOUSA000069981349	2010-12-28	SEAGULL-BAY SUPERSIRE-ET	2	58k
			HOUSA000066228178	2009-04-16	AMMON-PEACHEY SHAUNA-ET	1	58k
		НО84000301		2013-12-02	OCD SUPERSIRE 9882-ET	17	140k
			HOUSA000064966739	2008-12-23	ROYLANE SOCRA ROBUST-ET	1	58k
			но840003008315320	2011-03-08	OCD ROBUST SHIMMER-ET	2	58k
			HOUSA000066228180	2009-04-18	AMMON-PEACHEY SHANA-ET	1	58k

# Can we do anything about it?

## Scientists are trying to understand what's been lost

- Almost all Y chromosomes in the Holstein bull population are from Elevation and Chief
- It's unclear what might have been lost along the way
- A small genetic base may translate to a fragile population that can't respond well to changes



Source: O'Hagan (2019), Scientific American, 20 June 2019.



## Al companies were trying to identify new bloodlines



Global and North American (NA) sire numbers, before and after genomics

			Post-genomics		
		Pre-genomics	Bulls entered Al	All genotyped buils	
Birth years		2002-2008	2011		
No of come halls	Global	5,300	3,290	28,440	
No. of young bulls	NA	1,660	1,335	10,685	
	Global	380	410	1,240	
No. of sires of young bulls	NA	105	155	450	
No. of most popular sires representing	Global	15	18	32	
50% of young bulls	NA	8	9	16	
August a month or of some new size	Global	14	8	23	
Average number of sons per sire	NA	15	9	24	

**Source:** Miglior and Beavers, *Progressive Dairyman*, 18 July 2014.



## There are many theoretically satisfying ideas...

- ...but nobody uses them
- Geneticists don't breed cows, farmers do
- Many cows now mated at random to a portfolio of bulls
- Everyone thinks their neighbor should use different bulls

#### Some methods for avoiding inbreeding

Optimal contribution theory

Minimization of progeny inbreeding

Linear programming

Look-ahead mate selection

Selection against lethal alleles

Index selection including Mendelian sampling variance

Genomic selection including dominance



# U.S. PTAs are adjusted for inbreeding

Trait	Inbreeding depression/1%	Trait value in NM\$	<b>\$ Value /1% F</b>
Milk	-63.9	-0.004	0.3
Fat	-2.37	3.56	-8.4
Protein	-1.89	3.81	<b>-7.2</b>
Productive life	-0.26	21	<b>-5.5</b>
Somatic cell score	0.004	<b>-117</b>	-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 \$	<b>-25</b>	1	<b>-25</b>



## Example EFI adjustment for Acura

- Difference of EFI − daughter F = 8.7 − 0.0 = 8.7%
- Economic loss (future past daughters) = 8.7 × \$25/1%F = \$217
- Acura's initial NM\$ = +\$1,282 before adjustment
- Acura's official NM\$ = +\$1,065 after adjustment
- As the population becomes more related to an animal, its evaluations decrease
- Progeny, grandprogeny, etc., also adjusted because their EFIs tend to be higher than breed average

# **Opportunities and Conclusion**

#### Conclusions

- Male genetic diversity is very limited in the Holstein population
- It's important to conserve female genetic variation
- Inbreeding depression may be responsible for some of the decrease in fitness traits, such as fertility
- If stacking of pedigrees continues dairy breeding will come to resemble pig and chicken breeding – without the controlled environments



## Acknowledgments

- The author was supported by USDA-ARS project 8042-31000-002-00-D, "Improving Dairy Animals by Increasing Accuracy of Genomic Prediction, Evaluating New Traits, and Redefining Selection Goals".
- The conference organizers funded the author's travel.
- USDA is an equal opportunity provider and employer.
- Mention of trade names or commercial products in this presentation is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the US Department of Agriculture.



# **Questions?**

