



Can
industry
\$251,000 dairy heifer sale?

Genetics: What

the beef
learn from

Sold in Australia
Flown to Canada
Bought by Sexing Technology, USA





LIGHTNING RIDGE-CMD JEDI GIGHMP-ET

Lightning Ridge-CMD JEDI GIGHMP-ET is a 2-year-old Friesian x Jersey heifer, born in 2014, with a predicted mature weight of 1,200 lbs. She is a member of the Lightning Ridge-CMD herd, which is a registered herd of the Lightning Ridge-CMD Herd Book. She is a member of the Lightning Ridge-CMD herd, which is a registered herd of the Lightning Ridge-CMD Herd Book. She is a member of the Lightning Ridge-CMD herd, which is a registered herd of the Lightning Ridge-CMD Herd Book.



PNAS

Tendon and cartilage development

Holsteins are the genomic selection poster cows



"Genomic selection was a technology waiting to be invented for the US dairy industry."



We're happy to have genomic information.

But it's a rapidly changing industry .



As the industry changes it influences how you model and analyze the data.

- Analyst - Data structure
- Everyone else – business opportunities, market share and livelihoods
- Some planning....followed by adjusting, adapting, and competing. With winners and less-than-winners.



How we're using genomics within the Holstein breed.

- Determine the **genetic merit** of elite animals at a young age.
- Manage the rate of **Inbreeding**.
- Keep **undesirable genetic defects** at a low level.
- Identify **Breed composition** of crossbreds. ½ HO, ¼ HO, etc.
- Verify or discover **Parentage**.
- **Herd Management**, cull low end replacement animals earlier, breed lower genetics to beef bulls.
- Having more animals genotyped allows us to more easily **investigate** other genetic issues.

USDA **Haplotype tests for recessive disorders that affect fertility and other traits**

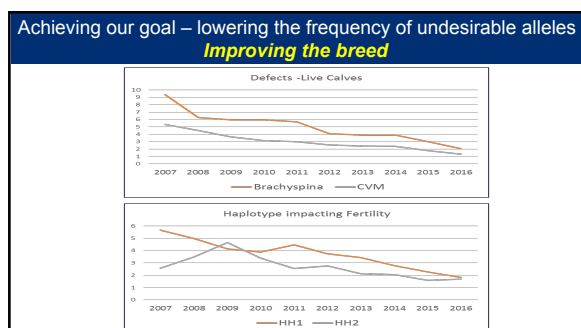
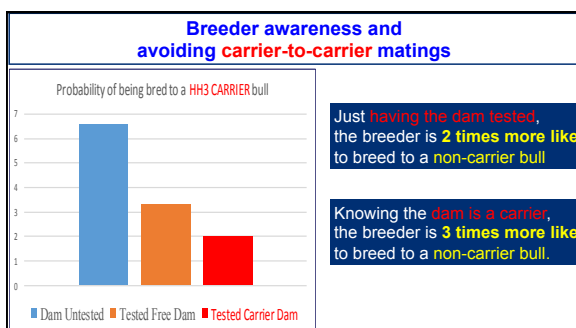
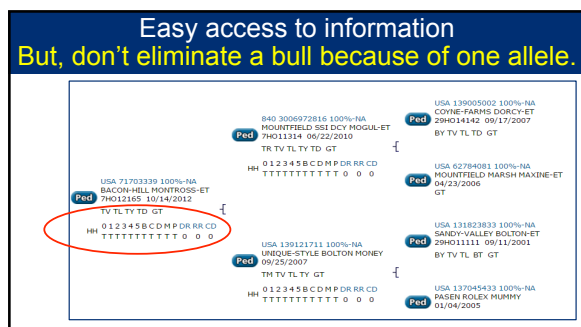
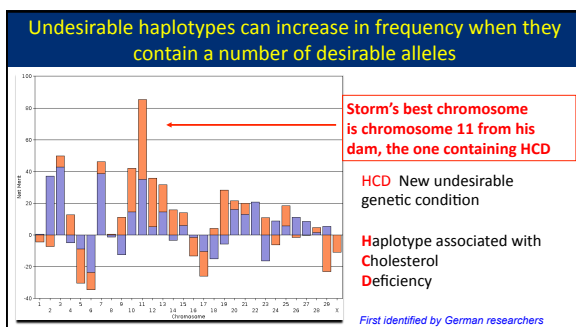
J.B. Cole, P.M. VanRaden, D.J. Nisell, J.L. Hutchison, T.A. Cooper, and R.M. Hubbard
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Updated Mar. 23, 2015

http://aigp.arsusda.gov/reference/recessive_haplotypes_ARR-G3.html

One in five animals are expected to be a carrier of a genetic defect causing early embryonic loss.

VanRaden and Miller, 2006

Breed	Haplotype	OMIA 9913 ID ¹	Functional/ gene name	Frequency (%)	Chromosome	Region (bp)	Reference
Holstein	HBR	001199	Black/red coat color/ NC2R(MSHR)	0.8	18	14,757,332 – 14,759,082	Lawlor et al. (2014)
	HDR	001529	Dominant red coat color	0.04	3	9,479,761	Lawlor et al. (2014), Capitani et al. (2014)
	HHO	000151	Brachypoda/FANCZ	2.76	21	21,184,869 – 21,188,198	Agarholn et al. (2006), Charlier et al. (2012)
	HH1	000061	APAF1	1.92	5	63,150,400	Adams et al. (2012)
	HH2	001823	—	1.66	1	94,860,836 – 94,953,359	VanRaden et al. (2011), McClure et al. (2014)
	HH3	001824	SMC2	2.95	8	95,410,507	Cooper et al. (2014), McClure et al. (2014)
	HH4	001826	GAT7	0.37	1	1,277,227	Pfütz et al. (2013)
	HH5	001941	—	2.22	9	92,350,052 – 93,910,957	Cooper et al. (2013)
	HH6	000595	BLAD/ITGB2	0.25	1	145,119,004	Shutter et al. (1992)
	HH7	001340	CUM/SLC35A3	1.37	3	43,411,473	Agarholn et al. (2001)
	HH8	000262	DUMPS/LAMP5	0.01	1	69,757,801	Shanks et al. (1984)
	HH9	000963	Mulefoot/LRN4	0.07	15	77,663,790 – 77,701,209	Eldridge et al. (1991), Duchesne et al. (2006)
	HHP	000483	Polledness/POLLED	0.71	1	1,705,634 – 1,969,480	Medugorac et al. (2012), Rothhammer et al. (2014)
	HHR	001199	Red coat color/ NC2R(MSHR)	5.42	18	14,758,207	Joerg et al. (1996)

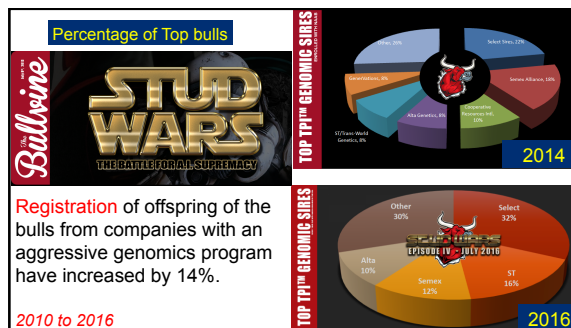
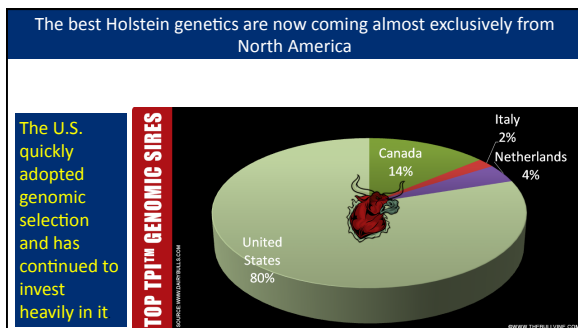
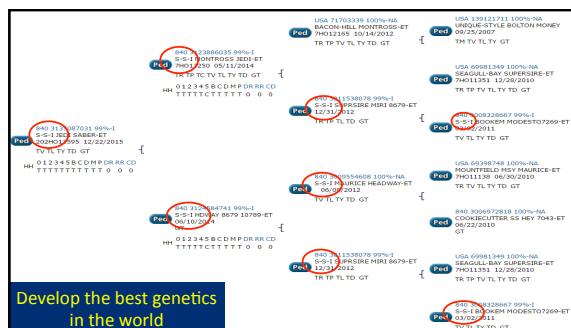
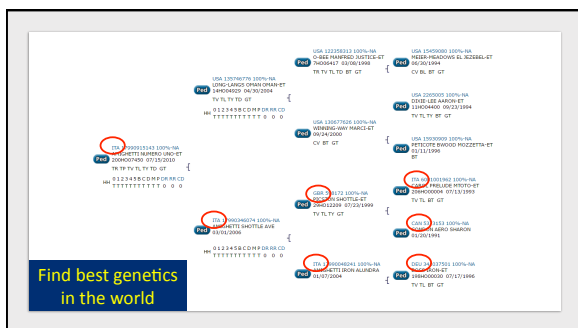
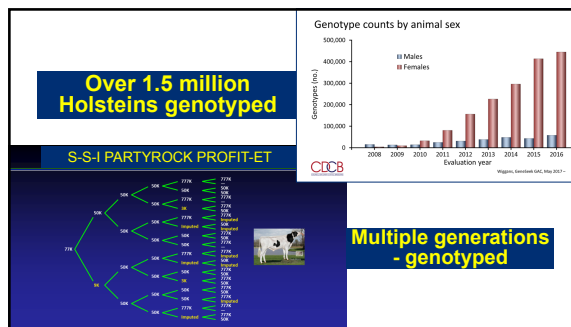
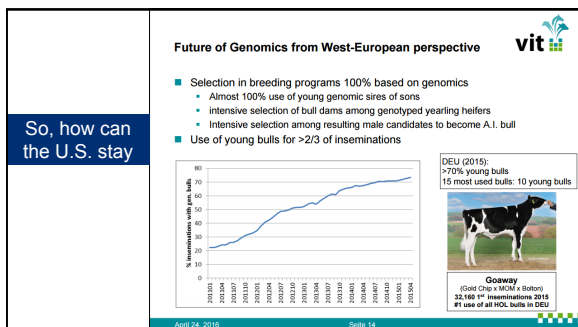


Germany

Genomic Selection: Revolution in dairy cattle breeding

- ca. 1950 – 2009:
 - Holstein breeding based on daughter proven A.I. bulls (test-waiting-proven bull system)
- from 2010 onward:
 - Selection based on genomic proofs
 - Same reliability for males and females
 - >90% young sires of sons
 - >90% yearling heifers as bull dams
 - 50-90% use of young genomic A.I. bulls in cow population
- Breeding based on genomic selection

Page 2



U.S. Registered Holsteins
FOR MAXIMUM PROFIT
REGISTRATION ASSOCIATION USA, INC.

Semen status is GENOMIC with no daughters in their proofs for Production or Type

NAME		TR	TRIA	TRAP	PRODUCTION	HEALTH			CONFORMATION		
						FE	TH	BT	FE	TH	BT
1	B LUMMENFELD JEN REASON-ET	TR TP	964	507H012941	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
2	WILCOX-ET BRENNAN 31-ET	TR TP	964	507H012942	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
3	SANDVOLDY PIZZAZ-ET	TR TP	964	507H012943	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
4	SANDVOLDY CADET-ET	TR TP	964	507H012944	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
5	WILCOX-ET BRENNAN 31-ET	TR TP	964	507H012945	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
6	SANDVOLDY CODEC-ET	TR TP	964	507H012946	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
7	SANDVOLDY MACHOUCH-ET	TR TP	964	507H012947	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
8	WILCOX-ET BRENNAN 31-ET	TR TP	964	507H012948	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
9	SANDVOLDY ALBERT-ET	TR TP	964	507H012949	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
10	WILCOX-ET BRENNAN 31-ET	TR TP	964	507H012950	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
11	SANDVOLDY JETT-ET	TR TP	964	507H012951	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
12	SANDVOLDY JETT-ET	TR TP	964	507H012952	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
13	SANDVOLDY JETT-ET	TR TP	964	507H012953	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
14	SANDVOLDY JETT-ET	TR TP	964	507H012954	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
15	SANDVOLDY JETT-ET	TR TP	964	507H012955	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
16	SANDVOLDY JETT-ET	TR TP	964	507H012956	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
17	SANDVOLDY JETT-ET	TR TP	964	507H012957	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
18	SANDVOLDY JETT-ET	TR TP	964	507H012958	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
19	SANDVOLDY JETT-ET	TR TP	964	507H012959	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
20	SANDVOLDY JETT-ET	TR TP	964	507H012960	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
21	SANDVOLDY JETT-ET	TR TP	964	507H012961	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
22	SANDVOLDY JETT-ET	TR TP	964	507H012962	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
23	SANDVOLDY JETT-ET	TR TP	964	507H012963	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
24	SANDVOLDY JETT-ET	TR TP	964	507H012964	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
25	SANDVOLDY JETT-ET	TR TP	964	507H012965	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
26	SANDVOLDY JETT-ET	TR TP	964	507H012966	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
27	SANDVOLDY JETT-ET	TR TP	964	507H012967	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
28	SANDVOLDY JETT-ET	TR TP	964	507H012968	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
29	SANDVOLDY JETT-ET	TR TP	964	507H012969	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
30	SANDVOLDY JETT-ET	TR TP	964	507H012970	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6
31	SANDVOLDY JETT-ET	TR TP	964	507H012971	908 208 211 5	2.0	8.7	1.1	2.9	6.9	1.6

- Female-sex-sorted semen
 - When semen is released to the mass market

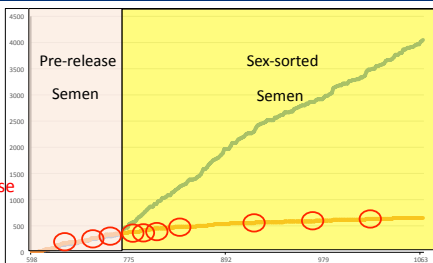
The graph shows the number of offspring (Y-axis, 0 to 4000) versus the age of bull in days (X-axis, 558 to 1003). Two lines are plotted: a blue line for Heifer and an orange line for Bulls. The Heifer line starts at approximately 500 offspring at age 558 and increases steadily to about 4000 offspring at age 1003. The Bulls line starts at approximately 500 offspring at age 558 and increases very slowly to about 800 offspring at age 1003.

Age of bull – in days	Heifer (Number of Offspring)	Bulls (Number of Offspring)
558	~500	~500
775	~1000	~600
882	~2000	~700
979	~3000	~750
1003	~4000	~800

Figure 1 is a line graph showing the relationship between the number of reads (Y-axis) and the number of SNPs (X-axis) for two samples: Semen and Sex-sorted Semen. The Y-axis ranges from 0 to 4500 reads, and the X-axis ranges from 568 to 1063 SNPs. The graph is divided into two regions: 'Pre-release' (left, light blue) and 'Sex-sorted' (right, light orange). The Semen sample (blue line) shows a linear increase in reads with SNPs, reaching approximately 4000 reads at 1063 SNPs. The Sex-sorted Semen sample (orange line) shows a much lower number of reads, reaching approximately 600 reads at 1063 SNPs.

Top 10
Sons

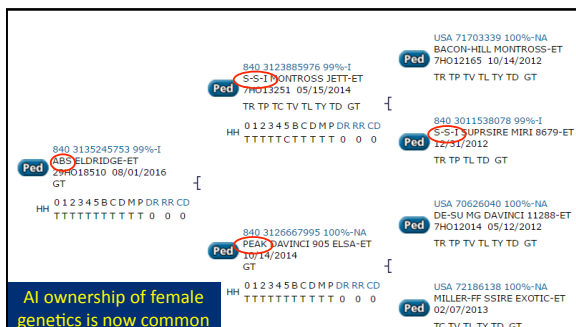
7 are
AFTER
Pre-release
period



U.S. Registered Holsteins
FOR MAXIMUM PRODUCTION
HOLSTEIN ASSOCIATION OF AMERICA

Bulls with no daughters in their genomic proofs for Production or Type. No requirement for semen status.

[illegible]



International competition amongst countries has caused the creation of genotype exchange consortiums.

Growth of large National Genetic Evaluations - move away from the Interbull model of "pooling data".

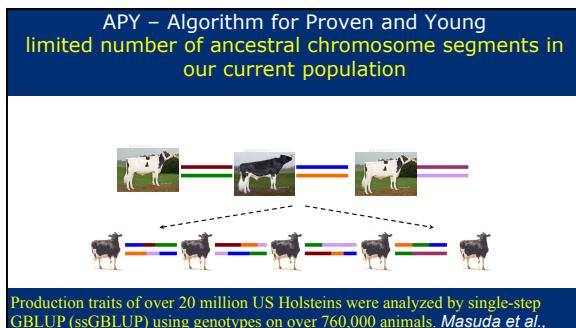
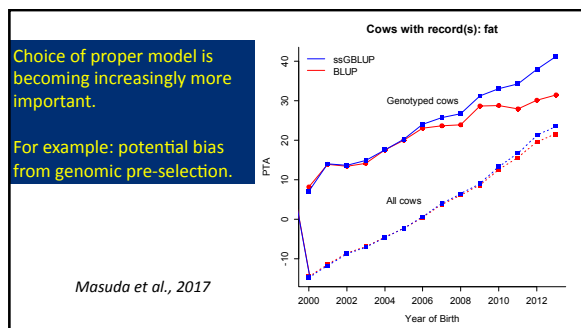
vit		CDCB	Initial	AI Service
German Holstein fee system for genomic evaluations		Full data contributor	\$15	\$575
		Non-Member of CDCB	\$150	\$575
		Approved Partners	\$15	\$575
		All others	\$150	\$1,200

Nominator	Initial male fee	AI service fee
Member of DGS	national policy	national policy
Approved partner 1 st	waived	0 €
Approved partner 2 nd	waived ¹	500 €
Third party bulls (nominated by DGS)	national policy ¹	1,000 €

J. Dairy Sci. 99:2405–2412
http://dx.doi.org/10.3181/journal.2016.99.2405
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Practical implications for genetic modeling in the genomics era¹
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¹ National Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, MD 20705-2350

Model Description	Reference
Iterative, nonlinear model with heavy-tailed prior for marker effects analogous to Bayes A	VanRaden, P.M. 2008. J. Dairy Sci. 91:4414–4423.
SNP-BLUP with polygenic effect	Liu, Z., et al. 2011. <i>Genet. Sel. Evol.</i> 43:19
Bayes C with no polygenic effect	Fernando & Garrick, 2009
Bayes multiple QTL	Meuwissen & Goddard, 2004
QTL detection with Bayes Cpi, Linear regression on IBS haplotypes	Croiseau P. et al., 2015. EAAP meeting.
Single-step GBLUP	Aguilar, I., et al. 2010 J. Dairy Sci. 93:743–752.



EASTERN DAIRYBUSINESS
USDA
Council on Dairy Cattle Breeding

Genetic Evaluations at a crossroads

PROGRESSIVE DAIRYMAN
Home News Organizations Dairy Business Genetics Livestock All Cattle
Dairy Health Feed & Nutrition A.I. & Breeding New Technology Management

Changes coming to who calculates, distributes genetic evaluations

U.S. needed a commercial entity to do genetic evaluations.

Proprietary data, procedures and genetic evaluations has caused a fragmentation within our industry

In addition to multiple sources of National Genomic Evaluations, we're seeing multiple sources of Domestic information for the same trait

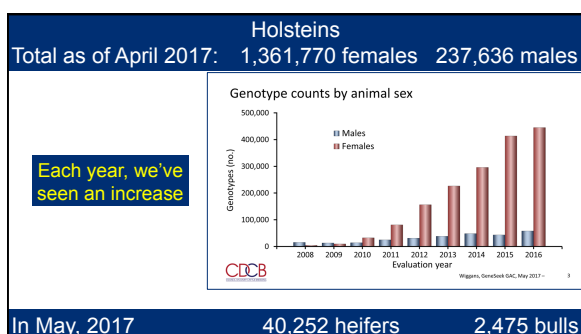
Health Monitor



Zoetis - Wellness Traits
ABS Global - TransitionRight
GENEX – Exclusive Health Traits
CDCB - soon to be released Health Traits
SEMEX – Immunity Plus

Competition amongst the breeds
Genomic testing - size matters

- Holstein 1.5 million
- Jersey 0.2 million
- Brown Swiss 0.03 million
- Ayrshire 0.007 million
- Guernsey 0.003 million



Genomic testing gives us an extra boost in improving the lowest heritable traits



Trait	Extra Daughter Equivalents from SNP effects
Production	25
Conformation	25
Calving Ease	38
Somatic Cell Score	58
Productive Life	80
Fertility	140

Renaissance Period
Rapid gains in health, fertility and production



Holstein's superiority over other breeds is GROWING with the use of genomics

USDA

Genetic Evaluation Summary

Genomic tested young bulls being marketed

Breed	Number	PTAM	PTAF%	PTAF	PTAP%	PTAP	SCS	PL	DPR	NMS	FMS	CMS
Holstein	2215	1105	0.06	58	0.03	42	2.81	5.2	1.6	635	586	656
Jersey	394	691	0.08	48	0.05	33	2.93	4.2	0	445	387	469
Ayrshire and Red	39	981	0.06	51	0.04	40	2.92	1.3	1.1	393	344	412
Brown Swiss	51	749	0.01	32	0.02	28	2.87	3.5	0.9	364	332	377
Red and White	28	335	0.05	25	0.04	21	2.88	2.8	0.7	332	278	354
Guernsey	8	504	-0.02	20	-0.02	12	2.96	1.4	-0.3	169	178	165

Just like Ancestry.com, breed purity is checked. Jersey breed has brought in Holstein genetics

This Top 100 Jersey bull is 20% Holstein

FARIA BROTHERS RAWLS (2)

Missing pedigree

BIF-SSF PARADE LOUIE-ET (5)
 JUSAM11488112
 Born: 23-DEC-02
 ET
 90%, 1%
 ALL LYNN LOUIE VALENTINO-ET (5)
 JUSAM110225813
 Born: 22-SEP-08
 ET
 99%, 1%
 DIE PARAMOUNT VIOLET (5)
 JUSAM220072718
 Born: 21-DEC-03
 ET
 1%, 1%
 FARIA BROTHERS MATINEE AUERBAC (5)
 JUSAM111981214
 Born: 25-MAY-01
 ET
 1%, 1%
 FARIA BROTHERS 21490 (5)
 JUSAM117245581
 Born: 30-DEC-06
 ET
 1%, 1%
 BIF-SSF PARADE LOUIE-ET (5)
 JUSAM11488112
 Born: 23-DEC-02
 ET
 90%, 1%
 WALDEN FARM ANGEL GRAYSON AVAI (5)
 JUSAM110292355
 Born: 14-JAN-99
 ET
 99%, 1%
 ROCK ELLA PARAMOUNT ET (5)
 JUSAM1102675
 Born: 01-JUN-95
 ET
 99%, 1%
 DIE ARE VIOLET (5)
 JUSAM110272724
 Born: 23-MAY-02
 ET
 1%, 1%
 WALDEN FARM M/T QUEST ANGEL-E (5)
 JUSAM1102675
 Born: 06-OCT-95
 ET
 99%, 1%
 TENN HADG E HADG (5)
 JUSAM11725063
 Born: 10-MAY-94
 ET
 99%, 1%
 FARIA BROTHERS 21490 (5)
 JUSAM117245581
 Born: 30-DEC-06
 ET
 1%, 1%

NAAB	Name	BBR or IX	NMS	REL NMS
029JE03866	SCHULTZ VOLCANO HARRIS (4)	100	779	91
001JE00957	FARIA BROTHERS BRAD STEVENS (5)	100	766	68
551JE01650	SUNSET CANYON GOT MAID (5)-ET	100	763	70
200JE00913	FARIA BROTHERS MESSI (5)-ET	100	737	69
001JE00935	CO-OP AD WORLD CUP (5)-ET	100	716	68
014JE00704	FARIA BROTHERS CALVIN HARRIS (4)	100	698	69
001JE00966	FARIA BROTHERS FUTURE (3)-ET	93	692	66
001JE00922	FARIA BROTHERS RONALDO (3)-ET	92	689	69
029JE04033	AHLEM FRISCO (5)	100	682	71
551JE01643	SEXING VALIDATE 60883 (5)-ET	100	680	70
001JE00962	FARIA BROTHERS DEGROM (3)-ET	100	677	66
014JE00652	FARIA BROTHERS MARLO (2)-ET	IX	674	70
007JE01503	FARIA BROTHERS RONALDINHO (3)	100	670	70
001JE00921	FARIA BROTHERS EUSEBIO (4)-ET	93	670	68
029JE03989	FOREST GLEN HARRIS HALT (5)	100	665	70
001JE00964	FARIA BROTHERS IODECI (3)	100	661	66
007X001535	FARIA BROTHERS SYNDERGAARD	IX	658	53
001JE00963	HEARTLAND HARRIS MAGLIO (5)	100	654	69
007JE01533	FOREST GLEN HARRIS RHUMBA (5)	IX	652	70
011JE01179	CDF VICEROY-ET	100	651	86
001JE00892	FARIA BROTHERS VANDRELL (2)-ET	IX	648	66
029JE04008	AHLEM HARRIS BALTAZAR (5)-ET	100	646	71

Bulls with Holstein genetics

(X) = Generation Count where X is the number of generations back to an unknown ancestor

BBR Breed Based Representation 93.75% or higher is rounded up to 100

February 4, 2017 Jersey-Cross Prefix

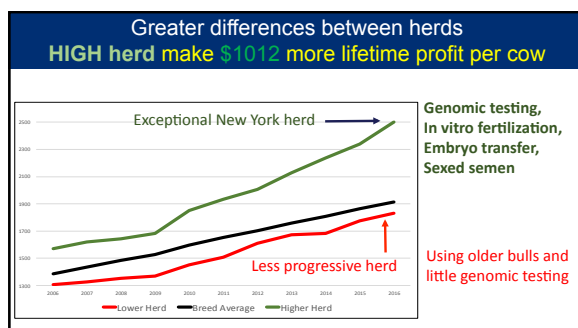
Herd Improvement

Genetic education, combination of technologies and economic analysis are more important than ever.

DAIRY HERD MANAGEMENT

WHICH IS THE BETTER HEIFER?

Genetic education, combination of technologies and economic analysis are more important than ever.



What's your genomics program?

Genomics Program

Basic theme:

- Top animals are IVF
- Next tier are bred with sexed semen or conventional semen (if bulls are wanted)
- Bottom 50% to 85% carry embryos

Variations:

- Many have On-farm IVF facility
- Several are selling embryos to other farms
- Low end animals bred to beef bulls

Large herds have an advantage – lots of recipients

Enough breeding to beef bulls that we can now do a fertility evaluation on Angus sires

Bull fertility evaluations for Angus service sires bred to Holstein cows

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¹Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD

²Council on Dairy Cattle Breeding, Bowie, MD

Sire Conception Rate (SCR): A Measure of Sire Fertility

So much flushing is going on, that a cow's ability to make eggs is now a trait of interest

Evaluation of genetic components in traits related to superovulation, in vitro fertilization, and embryo transfer in Holstein cattle

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³Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, MD 20705-2350

Table 1. Summary statistics including total, average per procedure, SD, minimum, and maximum of unfertilized data for superovulation, in vitro fertilization, and embryo transfer data sets

Item	Total	Average	SD	Minimum	Maximum
Superovulation data set					
Number of records	926	—	—	—	—
Number of donors	725	—	—	—	—
Total structures recovered	6,822	7.50	6.83	0	51
Total good embryos	6,017	5.11	4.84	0	26

LOT 11G

No-Fla Stoic Anne 40873-ET

846003129448990 96%GRITA-1

Born 3/2/15 4/16 PTA+2683GTPI

+1894M + 00% + 70F + 02% + 64P

+8678MIS + 7.7TPI + 2.40WPC 2.74SCS

+1.65T +1.47UDC + 73FLC

+1168DWPS +233WTIS

Bred 4/7/16, Due 1/13/17 to

710013093 Damaris +2644GTPI

*Sells ready to IVF

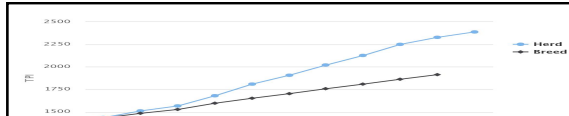
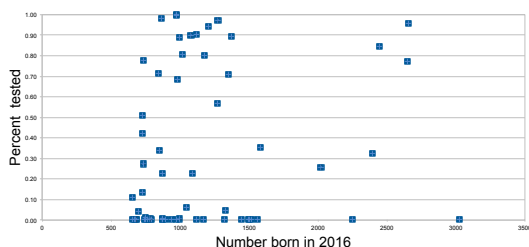
*Donor Dam

4/26/16 IVF: 7 frozen

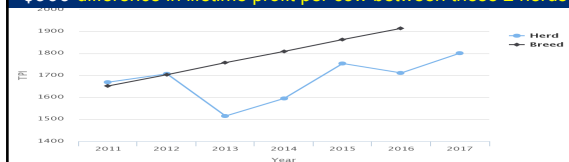
5/10/16 IVF: 7 frozen & sold!

Large Herd Genomic Testing

no set practice has been established



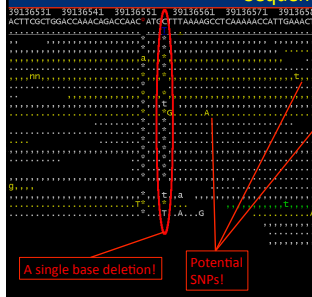
\$900 difference in lifetime profit per cow between these 2 herds



Future projects:



Sequencing



Finding informative SNPs linked to important QTLs

Add BEST SNPs to our current SNP chips.

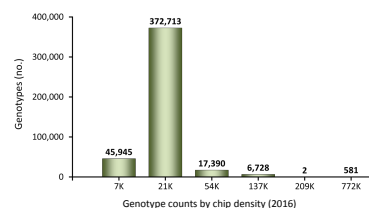
Not selecting for any specific genetic variant

Gains in reliability from adding imputed sequence variants

Trait	60K + selected (reliability %)		
	60K only	60K + 17K	Improvement
PL	35.6	38.2	2.6
SCS	35.1	37.0	1.9
DPR	29.0	33.0	4.0
CCR	28.9	31.8	2.9
HCR	20.5	21.5	1.0

Average trait reliability improvement: 2.7%

Slide adapted from a presentation by Mel Tooker at ADSA, Salt Lake City, UT, 2016

Key to success is *good* Imputation
Low cost, still informative

(S&K)	00 = Imputed data
(S&K_V2)	01 = S&K
(S&K)	02 = S&K (version 2)
(S&K)	03 = S&K
(S&K)	04 = Illumina 177K
(S&K)	05 = Affymetrix 440K
(LD)	06 = Bovine LD 7K
(G&P)	07 = Geneset Geneset Profile 7K
(G&P)	08 = Geneset Geneset Profile 10K
(G&P)	09 = Geneset Geneset Profile (version 2)
(ZLD)	10 = ZLD Low Density
(ZLD)	11 = ZLD Medium Density
(ZLD)	12 = ZLD High Density
(ZLD)	13 = ZLD Low Density (version 2)
(ZLD)	14 = ZLD Medium Density (version 2)
(ZLD)	15 = ZLD High Density (version 2)
(ZLD)	16 = ZLD Low Density (version 3)
(ZLD)	17 = ZLD Medium Density (version 3)
(ZLD)	18 = ZLD High Density (version 3)
(ZLD)	19 = ZLD Low Density (version 4)
(ZLD)	20 = ZLD Medium Density (version 4)
(ZLD)	21 = ZLD High Density (version 4)
(ZLD)	22 = ZLD Low Density (version 5)
(ZLD)	23 = ZLD Medium Density (version 5)
(ZLD)	24 = ZLD High Density (version 5)
(ZLD)	25 = ZLD Low Density (version 6)
(ZLD)	26 = ZLD Medium Density (version 6)
(ZLD)	27 = ZLD High Density (version 6)

Journal of Animal Breeding and Genetics

Use of haplotypes to estimate Mendelian sampling effects and selection limits

J.B. Cole & P.M. VanRaden

Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD, USA

RESEARCH **Open Access**

Prediction of expected genetic variation within groups of offspring for innovative mating schemes

Dierck Segelke^{1,2}, Friedrich Reinhardt¹, Zengting Liu³ and Georg Thaller²

RESEARCH ARTICLE

Mendelian sampling covariability of marker effects and genetic values

Sarah Bonk¹, Maruola Reichelt¹, Friedrich Teuscher¹, Dierck Segelke² and Norbert Reisch^{1*}

2011

2014

2016

Why do these two bulls have different progeny distribution?

If we can predict "expected progeny distribution" ahead of time we use it in a mating program

	PTA Fat		
	< 0 lbs	0 to 60	> 60 lbs
Denim	3 %	92 %	5 %
Baxter	9 %	82 %	9 %

Higher percentage of extreme daughters for AltaBaxter

Large farms can provide a tanker truck full of milk with a specified genotype

Personalized Nutrition

Our farmers say.... tell us what you want and we'll produce it.

Tufts

Study volunteers please check-in here for escort

Genomic information is being used in many ways
within the U.S. dairy industry.

Any questions ?

