Current Reality of the Ayrshire Breed and the Opportunity of Technology for Future Growth

First Current Reality

August 2016 US CDCB-AGIL Genetic Breed Difference From Holstein

Breed	Milk	Fat	Protein	Productive Life	Somatic Cell Score	Daughter Pregnancy Rate	Heifer Conception Rate	Cow Conception Rate	Livability
Ayrshire	-2563	-74	-68	-0.1	-0.04	1.3	-3.3	0.2	1.7
Brown Swiss	-2045	-48	-38	-0.4	0.01	0.0	-4.5	-2.2	0.4
Guernsey	-2957	-45	-72	-4.3	0.13	0.0	-5.4	-3.9	-6.1
Jersey	-2689	-26	-46	1.3	0.15	3.1	-0.5	2.6	0.6
Milking Shorthorn	-2702	-99	-81	-0.6	0.05	2.3	-0.8	1.3	2.5

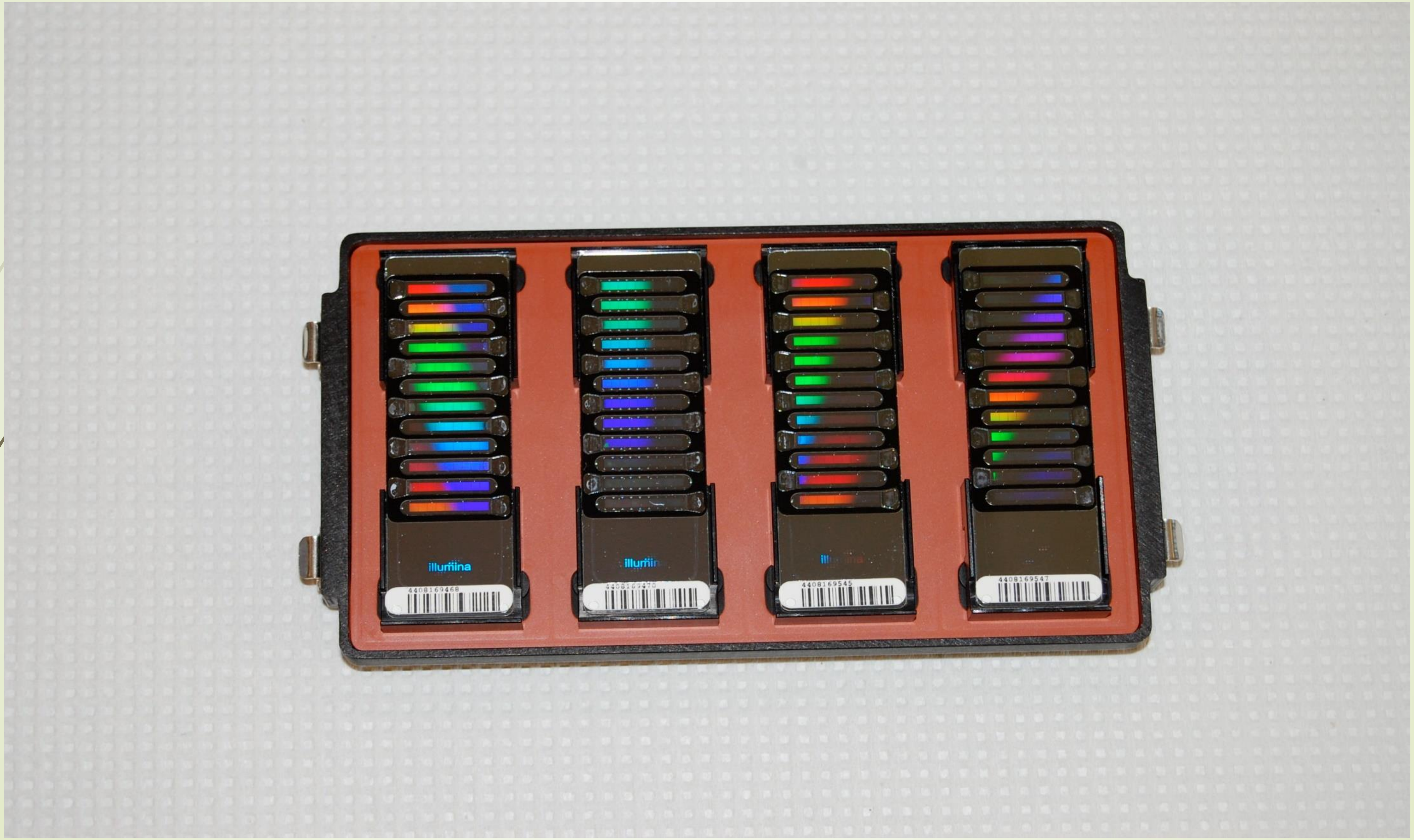
August 2016 US CDCB-AGIL Trait Means Base Cows

Breed	Milk	Fat	Protein	ECM	Productive Life	Somatic Cell Score	DPR	HCR	CCR	Livability
Ayrshire	18,585	723	587	19,666	28.7	2.43	25.7	47.1	39.9	85.3
Brown Swiss	22,639	916	751	24,672	27.2	2.55	24.5	47.2	31.7	83.9
Guernsey	17,459	781	570	19,924	25.7	3.01	24.0	41.5	28.5	76.7
Holstein	26,996	1006	822	27,774	26.0	2.37	28.5	57.2	35.1	84.9
Jersey	19,733	938	709	23,705	29.7	2.77	35.3	54.8	41.6	87.2
Milking Shorthorn	18,848	696	583	19,374	26.8	2.75	29.4	55.4	40.4	89.6

Domestic Semen Sales US

BREED	2015	2014	2013	2012	2011	2010	2009	2008	2000
HOLSTEIN	19,883,218	19,650,938	19,561,599	19,965,250	19,826,027	19,188,460	17,714,898	18,833,845	12,180,243
JERSEY	3,050,136	2,960,434	2,747,482	2,478,636	2,156,285	1,940,795	1,547,755	1,752,154	771,160
HOLSTEIN-RED CARRIER	302,910	231,157	111,572	86,097	79,967	59,131	66,524	69,427	91,487
R&W/RED HOLSTEIN	240,740	316,688	290,478	274,477	250,302	223,413	274,644	286,292	122,739
BROWN SWISS	103,232	104,754	108,071	111,877	120,833	119,119	138,706	160,924	118,954
AYRSHIRE	41,217	40,327	35,722	39,595	42,709	52,462	46,519	52,311	33,955
GUERNSEY	30,093	30,534	29,865	30,784	31,068	33,870	34,063	39,155	55,662
Mshort	21,951	23,830	24,846	26,430	26,946	25,879	25,639	27,910	13,323
NRF	100,616	98,169	77,262	59,333	40,375	19,450			
SRB	26,677	22,861	28,206	54,219	35,055	37,024	41,409	60,617	90,705

Technology-The Power of Genomics and Sexed Semen to Grow the Ayrshire Breed



First a Thought Experiment

X

Awesome is rr

Hailey is BB

As you know all the offspring from an Awesome and a Hailey flush will be Black, each calf will have the combination of Br for coat color.

A question for you: Suppose that you breed an Awesome x Hailey son to an Awesome x Hailey daughter, what would you expect from four calves for color?

Hailey’s Awesome-ET
(Br)

X

Awesome’s Hailey-ET
(Br)

From the above and from what all of us know we expect one calf to be rr and Red, one calf to be BB and Black and two calves to be Br and Black. The question that I present to you is:

What percentage of the red calf is Awesome and what percentage is Hailey for color?

How many of you had 50% Awesome and 50% Hailey?

How many of you had 100% Awesome?

Red coat Color is a Qualitative Trait

A More Complex Example

O-Style Haplotypes Chromosome 15

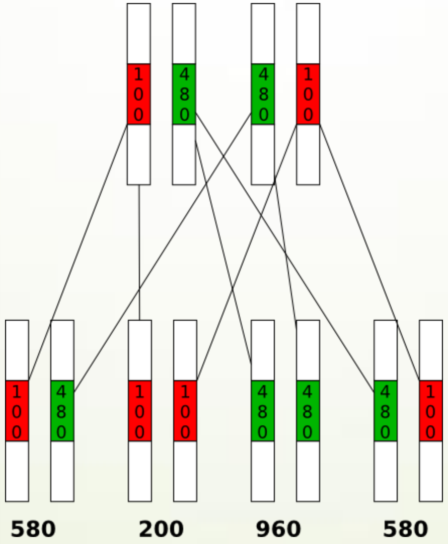
Provided by John Cole USDA-AGIL

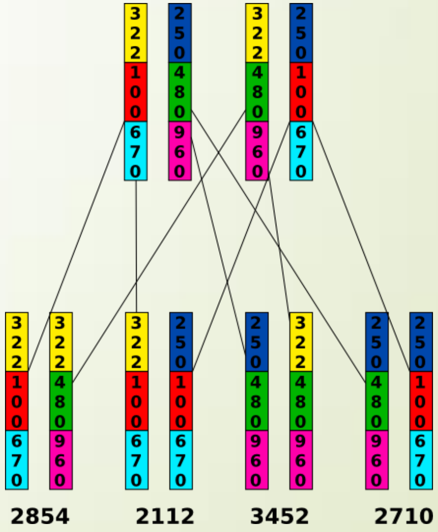
From qualitative to quantitative traits

- The trait “Coat Color" is defined by one gene located on some chromosome.
- The phenotypic expression of that trait is totally determined by the inheritance of that gene (Heritability = 1)
- In the quantitative case, we find a high number of genes, all of them contributing to the phenotypic expression

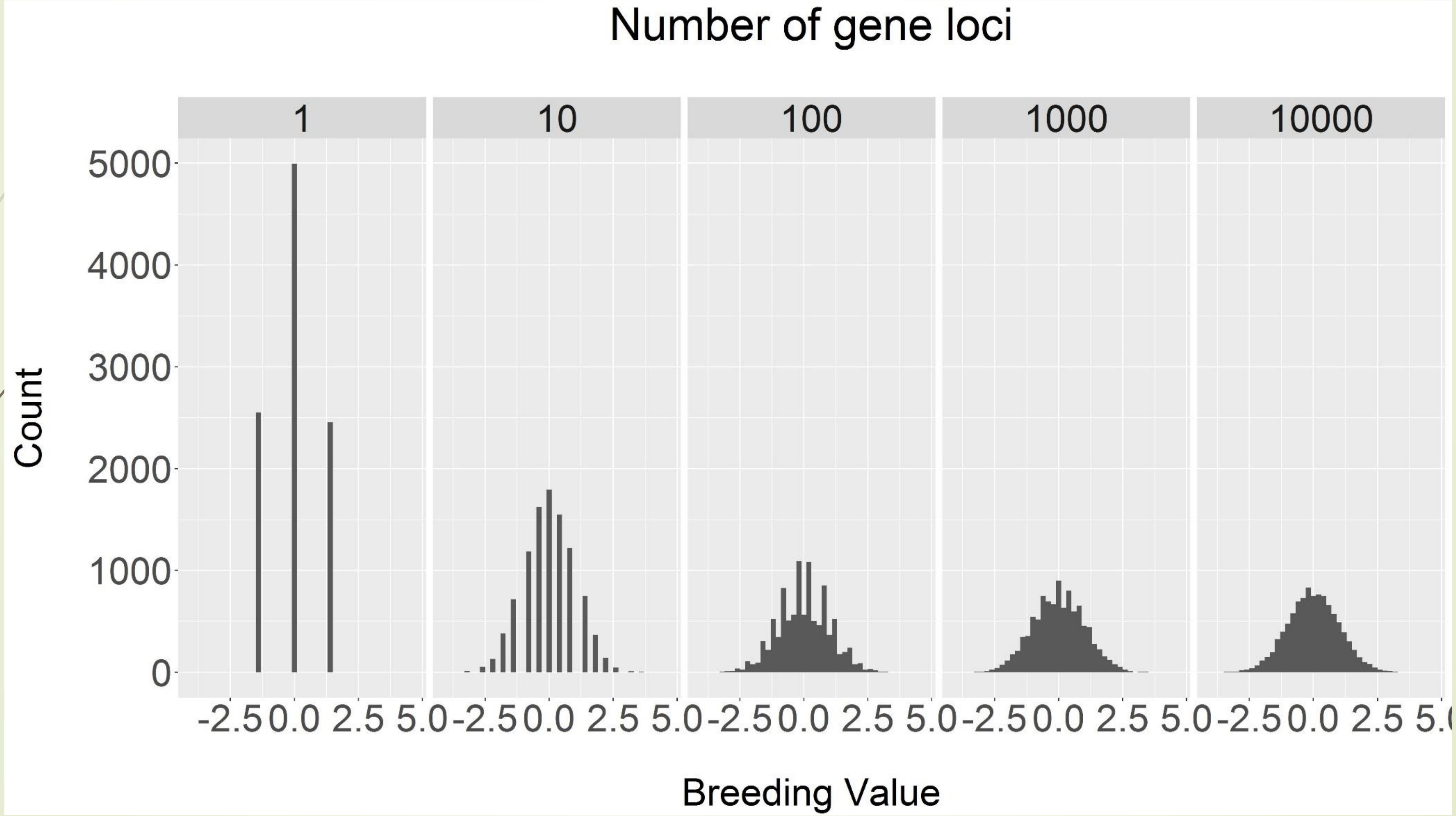
Quantitative Genetics

- The number of possible "gene configurations" grows exponentially with the number of genes having an impact on a trait
- The chances of observing one particular configuration is very low
- Therefore we describe quantitative traits not by discrete states but by a Gaussian distribution





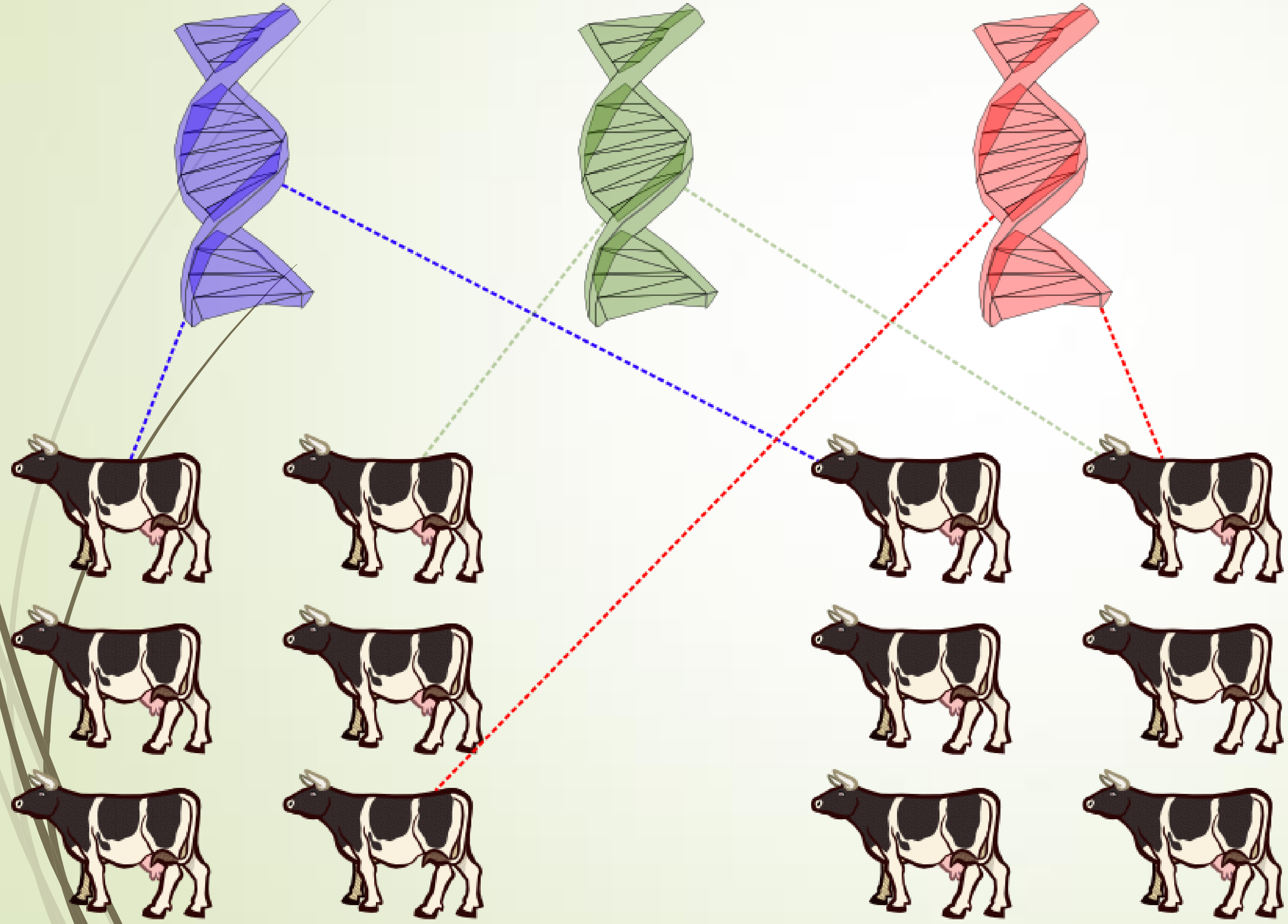
How many gene loci form a quantitative trait



Traditional Livestock Breeding

- Traditional breeding is solely based on the concept of Mendelian inheritance of a potentially unlimited number of genes for a given trait
- Selection decision are based on "conventional breeding values"
- The predicted breeding value of an unborn offspring is the parent average

What is Genomic Prediction?



- In genomic prediction we look at the actual DNA (SNP markers ~ genes) and not sires
- Every animal with phenotypic information contributes to all the ~50k SNP markers used
- The breeding value of a sire is then the sum of SNP effects
- Genomic prediction is therfore progeny testing of genes

Genomics helps in two ways to leverage genetic progress

Breeders Equation

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

- ΔG = Genetic progress per year
- i = selection intensity or number of animals you can choose from
- r = accuracy of selection
- σ = additiv genetic standard deviation
- GI = generation interveral

What can genomics do on Ayrshire farms?

- Traditionally, dairy 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

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

- ΔG = Genetic progress per year
- i = selection intensity
- r = accuracy of selection
- σ = additiv genetic standard deviation
- GI = generation interveral

- Sexed semen leverages selection intensity (i)
- Genomic prediction increases accuracy of selection (r)

Example

1) Sexed semen – Select from more females

2) Genomics – Select more accurately

Traditional	
σ	1100.00
i	0.35
r	0.40
p	0.80
GI	4.00
ΔG	**38.5**

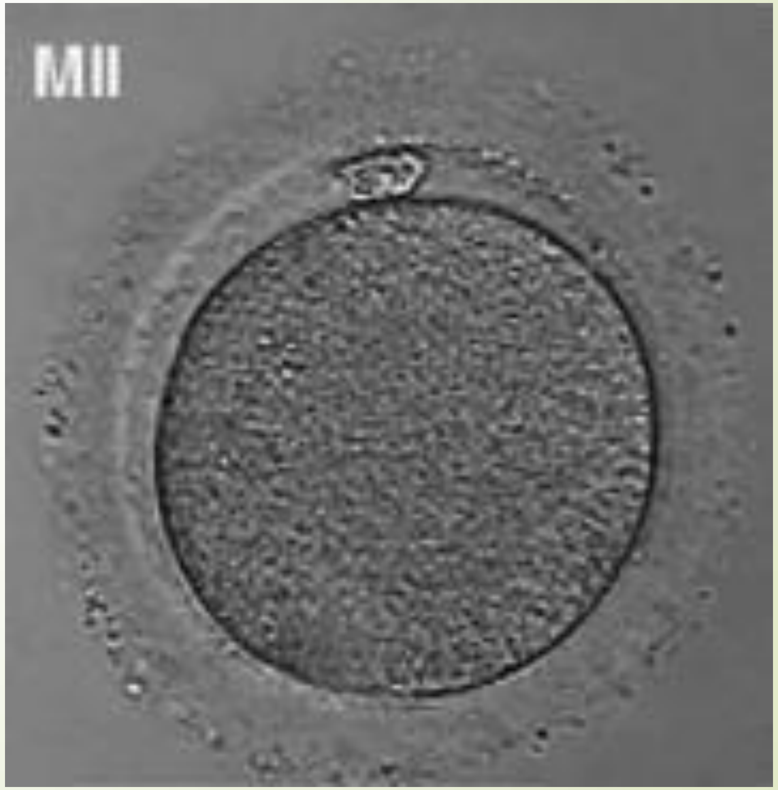
Sexed Semen	
σ	1100.00
i	**0.96**
r	0.40
p	**0.40**
GI	4.00
ΔG	**105.6**

Sexed Semen + Genomics	
σ	1100.00
i	**0.96**
r	**0.48**
p	**0.40**
GI	4.00
ΔG	**184.8**

Genomics and Sexed Semen Applied to the Ayrshire Breed

- Exploiting hidden selection potential on the female side
- Increase selection intensity (or introduce selection in the first place) by sexed semen
- Get higher selection accuracies by genomics (correct pedigrees, Mendelian segregation)

The other important avenue to increase selection is embryo transfer



Most Current Research Regarding Sexed Semen from USDA-AGIL Presented at ADSA 2016

0372 Sexed-semen usage for Holstein AI in the United States. J. L. Hutchison[*1] and D. M. Bickhart[2],

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Beltsville, MD.

The dairy industry has used sexed-semen to increase the number of heifer calves born on the farm for over a decade. While the efficacy of sexed-semen has been determined experimentally, we sought to tabulate statistics on the generalized use of the technology in the U.S. dairy herd and determine its effectiveness in the field Sexed-semen breeding status was determined by a National Association of Animal Breeders' 500-series marketing code or by individual breeding information in a cow or heifer reproduction record from a dairy records processing center. Only breedings from 2007 through 2015 with confirmed outcomes (pregnant or not pregnant) were included: 5,963,876 heifer breedings (1,323,721 to sexed semen) and 42,232,502 cow breedings (253,586 to sexed semen). Sexed-semen breedings resulted in 87 and 89% female offspring, for cows and heifers, respectively. This was a notable improvement over conventional Artificial Insemination (AI), which results in 48% female births, on average. Usage of sexed-semen in heifers has increased from 9% in 2007 to 31% in 2015. Furthermore, mean conception rates for heifer sexed-semen breedings has recently increased due to improved technology (42% in 2007 compared with 49% in 2015). Comparable conception rates for heifer conventional breedings were 56, and 59% for 2007, and 2015, respectively. Smaller increases were seen in sexed-semen breedings to cows where 0.2% of all breedings used sexed semen in 2007, and 1% in 2015. Conception rates for sexed-semen breedings to cows were 26% in 2007, and 30% in 2015 compared with 30, and 32% for conventional breedings during the same years, respectively. Usage of sexed-semen for both heifers and cows has increased, with a bigger increase seen in heifers. Mean conception rates for sexed-semen breedings have also increased for both heifers and cows.

Key Words: sexed semen, conception rate, breeding

Number of Animals Bred with Sexed Semen with Confirmed Pregnancy Status 2007 to 2015

Animals Bred 2007 to 2015	Heifers	Cows
Total	5,963,876	42,232,502
Conventional	4,640,155	41,978,916
Sexed	1,323,721	253,586
Percentage Bred Sexed Semen 2007	9%	.06%
Percentage Bred Sexed Semen 2015	31%	1%

Constantly Improving Conception of Sexed Semen produced by Sexing Technologies

Year	Heifer Sexed	Heifer Conventional	Confirmed Pregnancy Rate Sexed Percentage of Conventional	Cow Sexed	Cow Conventional	Confirmed Preganacy Rate Sexed Percentage of Conventional
2007	**42%**	**56%**	**75%**	**26%**	**30%**	**86%**
2015	**49%**	**59%**	**83%**	**30%**	**32%**	**93%**

Using Genomics to Determine Breed

Yesterday it was mentioned that using Genomics may be a possibility for part of breed definition.

This is complicated and requires the assistance of a geneticist.

It must be remembered that almost all SNPs are found in some member of every Bos Taurus breed.

Holstein, Jersey and Brown Swiss have approximately 230 SNPs that can be utilized to define the breed.

These SNPs are not unique to the breed, they are recognized as being breed ID as the homozygous states of a SNP appear very often in the breed and only rarely in the other breeds.

Ayrshire has only 12 such SNPs.

The following is from the article: "Genomic evaluation, breed identification, and discovery of a haplotype affecting fertility for Ayrshire Dairy Cattle Journal of Dairy Science 97: 3878-3882"

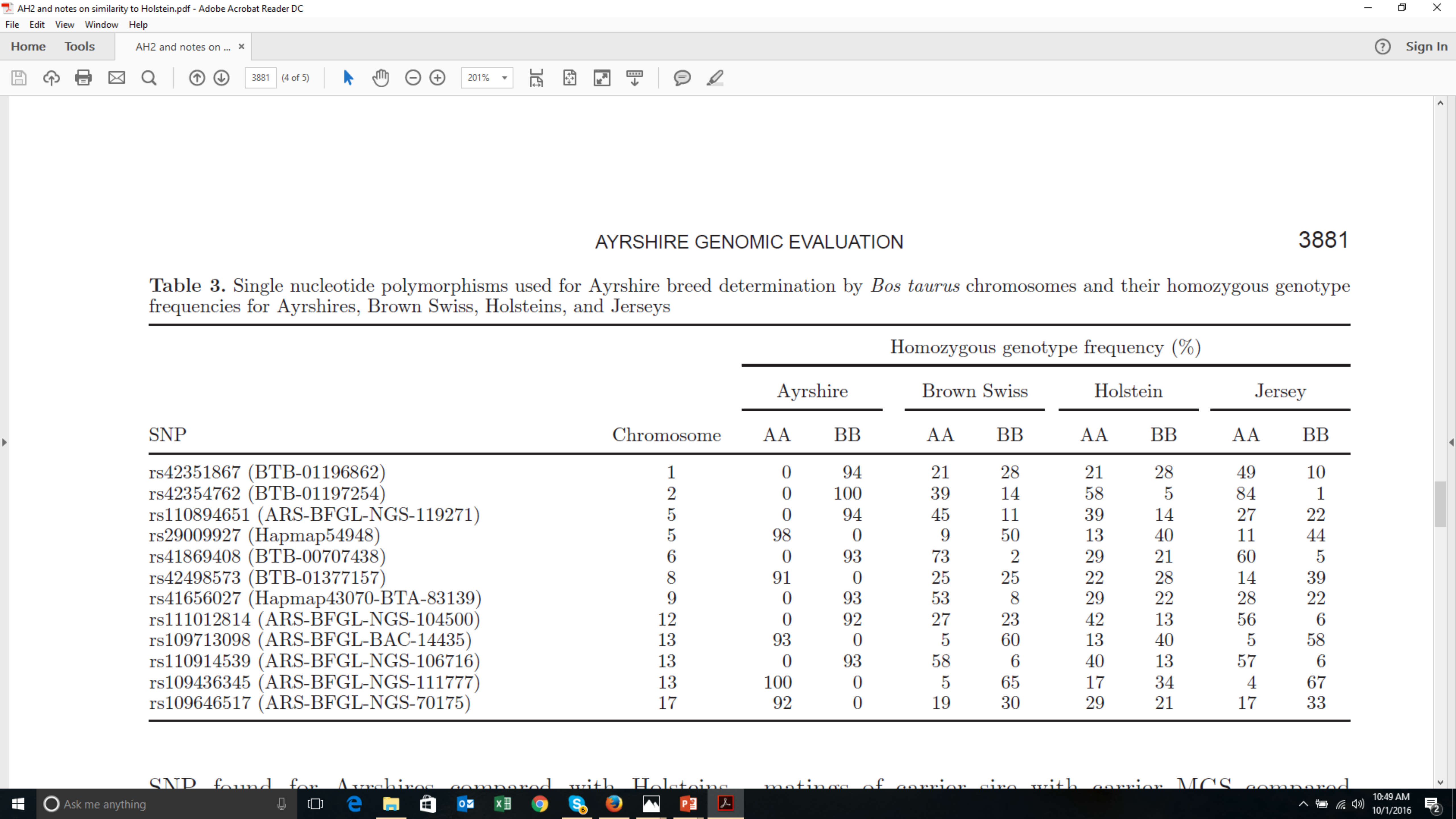

Table 3. Single nucleotide polymorphisms used for Ayrshire breed determination by *Bos taurus* chromosomes and their homozygous genotype frequencies for Ayrshires, Brown Swiss, Holsteins, and Jerseys

		Homozygous genotype frequency (%)							
		Ayrshire		Brown Swiss		Holstein		Jersey	
SNP	Chromosome	AA	BB	AA	BB	AA	BB	AA	BB
rs42351867 (BTB-01196862)	1	0	94	21	28	21	28	49	10
rs42354762 (BTB-01197254)	2	0	100	39	14	58	5	84	1
rs110894651 (ARS-BFGL-NGS-119271)	5	0	94	45	11	39	14	27	22
rs29009927 (Hapmap54948)	5	98	0	9	50	13	40	11	44
rs41869408 (BTB-00707438)	6	0	93	73	2	29	21	60	5
rs42498573 (BTB-01377157)	8	91	0	25	25	22	28	14	39
rs41656027 (Hapmap43070-BTA-83139)	9	0	93	53	8	29	22	28	22
rs111012814 (ARS-BFGL-NGS-104500)	12	0	92	27	23	42	13	56	6
rs109713098 (ARS-BFGL-BAC-14435)	13	93	0	5	60	13	40	5	58
rs110914539 (ARS-BFGL-NGS-106716)	13	0	93	58	6	40	13	57	6
rs109436345 (ARS-BFGL-NGS-111777)	13	100	0	5	65	17	34	4	67
rs109646517 (ARS-BFGL-NGS-70175)	17	92	0	19	30	29	21	17	33

SNP found for Ayrshires compared with Holsteins,

matings of carrier sire with carrier MCS compared

Thank you!