

Unraveling high progeny performance sired by 20th century bulls

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**Agricultural
Research
Service**

USDA's Gene Bank

Substantial collection of multibreed cattle genetics has been developed

- 11,990 animals and 270,768 samples
- Bull birth years range from 1943 to the 2022

Collection use

- Introduce genetic diversity
 - Alleviate inbreeding depression or introducing allelic combinations of interest
- Address genetic improvement goals or corrective mating
- Reestablish breeds/population lost due to disease

Major Question

Can bulls from the collection be used without compromising performance?

Unexpected Results From Holstein Collection Use

Two 1960-70's era bulls were used to reintroduce Y chromosomes missing from today's Holstein

Progeny compared to Penn State Herd and commercial herds

Trait	Old	Modern	
Genomic PTA Milk	-785	321	
Genomic NM\$	-176	236	
Lifetime milk lbs	82,147	62,866	
	Modern	Pilot F1	Cuthbert F1
Ave total length Kb	435,334	84,553	99,543
% homozygosity base pairs	17%	3%	4%

Case study: Jorgensen

Breeder's goals improve maternal characteristics of herd

Use of historically significant Angus bulls from the USDA National Animal Germplasm Program (NAGP) collection



BY 1997



BY 1958

Objectives

Evaluate the performance of progeny using older sire genetics

Characterize genomic properties of older and contemporary bulls and their progeny

Detect selection signatures

Evaluate more progeny than Holstein study

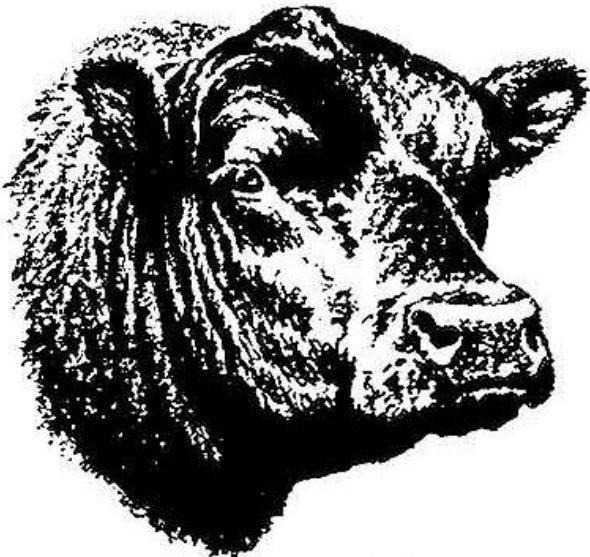
Pedigree



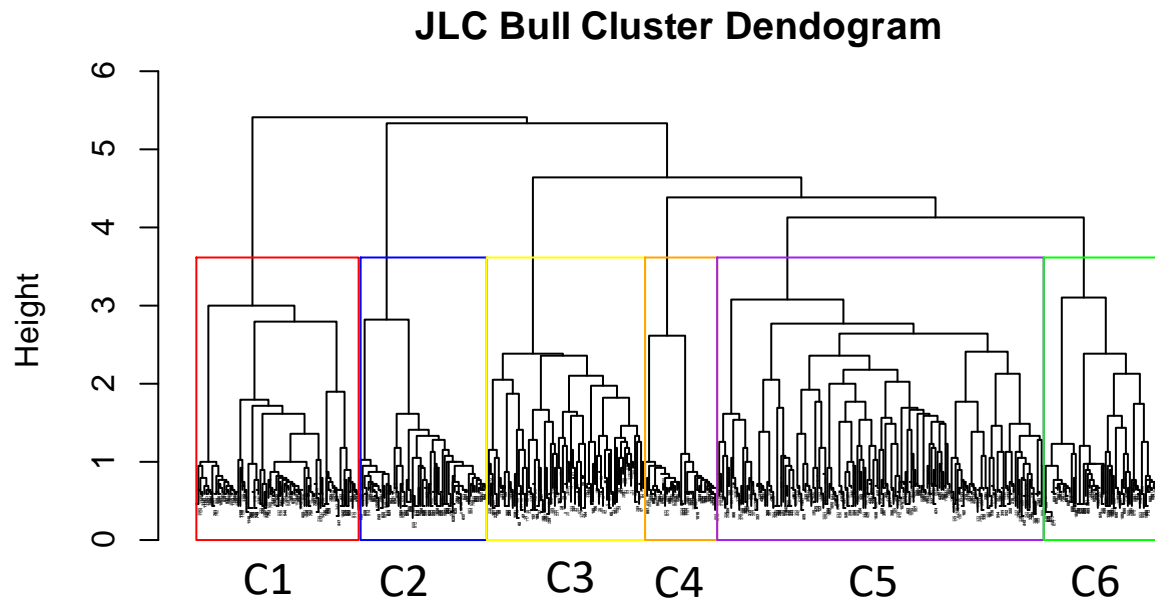
Pedigree included 88,721 animals with birth years from 1937 to 2023

Pedigree quality was evaluated

Primary focus on data from nucleus herd



Clustering Analysis



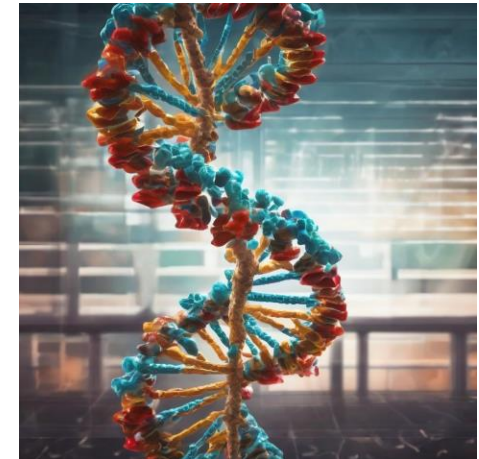
Pedigree relationships used Wards minimum variance clustering method was used. Six clusters identified using pseudo-t test.

Suggests genetic variability among breeding program within the herd

Phenotypic and genomic data available

Number of phenotypes of progeny out of ≥ 2016 dams

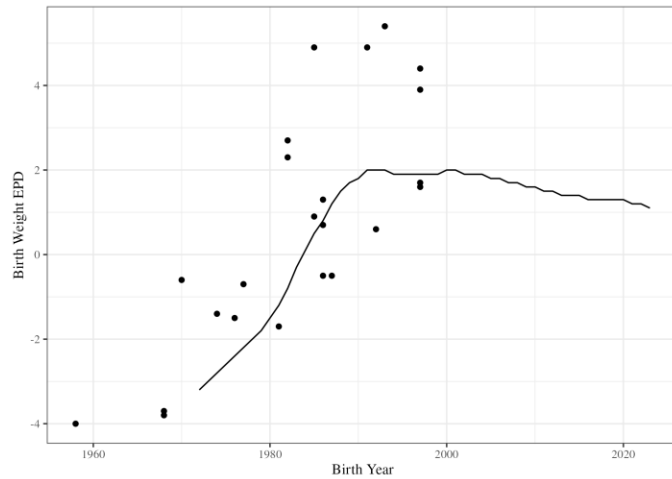
Bulls	Birth Weight	Weaning Weight	Yearling Weight
Older	214	137	18
Recent	4791	3144	1181



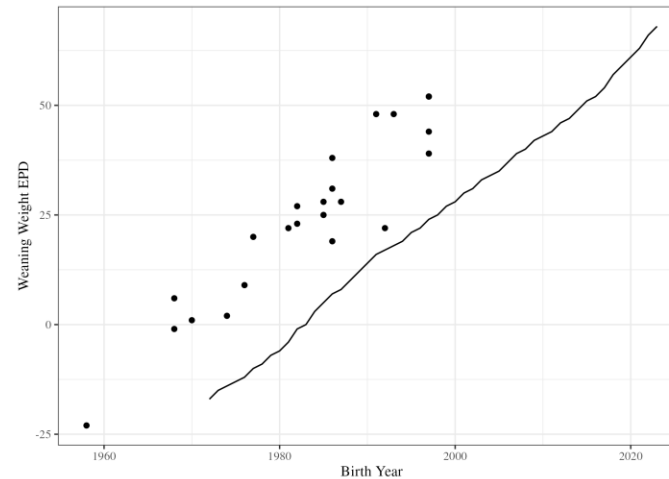
Genomic data included 40,647 SNP markers on 28,916 individuals. Birth year of genotyped animals ranged from 2010 to 2021

Genetic Trends - AAA Overall Genetic Trend for Growth Traits and AAA EPDs of Old Sires with Modern JLC Progeny

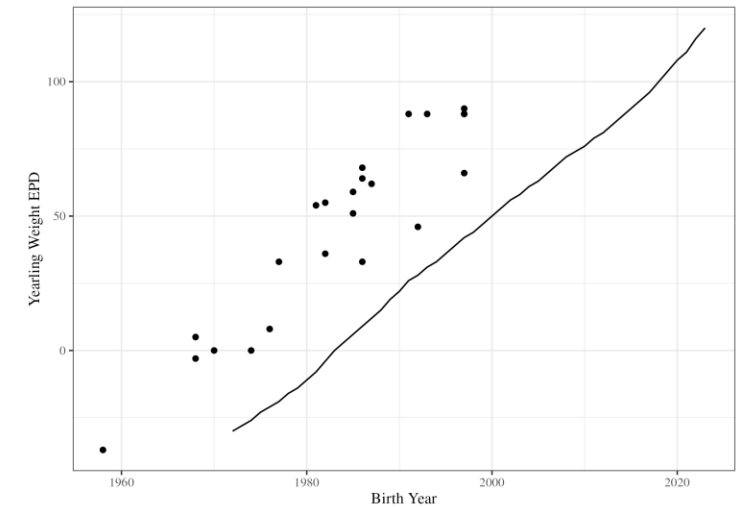
Birth Weight



Weaning Weight



Yearling Weight



Genomic estimated breeding values

Mixed model

Fixed Effects

- Mean
- Sex
- Dam Heifer/Cow Status
- IVF status
- HYS
- Age (for weaning and yearling traits)

Random Effects

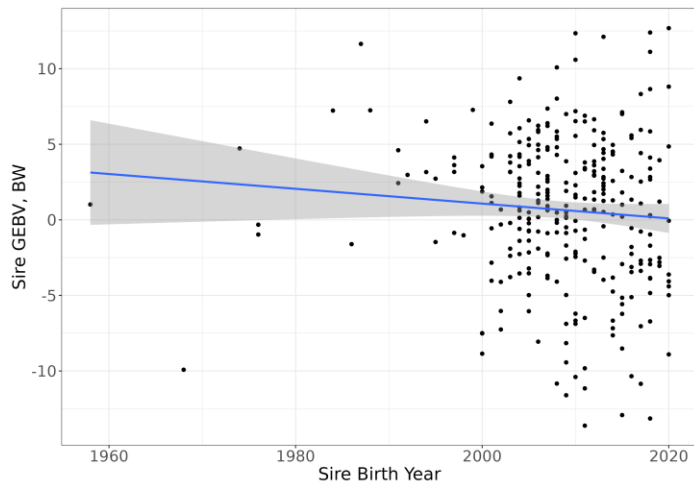
- Animal
- Maternal

GEBVs were estimated using genomic data and single-step GBLUP as implemented in BLUPF90

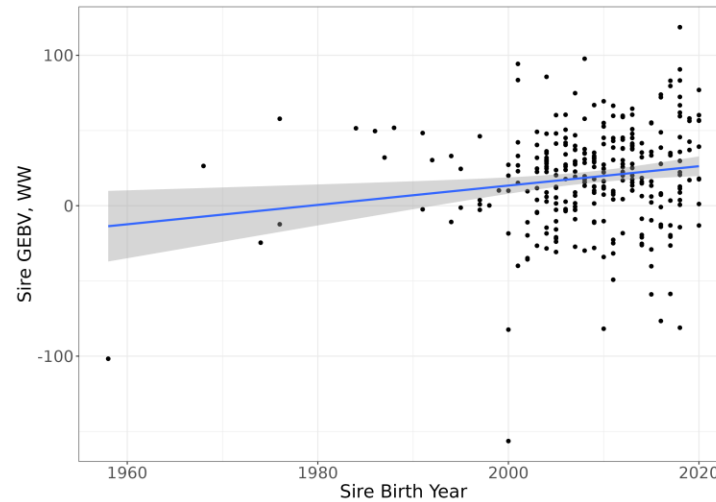
Adjusted phenotypes were corrected for all fixed effects in predictf90

Genetic Trends for JLC Bulls over time

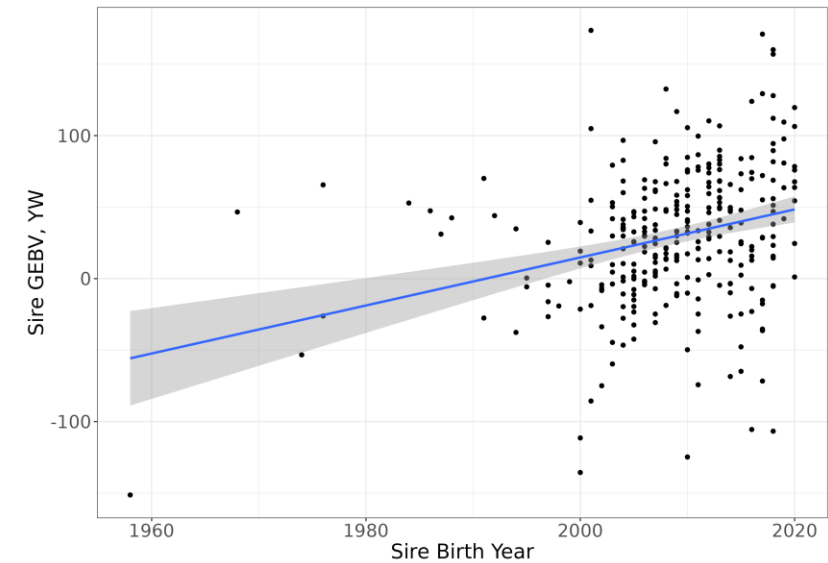
Birth Weight



Weaning Weight

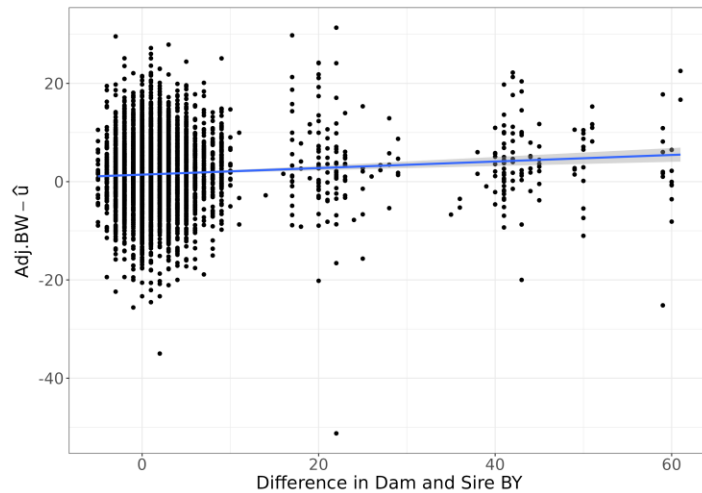


Yearling Weight

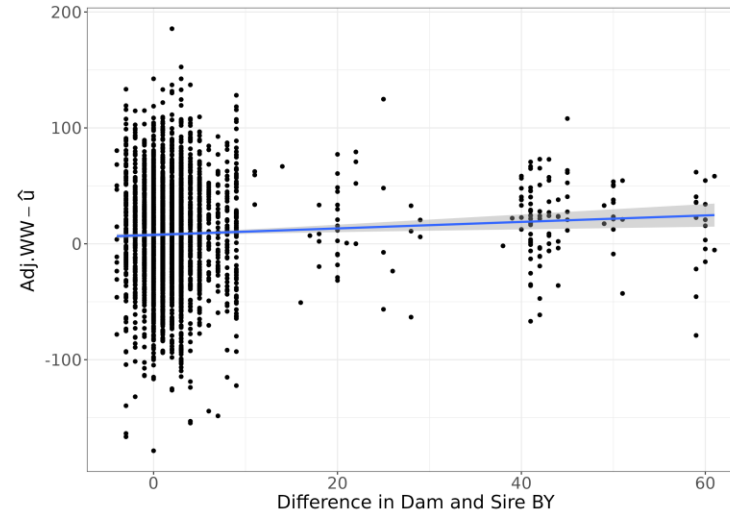


Adjusted body weights based upon difference in the sire and dam's age

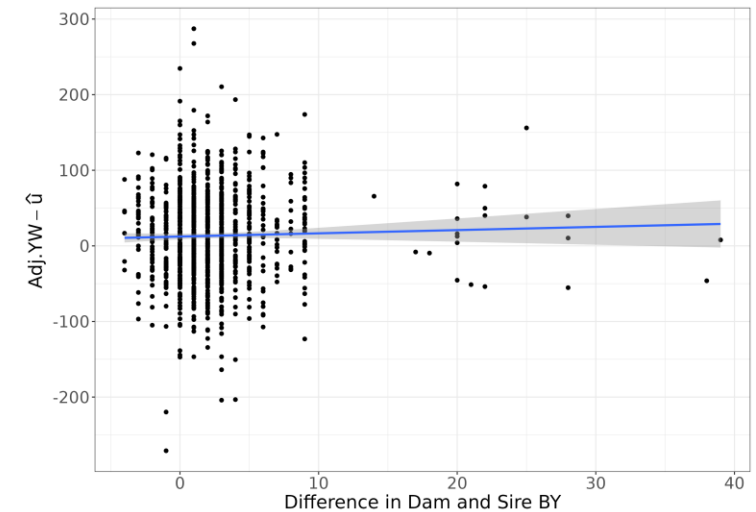
Birth Weight



Weaning Weight



Yearling Weight



Analyzing Inbreeding

Inbreeding and Heterozygosity

Pedigree inbreeding

Trait	Recent bulls' progeny		Older bulls' progeny	
	Pedigree	Genomic	Pedigree	Genomic
BWT, lbs	-2.75 (4.41)	0.0057 (0.01)	25.55 (72.16)	0.59 (0.32)
WWT, lbs	-20.54 (31.70)	-1.06(0.15)***	41.18 (36.10)	8.02 (2.31)**
YWT, lbs	-54.72 (84.70)	-1.55 (0.46)***	107.4 (87.30)	30.25(7.08)*

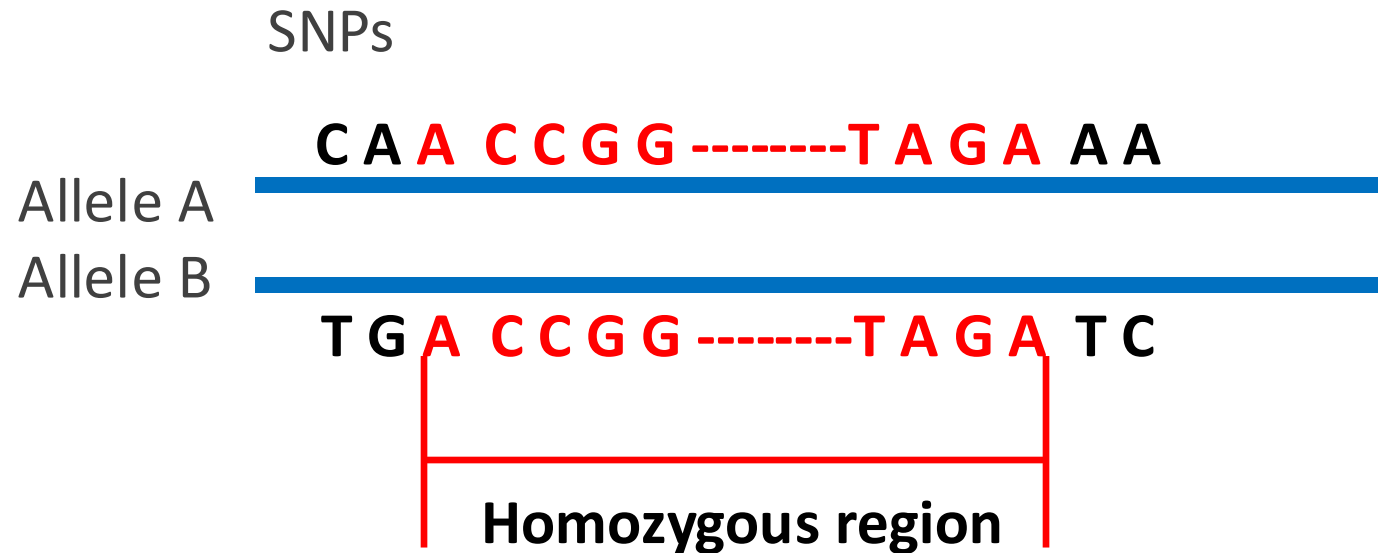
Genomic heterozygosity

Trait	Recent bulls' progeny	Older bulls' progeny
BWT, lbs	0.09 (0.06)	-18.9(0.83)*
WWT, lbs	2.98 (0.54)***	-21.20(5.98)**
YWT, lbs	7.4(1.64)***	-72.63(18.80)***

* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$

Runs of Homozygosity

Runs of homozygosity (ROH)



Obtaining Runs of Homozygosity

Used PLINK to obtain ROH

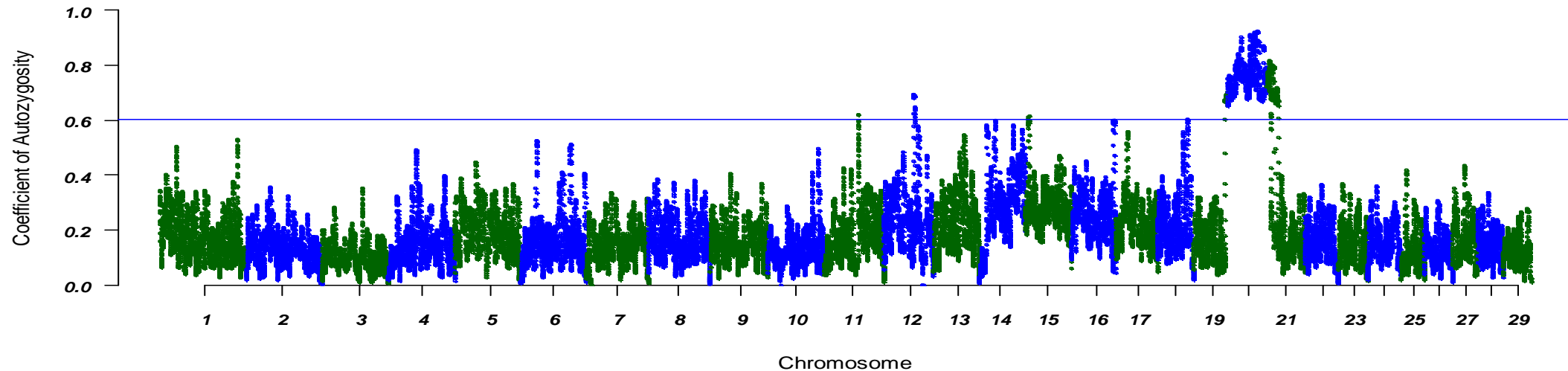
- Scanning window parameters
 - Window size = 1Mbp
 - Window heterozygous SNP = 2
 - Window missing SNP = 1
- ROH parameters
 - Density = 1 SNP/200kbp
 - Maximum gap of 1 Mbp between SNP in ROH
 - Minimum ROH size = 1 Mbp and 15 SNP
 - ROH heterozygous SNP = 2

ROH summary statistics

Parameter	Mean	Median	Standard deviation	Minimum	Maximum
Number of ROH	258	252	51.09	101	592
Average ROH length	1.88	1.95	0.16	1.44	2.79
Average combined ROH length	486.65	476.46	116.34	160.52	1584.02

Runs of Homozygosity

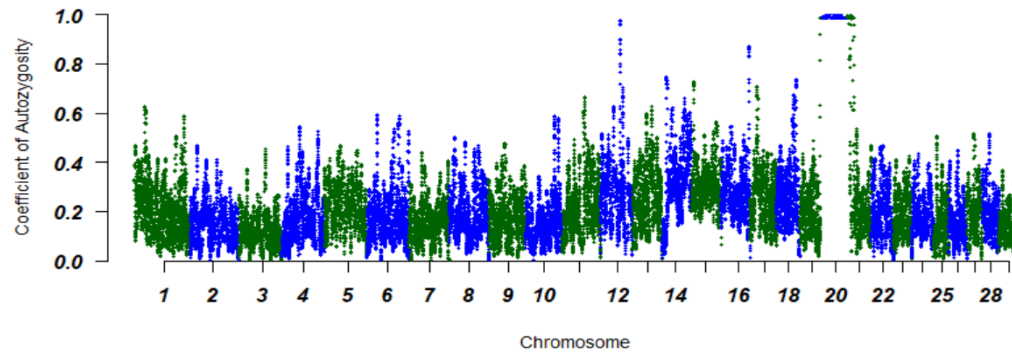
For every marker we calculated the proportion of animals that have an ROH.



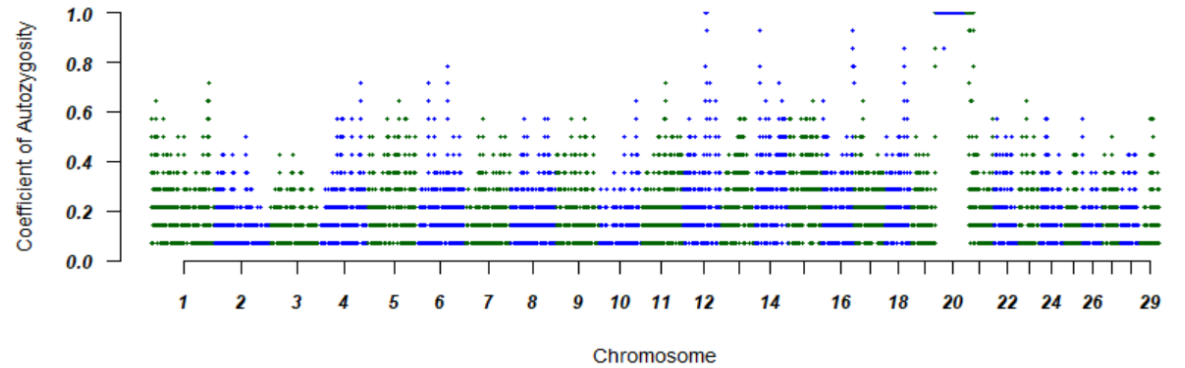
- Significance threshold is based on the 1st percentile of homozygosity on the marker (excluding chromosome 20).

Runs of Homozygosity

Recent Bulls



Old Bulls



Enrichment of QTL regions in chr 20 and 21

Top 5 enriched trait-chromosome

Trait	QTL Type	LogP
Age at puberty (21)	Reproduction	5.27
Average daily gain (21)	Production	1.37
Maturity rate (21)	Reproduction	2.10
Sexual precocity (21)	Reproduction	2.97
Shear force (21)	Meat	15.11

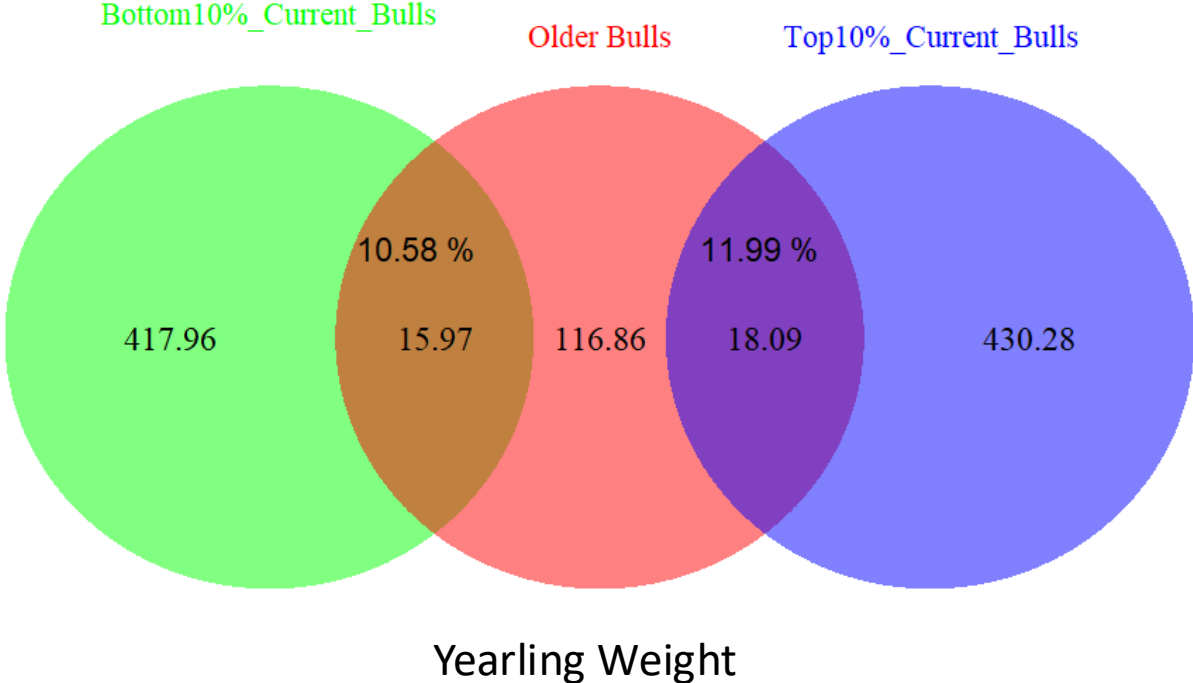
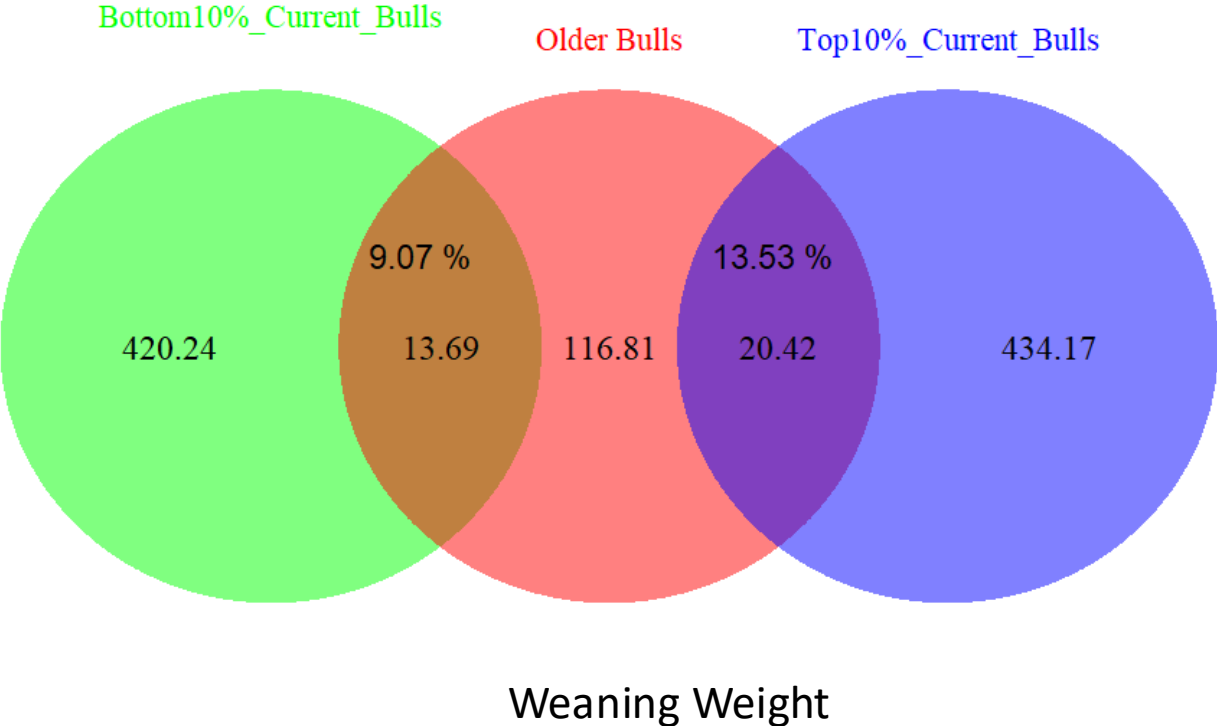
Top 5 enriched traits

Trait	QTL Type	LogP
Age at puberty	Reproduction	9.19
Maturity rate	Production	3.13
Sexual precocity	Reproduction	4.10
Shear force	Meat	11.09

Top enriched type

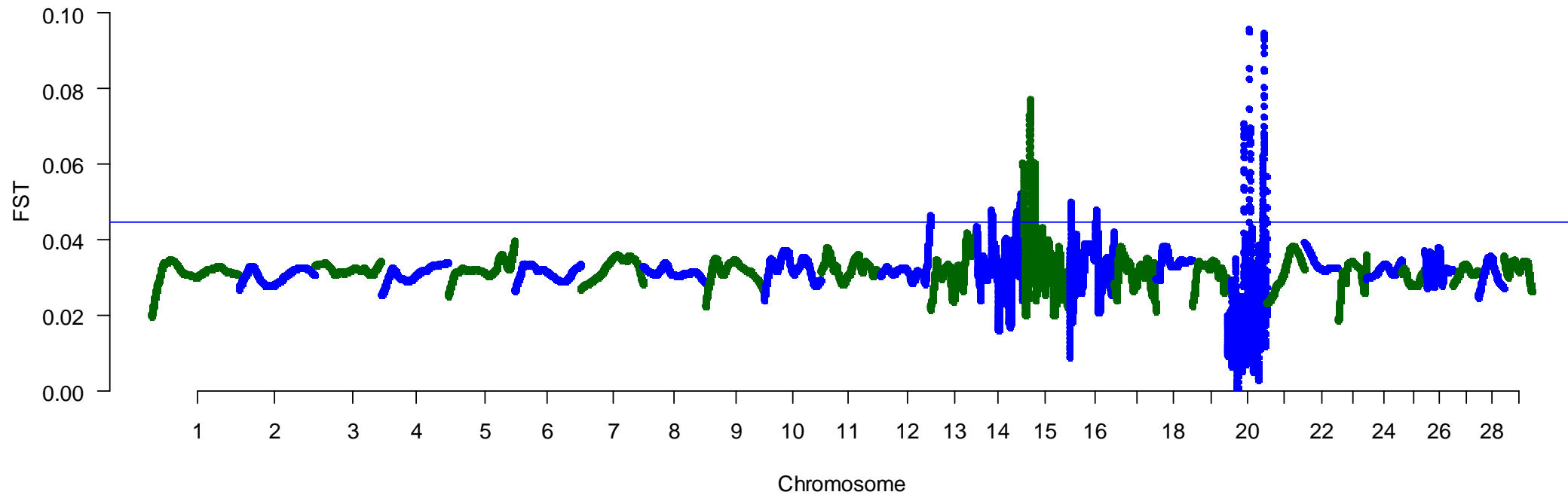
QTL Type	LogP
Meat and Carcass	3.80
Reproduction	1.99

Shared runs of homozygosity regions



F_{ST} Analysis

Global estimate between older and recent bulls offspring = 0.03



Enrichment of QTL regions

Top 5 enriched trait-chromosome

Trait	QTL Type	QTL Ratio
Milk fat % (20)	Milk	0.42
Milk glycosylated kappa-casein percentage (15)	Milk	0.94
Milk linoleic acid content (15)	Milk	1.00
Meat color (14)	Meat and carcass	1.00
Milk yield (20)	Milk	0.32

Final remarks

Selection works

- The additive model is not perfect

Performance of progeny was not negatively impacted – opens new opportunities in selection programs

Use of older genetics beneficial

- Corrective mating
- Injecting genetic diversity
- Alleviate inbreeding depression

NAGP collection is a valuable resource for breeders

Acknowledgments

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PennState Department of
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Questions



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