# Unraveling high progeny performance sired by 20th century bulls

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# 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

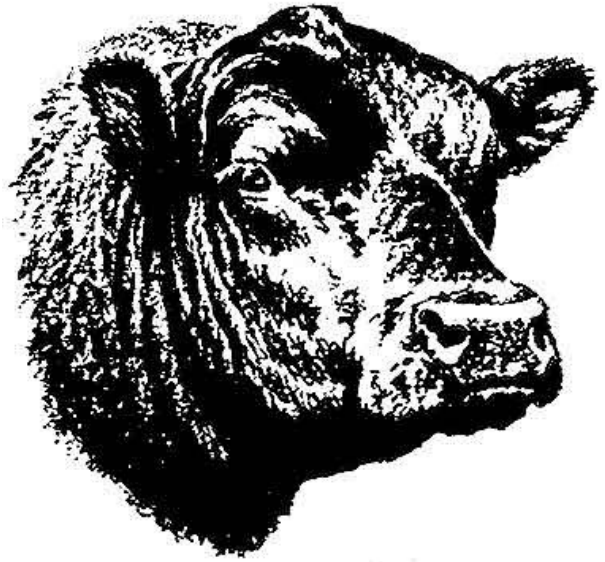
Characterize genomic properties of older and contemporary bulls and their progeny

Detect selection signatures

Evaluate more progeny than Holstein study

# Pedi gr ee

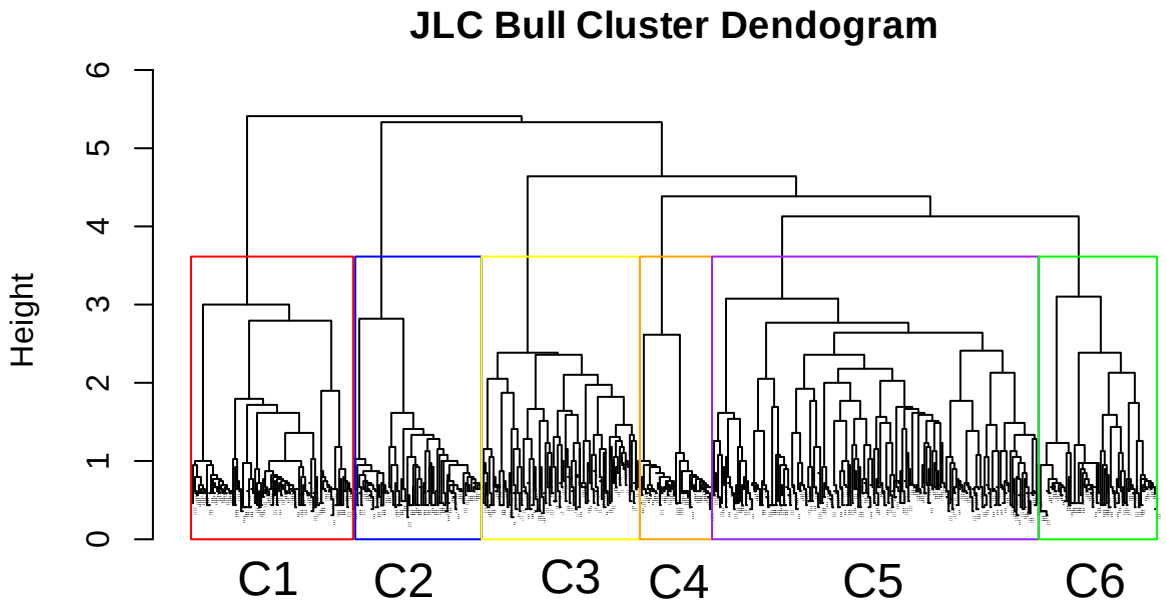
Jorgensen Land & Cattle PARTNERSHIP



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

Primary focus on data from nucellus 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

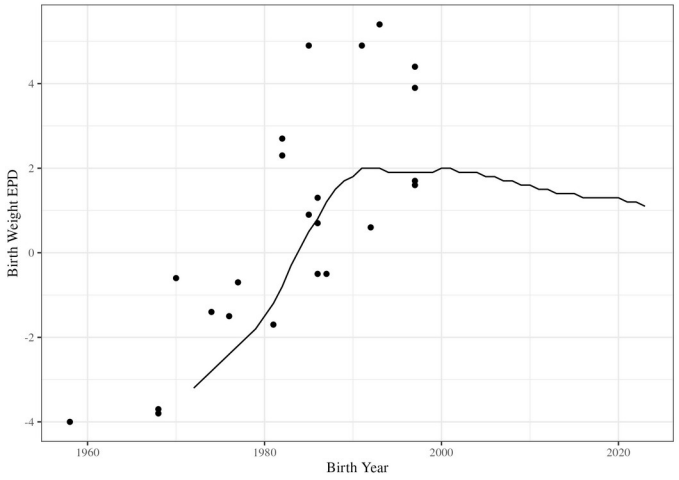
| Bulls | Birth Weight | Weaning Weight | Yearling Weight |
|---|---|---|---|
| Older | 214 | 137 | 18 |
| Recent | 4791 | 3144 | 1181 |

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

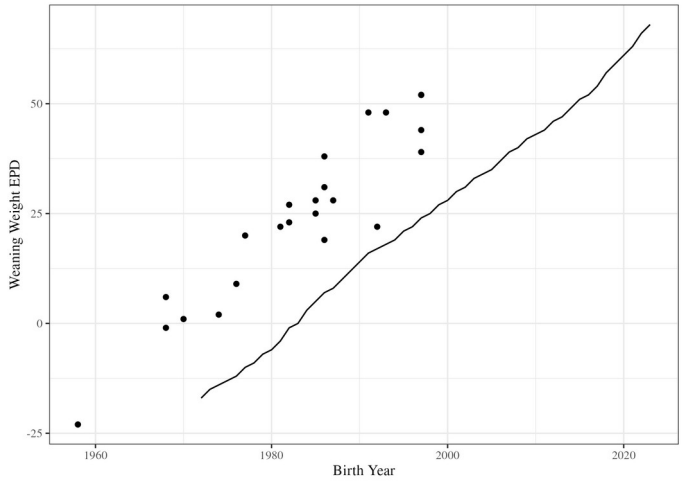


# Genetic Trends - AAA Overall Genetic Trend for Growth Traits and AAA EPDs of Old Sires with Modern JLC Progeny

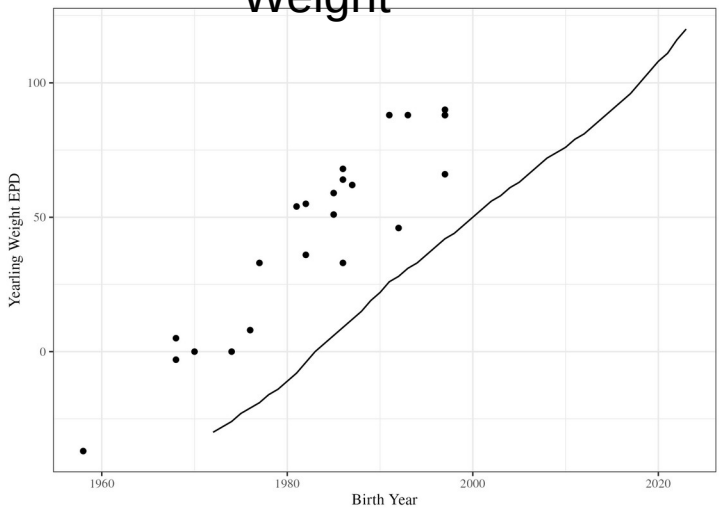
Birth Weight




Weaning Weight




Yearling Weight



# Mixed Model Analysis

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

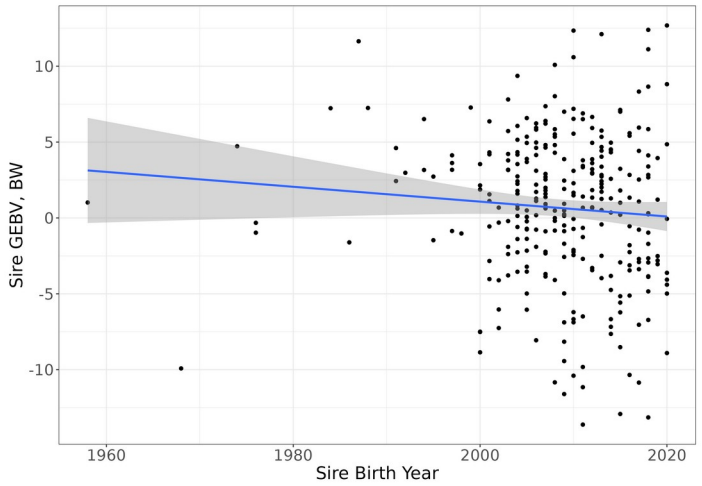
Random Effects
- Animal
- Maternal

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

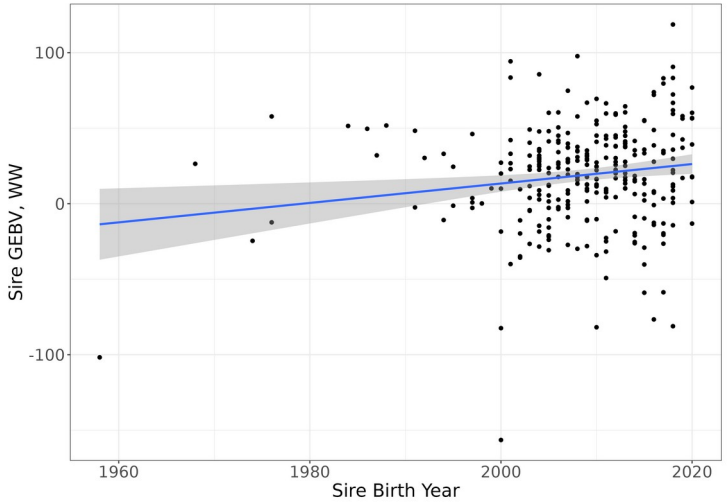
Adjusted phenotypes were corrected for all fixed effects in predictf90

# Genetic Trends for JLC Bulls over time

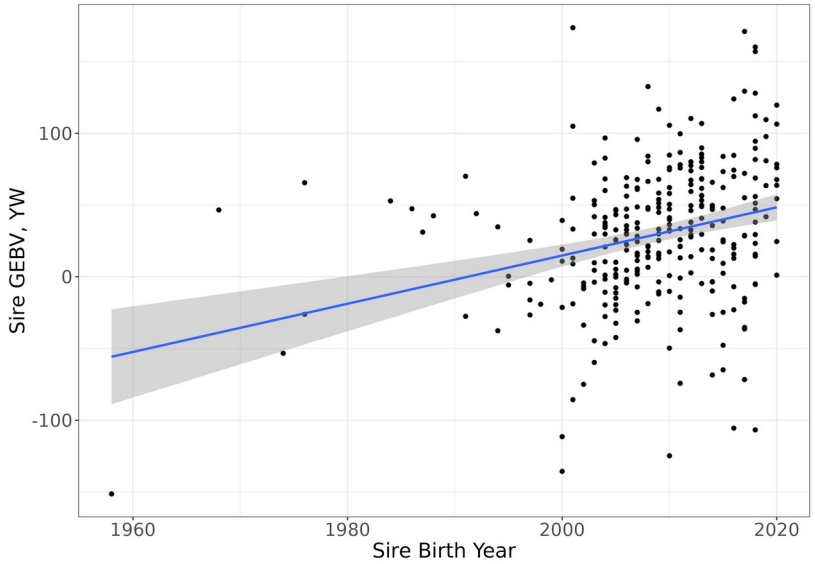
Birth Weight




Weaning Weight

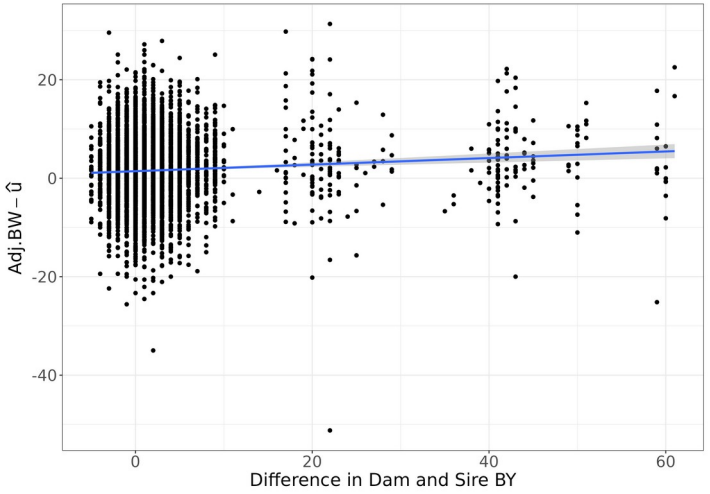



Yearling Weight

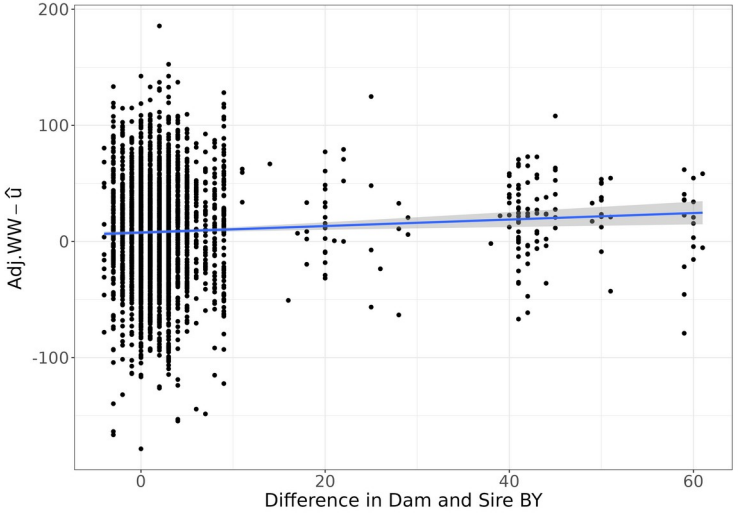


# Adjusted body weights based upon difference in the sire and dam's age

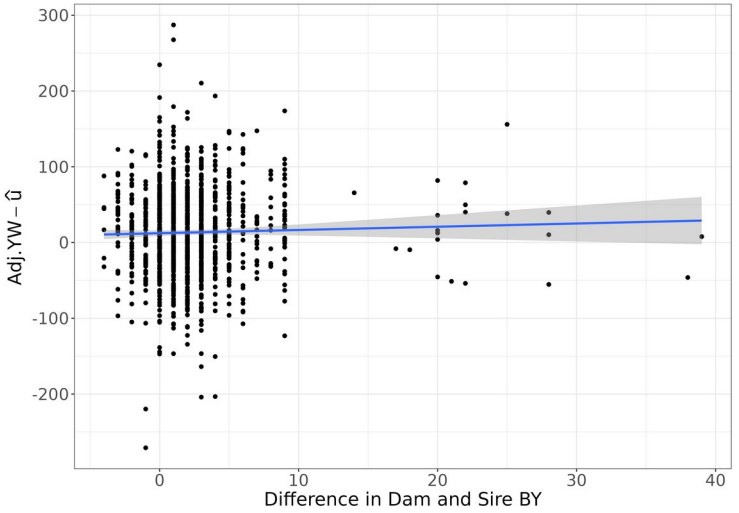
Birth Weight




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

# Obtaining Runs of Homozygosity

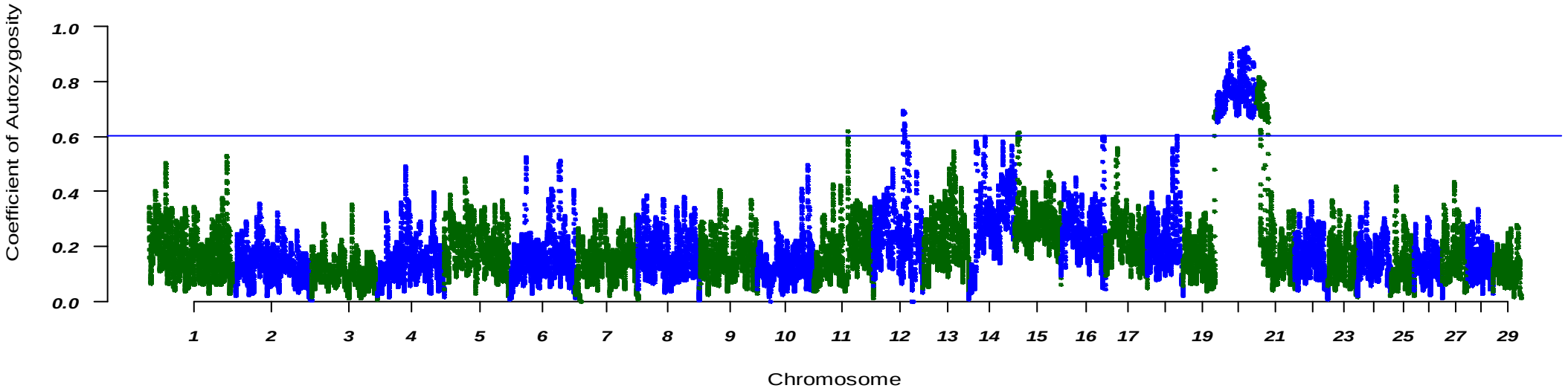
Used PLINK to obtain ROH

- 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

# Runs of Homozygosity

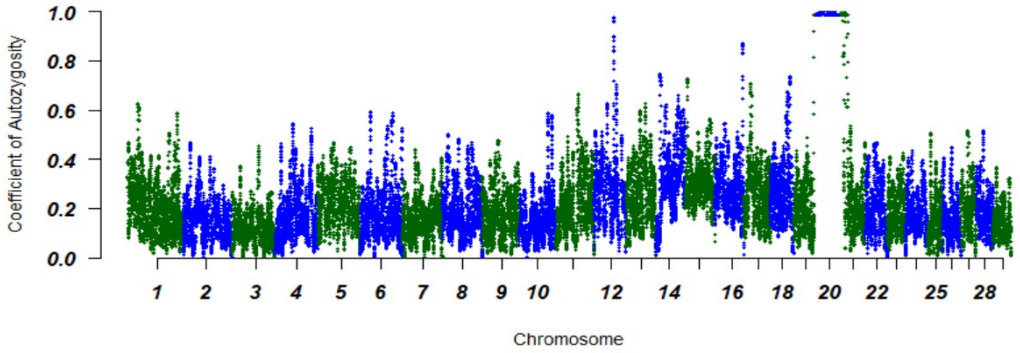
For every marker we calculated the proportion of animals that have an ROH.



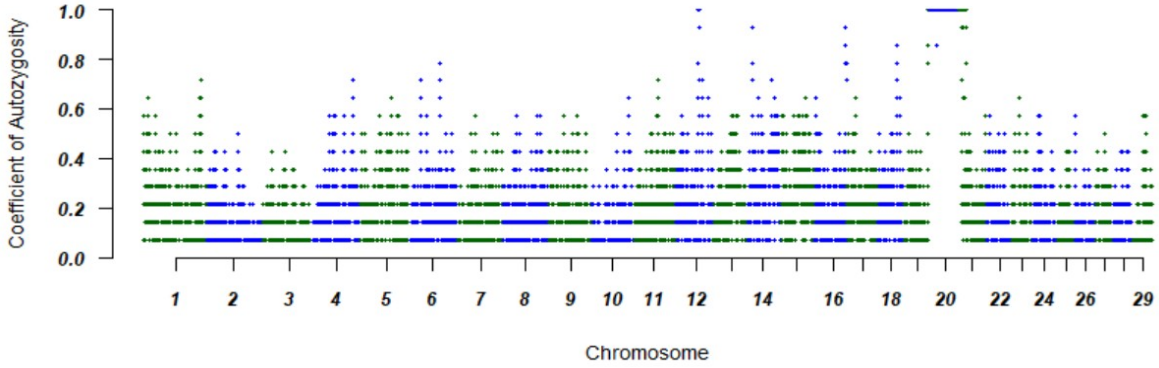

- Significance threshold is based on the 1st percentile of homozygosity on the marker (excluding chromosome 20).

# 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**

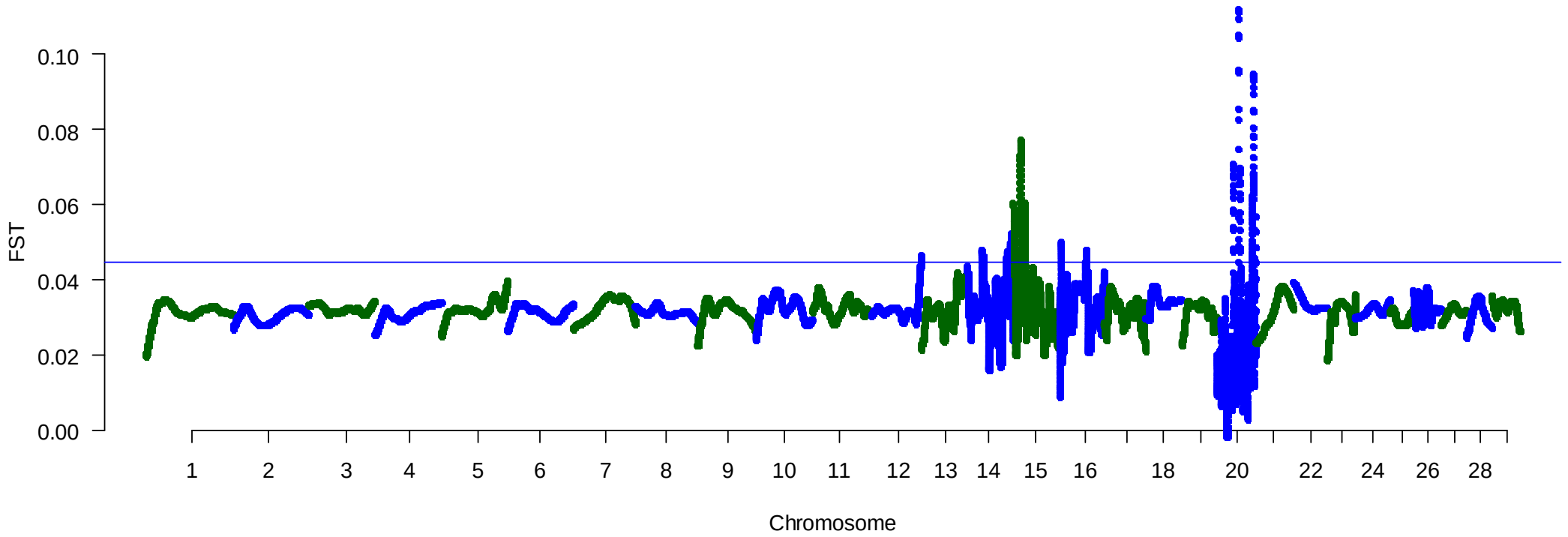
| Trait | QTL Type | LogP |
|---|---|---|
| Age at puberty | Reproduction | 9.19 |
| Maturity rate | Production | 3.13 |
| Sexual precocity | Reproduction | 4.10 |
| **Shear force** | **Meat** | **11.09** |

**Top 5 enriched type**

| QTL Type | LogP |
|---|---|
| **Meat and Carcass** | **3.80** |
| Reproduction | 1.99 |

# $F_{ST}$ Analysis

Global estimate between older and recent bulls offspring = 0.03



# Enrichment of QTL regions

**Top 5 enriched traits**

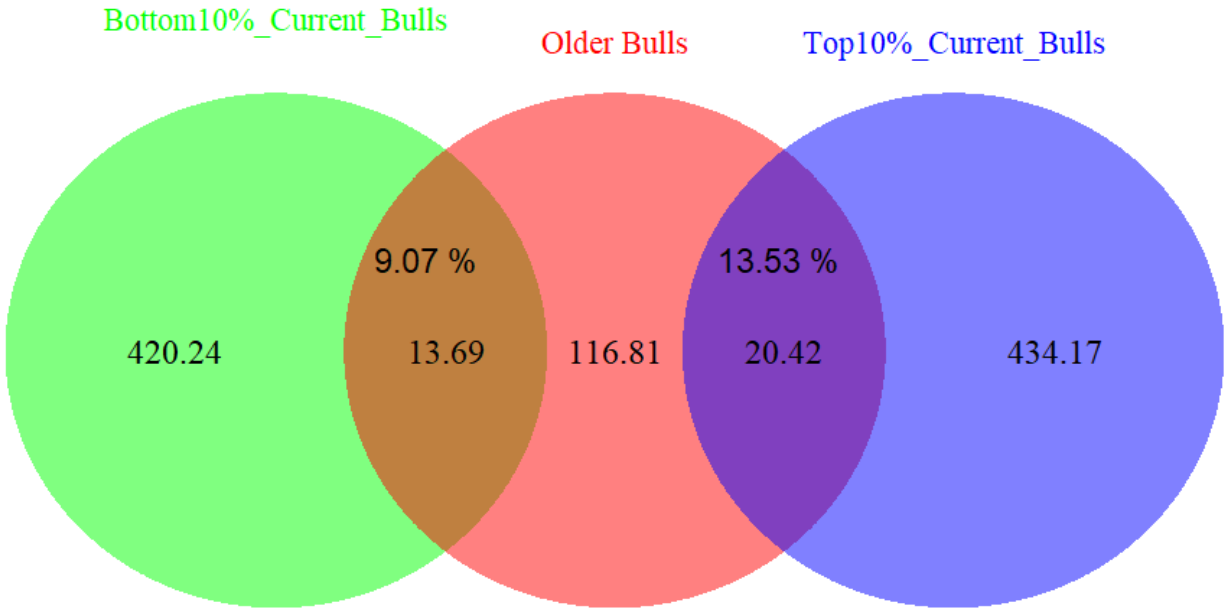
| Trait | QTL Type | QTL Ratio |
|---|---|---|
| Milk protein percentage | Milk | 0.07 |
| Milk yield | Milk | 0.06 |
| Milk fat % | Milk | 0.04 |
| Lactation persistency | Milk | 0.11 |
| Calf suckling reflex | Exterior | 0.15 |

# Enrichment of QTL regions

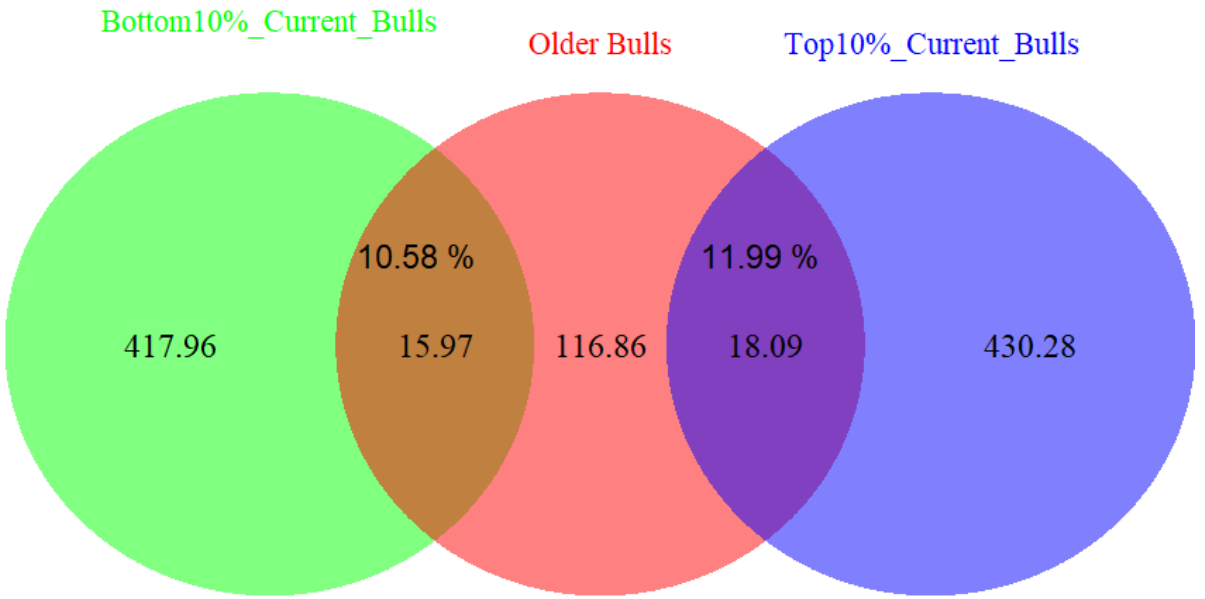
**Top 5 enriched trait-chromosome**

| 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 |

# Shared Runs of Homozygosity Regions




Weaning Weight




Yearling Weight

# Final remarks

Selection works

- The additive model is not perfect, thus difference in EBV estimation

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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Collaborators







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PennState Department of Animal Science

# Questions





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