Inbreeding in Line 1 Hereford

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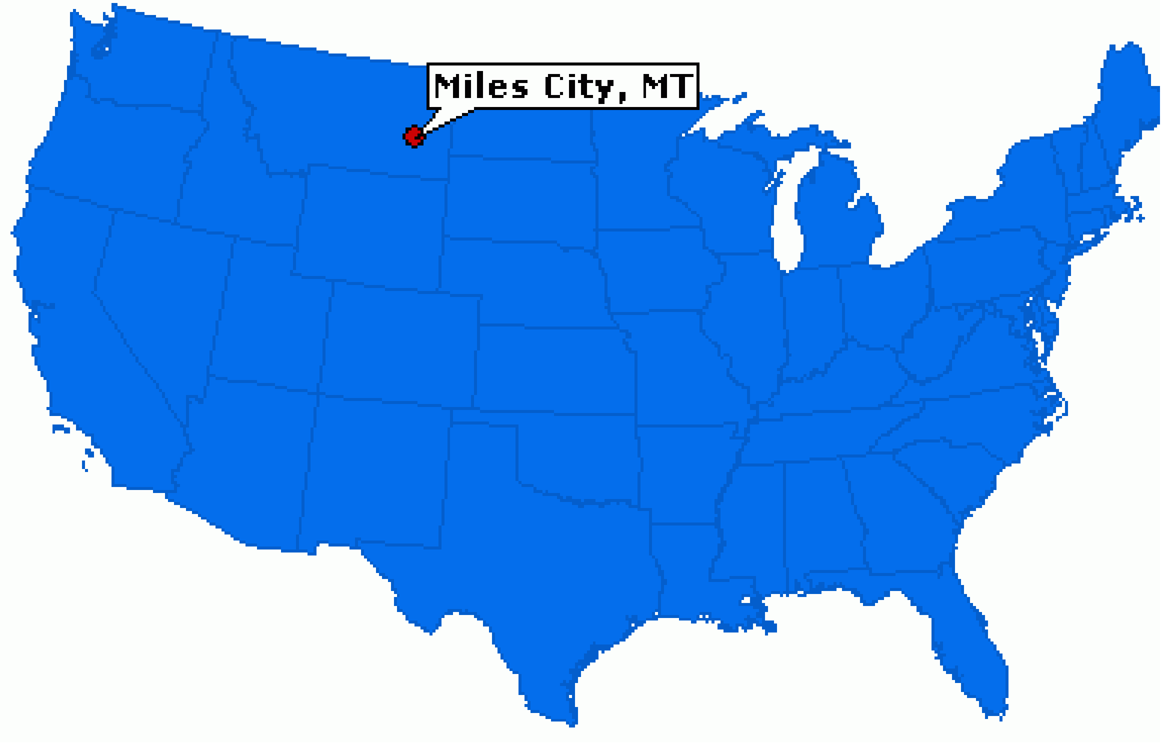

Miles City, MT


FREEWAY ENTRANCE

Line 1 Hereford

- Line 1 history:
  - Started more than 80 years ago
    - 50 cows from Montana
    - 2 paternal half sib bulls from Colorado
  - Selection based:
    - Linear measurements
    - Pre-weaning gain
      - Progeny testing

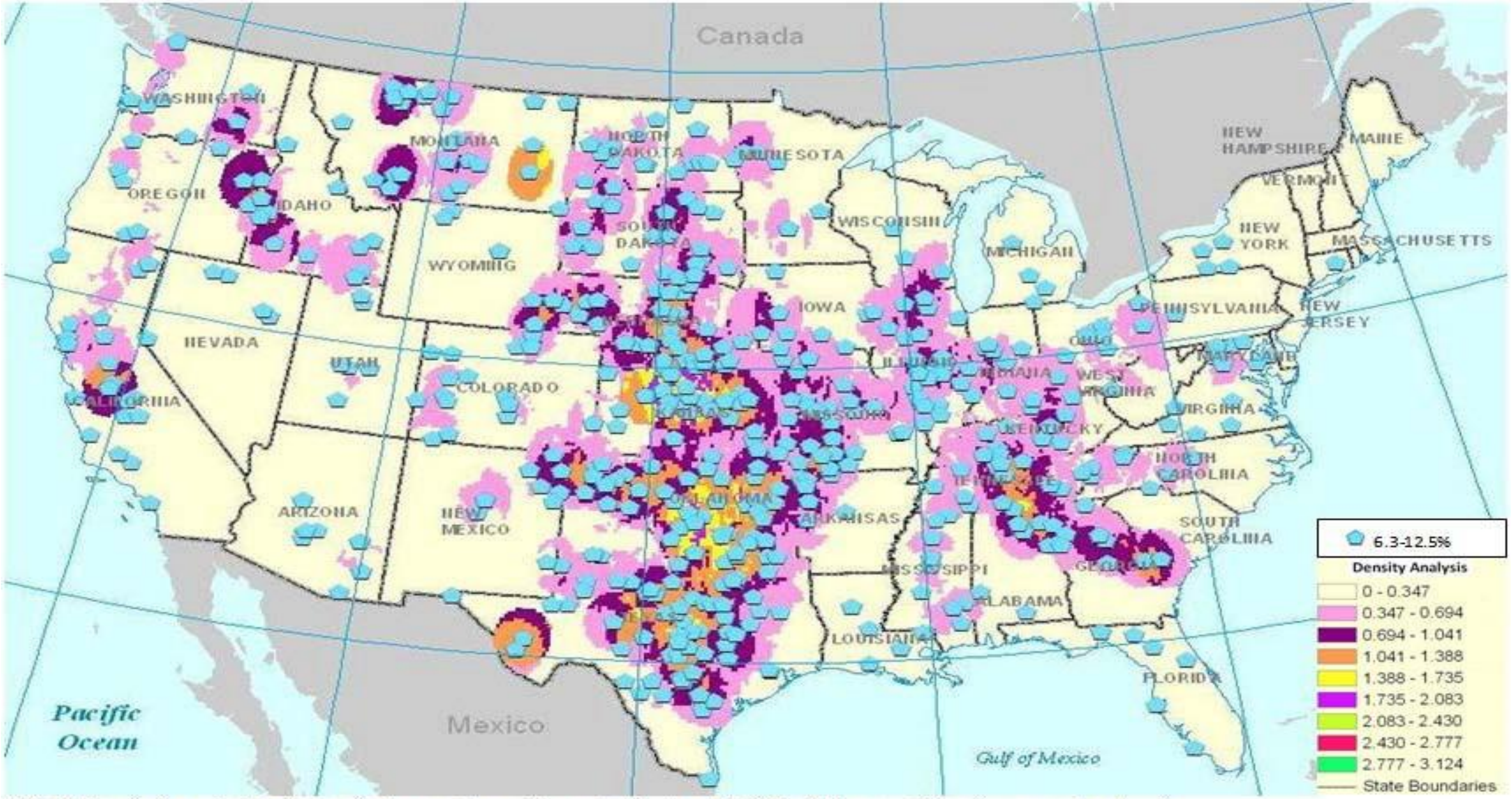
Advance Domino 20

Advance Domino 54

Impact

- Development of correction factors (Knapp et al., 1940; Koch and Clark, 1955)
- Early estimates of variance components for beef cattle traits (Knapp and Nordskog, 1946; Knapp and Clark, 1947,1950)
- Genetic x environment interaction (Burns et al. 1979)

Impact



^^Point density is a calculated magnitude per unit area from point features that fall within a specific region around each cell.

Figure 4.4 Density of Hereford cattle recorded by the American Hereford Association that are 6.3% to 12.5% related to Line 1.

Leesburg et al. 2012

Study

- Objective
    - Evaluate inbreeding in Line 1 using pedigree and genomic information and assess its impact on growth and fertility traits

Data

- Line 1 Hereford data
  - 10,186 pedigree
  - 30,220 SNP markers
  - 785 genotyped animals
  - Phenotypes
    - Animals born between 1990 and 2016 (n=3,866)
    - Birth weight (BW), weaning weight (WW), yearling weight (YW), average daily gain (ADG) and age at first calving (AFC).

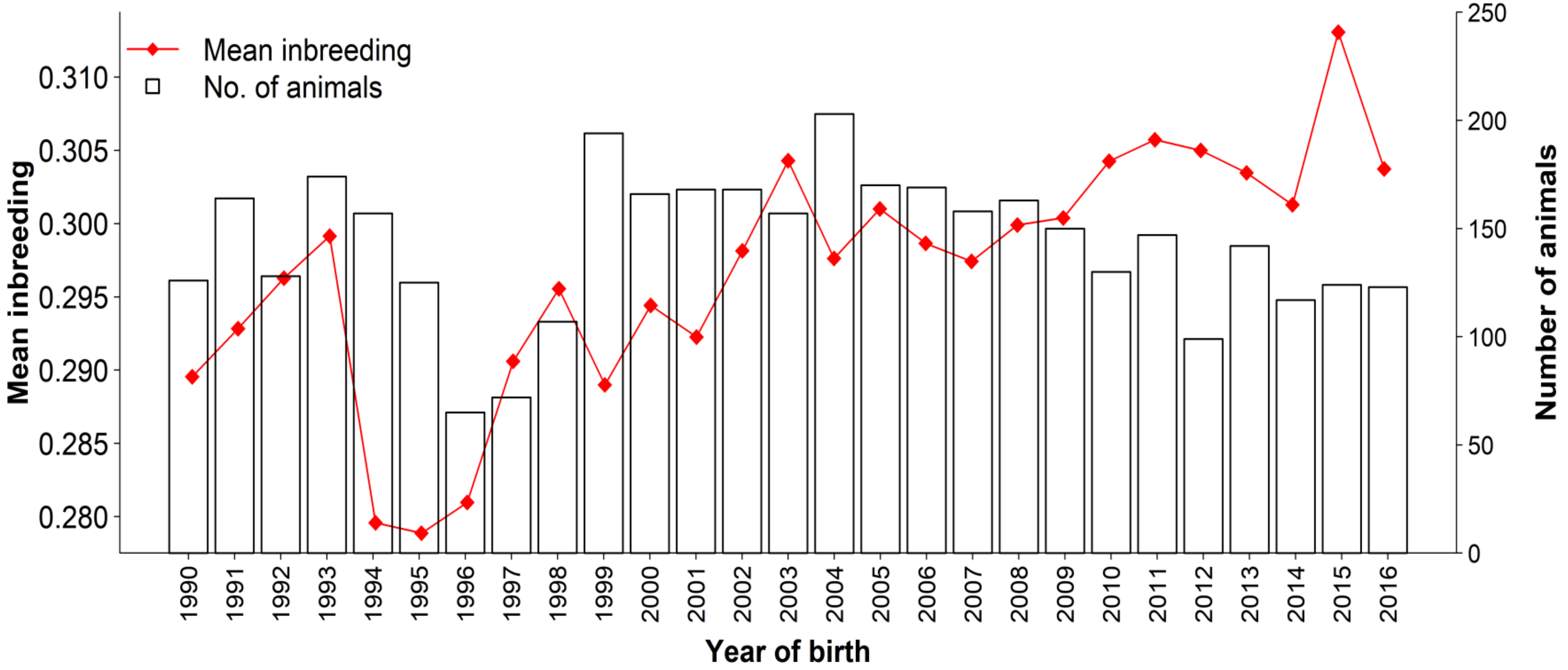
Pedigree

Depth and completeness of the pedigree for all phenotyped and genotyped animals

Animals	**Parameter**[1]	**Mean**	**Min**	**Max**
All	Maximum generations traced back	31.05	0.00	48.00
	Equivalent complete generations (ECG)	17.15	0.00	28.64
	Pedigree completeness index (PCI)	0.92	0.00	1.00
Phenotyped	Maximum generations traced back	41.72	35.00	48.00
	Equivalent complete generations (ECG)	24.25	17.27	28.64
	Pedigree completeness index (PCI)	0.99	0.77	1.00
Genotyped	Maximum generations traced back	44.69	22.00	48.00
	Equivalent complete generations (ECG)	25.36	10.92	28.64
	Pedigree completeness index (PCI)	0.98	0.00	1.00

Pedigree Inbreeding

Pedigree-based inbreeding, % (1990-2016)



Runs of Homozygosity

- PLINK used to determine ROH
  - Minimum of 30 consecutive SNPs
  - Minimum density of 1 SNP per 500 kb inside a ROH
  - Maximum gap of 500 kb between consecutive homozygous SNPs
  - Minimum length of 1000 kb
  - Maximum of 2 heterozygous SNPs

Runs of homozygosity

Summary description of the number, individual and total length of ROH segments (in Mb) per animal

Parameter	Mean	SD	Min	Max
[1]ROH$_{\_n}$	82.92	16.89	6.00	119.00
[2]ROH$_{\_L}$	6.83	4.45	1.36	64.86
[3]ROH$_{\_T\_L}$	574.66	128.51	21.61	964.66

[1] Number of individual ROH segments per animal.

[2] Length of an individual ROH in Mb.

[3] Total length ROH segments, in Mb, per animal.

ROH based inbreeding

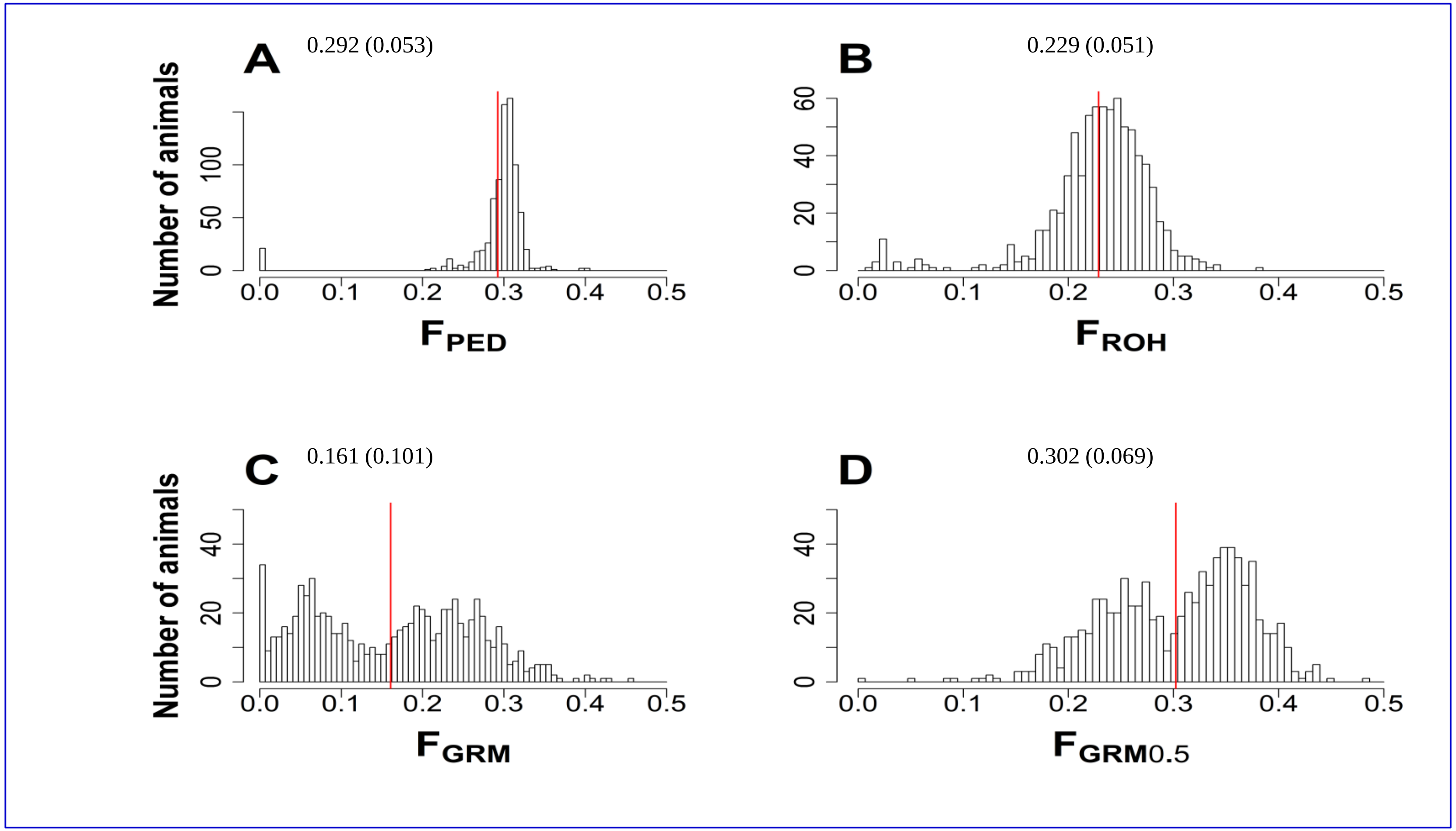
- $\mathbf{F_{ROH}}$ represents true or realized autozygosity (introduced by McQuillan et al. 2008)

$$\mathbf{F_{ROH}} = \frac{\sum \mathbf{L_{ROH}}}{\mathbf{L_{autosome}}}$$

McQuillan et al. (2008)

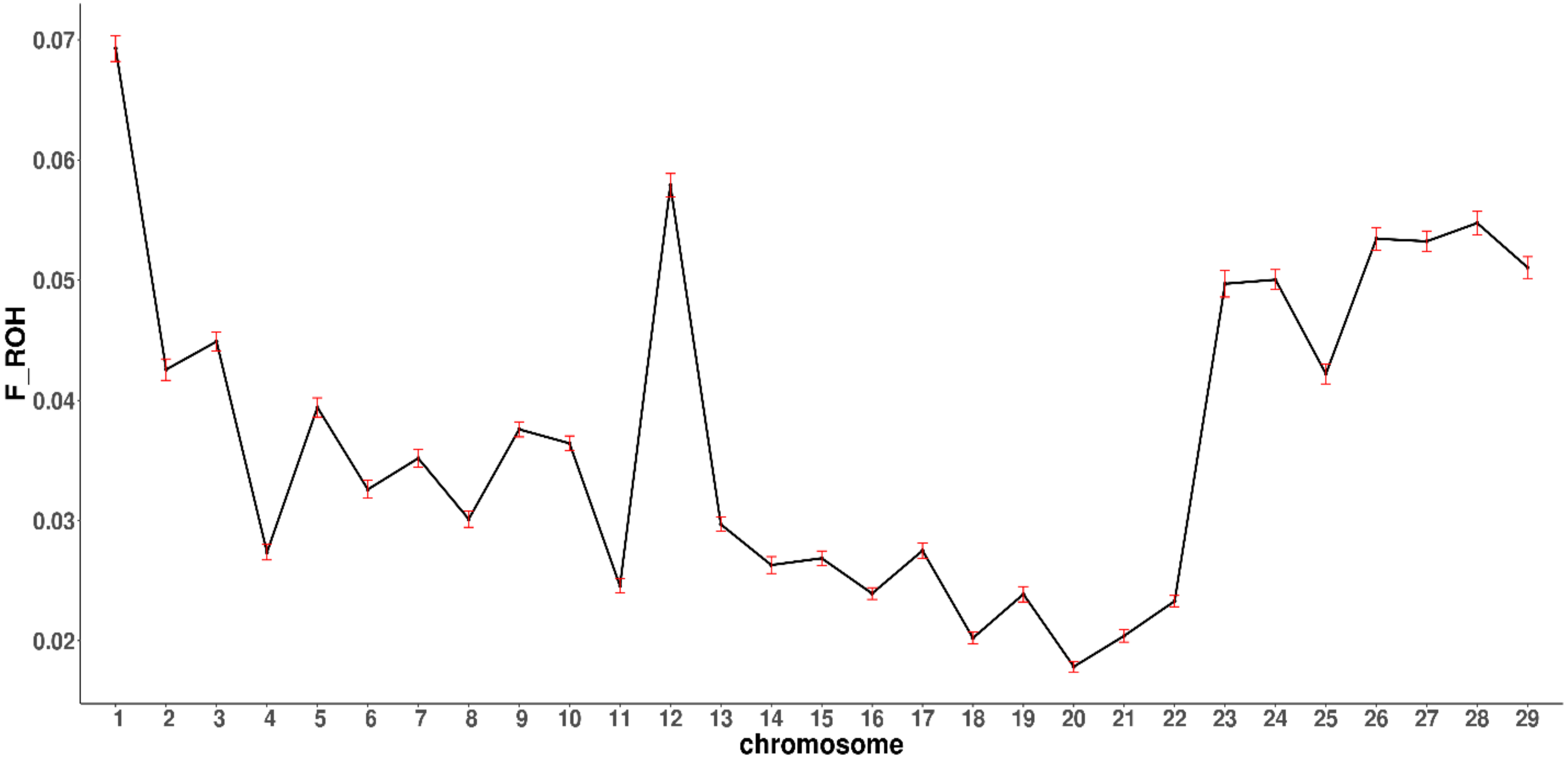
- Standard procedure for quantifying autozygosity
  - Can distinguish between markers that are IBD and IBS
- Inbreeding depression detection
  - Sensitive to selection, easy to interpret

Inbreeding measurements



Distribution of inbreeding coefficients based on different inbreeding measurments

Runs of homozygosity



Average runs of homozygosity based inbreeding (SE in red bars) across the 29 autosomal chromosomes ($F_{ROH\text{-}CHR}$) calculated as the proportion of chromosomal F_{ROH}

Inbreeding

Correlations between pedigree and genomic based inbreeding coefficients using genotyped animals

Inbreeding[1]	**Correlation**	**CI**[2]
(F_{PED}, F_{GRM})	0.250	0.183 - 0.314
(F_{PED}, $F_{GRM0.5}$)	0.434	0.376 - 0.490
(F_{PED}, F_{ROH})	0.661	0.620 - 0.700
(F_{GRM}, $F_{GRM0.5}$)	0.804	0.777 - 0.827
(F_{GRM}, F_{ROH})	0.567	0.518 - 0.613
($F_{GRM0.5}$, F_{ROH})	0.827	0.804 - 0.848

Inbreeding depression

Summary description of the phenotypic data

Data[1]	**Trait[2]**	**n[3]**	**Mean**	**SD**	**Minimum**	**Maximum**
All	BWT, kg	3,866	36.68	5.12	19.05	58.06
	WWT, kg	3,639	191.14	33.78	71.67	309.35
	YWT, kg	3,358	348.53	70.36	150.14	572.43
	ADG, kg/d	3,358	0.91	0.30	0.14	2.66
	AFC, d	1,153	763.13	104.94	638	1,485
Genotyped	BWT, kg	743	37.30	4.64	21.77	53.52
	WWT, kg	736	197.68	34.12	96.62	293.02
	YWT, kg	687	338.14	81.30	169.64	555.65
	ADG, kg/d	687	0.844	0.352	0.149	1.625

Inbreeding depression – Pedigree

Estimates of the regression coefficients (SE) of pedigree inbreeding on growth and fertility traits

Trait	**Model M1**	**Model M2**	
	F	F	F_D
BWT, kg	-0.053 (0.044)	-0.031 (0.045)	-0.089 (0.039)*
WWT, kg	-1.200 (0.290) ***	-0.867 (0.295)**	-1.424 (0.257)***
YWT, kg	-2.033 (0.431)***	-1.724 (0.441)***	-1.303 (0.382)***
ADG, kg/d	-0.004 (0.002)**	-0.004 (0.002)**	0.0004 (0.001)
AFC, d	1.654 (1.403)	1.426 (1.442)	0.817 (1.190)

M1: Only animal's inbreeding coefficients (F) was fitted in the regression model.

M2: Animal (F) and maternal (F_D) inbreeding coefficients were fitted in the regression model.

* *P* < 0.05; ** *P* < 0.01; *** *P* < 0.001.

Inbreeding depression (genotyped animals)

Estimates of the regression coefficients (SE) of genomic inbreeding on growth and fertility traits

Trait	**Regression coefficient**			
	F_{PED}	**F_{GRM}**	**$F_{GRM0.5}$**	**F_{ROH}**
BWT, kg	-0.003 (0.032)	0.009 (0.021)	-0.012 (0.027)	-0.014 (0.031)
WWT, kg	-0.114 (0.203)	-0.212 (0.135)	-0.529 (0.172)**	-0.387 (0.198)
YWT, kg	-1.060 (0.268)***	-0.458 (0.183)*	-0.923 (0.234)***	-1.133 (0.266)***
ADG, kg/d	-0.006 (0.001)***	-0.002 (0.001)**	-0.003 (0.001)***	-0.006 (0.001)***

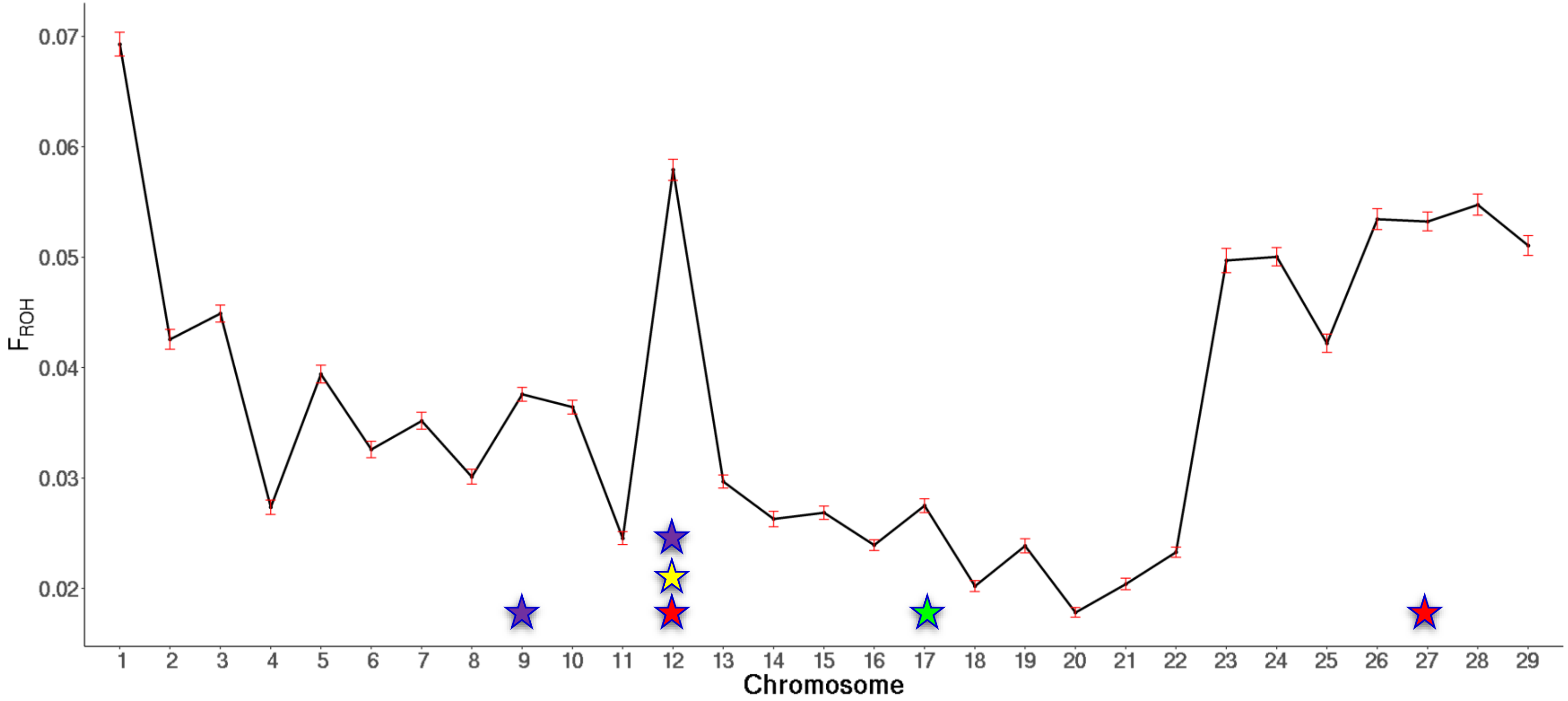
Inbreeding depression-ROH

Estimates of the regression coefficients of ROH based chromosomal inbreeding on growth trait

Trait	**Chromosome**	**$F_{ROH\text{-}CHR}$**	**SE**
BWT, kg	12	-0.676*	0.289
	27	-0.855**	0.306
WWT, kg	17	-6.827*	3.011
YWT, kg	12	-5.576*	2.512
ADG, kg/d	9	-0.032*	0.014
	12	-0.022*	0.010

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

Contribution of chromosomal inbreeding to total inbreeding



Top 5 chromosomes with high proportion of inbreeding: 1, 12, 28, 26, 27

★ BWT-Significant; ★ WWT-Significant; ★ YWT-Significant; ★ ADG-Significant

Final remarks

- Inbreeding was around 30% which is significantly higher than estimates in beef cattle.
- Despite of inbreeding, growth traits were not as negatively impacted as expected
  - Purging of deleterious alleles
- Genomic inbreeding estimates could be used in mating decisions
  - Missing or incomplete pedigree
  - Discrimination of same order relationships

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Thank you