Application of genetic tools to utilize reproductive records from cattle populations

Tara McDaneld

USDA/ARS Meat Animal Research Center
Clay Center, NE, 68933, USA

Background

- Reproductive efficiency
  - Lifetime production of the cow
  - Important element of cow-calf component of cattle industry
  - Female becomes a liability in the herd with no calf for producer to market

Objective

- Identify regions of the genome associated with reproductive efficiency in beef cattle

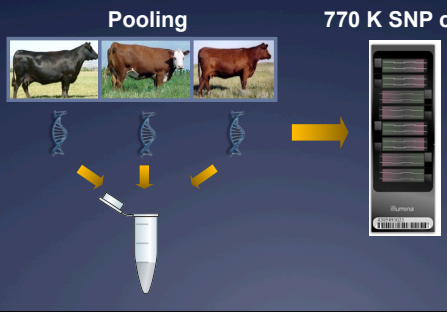
Background

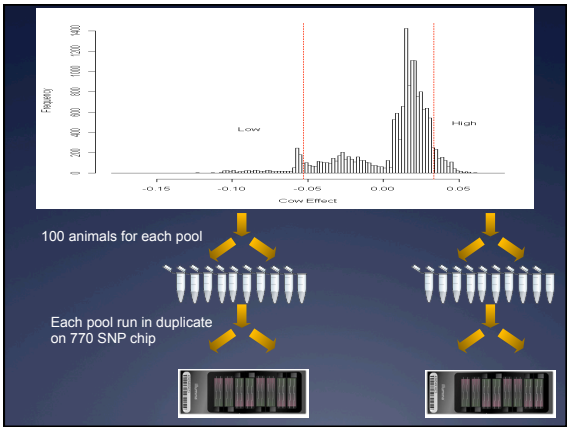
- Previous research has identified chromosomal regions associated with reproductive efficiency
  - BTA 5, 14
    - Twinning (Kim, et al., 2009; Allan et al., 2009; Cobanoglu, et al., 2005)
  - Significant SNP on 8 chromosomes
    - Fertilization rate (Huang et al., 2010)
  - BTA 16
    - Blastocyst rate (Huang et al., 2010)

Challenges when evaluating reproductive traits

- Low heritability (0.10-0.40)
- Complex trait
  - Influenced by multiple genes
  - Creates difficulty when identifying genomic regions

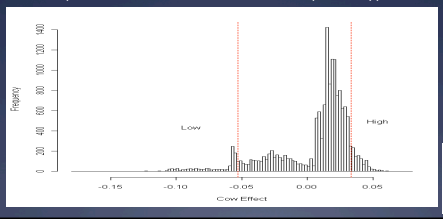
Tools for overcoming challenges





Cattle populations

- USMARC
  - Genetically diverse populations
    - British and Continental breeds
  - 1000 females of low reproductive efficiency
  - 1000 females of high reproductive efficiency
  - 10 pools of 100 individuals for each phenotype



Cattle populations

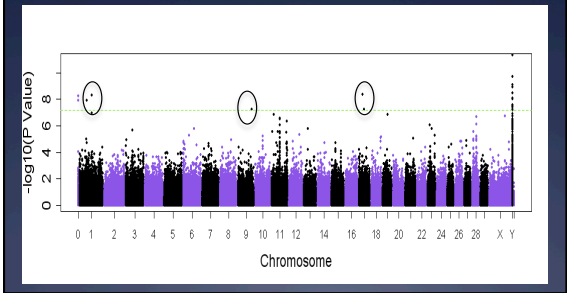
- Deseret ranch in Florida
  - *Bos indicus* influence
    - Brangus
    - Simbrah
    - Braford
  - Reproductive records from 2 breeding seasons
    - Open/open
    - Open/pregnant
    - Pregnant/open
    - Pregnant/pregnant

Deseret Ranch

Brangus	Second = No	Second = Yes
First = No	199	461
First = Yes	163	437
Braford	**Second = No**	**Second = Yes**
First = No	96	246
First = Yes	204	603
Simbrah	**Second = No**	**Second = Yes**
First = No	123	372
First = Yes	207	543

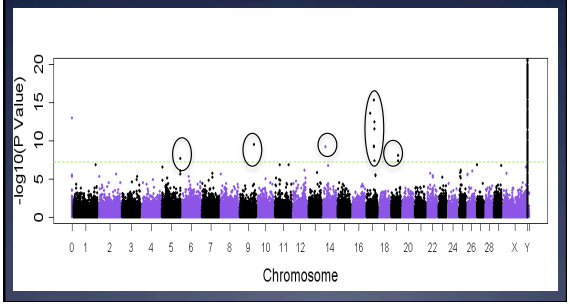
MARC population

- Identified multiple regions across genome associated with reproductive efficiency
  - BTA 1, 9, 17



Deseret population

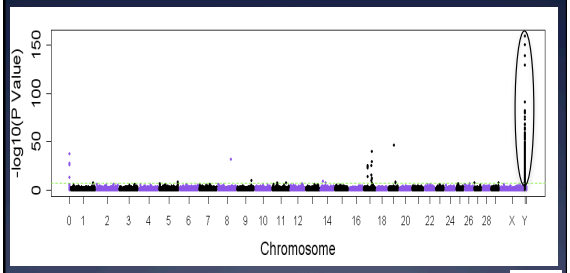
- Identified multiple regions across genome associated with reproductive efficiency
  - BTA 5, **9**, 14, **17**, and 19



Results

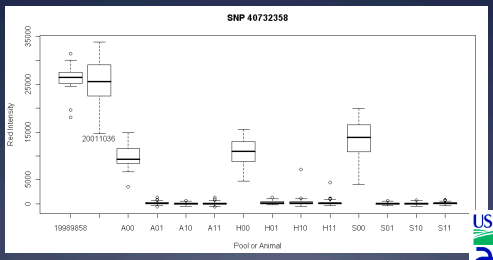
- BTA 5
  - Twinning (Kim, et al., 2009; Allan et al., 2009; Cobanoglu, et al., 2005)
- BTA 14
  - Twinning (Bierman et al., 2010,; Cobanoglu et al., 2005)

Y are there Y SNP in females?



Y SNP in males and females?

- Only see Y SNP in open Deseret pools and MARC low reproductive pools



Why do we see Y SNP in the open females?

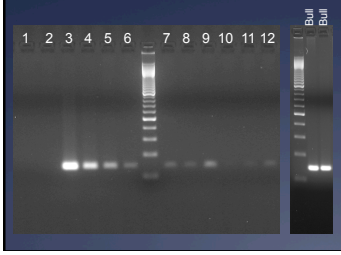
- Can we determine which females that possess the Y SNP?
- What would it mean to the industry to identify females that will not get pregnant?

Y SNP in females?

- Evaluate individual females that make up open pool
  - Are all the open females contributing to the Y SNP?

Y chromosome in the pools

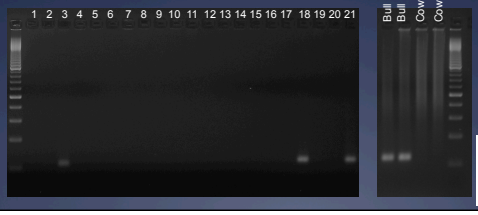
- Evaluate individuals of pools
  - PCR test specific to Y chromosome
    - PCR test is used to sex embryos
    - Only positive for males



% pool positive for sexing test	
Brangus	21%
Simbrah	27%
Braford	29%

Y SNP in pools

- Evaluate specific Y SNP on 770 K SNP chip
  - Developed PCR tests for Y SNP that are significant
  - We see different patterns in females that are positive for sexing PCR test
  - Different fragments of Y chromosome?

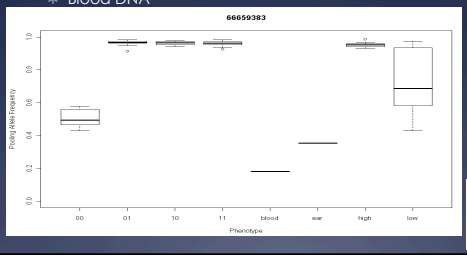


What is causing the Y SNP in females?

- Undetected freemartins?
  - Females commonly calve on pasture
    - May miss calves that are born twins
  - Reproductive tracts are checked in Deseret population at prebreeding check
  - Twins are recorded at USMARC

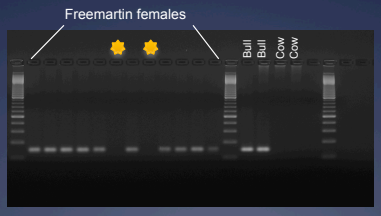
Freemartins in pools?

- Evaluate known freemartin pools with 770 SNP chip
  - Ear DNA
  - Blood DNA



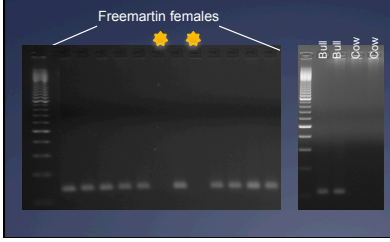
Freemartins in pools?

- Use PCR to test for genomic regions of Y in individuals that made up pool
  - Sexing PCR test



Freemartins in pools?

- Use PCR to test for Y SNP that are significant
  - All females that are positive for sexing primers are also positive for Y-SNP tests
  - Are freemartins the only cause of the Y?



% + Sexing primer test	% + Y-SNP primer test
96%	96%

Conclusions

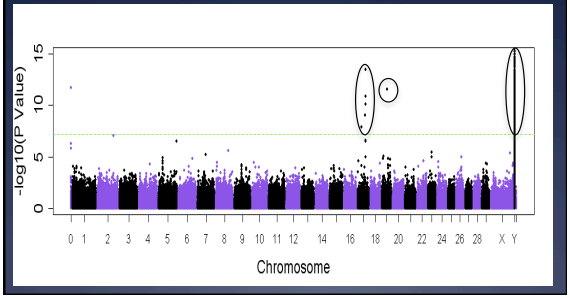
- Identified regions of the genome associated with reproductive efficiency
- Able to replicate these results in additional populations
- Identified Y SNP in individuals of open pools that may contribute to low reproductive efficiency (approx. 3-20% of the open population)

Additional populations

- Rex ranch, Ashby, NE
  - Records from 2007, 2008, and 2009
    - Three breeding seasons for each year
    - Open females are culled after first failure
- Milt Thomas at NMSU
  - Camp Cooley
  - Suhn
  - Branch Ranch
  - UC Davis
  - Carona

Rex population

- Identified multiple regions across genome associated with reproductive efficiency
  - BTA 17, 19, Y



Acknowledgements

- Deseret Ranch
- MARC cattle operations
- Rex Ranch
- Bonnie Long
- John Keele
- Larry Kuehn
- Warren Snelling
- Milt Thomas and lab personal
- Tammy Sorensen
- Steve Simcox

2000 bull project results

- Larry Kuehn will be presenting at the end of both of his talks tomorrow
  - Emerging technology and Genetic Prediction
  - Information on MBV release and prediction equations

Thank You!