Tackling fertility using pooled DNA information

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Reproductive efficiency in cattle is an important element of the cow-calf component of the beef production industry. If the female does not become pregnant after breeding she becomes a liability in the herd with no calf for the producer to market. As a result, reduction in unproductive periods in the reproductive females life would significantly impact production costs. **Therefore, we set out to identify regions of the genome that are associated with reproductive efficiency in beef cattle.**

Traditionally, heritability of reproductive traits is low (0.04-0.16), creating a challenge when identifying genomic regions that may harbor genetic markers that could be used for selection. With the development of **high-density SNP arrays**, it is possible to perform genome wide association studies for lowly heritable traits such as reproductive efficiency. However, high cost of genotyping with SNP arrays can result in smaller sample sizes being genotyped limiting the power of the study. To overcome this, we have utilized **DNA pooling (Figure 1)** of individual animals based on reproductive efficiency.


Figure 1
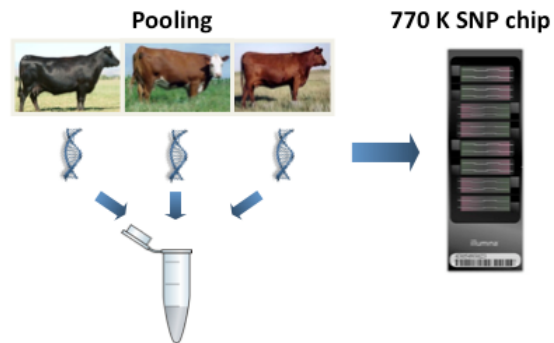
Cattle populations: Several populations have been evaluated for this study including **commercial ranches** and the **USMARC** population. Animals from the commercial ranches include populations from across the United States. For al populations evaluated, reproductive data was collected at first breeding for success of pregnancy. Reproductive data was also collected for a second breeding season from a single ranch.

Pooling: DNA was pooled based on open/pregnant phenotype for each population **(Figure 2)**. Equal concentrations of each individual sample

Figure 2
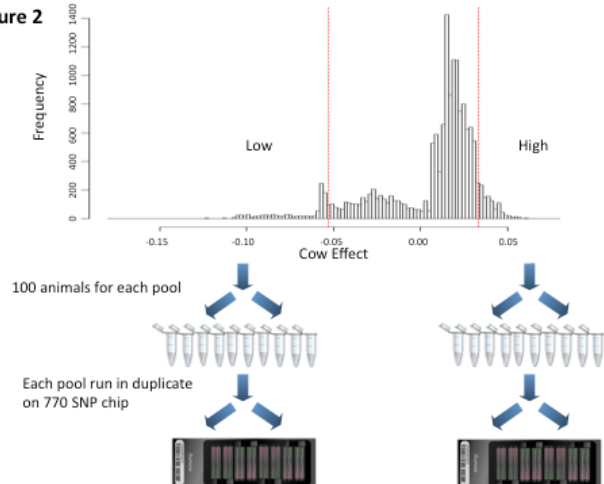
were added to the respective pool to ensure that each animal is represented equally within the pool. Pools were then evaluated using the BovineHD 770 SNP chip.

Results: Utilizing **pooling** and the **770 HD SNP chip** we were able to identify regions of the genome associated with reproductive efficiency in breeding females. Genomic regions associated with reproductive efficiency for the USMARC population included **BTA 1, 9, and 17 (Figure 3)**. Two of these regions **(BTA 9 and 17)** were also significant in the Deseret population with the addition of **BTA 5, 14, and 19 (Figure 4)**.

Figure 3 — USMARC Population

Figure 4 — Deseret Population
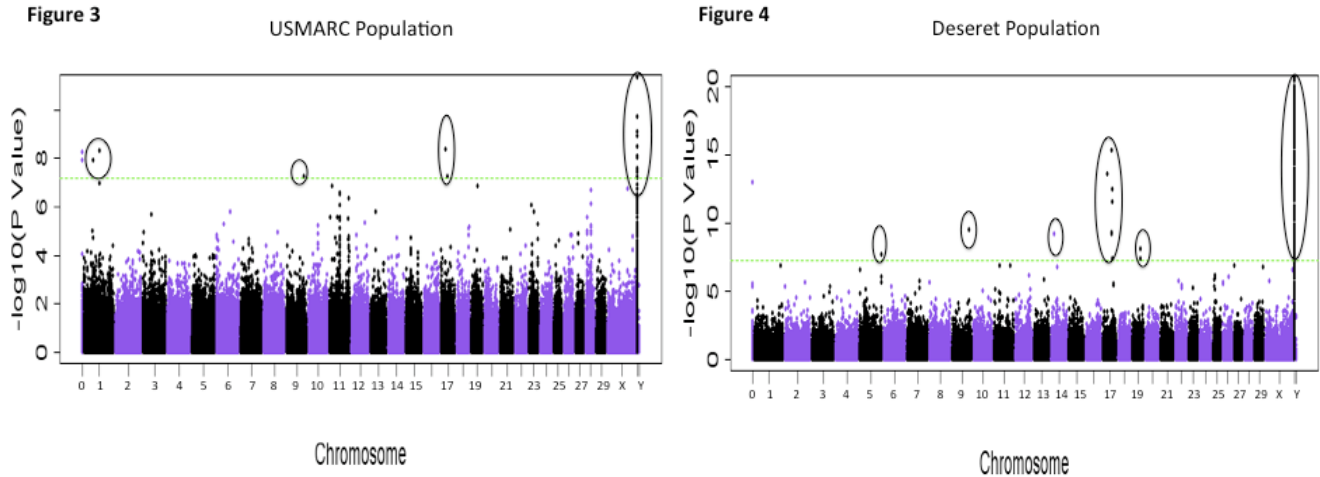
Additionally, **SNP on the Y chromosome** were identified to be associated with decreased reproductive efficiency in both the USMARC and Deseret populations **(Figure 3 and 4)**. The significance of Y was an unexpected result in the female populations, and was only associated with reproductive efficiency in the **open (00)** pools **(Figure 5)**. To assess these results, 10 Y SNP that were identified to be associated with reproduction were selected for further evaluation in individual animals that comprised each pool. Of the animals with low reproductive efficiency, 3-20% had at least 1 significant Y SNP. Additionally, none of the highly reproductive animals showed incidence of the Y SNP on an individual basis.

Figure 5 — Y SNP in the Deseret Populations

This research is the first to identify a group of Y SNP that can be used to evaluate breeding females for reproductive potential and as a result can select against those females with a greater propensity for reproductive failure.

From these results, producers will have a tool to identify replacement heifers that have no potential to rebreed and direct these females to a different management strategy.