

# Genomic Characterization of the McNay Angus Beef Cattle Herd

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### Summary and Implications

Recent calf crops and their sires and dams from the University Angus herd are currently being characterized for high-density SNP genotypes. Some 30 of the herd sires are being individually sequenced. This will be the first purebred beef herd to be so characterized and the data will aid many research and graduate teaching programs, and improve predictions of breeding performance at State and National levels.

### Introduction

The 400-cow purebred American Angus herd is run at the McNay R&D Farm in Lucas County and has been selected since 1996 for increased marbling. The herd has been a valuable resource for the collection of phenotypic data for use in both short- and long-term research. The herd has previously been used to research and showcase the use of ultrasound technology to select for marbling, to research the inheritance of pinkeye resistance, to research genetic variation in vaccine response, and to study the genetic basis of mineral and fatty acid concentrations in beef.

Selection is most effective when it is applied to rankings of animals based on statistical analysis of the performance of the selection candidates, their ancestors and other relatives. This information for ranking is known in the industry as Expected Progeny Differences (EPD) and from a multi-trait perspective is often weighted by economic values for each trait and combined into selection indexes.

The statistical method used to predict EPD takes non-genetic fixed effects such as year-season of birth, sex of calf and age of dam into account and is known as Best Linear Unbiased Prediction (BLUP). It determines the emphasis to place on relatives records based on the additive genetic variance-covariance matrix, which has traditionally been constructed from pedigree information. That method assumes average relationships, for example non-inbred half-sib offspring of the same sire would have a one-half share of the sires genome, but be expected to share one-quarter of their genes with another half sib. In reality, some half-sib pairs could share more than this while others share less.

Actual relationships can be determined by estimating the proportion of the genome shared in common, which can be carried out using DNA markers. The most common markers currently used are single-nucleotide polymorphisms (SNP) and these can be interrogated using high-density SNP chips.

Variation in performance does not result from variation in markers, but from causal changes to the genome, such as those that alter protein sequence or gene expression. Such variants can be catalogued using whole genome sequence (WGS) data that is becoming more effective to obtain on individuals using next generation sequencing (NGS).

### Materials and Methods

Entire calf crops recorded in the McNay herd in recent years will be high-density genotyped at GeneSeek using SNP chips comprising 20k markers (GGP-LD). Their sires and dams will be genotyped for 70k markers (GGP-HD). The data is now available on the first batch of samples.

Some 30 of the 65 sires that have been used in the herd in recent years will be WGS using NGS technology. The sequencing libraries are currently being prepared.

### Results and Discussion

The SNP data will allow us to accurately quantify the sharing of genome fragments between individuals that have been performance recorded in the McNay Angus herd. The sequence data will allow us to impute loss-of-function and other variants that have been inherited by different individuals. Collectively, this data will allow us to discover causal variants from genome-wide association studies (GWAS) and to more accurately predict the performance of selection candidates.

The McNay herd will be the first pure-bred beef cattle herd to be extensively characterized from a genomic perspective. The data will prove invaluable to many research projects and to the education of many graduate students.

### Acknowledgments

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