

Final Technical Report
FCEB Project #46

FINAL REPORT – Project # P0324619 (FCEB #46)

Percentage completion of project deliverables: 100%

Title: Using genomics to estimate heterosis effect on growth and carcass traits

Principle Investigator: Raluca G. Mateescu^{1*} (PD/PI), Co-PI: Fernanda Rezende

¹Department of Animal Sciences, University of Florida, Gainesville, FL 32611-0910.

*Email: raluca@ufl.edu; Tel: 352-392-2367

Relevance to Florida Cattle Industry: Crossbreeding is a common strategy used in tropical and subtropical regions to enhance beef production. Planned crossbreeding programs, such as two and three- breed rotations, have probably been used longer and more effectively in Florida than in any other part of the United States. The economic benefits obtained from a crossbreeding system can be great, but efficacy of the system depends upon the proper mating of cows to superior, unrelated bulls. Heterosis, which is one benefit of crossbreeding, arises from combining the genes from different breeds in such a way that inferior recessive genes are concealed. Heterosis may result in the crossbred being better than either parental breed or simply better than the average of the two. While the maximum heterosis is achieved in the first cross of purebred animals (F1), retained heterosis in subsequent matings is not accurately known.

This proposal will benefit the Florida Beef Cattle Industry by developing the resources needed to develop management tools for *Bos indicus* influenced cattle. Genomic technologies, such as marker assisted management, offer the opportunity to increase productivity (i.e. using genetic information for mating decisions where parents are selected to optimize the level of heterosis for specific traits). Developing a reliable method of predicting heterosis for crossbred beef cattle could improve the efficiency of crossbreeding and improve the accuracy of estimated breeding values (EBV) by accounting for non- additive genetic effects in the genomic evaluation model.

Objectives:

This proposal had three objectives:

- 1) Select a new set of 350 animals from our database: purebred Brahman, purebred Angus, and F1 (50%Brahman – 50%Angus) animals. Sequence the entire genome of these animals to provide a higher resolution of the genomic architecture.
- 2) Use the statistical method developed by our group to assign a breed of origin for all chromosomal fragments in a crossbred animal based on 250K high-density genotypes.
- 3) Estimate genomic heterosis based on the percentage of chromosomal fragments which have different breed origin along the genome. Existing commercial tests on the market can estimate heterozygosity which is a proxy of heterosis. Our method will provide a more accurate estimate of the true heterosis.

Results

Individual breed composition was estimated from genomic data using a maximum likelihood model implemented in the software ADMIXTUREv1. Since fractional subgroup membership is allowed, membership coefficients can also be conveniently interpreted as the proportion of an animals' genome with a particular breed ancestry. In addition to not requiring allele frequency estimates from external reference populations, this method allows inference on the correct number of ancestral populations, an important feature when the full range of parental breeds involved is not certain.

The approach that we developed to assign breed of origin to alleles of crossbred animals, consists of three steps: (1) phasing the genotypes of both purebred and crossbred animals, (2) assigning breed origin to the phased haplotypes, and (3) assigning breed origin to alleles of crossbred animals based on the library of assigned haplotypes, the breed composition of the cross-bred animals and the zygosity (i.e., homozygosity or heterozygosity).

The traditional heterosis is estimated at the population level. The formula for heterosis is based on the average of the crossbred animals and the average of the purebred animals for a particular trait of interest. This requires generation of crossbred (F1) animals and measuring the trait of interest on large numbers of both purebred and crossbred animals. Although this method generates a fairly accurate heterosis value for a particular trait, it doesn't allow an estimation of heterosis on an individual basis.

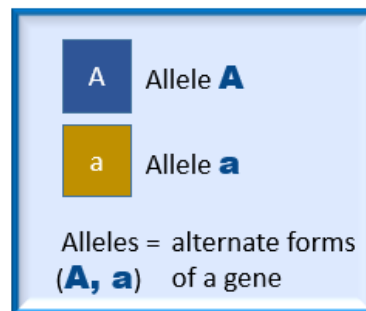
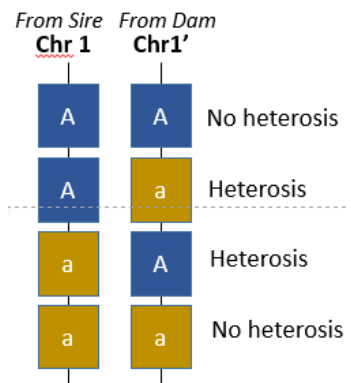


Figure 1. Using genomic information (250K genetic markers) we can calculate heterozygosity at the individual level as the percentage of markers in heterozygous state (Aa).

$$\text{HET} = 2/4 = .5$$

Estimate genomic heterosis based on the percentage of chromosomal fragments which have different breed origin along the genome. Existing commercial tests on the market can estimate heterozygosity which is a proxy of heterosis. Our method will provide a more accurate estimate of the true heterosis. More research is needed to be able to estimate the heterosis based on breed of origin information.

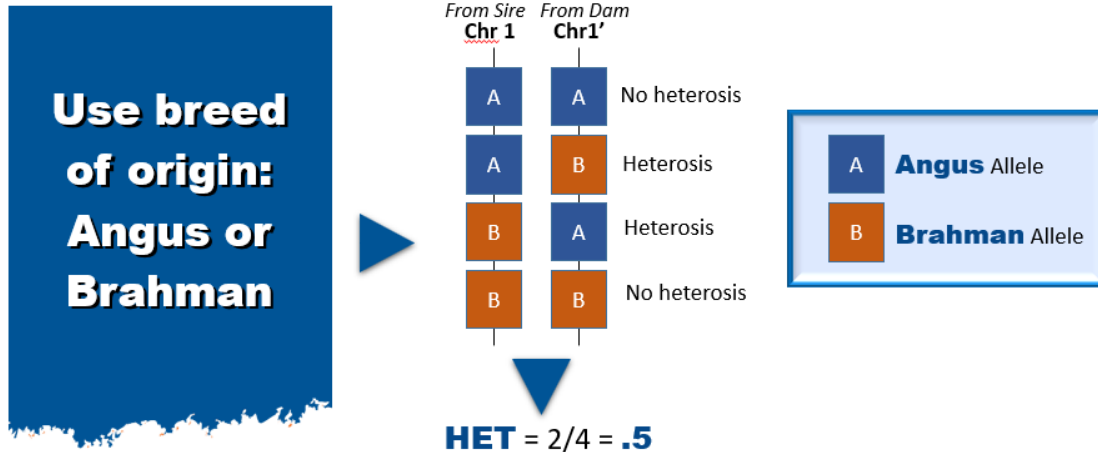
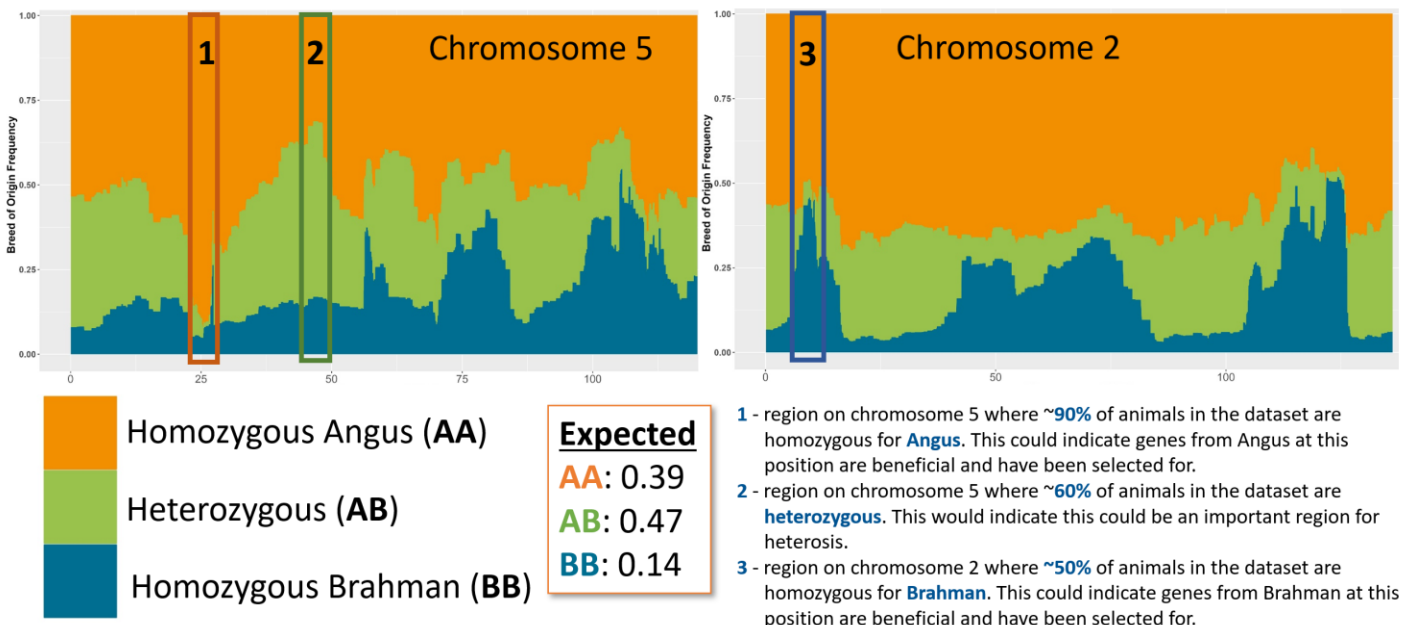


Figure 2. For a more accurate estimation of heterosis, the breed of origin (Angus or Brahman) for each allele at each of the 250K genetic markers has to be estimated. Using the breed of origin information, we can then calculate heterozygosity at the individual level as the percentage of markers in heterozygous state (one Angus allele and one Brahman allele).

Individual breed composition was estimated from genomic data using a maximum likelihood model implemented in the software ADMIXTUREv1. The approach that we developed to assign breed of origin to alleles of crossbred animals, consists of three steps: (1) phasing the genotypes of both purebred and crossbred animals, (2) assigning breed origin to the phased haplotypes, and (3) assigning breed origin to alleles of crossbred animals based on the library of assigned haplotypes, the breed composition of the crossbred animals and the zygosity (i.e., homozygosity or heterozygosity).



PLEASE REMIT TO:

UNIVERSITY OF FLORIDA BOARD OF TRUSTEES
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 PO Box 931297
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Invoice Date: 08/15/2024
 Invoice Period: 05/01/2024 - 07/31/2024
 Principal Investigator: Mateescu,Raluca
 Award Begin Date: 10/30/2023
 Award End Date: 07/31/2024

SPONSOR:

FL CATTLE ENHANCEMENT BOARD
 P.O. Box 421929
 Kissimmee FL 34742-1929
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UF FEIN: 59-6002052

Sponsor Award ID: 46
 Award Title: Using genomics to estimate heterosis effect on growth and carcass traits
 Award Amount: \$46,863.00

Invoice #	1000130488
UF Award #	AWD15803
Primary Project #	P0324619
Primary Department:	60090000
Current Invoice Amount:	\$34,016.02

Description	Current	Cumulative
Personnel - Salary	(\$4,430.89)	\$0.00
Personnel - Fringe Benefits	(\$522.85)	(\$0.04)
Other Expenses	\$35,325.18	\$41,829.93
Direct Cost	\$30,371.44	\$41,829.89
Facilities and Administrative Costs	\$3,644.58	\$5,019.59
Total	\$34,016.02	\$46,849.48

For billing questions, please call 352.392.1235
 Torres,Kannika S kannika@ufl.edu
 Please reference the UF Award Number and Invoice Number in all correspondence

By signing this report, I certify to the best of my knowledge and belief that the report is true, complete, and accurate, and the expenditures, disbursements and cash receipts are for the purposes and objectives set forth in the terms and conditions of the federal award. I am aware that any false, fictitious, or fraudulent information, or the omission of any material fact, may subject me to criminal, civil, or administrative penalties for fraud, false statements, false claims or otherwise. (U.S Code Title 18, Section 1001 and Title 31, Sections 3729-3730 and 3801-3812).

Kannika Torres

 Certifying Official

Payment History	
Cumulative Invoices:	\$46,849.48
Payments Received:	\$12,833.46
Outstanding Balance:	\$34,016.02
Note: Outstanding balance includes current invoice amount	

FOR UF USE ONLY			Additional Projects: N	
Project ID	Deptid	Department Name	Current	Cumulative
P0324619	60090000	AG-ANIMAL SCIENCES	\$34,016.02	\$46,849.48