

# UF-Gainesville Beef Cattle News Corner

## Predicting breed composition from genetic marker information

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### Introduction

Crossbreeding is a common strategy used in tropical and subtropical regions to enhance beef production and this is evident with our beef cattle in the state of Florida. Having accurate knowledge of breed composition is essential for the success of a crossbreeding program. Although pedigree records have been traditionally used to obtain the breed composition of crossbred cattle, inaccurate and/or incomplete records and other factors such as Mendelian sampling (see [Figure 1](#)) can reduce the accuracy of pedigree-based breed composition.

Our group at University of Florida (UF) has been tackling this problem with the goal of developing the strategy and the tools to predict breed composition accurately. Research funding from Florida Beef Council and FL Cattlemen Enhancement Fund allowed genotyping of a large number of animals from the UF purebred Brahman herd and UF Multibreed herd (population of animals ranging from 100% Angus to 100% Brahman, with historic pedigree data, growth, production, reproduction and meat quality information). Research funding and collaborations with the Seminole Tribe of Florida, along with funding from USDA-NIFA allowed genotyping of thousands of commercial Brangus animals.

Animals in these populations were genotyped with the 250K SNP chip (assay for genotyping 250,000 genetic markers). The initial study was conducted in the UF Multibreed herd where we have extensive pedigree information and a perfect breed composition structure for this type of study (gradient from 100 – 0% Brahman and Angus). The main result of the study was the development of a statistical method to predict breed composition strictly from genomic data. Breed composition estimation from genomic data has higher accuracy as missing, incomplete or inaccurate pedigree records do not affect it and it accounts for a substantial proportion of Mendelian sampling. Last year, our group published the results of this research in an article in the “Frontiers in Genetics” journal (Population Structure and Genomic Breed Composition in an Angus–Brahman Crossbred Cattle Population) where we presented a new method to accurately predict breed composition using genomic data. Because of its high accuracy, genomic breed composition methodology can be used as independent authentication of breed in breed-labeled beef products.

One disadvantage of using genomic data to determine breed composition is the cost of genotyping, but this cost has been declining and, as genetic and genomic methods are becoming widely adopted and increasingly accessible, it is likely to decrease even more in the future. Only genotyping breed-informative markers can also further reduce the genotyping cost. This has been the focus of our research since this method has been developed and we were able to identify a small number of carefully selected breed-informative markers to predict breed composition. Our work contributed to the development of a breed composition product which will be released soon for certain composite breeds.

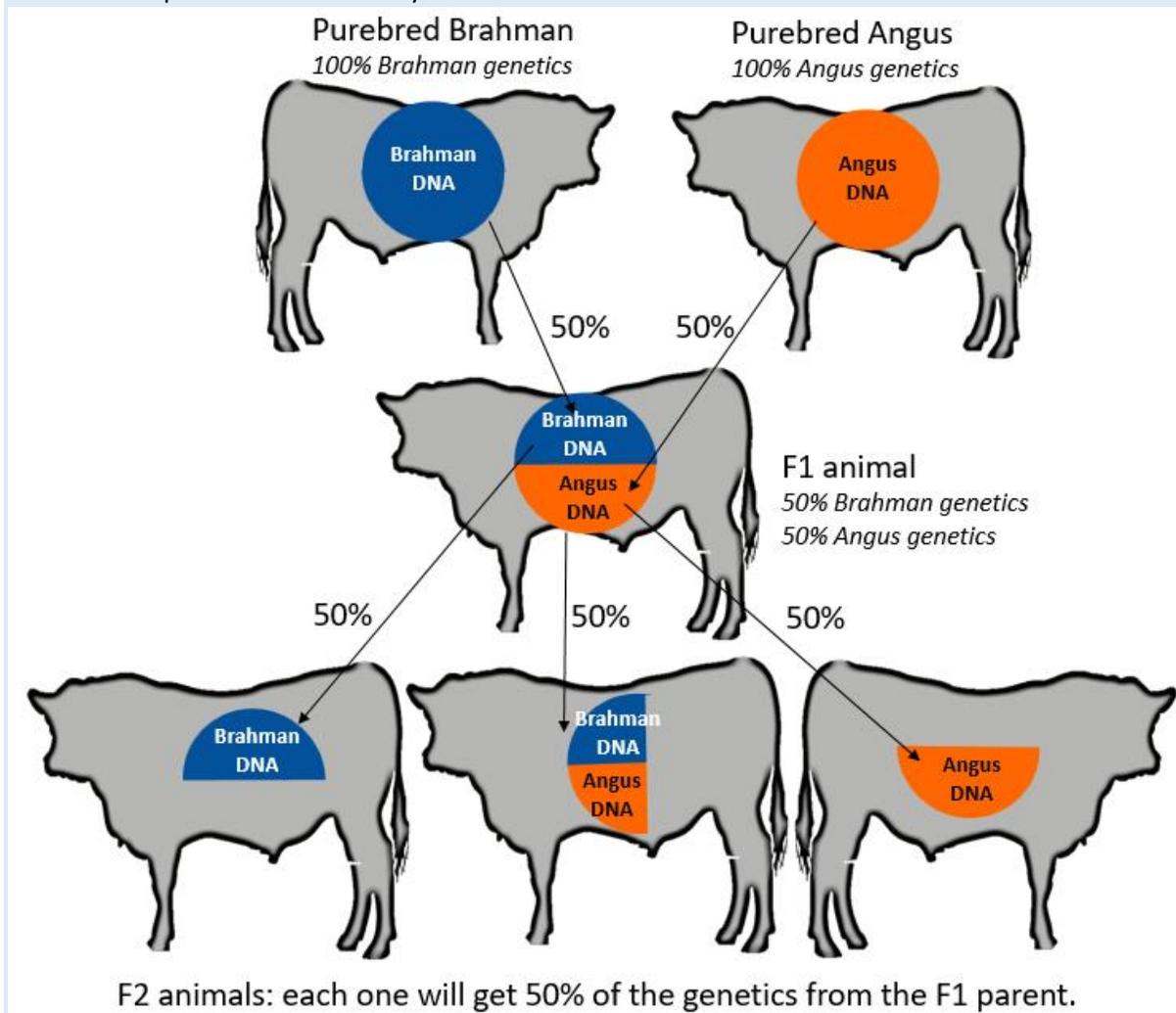
An additional and interesting result from our study was the ability to infer the distance of animals from a first-generation crossbred animal. This could be of particular importance for composite breeds like Brangus, where producers might be interested in knowing how far away certain animals are from a first-generation Brangus. In the UF Multibreed population we do have a specific breed group of Brangus animals ranging from first-generation to multi-generation ([Figure 2](#)). The ability to determine this composite breed progression will be important for producers interested in knowing if they are losing heterosis in their animals. More information on the possibility to use genomics to estimate heterosis in

composite breeds such as Brangus will come soon – but for now it is important to point out that information on breed composition will not indicate the level of heterosis.

Article published in *The Florida Cattleman & Livestock Journal*, May 2019

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**Figure 1.** Mendelian sampling – fancy name for a simple genetics concept. An offspring will always get half of its genetics from the mother and half from the father. In crossbreeding, and F1 offspring will always get EXACTLY 50% of the genetics from each breed (parent). However, offspring resulting from any matings involving the F1 will have varying % from the initial breed. In this diagram you can see that F2 will get 50% of genetics from the F1 (the other half would come from the other parent). However, the half the F2 gets from the F1 can range in breed composition all 50% Brahman genetics to all 50% Angus genetics. In the pedigree calculation, the F2 progeny will be assumed to have received 25% Brahman and 25% Angus genetics from the F1 parent. Therefore, pedigree estimations of breed composition can be widely inaccurate.



**Figure 2.** Plot of UF Multibreed animals ranging from 100% Brahman (dark blue dots on the left side of the graph) to 100% Angus (purple dots at the right end of the graph). First generation Brangus (brown circles) align close to the vertical blue line connecting purebred Brahman and purebred Angus. Brangus cattle from one or more generations of Brangus–Brangus matings (big red dots) will align on the vertical red line, with the higher generation Brangus animals further away from the vertical blue line.

