UF-Gainesville Beef Cattle News Corner

**Genomic heterosis estimation in crossbred cattle.**

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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.

Our UF research group has a strong interest in developing a reliable method of predicting heterosis for crossbred beef cattle. With financial support from the Florida Cattlemen Enhancement Fund and Town Creek Farm, we were able to start this work and develop a statistical method to assign a breed of origin for all chromosomal fragments in a crossbred animal. We used animals from the University of Florida (UF) Multibreed Angus-Brahman herds. High density 250K genotypes (GeneSeek GGP250k chip) on more than 1,500 DNA samples from the multibreed herd were already available for this project. Breed composition for each animal on this population was estimated using a procedure developed by our group. Three groups of animals with phenotypic data were then selected for subsequent analyses: purebred Angus (>90% Angus, N = 152), F1 (49%-51%Angus, N = 36) and purebred Brahman (>90 Brahman, N = 341).

Breed-of-origin heterozygosity was calculated for each animal using the breed-of-origin assignment of chromosomal fragments based on a statistical algorithm developed by our UF group. Genotypes for purebred Angus and purebred Brahman animals (>99%) were used as reference for calling chromosomal segments originating from either Brahman or Angus genome. Similar to the genotypic data, for one specific chromosomal segment, an animal could be homozygous for the Angus allele (AA), heterozygous (AB) or homozygous for the Brahman allele (BB). These are called breed-of-origin genotypes. Heterozygosity for all animals was calculated from the breed-of-origin genotypes (breed-of-origin heterozygosity). This represents the percentage of heterozygous alleles (Aa or AB) out of all alleles across the entire genome in an individual.
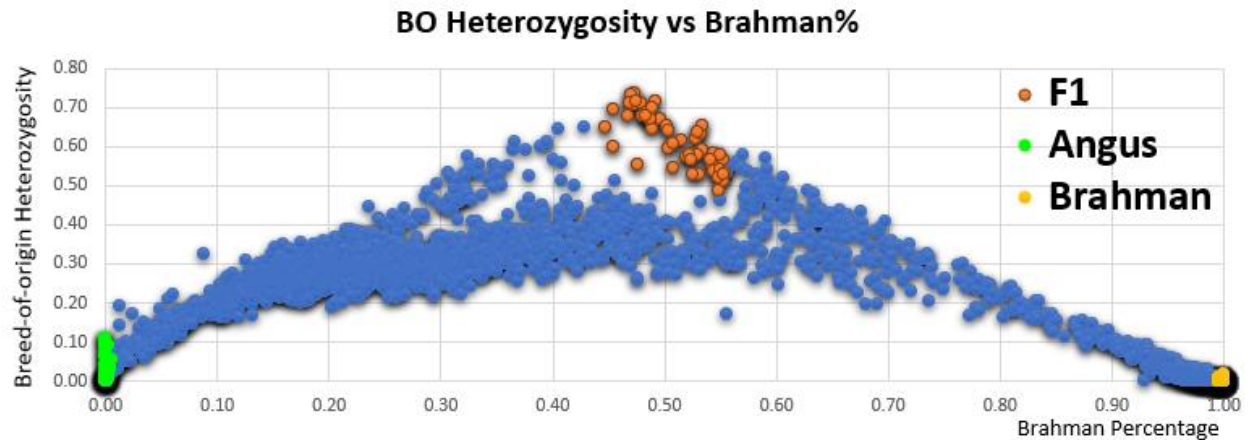
Figure 1. *Breed-of-origin (BO) heterozygosity across the UF multibreed population* ranging from 100% Angus (green dots left side) to 100 Brahman (yellow dots, right side). The breed-of-origin heterozygosity increases as the purebred % decreases from 100 to 50% and reaches a maximum in the F1s. However, more variation is observed in the breed-of-origin indicating this measure would provide a higher resolution for differentiating different level of heterozygosity in the crosses.

We expected an increase in heterozygosity in crossbred animals compared with purebred and this can be observed in **Figure 1**. The heterozygosity reaches a maximum in the F1 animals. However, a great amount of variation is observed in the group ranging from 45-55% Angus/Brahman (F1 animals). It is also interesting to notice that this variation is related to the number of generations of these animals, with the first generation F1 (produced from crossing purebred Angus x purebred Brahman) have the highest genotypic heterozygosity (orange dots, middle top). This indicates that the genotypic heterozygosity could be used as an indicator of the distance from the first cross of crossbred animals.