

# **Genomic EBV for reproduction traits in beef cattle ranging from 100% Brahman to 100% Angus**

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## **Introduction**

Florida beef cattle operations routinely perform the task of choosing replacement heifers to be added to the breeding cow herd. Identification of sexually mature heifers is particularly important for reproduction strategies involving estrous synchronization and seasonal matings that require cows to calve once a year. Reproductive tract score, an indirect measure of sexual maturity that is positively correlated with yearling weight, can be used to identify early maturing heifers instead of directly measuring age at puberty. Two other important reproduction traits are age at first calving and first calving interval. These traits can be effectively used to identify fertile early maturing replacement heifers and reduce age at first calving in Brahman and Brahman influenced cattle under Florida subtropical environmental conditions.

Thus, the objectives of this study were to compute heritabilities and to compare genomic estimated breeding values (genomic EBV) for yearling weights (YW; n = 1,758), yearling reproductive tract score (RTS; n = 381), age at first calving (AFC; n = 1,082), and first calving interval (FCI; n = 387) in cattle ranging from 100% Angus to 100% Brahman belonging to the Angus-Brahman multibreed herd from the University of Florida. Animals used in this research were under feeding and management conditions comparable to those in commercial beef operations in Florida. The breeding protocol consisted of an initial period of estrous synchronization (progesterone CIDR followed by a Lutalyse injection) and artificial insemination followed by a period of natural service of 60 days. Genomic EBV were obtained using production records (YW, RTS, AFC, and FCI), pedigree records, and genotype records. Animals with genotypes (n = 1,547) contained information on 115,711 actual and imputed single nucleotide polymorphisms (SNP).

## Results

Table 1 shows numbers of animals and means for YW, RTS, AFC, and FCI by breed group and total. Breed groups are defined as follows: BG1 = 100% A to (80% A 20% B); 2) BG2 = (60% A 40% B) to (79% A 21% B); 3) BG3 = Brangus = (62.5% A 37.5% B); 4) BG4 = (40% A 60% B) to (59% A 41% B); 5) BG5 = (20% A 80% B) to (39% A 61%B); and 6) BG6 = (19% A 81% B) to 100% B; where A = Angus, B = Brahman.

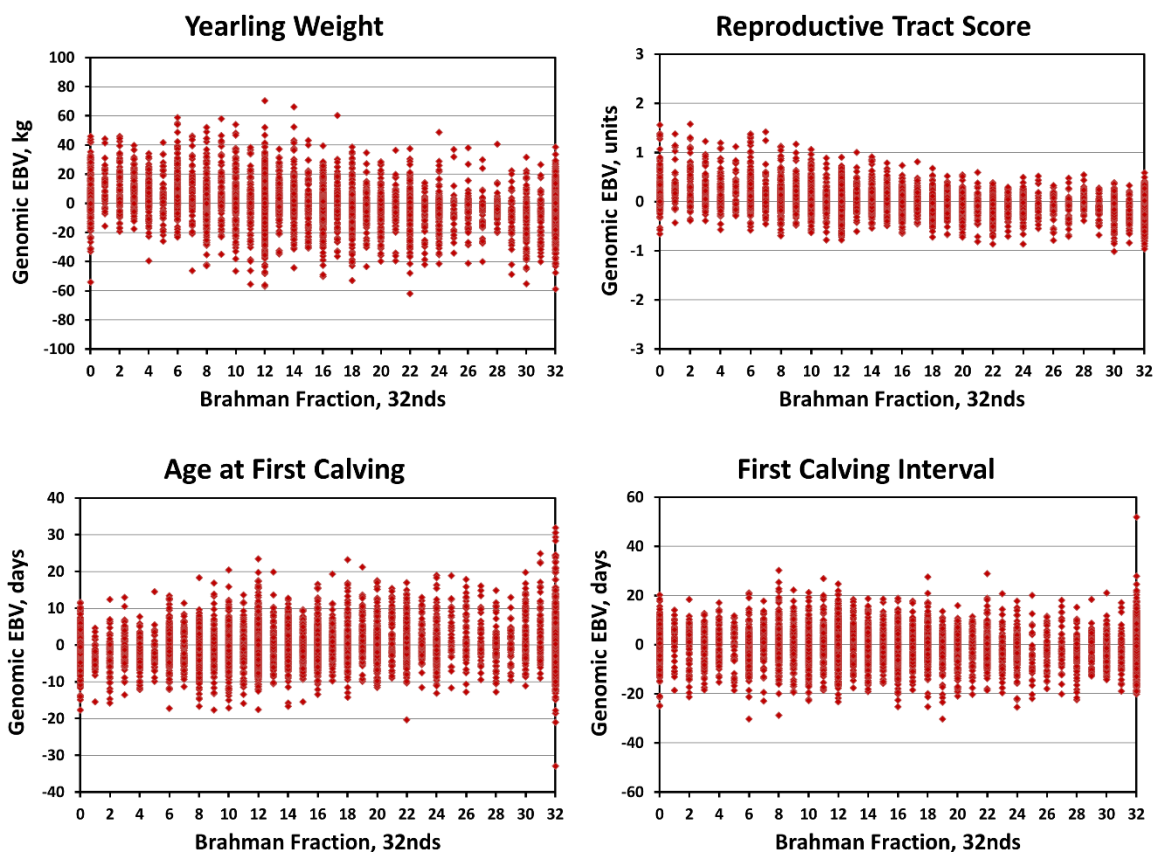
**Table 1.** Numbers of calves, means and standard deviations per breed group and total.

Breed group	Trait							
	YW, kg		RTS, units		AFC, days		FCI, days	
	N	Mean	N	Mean	N	Mean	N	Mean
<b>BG1</b>	251	354	62	3.6	180	1,078	143	390
<b>BG2</b>	286	366	42	3.5	218	1,083	162	388
<b>BG3</b>	250	358	37	2.8	164	1,081	116	389
<b>BG4</b>	380	364	63	3.2	363	1,084	263	385
<b>BG5</b>	196	355	46	2.7	205	1,087	129	379
<b>BG6</b>	395	322	131	2.4	255	1,078	172	390
<b>Total</b>	1,758	352	381	2.9	1,385	1,082	985	387

Heritabilities were equal to 0.47 for YW, 0.31 for RTS, 0.14 for AFC, and 0.31 for FCI. Values of heritability were medium to high for all traits. This means that selection for these 4 traits using genomic EBV would change the population of animals in the desired direction. Traits with higher heritability such as YW and RTS would change faster than traits with lower heritability such as AFC.

Genomic EBV for YW, RT, AFC, and FCI are presented in Figure 1, where each red diamond is the genomic EBV of a single animal. Animals with Brahman fraction equal to 0 are 100% Angus, animals with Brahman fraction equal to 32 are 100% Brahman, animals with Brahman fraction equal to 12 are Brangus, and the remaining animals are crossbreds

of other Angus and Brahman fractions (e.g., 22 is an animal that is 22/32 Brahman and 10/32 Angus). Figure 1 clearly shows that there is an enormous amount of variation among genomic EBV in the Angus-Brahman multibreed population. More importantly, the range of genomic EBV is similar across animals of all Brahman fractions, including purebred Brahman. This fact, along with the medium-high heritabilities, indicates that selection for these 4 traits is feasible in this population. Considering that the Angus-Brahman herd is a one-herd representation of the type of Brahman, Brangus, Angus, and Brahman-Angus crossbred animals present in Florida, we would expect within-herd selection for these 4 traits in private herds to be effective at increasing yearling weights and decreasing age at puberty, age at first calving, and calving interval in the state-wide Florida population.



**Figure 1.** Genomic EBV for yearling weight, reproductive tract score, age at first calving, and calving interval in animals with Brahman fraction ranging from 0% (purebred Angus) to 100% (purebred Brahman)

This research was published in Livestock Science in 2016. The complete publication can be viewed at <http://animal.ifas.ufl.edu/elzo/publications/refereed/index.shtml>.