Livestock Science 175 (2015) 18–26

Contents lists available at ScienceDirect

Livestock Science

journal homepage: www.elsevier.com/locate/livsci

Genomic–polygenic evaluation of multibreed Angus–Brahman cattle for postweaning ultrasound and weight traits with actual and imputed Illumina50k SNP genotypes

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ARTICLE INFO

Article history:
Received 15 April 2014
Received in revised form
24 February 2015
Accepted 3 March 2015

Keywords:
Beef
Imputation
Multibreed
Ultrasound

ABSTRACT

The objectives were to estimate additive genetic variance fractions for 4 postweaning ultrasound and weight traits explained by 46,839 actual and imputed SNP genotypes, to compare rankings of calf additive genetic predictions from genomic–polygenic (GP), genomic (G), and polygenic (P) models, and to assess trends for GP, G, and P predicted additive genetic values as functions of calf Brahman fractions in a multibreed Angus–Brahman population. Traits were postweaning ultrasound ribeye area (UREA), backfat thickness (UBF), and percent intramuscular fat (UPIMF), and weight (UW). Phenotypes and Illumina3k genotypes were from 812 bull, heifer, and steer calves housed at the Feed Efficiency Facility of the University of Florida from 2006 to 2010. Program Findhap2 was used to impute from 2899 Illumina3k SNP to 46,839 Illumina50k SNP using a reference population of 828 Brangus heifers. Fixed effects for all models were contemporary group (year-pen), age of dam, sex of calf, age of calf, Brahman fraction of calf, and heterozygosity of calf. Random effects were additive SNP (GP and G models), additive polygenic (GP and P models), and residual. Software GS3 was used to compute variance components and heritabilities, and additive genetic predictions. Additive genetic variance fractions explained by the 46,839 actual and imputed SNP were 0.17 for UREA, 0.32 for UBF, 0.25 for UPIMF, and 0.19 for UW. Heritabilities were 0.33 for UREA, 0.22 for UBF, 0.43 for UPIMF, and 0.54 for UW. These additive genetic variance fractions were 1.8, 1.0, 4.4, and 2.1 times greater and heritabilities were 1.0, 1.2, 1.0, and 1.2 times greater than those obtained for these 4 traits using only the 2899 Illumina3k SNP. Rank correlations between EBV from GP and P models were the highest (0.93 to 0.96), followed by those between EBV from GP and G models (0.81 to 0.94), and by those between EBV from G and P models (0.66 to 0.81). Regression coefficients of EVB on Brahman fraction were small for all traits and models indicating that animals of comparable EBV existed in all breed groups. Imputation from Illumina3k to 50k increased the explained fraction of additive SNP variance resulting in higher rank correlations between additive genetic predictions from G and GP, and from G and P models for all ultrasound traits in this Angus–Brahman multibreed population.

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http://dx.doi.org/10.1016/j.livsci.2015.03.002
1871-1413/

1. Introduction

Brahman and Brahman-*Bos taurus* crossbred cattle are widely used in Florida and other subtropical regions of the United States because of their superior adaptability to hot and humid climatic conditions. However, Brahman and high-percent crossbred Brahman cattle tend to have smaller ribeye areas, less marbling, and lower tenderness than *B. taurus* cattle (Elzo et al., 2012a; Johnson et al., 1990; Pringle et al., 1997; Wheeler et al., 2010), hence the pressing need for accurate genetic predictions for carcass traits in Brahman and Brahman-*B. taurus* crossbred populations. Although high cost has restricted the availability of carcass data, ultrasound carcass measurements are widely used because they are cheaper, easier to measure, and closely associated with carcass traits (Houghton and Turlington, 1992). Genotypic data from low and high density SNP chips could also be used to help increase accuracies of prediction for carcass traits. However, the cost of high-density chips likely remains an issue for most beef production systems. Thus, a combination of low and high-density chips plus imputation (Dassonneville et al., 2011; Khatkar et al., 2012; Sargolzaei et al., 2011a, b, c; VanRaden et al., 2011, 2013; Weigel et al., 2010) may be a cost-effective alternative to the use of high-density chips throughout a population. Consequently, the objectives of this research were: (1) to estimate fractions of additive genetic variances for postweaning ultrasound ribeye area (UREA), backfat thickness (UBF), percent intramuscular fat (UPIMF), and weight (UW) explained by 46,839 actual and imputed SNP genotypes, (2) to compare rankings of calf additive genetic predictions from genomic–polygenic (GP), genomic (G), and polygenic (P) models, and (3) to assess trends for GP, G, and P predicted additive genetic values as functions of Brahman fractions in a multibreed Angus–Brahman population.

2. Materials and methods

2.1. Animals, feeding, and management

The research protocol for this project was approved by the University of Florida Institutional Animal Care and Use Committee (IACUC protocol number 201003744). Calves were from the multibreed Angus–Brahman (MAB) herd of the University of Florida, Gainesville. A total of 812 calves (66 bulls, 413 heifers, and 333 steers) born from 2006 to 2010 were used in this study. Calves were the offspring of 64 sires from 6 breed groups mated to 364 dams from these same 6 breed groups according to a diallel mating design (Elzo and Wakeman, 1998). Breed groups were as follows: Angus=(1.0 to 0.80) A (0.0 to 0.20) B, 3/4 A 1/4 B=(0.79 to 0.60) A (0.21 to 0.40) B, Brangus=(0.625) A (0.375) B, 1/2 A 1/2 B=(0.59 to 0.40) A (0.41 to 0.60) B, 1/4 A 3/4 B=(0.39 to 0.20) A (0.61 to 0.80) B, and Brahman: (0.19 to 0.0) A (0.81 to 1.00) B. Numbers of calves per breed group were 121 Angus, 163 3/4 A 1/4 B, 143 Brangus, 192 1/2 A 1/2 B, 87 1/4 A 3/4 B, and 106 Brahman calves. Calves were reared at the Beef Research Unit (BRU) of the University of Florida from birth to weaning. Calves received a preconditioning diet for 3 to 4 wk postweaning before moving to the University of Florida Feed Efficiency Facility (UFFEF) in Marianna, Florida. The preconditioning diet consisted of concentrate (1.6 kg to 3.6 kg/d; 14.0% CP; 488 Pellet, Medicated Weaning Ration, Lakeland Animal Nutrition, Lakeland, Florida; and soy hull pellets), ad libitum mineral supplement, and bahiagrass (*Paspalum notatum*) hay. Upon arrival to UFFEF, calves were identified with half-duplex passive transponder ear tags (Allflex USA Inc., Dallas-Fort Worth, TX). The feed efficiency trial at UFFEF consisted of an adjustment period of 21 d and a trial period of 70 d. Calves from each sire group (Angus, 3/4 A 1/4 B, Brangus, 1/2 A 1/2 B, 1/4 A 3/4 B, and Brahman) by sex (bull, heifer, and steer) category were randomly allocated to pens (108 m^2/pen; 2 GrowSafe nodes per pen; mean stocking rate=15 calves/pen; 7.5 calves/GrowSafe node). The components of the ad libitum ration at UFFEF were whole corn or corn gluten, cottonseed hulls, molasses, chopped grass hay, and a vitamin–mineral–protein supplement. Average values of dry matter, crude protein, net energy for maintenance, and net energy for gain were 89.2%, 12.9%, 1.6 mcal/kg DM, and 1.0 mcal/kg DM from 2006 to 2010, respectively.

2.2. Traits

Traits were postweaning ultrasound ribeye area (UREA, cm^2), ultrasound backfat thickness (UBF, cm), ultrasound percent of intramuscular fat (UPIMF, %), and body weight on the day that ultrasound measurements were taken (UW, kg). Ultrasound traits were measured by a certified technician using an Aloka 500 ultrasound system (Hitachi Aloka Medical, Ltd., Wallinford, Connecticut, USA) at the conclusion of the 70-d feed efficiency trial. Phenotypic data for UREA, UBF, and UPIMF were obtained by analyzing the ultrasonic images with UICS Scanning Software by Walter and Associates, LLC (Ames, Iowa, USA).

2.3. Tissue sampling, genotyping, and imputation

Blood samples were collected at weaning using 10 mL EDTA vacutainer tubes. Samples were processed at New Mexico State University (NMSU) and stored at −80 °C. Processing consisted of centrifugation for 30 min at 1875*g* at 4 °C, recovery of white blood cell supernatant, and addition of sterile phosphate-buffered saline up to a volume of 1.0 mL (Beauchemin et al., 2006). Subsequently, genotyping with the Illumina3k (Illumina, Inc., 2011a) was done at GeneSeek (Gene Seek, Inc., Lincoln, NE, USA). Imputation from the Illumina3k to the Illumina50k (Illumina, Inc., 2011b) was done with program Findhap2 (VanRaden, 2011) using a reference population (RP) of 828 registered Brangus heifers (Fortes et al., 2012; Peters et al., 2012, 2013) genotyped with version 1 of the Illumina50k chip. Relationships among animals within MAB and RP were accounted for. However, pedigree data relating animals from the MAB and RP populations were unavailable. Consequently, MAB animals were assumed to be unrelated to RP animals. The combined MAB-RP pedigree file had 8720 animals (6674 from MAB and 2046 from RP).

The SNP markers from the Illumina3k (n=2900) were matched to a subset of SNP markers in common in