

193. Genetic architecture of a composite beef cattle population

E. Hay^{1*}, S. Toghiani², A.J. Roberts¹, T. Paim³, L.A. Kuehn⁴ and H.D. Blackburn⁵

¹USDA Agricultural Research Service, Fort Keogh Livestock and Range Research Laboratory, Miles City, MT 59301, USA; ²USDA Agricultural Research Service, Beltsville Agricultural Research Center, Beltsville, MD, 20705, USA; ³Instituto Federal de Educação, Ciência e Tecnologia Goiano, Campus Rio Verde, Rio Verde, Goiás, Brazil, 76200-000; ⁴USDA, Agricultural Research Service, US Meat Animal Research Center, Clay Center, 68933, USA; ⁵National Animal Germplasm Program, USDA, Fort Collins, CO, 80521, USA; elhamidi.hay@usda.gov

Abstract

In this study, genomic information was used to evaluate the genetic composition and characteristics of a composite beef cattle population. This composite population consisted of 50% Red Angus, 25% Charolais, 25% Tarentaise. The results showed an increase in the proportion of Tarentaise to approximately 57% while Charolais decreased to approximately 5%, and Red Angus decreased to 38%. Evaluating runs of homozygosity showed the formation of new haplotypes in the composite population around the sixth generation. The study showed that progenitor combinations are not stable over generations and that either direct or natural selection plays a role in modifying the proportions. Furthermore, the results showed that Tarentaise contributed useful attributes to the composite in a cool semi-arid environment and suggests a re-exploration of this breed's role may be warranted.

Introduction

Composite breeds are traditionally developed by combining two or more breeds that have complementary traits. In 1979, the USDA Agricultural Research Service's station in Miles City, Montana, US developed a composite population using *Bos taurus* breeds with distinct production characteristics. For this cold semi-arid environment, a three-breed composite (50% Red Angus, 25% Charolais, 25% Tarentaise) was formed to evaluate its performance in a limited nutrient production system. In brief, the CGC was started with breeding 300 Red Angus dams to either 14 Charolais sires or 12 Tarentaise sires using artificial insemination. The F₁ individuals were produced between years 1980 to 1984. Crossing of F₁ individuals began in 1981 and F₂ individuals were generated from 1982 until 1988. The F₃ generation was produced between 1984 and 1990. With this mating plan the CGC effective population size was computed to be 95.7. Subsequent generations have been produced since 1987.

The objective of this study was to evaluate the genetic composition of CGC, if changes have occurred, what parental populations were favored/disfavored and given the small population size can it adequately be a research model for composite beef populations.

Materials & methods

The dataset consisted of a total of 248 animals, where 10 were founder crosses to form CGC, 69 were CGC, 61 Red Angus, 79 Charolais and 29 Tarentaise. The ten early founder crosses were born in 1980 and were 50% Charolais and 50% Red Angus or 50% Tarentaise and 50% Red Angus. The CGC animals were born between 1986 and 2017. All animals were genotyped with High-density SNP panel (777,962 SNP, BovineHD Beadchip, Illumina, San Diego, CA, USA). Markers with minor allele frequency lower than 1% were removed. In addition, markers with a call rate lower than 95% or not physically mapped to the bovine genome assembly UMD3.1 were discarded from the analyses. Markers on sex chromosomes were also removed, the final number of SNP genotypes used was 203,297.

To evaluate the genetic relationship between the pure breeds and CGC, principal component and ADMIXTURE (Alexander *et al.* 2009) analyses were conducted. Additionally, runs of homozygosity (ROH) analysis was conducted using PLINK (Purcell *et al.* 2007). The parameters were set to be a minimum run length equal to 1 Mb with a minimum of SNP markers calculated using the equation in Lencz *et al.* (2007) and allowing runs to contain up to two heterozygotes and five missing genotypes with a maximum gap equal to 50 kb and a minimal SNP density of 1 SNP per 50 kb.

Results

The principal components analysis showed population divergence with CGC clustered intermediately among the progenitor breeds (Figure 1). Furthermore, the progenitor breed proportions of CGC animals were estimated by ADMIXTURE and evaluated according to the generation number. The results showed decreased proportions of Charolais and Red Angus and an increase in Tarentaise in subsequent generations of CGC. As shown in Figure 2, there was an increase in the proportion of Tarentaise to approximately 57% while Charolais decreased to approximately 5%, and Red Angus decreased to 38%.

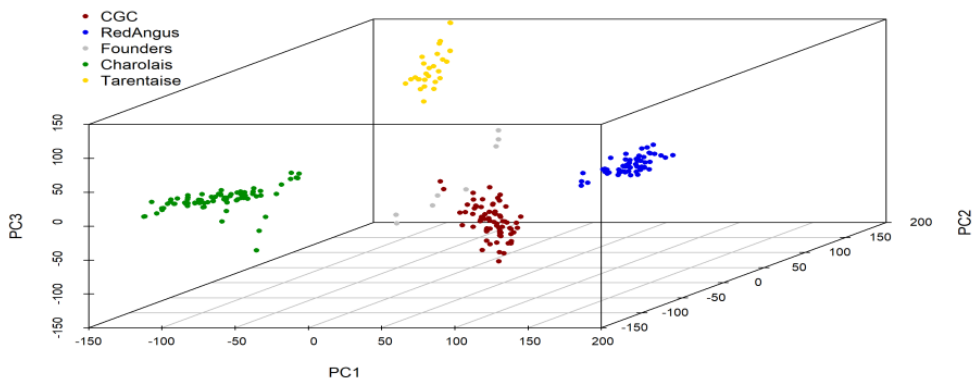


Figure 1. PCA plot for CGC founders, CGC, Red Angus, Charolais and Tarentaise.

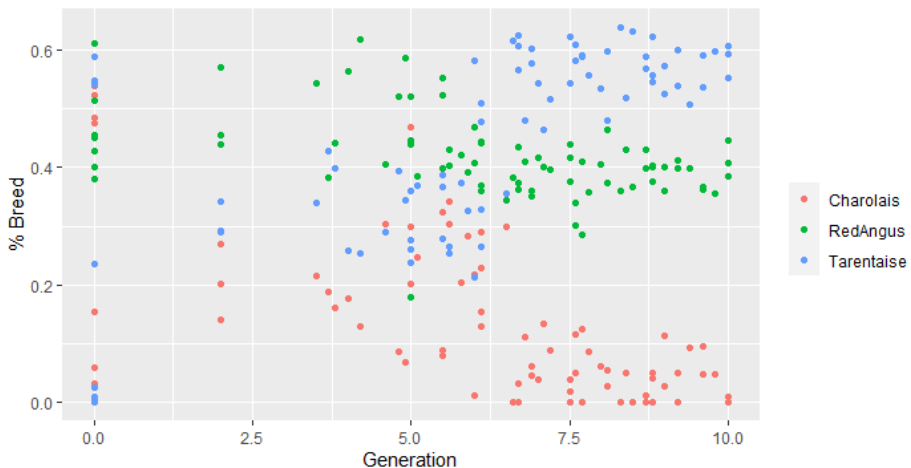


Figure 2. Genomic breed composition of CGC animals according to their equivalent generation number using Admixture analysis.

The ROH analysis showed Red Angus to have the highest number of ROH per animal and the longest total length of ROH (Table 1). Additionally, runs of homozygosity were classified according to the expected number of prior generations tracing back to a common ancestor. Figure 3 shows the change in the average ROH length according to the equivalent generation number of animals. Around the sixth-generation formation of longer ROH was observed.

Table 1. Summary description of the number, individual and total length of ROH segments (in Mb) per animal.

Parameters ¹	Breeds	Mean	SD	Min	Max
ROH _n	CGC	40.76	10.86	2	65
	Charolais	45.21	9.80	19	78
	Red Angus	92.26	12.09	70	127
	Tarentaise	70.72	10.99	50	98
ROH _L	CGC	3.33	3.60	1	55.41
	Charolais	3.70	4.40	1	100.54
	Red Angus	3.79	3.99	1	85.66
	Tarentaise	2.97	3.22	1	52.87
ROH _{T_L}	CGC	141.10	56.93	4.55	262.47
	Charolais	172.46	88.49	37.99	525.16
	Red Angus	349.92	81.52	226.98	738.47
	Tarentaise	209.27	44.21	115.42	304.64

¹ ROH_n = number of individual ROH segments per animal, ROH_L = length of individual ROH segments in Mb, ROH_{T_L} = total length of ROH segments in Mb per animal.

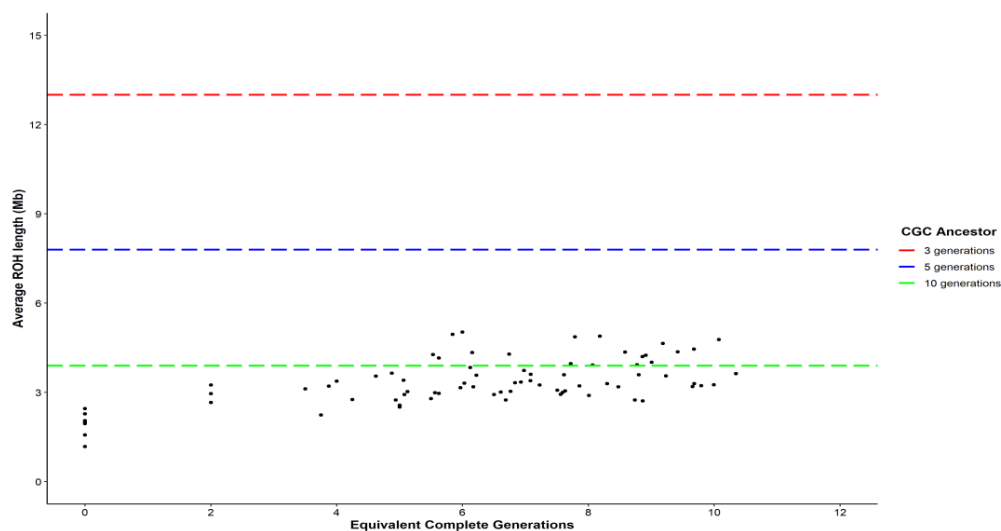


Figure 3. Runs of homozygosity observed in CGC cattle according to the equivalent generation number. Dashed lines indicate the length threshold for ROH that relates to a common ancestor at 3, 5, and 10 prior generations (red, blue, and green, respectively).

Discussion

Our results suggest several points about composite population development and potential use. As with other studies (Blackburn *et al.* 2017; Paim *et al.* 2020a; Paim *et al.* 2020b) with advancing generations the composite population develops its own unique cluster when compared to progenitor breeds (Figure 1). The formation of CGC cluster (generation 6) appears to be in concordance with previous work where a Brangus cluster occurred between generation 5 and 6 (Paim *et al.*, 2020a).

Evaluating runs of homozygosity showed new islands in CGC formed around generation 6 (Figure 3). This could be interpreted as when new breed formation occurred. The ROH based genomic inbreeding also showed a sharp increase to 10% in generation 6 and is different than the UN Food and Agriculture Organization (FAO) Guidelines for *in vivo* conservation of animal genetic resources (FAO 2013) which suggest three generations of inter se mating are required to establish a new composite breed after the initial crosses have been made.

The CGC population was constructed for increased cow productivity with the ability to perform in the northern Great Plains and has not been selected for meat quality, feedlot performance, nor increased mature size. Rather, the emphasis on selection tended to focus upon cow fertility and calf weaning weight. Given these selection objectives it is not surprising that the composition of the progenitor breeds shifted with time for CGC. Specifically, the proportion of Tarentaise shifted from a target of 25% to an average 57% in the last two generations, Red Angus decreased from a target of 50% to approximately 38%, and Charolais decreased from a target of 25% to approximately 4% (Figure 2).

References

- Alexander, D. H., J. Novembre and K. Lange, 2009 Fast model-based estimation of ancestry in unrelated individuals. *Genome research* 19: 1655-1664.
- Blackburn, H., B. Krehbiel, S. Ericsson, C. Wilson, A. Caetano *et al.*, 2017 A fine structure genetic analysis evaluating ecoregional adaptability of a *Bos taurus* breed (Hereford). *PLoS one* 12: e0176474.
- Lencz, T., C. Lambert, P. DeRosse, K. E. Burdick, T. V. Morgan *et al.*, 2007 Runs of homozygosity reveal highly penetrant recessive loci in schizophrenia. *Proceedings of the National Academy of Sciences* 104: 19942-19947.
- Paim, T. d. P., E. Hay, C. Wilson, M. Thomas, L. Kuehn *et al.*, 2020a Dynamics of genomic architecture during composite breed development in cattle. *Animal genetics* 51: 224-234.
- Paim, T. d. P., E. H. A. Hay, C. Wilson, M. G. Thomas, L. A. Kuehn *et al.*, 2020b Genomic breed composition of selection signatures in Brangus beef cattle. *Frontiers in genetics* 11: 710.
- Purcell, S., B. Neale, K. Todd-Brown, L. Thomas, M. A. Ferreira *et al.*, 2007 PLINK: a tool set for whole-genome association and population-based linkage analyses. *The American journal of human genetics* 81: 559-575.