




## ORIGINAL ARTICLE

# Genome-wide scan for runs of homozygosity in the composite Montana Tropical<sup>®</sup> beef cattle

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## Abstract

The aim of this study was to assess the distribution of runs of homozygosity (ROH) and autozygosity islands in the composite Montana Tropical<sup>®</sup> beef cattle to explore hotspot regions which could better characterize the different biological types within the composite breed. Montana animals ( $n = 1,436$ ) were genotyped with the GGP-LD BeadChip (~30,000 markers). ROH was identified in every individual using the PLINK v1.90 software. Medium and long ROH prevailed in the genome, which accounted for approximately 74% of all ROH detected. On an average, 2.0% of the genome was within ROH, agreeing with the pedigree-based inbreeding coefficient. The Montana cattle with a higher proportion of productive breed types showed the highest number of autozygosity islands ( $n = 17$ ), followed by those with a higher proportion of breeds adapted to tropical environments ( $n = 15$ ). Enriched terms ( $p < .05$ ) associated with the immune and inflammatory response, homeostasis, reproduction, mineral absorption, and lipid metabolism were described within the autozygosity islands. In this regard, over-represented GO terms and KEGG pathways described in this population may play a key role in providing information to explore the genetic and biological mechanisms together with the genomic regions underlying each biological type that favoured their optimal performance ability in tropical and subtropical regions.

## KEYWORDS

autozygosity, *Bos indicus*, *Bos taurus*, Brazilian cattle, crossbreed, heterosis

## 1 | INTRODUCTION

Most livestock production in the world occurs in tropical and subtropical areas, in a wide range of heterogeneous production systems that can range from grassland-based to feedlot systems. Animal husbandry faces many conflicting challenges since several environmental factors can affect the livestock production, especially in tropical regions where

the air temperature and relative humidity directly influence the animal's production potential (Marino et al., 2016). Given the variable climates and landscapes, it is essential to match the animal biological type to the environment of which it will be raised, increasing its optimal performance ability to the challenging environment. Climatic adaptation in the cattle is a complex issue, and there are strong differences between breeds regarding heat tolerance (Beatty et al.,

2006; Cartwright, 1955; Renaudeau et al., 2012; Ribeiro et al., 2009) and other efficiency and adaptive-related traits (Prayaga et al., 2009; Wolcott, Johnston, & Barwick, 2014).

The Montana Tropical<sup>®</sup> is a composite breed developed for tropical and subtropical beef cattle systems under grazing conditions. The composite system of the Montana Tropical<sup>®</sup> beef cattle proposes the formation of clusters defined by biological types according to likeness, physiology, growth and reproduction traits, combining both *Bos taurus indicus* and *Bos taurus taurus* individuals. The base population is mainly centered on four different biological types defined as the NABC system, where: **N** is *B. taurus indicus* cattle breeds already adapted under tropical conditions (heat tolerance, resistance to parasites, and poor feeding management); **A** is *B. taurus taurus* cattle breeds known by their fertility and adaptive traits under tropical conditions; **B** is *B. taurus taurus* British breeds notorious for sexual precocity, carcass quality traits, and high growth rate; and **C** is European Continental breeds recognized by their high growth rates and carcass quality traits.

The composite Montana Tropical<sup>®</sup> beef cattle can be classified into sixteenths of the breed proportion from the NABC system. In this regard, the traditional cattle have the same proportions of NABC biological types (4:4:4:4, N = 4, A = 4, B = 4, and C = 4), always summing up a value of 16 in the total composition. However, the composition of these cattle may vary due to regional climates and breeder's preference, and as a result, they can be empirically classified into two main biological types (adaptive and productive) given the proportion of the NABC biological types that make them up. The adaptive group has a high proportion ( $\geq 50\%$ ) of adapted (**A**) biological types breeds (i.e., 4:8:2:2 and 4:8:4:0), whereas animals that present  $< 50\%$  of **A** together with a high proportion of **B** and **C** productive biological type breeds (i.e., 4:6:2:4 and 4:6:4:2) are classified as productive. At the beginning of the breed establishment, several breeds have been used to make up the genetic basis of the Montana Tropical<sup>®</sup> beef cattle, however, fewer breeds are predominant within the composite breed nowadays (i.e. Nellore, Senepol, Bonsmara, Limousin, and Hereford). It is noteworthy to high point that Montana animals are now well established and can be used as a purebred without the need for any ongoing crossbreeding programmes.

The great limiting factor of newly composite programmes, such as the composite Montana Tropical<sup>®</sup> beef cattle which started in 1994 (Ferraz, Eller, Dias, & Golden, 2002), is the effective population size when compared to ancient breeds and the availability of genomic information. In this regard, it is essential to define mating strategies to preserve the genetic diversity and avoid high inbreeding rates (Zhang, Calus, Gulbrandsen, Lund, & Sahana, 2015a) so as to maintain long-term viability and sustainability of breeding

programmes. One of the main advantages of a composite breed is that it maintains heterosis over time that we normally associate with continuous crossbreeding and it also explores the complementarity amongst breeds to achieve an optimum additive genetic composition. It is worth to highlight that the retention of heterosis in composite breeds is influenced by inbreeding levels. In this regard, inbreeding should be avoided in order to retain high levels of heterozygosity and heterosis in composite breeds (Gregory, Cundiff, & Koch, 1993, 1999).

With the widespread use of whole-genome marker panels, an increasing interest in identifying autozygosity from molecular information has aroused. Autozygosity occurs when chromosomal segments identical by descent (IBD) arising from a common ancestor are inherited from both parents onto the offspring genome (Broman & Weber, 1999), resulting in continuous IBD homozygous segments characterized as runs of homozygosity (ROH; Gibson, Morton, & Collins, 2006). The autozygosity based on ROH can disclose the genetic relationships amongst individuals, being an accurate estimator for detecting the effects of inbreeding (Ferenčaković, Hamzić, Gredler, Curik, & Sölkner, 2011; Ferenčaković, Hamzić, et al., 2013). Besides, it can reveal selection pressure events (Kim et al., 2013; Zhang, Gulbrandsen, Bosse, Lund, & Sahana, 2015b) since selection is one of the main forces triggering homozygous stretches on the genome (Marras et al., 2015). The selection also tends to generate autozygosity islands, which can be defined as ROH shared regions amongst individuals with reduced genetic diversity and, consequently, high homozygosity around the selected locus that might harbour targets of positive selection and are under strong selective pressure (Pemberton et al., 2012). ROH has not yet been widely applied in crossbred or composite population, however, Howard, Tiezzi, Huang, Gray, and Maltecca (2016) characterized the frequency of ROH in a swine population within purebred breeds and its persistence within the crossbred progeny.

The aim of this study was to assess the distribution of ROH in the composite Montana Tropical<sup>®</sup> beef cattle to describe the genome-wide autozygosity. It also attempts to investigate ROH hotspot regions for traces of selection and gene content which could better characterize different biological types contributing to the composite Montana Tropical<sup>®</sup> beef cattle raised in tropical and subtropical regions.

## 2 | MATERIALS AND METHODS

### 2.1 | Samples, genotyping, and data editing

The animals used in this study comprise a dataset from the composite Montana Tropical<sup>®</sup> cattle breeding programme. Montana animals were genotyped with the GeneSeek<sup>®</sup> Genomic Profile Low-Density BeadChip containing over

30,105 markers ( $n = 1,436$  animals). Animals were sampled from 14 farms located in Brazil (South, Southeast, and Midwest regions) and one in Uruguay. The biological type composition according to the NABC system for the animals sampled in this study is described in Table 1. For all samples, markers unsigned to any chromosome and those assigned to sexual chromosomes were removed from the dataset. Additionally, markers and samples were edited for a call rate frequency higher than 0.90.

## 2.2 | Effective population size

The effective population size ( $N_e$ ) was estimated using the SNP1101 v1.0 software (Sargolzaei, 2014). The analysis was based on the extent of linkage disequilibrium (LD) using the  $r^2$  statistic (Sved, 1971), represented as follows:

$$N_e = \left[ \left( \frac{1}{E(r^2)} \right) - 1 \right] \frac{1}{4c}$$

where  $c$  is the distance in Morgans between two markers estimated for each chromosome in the LD. The  $E(r^2)$  is the expected  $r^2$  at a distance  $c$ , calculated as follows:

$$E(r^2) = \frac{1}{1 + 4N_e c}$$

Each genetic distance ( $c$ ) corresponds to a value of  $t$  generations in the past (Hayes, Visscher, McPartlan, & Goddard, 2003), obtained as follows:

$$t = \frac{1}{2c}$$

The  $N_e$  was investigated at four time points: 5, 10, 20, and 50 generations ago. Studies have shown that including

**TABLE 1** The biological type composition according to the NABC system for the composite Montana Tropical<sup>®</sup> beef cattle sampled in this study

Number of samples	Biological type	Biological type proportion <sup>a</sup>			
		N	A	B	C
155	Productive/adaptive	4	4	4	4
40	Productive	4	6	2	4
228	Productive	4	6	4	2
769	Adaptive	4	8	2	2
244	Adaptive	4	8	4	0

<sup>a</sup>Comprises the NABC system classification based on pedigree records: **N** is the *Bos taurus indicus* cattle breeds already adapted under tropical conditions, **A** is the *Bos taurus taurus* cattle breeds known by their adaptive traits under tropical conditions, **B** is the *B. taurus taurus* British breeds, and **C** is the European Continental breeds.

markers with low minor allele frequencies (MAF) can bias LD estimates (Espigolan et al., 2013; Goddard, Hopkins, Hall, & Witte, 2000; Qanbari et al., 2010), therefore, a MAF threshold of 0.01 was applied on the data for this analysis. After the quality control, a total of 27,560 markers and 1,391 samples were left for  $N_e$  analysis.

## 2.3 | Pedigree-based inbreeding coefficient

Pedigree-based inbreeding coefficients ( $F_{PED}$ ) were estimated using pedigree records from a dataset containing information from 6,169 sires and 366,353 dams. The pedigree data was provided by the Animal Breeding and Biotechnology Group of the College of Animal Science and Food Engineering (Pirassununga, São Paulo, Brazil). The pedigree ranged from one to nine generations. The  $F_{PED}$  was estimated through the software INBUPGF90 (Aguilar & Misztal, 2008).

## 2.4 | Runs of homozygosity

Runs of homozygosity were estimated in every individual using the PLINK v1.90 software (Purcell et al., 2007) and no pruning was performed based on the MAF. High LD estimates lead to short and common ROH throughout the genome (Purfield, Berry, McParland, & Bradley, 2012), whereas a low value allows the identification of short segments that are more likely to be IBD rather than derived from LD. In this regard, the average LD estimate (0.13) for all autosomes was used to determine the minimum length of an ROH, allowing us to lower down the minimum length of an autozygous segment to 0.5 Mb. The criterion and thresholds used to define ROH are described in Table 2. ROH were classified into four length classes: 0.5–2, 2–4, 4–8, and >8 Mb, identified as ROH<sub>0.5–2 Mb</sub>, ROH<sub>2–4 Mb</sub>, ROH<sub>4–8 Mb</sub>, and ROH<sub>>8 Mb</sub>, respectively. The average level of autozygosity per animal was calculated as the ratio of the total length of the genome covered by ROH to the total length of the genome covered by autosomes markers, as proposed by McQuillan et al. (2008). After filtering, Montana animals held 27,929 markers and 1,391 samples for ROH analysis.

## 2.5 | Detection of autozygosity islands

As described in the introduction, the composite Montana Tropical<sup>®</sup> beef cattle can be classified into sixteenths of the breed proportion from the NABC system. This categorization was based on pedigree records from 680,552 animals containing the breed composition information. The animals were classified into two main biological types (adaptive and productive) according to their NABC system (Table 1). The first group comprised animals with a high proportion of adapted biological type breeds (**A**) (4:8:2:2 and 4:8:4:0). The second one also encompassed animals with

**TABLE 2** Preset parameters and criterion to define the runs of homozygosity (ROH) in the composite Montana Tropical<sup>®</sup> beef cattle

Parameters	Threshold
Sliding window (number of SNPs)	40
Minimum number of consecutive SNPs	15
Minimum length of an ROH	0.5 Mb
Maximum gap between consecutive homozygous SNPs	1 Mb
Density (SNP/Kb)	1/120
Missing genotypes	2
Heterozygous genotype	0

a considerable proportion of adapted cattle, however, with a high proportion of British (B) and Continental (C) biological type breeds (4:6:2:4 and 4:6:4:2). The traditional composite Montana Tropical<sup>®</sup> beef cattle (4:4:4:4) was included in both biological types of analysis as they have the same proportion of the NABC biological types.

Autozygosity islands were identified using an outlier approach. The boxplot distribution for each autosome displaying the number of time each SNP fell within an ROH was used to define the regions where SNPs were outliers in the upper quartile (Figure S1). A file generated by the PLINK v1.90 software (Purcell et al., 2007) which specifies how many times each SNP appeared in an ROH was used and regions displaying at least 15 consecutive outlier SNPs were then classified as an autozygosity island. Autozygosity islands were identified separately for adaptive and productive biological types groups.

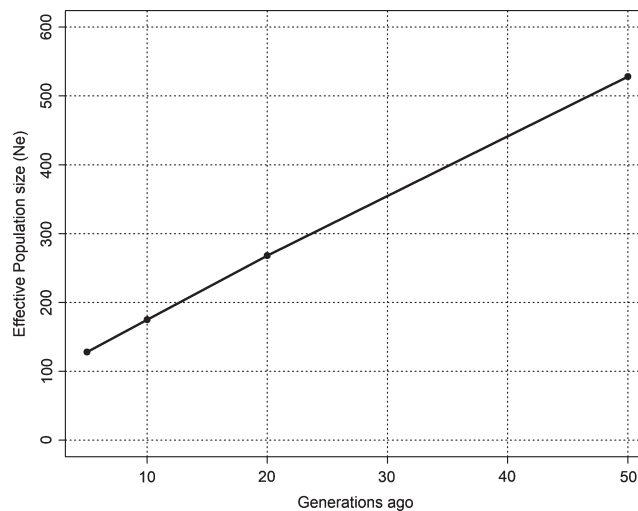
## 2.6 | Gene searching and functional annotation analysis

The gene content of the autozygosity islands for each biological type (adaptive and productive) was identified using the Ensembl Biomart tool (Haider et al., 2009; Genes 94, *Bos taurus* UMD3.1). The database for Annotation, Visualization, and Integrated Discovery (DAVID) v. 6.8 tool (Huang Sherman, & Lempicki, 2009a, 2009b) was used to identify significant ( $p < .05$ ) Gene Ontology (GO) terms and KEGG (Kyoto Encyclopedia of Genes and Genomes) pathways using the list of genes from the autozygosity islands from each biological type and the *B. taurus taurus* annotation file as a background.

## 3 | RESULTS AND DISCUSSION

### 3.1 | Effective population size

The  $N_e$  obtained in this population was estimated from 5 to 50 generations ago (Figure 1) and its decay over time indicates that the ancestral population based on 50 past generations had a much larger  $N_e$  ( $n = 528$  animals) compared to the

**FIGURE 1** Estimated an effective population size ( $N_e$ ) over time for the composite Montana Tropical<sup>®</sup> beef cattle

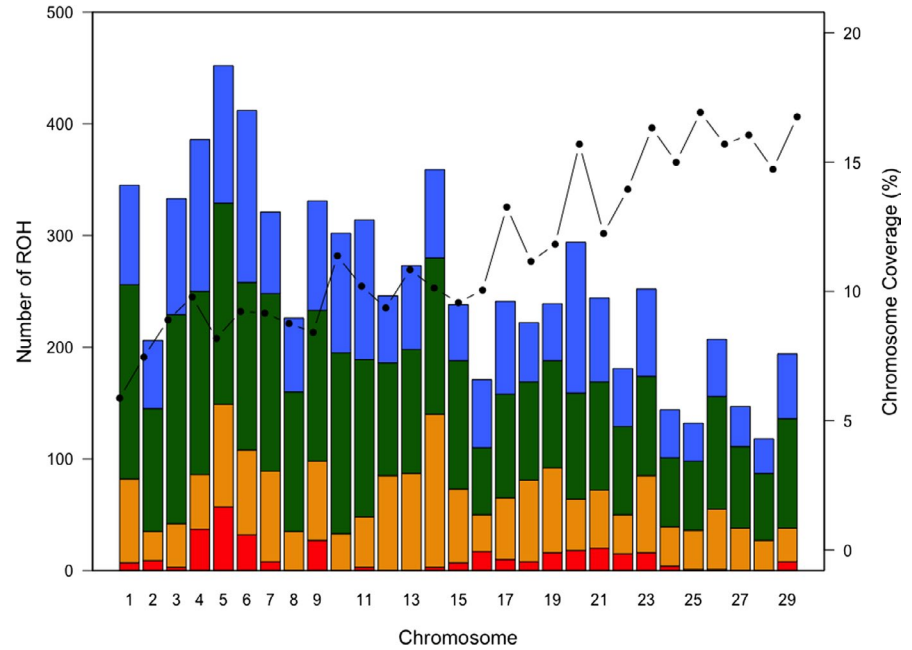
most current generations. The  $N_e$  for the last five generations showed a value of 128 animals, falling within the minimum value of 50 individuals for any livestock species to ensure the viability and genetic improvement in breeding programmes (FAO, 2004). Furthermore, the maintenance of a sufficiently large  $N_e$  is essential for the retention of heterozygosity and heterosis in composite breeds (Gregory, Cundiff, & Koch, 1999).

The average  $r^2$  in all autosomes was .13 by considering a maximum distance of 100 kb between adjacent SNPs. Since there were no previous results from the composite Montana Tropical<sup>®</sup> beef cattle regarding LD analysis, our results were compared to those described for other cattle and composite breeds. Studies have described an  $r^2$  value of .17 for a distance of 100 kb in the Nellore cattle (Espigolan et al., 2013) and values varying between .20 and .22 in Angus, .13 and .16 in Brahman and .15 and .26 in Limousin cattle breeds when considering a physical distance close or equal to 100 kb (McKay et al., 2007; Porto-Neto, Kijas, & Reverter, 2014). Additionally, an  $r^2$  value varying from .13 to .16 has been reported in the composite cattle (Tropical Composite, Santa Gertrudis, and Belmont Red) within a distance of 70 kb between adjacent SNPs (Porto-Neto et al., 2014).

### 3.2 | Distribution of ROH

Runs of homozygosity was identified in almost all Montana individuals with the exception of 60 samples. A total of 7,530 ROH was identified to be distributed amongst 1,331 Montana individuals with an average value of 5.65 ROH per animal. An average ROH length of 7.73 Mb was estimated across all the autosomes with a maximum value of 73.18 Mb in length (708 SNPs) in *B. taurus* autosome (BTA) 11. Similar results regarding the average and maximum ROH length were

**FIGURE 2** Runs of homozygosity distribution and coverage for each autosome in the composite Montana Tropical<sup>®</sup> beef cattle. Barplot: Frequency distribution of the number of runs of homozygosity in different length classes: red (ROH<sub>0.5–2 Mb</sub>), orange (ROH<sub>2–4 Mb</sub>), green (ROH<sub>4–8 Mb</sub>), and blue (ROH<sub>>8 Mb</sub>). Lines: The average percentage of chromosome coverage by the runs of homozygosity of minimum length of 0.5 Mb



**TABLE 3** Descriptive statistics of runs of homozygosity number ( $n$  ROH) and mean length (in Mb) for four different length classes (ROH<sub>0.5–2 Mb</sub>, ROH<sub>2–4 Mb</sub>, ROH<sub>4–8 Mb</sub>, and ROH<sub>>8 Mb</sub>) in the composite Montana Tropical<sup>®</sup> beef cattle

Class	$n$ ROH	(%)	Mean length	Cumulative ROH length (%)
ROH <sub>0.5–2 Mb</sub>	327	4.34	1.44	0.81
ROH <sub>2–4 Mb</sub>	1,655	21.98	3.15	8.97
ROH <sub>4–8 Mb</sub>	3,307	43.92	5.62	31.96
ROH <sub>&gt;8 Mb</sub>	2,241	29.76	15.14	58.26

reported by the Mastrangelo et al. (2017) study in sheep using the medium density SNP array. According to the authors, values of the total ROH length and number might have been underestimated since many ROH remain undetected when using the low- and medium-density SNP array. Therefore, our results may be slightly biased since a low-density array was used to characterize ROH, not accurately identifying the total ROH number per animal due to the lack of power to detect these segments when using a shallow density panel.

The number of ROH per chromosome was greater for BTA5 (532 segments) and the greater fraction of chromosome covered with ROH was found on BTA25 (16.91% of chromosomal length within an ROH; Figure 2). Our previous studies in indicine cattle (Peripolli, Metzger, et al., 2018; Peripolli, Stafuzza, et al., 2018) also have described the greatest number of ROH on BTA5, whereas others have found on BTA1 (Gurgul et al., 2016; Mastrangelo et al., 2016; Purfield et al., 2012).

Runs of homozygosity analysis for the different length classes revealed that medium (ROH<sub>4–8 Mb</sub>) and long (ROH<sub>>8 Mb</sub>) segments prevailed in the genome of the composite Montana Tropical<sup>®</sup> beef cattle, which accounted for approximately 74% of all ROH detected and greatly contributed to 90% of the cumulative ROH length (Table 3).

The high proportion of medium and long ROH described in our study might reflect the reduced power of low-density arrays in identifying ROH between 0.5 and 2 Mb in length ( $n = 327$  segments), as discussed by Purfield and colleagues (Purfield et al., 2012). Additionally, by not allowing any heterozygous call within an ROH, long ROH might not have been overestimated. In fact, these results contradict those reported in the cattle (Ferenčaković et al., 2011; Ferenčaković, Hamzić, et al., 2013; Marras et al., 2015; Peripolli, Metzger, et al., 2018; Peripolli, Stafuzza, et al., 2018; Szmatoła et al., 2016; Zhang, Calus, et al., 2015a), sheep (Purfield, McParland, Wall, & Berry, 2017), and pigs (Saura et al., 2015), in which the total length of ROH was composed mostly of high number of shorter ROH. It is noteworthy to highlight that the inconsistency amongst the criteria for defining ROH make the comparison of ROH studies not straightforward. The lack of consensus allows different thresholds across studies (Howrigan, Simonson, & Keller, 2011; Ku, Naidoo, Teo, & Pawitan, 2011) and it may be responsible for bias in ROH-based estimates of autozygosity (Ferenčaković, Sölkner, & Curik, 2013). The studies described above reported a high number of shorter ROH and most of them made use of medium-density arrays (50K). According to Ferenčaković, Hamzić, et al. (2013),

the 50K array tends to reveal an abundance of small segments, however, it overestimates the numbers of segments between 1 and 4 Mb, suggesting that it is not sensitive enough for its accurate determination. In this regard, a strict comparison has to be made when assessing different studies, taking into account the parameters used to define ROH since they may cause biased estimation.

It should be noted that, it is unclear how frequently ROH persists in a crossbred population and whether longer ROH exists. In this context, the persistence of ROH in the crossbred and composite population likely results in decreased heterozygosity for that region, which reduces the degree of heterosis. Furthermore, long ROH reduces the probability of creating new favourable haplotype combinations by recombination, then, managing these populations to maintain genetic diversity and reduce the length and frequency of ROH is a desirable effect regarding the genetic diversity (Howard et al., 2016).

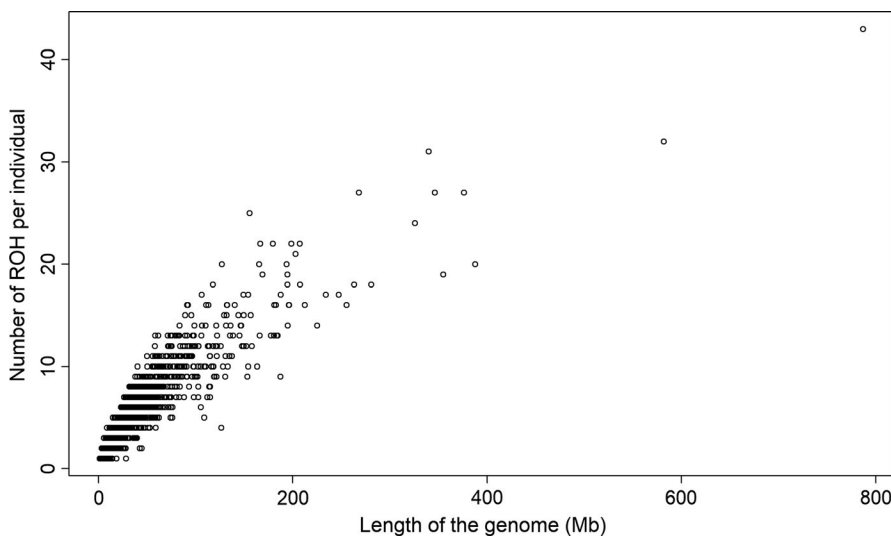
The extension and frequency of ROH can disclose the number of generations of inbreeding given that the approximate correlation between the length of the ROH and the distance with the common ancestor due to recombination events. By considering 1 cM equals to 1 Mb, the expected length of autozygous segments follows an exponential distribution with mean equal to  $1/2g$  Morgans, where  $g$  is the number of generations since the common ancestor (Howrigan et al., 2011). Therefore, by considering that  $ROH_{>8 \text{ Mb}}$  are expected to correspond to the reference ancestral population dating six generations ago or less together with the higher frequencies of ROH in this length category, we can disclose that the recent inbreeding was observed in the studied population. Further, the ROH pattern in this population is consistent with the recent development of the composite breed in 1994 (Ferraz et al., 2002), reinforcing the idea of not long past inbreeding events in such population. The small number of proven sires mated to disseminate the breed presumably triggered the autozygosity in this population, however, when

assessing the proportion of the genome under autozygosity, an average value close to 2% was observed. Concurring with this result,  $F_{PED}$  estimates were low in this population, with a mean value of 0.6%. These results might reflect the recent establishment of the breed together with the introduction of new genes through genic combinations to explore the complementarity amongst the breeds within each biological type, resulting in decreased inbreeding rates. However, it should be taken into consideration that the average level of autozygosity described here might not reflect the true level of autozygosity since many ROH remain undetected when using a low-density panel, as discussed previously.

Animals exhibiting the same homozygous genome length displayed a variable number of ROH (Figure 3) and this pattern can be attributed as a consequence of the distinct distances from the common ancestor (Mészáros et al., 2015). Hence, when considering animals with the same homozygous genome length, we can infer that those displaying a lower number of ROH have a higher proportion of longer segments and then a decreased distance with the common ancestor than those exhibiting a higher number of ROH. The most extreme animal exhibited an ROH genome coverage encompassing 786.84 Mb of the total autosomal genome extension (UMD3.1) covered by markers (31.47% of the cattle genome). Similar results were described in several cattle breeds, whose findings reported a coverage varying from 25% to 29.20% of the cattle genome (Marras et al., 2015; Mastrangelo et al., 2016; Peripolli, Metzger, et al., 2018; Peripolli, Stafuzza, et al., 2018; Purfield et al., 2012; Szmatoła et al., 2016).

### 3.3 | Autozygosity islands

Autozygosity islands were evident across the genome and their distributions varied in length and position across chromosomes for both biological types (Table S1). The number



**FIGURE 3** Number of runs of homozygosity (ROH) per individual and the total length of the genome covered by ROH

of islands did not differ considerably between biological types, resulting in 15 islands identified for the adaptive types and 17 for the productive. Additionally, the longest island found on the adaptive biological type encompassed 5.95 Mb (199,195:6,154,638 bp) in length on BTA1. This region was screened for the gene content and no genes with described functions were identified. For the productive biological type, the longest island was found covering 4.34 Mb (32,861,744:37,203,531 bp) in length on BTA22 and harboured five genes with described functions (FAM19A4, FAM19A1, SUCLG2, KBTBD8, and LRIG1).

### 3.4 | Functional annotation of genes

A total of 487 protein-coding genes (adaptive = 273 and productive = 217) were identified within the autozygosity islands regions using the bovine reference genome assembly UMD3.1. Only three genes (*XKR4*, *MT1E*, and *CSMD3*) were identified in both biological types and the first two are noteworthy to highlight given their role in cattle productive traits. The *XKR4* (XK, Kell blood group complex subunit-related family, member 4) gene has been associated with several economically important traits in the beef cattle such as intramuscular fat (Ramayo-Caldas et al., 2014) and subcutaneous rump fat thickness (Bolormaa et al., 2011; Porto Neto, Bunch, Harrison, & Barendse, 2012). This gene has also been described to have functions associated with serum prolactin concentrations in the Angus–Simmental–Charolais crossbred (Bastin et al., 2014), feed intake in crossbred steers (Lindholm-Perry et al., 2012), age at puberty in Brahman (Fortes et al., 2012), and backfat thickness (Silva et al., 2017), birth weight (Terakado et al., 2018) and meat tenderness (Magalhães et al., 2016) in the Nellore cattle. The second gene (*MT1E*, metallothionein 1E) encodes a protein that exhibits antioxidant activity (Chung, Hogstrand, & Lee, 2006) and displayed a significant negative correlation with dry matter intake in beef steers (Sun, Zhao, Zhou, Chen, & Guan, 2019).

The analyses set to study the functional enrichment using the DAVID tool that revealed significant ( $p < .05$ ) GO terms and KEGG pathways for each biological type (Tables S2 and S3) and it was used to give an insight about the predicted gene networks. No significant GO term neither KEGG pathway was found to be shared between biological types. For the adaptive biological type, the analysis showed 20 GO terms and six KEGG pathways as significant ( $p < .05$ , Table S2) for the gene list. Amongst them, we highlight terms involved in the immune system activation in response to pathogens and those associated with adaptive traits related to homeostasis, briefly described below.

The type I interferon receptor activity (GO:0004905) and type I interferon signalling pathway (GO:0060337) terms have functions linked to molecular signals that act to initiate

changes in the cell activity to promote the first line of defense against the viral infection, i.e., foot-and-mouth disease virus (Ma et al., 2018), bovine herpesvirus 1 (Jones, 2019), and bovine viral diarrhoea virus (Van Wyk, Snider, Scruten, van Drunen Littel-van den Hurk, & Napper, 2016). The natural killer cell-mediated cytotoxicity (bta04650) was identified in the adaptive biological type associated with the immune system activities since natural killer cells are lymphocytes of the innate immune system involved in early defense against both allogeneic and autologous cells undergoing infection with bacteria, viruses or parasites. The JAK-STAT signalling pathway (bta04630) is one pleiotropic cascade used to transduce several signals for the development and homeostasis in animals, acting as a central pathway for the improvement and function of the immune system and playing important roles in other biological systems (Liongue, O'Sullivan, Trengove, & Ward, 2012).

The blood coagulation, fibrin clot formation (GO:0072378), platelet activation (GO:0030168), complement and coagulation cascades (bta04610), respiratory chain (GO:0070469), oxidoreductase activity (GO:0016491), and cAMP signalling pathway (bta04024) were identified as over-represented in the adaptive biological type which functions related to several physiological processes in order to maintain homeostasis. Homeostasis is the state of equilibrium that the body reaches after responding to a foreign antigen and the immune system plays a remarkable role by providing several functions to maintain homeostasis to respond effectively to a new antigenic challenge (Taniguchi et al., 2009; Van Parijs & Abbas, 1998).

The functional enrichment analysis for the productive biological type gene list covered a total of 17 GO terms and four KEGG pathways ( $p < .05$ , Table S3), in which we highlight those related to the immune system, reproductive, and productive functions. The GO terms related to inflammatory immune response included innate immune response (GO:0045087), lymphocyte chemotaxis (GO:0048247), monocyte chemotaxis (GO:0002548), CCR chemokine receptor binding (GO:0048020), and chemokine signalling pathway (bta04062). Chemokines are a family of small signalling peptides that have a crucial role in the development and maintenance of the innate and adaptive immune response against pathogens, showing vital roles in inflammation, disease modulation, and homeostasis (Widdison & Coffey, 2011). During the inflammation process, chemokines and adhesion molecules work together to promote the differential leukocyte trafficking between circulation and the tissue through chemotaxis (Raman, Sobolik-Delmaire, & Richmond, 2011; Thelen, 2001). Chemokines are also involved in embryo implantation, development, and growth (Raman et al., 2011).

The endodermal cell differentiation (GO:0035987) is a biological process related to reproduction, in which relatively

unspecialized cells acquire the specialized features of endoderm cells, one of the three germ layers of the embryo. Platelet activation (bta04611) pathway plays a key role for primary homeostasis in the disruption of the integrity of vessel wall and has been associated with the establishment of pregnancy in cows through the maternal platelet activation during early pregnancy (Kojima, Akagi, Zeniya, Shimizu, & Tomizuka, 1996).

Regarding the mineral absorption (bta04978) pathway, the animal's tissues need moderate quantities of some minerals (Ca, P, K, Na, Mg, S, and Cl) and smaller amounts of others (Mn, Fe, I, Co, Cr, Cu, Zn, and Se). Minerals in the diet must be absorbed by either passive or active transport system across the gastrointestinal mucosa to enter into the blood flow for maintenance, growth, and reproduction. Amongst the minerals, Mg is vital to the bone mineral formation, nerve, and muscle functions; Na plays a crucial role in the absorption of dietary sugars, amino acids, and water; Cl is the main anion related to the regulation of osmotic pressure, responsible for the low pH in the lumen of the abomasum; while Ca plays several roles in the animal's body, acting as a main component of bone and as an intracellular messenger in muscle contraction/relaxation allowing normal muscle and nerve functions, and play important functions in neural networks and immune system (Goff, 2018).

Propanoate (propionic acid) metabolism (bta00640) is an essential metabolic pathway since propionate, a by-product of ruminal fermentation, is the main precursor for glucose synthesis through gluconeogenesis in the liver of ruminants (Hocquette & Bauchart, 1999). In ruminants, glucose is one of the main forces triggering lipogenesis and marbling, and it also plays a key role in providing fuel for cellular and tissue functions. In this regard, mechanisms involved in the glucose absorption in the small intestine, liver gluconeogenesis, and glucose retention by the tissues are essential to produce high marbling meat and to increase meat quality traits in ruminants (Ladeira et al., 2018). Lee, Park, Kim, Yoon, and Seo (2014), studying metabolic differences between muscle and intramuscular adipose tissues in the *Longissimus dorsi* of Hanwoo beef cattle, identified the propanoate metabolism downregulated in the intramuscular adipose tissue. Nguyen, Zacchi, Schulz, Moore, and Fortes (2018) identified the propanoate metabolism pathway working together with other pathways influencing the adipose tissue in Brahman heifers.

Enriched terms associated with the immune response and homeostasis described for the adaptive biological type can help to better elucidate the mechanisms underlying the cattle adaptation in hostile environments since the survivability benefit could be achieved with the evolutionary success of the immune system (Lemos et al., 2018; Stothard et al., 2011). Besides describing terms related to the immune response, the

productive biological type also displayed terms associated with reproduction, glucose synthesis, and lipid functions as well, most likely reflecting the fixation of genomic regions harbouring genes related to the higher productive potential in those specialized breeds that compose the **B** and **C** biological types. According to Frisch and Vercoe (1979), there is an antagonism between some components of adaptation and production potential, which preclude the possibility to create an animal which has both high production potential coupled with a high level of adaptation.

## 4 | FINAL CONSIDERATIONS

This study describes, for the first time, ROH patterns and autozygosity islands in the composite Montana Tropical<sup>®</sup> beef cattle so as to better characterize the composite breed and the biological types within the NABC system. The ROH patterns described in this population suggested not long past inbreeding events, agreeing with such recent development of the composite Montana Tropical<sup>®</sup> beef cattle. Despite our results indicate recent inbreeding, autozygosity levels in such population were considered low, agreeing with  $F_{PED}$  estimate.

Autozygosity islands were assessed to better identify regions of the genome that have undergone directional selection and how they differ between biological types selected for different objectives within the NABC system. Overrepresented GO terms and KEGG pathways provided important genomic information to explore the genetic mechanisms underlying the biological types and the environment that favoured their optimal performance ability. The challenge to increase productivity in tropical environments is to combine in one breed several desirable traits, i.e., sexual precocity, resistance to parasites, heat tolerance and growth traits, adapted to pasture-based systems. In this regard, composite breeds such as the Montana Tropical<sup>®</sup> beef cattle can be an alternative for production systems in challenging environments as a unique genetic resource since it is possible for the breeder to choose what biological type should better adapt to the environmental conditions where the animals will be raised.

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## CONFLICT OF INTEREST

The authors declare that they have no conflict of interests.



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## SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section at the end of the article.

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