UNIVERSIDADE DE BRASÍLIA
INSTITUTO DE CIÊNCIAS HUMANAS
DEPARTAMENTO DE GEOGRAFIA
PROGRAMA DE PÓS-GRADUAÇÃO EM GEOGRAFIA

Mapeamento Genético e Espacialização Geográfica: Uma Análise da Raça Montana Tropical

Tese de Doutorado

Nathalia Silva da Costa

Brasília/DF, 30 de Outubro de 2023

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Orientador: Prof. Dr. Renato Fontes Guimarães
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Tese de Doutorado submetida ao Departamento de Geografia da Universidade de Brasília, como parte dos requisitos necessários para a obtenção do Grau de Doutor em Geografia, área de concentração Geoprocessamento e análise regional.

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Nathalia S. Costa

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Nathalia Silva da Costa

DEDICATÓRIA

Dedico esse trabalho a minha família, e
aos meus amigos verdadeiros.

AGRADECIMENTOS

SUMÁRIO

RESUMO

Valores genéticos de produção em 571,424 animais Montana Tropical, nascidos entre 1950 e 2019, juntamente com informações ambientais de 63 fazendas, possibilitaram a realização de diversas análises. Uma revisão bibliográfica focada em gado composto fornece contexto sobre o desenvolvimento de pesquisas e a contribuição de diferentes países apresentando maior interesse e número de publicações sobre o tema. Com o auxílio de análises estatísticas e técnicas de geoprocessamento associadas com diferentes variáveis ambientais como tipo de solo, altitude, precipitação, umidade relativa, Índice de Vegetação por Diferença Normalizada, Índice de Temperatura e Umidade, e temperatura do ar, foram realizados estudos para compreender como interações genótipo x ambiente afetam os valores genéticos da raça Montana Tropical no Brasil. Além disso, um mapeamento específico do gene Slick Hair foi conduzido, utilizando ferramentas que analisam distâncias genética e geográfica para investigar como a prevalência desse gene, relevante para a indústria pecuária, varia geograficamente.

Palavras chave: Montana Tropical, Mapeamento Genético, Análise da paisagem, Geoprocessamento.

ABSTRACT

Genetic production values in 571.424 Montana Tropical animals, born between 1950 and 2019, along with environmental information from 63 farms, enabled the conduct of various analyses. A bibliographic review focused on composite cattle provides context about the development of research and the contribution of different countries showing greater interest and number of publications on the topic. With the aid of statistical analyses and geoprocessing techniques associated with different environmental variables such as soil type, altitude, precipitation, relative humidity, Normalized Difference Vegetation Index, Temperature and Humidity Index, and air temperature, studies were carried out to understand how genotype x environment interactions affect the genetic values of the Montana Tropical breed in Brazil. In addition, a specific mapping of the Slick Hair gene was conducted, using tools that analyze genetic and geographic distances to investigate how the prevalence of this gene, relevant to the livestock industry, varies geographically.

Keywords: Montana Tropical, Genetic Mapping, Landscape Analysis, Geoprocessing.

1. INTRODUÇÃO

O Brasil é um país de grande extensão territorial, consequentemente, o estudo das características ambientais da paisagem e o uso de geotecnologias se tornam ferramentas importantes para identificar as regiões brasileiras que necessitam de mais investimentos em pesquisas, buscando dessa forma aproveitar melhor a capacidade de produção dos animais. A sustentabilidade econômica e ambiental da pecuária brasileira é de grande importância para garantir o fornecimento de proteína animal e segurança alimentar mundial, pois, espera-se grande aumento na demanda de alimentos nas próximas décadas (McManus et al., 2016)

Dentro do setor primário da economia, a pecuária brasileira apresenta um papel de destaque inserindo o país entre os principais produtores e exportadores mundiais de carne bovina. O relatório da OCDE/FAO (2021) projeta que a oferta global de carne bovina será expandida até 2030, com aumento dos rebanhos nas Américas e China, combinado com o crescimento da produtividade animal (peso médio de abate, melhoramento genético, e melhores formulações de ração). O Brasil é o terceiro maior consumidor de carne bovina do mundo atrás dos EUA e China, sendo responsável pela produção de aproximadamente 14,4% da carne bovina mundial (FAO, 2021).

Os Sistemas de Informações Geográficas- SIG vêm ao longo do tempo contribuindo para o desenvolvimento de diferentes áreas do conhecimento. Trabalho desenvolvido por Robinson et, al (2014) mostra o potencial dos sistemas de informações geográficas associados com bancos de dados animais voltado para representação populacional de rebanhos no mundo. De acordo com Mendes et al. (2018) a junção de ferramentas de sistema de informação geográfica com dados de sensoriamento remoto permite compreender os fenômenos que ocorrem na superfície terrestre em larga escala, e ainda analisar e até correlacionar com eventos naturais ou antrópicos.

No Brasil o estudo voltado para o melhoramento animal vem se desenvolvendo com o objetivo de aumentar a produtividade no território, ainda de acordo com Lobo et al, (2010) os estudos vão desde os clássicos trabalhos de estimativas de componentes de variância e parâmetros genéticos, passando por trabalhos de modelagem estatística até chegar aos trabalhos mais recentes envolvendo genética molecular aplicada ao melhoramento animal. Um desafio enfrentado no Brasil, segundo Ferraz et al. (2010), são às diferenças de ambiente, de tecnologia e de recursos presentes em diferentes sistemas de produção e, portanto, demanda diferentes tipos de animais, com genética diferenciada.

Com objetivo de melhorar a produção bovina, tentando superar as adversidades do território brasileiro, o uso de raças compostas formadas por animais resultantes de cruzamento entre raças distintas é uma excelente alternativa. Segundo Eler (2017), a utilização de bovinos compostos permite a democratização destes acasalamentos, e possibilita ao pequeno criador a utilização de animais com material genético eficiente e com maior capacidade de adaptação ao local.

O Composto Tropical Montana® é uma população que foi desenvolvida em 1994, depois de estudos desenvolvidos por pesquisadores e produtores no Brasil em parceria com o Centro de pesquisa em animais de corte dos Estados Unidos no Clay Center, Departamento de Agricultura dos Estados Unidos (USDA). Os bovinos adaptados ao clima são conhecidos por sua capacidade de tolerar o estresse térmico mantendo os padrões de produção e a resistência a doenças (Huson et al., 2014).

A análise da produção cientifica é um processo fundamental para compreensão dos trabalhos que estão sendo desenvolvidos. A análise bibliométrica pode ajudar a entender diferentes áreas de pesquisa e identificar os principais grupos de pesquisa, publicações e mudanças nos tópicos de pesquisa ao longo do tempo (Yu et al., 2020). As análises

bibliográficas permitem o estabelecimento de interconexões entre artigos e tópicos de pesquisa.

1.1. OBJETIVOS

1.1.1. Objetivos Gerais

Diante do exposto, o objetivo da presente pesquisa é realizar uma análise genética e espacial da distribuição dos animais na raça Montana no Brasil.

1.1.2. Objetivos Específicos

a). Compreender como estão sendo desenvolvidos os estudos e revisões bibliográficas sobre bovinos compostos.

b). Analisar as características das paisagens que podem influenciar a produção dos animais da raça Montana.

c). Avaliar a dispersão genética e geográfica dos animais da raça Montana em todo território brasileiro.

d). Avaliar a expressão do gene "Slick Hair" nos animais da raça Montana.

1.2. APRESENTAÇÃO

O presente trabalho será dividido da seguinte forma:

- O capítulo 2 apresenta o artigo de análise bibliométrica que tem como objetivo entender como está o desenvolvimento das pesquisas dos animais de raças compostas. Título do artigo: MAPPING THE COMPOSITE CATTLE WORLDWIDE USING BIBLIOMETRIC ANALYSIS**.**

- O capítulo 3 apresenta o artigo desenvolvido a partir da análise de elementos da paisagem e avaliação estatística de dados genéticos de animais da raça Montana.

Título do artigo: **Spatial distribution of Genetic Values for the Brazilian Montana Tropical cattle Breed.**

- O capítulo 4 apresenta o artigo de mapeamento do gene "slick hair" gene responsável pelo conforto térmico animal. Título do artigo: **Spatialization for Slick Hair gene in Montana Cattle in Brazil.**

- O capítulo 5 apresenta o artigo com análise espacial da distribuição dos animais da raça Montana a partir dos valores genéticos. Título do artigo: **Genetic Spatialization in Montana Cattle.**

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2. MAPPING THE COMPOSITE CATTLE WORLDWIDE USING BIBLIOMETRIC ANALYSIS

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Abstract

Bibliographic mapping can help us understand publication networks and how a specific area of knowledge is developing. Here, we analysed citation, co-occurrence of keywords, co-citation and bibliographic coupling networks for composite cattle worldwide. Data was collected from Scopus® and analysed in Vosviewer®. The highest cited authors are from Brazil and Australia, but the USA has the highest number of publications and citations. Recent advances have seen the appearance of Chinese research groups. Keyword analysis shows a shift from quantitative to molecular genetics. Multi-focal journals such as Journal of Dairy Science, Journal of Animal Science and Livestock

Science have the highest numbers of publications and citations in this field. This analysis can help us identify major changes in future research pathways and identify new groups that working on it. It is useful in network building and identifying up-to-date topics in the research field.

Keywords: Bibliographic coupling, Co-citations, Genetics, Country, Research group

2.1 Introduction

Bibliometric analysis is a quantitative scientific computer-assisted review methodology used to analyze all related publications on a specific topic providing a more abundant, relational, contextual, and holistic intellectual landscape knowledge (Han et al., 2020). In this context, a bibliometric analysis may also be considered a proxy for measuring economic and social indicators due to the resource investment necessary to produce the final result (McManus et al., 2023). Initially, the bibliometric analysis is mostly based on the author or citation information and examines their intellectual flow and most influential publications, and lately, bibliometric analysis adopts network and sociometric analyses based on the titles, keywords, and abstract data (Han et al., 2020).

In this context, bibliometric tools allow us to conduct a systematic, transparent and replicable review of the existing research and provide a comprehensive knowledge map of the research field (Brito-Ochoa et al., 2020; Kraus et al., 2020). Through clustering algorithms, bibliometrics systematizes and automates the selection, ordination and visualization of information, enabling the process replication (Cobo et al., 2011). Science mapping techniques are one of the main pillars of bibliometrics. They explore relational aspects that identify document-to-document similarities. Bibliographic coupling and co-citation analyses are the most widely used because each one can successfully cluster over 92% of the scientific corpus (Boyack and Klavans, 2010). While bibliographic coupling

analyses cite documents, co-citation analysis focuses on cited documents (Cobo et al., 2011).

Co-citation analysis associates papers that have been co-cited in the reference list of previous papers, so that the information used to establish the similarity relationship between documents is retrospective. This technique is widely used to identify key papers in a research field, capturing the origins of that field (Kovacs et al., 2015). On the other hand, bibliographic coupling links documents that reference the same set of cited documents and is used to assess the similarity between citing articles. This technique is forward-looking and is more appropriate for studying emergent literature fields and capturing current research trends within a field (Boyack and Klavans, 2010; Vogel and Güttel, 2013).

The biometric review work is an important tool to understand how studies are being developed around the world. Future food production systems need to be integrated with the challenges of sustainable development, biodiversity conservation, water security, climate change adaptation and mitigation, poverty reduction and social inclusion (Herrero et al., 2021). Animal production, especially of ruminants, varies depending on species and breed. Understanding the parameters that can influence production is vital to understanding protein needs, malnutrition and nutrient deficiencies in low-income countries (Perignon et al., 2017; Van Zanten et al., 2018). Several countries are seeking different breeding strategies (Mokolobate et al., 2014; Leroy et al., 2016) and formation of composite breeds (Santana Jr et al., 2013; Hay et al., 2022) to maintain high production despite adversities (Toghiani et al., 2020). The objective of this study was to investigate trends and patterns of bibliographic measurements for studies in composite cattle.

2.2 Material and Methods

Global literature on composite cattle was identified in Scopus (Elsevier data). The search parameters are in ANNEX. The information included year of publication, language, journal, title, author, affiliation, keywords, document type, abstract and citations which were exported in CSV format. The date of the retrieval was 26th August 2022. Data were cleaned in OpenRefine (https://openrefine.org/). This involved joining variations of the same author (for example, McManus, C. and McManus, C.M.). We excluded the research parameters from the keywords section. Duplicate terms such as *Bos indicus* or Zebu were joined, as were singular and plural words.

VOSviewer (version 1.6.18) was used to map Co-authorship, Co-occurrence, Citation, Bibliographic coupling, Co-citation and keywords (van Eck and Waltman, 2010), using normalization of associations and the full counting algorithm (Prashar and Sunder, 2020). In bibliographic coupling, two works reference a third common work, while co-citation is when two documents receive a citation from the same third document (Fig. 1). Parameters for analyses are in Table 1. The circle size in VosViewer positively correlates with the keyword occurrence or countries in the title and abstract. The colour is more vibrant if the word/researcher/country is commonly found in different studies. If the connection is small, then the colour is more transparent. It was possible to download cluster information for further analyses.
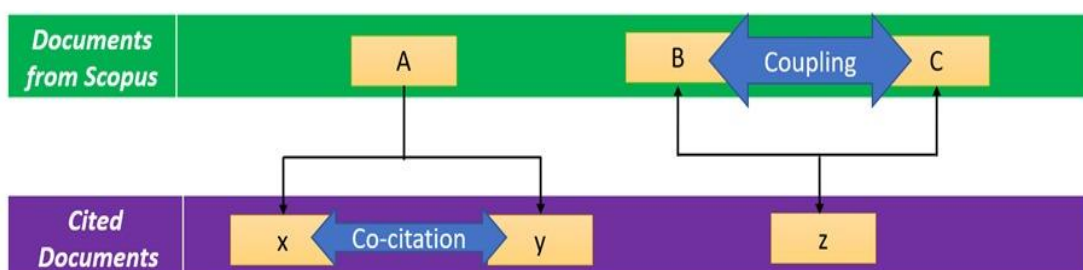
Fig 1. Bibliographic coupling and co-citation analyses.

2.3 Results

In total 351 documents were found, with 1384 co-authors (Table 1). There was a steady quadratic increase in this topic over the years (Fig. 2a). The Animal and Dairy Science Journals showed the highest number of papers published, followed by Animal Production Science and Livestock Science.

Table 1. Bibliometric parameters for publications on composite cattle breeds.

	Total	Minimum Documents	Number met threshold	With links	Clusters
Co-Authors	1384	2	204	141	11
Countries	76	5	21	21	5
Keywords	1006	2	157	103	11
Citation – Docum.	351	3	273	49	10
Sources	146	2	45	18	6
Authors	1384	2	204	104	8
Countries	76	5	21	18	7
Biblio. Coupling-	351	5	232	155	12
Sources	146	3	27	24	4
Authors	1384	2	204	195	12
Countries	76	3	31	31	7
Co-citation – ref.	11822	2	210	138	10
Sources	4448	20	56	38	6
Authors	21373	20	150	150	5

There were 126 funding agencies listed, with Brazilian agencies FAPESP (São Paulo State Funding Agency), CNPq (Ministry of Science and Technology) and CAPES (Ministry of Education) having the highest number of papers. The USA and Brazil were the major publishers, followed by Australia, Canada and South Africa. This is in line with the top researchers in the area (Fig. 2c).

a
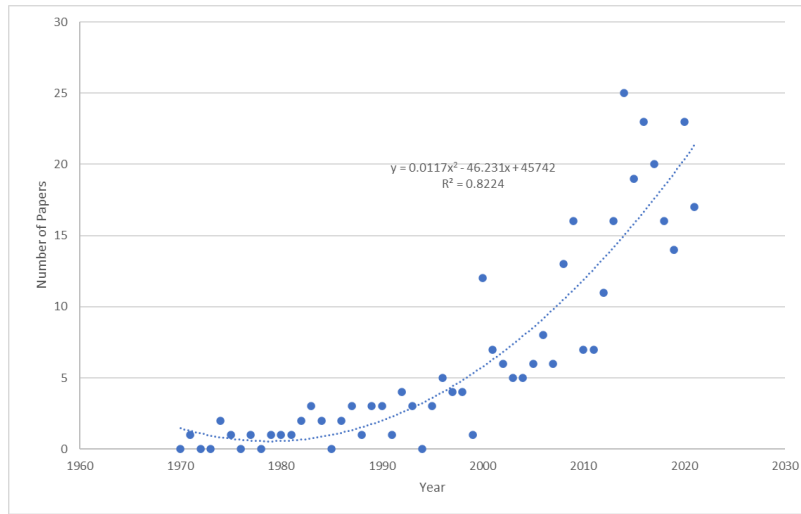
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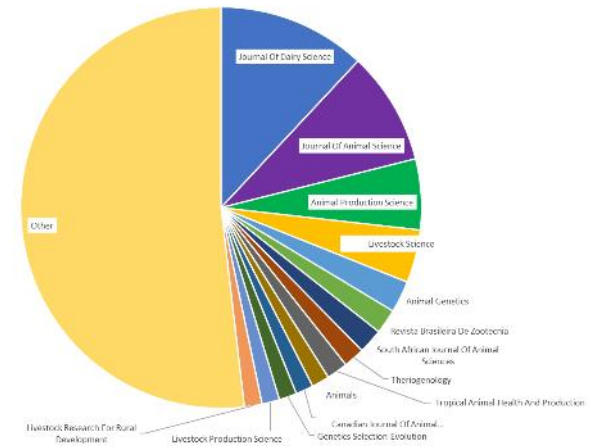
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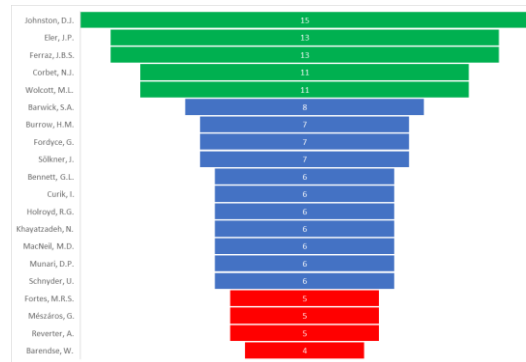
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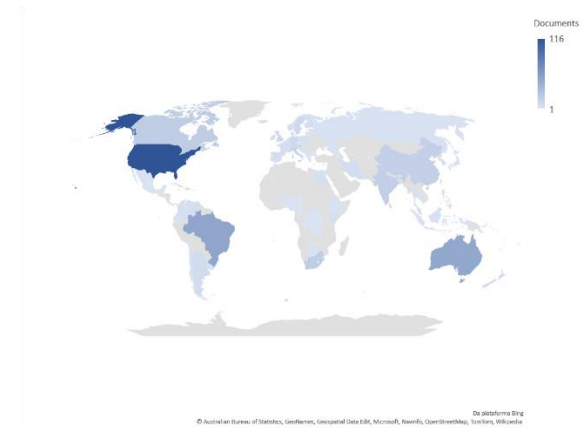
Fig. 2. Information on composite cattle breeds publications for a) the number of papers per year; b) journals; c) top 20 authors and d) countries.

1   Distinct groups of co-authors were formed (Fig. 3a). The Brazilian researchers

2   (purple and light blue) showed links to the USDA and the University of Wisconsin, while

3   the South African group (red) were linked through Michael MacNeil to USDA. Two

4   closely linked Australian researchers (yellow and green) were seen, linked to various

5   other worldwide research groups. Newer groups (Figs. 3 a and 3b) are seen in China, but

6   most groups are well established.
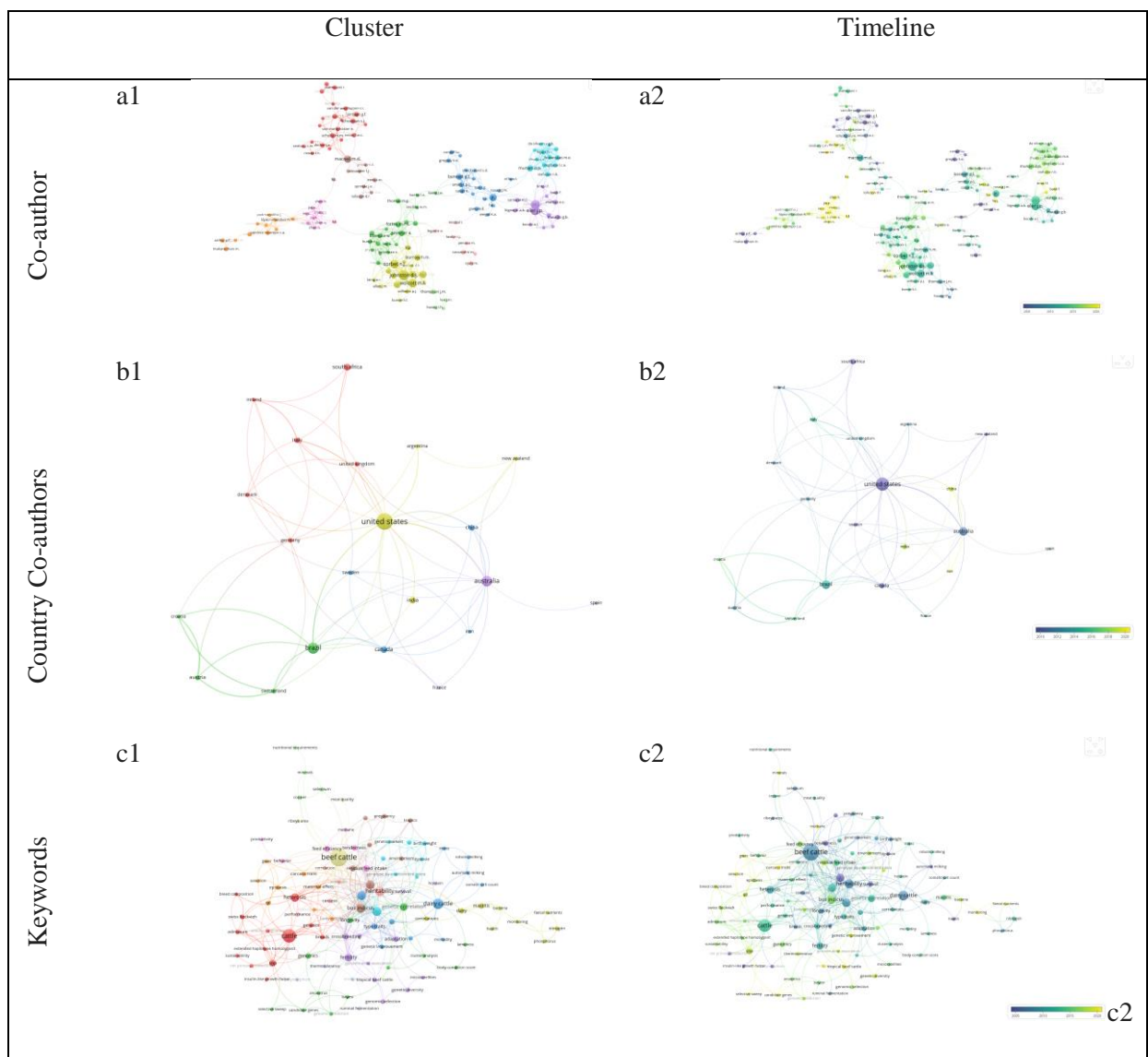
7   **Fig. 3.** Publication parameters for publications on composite cattle breeds by cluster and

8   timeline for a) co-author; b) country co-autor and c) keywords.

9   **Table 2.** Top 20 researchers by link strength on composite cattle breeds

Researcher	Country	Cluster	Total link strength	Documents	Citations	Norm. citations	Avg. pub. Year	Avg. Citations	Avg. norm. citations
Johnston D.J.	Australia	4	60	15	439	20.77	2012.27	29.27	1.38
Corbet N.J.	Australia	4	55	11	232	10.46	2014.00	21.09	0.95
Wolcott M.L.	Australia	4	43	11	320	14.58	2011.73	29.09	1.33
Eler J.P.	Brazil	5	42	13	120	9.20	2012.69	9.23	0.71
Ferraz J.B.S.	Brazil	5	41	12	95	8.20	2013.33	7.92	0.68
Barwick S.A.	Australia	4	33	8	221	11.18	2012.13	27.63	1.40
Fordyce G.	Australia	4	33	7	198	10.25	2013.86	28.29	1.47
Holroyd R.G.	Australia	4	33	6	180	6.99	2012.67	30.00	1.16
Munari D.P.	Brazil	6	30	6	125	8.76	2015.83	20.83	1.46
Burns B.M.	Australia	4	27	4	81	2.82	2016.00	20.25	0.71
McGowan M.R.	Australia	4	27	4	81	2.82	2016.00	20.25	0.71
Burrow H.M.	Australia	4	26	6	213	10.38	2011.17	35.50	1.73
Buzanskas M.E.	Brazil	6	26	4	109	7.80	2016.00	27.25	1.95
de Alencar M.M.	Brazil	6	25	3	85	5.88	2015.67	28.33	1.96
Higa R.H.	Brazil	6	25	3	85	5.88	2015.67	28.33	1.96
Bennett G.L.	USA	3	22	6	316	10.11	2009.33	52.67	1.69
Li Y.	China	4	22	4	114	2.07	2014.75	28.50	0.52
Reverter A.	Australia	2	22	5	236	9.48	2015.60	47.20	1.90
Stafuzza N.B.	Brazil	6	22	3	60	6.03	2017.67	20.00	2.01
Hayes B.J.	Australia	2	21	3	139	3.88	2017.00	46.33	1.29

10

11   In the keyword analysis (Fig. 3c) we see clusters linked to dairy as well as beef

12   cattle. Keyword analysis shows a shift from quantitative to molecular genetics. There was

13   an increase in recent publications on tropical breeds and SNPS, including questions

14   related to thermotolerance. Although the USA dominates with the number of papers on a

15   country basis (Fig. 3b1), Australia and Brazil (Table 2) are more interactive.

16   Cited papers (Fig. 4 and Table 3) show the importance of Heather Burrow's (2001)

17   paper on productive and adaptive traits and temperament in a composite breed of tropical

18   beef cattle as well as Bolormaa et al. (2013) paper on residual feed intake. Clear clustering

19   of citations is seen. Publication sources are similar to those seen above with the

20   dominance of the Journal of Dairy Science and the Journal of Animal Science. Citation

21   clusters include those involved with candidate genes, production traits, genetic ×

22   environment interactions, among others. Once again, the USA, Australia and Brazil

23   dominate the citation analysis, and distinct groups are seen within these countries (such

24   as Brazil- purple and green, USA- dark blue and South Africa - orange).
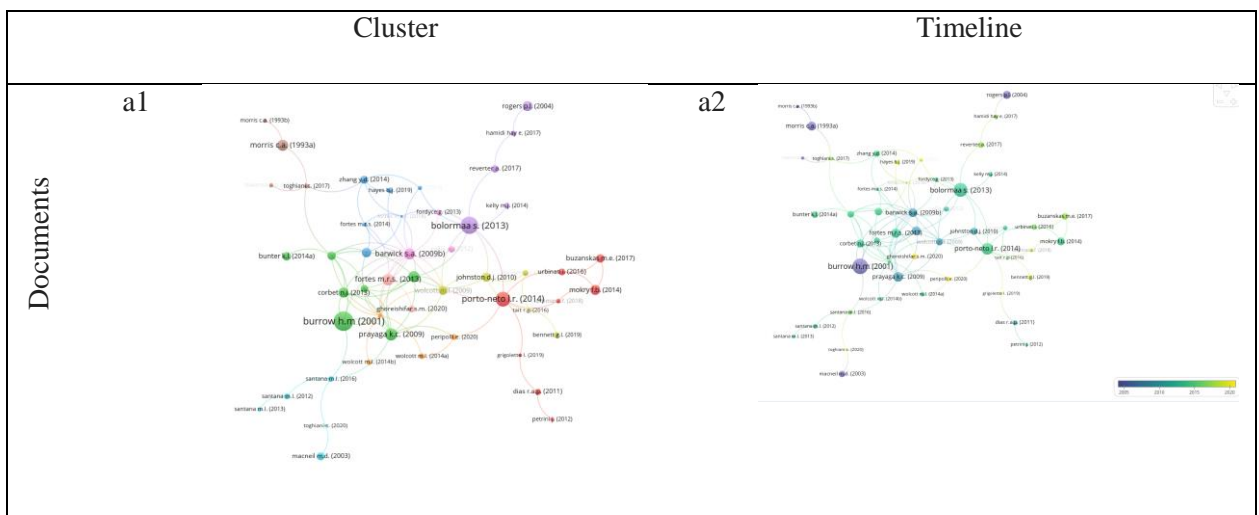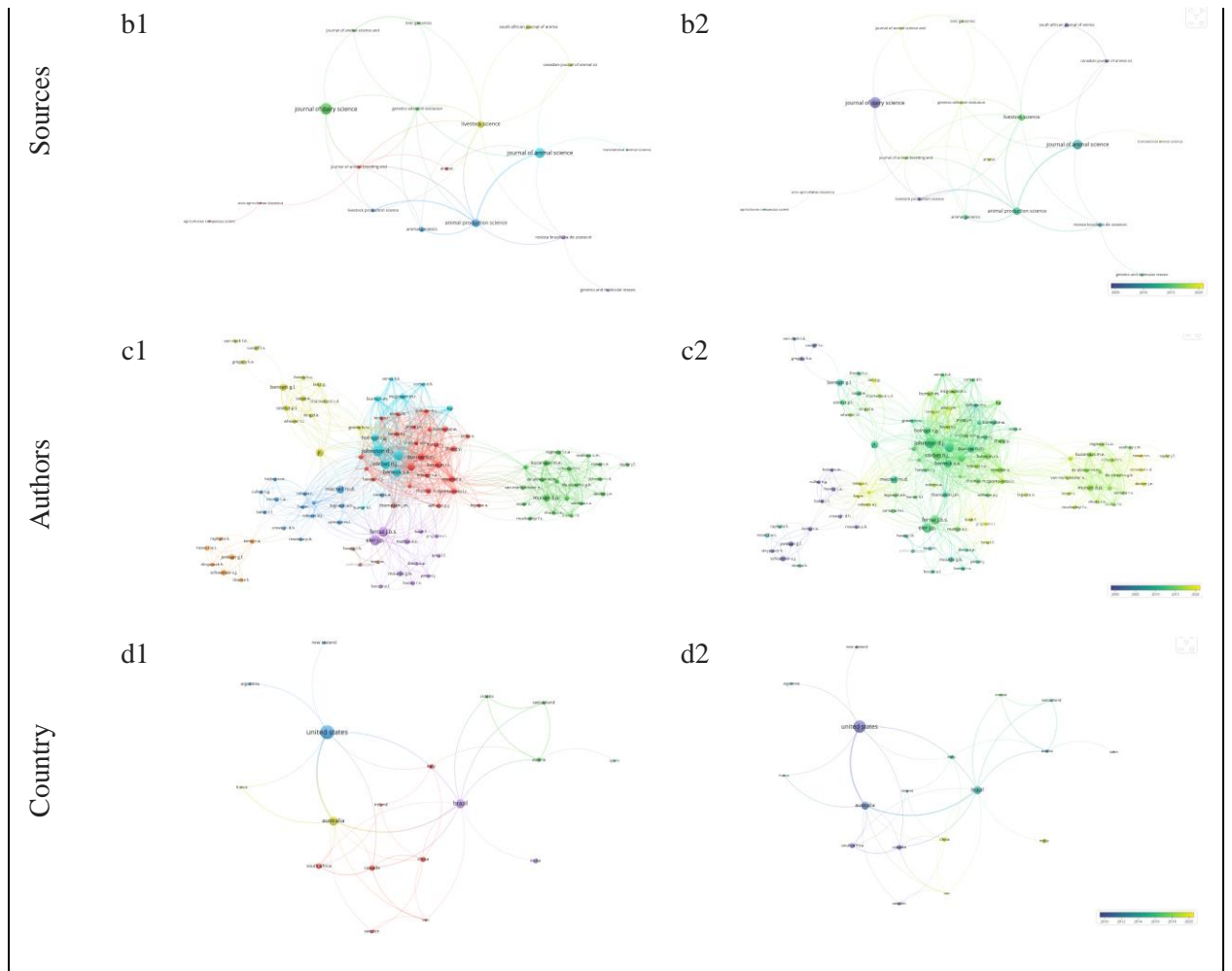
Cluster	Timeline

Fig. 4. Citation Analysis for publications on composite cattle breeds by cluster and timeline for a) documents; b) sources; c) authors and d) country.

Table 3.

Top 20 Cited Papers on composite cattle breeds.

Paper	URL
Burrow H.M. Variances and covariances between productive and adaptive traits and temperament in a composite breed of tropical beef cattle; Livest. Prod Sci, 70(3), 213-233, 2001	https://doi.org/10.1016/s0301-6226(01)00178-6
Bolormaa S.; et al. Accuracy of prediction of genomic breeding values for residual feed intake and carcass and meat quality traits in *Bos taurus*, *Bos indicus*, and composite beef cattle. J. Anim. Sci., 91(7), 3088-3104; 2013	https://doi.org/10.2527/jas.2012-5827
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Prayaga k.c.; et al. Genetics of adaptive traits in heifers and their relationship to growth, pubertal and carcass traits in two tropical beef cattle genotypes, Anim. Prod. Sci., 49(6), 413-425, 2009	https://doi.org/10.1071/ea08247
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In Bibliographic coupling (Fig. 5) we see some newer papers, such as Rowan et al. (2019), Soufleri et al. (2019) and Peripolli et al. (2020). Peripolli´s study assessed the distribution of runs of homozygosity (ROH) and autozygosity islands in the composite Montana Tropical® beef cattle to explore hotspot regions which could better characterize the different biological types within the composite breed. This paper is published in Journal of Animal Breeding and Genetics, with an impact factor of 2.6 and has an Article Processing Charge (APC) of $4330 USD. This is a consolidated journal with publications since 1924.

The Journal of Dairy Science remain the most important (Fig. 5). Still, we see a recent increase in journals such as Animal, Animals and Animal Production Science. Coupling is well defined by the researcher's country in general, with the more recent appearance of Chinese, Indian, Iranian and Egyptian references.
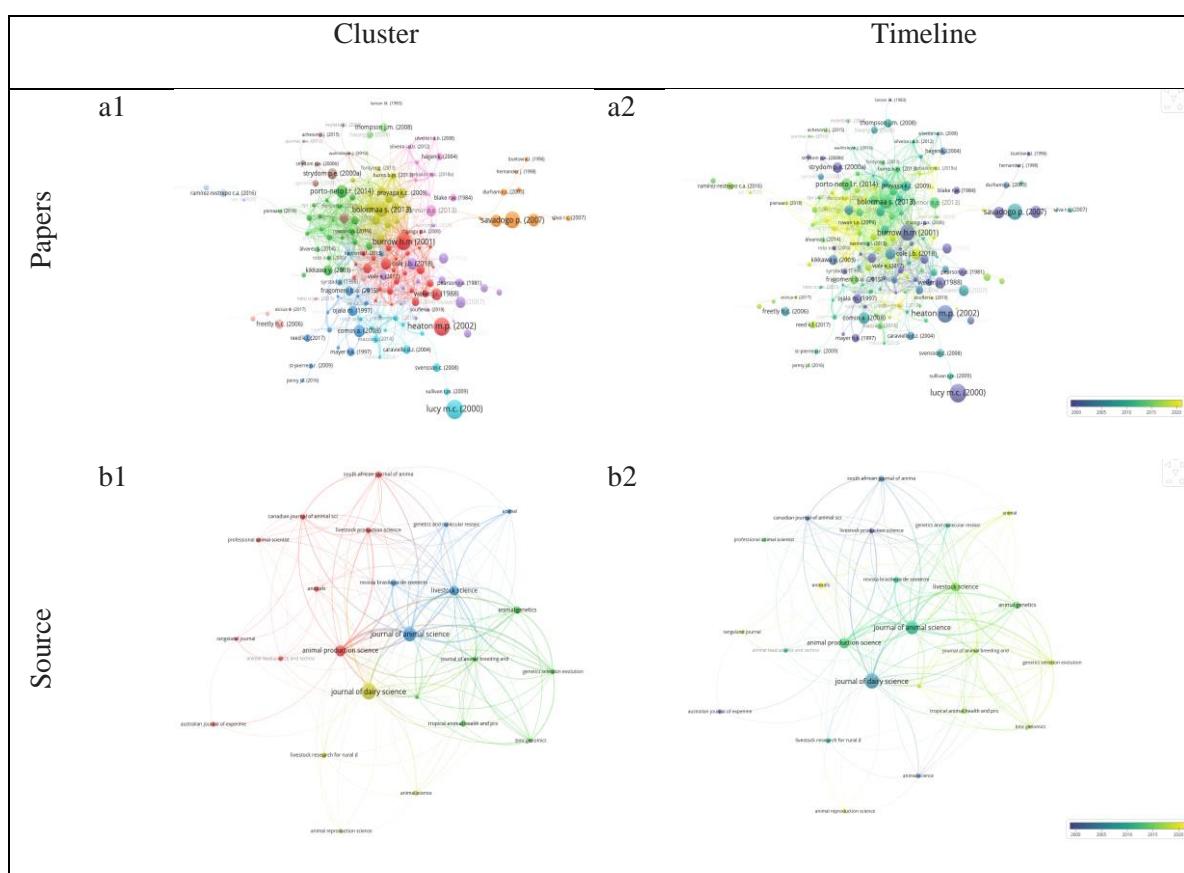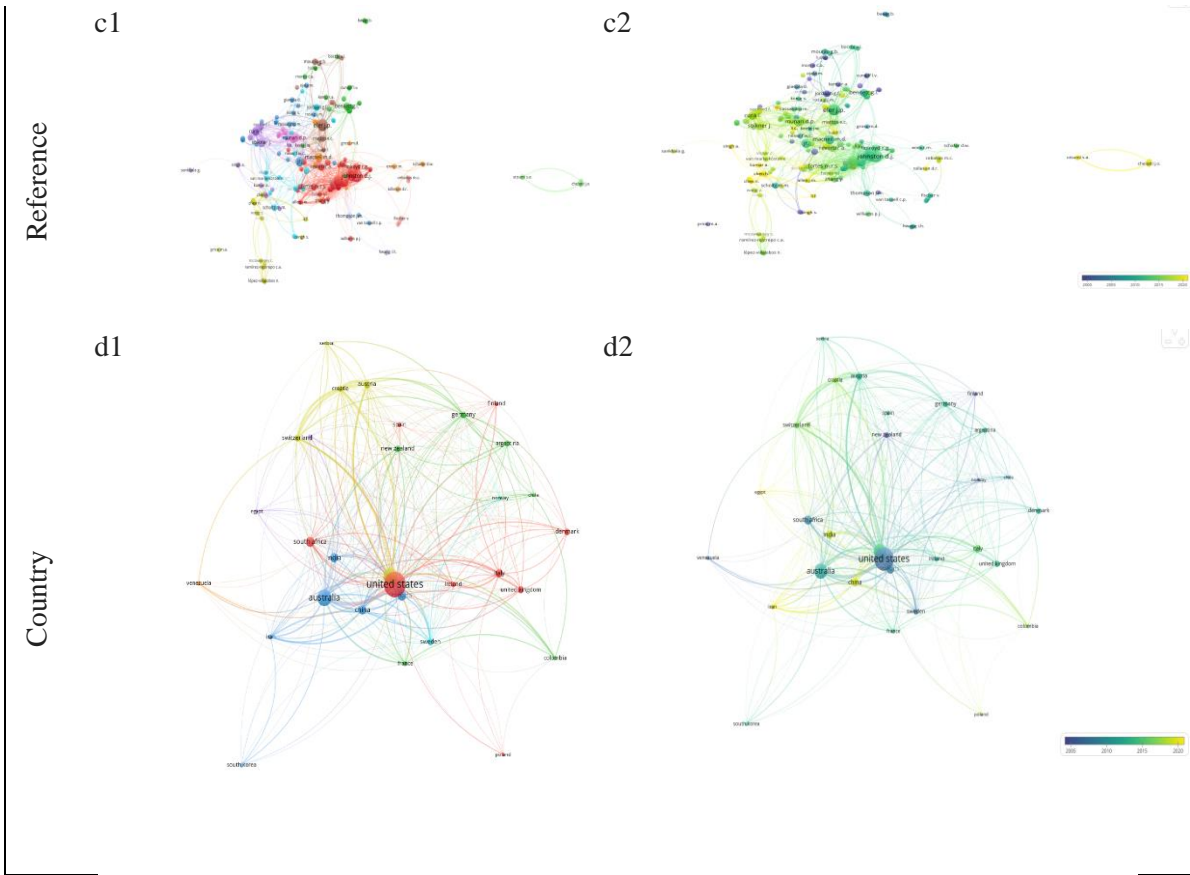
Fig. 5. Bibliographic Coupling Analysis for publications on composite cattle breeds by cluster and timeline for a) papers; b) source; c) reference and d) country.

For co-citation analysis, papers are cited in distinct groups, possibly because of the breed involved (for example, Tropical Composite in Brazil – green – or Australia). Given the large number of papers cited (11,800) these groups are small with weak linkages, but country and research groups can be observed (Fig. 6b and c).
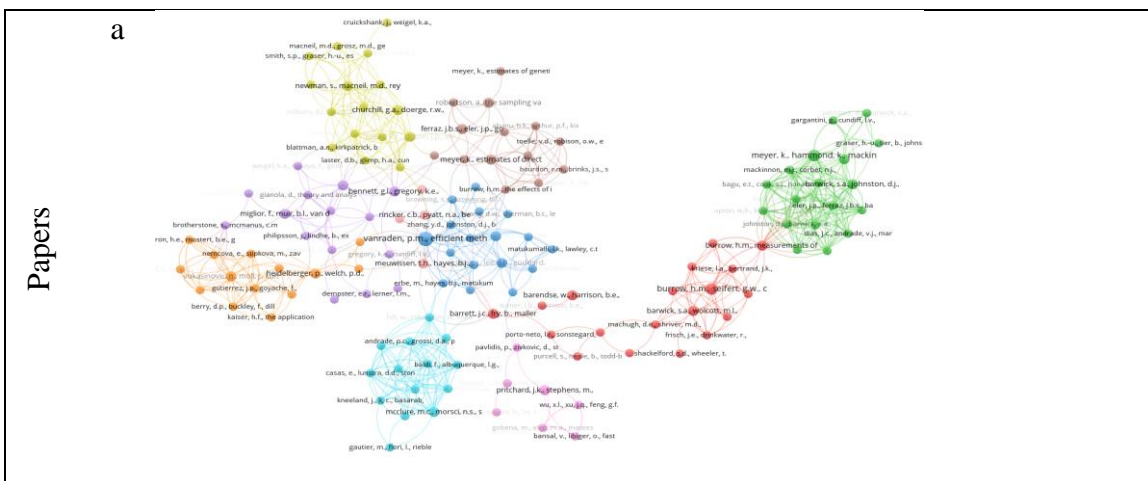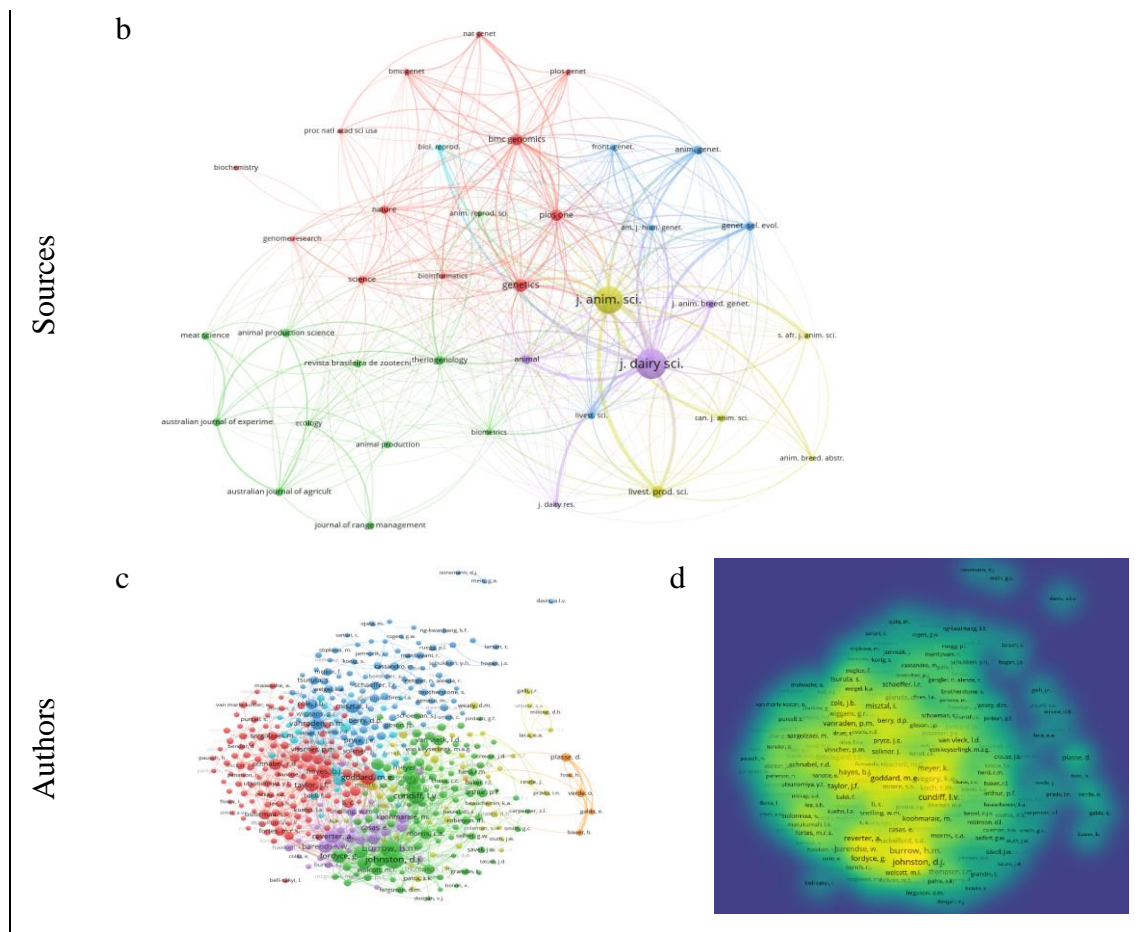
Fig. 6. Co-citation Analysis for publications on composite cattle breeds for a) papers; b) sources, c) authors and d) density network for authors

The dominance of Australia and USA researchers in the cited works is again evident (Table 4). Looking at their institutions, the University of New England in Amidale, University of Queensland, and ARS-USDA.

Table 4. Top 20 Cited Authors for publications on composite cattle breeds[1].

Author	Country	Institution	Cluster	Links	Total link strength	Citations
Johnston, D.J.	Australia	UNE	2	302	11625	135
Burrow, H.M.	Australia	UNE	2	315	10184	134
Cundiff, L.V.	USA	ARS-USDA	2	362	5784	106
Goddard, M.E.	Australia	Melbourne	1	382	9332	102
Gregory, K.E.	USA	ARS-USDA	2	376	5351	94
Fordyce, G.	Australia	Queensland	2	323	6365	83
Reverter, A.	Australia	CSIRO	5	353	7561	80

Misztal, I.	USA	Georgia	3	340	4676	76
Taylor, J.F.	USA	Missouri	1	371	6683	75
Koch, R.M.	USA	ARS-USDA	2	350	4236	74
Hayes, B.J.	Australia	Queensland	1	353	7078	73
Barendse, W.	Australia	Queensland	5	327	6017	70
Barwick, S.A.	Australia	UNE	2	278	6014	67
Holroyd, R.G.	Australia	UNE	2	265	5267	67
Meyer, K.	Australia	UNE	2	298	4396	67
VanRaden, P.M.	USA	ARS-USDA	3	354	6515	65
Corbet, N.J.	Australia	CQUni	2	322	5621	64
Koohmaraie, M.	USA	IEH Labs & Consult	5	298	4143	59
Schnabel, R.D.	USA	Missouri	1	347	6122	56
MacNeil, M.D.	USA/SA	Delta G	2	300	2488	55

[1]Number of citations is relative to this data set, not to all citations for the authors

Citation accumulation takes time (Fig. 7), showing a quadratic response. No papers after 2020 appeared with significant citation indices. This is not unusual as accumulation of citations takes time.
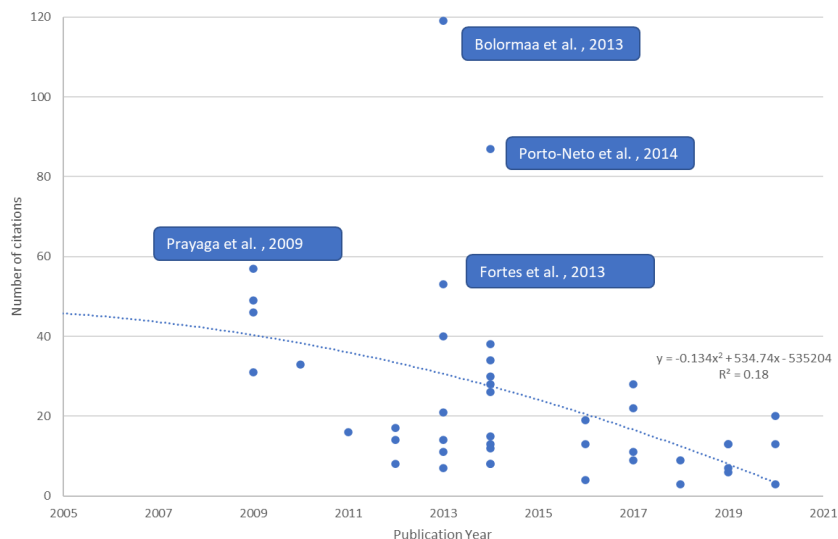
Fig. 7. Number of citations by year of publication for papers on composite cattle breeds (2005-2020).

2.4 Discussion

The overall increase in documents may reflect the overall scientific production worldwide (Fire and Guestrin, 2019). Regarding the dataset, Rogers et al. (2020) have indicated that bibliometric analysis needs at least 200 references, whereas our set had 351. Several trends were seen in the study. Keyword co-occurrence helps in understanding patterns in the document-set that underlie the research. These include the growing interest in genetic aspects of heat stress, especially with SNPs, sequencing and selection signatures. Within this area, there has been a move away from quantitative toward molecular genetics, crossbreeding, and heterosis. Unlike other areas (Fire and Guestrin, 2019), there has been no move towards "super-journals" such as PlosOne.

Through the bibliometric analysis, we can also see the networks in co-authorships, thereby understanding how groups work together. Co-authorship reveals the interactions of authors, contributing countries, or affiliations for advancing research fields (Tamala et al., 2022).

According to Mörschbächer and Granada (2022), high-income countries tend to dominate publishing ranks (produce and publish more documents) as they tend to have higher funding and suitable tools, equipment, and structure. Although this was true here in general, with countries such as the USA, Brazil is seen as a major publisher in this field, especially with researchers from São Paulo state.

Citations of publications from these developing countries are relevant in the present study. These may be especially interesting worldwide for the current research topic due to unfavorable production environments (Bayssa et al., 2021; Sejian et al., 2021), the presence of locally adapted species and breeds (McManus et al., 2020), and local knowledge (Makondo and Thomas, 2018).

Bibliographic coupling shows references shared by two documents as a measure of comparison, while co-citations determine the conceptual structure of the study topic. As such, trends here follow publishing and citation trends as described above. Since method selection depends on the questions the literature review sets out to answer, in this review we used bibliographic coupling to provide a prospective approach. Bibliographic coupling associates papers that have similarities in their reference lists, indicating the probability of a shared related topic. Bibliographic coupling analysis groups articles in accordance with the similarities between citing documents that reference the same set of cited documents. The larger the number of references cited in common in two publications, the stronger the bibliographic coupling relationship between these documents (Van Eck and Waltman, 2010).

As science becomes more collaborative the identification of individuals, teams, and institutions is crucial for scientific progress (Schleyer et al., 2012). Bibliometric research as seen here can help identify researchers with particular areas of expertise, affiliations, interests, or resources (Weber and Yuan, 2019). Here we were able to identify links between research groups and countries and the people responsible for these links. The increased network has also been enhanced by the use of the internet (Yu, 2021).

The results of the bibliographic coupling analysis are presented visually in Fig. 5 by means of a map indicating thematic clusters. The nodes (circles) represent the articles that were labelled with the surname of the first author. The location of each node and its colour are used to group the articles from the same cluster, while the size of each node depends on the weight of the articles (citations of each article).

The current Article Processing Charge (APC) in the Journal of Dairy Science is USD 3,500 (the most important journal in the present analysis), reflects almost double a

university lecturer's monthly liquid salary. Many Global South researchers, therefore, publish behind paywalls or in local and non-English journals, making international citations more difficult. Many of the top journals in co-citation or bibliographic coupling are open access, so their appearance on these lists, as well as the predominance of certain research groups and countries, may reflect the ability to pay APCs.

Quality articles that have been published more recently may not be identified because of, as yet, low citation frequency. The research is biased by the keywords used and may not cover all of the literature. The study was also limited by language use, with only publications in English or the Scopus database included in the analysis. Nevertheless, we feel it helps in understanding tendencies in this field of research and may point to future actions within the research community.

2.5 Conclusions

This bibliometric analysis provides a basic worldwide overview of research publications on composite cattle. It can help direct future research and construct structured reviews on the subject of interest. The most important papers in the research area were cited, and bibliographic coupling showed the linkages between research groups. Major research groups were identified in Australia, United States of America and Brazil.

Data availability

Data will be made available on request.

Declaration of generative AI and AI-assisted technologies in the writing process

None

CRediT authorship contribution statement

Concepta McManus: Conceptualization, Methodology, Formal analysis, Supervision, Writing - Review & Editing, Project administration, Funding acquisition. **Felipe Pimentel:** Investigation, Data Curation, Writing - Original Draft. **José Bento Ferraz:** Conceptualization, Methodology, Resources. **Rafael Núñez-Domínguez:** Conceptualization, Writing - Review & Editing. **Renato Fontes Guimarães:** Conceptualization, Methodology, Formal analysis, Supervision, Writing - Review & Editing. **Daniel Pimentel:** Investigation, Data Curation, Writing - Original Draft. **Luis Telo da Gama:** Conceptualization, Writing - Review & Editing. **Nathalia da Silva Costa:** Conceptualization, Methodology, Investigation, Data Curation, Writing - Original Draft, Project administration. **Vanessa Peripolli:** Conceptualization, Writing - Review & Editing.

Conflict of Interest

The authors declare no conflict of interest.

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Ethics Committee Approval

Animal Care Committee approval was not obtained for this study as all the analyses were performed using pre-existing databases.

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2.7 Annex: Research Terms

(TITLE-ABS-KEY (composite) AND TITLE-ABS-KEY (cattle)) AND (LIMIT-TO (PUBSTAGE , "final")) AND (LIMIT-TO (DOCTYPE , "ar")) AND (LIMIT-TO (SRCTYPE , "j")) AND (EXCLUDE (EXACTKEYWORD , "Chemistry") OR EXCLUDE (EXACTKEYWORD , "Resin") OR EXCLUDE (EXACTKEYWORD , "Composite Resins") OR EXCLUDE (EXACTKEYWORD , "Dental Bonding") OR EXCLUDE (EXACTKEYWORD , "Materials Testing") OR EXCLUDE (EXACTKEYWORD , "Comparative Study") OR EXCLUDE (EXACTKEYWORD , "Methodology") OR EXCLUDE (EXACTKEYWORD , "Resin Cements") OR EXCLUDE (EXACTKEYWORD , "Resin Cement") OR EXCLUDE (EXACTKEYWORD , "Priority Journal") OR EXCLUDE (EXACTKEYWORD , "Human") OR EXCLUDE (EXACTKEYWORD , "Surface Property") OR EXCLUDE (EXACTKEYWORD , "Surface Properties") OR EXCLUDE (EXACTKEYWORD , "Dentin") OR EXCLUDE (EXACTKEYWORD , "Humans") OR EXCLUDE (EXACTKEYWORD , "Enamel") OR EXCLUDE (EXACTKEYWORD , "Scanning Electron Microscopy") OR EXCLUDE (EXACTKEYWORD , "Dental Enamel") OR EXCLUDE (EXACTKEYWORD , "Dentin-Bonding Agents") OR EXCLUDE (EXACTKEYWORD , "Dentin Bonding Agent") OR EXCLUDE (EXACTKEYWORD , "Tensile Strength") OR EXCLUDE (EXACTKEYWORD , "Dental Stress Analysis") OR EXCLUDE (EXACTKEYWORD , "Ultrastructure") OR EXCLUDE (EXACTKEYWORD , "Procedures") OR EXCLUDE (EXACTKEYWORD , "Time Factors") OR EXCLUDE (EXACTKEYWORD , "Microscopy, Electron, Scanning") OR EXCLUDE (EXACTKEYWORD , "Analysis Of Variance") OR EXCLUDE (EXACTKEYWORD , "Stress, Mechanical") OR EXCLUDE (EXACTKEYWORD , "Dental Surgery") OR EXCLUDE (EXACTKEYWORD , "Mechanical Stress") OR EXCLUDE (EXACTKEYWORD , "Time") OR EXCLUDE (EXACTKEYWORD , "Acid Etching, Dental") OR EXCLUDE (EXACTKEYWORD , "Methacrylates") OR EXCLUDE (EXACTKEYWORD , "Unclassified Drug") OR EXCLUDE (EXACTKEYWORD , "Drug Effect") OR EXCLUDE (EXACTKEYWORD , "Dental Restoration, Permanent") OR EXCLUDE (EXACTKEYWORD , "In Vitro Study") OR EXCLUDE (EXACTKEYWORD , "Dental Care") OR EXCLUDE (EXACTKEYWORD , "Bisphenol A-Glycidyl Methacrylate") OR EXCLUDE (EXACTKEYWORD , "Random Allocation") OR EXCLUDE (EXACTKEYWORD , "Collagen") OR EXCLUDE (EXACTKEYWORD , "Cytology") OR EXCLUDE (EXACTKEYWORD , "Randomization") OR EXCLUDE (EXACTKEYWORD , "Methacrylic Acid Derivative") OR EXCLUDE (EXACTKEYWORD , "Dental Materials") OR EXCLUDE (EXACTKEYWORD , "Dental Acid Etching") OR EXCLUDE (EXACTKEYWORD , "Shear Strength") OR EXCLUDE (EXACTKEYWORD , "Bisphenol A Bis(2 Hydroxypropyl) Ether Dimethacrylate") OR EXCLUDE (EXACTKEYWORD , "Bovine Serum Albumin") OR EXCLUDE (EXACTKEYWORD , "Serum Albumin, Bovine") OR EXCLUDE (EXACTKEYWORD , "Dental Cements") OR EXCLUDE (EXACTKEYWORD , "Tissue Engineering") OR EXCLUDE (EXACTKEYWORD , "Animal Cell") OR EXCLUDE (EXACTKEYWORD , "Animal Experiment") OR EXCLUDE (EXACTKEYWORD , "Tooth Cement") OR EXCLUDE (EXACTKEYWORD , "Tooth Disease") OR EXCLUDE (EXACTKEYWORD , "Isolation And Purification") OR EXCLUDE (EXACTKEYWORD , "Incisor") OR EXCLUDE (EXACTKEYWORD , "Dental Procedure") OR EXCLUDE (EXACTKEYWORD ,

"Biocompatible Materials") OR EXCLUDE (EXACTKEYWORD , "Biomechanics") OR EXCLUDE (EXACTKEYWORD , "Adhesion") OR EXCLUDE (EXACTKEYWORD , "Composite Material") OR EXCLUDE (EXACTKEYWORD , "Cell Culture") OR EXCLUDE (EXACTKEYWORD , "Cementation") OR EXCLUDE (EXACTKEYWORD , "Proteins") OR EXCLUDE (EXACTKEYWORD , "Glass Ionomer") OR EXCLUDE (EXACTKEYWORD , "Pathology") OR EXCLUDE (EXACTKEYWORD , "Polymers") OR EXCLUDE (EXACTKEYWORD , "Instrumentation") OR EXCLUDE (EXACTKEYWORD , "Biomaterial") OR EXCLUDE (EXACTKEYWORD , "Glass Ionomer Cements") OR EXCLUDE (EXACTKEYWORD , "Hydroxyapatite") OR EXCLUDE (EXACTKEYWORD , "Polymer") OR EXCLUDE (EXACTKEYWORD , "PH") OR EXCLUDE (EXACTKEYWORD , "Adhesives") OR EXCLUDE (EXACTKEYWORD , "Tissue Scaffolds") OR EXCLUDE (EXACTKEYWORD , "Cell Count") OR EXCLUDE (EXACTKEYWORD , "Cell Proliferation") OR EXCLUDE (EXACTKEYWORD , "Acrylic Resins") OR EXCLUDE (EXACTKEYWORD , "Body Fluids") OR EXCLUDE (EXACTKEYWORD , "Nonparametric Test") OR EXCLUDE (EXACTKEYWORD , "Hardness") OR EXCLUDE (EXACTKEYWORD , "Particle Size") OR EXCLUDE (EXACTKEYWORD , "Polymethacrylic Acids") OR EXCLUDE (EXACTKEYWORD , "Dental Leakage") OR EXCLUDE (EXACTKEYWORD , "Phosphoric Acid") OR EXCLUDE (EXACTKEYWORD , "Polymethacrylic Acid Derivative") OR EXCLUDE (EXACTKEYWORD , "Single Bond") OR EXCLUDE (EXACTKEYWORD , "Tooth Crown") OR EXCLUDE (EXACTKEYWORD , "Adhesive Agent") OR EXCLUDE (EXACTKEYWORD , "Tissue") OR EXCLUDE (EXACTKEYWORD , "Tissue Scaffold") OR EXCLUDE (EXACTKEYWORD , "Classification") OR EXCLUDE (EXACTKEYWORD , "Biocompatibility") OR EXCLUDE (EXACTKEYWORD , "Acrylic Acid Resin") OR EXCLUDE (EXACTKEYWORD , "Orthodontic Brackets") OR EXCLUDE (EXACTKEYWORD , "Polymerization") OR EXCLUDE (EXACTKEYWORD , "Porosity") OR EXCLUDE (EXACTKEYWORD , "Silicon Dioxide") OR EXCLUDE (EXACTKEYWORD , "Phosphoric Acids") OR EXCLUDE (EXACTKEYWORD , "Cells, Cultured") OR EXCLUDE (EXACTKEYWORD , "Durapatite") OR EXCLUDE (EXACTKEYWORD , "Light") OR EXCLUDE (EXACTKEYWORD , "Dental Material") OR EXCLUDE (EXACTKEYWORD , "Mice") OR EXCLUDE (EXACTKEYWORD , "Dental Caries") OR EXCLUDE (EXACTKEYWORD , "Histology") OR EXCLUDE (EXACTKEYWORD , "Hydrogen-Ion Concentration") OR EXCLUDE (EXACTKEYWORD , "Drug Effects") OR EXCLUDE (EXACTKEYWORD , "Growth, Development And Aging") OR EXCLUDE (EXACTKEYWORD , "Antiinfective Agent") OR EXCLUDE (EXACTKEYWORD , "Nanoparticles") OR EXCLUDE (EXACTKEYWORD , "Orthodontic Device") OR EXCLUDE (EXACTKEYWORD , "Bone And Bones") OR EXCLUDE (EXACTKEYWORD , "Mouse") OR EXCLUDE (EXACTKEYWORD , "Nanocomposite") OR EXCLUDE (EXACTKEYWORD , "Adhesiveness") OR EXCLUDE (EXACTKEYWORD , "Cell Adhesion") OR EXCLUDE (EXACTKEYWORD , "Dental Cavity Preparation")) AND (EXCLUDE (SUBJAREA , "MEDI") OR EXCLUDE (SUBJAREA , "ENGI") OR EXCLUDE (SUBJAREA , "CHEM") OR EXCLUDE (SUBJAREA , "EART") OR EXCLUDE (SUBJAREA , "MATE") OR EXCLUDE (SUBJAREA , "BUSI") OR EXCLUDE (SUBJAREA , "MULT") OR EXCLUDE (SUBJAREA , "CENG") OR EXCLUDE (SUBJAREA , "ARTS") OR EXCLUDE (SUBJAREA , "PHYS") OR EXCLUDE (SUBJAREA

, "DECI") OR EXCLUDE (SUBJAREA , "MATH") OR EXCLUDE (SUBJAREA , "ECON") OR EXCLUDE (SUBJAREA , "NURS") OR EXCLUDE (SUBJAREA , "DENT")) AND (EXCLUDE (EXACTKEYWORD , "Controlled Study") OR EXCLUDE (EXACTKEYWORD , "Ovis Aries") OR EXCLUDE (EXACTKEYWORD , "Zea Mays") OR EXCLUDE (EXACTKEYWORD , "Friesia") OR EXCLUDE (EXACTKEYWORD , "Eating") OR EXCLUDE (EXACTKEYWORD , "Sheep") OR EXCLUDE (EXACTKEYWORD , "Streptococcus") OR EXCLUDE (EXACTKEYWORD , "Escherichia Coli") OR EXCLUDE (EXACTKEYWORD , "Staphylococcus") OR EXCLUDE (EXACTKEYWORD , "Enzyme Linked Immunosorbent Assay") OR EXCLUDE (EXACTKEYWORD , "Enzyme-Linked Immunosorbent Assay"))

3. SPATIAL DISTRIBUTION OF GENETIC VALUES FOR THE BRAZILIAN MONTANA TROPICAL CATTLE BREED

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Abstract

The article analyzed genetic values on 571,424 Montana Tropical animals born between 1950 and 2019 from 63 farms located in 10 Brazilian states. The following characteristics were analyzed, birth, weaning and yearling weights, daily weight gain, scrotal circumference, navel, muscle and height scores, index Montana, and maternal effect. Data were spatialized in ArcGIS together with environmental and socioeconomic information, including soil type, altitude, rainfall precipitation, relative humidity, Normalized Difference Vegetation Index (NDVI), Temperature and Humidity Index (THI), air

temperature and solar radiation as well as population density and gross domestic product. Analyses showed that most environmental and socioeconomic characteristics affected genetic values, with significant changes over the years. Cluster groups for high genetic value were in regions with higher altitudes, medium to high NDVI, especially after weaning, low THI, lower population density, higher mean air temperature and lower relative humidity, but lower solar radiation. All traits had significant autocorrelations, except birth weight. Environmental and socioeconomic conditions showed regional variation over time and these affected genetic values in Montana Tropical cattle breed.

Keywords: Cattle, Genetic landscape shape, Georeference, Spatial correlation

3.1 Introduction

Most livestock production in the world occurs in tropical and subtropical areas, in a wide range of heterogeneous production systems ranging from grassland-based to feedlot systems. Animal husbandry faces many challenges since several environmental factors can affect livestock production, especially in tropical regions where the air temperature and relative humidity directly influence the production potential of the animals (Marino et al., 2016). Given the variability of climates and landscapes, matching the animal's biological type to its environment is essential, increasing its optimal performance in a challenging environment. Climatic adaptation in cattle is a complex issue, and there are strong differences between breeds regarding heat tolerance (Beatty et al., 2006; McManus et al., 2009; Renaudeau et al., 2011; 2012; Cardoso et al., 2015; 2016) and other efficiency and adaptive-related traits (Prayaga et al., 2009; Wolcott et al., 2014; Alfonzo et al., 2016).

The Montana Tropical is a composite breed developed for tropical and subtropical beef cattle systems under grazing conditions. The breeding system for this breed proposes

the formation of clusters defined by biological types according to phenotype similarity, physiology, growth and reproduction traits, combining both *Bos taurus indicus* and *Bos taurus taurus* individuals.

The base population is centred on four different biological types (NABC), where: N is *B. taurus indicus* cattle breeds already adapted to tropical conditions (heat tolerance, resistance to parasites, and poor feeding management); A is *B. taurus taurus* cattle breeds known for their fertility and adaptive traits under tropical conditions; B is *B. taurus taurus* British breeds indicated for sexual precocity, carcass quality, and high growth rate; and C is European Continental breeds recognised for high growth rates and carcass quality. However, the composition of these cattle may vary due to regional climates and breeder preferences. As a result, they can be empirically classified into two main biological types called adaptive or productive (Peripolli et al., 2020).

Development of the livestock industry within a country or region (McManus et al., 2016) has implications on several aspects (genetics, adaptation, welfare, nutrition). Regions in Brazil differ in farmer profiles, and types of agriculture and livestock farming practised (Cervo et al. 2018). Silva et al. (2013) state that environmental and climatic factors associated with solar incidence oscillations, rainfall precipitation, and different soils also interfere in animal production. Worldwide, studies related to animal production have demonstrated that there will be a need to replace breeds and species in production systems in the next 30 years due to changes in the environment and market demands (Yahdjian and Sala, 2008). Therefore, the study of landscape genetics helps to promote the understanding of how environmental characteristics interfere with the structure of the animals' genetic variation. For example, Costa et al. (2014; 2020) looked at the spatialisation of genetic values of Girolando and Holstein cattle in Brazil and observed that these were related to environmental and social parameters.

Given the racial diversity of Brazilian Montana Tropical cattle breed and its diffusion throughout the Brazilian territory, the present study aimed to analyse the influence of environmental and socioeconomic conditions of counties in its genetic distribution.

3.2 Material and Methods

The animals used in this study comprise a dataset from the Brazilian Montana Tropical cattle breeding program. Genetic values (Expected Progeny Differences - EPD) for production traits on 571.424 male and female animals born between 1950 and 2019 from 63 farms located in 10 Brazilian states were used.

The data were georeferenced through the Geographic Information System (ArcGis 10.8 software), using a geographic coordinate system and Sirgas 2000 datum. Data included BW (birth weight - kg), WW (weaning weight corrected for 205 days - kg); YW (yearling weight at 12 months– kg), Mat (maternal effect obtained by adding half EPD for weaning weight - direct effects - with EPD for maternal ability - difference expected for milk production and protection of the calf), DWG (daily weight gain from weaning to 12 months - kg), SC12 (scrotal circumference at 12 months - cm); Musc (muscle score at 12 months obtained by visual assessment - ranging from 1 to 6 following the standard procedure established by the Montana Program); Height (height score taken on the rump at 12 months - cm); Navel (navel score at 12 months obtained in males by visual assessment - ranging from 1 to 5, where higher scores are assigned to animals with longer or more pendulous navels, and lower scores to the more adherent navel (Koury Filho, 2003)) and Index (index Montana at 12 months, based on the following formula, $I_{Montana}= 2WW+2DWG+3YW+SC+2MS$, in which values are standardized - each EPD is divided by the genetic standard deviation of the trait).

Environmental and socioeconomic data were acquired from different sources as follows and detailed by Hermuche et al. (2013). For plant cover, the annual average of the Normalised Difference Vegetation Index (NDVI), derived from MODIS (Moderate Resolution Imaging Spectroradiometer) sensor images acquired from the NASA (2012) website and processed in the ENVI 4.7 software, was used. NDVI is the ratio between the difference of the reflectance measurement in the near-infrared (NIR) and red (RED) channels specified by the equation: $NDVI = (NIR - RED)/(NIR + RED)$. This index is sensitive to chlorophyll, and the presence of healthy vegetation and its range varies between -1 and 1, with the value of 1 being the highest response of photosynthetically active vegetation (Rouse et al., 1973).

Mean rainfall precipitation (mm/day) was acquired from TRMM (Tropical Rainfall Measuring Mission) images from 2000 to 2010, with a spatial resolution of 0.25 °C, approximately 27 km, downloaded from NASA (2012) and processed in Envi 4.7 software. Average air temperatures (°C) from 2000 to 2010 were obtained from images of the MODIS sensor, product MOD11, which consists of the average monthly surface temperature with a spatial resolution of 1 km. The original images were acquired on NASA's website (2012) and redesigned in the MODIS Reprojection Tool (MRT) program with geotif extension, latitude/longitude geographic projection, and WGS 84 Datum. Solar radiation (W/m2) was calculated in ArcGis from data from the SRTM topography.

Average altitude (meters above sea level) was obtained based on the SRTM (Shuttle Radar Topography Mission), which consisted in the acquisition of radar data of the entire earth's surface (except for extreme latitudes) with a resolution of 90 m acquired from the NASA (2012) website from the internet. Relative humidity (%) was obtained from the National Institute of Meteorology (INMET 2012), consisting of an average of approximately 30 years of observation from 283 climatological stations distributed throughout the national territory.

Soil type classification throughout the Brazilian territory followed the Brazilian Soil Classification System (SiBCS) (Santos et al., 2018) and corresponding World Reference Base (WRB) (IUSS Working Group WRB, 2014) and Soil Taxonomy classes (Soil Survey Staff, 2014) are shown in supplementary Table 1.

Temperature and Humidity Index (THI) was calculated from the data of temperature and humidity as follows:

THI = AT + (0.36 × DT) + 41.5, where AT = ambient temperature (°C) and DT = dew point temperature (°C).

The socioeconomic variables considered included population density (number of people/year) and GDP (gross domestic product, $/person/year) and were obtained from the IBGE website (ibge.gov.br).

For the statistical analysis, the environmental and socioeconomic variables were normalised by the Z-score method to minimise problems caused using different units considering the following formula f (X) = X −X/ δ =, where δ = standard deviation. The maps in Fig. 1 show the values of NDVI, Altitude, THI and soil type by state. Also in Fig. 1, the soil map was developed using municipal data to facilitate the visualization of the location of different types of soil in the same region.
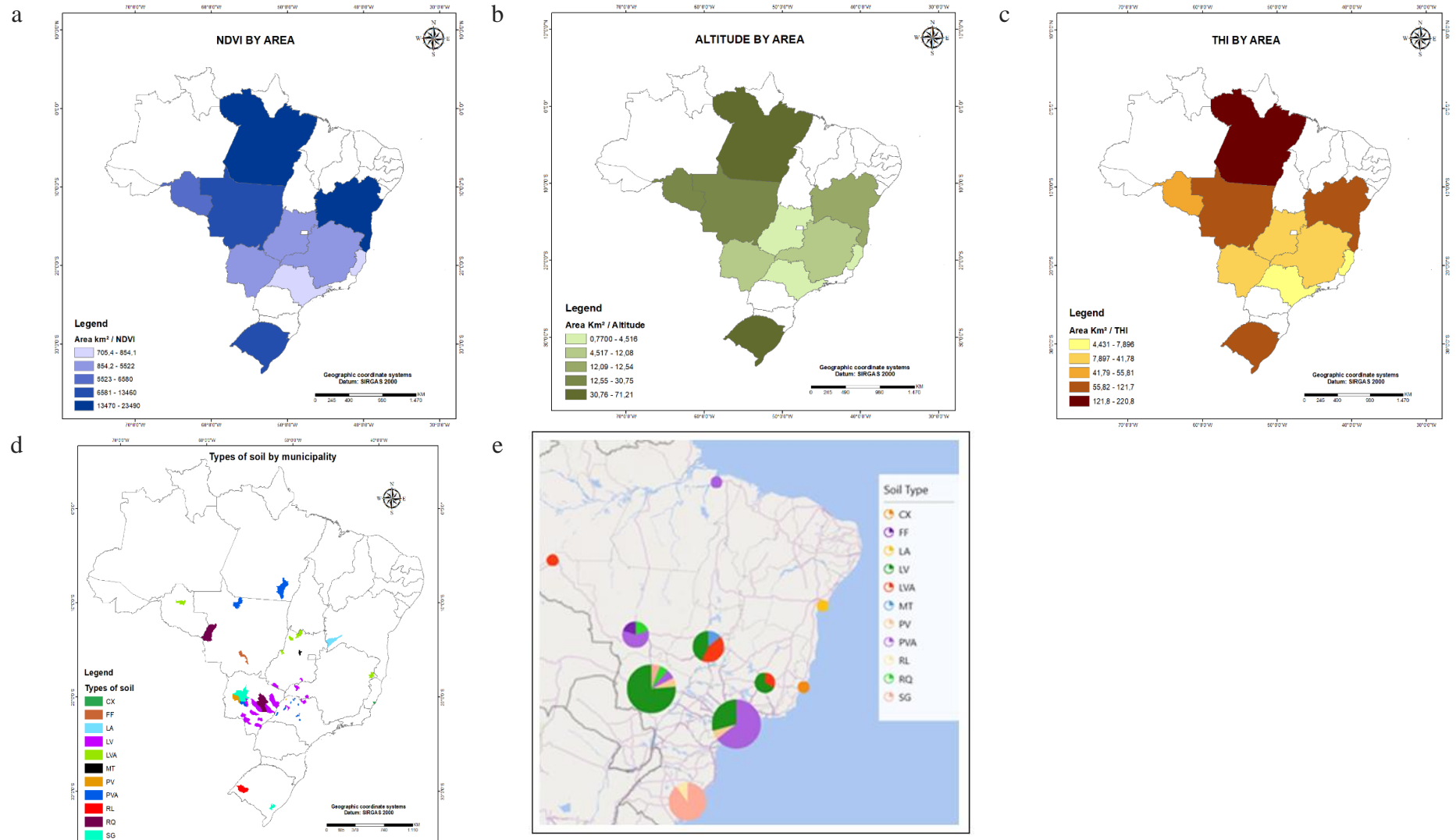
Fig. 1. Maps for average a) NDVI, b) Altitude, c) THI for Montana Tropical cattle farms in this study, d) Soil type (Supplementary Table 1) and d) states farms per soil type (the size of bubble represents the number of farms in the state). NDVI: Normalised Difference Vegetation Index, THI: Temperature and Humidity Index.

2   The averages of genetic value and accuracy were calculated by municipality based

3   on the cluster analysis method (PROC FASTCLUS) of the Statistical Analysis System

4   SAS® software (Statistical Analysis System, Cary, NC) and using the K method in

5   ArcGIS software. Two further cluster analyses were performed: i) with genetic values

6   up to weaning and ii) after weaning. The objective was to form groups minimising the

7   variability within groups and maximising the variability between groups.

8   Analyses of variance (Proc GLM) were performed to determine the effect of

9   environmental variables, soil, sex, and year of birth of the animals on genetic values as

10   well as differences between clusters. Variance Inflation factor (VIF) was identified using

11   stepwise regression analysis (PROC REG and PHREG). Clusters were formed using the

12   genetic variables (FASTCLUS and CLUSTER) and then Canonical (CANDISC) and

13   discriminant (DISCRIM; STEPDISC) analyses were also performed using Statistical

14   Analysis System SAS® software (Statistical Analysis System, Cary, NC, v.9.4). Maps

15   were created for changes in genetic values over time. Autocorrelations, Moran´s I (Moran,

16   1950) and Geary´s G (Geary, 1954) were calculated using PROC VARIOGRAM.

17   Moran's I is a measure of global spatial autocorrelation, while Geary's G is more sensitive

18   to local spatial autocorrelation. Exploratory analyses used up to 20 distance classes.

19   Omnidirectional semivariograms were fitted using exponential, Gaussian and Matérn

20   models.

21   **3.3 Results**

22   The four major states for Montana Tropical cattle herds are São Paulo (SP), with

23   16 farms, Mato Grosso do Sul (MS) with 15 and Minas Gerais (MG) and Rio Grande do

24   Sul (RS), with six each. Soil, sex, year, altitude, and solar radiation were significant for

25   all traits (Table 1). Relative humidity (RH) was the less frequent environmental effect in

26   the analysis but had a VIF > 10 together with air temperature. Normalised Difference

Vegetation Index (NDVI) was positively correlated with rainfall precipitation (r = 0.59)

and RH (r = 0.76) and negatively with Temperature and Humidity Index (THI) and air

temperature (r=-0.46 and r = -0.42). Correlations between genetic values were generally

high (r = >0.6) but lowest for navel score (r = <0.50). The correlation between genetic

values and environmental characteristics was generally low but significant (not shown;

P<0.01). Increased THI, solar radiation, and air temperature decreased genetic values (r

= 0.3). WW and SP12 had positive correlations with WW and SP12, while DWG and

maternal effect had positive correlations with altitude (r = 0.2).

Table 1. Levels of significance for environmental effects on genetic values of Montana

Tropical cattle breed in Brazil.

Environmental	Genetic values									
	BW	WW	Mat	DWG	YW	SC12	Musc	Height	Navel	Index
Soil type	*	*	*	*	*	*	*	*	*	*
Sex	*	*	*	*	*	*	*	*	*	*
Year	*	*	*	*	*	*	*	*	*	*
Solar radiation	*	*	*	*	*	*	*	*	*	*
Rainfall precipitation	*		*	*	*		*	*	*	*
Altitude	*	*	*	*	*	*	*	*	*	*
Air temperature	*	*		*			*	*	*	*
NDVI	*	*		*		*	*	*	*	*
THI			*	*	*	*		*	*	*
Relative humidity						*	*		*	

NDVI: Normalised Difference Vegetation Index, THI: Temperature and Humidity Index,
BW: birth weight, WW: weaning weight, DWG: daily weight gain, YW: yearling weight
at 12 months, SC12: scrotal circumference at 12 months, Musc: muscle score, index:
index Montana.

Soil types such as LV (Red Latosol) and LVA (Red-Yellow Latosol) showed

higher genetic values (Table 2). Yellow latosol (LA) has few animals. The distribution of

46   soil types and environmental variables is shown in Fig. 1. Higher NDVIs are seen in

47   southern states with higher THI in more northern regions.

48   **Table 2.**
49   Mean genetic values for soil type on genetic values of Montana Tropical cattle breed in
50   Brazil.

Soil	Genetic values									
	BW	WW	Mat	DWG	YW	SC12	Musc	Height	Navel	Index
CX	-0.06[d]	1.41[a]	-0.95[d]	0.09[c]	1.12[b]	0.08[b]	0.02[b]	0.04[c]	0.00[b]	2.60[b]
FF	0.16[b]	-1.04[f]	-0.11[c]	-0.46[d]	-1.39[c]	-0.22[d]	-0.04[c]	-0.20[c]	0.00[b]	1.22[c]
LA	0.25[a]	-0.26[e]	4.96[a]	3.67[a]	6.09[a]	0.24[a]	0.12[a]	1.04[a]	-0.03[c]	3.91[a]
LV	0.07[c]	0.96[b]	0.20[b]	0.03[c]	1.25[b]	0.07[b]	0.02[b]	0.14[b]	0.02[a]	2.53[b]
LVA	0.08[c]	1.07[b]	0.50[b]	0.48[b]	2.38[b]	0.14[b]	0.05[b]	0.19[b]	0.02[a]	2.95[b]
MT	-0.07[d]	-0.31[e]	-0.59[d]	0.16[b]	-0.55[c]	-0.03[c]	-0.01[c]	-0.11[c]	0.00[b]	1.80[b]
PV	-0.14[e]	-1.55[f]	0.02[c]	0.00[c]	-2.01[c]	-0.12[c]	-0.03[c]	-0.21[c]	0.00[b]	1.13[c]
PVA	0.08[c]	0.85[c]	-0.18[c]	0.13[b]	1.17[b]	0.08[b]	0.03[b]	0.08[c]	0.01[a]	2.54[b]
RL	0.06[c]	0.85[c]	-0.10[c]	0.48[b]	2.00[b]	0.08[b]	0.04[b]	0.09[b]	0.01[b]	2.76[b]
RQ	-0.08[d]	0.08[d]	-0.88[d]	0.03[c]	-0.38[c]	0.01[b]	-0.01[c]	-0.08[c]	0.01[a]	1.90[b]
SG	0.09[c]	0.64[c]	-0.12[c]	0.04[c]	0.77[b]	0.04[b]	0.01[c]	0.02[c]	0.02[a]	2.35[b]

51   CX: Haplic Cambisol, FF: Petric Plinthoil, LA: Yellow Latosol, LV: Red Latosol, LVA:
52   Red-Yellow Latosol, MT: Argiluvian Chernosol, PV: Red Argisol, PVA: Red-Yellow
53   Argisol, RL: Litholic Neosol, RQ: Quartzite Neosol, SG: Hydromorphic Planosol, BW:
54   birth weight, WW: weaning weight, DWG: daily weight gain, YW: yearling weight at 12
55   months, SC12: scrotal circumference at 12 months, Musc: muscle score, index: index
56   Montana. Means with different letters in the same columns are statistically different by
57   Tukey test (P<0.05).

58
59
60   The clusters formed (Table 3) showed significant differences between means for

61   genetic values and soil types, with medium cluster with values close to zero.

62   Approximately 20 (3%) animals were in both high and low clusters when all

63   characteristics were considered together. These proportions changed when traits were

64   analysed up to and after weaning. The proportion of soil types also varied by cluster.

Table 3. Means between clusters for genetic values in Montana Tropical cattle breed for (a) all values, up to and after weaning, and b) soil type.

a)

Cluster	Genetic values										
	No. obs.	BW	WW	Mat	DWG	YW	SC12	Musc	Height	Navel	Index
All											
High	19284	0.67	8.46	3.49	1.43	14.66	0.61	0.21	1.59	0.05	7.47
Medium	663848	0.01	0.20	0.08	0.04	0.38	0.02	0.01	0.03	0.01	2.16
Low	16550	-0.49	-5.94	-3.58	0.22	-10.20	-0.41	-0.12	-1.40	-0.03	-1.66
Up to weaning											
High	93315	0.542	6.226	2.732							
Medium	408584	-0.022	-0.171	-0.498							
Low	5154	-0.652	-8.481	-3.782							
After weaning											
High	11697				2.235	16.067	0.667	0.226	1.709	0.017	7.832
Medium	454023				0.064	1.767	0.098	0.030	0.175	0.013	2.734
Low	41333				-0.085	-8.026	-0.324	-0.097	-1.071	0.012	-0.815

BW: birth weight, WW: weaning weight, DWG: daily weight gain, YW: yearling weight at 12 months, SC12: scrotal circumference at 12 months, Musc: muscle score, index: index Montana, YW: yearling weight. All means in the same columns are statistically different by Tukey test ($P<0.05$).

b)

Cluster	Soil type										
	CX	FF	LA	LV	LVA	MT	PV	PVA	RL	RQ	SG
All											
High	0.01	0.00	0.00	1.46	0.66	0.00	0.00	0.64	0.11	0.00	0.09
Medium	0.97	0.03	0.00	51.03	10.50	1.11	0.36	20.13	2.09	0.43	6.60
Low	0.01	0.00	0.00	1.94	0.31	0.04	0.01	0.98	0.09	0.01	0.39
Up to weaning											
High	0.15	0.00	0.00	9.93	2.52	0.07	0.00	3.22	0.36	0.03	0.79
Medium	0.84	0.03	0.00	43.99	8.81	1.08	0.37	18.22	1.90	0.41	6.18
Low	0.00	0.00	0.00	0.51	0.14	0.01	0.00	0.30	0.02	0.00	0.11
After weaning											

High	0.01	0.00	0.00	1.04	0.57	0.00	0.00	0.52	0.11	0.00	0.07
Medium	0.93	0.03	0.00	49.04	10.18	1.04	0.33	19.21	1.98	0.40	6.26
Low	0.05	0.00	0.00	4.34	0.72	0.12	0.04	2.02	0.20	0.04	0.75

CX: Haplic Cambisol, FF: Petric Plinthoil, LA: Yellow Latosol, LV: Red Latosol, LVA: Red-Yellow Latosol, MT: Argiluvian Chernosol, PV: Red Argisol, PVA: Red-Yellow Argisol, RL: Litholic Neosol, RQ: Quartzite Neosol, SG: Hydromorphic Planosol. All means in the same columns are statistically different by Tukey test ($P<0.05$).

73   The medium cluster had the poorest percentage classification (Table 4) and the

74 high cluster had the best. There was an overlap between clusters, as expected. Stepwise

75 analyses indicated that all environment variables, except relative humidity, were essential

76 for discrimination between clusters.

77 **Table 4.**
78 Percentage of animals correctly classified by cluster for Montana Tropical cattle breed in
79 Brazil.

From CLUSTER	Percent Classified into CLUSTER		
	High	Medium	Low
High	74.53	7.2	18.27
Medium	18.33	51.49	30.18
Low	25.53	5.88	70.59

80
81
82   Mean comparison by cluster for environmental and socioeconomic variables

83 (Table 5) showed that, in general, the high cluster groups for genetic value were in regions

84 with higher altitudes, medium to high NDVI, especially after weaning, low THI, lower

85 population density, higher average air temperature and lower relative humidity, but lower

86 solar radiation.

87

88   **Table 5.** Means of environmental and socioeconomic characteristics by Cluster for Montana Tropical cattle breed in Brazil.

	All		Up to weaning		After weaning	
	Mean	CLUSTER	Mean	CLUSTER	Mean	CLUSTER
Altitude (m)	355.27[b]	Low	356.04[b]	Medium	353.38[b]	High
	358.13[ab]	Medium	358.47[b]	Low	354.81[b]	Low
	359.96[a]	High	366.99[a]	High	358.50[a]	Medium
Rainfall Precipitation (mm/day)	0.1702[c]	Low	0.1691[c]	Low	0.1704[c]	High
	0.1709[b]	High	0.1716[b]	Medium	0.1709[b]	Low
	0.1718[a]	Medium	0.1723[a]	High	0.1718[a]	Medium
NDVI	0.564[b]	Low	0.562[c]	Low	0.567[c]	Low
	0.569[a]	High	0.566[b]	High	0.570[b]	Medium
	0.570[a]	Medium	0.571[a]	Medium	0.573[a]	High
THI	78.48[c]	High	78.52[c]	High	78.46[c]	High
	78.75[b]	Medium	78.79[b]	Medium	78.74[b]	Medium
	78.94[a]	Low	79.04[a]	Low	78.86[a]	Low
GDP ($/person/year)	446196[c]	High	451953[c]	High	465100[b]	High
	589712[b]	Low	621118[b]	Low	612304[a]	Low
	637570[a]	Medium	670726[a]	Medium	635815[a]	Medium
Population density (number)	33388[c]	High	34367[c]	High	34675[b]	High
	44347[b]	Low	45084[b]	Low	46610[a]	Low
	48118[a]	Medium	50565[a]	Medium	47944[a]	Medium
Relative humidity (%)	70.26[c]	Low	70.02[b]	Low	70.51[c]	Low
	70.85[b]	Medium	70.79[a]	High	70.85[b]	Medium
	71.01[a]	High	70.85[a]	Medium	71.19[a]	High
Air temperature (ºC)	28.72[c]	High	28.75[c]	High	28.70[c]	High
	28.92[b]	Medium	28.96[b]	Medium	28.92[b]	Medium
	29.10[a]	Low	29.19[a]	Low	29.03[a]	Low
Solar radiation (W/m²)	838322.1[c]	High	840212.5[c]	High	838556.8[c]	High
	851003.5[b]	Medium	853311.5[b]	Medium	850607.6[b]	Medium
	868313.9[a]	Low	872659.1[a]	Low	862120.5[a]	Low

89   NDVI: Normalised Difference Vegetation Index, THI: Temperature and Humidity Index, GDP: gross domestic product. Means with different

90   letters in the same columns are statistically different by Tukey test (P<0.05).

91   In the canonical analysis (Fig. 2), the high cluster was associated with altitude and

92   the low cluster with higher solar radiation and air temperatures. The medium cluster was

93   associated with higher NDVI, rainfall precipitation and relative humidity. High and

94   medium clusters were in the regions of lower THI and air temperature, giving the animal

95   greater thermal comfort.
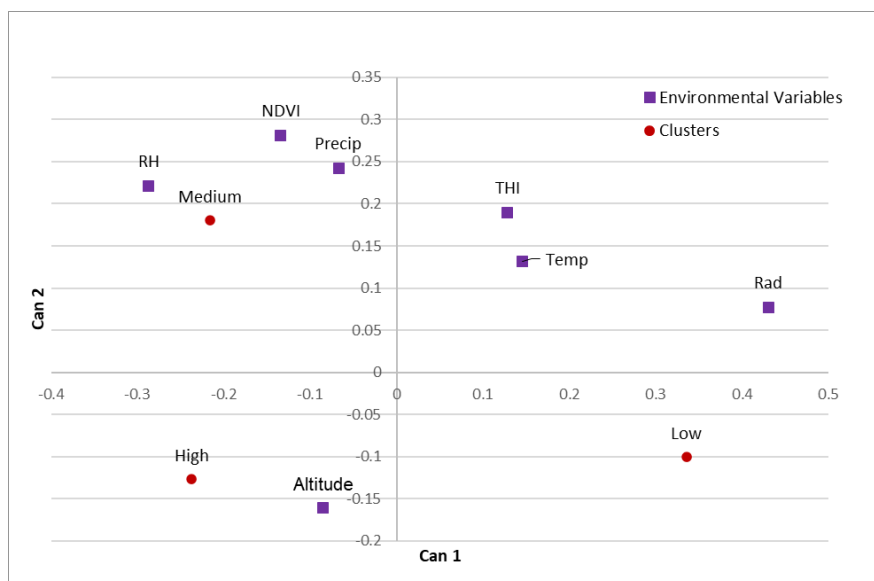
96 **Fig. 2.** Canonical distribution of production clusters and environmental characteristics
97 for Montana Tropical cattle breed in Brazil. NDVI: Normalised Difference Vegetation
98 Index, RH: relative humidity, Precip: rainfall precipitation, THI: Temperature and
99 Humidity Index, Temp: air temperature, Rad: solar radiation.
100

101   In the canonical correlations (Table 6), solar radiation had a high correlation with

102 production traits in the first correlation (V1), while NDVI, THI and air temperature had

103 high correlations with V2 and V3. WW and index Montana showed a negative correlation

104 with W1 while in W2 Maternal effect, DWG and Muscle score were positive.

105

106

107

108   **Table 6.** Canonical correlations between environmental characteristics and genetic values

109   for Montana Tropical cattle breed in Brazil.

	Correlations Between the V Variables and Their Canonical Variables				Correlations Between the W WITH Variables and Their Canonical Variables		
	V1	V2	V3		W1	W2	W3
Altitude	-0.06	-0.11	-0.09	**BW**	0.23	-0.02	0.20
Precip	-0.26	-0.27	0.10	**WW**	-0.52	-0.04	-0.10
NDVI	0.01	0.32	0.44	**Maternal**	-0.36	0.45	0.40
Temp	0.16	-0.20	0.49	**DWG**	-0.14	0.63	-0.29
Rad	0.86	-0.37	0.24	**YW**	-0.34	0.28	-0.27
THI	0.14	-0.21	0.53	**SC12**	-0.38	0.08	-0.30
RH	-0.34	0.03	0.14	**Musc**	-0.27	0.46	-0.37
				Height	-0.26	0.20	0.05
				Navel	-0.22	-0.16	-0.48
				Index	-0.40	0.25	-0.28

110   Precip: rainfall precipitation, NDVI: Normalised Difference Vegetation Index, Temp: air
111   temperature, rad: solar radiation, THI: Temperature and Humidity Index, RH: relative
112   humidity, BW: birth weight, WW: weaning weight, maternal: maternal effect, DWG:
113   daily weight gain, YW: yearling weight at 12 months, SC12: scrotal circumference at 12
114   months, Musc: muscle score, index: index Montana.

Farm clusters changed by genetic values analysed (Fig. 3). Farms MF, JP, and CI, had the highest percentage of animals in the high cluster (> 17%) when all traits were considered. These farms had soil type PVA or LV, medium to high NDVI, low relative humidity and medium rainfall precipitation. JP and MF were also at relatively higher altitudes.
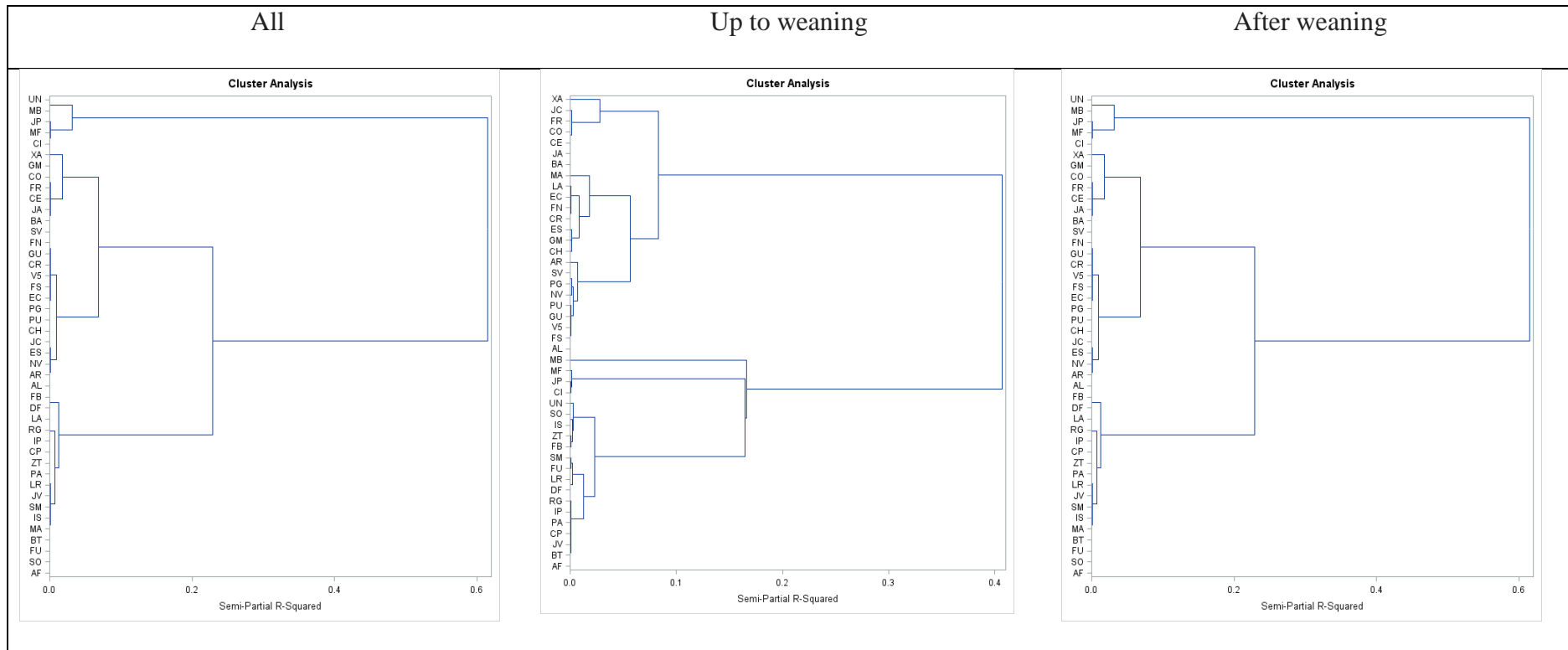
Fig. 3. Farm Clusters for a) all genetic values; b) up to weaning and c) after weaning for Montana Tropical cattle breed in Brazil.

1   In the autocorrelation analysis lag class was found as 2, Maximum X coordinate

2   as 23.38, Maximum Y coordinate as 22.41 and Maximum data 32.38 (Fig. 4;

3   Supplementary Table 2).

53

g

Spatial Distribution of Navel Observations

h

Spatial Distribution of Index Observations

i

Spatial Distribution of MS Observations

j

Spatial Distribution of SC Observations
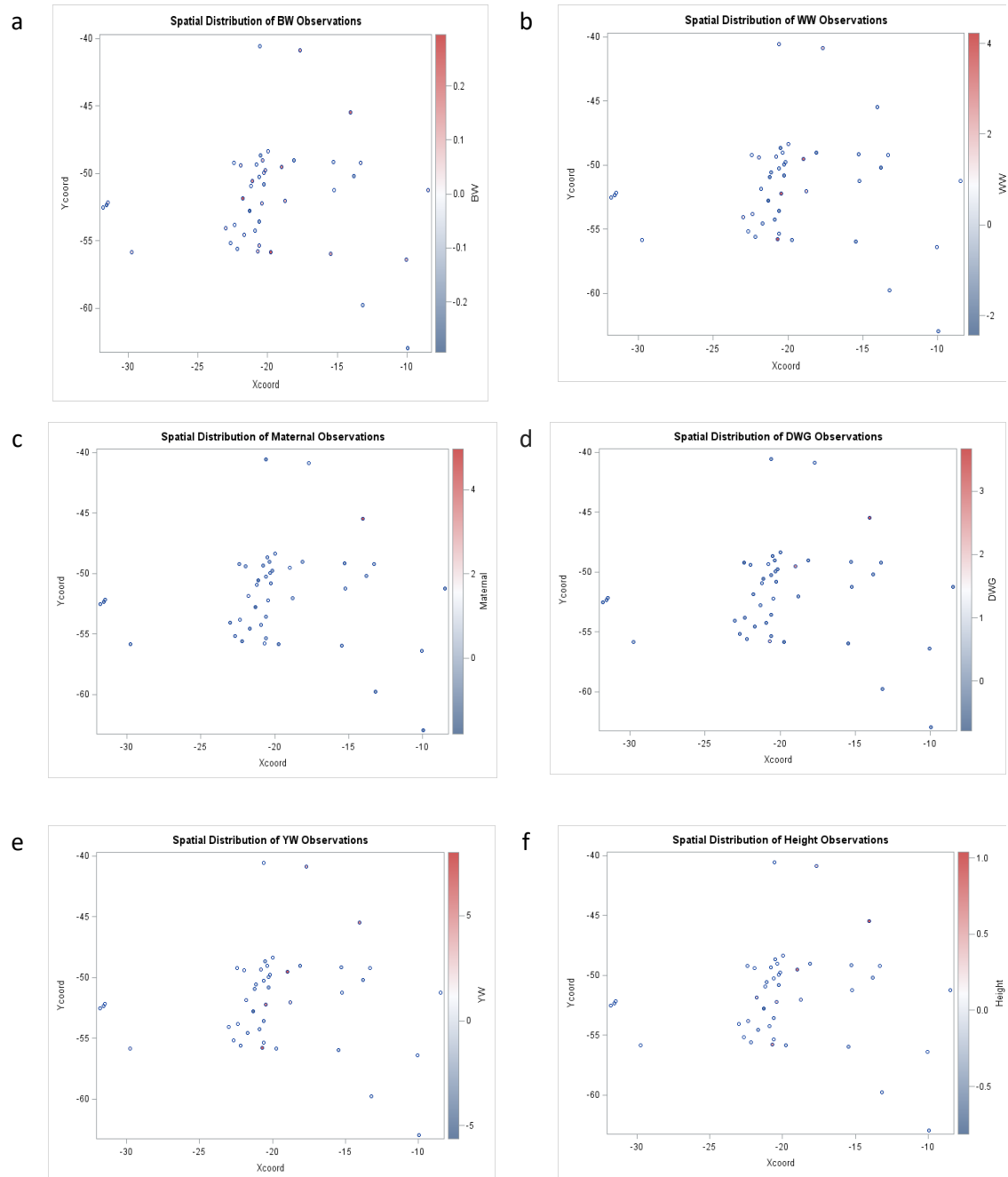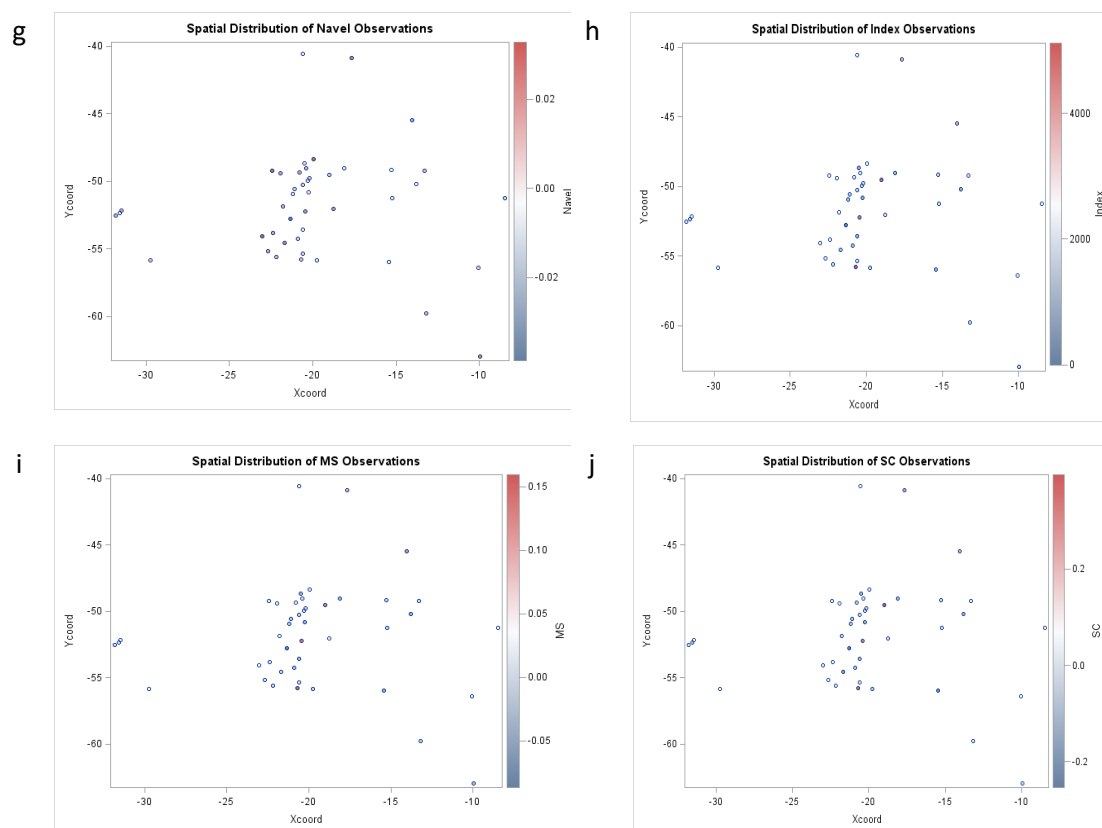
Fig. 4. Spatial distribution of genetic values observations for a) birth weight (BW), b) weaning weight (WW), c) maternal effect, d) daily weight gain (DWG), e) yearling weight, f) height, g) navel score, h) Index Montana, i) muscle score (MS) and j) scrotal circumference (SC) for Montana Tropical cattle breed in Brazil.

Spatial autocorrelations (Table 7; Supplementary Fig. 1) were significant for all traits except birth weight. In terms of fitted semivariograms (Supplementary Fig. 2), BW and WW, did not converge. The Gaussian model was the best fit for the other traits. The significant range values estimated for most traits was approximately one (1) (YW, Height, Navel, Muscle score), while for DWG range was 4 (four). This indicates a high correlation of genetics with distances between one and four distance classes (111 to 444 km).

Table 7.

Moran´s I and Greary´s G for genetic values in Montana Tropical cattle breed in Brazil.

	Moran´s I	Moran Z	Greary´s G	Greary Z
BW	-0.072^{ns}	-0.54	0.975^{ns}	-0.17
WW	0.327^{**}	-1.84	0.770^{**}	1.29
YW	0.322^{**}	-1.71	0.694^{**}	1.06

DWG	0.101**	-1.31	1.012**	0.86
Maternal	0.291**	-2.06	0.670**	1.43
Height	0.251**	-1.82	0.772**	0.99
Navel	0.339**	-0.15	0.359**	0.09
Index	0.288**	-1.86	0.697**	1.18
Musc	0.259**	-1.75	0.666**	0.97
SC12	0.304**	-1.70	0.694**	1.33

BW: birth weight, WW: weaning weight, YW: yearling weight, DWG: daily weight gain, maternal: maternal effect, index: index Montana, Musc: muscle score, SC12: scrotal circumference at 12 months. [ns] – not significant; ** $P<0.001$.

Fig. 5 shows changes in genetic values over time. The size of the bubble represents the mean genetic value on the date shown. Overall, all characteristics started in SP (São Paulo) state followed by MG (Minas Gerais), and over time spread to the other states. The major positive genetic values were seen in the final period in MS (Mato Grosso do Sul), BA (Bahia) and MG states, followed by RS (Rio Grande do Sul). Up to weaning characteristics were different, as higher genetic values were seen in MS, MT (Mato Grosso), BA and MG, while for Navel Score this was in RS state. After weaning characteristics also included SP state. Negative values for maternal values were seen in ES (Espirito Santo), AC (Acre) and RO (Roraima).

c
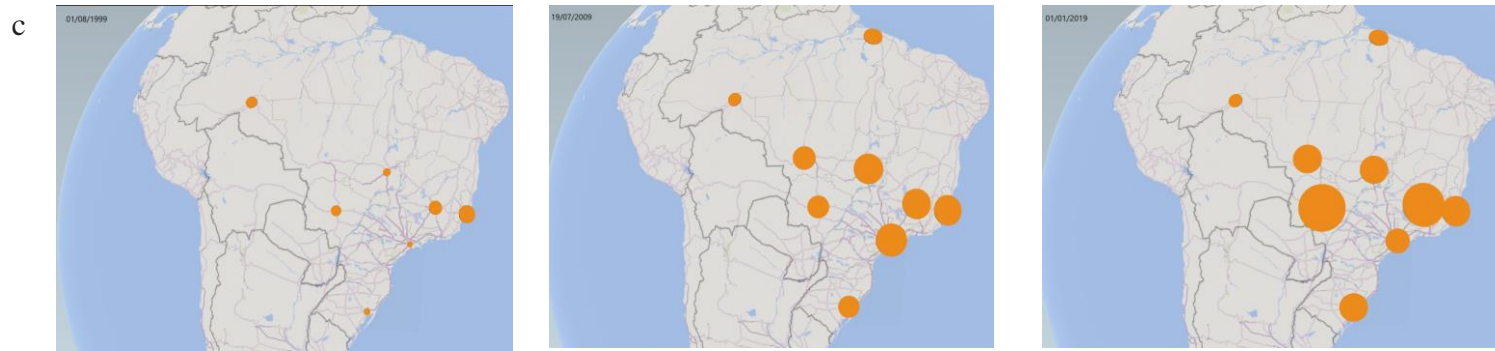
Fig. 5. Temporal analysis of genetic values for a) all; b) up to weaning, and c) after weaning characteristics for Montana Tropical cattle breed in Brazil.

3.4 Discussion

Expected progeny differences (EPD) are predictions of the genetic transmitting ability of a parent to its offspring and take several factors into consideration such as animal's actual performance, performance of progeny, and performance of other relatives. In the case of the Montana Tropical cattle breed they are calculated using a full Animal Model (Dias et al., 2011), including biological type, julian day, age of dam and contemporary groups as well as random additive maternal effects and uncorrelated random effects of maternal permanent environment. As seen in the present study, and in line with previous studies (Lima et al., 2021; Silva et al., 2021), this is not sufficient to remove spatial and other effects affecting EPDs. Silva et al. (2013) state that environmental and climatic factors associated with solar incidence, rainfall precipitation and different soils interfere with animal production, as seen here.

Climate changes drive changes in production systems, and identifying animals adapted to broad environmental challenges can aid in developing sustainable production systems. Several studies have shown the effect of environmental conditions on genetic values in Brazil (Costa et al., 2014; Alfonzo et al., 2021; Lima et al., 2021), indicating a genotype by environment interaction not evaluated in standard genetic analyses (Silva et al., 2021). Santana Jr. et al. (2015), working with Montana and other breeds, showed that accumulation of THI units from birth to weaning negatively affected the WW, with substantial heterogeneity in the (co)variance components for WW across the environmental gradient. In the present study, high weaning weights were seen in regions with lower air temperatures but overall higher THIs. On the other hand, looking at clusters up to weaning and after weaning, the high cluster groups for genetic value were in regions with higher altitudes, medium to high NDVI, especially after weaning, low THI, lower

population density, higher average air temperature and lower relative humidity, but lower solar radiation.

NDVI is an indicator of pasture production and has been used as an indicator of pasture degradation (Pereira et al., 2018) and quality (Serrano et al., 2021). In the USA, McManus et al. (2021) saw that lower NDVIs were more associated with commercial and *Bos indicus* than purebred cattle production. Higher genetic values were associated with higher NDVI here, indicating the contribution of improved pastures to animal production. The high solar radiation correlation with production parameters may be related to on-farm measures to protect the animals from the effects of the environment such as providing shade, silvopastoral systems or housing. On the other hand, the negative effects of combined high THI, air temperature and relative humidity on production traits is expected (McManus et al., 2022).

Latosols and Agisols have low natural fertility but occur in relatively flat areas and respond well to fertilization (Batista et al., 2014). Neosols can have poor water retaining capacity (Pes and Arenhardt, 2015), while planosols are poorly drained (Sousa et al., 2013). Cambisols and chernosols can have higher organic matter had higher natural fertility (Pes and Arenhardt, 2015; Santos et al., 2018). As such, the soils here differ in their texture, base saturation, drainage etc, which affect the capacity to grow pastures and crops for use in animal production.

Understanding how environmental characteristics interfere with the structure of the animals' genetic variation can help construct animal improvement programs. Rexroad et al. (2019) and McManus et al. (2021) showed that genetic by environment and/or management interactions are needed to tailor cattle productivity and genetic improvement. In the present study, Montana Tropical cattle breed is seen to have diverse genotypes that can be selected for different environmental conditions.

Looking at change over time (Fig. 5, white centers indicate mean negative genetic values), different regions of the country and production systems become more prevalent for higher genetic values. This may be because of new breeders entering the program, changing production systems or a better environment, and improving the selection program. The move toward rearing this breed in Mato Grosso and Mato Grosso do Sul is in line with the overall change in cattle production in Brazil (McManus et al., 2016), which brings new challenges and challenging adaptations. The current trend is towards higher genetic weight values in Mato Grosso do Sul and Minas Gerais states, and Maternal effects in Bahia state. Rio Grande do Sul state has higher Navel scores and Minas Gerais for Scrotal circumference. Variation over the years can help farmers associate climate conditions with genetic values when looking for replacement animals. Rust (2019) states that relevant decisions should be based on all relevant data including trends in practice within production systems. These trends, as shown here, are both spatial and temporal.

3.5 Conclusion

Environmental and socioeconomic conditions (including soil type, altitude, Normalised Difference Vegetation Index, Temperature and Humidity Index and population density) showed regional variation over time and these affected genetic values in Montana Tropical cattle breed. Regional differences may also help new breeders select adapted animals for their production system. Space and time should be considered when calculating genotype×environment interactions.

Data availability

Data will be made available on request.

Declaration of generative AI and AI-assisted technologies in the writing process

None

CRediT authorship contribution statement

Nathalia da Silva Costa: Conceptualization, Methodology, Investigation, Data Curation, Writing - Original Draft, Project administration. **Renato Fontes Guimarães:** Conceptualization, Methodology, Formal analysis, Supervision, Writing - Review & Editing. **Osmar Abilio de Carvalho Junior:** Conceptualization, Methodology, Formal analysis, Writing - Review & Editing. **Potira Hermuche:** Conceptualization, Methodology, Formal analysis, Supervision, Writing - Review & Editing. **José Bento Ferraz:** Conceptualization, Methodology, Resources. **Felipe Pimentel:** Investigation, Data Curation, Writing - Original Draft. **Daniel Pimentel:** Investigation, Data Curation, Writing - Original Draft. **Luis Telo da Gama:** Conceptualization, Writing - Review & Editing. Rafael Núñez-Domínguez: Conceptualization, Writing - Review & Editing. **Vanessa Peripolli:** Conceptualization, Writing - Review & Editing. **Concepta McManus:** Conceptualization, Methodology, Formal analysis, Supervision, Writing - Review & Editing, Project administration, Funding acquisition.

Conflict of Interest

The authors declare no conflict of interest.

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Ethics Committee Approval

Animal Care Committee approval was not obtained for this study as all the analyses were

performed using pre-existing databases.

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4. SPATIALIZATION FOR SLICK HAIR GENE IN MONTANA CATTLE IN BRAZIL

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Abstract

Amidst rapidly escalating global temperatures, understanding the multifaceted implications of climate change has never been more crucial. For animal husbandry, the prevailing warmer conditions pose unique challenges and necessitate a renewed perspective on livestock management and breeding strategies. This study focuses on the 'slick hair' phenotype as a potential strategy to address thermal stress in cattle. We analyzed 120 genetic markers, derived from genotyping via a 100,000 SNP chip, specifically between 35,029,690 bp and 40,588,890 bp on BTA20. Through georeferencing the collection sites and using the Alleles in Space software, we established correlations between environmental variables, geographical characteristics, and genetic expressions. The findings highlight particularly sensitive areas among the 120 markers and the most influential landscape features. Notably, from a distance of 500 km, a higher genetic variability associated with 'slick hair' was observed. These insights provide valuable strategies for optimizing livestock in tropical regions, aiming for more resilient production against climate challenges.

Keywords: cattle, genetic landscape shape, spatial correlation, slick hair phenotype, georeferencing, genetic variability, tropical regions.

4.1 Introduction

Animal production faces new challenges imposed by the scarcity of resources due to climate change (Weindl et al., 2015), which will negatively reflect on the health and well-being of animals. Among the expected changes are rising temperatures, changes in sea levels and precipitation, which will lead to prolonged droughts, increasing the incidence of extreme events, including floods and frosts, interruption of food supply, disease outbreaks, among others (Hoffmann, 2013). Thus, the management of agricultural systems and natural resources needs to be better planned to ensure that communities and agricultural practices are resilient and sustainable enough to deal with the impacts of climate change.

In recent years, the appearance of disease vectors and invasive species has occurred due to increased precipitation and temperatures (IPCC, 2014) which, in turn, have a negative impact on the health of animals (Hoffmann, 2010). On the other hand, in animal production, the greater intensity of selection to increase productivity with the use of animal breeding techniques and reproductive technologies, results in a reduction in disease resistance, as well as in tolerance to many of these challenges. Climate change is a reality and, therefore, it is important to understand how producers perceive and adapt to it, as this data will help in the development of adaptation and mitigation strategies (Deressa et al., 2011). Future research should also evaluate the possibility of adopting cattle breeds that are more tolerant of hot environments, thereby minimizing the duration of welfare impairment under HS (Polsky & Von Keyserlingk, 2017). The choice of breeds and racial composition in mestizos must be carried out according to the local edaphoclimatic environment and sociocultural context, giving priority to animals that adapt to adverse climatic, nutritional and health conditions.

Landscape genomics aims to reveal the relationship between adaptive genetic markers in genomes and environmental heterogeneity and system production between natural populations or livestock/agricultural species. Landscape genomics is the spatially explicit study of geographic patterns of genetic variation across the genome (Sork et al., 2013). This technique is a combination of landscape ecology and population genetics, which aims to provide information about the interaction between geographic coordinates, their associated biotic and abiotic environmental features, and evolutionary processes,

including gene flow, genetic drift, adaptation, and selection Manel et al., 2003; Holdereguer & Wagner, 2008).

The definition of a heat tolerant animal is complex (McManus et al., 2020a, b). In principle, a heat tolerant animal is one that maintains homeothermy under high environmental heat loads. However, from a livestock perspective, the objective is to maintain productive and reproductive levels in hot conditions (Carabaño et al., 2016) and the animal's performance under heat stress can be an indicator of the animal's general ability to deal with heat. Homeothermy in hot conditions depends on the animal's ability to balance thermogenesis and heat dissipation. Among the evaluations that have been proposed as criteria to identify heat-tolerant animals are body temperature, respiratory rate, heart rate and sweating rate (McManus et al., 2009a, b; 2011). However, their use in large-scale selection programs is still limited due to the high cost of obtaining these measures. Skin and coat characteristics, including the rate of shedding and the ratio of body surface area to mass, are related to the animal's ability to dissipate internal heat (Gray et al., 2011).

In cattle, there is a gene that is associated with a particular hair coat pattern called "slick hair" (Olson et al., 2003; Mariasegaram et al., 2007; Landaeta-Hernandez et al., 2011). These studies show that the Slick gene is dominant, which means that if an animal inherits a copy of the gene from one of its parents, it will exhibit the slick hair coat pattern. Cattle with the Slick gene have shorter, smoother hair that lies flat against their skin, which makes them better adapted to hot, humid environments. The slick hair coat allows for better heat dissipation and helps to reduce the risk of heat stress in these animals.

The Slick gene has been identified in several cattle breeds, including Brahman, Brangus, and Santa Gertrudis. However, it should be noted that not all individuals within these breeds may have the gene, as it is possible for an animal to inherit two copies of the non-slick gene and not express the slick hair coat pattern. Based on studies at the Clay Center, the Compost Montana project emerged, a franchise involving Companhia Agropecuária CFM, from São José do Rio Preto/SP, and the family Leachman (compost producers in the state of Montana, in the United States). Other partners (franchisees) emerged: a group of traditional cattle ranchers from different regions of Brazil, with more than 40 thousand dams, in addition to the participation of cattle ranchers from the north of Uruguay. The program brought breeds from countries such as Africa, Australia,

Central America, the Caribbean and the United States, some of which had never set foot on Brazilian soil and, in some cases, little known in the country of origin:

- Zebu: Boran and Nellore – high rusticity, resistance to parasites and good carcass yield;
- Adapted: Belmont Red, Bonsmara, Caracu, Romo, Sinuano, Senepol, Tuli – high degree of climate adaptability tropical climate and fertility, in addition to other traits related to meat quality. They derive from the Sanga family (Africa) and from the Creole lines (South America);
- British: Red Angus, South Devon – originally from the United Kingdom, they have excellent sexual precocity and very easy finishing. Their meat is excellent with high marbling. The bulls used in Montana were selected for high growth;
- Continental: Gelbvieh, Limousin, Simmental – originating from the European continent, exhibit high growth and muscularity.

Overall, the slick hair gene in cattle is a useful adaptation for animals living in hot and humid climates, and it is a good example of how genetic variation can contribute to the survival and success of a particular species or breed. The objective of the current study is to examine the effect of environmental factors on markers defined by Huson et al. (2014) as the localization of the Slick hair gene. These authors identified a 0.8 Mb (37.7–38.5 Mb) consensus region for the SLICK locus on BTA20 and haplotype blocks from 35,029,690 bp to 40,588,890 bp.

4.2 Material and Methods

A total of 3233 Montana cattle from 16 farms were phenotyped for Slick hair (on a 1 to 5 scale (Durbin et al., 2020) where 1 is very hairy to 5 little hair). The data were georeferenced through the Geographic Information System (ArcGis 10.3 software), considering a geographic coordinate system and WGS 84 datum.

These animals were genotyped using a 100,000 SNP chip and the SNPs between 35,029,690 bp and 40,588,890 bp on BTA20 were separated giving 120 markers (V1 to V120). The markers were coded as A_A = -1; A_B = 0 and B_B = 1. The effect of altitude, precipitation, NDVI, Relative Humidity, Temperature, Radiation, and THI on genotype on were evaluated using logistic regression.

Environmental and socioeconomic data were acquired from different sources. The annual average of the normalized difference vegetation index (NDVI) and Average temperatures were obtained using MODIS (Moderate Resolution Imaging Spectroradiometer) sensor (NASA, 2012). These were processed in ENVI 4.7 software and MODIS Reprojection Tool (MRT) program with geotif extension, latitude/longitude geographic projection and WGS 84 Datum. NDVI was determined as NDVI = (NIR-RED) / (NIR + RED) where NIR is near infrared and RED is the red channel. This is a chlorophyll sensitive index with values ranging between -1 and 1, where 1 is the highest response of photosynthetically active vegetation (Rouse et al., 1973). TRMM (Tropical Rainfall Measuring Mission) provided mean rainfall precipitation, with a spatial resolution of 0.25°C, (~27 km), from NASA (2012) and processed in ENVI 4.7.

Average altitude was from the SRTM (Shuttle Radar Topography Mission). This consisted of radar data of the entire earth's surface (except for extreme latitudes) with resolution of 90 meters (NASA, 2012).

Humidity was obtained from 283 climatological stations distributed throughout Brazil from the National Institute of Meteorology (INMET, 2012). This consisted of approximately 30 years observations. Temperature and Humidity Index (THI) was calculated: THI = AT + (0.36 x DT) + 41.5, where: AT = ambient temperature (ºC) and DT = dew point temperature (ºC).

Environmental and socioeconomic variables were normalized by the Z-score as formula f(X)= ((X-‾X))/δ, where δ = standard deviation. This was to minimize problems caused by different units of measurement. The Statistical Analysis System SAS® software (Statistical Analysis System, Cary, North Carolina) was used for statistical analyses. The significant genes were then identified using BovineHD Annotation Files (https://support.illumina.com/downloads/bovinehd_product_support_files.html) and then in the NCBI database (https://www.ncbi.nlm.nih.gov/genome/gdv/browser/genome/?id=GCF_000003055.6)

The Alleles in Space (AIS) software (Miller, 2005) allowed a study regarding genetic SNP data and geographic distances between genotypes. The Mantel test identified the similarity and dissimilarity matrices with logarithm in base 10 (Mantel, 1967), used by Sokal (1979). The Monmonier algorithm (1973) was used to identify genetic barriers. This method delineates barriers where there was maximum genetic differentiation

between sample locations. Spatial Auto Correlation verified the spatial relationship between genetic values and geographic distances, using classes with similar distances but different numbers of observations (Equal), and classes with different distances but similar number of observations (Unequal).

4.3 Results

Sixteen farms were mapped (Figure 1), distributed across 5 states in Brazil: Minas Gerais (MG), Goiás (GO), Mato Grosso do Sul (MS), São Paulo (SP), and Rio Grande do Sul (RS). The properties are located in the following municipalities: Carlos Chagas (MG), Ituiutaba (MG), Aporé (GO), Aquidauana (MS), Miranda (MS), Dois Irmãos do Buriti (MS), Rio Brilhante (MS), Três Lagoas (MS), Santa Rita do Pardo (MS), Araçatuba (SP), Pomissão (SP), Pirajuí (SP), São José do Rio Preto (SP), Alegrete (RS), Turuçu (RS) and Capão do Leão (RS).
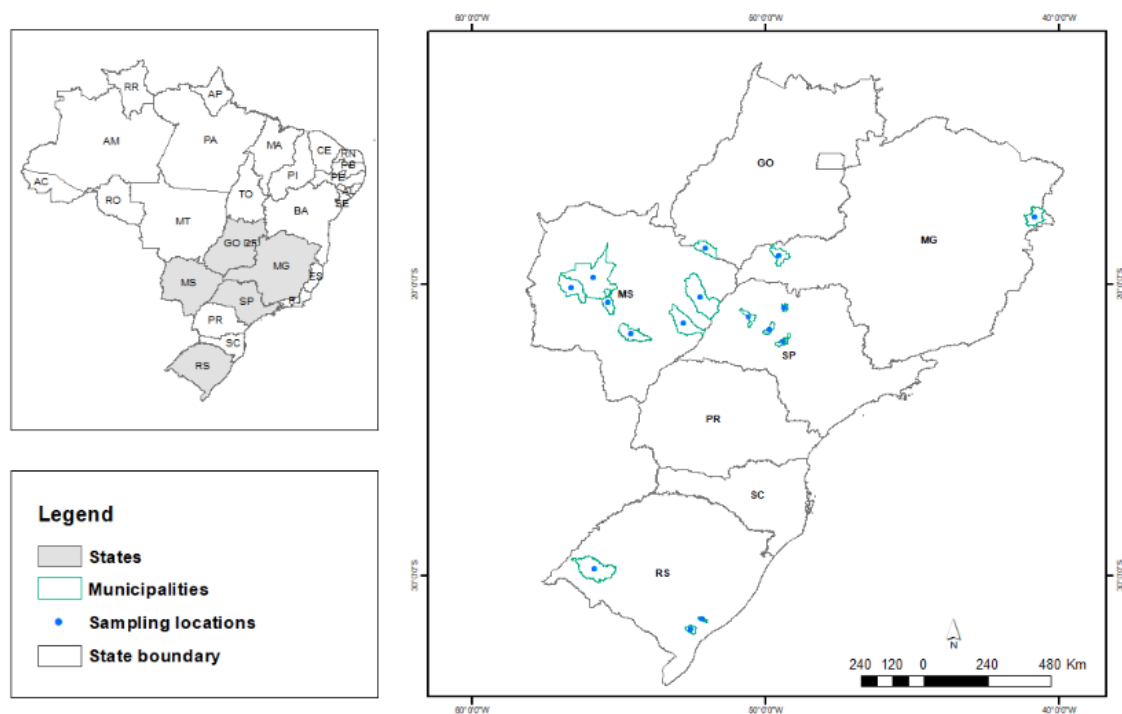
Figure 1- Map of the data collection point locations.

Differences of hair types depending on soil type (Table 1) showed that most animals were in type LV.

Table 1 . Percentage of Soil Type by Slick Hair Phenotype

	LV	LVA	PVA	RL	SG
1	0.06	0.00	0.18	0.00	0.23
2	0.59	0.00	0.12	0.00	0.12
3	4.28	0.12	1.35	0.76	0.53
4	30.56	1.94	3.34	2.76	2.23
5	45.92	0.53	0.12	2.35	1.94

LV *(Red Latosol)* /LVA *(Red-Yellow Latosol)*/PVA *(Red-Yellow Argisol)* /RL *(Lithic Neosol)/*SG *(Hydromorphic Planosol)*

Higher altitudes, more precipitation, lower NDVI and Relative humidity, higher air temperatures and THI showed a higher % of animals with slicker hair (Table 2).

Table 2 . Differences between environments for Slick Hair Phenotype

Slick Phenotype	N	Altitude m	Precipitation mm/day	NDVI	RH %	Temp ^{o}C	THI	Rad (MH/m²)
1	24	230.71a	0.1690a	0.62	73.99a	23.82a	72.22a	806984
2	21	252.42a	0.1721a	0.57	72.63b	28.39b	77.91b	829279
3	203	277.07a	0.1748ab	0.57	72.56b	28.08b	77.52b	834310
4	886	408.60b	0.1795b	0.55	70.38b	29.22b	79.06b	824599
5	1947	399.19b	0.1745ab	0.56	70.96b	26.59b	75.84b	817118

Different letters in the same column mean significant difference by Tukey Test (P<0.05)

The results of the logistic regression the slick hair genotype (Annex 1) show that V75 to V85, in particular, show a concentration of environmental effects on the markers. These represent markers BTA 20 00011097 to BTA 20 00011168 and ARS_BFGL_NGS_116981. These genes lie between 39035407 and 39268439bp. Genes in this region include PRLR, AGXT2, DNAJC21, BRIX1, and RAD1 (Figure 2).
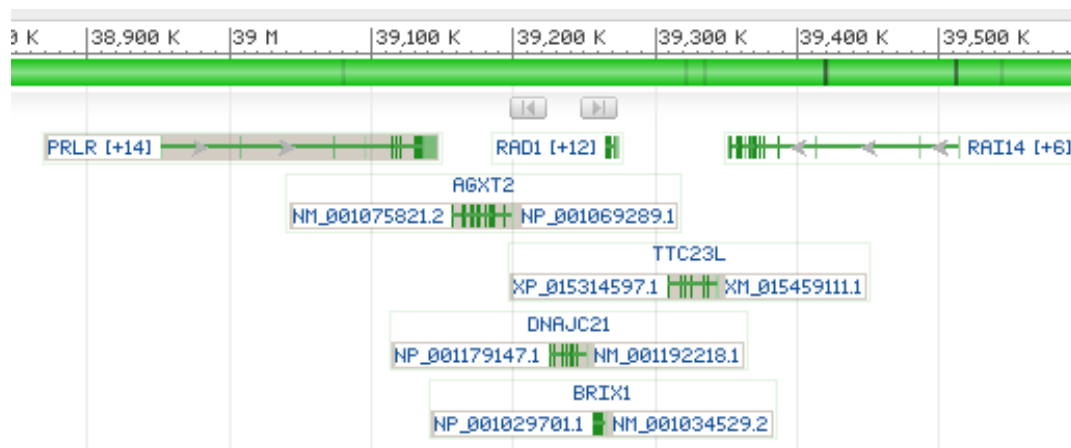
Figure 2- Location of the main markers on the chromosome.

The odds ratio for these markers and environmental effects are in Table3 and Figure 3 in the study conducted, 120 markers associated with the slick hair trait were evaluated. However, a subset of these, particularly markers V75 through V85, showed statistical relevance when correlated with environmental variables. These findings highlight the significance of these markers in influencing the "slick hair" trait in response to various environmental conditions or stimuli. Values greater than 1 indicate that an increase in the environmental variable indicates a higher frequency of the slick genotype. As such, the slick hair occurs in low at higher altitudes, with lower vegetation density (low NDVI), lower relative humidity, higher temperatures, and higher temperature and humidity index (THI).

27   Table 3. Odds ratios for environmental effects on slick hair SNPs

	NDVI	Altitude	Precipitation	Relative Humidity	Temperature	Radiation
V75	0,001***	0,991**	293**	1,240**	1,703**	NS
V76	0.001****	0,993***	NS	1,26*	1,50*	NS
V77	NS	0,996*	110***	1,278**	1,463**	ns
V78	ns	0,996*	999	1,289**	1,540**	Ns
V79	0.001**	0,994*	0,933*	1,357**	1,496***	ns
V80	0,001**	0,993*	NS	1,102**	1,377**	NS
V81	NS	1,002	NS	NS	NS	NS
V82	0,001*	0,990*	999**	1,321**	1,569*	ns
V83	0,001*	1,003	NS	NS	NS	NS
V84	NS	NS	NS	NS	NS	NS
V85	NS	0,993	999	NS	1,735	NS

28

29   As can be seen in Figure 3, the heterozygote always accompanies one of the homozygote

30   genotypes at the marker, with slick hair genotypes being in accordance with Table 3.

31

32

NDVI

Percipitation
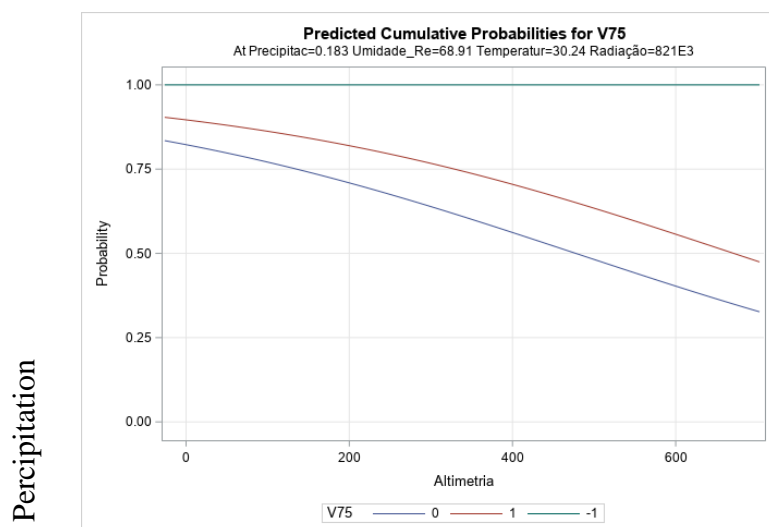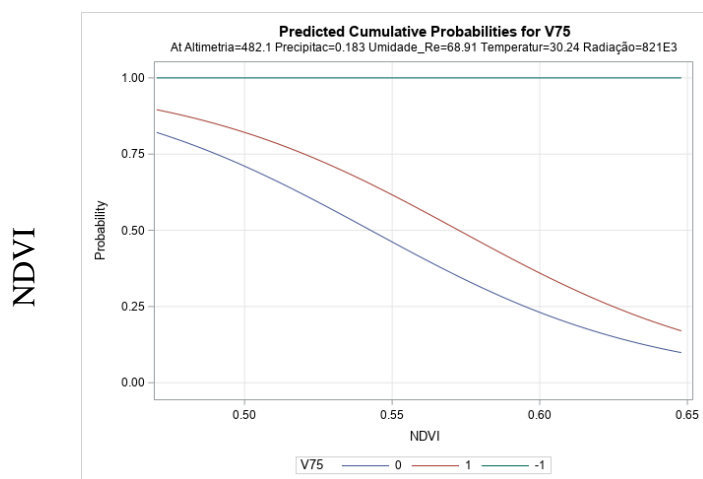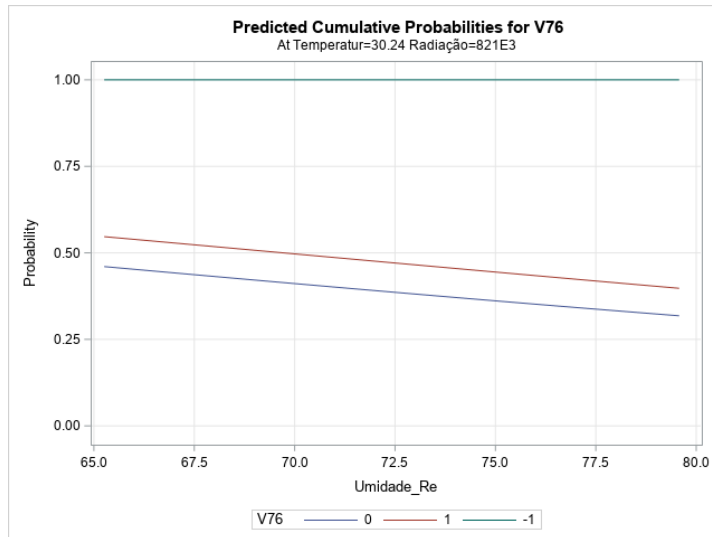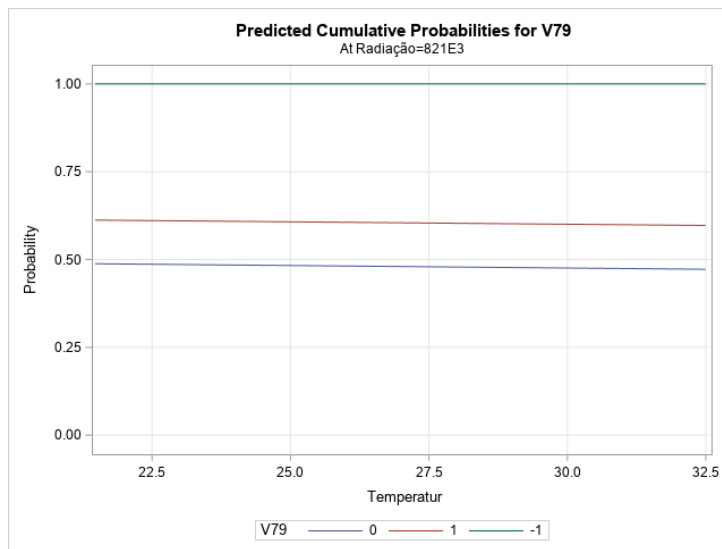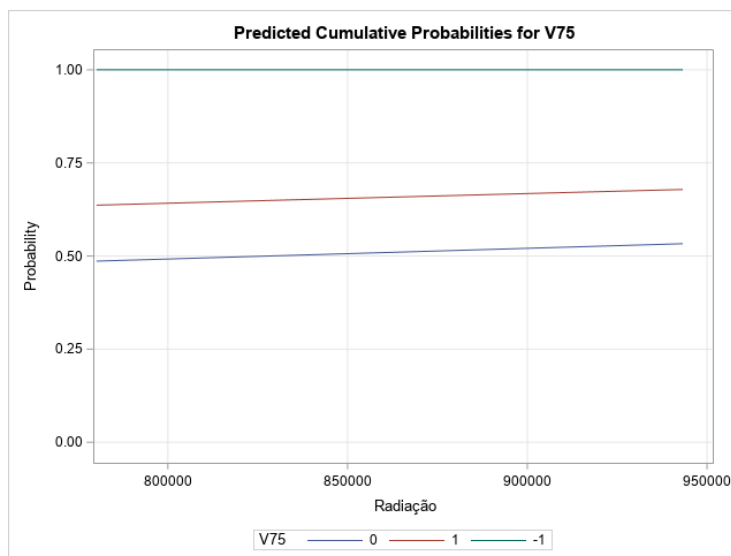
33
Figure 3- Analysis of the interaction of the V75-V85 markers associated with
environmental effects on slick hair SNPs

The first two eigenvalues explained most of the variance for the markers studied (Figure 4 a), although no distinct separation can be seen between farms (figure 4b).
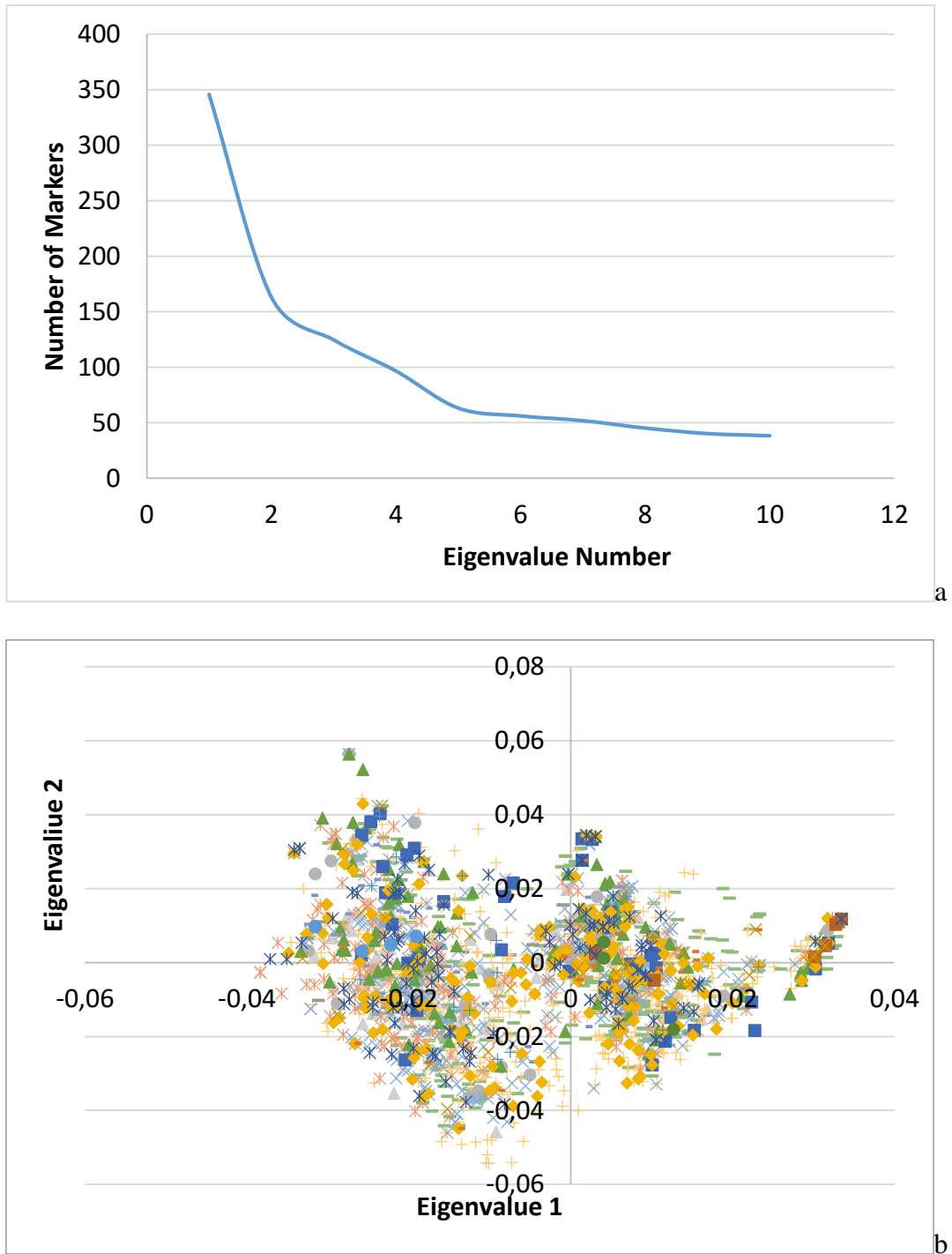
Figure 4. Eigenvalues (a) for slick hair (120 markers) and Two eigenvalues per farm (b)

Alleles in Space for Slick Hair

Alleles in Space software was utilized with the aim of conducting a more in-depth investigation of the data associated with the slick hair trait. In the Mantel test (Figure 5), 1000 permutations were conducted for the analysis, suggesting a robust test that accounted for the variability in the data to confirm the significance of the results. The Mantel test showed a low but significant correlation of genetic and geographical distances: $r = .094$ ($P<0.001$).
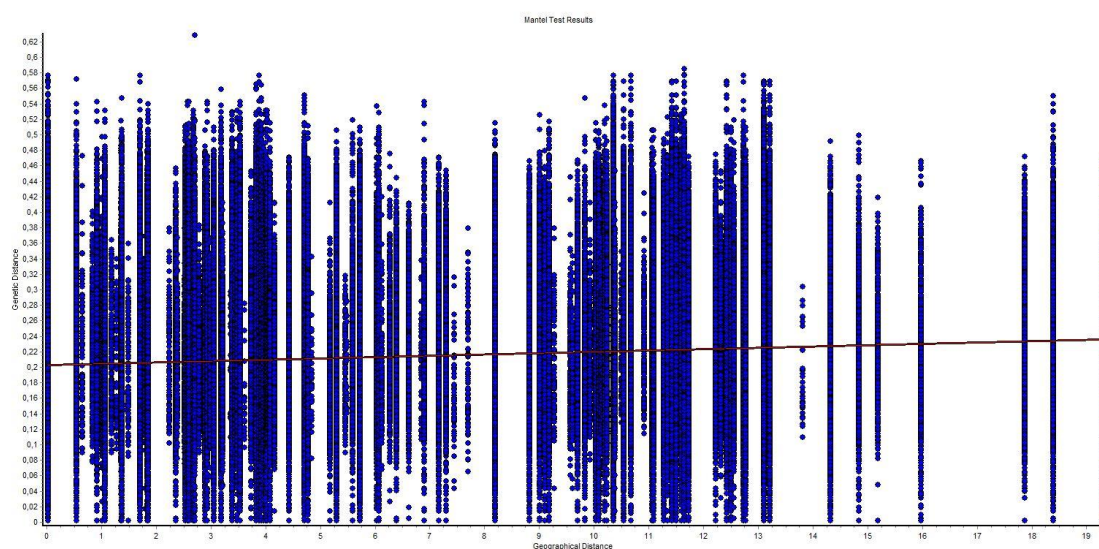
Figure 5- Relationship between geographical and genetic distances using Mantel test (1000 permutations).
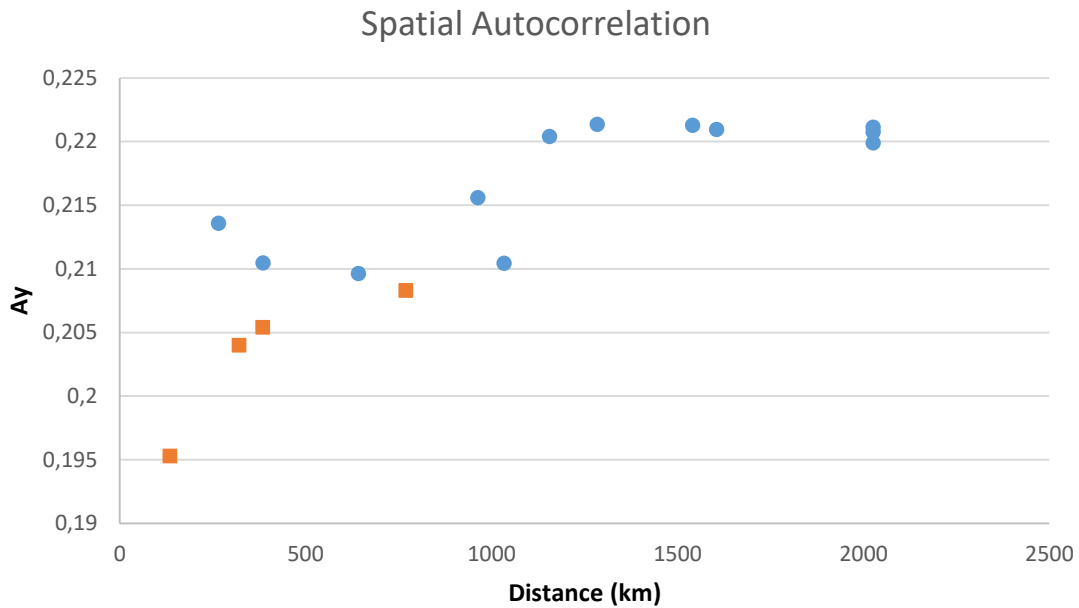
Figure 6- Spatial autocorrelation between geographical and genetic distances.

The Mantel test and the spatial autocorrelation analysis each provide unique perspectives on the relationship between genetic and geographical distances. Both tests suggest a non-random association between geographic and genetic distance, although the strength of this relationship low but significant (V = ,008 and P = 0.001).

Figures 7 represents the distribution pattern of Montana breed animals associated with the slick hair characteristic, under three perspectives. The peaks (dark blue) represent areas with high genetic distance, while the valleys (light blue and gray) indicate lower genetic distance between the animals.
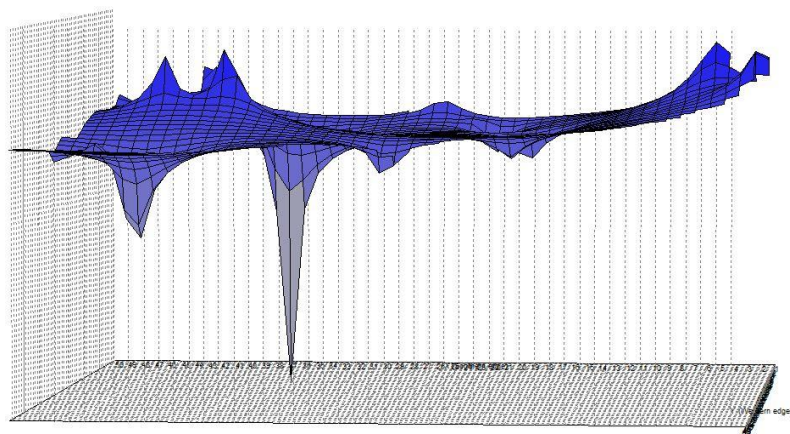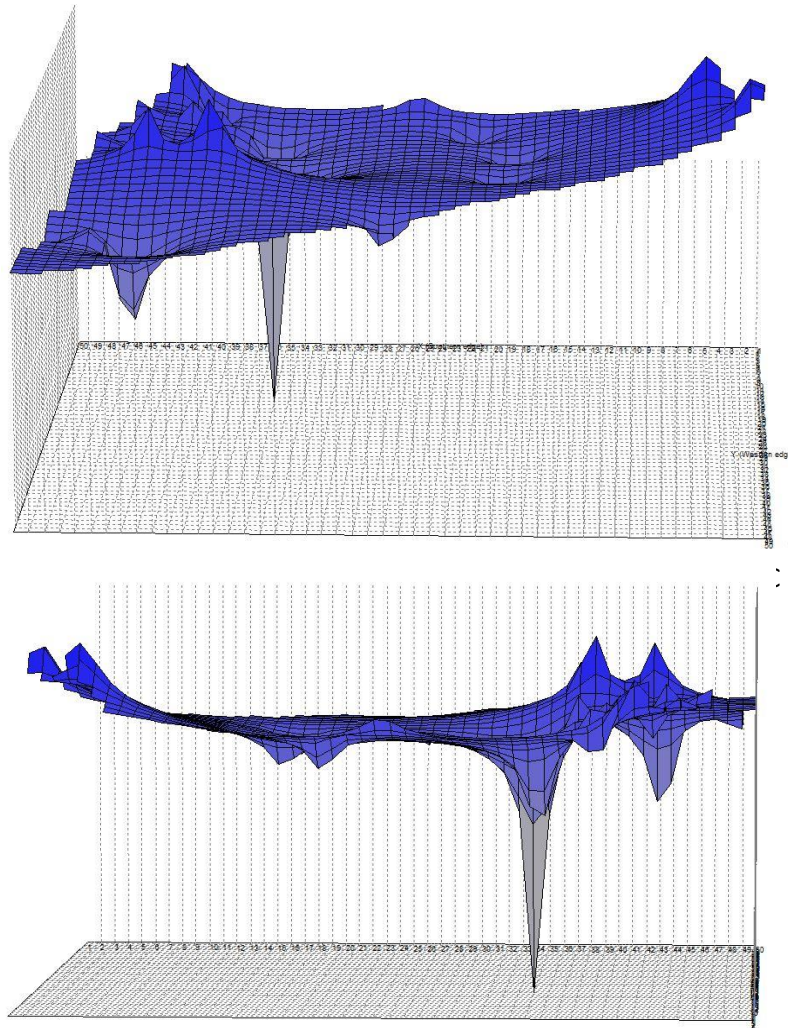
Figure 7 –Three perspectives of the Landscape space.

The Monmonier algorithm (Figure 8) is used to detect the locations of potential barriers to gene flow. These genetic barriers are regions where there is a significant separation between different genetic groups, specifically associated with the slick hair characteristic. The barriers show major separations between farms in Sao Paulo and Mato Grosso do Sul states, and later with southern states.
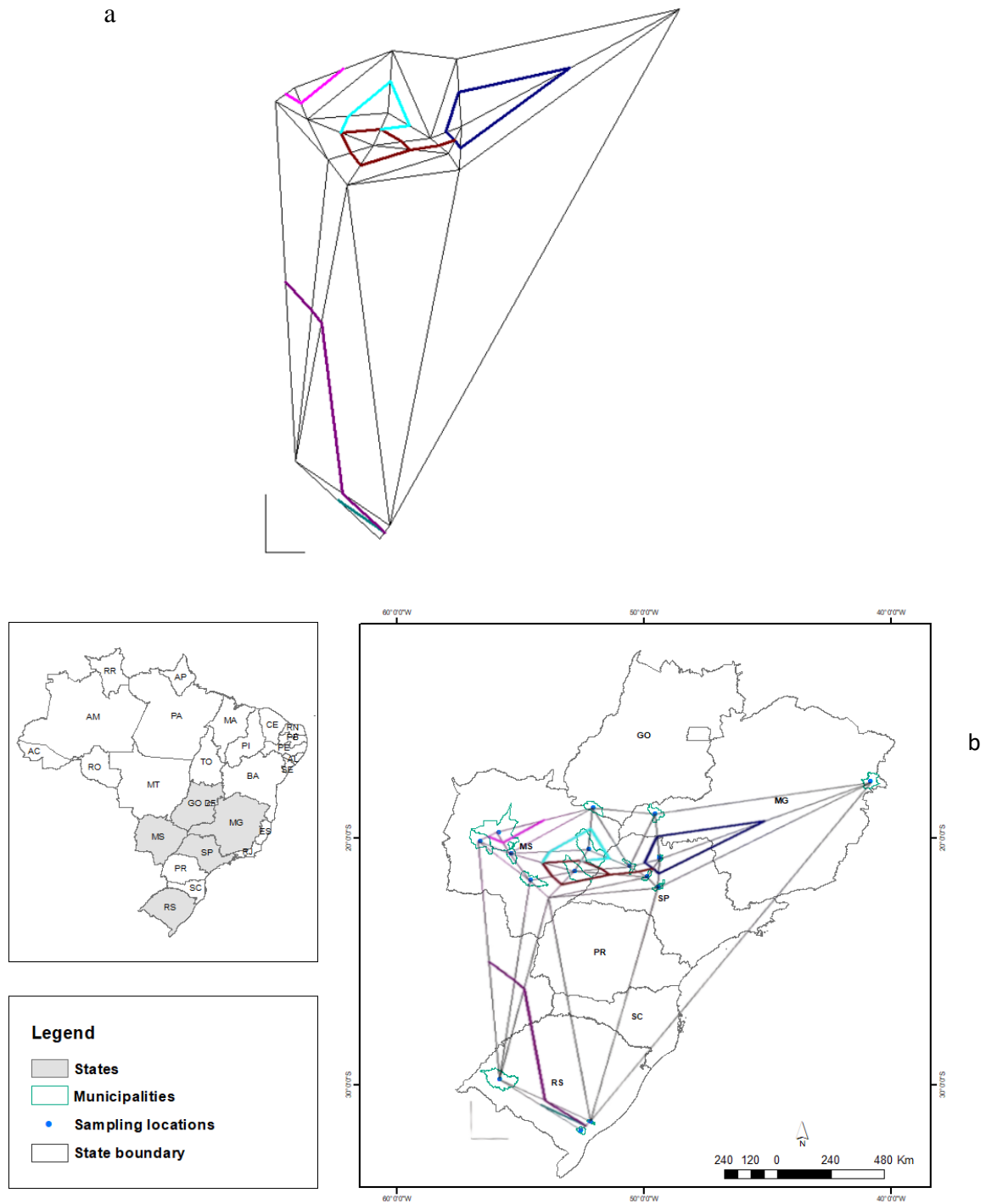
Figure 8- Monmonier genetic barriers for the slick hair gene in Montana associated with collection points in Brazil. (1ˢᵗ barrier Dark blue, 2ⁿᵈ light green, 3ʳᵈ pink, 4ᵗʰ red, 5ᵗʰ purple, 6ᵗʰ light blue)

4.4 Discussion

Geographical analysis is crucial for understanding the manifestation of the slick hair gene in cattle, as it helps identify the relationship between geographic characteristics

and the phenotype associated with the gene. Geography is closely linked to the climate of a specific region. The slick hair gene provides a short and shiny coat that is adaptive in hot environments. Analyzing the relationship between climate (temperature, humidity, radiation, precipitation) and the expression of this gene helps understand how cattle adapt to different climatic conditions.

The highest frequency of slick hair is observed within the variations of the latosol, a factor closely tied to the geographic location of the farm where the animals are raised. Research on various cattle breeds underscores the significance of comprehending the specific soil type for effective animal husbandry. As stated by Scherer et al. (2007), a comprehensive understanding of alterations in soil chemical attributes can provide valuable insights for sustainable production practices without detrimental impacts on the environment.

The most significant landscape characteristics for separating the groups (Table 2) highlight that the "slick hair" phenotype is more expressed at higher altitudes, with lower vegetation density (low NDVI), lower relative humidity, higher temperatures, and higher temperature and humidity index (THI). The primary function of the "slick hair" phenotype is to assist the animal in adapting to warm climates. This type of hair, being shorter and finer, facilitates more efficient heat dissipation. Such a trait translates into a significant adaptive advantage in tropical environments.

As highlighted by Olson et al. (2003), the identification of a predominant gene in cattle that mitigates the effects of heat stress, and its subsequent incorporation into temperate breeds, could greatly impact cattle productivity in warm climates. As highlighted by Sonstegard and Bickhart (2014), the trait is of particular interest in relation to climate change due to its association with enhanced thermo-tolerance and subsequent increased productivity.

The region noted here 39035407bp and 39268439bp has been seen in previous studies with slick hair. Genes in this region include PRLR (Prolactiin Receptor - Sarlo Davila et al., 2020; Soso et al., 2022), AGXT2 (Freitas et al., 2021), DNAJC21, BRIX1 (also called BXDC2), and RAD1. Saravanan et al. (2021) saw selection signatures for RAD1, DNAJC21 and BRIX1 in Garole sheep in India. Alanine glyoxylate aminotransferase-2 (AGXT2) metabolizes asymmetric dimethylarginine (ADMA) and symmetric dimethylarginine (SDMA). According to Yudin et al. (2017) has two enriched

terms related to regulation of reactive oxygen species metabolic process and transition metal ion transport. DNAJC21 codes a member of the DNAJ heat shock protein 40 family of proteins. BRIX1 has linked to the biogenesis of ribosomes and been seen to have a potential role in disease resistance in chickens (Zhu et al., 2019). RAD1 has been seen to protect fungal cells from solar UV damage (Yu et al., 2022). Prolactin (PRL) is known to regulate the hair follicle (Hansen et al., 2020).

Figure 3 shows the biallelic response of the slick hair to the environment. Crossbreeding and selection for a slick hair coat seem as appropriate strategies to improve cattle performance in tropical and subtropical zones (Landaeta-Hernandez et al., 2011). Dikmen et al. (2012) concluded that slick hair cattle have superior thermoregulatory ability compared with non-slick animals. In general, Figure 3, which presents the different behavior of the most significant odd ratios associated with environmental effects on the slick hair trait, showed high values for the AA base (-1) regardless of the environmental characteristic in all markers. On the other hand, the AB and BB bases showed different variations according to the markers and specific characteristics.

In simpler terms, when looking at a dataset (figure 4 a), the first two eigenvalues accounted for a significant portion of the variation in the markers studied. When examining the farms (figure 4 b), a clear distinction was not observed. Therefore, the "Alleles in Space" program was used for a more detailed analysis of the spatial genetic structure, considering the geographical location of the sampled individuals.

The Mantel test (Figure 5) shows a significant, albeit modest, correlation between the genetic and geographic distances of the animals. When evaluated alongside Figure 6, it becomes evident that from a geographical distance of approximately 500 km, the genetic variation of animals associated with the slick hair trait increases. According to Diniz et al. (2013), Mantel tests can overcome certain potential statistical issues and provide a simple and useful tool for the multivariate analysis of spatial patterns of genetic divergence.

It is important to emphasize that, despite the differences in classification methods, the Mantel and autocorrelation tests point to the existence of genetically distinct subpopulations. According to McManus et al. (2020) there is increased interest in the use of georeferencing technologies in combination with genetic information in the management and planning of livestock production and conservation systems, as well as

prediction of the adaptive potential of specific livestock populations (i.e., breeds, selection lines, genetic groups, etc.).

Figures 7 reveals variations in characteristics related to the straight hair phenotype in Rio Grande do Sul, as evidenced by the blue peaks in different perspectives, while there is a greater genetic similarity in the farms located in Mato Grosso do Sul. This may be related to the varying subtropical climate in Rio Grande do Sul compared with a tropical and therefore hotter climate in Mato Grosso do Sul. Just as demonstrated in Figure 6, where the squares show greater genetic similarity in the animals located on farms in Mato Grosso.

Figure 8a presents the genetic barriers identified by the Monmonier algorithm, while Figure 8b provides a geographical view of the locations of these barriers in relation to the data collection points. In all three municipalities of Rio Grande do Sul, we observe the formation of two distinct barriers. These barriers separate the municipalities of Turuçu and Capão do Leão, located in the southeast of the state, characterized by lower average temperatures and lower rainfall indices (Reisser Junior et al., 2012), from the municipality of Alegrete, situated in the southwest of the state.

4.5 Conclusion

Studying and understanding the factors that can affect the 'slick hair' trait is essential for optimizing cattle breeding in tropical areas. This phenotype acts as a valuable ally in controlling thermal stress, thereby enhancing the productive process of these animals. The decoding of BTA20 resulted in 120 markers, revealing the expression of the chromosome region that has a stronger interaction with geographic characteristics. Based on statistical analyses, it was observed that, from a geographical distance of 500 km, there is a greater genetic differentiation of the animals concerning the 'slick hair' trait.

Conflict of Interest

The authors declare no conflict of interest.

Ethics Committee Approval

Animal Care Committee approval was not obtained for this study as all the analyses were performed using pre-existing databases.

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4.7 Annex

Annex 1.

Table 1. Summary of Logistic Regression for environmental effects on Slick hair markers

	Marker	NDVI	Altiude	Precip	RH	Temp	Rad
V1	BOVINEHD2000010048	***	*	*	**	ns	P<0.10
V2	BOVINEHD2000010073						
V3	BOVINEHD2000010074		*				*
V4	BTB_00778141						
V5	BOVINEHD2000010095						
V6	BOVINEHD2000010098						
V7	BOVINEHD2000010115						
V8	ARS_BFGL_NGS_84088		P<0,1	*		**	
V9	BOVINEHD2000010170						
V10	BOVINEHD2000010191						
V11	BOVINEHD2000010192	*					
V12	BOVINEHD2000010201						
V13	BOVINEHD2000010208	*			*		
V14	BOVINEHD2000010209	***	***	**	***	***	***
V15	BOVINEHD2000010231	*	*	*			**
V16	BOVINEHD2000010242						
V17	BOVINEHD2000010250						
V18	HAPMAP45498_BTA_50448	P<0,1					
V19	HAPMAP52690_SS46526609	*	**	*	*	**	**
V20	BOVINEHD2000010285					P,0,1	

V21	BOVINEHD2000010292						
V22	BOVINEHD2000010308						
V23	BOVINEHD2000010316						P<0,1
V24	BTA_50420_NO_RS						
V25	BOVINEHD2000010329	*				P<0,1	
V26	HAPMAP24145_BTA_135146		**				P<0,1
V27	BOVINEHD2000010381						
V28	BOVINEHD2000010409						
V29	BOVINEHD2000010410						P<0,1
V30	BOVINEHD2000010417						
V31	BTA_50482_NO_RS						
V32	BOVINEHD2000010446		*				*
V33	BOVINEHD2000010451						
V34	BOVINEHD2000010480	**	**	*	*	P<0,1	
V35	ARS_BFGL_NGS_2860						
V36	ARS_USMARC_PARENT_DQ990835_RS29012811						
V37	BOVINEHD2000010510						
V38	BOVINEHD2000010515						
V39	BOVINEHD2000010556						
V40	BOVINEHD2000010571	*	**			P<0,1	**
V41	BOVINEHD2000010621						
V42	HAPMAP53150_SS46526297	P<0,1	*				*
V43	BOVINEHD2000010665						
V44	BOVINEHD2000010676	P<0,1	**			P<0,1	**
V45	INRA_620	P<0,1	**	*		*	***
V46	BOVINEHD2000010708						
V47	BOVINEHD2000010715						P<0,1

V48	BOVINEHD2000010760						
V49	BOVINEHD2000010761		*	*	P<0,1	**	P<0,1
V50	BOVINEHD2000010780	P<0,1	**				***
V51	BTA_50515_NO_RS						
V52	BOVINEHD2000010836	*	*				
V53	BOVINEHD2000010842					**	
V54	BTB_01565998						
V55	BOVINEHD2000010857	P<0,1	*			P<0,1	P<0,1
V56	BOVINEHD2000010863		P<0,1				*
V57	BOVINEHD2000010868						
V58	BOVINEHD2000010869						
V59	BOVINEHD2000010875	P<0,1		P<0,1	*	P<0,1	
V60	BOVINEHD2000010900						
V61	BOVINEHD2000010903				*		
V62	BOVINEHD2000010911	*	*		**	*	**
V63	BOVINEHD2000010913						
V64	BOVINEHD2000010914				P<0,1		
V65	BOVINEHD2000010920	*	P<0,1				
V66	BOVINEHD2000010928	P<0,1			*		
V67	BOVINEHD2000010933						
V68	BOVINEHD2000010978		P<0,1				
V69	BOVINEHD2000011006	*	*			*	
V70	HAPMAP30570_BTA_152778	P<0,1	P<0,1				
V71	BOVINEHD2000011021				P<0,1		
V72	BOVINEHD2000011046		*	P<0,1			*
V73	BOVINEHD2000011089						
V74	BOVINEHD2000011094						

V75	BOVINEHD2000011097	***	***	***	*	***	***
V76	BOVINEHD2000011098	***	***		*	**	***
V77	BOVINEHD2000011103	*	*	**	**	**	*
V78	ARS_BFGL_NGS_116981		*	***	**	***	*
V79	BOVINEHD2000011106	***	***	*	***	**	**
V80	BOVINEHD2000011112	***	***			*	**
V81	BOVINEHD2000011113	P<0,1					
V82	BOVINEHD2000011152	P<0,1	**	***	**	***	***
V83	BOVINEHD2000011165		P<0,1	P<0,1		P<0,1	
V84	BOVINEHD2000011167	P<0,1					
V85	BOVINEHD2000011168		***	***	P<0,1	***	***
V86	BOVINEHD2000011170		P<0,1	P<0,1		P<0,1	
V87	BOVINEHD2000011171	P<0,1					
V88	BOVINEHD2000011172		P<0,1	P<0,1		P<0,1	
V89	BOVINEHD4100014689		P<0,1	P<0,1		P<0,1	
V90	BOVINEHD2000011179	P<0,1					
V91	BOVINEHD4100014690		P<0,1				
V92	BOVINEHD2000011180	P<0,1					
V93	BOVINEHD2000011185		P<0,1	*		*	
V94	BTA_110053_NO_RS			P<0,1			*
V95	BOVINEHD2000011197		***	*		*	***
V96	BOVINEHD2000011201		*	*		P<0,1	**
V97	BOVINEHD2000011217						***
V98	ARS_BFGL_BAC_34879						*
V99	ARS_BFGL_NGS_36606		**				**
V100	BOVINEHD2000011266				P<0,1		
V101	BOVINEHD2000011279		*			P<0,1	***

V102	BOVINEHD2000011282				P<0,1		
V103	BOVINEHD2000011290	P<0,1	**				*
V104	BOVINEHD2000011300						
V105	BOVINEHD2000011341						
V106	HAPMAP47541_BTA_22031						
V107	BOVINEHD2000011383			P<0,1			
V108	BOVINEHD2000011393				P<0,1		P<0,1
V109	BOVINEHD2000011415						
V110	BOVINEHD2000011418						
V111	ARS_BFGL_NGS_41834						
V112	BOVINEHD2000011461				P<0,1		
V113	BOVINEHD2000011465						
V114	BOVINEHD2000011491						
V115	BOVINEHD2000011538						
V116	HAPMAP39921_BTA_44918						
V117	BOVINEHD2000011580						
V118	BOVINEHD2000011622					P<0,1	
V119	BOVINEHD2000011627						
V120	ARS_BFGL_NGS_56135	P<0,1					

Annex 2

Table 2- Correlation of slick hair and soil type.

Table of pelos12 by Solos							
		Solos					Total
		LV	LVA	PVA	RL	SG	
pelos12							
1	Frequency	0	0	0	0	2	2
	Percent	0	0	0	0	0,12	0,12
	Row Pct	0	0	0	0	100	
	Col Pct	0	0	0	0	2,33	
2	Frequency	1	0	3	0	2	6
	Percent	0,06	0	0,18	0	0,12	0,35
	Row Pct	16,67	0	50	0	33,33	
	Col Pct	0,07	0	3,45	0	2,33	
3	Frequency	10	0	2	0	2	14
	Percent	0,59	0	0,12	0	0,12	0,82
	Row Pct	71,43	0	14,29	0	14,29	
	Col Pct	0,72	0	2,3	0	2,33	
4	Frequency	73	2	23	13	9	120
	Percent	4,28	0,12	1,35	0,76	0,53	7,04
	Row Pct	60,83	1,67	19,17	10,83	7,5	
	Col Pct	5,26	4,55	26,44	13	10,47	
5	Frequency	521	33	57	47	38	696
	Percent	30,56	1,94	3,34	2,76	2,23	40,82
	Row Pct	74,86	4,74	8,19	6,75	5,46	
	Col Pct	37,54	75	65,52	47	44,19	
6	Frequency	783	9	2	40	33	867
	Percent	45,92	0,53	0,12	2,35	1,94	50,85
	Row Pct	90,31	1,04	0,23	4,61	3,81	
	Col Pct	56,41	20,45	2,3	40	38,37	
Total	Frequency	1388	44	87	100	86	1705
	Percent	81,41	2,58	5,1	5,87	5,04	100

Annex 3.

Table 3- Important phenotypic characteristics for Phenotype.

Characteristic	Source	DF	F Value Pr > F
Altimetry	pelos12	5	24.38 <.0001
Precipitation	pelos12	5	21.56<.0001
NDVI	pelos12	5	15.57<.0001
Relative humidity	pelos12	5	17.29<.0001
Temperature	pelos12	5	76.29<.0001
THI	pelos12	5	72.11<.0001
Radiation	pelos12	5	9.93<.0001
Temperature nor	pelos12	5	12.01<.0001
Precipitation nor	pelos12	5	9.92<.0001

5. GENETIC SPATIALIZATION IN MONTANA CATTLE

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Abstract

Brazil holds a prominent position among the world's leading beef producers and exporters, playing a significant role in the trade balance. The Montana breed has been gaining prominence in Brazilian livestock due to its meat quality and adaptability to the tropical climate, distinguishing itself from other breeds such as Zebu and Taurine. The adopted methodology mapped sixteen farms across five Brazilian states. The data was georeferenced using the Geographic Information System and the ArcGIS 10.3 software, considering a geographic coordinate system and the WGS 84 datum. The Alleles in Space (AIS) software was used to study the relationship between the SNP genetic data and the animal collection location. Various analyses were conducted, including the Mantel correlation, genetic barrier identification, and spatial autocorrelation. The results indicate a correlation between genetic and geographical distances, reinforcing the idea that geographical distance can influence genetic diversity. This information is vital to understand the genetic structure of populations concerning geographical space and is crucial for optimizing Brazilian agricultural production.

Keywords: Genetic landscape shape, Georeference, Mantel, spatial correlation, Montana breed

5.1 Introduction

Brazil ranks among the world's leading producers and exporters of beef, holding a significant influence over its trade balance. ABIEC (2021) reported an increase in exports compared to 2020, reaching 2.02 million tons, generating a revenue of US$ 8.50 billion. The livestock industry plays a pivotal role in the Brazilian economy, not only as a primary source of food but also as a job creator, a source of foreign exchange, and a driving force behind technological innovations in the agricultural sector. According to Gomes et al. (2017), Brazil's prominent position in this market is attributed to the structured development process of the industry, which has not only elevated productivity but also enhanced the quality of the meat.

The Montana breed has been gaining increasing prominence in Brazilian livestock farming. With Brazil recognised as one of the world's top beef producers, this breed presents an opportunity to enhance the quality and quantity of production further. According to Grigoletto et al. (2020), the expansion of the Montana breed in Brazil and other tropical countries is primarily attributed to its superior meat quality and adaptability to the tropical climate, compared to the Zebu and Taurine breeds. This adaptability is pivotal for the success of the Montana breed in the Brazilian context.

Research focused on the development of the Montana breed in Brazil began in the 1990s, driven by the quest for livestock that could thrive in Brazilian tropical conditions while retaining the ability to produce high-quality meat. The Montana Tropical Composite was first established in 1994, drawing from studies conducted by the U.S. Meat Animal Research Center in Clay Center, under the guidance of the United States Department of Agriculture (USDA), as highlighted by Gregory et al. (1993) and Gregory et al. (1994). This composite population was formulated by interbreeding animals from four distinct biological types or breed groups (Ferraz et al., 1999): 1) Zebu breeds (*Bos taurus indicus*), 2) Adapted Taurine breeds (*Bos taurus taurus*), 3) British breeds (*Bos taurus taurus*), and 4) Continental European breeds (*Bos taurus taurus*).

The Montana breed has proven to be versatile and adaptable to various breeding methods, solidifying its prominent position in Brazilian agriculture. This article aims to map the distribution of animals of this breed while exploring their genetic potentialities concerning variables such as geographical distance between different animal groups.

5.2 Material and Methods

Sixteen farms were mapped (Figure 1), distributed across 5 states in Brazil: Minas Gerais (MG), Goiás (GO), Mato Grosso do Sul (MS), São Paulo (SP), and Rio Grande do Sul (RS). The farms are located in the following municipalities: Carlos Chagas (MG), Ituiutaba (MG), Aporé (GO), Aquidauana (MS), Miranda (MS), Dois Irmãos do Buriti (MS), Rio Brilhante (MS), Três Lagoas (MS), Santa Rita do Pardo (MS), Araçatuba (SP), Pomissão (SP), Pirajuí (SP), São José do Rio Preto (SP), Alegrete (RS), Turuçu (RS) and Capão do Leão (RS).

The data were georeferenced through the Geographic Information System (ArcGIS 10.3 software), considering a geographic coordinate system and WGS 84 datum, and the SNP data from a 500,000 SNP chip was available on 6551 markers and 1607 animals distributed throughout Brazil (figure 1).
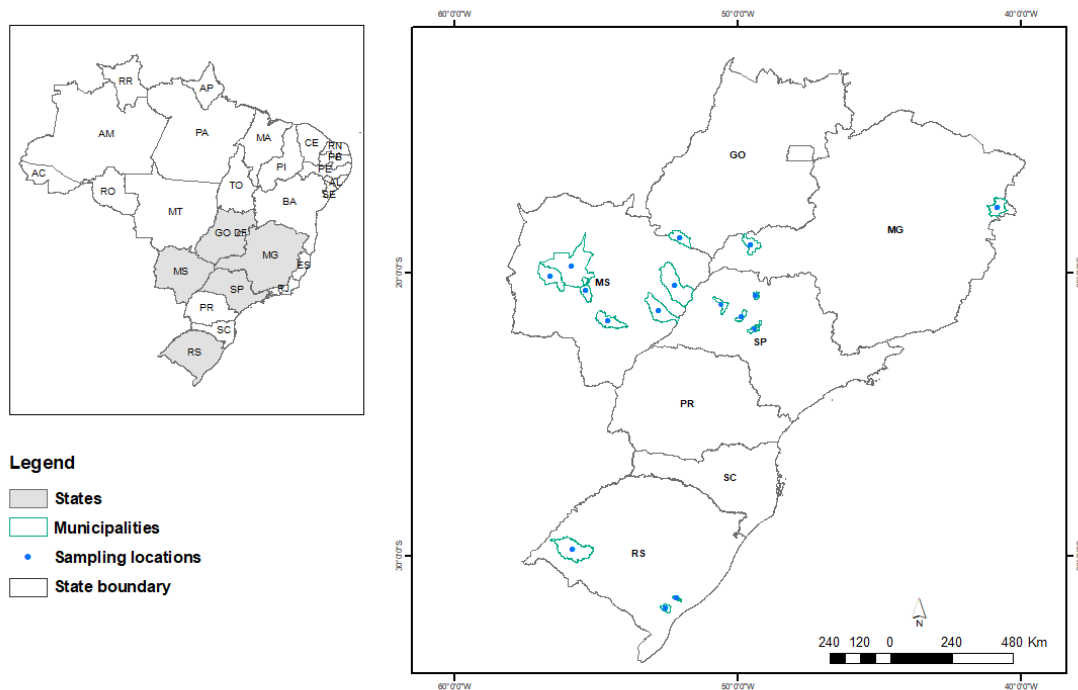

Figure 1- Collection points using the SNP markers.

Alleles in Space (AIS) software (Miller, 2005) was used to study the relationship between genetic SNP data and animal collection location. The following analyses were carried out: Mantel correlation (Mantel, 1967) was carried out with 1000 replications to calculate the correlation between genetic and geographic distances; Genetic barriers were identified using the Monmonier algorithm (1973); Spatial autocorrelation was used to verify the spatial dependence of the genetic values on geographic distances. For the Spatial autocorrelation

analysis, distance classes were constructed using equal distances with unequal sample sizes and 1000 permutations performed.

5.3 Results

The Mantel test is a statistical method frequently used in genetic studies to assess the correlation between two distance matrices, especially when analyzing the relationship between genetic and geographic distances. In (Figure 2), the test results are displayed: The X-axis represents the geographic distance between pairs of animals, while the Y-axis illustrates the genetic distance based on SNP markers. Mantel correlation: Correlation of genetic and geographical distances: $r = 0.12$ and probability of observing a correlation greater than or equal to observed: $P = 0.001$.
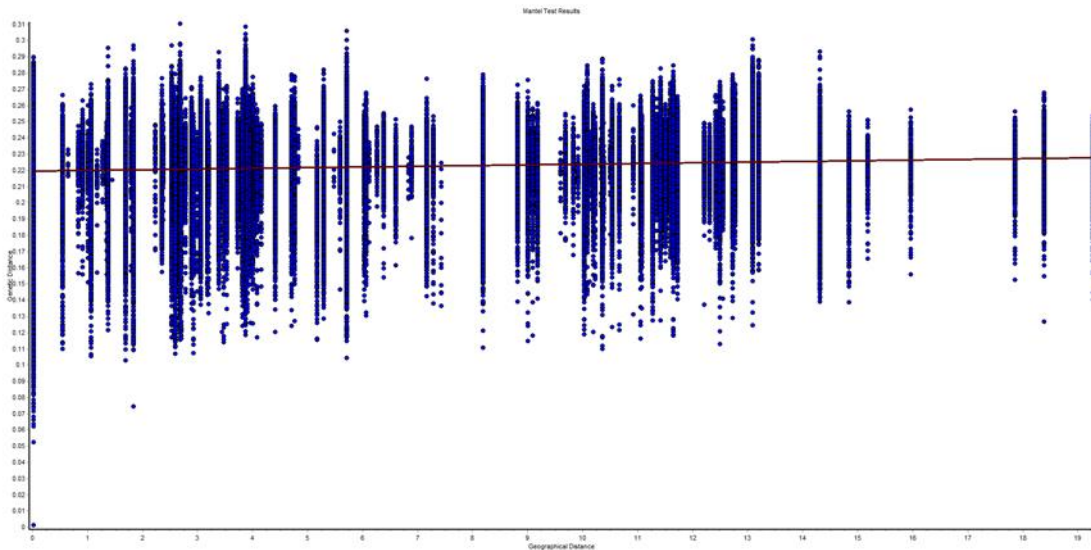

Figure-2 Relationship between geographical and genetic distances in the mantel test (1000 permutations)

The spatial autocorrelation analysis is crucial for understanding the genetic structure of populations concerning geographical space. Figure 3 was generated using two distinct methods: Figure 3a employs the equal interval method with 1,000 permutations and 5 classes presents similar distances with different number of samples, while Figure 3b was obtained using the unequal interval method, also with 1,000 permutations and 5 classes presents different distances and equal number of samples.
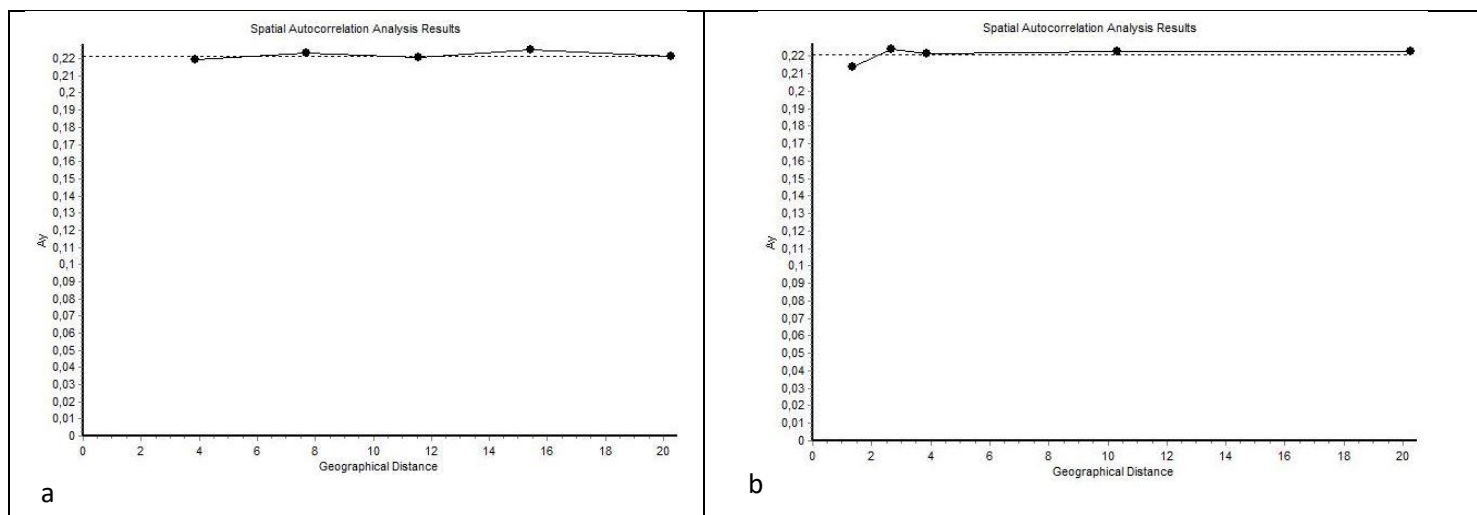
Figure 3- Graphs with spatial autocorrelation: a) equal method with 5 classes b) unequal method with 5 classes.

The Monmonier genetic barriers were identified among the farms participating in the collection points. The aim of using this method was to determine potential genetic separation zones that could affect the diversity and distribution of the breed. Figure 4a displays the overall polygon of the collection area, with the blue points representing the farms. Figure 4b was constructed by correlating the genetic barriers with the collection points.
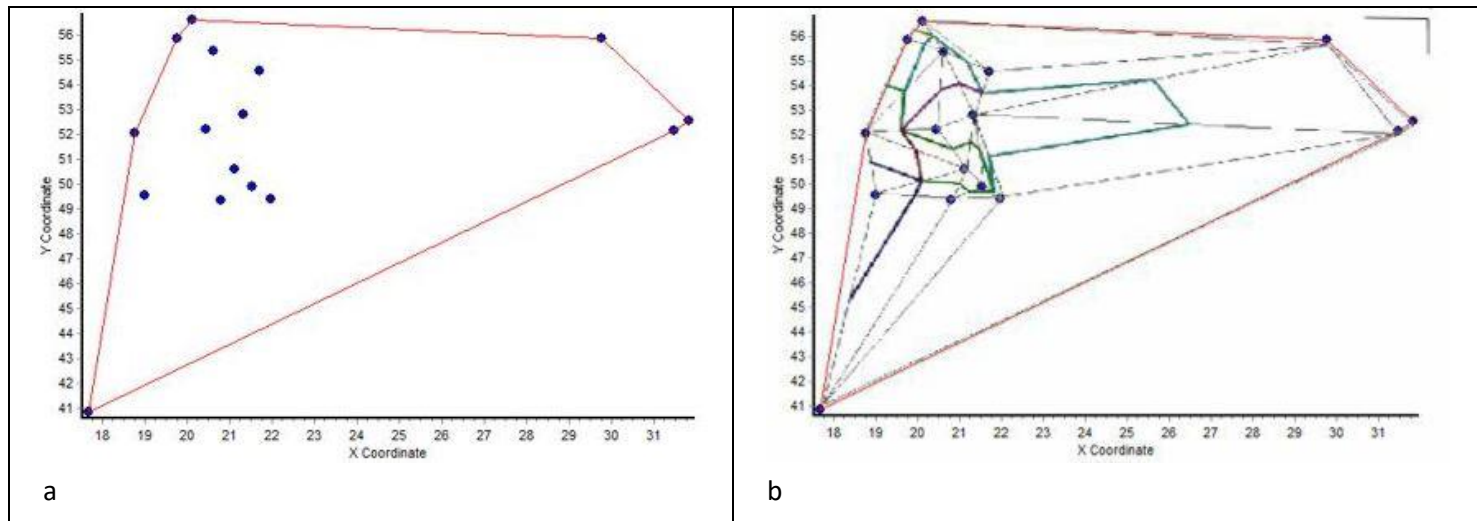

Figure 4 - Application of the Monmonier Method: a) Polygon connecting the collection points; b) Genetic barriers fitted within the polygon and the collection points. To provide a more precise visualization and interpretation of the data across Brazilian territory, Figure 5 highlights the main genetic barriers established by the Monmonier method, distributed according to the collection points throughout the region.
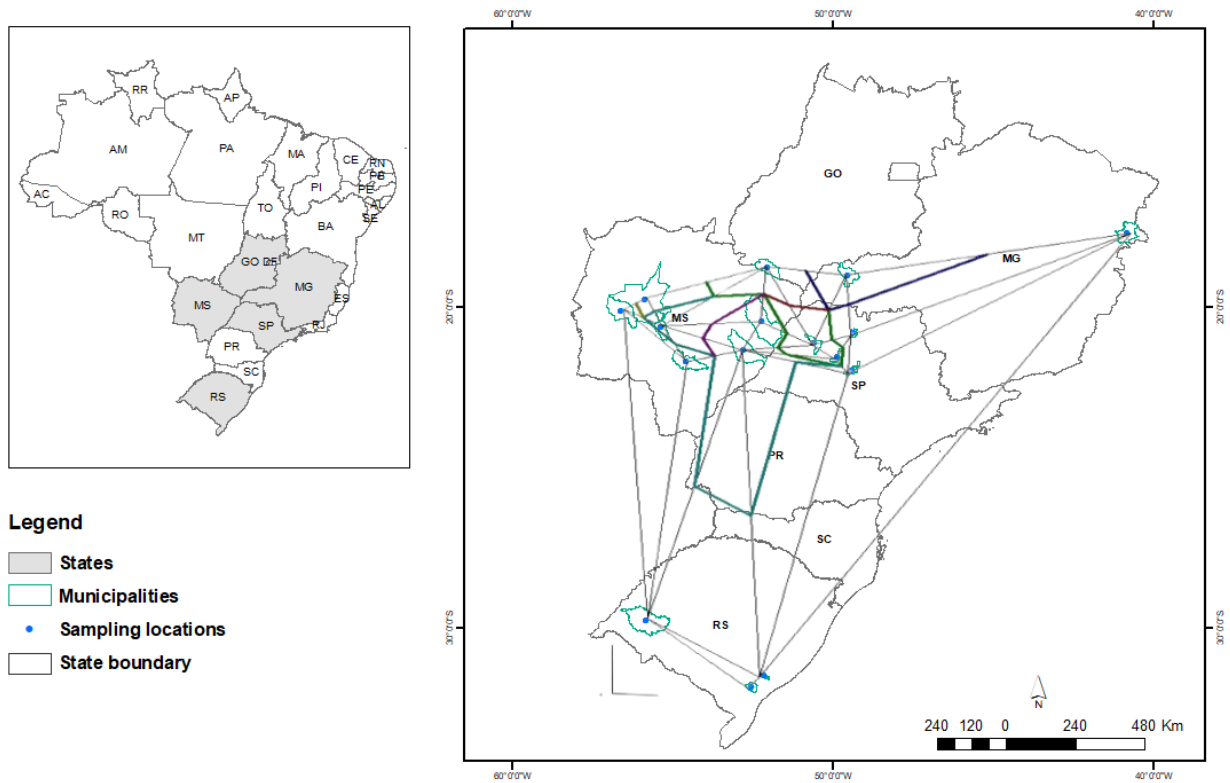
Figure 5- Overlaid on a Brazilian map. 1st, dark blue 2nd dark green, 3rd purple, 4th dark red, 5th Turquoise, and 6th olive green.
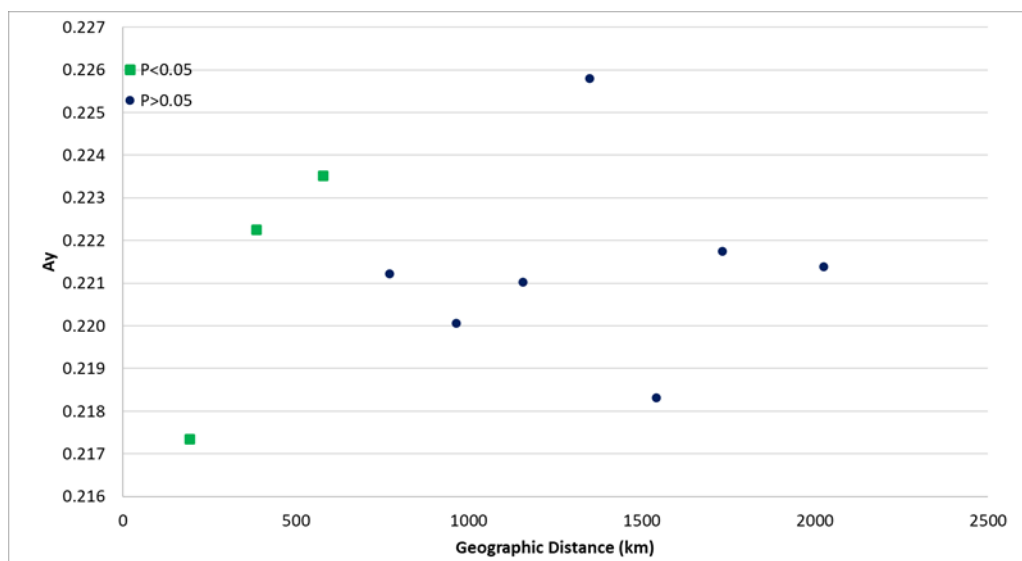

Figure 6: Scatter plot between geographic distances and genetic values

Figures 7 A and B represent the distribution pattern of Montana breed animals under two perspectives. The rising peaks indicate areas with high genetic discontinuity among the animals, while the descending peaks show high genetic similarity. The genetic proximity among the animals found in the southern region and also highlights significant valleys, which demonstrate this genetic closeness at the collection points situated in Mato Grosso do Sul. The major peaks indicating greater genetic divergence are found near the southern region of Goiás, the western part of Minas Gerais, and certain points within São Paulo.
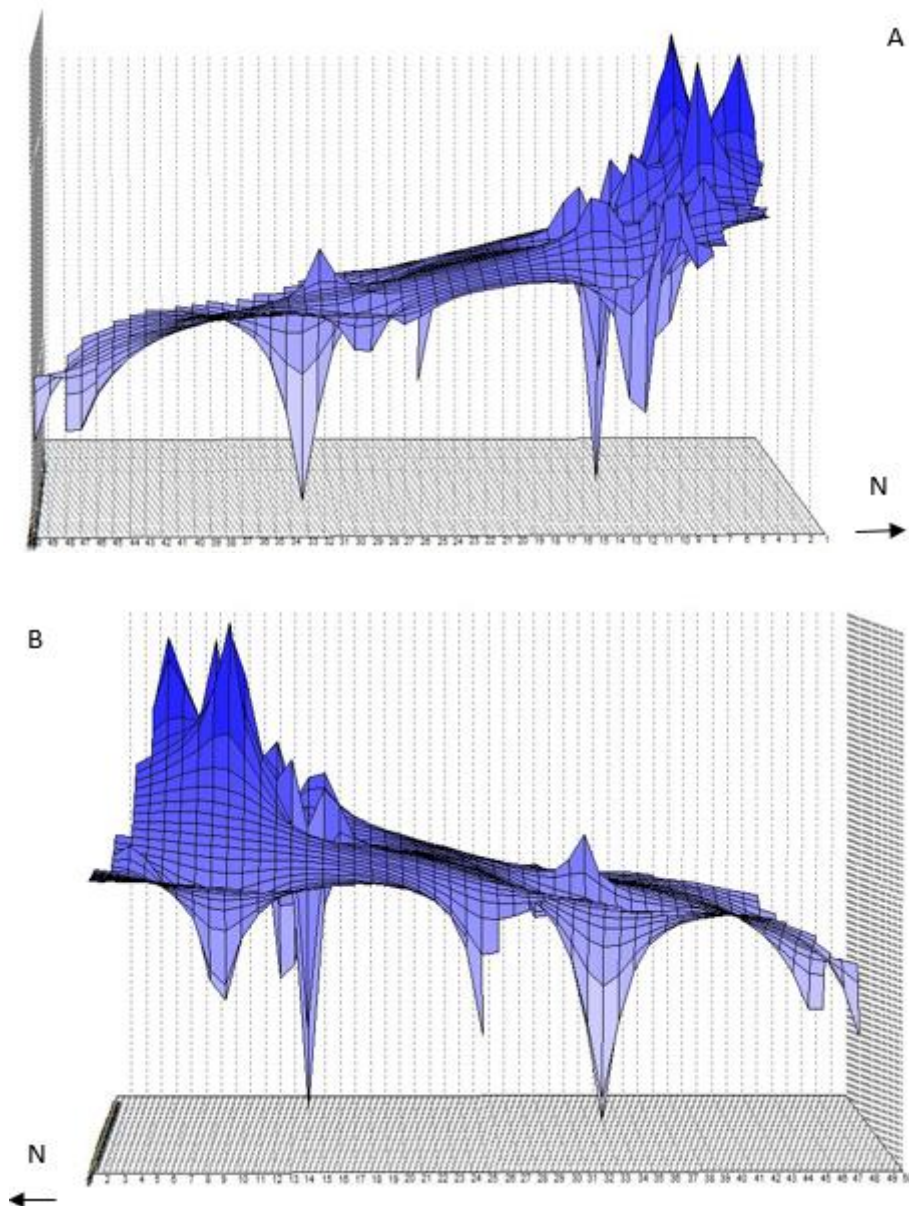
Figure 7 - Interpolation of the genetic landscape using a 50x50 grid and a distance weighting parameter (a) equal to 1, under two perspectives (A and B), of the 3D surface of spatialized genetic distances for Montana breed cattle in Brazil.

5.4 Discussion

Following the analysis of the Mantel test (Figure 2), a linear relationship between the genetic and geographic distances represented on the graph's axes is observed. This suggests that as the geographic distance between animals increases, their genetic distance also increases. This indicates a spatial structuring, where animals geographically closer are also more genetically similar. According to Teixeira et al. (2006), the performance of different genetic groups was influenced by the regional effect, and contrasts between the estimated averages indicated an environmental limitation for the full expression of productive potential.

This visualization shows that a more pronounced genetic disparity emerges in samples separated by a distance exceeding 500 km. Based on the analysis of figures 3a and 3b, the equal and unequal methods indicated that there isn't a strong spatial autocorrelation in the SNP genetic data for these animals. The genetic autocorrelation appears to be relatively constant across various geographical distances, although there are some differences that become more significant from 500 km onwards.

Brazil is a country with a vast territorial expanse and significant variation in physical aspects. To provide a more coherent analysis of the data collection points, the main geographical aspects of each area were examined. According to Zavattini (2009), the state of Mato Grosso do Sul exhibits low altitude levels in the regions corresponding to the area of the Pantanal in southern Mato Grosso do Sul, with average altitudes ranging between 200 and 600 meters. Most of the state's territory is dominated by a tropical climate, with summer rains and a dry winter, characterized by average temperatures that vary between 26°C in the Paraguay lowlands and 23°C in the plateau. The annual rainfall is approximately 1,500 mm, and the primary biome associated with the municipalities is the Cerrado, according to IBGE (2012).

The southern portion of Rio Grande do Sul, known for its vast plains called the Pampa, has an average altitude that rarely exceeds 100 meters. Valério et al. (2018) note that this part of the State displays moderate to low altitudes. The climate is predominantly humid subtropical. Brito et al. (2006) state that this region is characterized by an annual rainfall index of approximately 1,200mm to 1,500mm, distributed throughout the year. The predominant

vegetation is the pampa, described by IBGE (2012) as a vast field that extends throughout the region, serving as an important biome for extensive livestock farming.

The northwest region of the state of São Paulo is characterized by a gently rolling topography, with altitudes ranging on average between 400 and 600 meters. According to Novais et al. (2022), the western part of the state has a drier climate, with a rainfall index fluctuating between 1,000mm and 1,200mm annually and average yearly temperatures around 22°C. Regarding vegetation, the northwest of São Paulo originally featured extensive areas of Cerrado (IBGE, 2012). However, with the advancement of agricultural activity, much of this vegetation has been replaced by crops and pastures.

The municipality of Carlos Chagas is located in the state of Minas Gerais, Brazil. Its annual rainfall index is approximately 1,000mm. According to Almeida et al. (2018), more than 50% of the annual precipitation occurs in the rainy trimester, while the driest trimester accounts for 16% of the annual precipitation. The prevailing climate in Carlos Chagas is tropical, with average annual temperatures ranging between 20°C and 28°C. The region has an average altitude of about 200 meters above sea level. The original vegetation is characteristic of the Atlantic Forest biome, as pointed out by IBGE (2012). However, much of the territory has been adapted for agricultural activities.

Figure 6 illustrates the relationship between the genetic and geographic distances of the Montana breed animals. Pairs of samples with statistically significant genetic differences at a significance level of P<0.05 are denoted by green points. In contrast, blue points symbolize pairs of samples whose genetic differences do not reach statistical significance (P>0.05).

The data presented in Figure 4 indicate patterns of genetic barriers within the Montana breed animal population. The first identified barrier is located near the collection points in São Paulo (SP) and the municipality of Carlos Chagas in Minas Gerais (MG), as illustrated in Figure 7. These regions host distinct biomes: while in São Paulo, the breeding predominantly occurs in the Cerrado, in Minas Gerais, the prevailing biome is the Atlantic Forest. As Baiardi et al. (2021) highlighted, Brazilian biomes have a rich diversity of natural potential, influencing investment decisions and the direction of agricultural research. However, it is crucial to understand that natural resources alone do not guarantee success. Antunes et al. (2021) also emphasise the importance of the Cerrado and Atlantic Forest biomes for the progress of Brazilian agriculture over the years. Thus, combining genetic studies with geographical analyses becomes a valuable tool for optimizing Brazilian agricultural production.

The three-dimensional graph shown in Figure 5 displays a genetic proximity among the animals found in the country's southern region. The geographical distance between the collection points is around 400km an important factor to consider when noting the genetic closeness despite the significant geographical distance is that the collection points in the southern region of Brazil share similar geographical characteristics.

5.5 Conclusions

The most pronounced genetic difference between the animals is observed in samples typically separated by a geographical distance exceeding 500 km. This observation is supported both by the Mantel test and by the analyses of the equal and unequal methods. When the geographical distance aligns with a biome transition at the collection points, a genetic differentiation between the animals is more likely to be found. Integrating genetic studies with geographical analyses is essential to optimize Brazilian livestock production.

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Conflict of Interest

The authors declare no conflict of interest

Ethics Committee Approval

Animal Care Committee approval was not obtained for this study as all the analyses were performed using pre-existing databases.

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CONCLUDING REMARKS

The four articles developed in this thesis provide a data survey and analysis of different characteristics of the Montana breed animals associated with the development of Brazilian livestock farming, offering a perspective on genetic diversity, adaptation, and the impact of the environment on phenotypic characteristics, which can be used as a basis for the improvement of livestock farming with composite animals in tropical regions.

The first article on bibliometric analysis provides an overview of the publications on composite cattle, highlighting the Montana breed as a significant focus of research. It also identified important research groups in Australia, the United States, and Brazil.

The second article brought an analysis of the environmental and socioeconomic conditions, revealing regional variations that influence the genetic values of Tropical Montana cattle. It was evidenced that differences in soil, altitude, vegetation indices, climatic conditions, and population density affect the breed, emphasizing the need to consider these variations when selecting animals adapted to different production systems.

The third article shows a more specific study related to the "slick hair" characteristic and presents the importance of this feature as an adaptive mechanism to thermal stress in tropical areas. The decoding of genetic markers on BTA20 revealed the expression of the chromosomal region and its interaction with geographic characteristics.

The fourth article presents the integration of genetic studies with geographical analyses, observing that the greatest genetic differentiation between the animals occurs in samples separated by geographic distances greater than 500 km, especially when this distance coincides with a biome transition.

The results presented in this thesis demonstrate the importance of multidisciplinary studies to improve livestock development, and it should be made clear that the Montana breed animals show high potential to enrich Brazilian livestock production.