

Gene bank collection strategies based upon geographic and environmental indicators for beef breeds in the United States of America[☆]

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HIGHLIGHTS

- Sampling for genebanks based upon environment adaptability could enrich germplasm collections.
- We mapped beef cattle DNA samples in the USDA germplasm bank to define new sampling regions.
- Sampling of continental and british breeds need to increase in westerly states.
- *Bos indicus* sampling needs to increase overall, but especially in the more northerly states.
- Methods here can be extended to promote sampling in environmentally unique areas.

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ABSTRACT

As gene bank collections develop, there are opportunities to collect germplasm using criteria other than random sampling or genetic relationships. For Brazil and the US, it has become apparent that sampling based upon environmental adaptability could enrich germplasm collections. Combining current US beef cattle germplasm collection with Geographical Information System (GIS) approaches, sample concentration and underrepresented areas were identified for *Bos taurus* and *Bos taurus indicus* (BI). BI samples were principally derived along the Gulf Coast region (not necessarily close to freshwater sources). In contrast, continental Europe (BTCE) and British, African and Asian (BAA) breed samples were more concentrated among the Great Plains/Mid-West (close to major rivers and lakes), with some samples being derived from the south-west and Gulf Coast areas. BTCE and BAA have been extensively sampled, but more is needed in the more westerly states of New Mexico, Nevada, California and Utah. In addition, BI sampling should increase in the more northerly states of Tennessee and Kentucky to capture allele frequencies that may better enable those breeds to perform outside the Deep South. The methods used in this evaluation can be extended to using genotypes within or among breeds to promote sampling in environmentally unique areas.

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1. Introduction

Genebanks are important resources for scientific and production advancements, especially when combining accessible and well-characterized biological samples of various types with associated data (Blackburn, 2012; Groeneveld et al., 2016). In addition, diversity of Animal Genetic Resources (AnGR) is needed to ensure adaptation potential in times of uncertainty, such as those associated with global climate change (Renaudeau et al., 2012). Over the last decade, substantial strides have been made in conserving animal genetic resources by gene banking, particularly in Brazil and the United States (Paiva, 2016; Blackburn et al., 2017; Blackburn et al., 2018). Presently, 80% of the USA beef cattle collection (Animal-GRIN: https://agrin.ars.usda.gov/collection_overview_page_dev?language=EN&record_source=US) has met or is approaching collection goals recommended by FAO (2012). The ability to regenerate entire breeds with an effective population size of 50 animals has been met for these breeds, based upon collection size. To date, most emphasis on gene bank collection development has been to assure the breadth of genetic diversity has been captured for any one breed. Such assessments have been conducted using pedigree or genomic data (Danchin-Burge et al., 2011; FAO, 2015). But these assessments deal with assessing genetic diversity in the broadest of terms by using genomic markers distributed across the genome at varying marker densities (Yue et al., 2015; Liu et al., 2019).

While meeting recommended FAO (2012) levels, our focus is now shifting to ensure the collections have specific environments represented. This particular focus takes on a new urgency as gene banks position themselves to address challenges such as climate change. Taking this step provides greater insurance that a richer representation of genetic diversity includes subpopulations emerging from different environments that pose different biological challenges or stressors. Such a step increases the utility of the gene bank collections for various stakeholders, particularly when taking a long-term view of decades or centuries.

Landscape genomics has not been utilized in the development of gene bank collections. It has, however, been useful in identifying the genetic basis for adaptation (Joost et al., 2007) and studying genetic diversity among African goats and cattle (Carson et al., 2009; Kim et al., 2016; Mdladla et al., 2016, 2017, 2018) and Brazilian sheep (McManus et al., 2014, 2016, 2020) and cattle (Alfonzo et al., 2021; Lima et al., 2021a,b; Souza et al., 2021) populations. These studies have focused mainly upon breed level analysis. That said, it has been well documented that most genetic diversity resides within populations (Groeneveld, 2010; Hoffmann, 2010).

Hoffmann (2010) has suggested that selection criteria for traits such as heat resistance and disease resistance will need to increase to cope with climate change. It has been assumed that breeds from harsh environments may be of the greatest interest for adaptation to climate change (Boettcher et al., 2010, 2014). But this suggests livestock have the genetic variability to use in selection. Within the USA, several breeds are widely dispersed among environments. For example, Blackburn et al. (2017) and Delgadillo Liberona et al. (2020) demonstrated the presence of subpopulations in Hereford cattle that vary significantly in allele frequencies for loci associated with an animal's ability to adapt to various environmental stressors and heritability for intramuscular fat.

The USA has considerable environmental variability in terms of ambient temperatures, humidity levels, precipitation, altitude, and forage production. How those potential stressors can impact cattle production is presented in Fig. 1, along with the impact on typically selected traits. Accordingly, cattle of different genetic backgrounds are used as environmental conditions dictate. For example, *Bos taurus indicus* are predominately used in the hot humid region along the Gulf of Mexico and in hot arid regions, representing approximately 34% of the national herd (USDA-NASS, 2021). *Bos taurus* have a broader geographic distribution than *Bos taurus indicus* however some *Bos taurus* breeds are primarily used in more temperate climates, vs those with a national

distribution (e.g., Hereford and Angus). While both subspecies are located in the hot dry or hot humid areas it is well known that *Bos indicus* better perform in hot humid environments than do *Bos taurus*. Therefore, under climate change scenarios it is anticipated that more heat and humidity stress, measured by temperature humidity index (THI), will likely change and potentially alter the range where cattle types are commonly used, assuming no genetic change in adaptation traits.

Both Brazil and the United States are environmentally diverse beef cattle producing countries, with 232 million and 31 million head of breeding cattle, respectively (<https://www.nass.usda.gov/>). As a result of such environmental diversity, researchers need to focus more on genetic by environment by management interactions to effectively tailor cattle productivity and genetic improvement (Rexroad et al., 2019), especially under climate change scenarios. Climate change is expected to impact production systems, through changes in precipitation, temperature, water and forage availability among others. Therefore, the breeds that can adapt to specific regions may change, or there will a need to mitigate environmental conditions to maintain the same breeds and production levels. Studies show (Costa et al., 2014; da Costa et al., 2020) that breeding values maintain an environmental influence, even after correction for location. Brazilian and USA collections have begun to explore how environmental conditions, as visualized through geographic information systems (GIS), might be used, in combination with current collection status, as a tool for further collection efforts (e.g., Hermuche et al., 2013; McManus et al., 2014, McManus et al., 2016; Paiva et al., 2016b), as well as for within-country changes in production environments (Lopes et al., 2012; McManus et al., 2014). This requires socioeconomic and production system information (Drucker, 2010; FAO/WAAP 2008) and data on soil, vegetation, climate, and water resources.

Here we report the first work combining the source of germplasm samples in a gene bank with environmental variables and explore the ramifications of combining these types of data. Specifically, we compared beef breeds originating from the United Kingdom, Africa, and Asia (all *Bos taurus*; BAA), Continental Europe (all *Bos taurus*; BTCE), and *Bos taurus indicus* (BI).

1.1. Material and methods

Data included information from the US beef cattle germplasm collection on 12,076 animals (Tissue, Whole Blood, Purified DNA, Semen/Sperm or Buffy Coat/White Blood Cells) from 1891 sampling locations. Breeds were assigned to one of three groups for mapping. They included: 20 *Bos taurus* British, African and Asian origin (BAA), 17 *Bos taurus* Continental Europe (BTCE), and 12 *Bos taurus indicus* (BI) breeds. A complete list of breeds in the collection is in Animal-GRIN (https://agrin.ars.usda.gov/main_webpage_dev/ars). In addition, the city and state of the breeder producing the animals sampled are maintained in the Animal-GRIN database. Breeds assigned to BTCE tended to be those imported into the USA after 1960. A previous publication illustrated the difficulty new breeds have in becoming established and utilized in the USA (Blackburn and Gollin, 2009). Therefore, it was of interest to determine if BTCE were limited in their geographic/environmental distribution. Contrary to BTCE some BAA breeds have achieved a broad geographic/environmental distribution. *Bos indicus* breeds and their composite breeds (e.g., Brangus) tend to be found in the southern USA, but it is of interest to determine how far north they have expanded.

County-level data for in-situ cattle inventory were obtained from USDA - National Agricultural Statistics Service for the years 2007, 2010 and 2012 (https://www.nass.usda.gov/Data_and_Statistics/County_Data_Files/Livestock_County_Estimates/index.php). Data were partitioned into counties (political and administrative divisions within a state). There are no set standards for county number and size across the 50 states. In the present study, only counties and equivalents within the

continental US border were considered, Alaska and Hawaii were excluded. Data was generated in Datum NAD 1983 and converted to Datum WGS 1984. Growth for in-situ cattle inventory per county was calculated as: $[(\text{Number cattle in 2012}) - (\text{Number cattle in 2007})] / (\text{Number cattle in 2007}) * 100$. Vegetation cover was obtained from the 2015 average annual Normalized Difference Vegetation Index (NDVI) derived from images of MODIS (Moderate Resolution Imaging Spectroradiometer) sensor. NDVI is defined as the ratio between the difference in the reflectance measurement in the near-infrared (NIR) and red (RED) channels and the sum of these, being expressed by the equation: $\text{NDVI} = (\text{NIR} - \text{RED}) / (\text{NIR} + \text{RED})$

This index is sensitive to chlorophyll and the presence of healthy vegetation, and its range varies between -1 and 1 , with value 1 being the highest response of photosynthetically active vegetation. Three hundred and twelve images (2 per month (24 per year) of each of the 13 tiles that cover the entire USA) were acquired from NASA's website (<https://earthobservatory.nasa.gov/features/MeasuringVegetation>) and, after converting the sinusoidal projection to geographic Lat / Long in the Modis software Reprojection Tool (MRT) (geographic projection Lat / Long and Datum WGS 84), the annual average was processed using the ENVI 4.7 software.

Precipitation and temperature data (<http://www.worldclim.org>) were processed by Hijmans et al. (2005), and data were interpolated using a Spline algorithm with a spatial resolution of 30 s (near 1 km). Elevation above sea level was derived from data obtained from the Shuttle Radar Topography Mission (SRTM) with a 30-meter resolution (<https://www2.jpl.nasa.gov/srtm/>). Relative humidity data were obtained from the Surface Meteorology and Solar Energy Laboratory (Zhang et al., 2010). It consists of the annual average of the relative humidity (%) captured 10 m above the earth's surface based on 22 years of observation (1983–2005), with a resolution of 1° (approximately 80 km). The original data was converted to points and reinterpolated using the IQD (Inverse Square Distance) algorithm, with a resolution of 10 km.

The Temperature Humidity Index (THI) relates animals' thermal comfort range to the ambient temperature and relative humidity. For its

calculation, the data of temperature and humidity acquired previously were used. THI was proposed by Thom (1959) and is based on the following equation: $\text{THI} = \text{Ta} + (0.36 \times \text{To}) + 41.5$ Where: Ta = air temperature ($^\circ\text{C}$); To = dew point temperature ($^\circ\text{C}$).

A simple approximation of the dew point temperature (To) was used, based on the following equation: $\text{To} = \text{Ta} - (100 - \text{RH}) / 5$ where RH is relative humidity.

All variables were spatialized in ArcGIS 10.1 with geographic projection Latitude/Longitude and Datum WGS 84 from the Zonal Statistics tool based on vector data relating to counties (<https://www.census.gov/programs-surveys/ces/data.html>). This tool calculates the average value for each county.

Beef cattle census maps were generated from the three years and then converted to a raster format (GRID) and processed in ENVI software (Version 4.5, ITT Visual Information Solution, www.itvis.com). Maps were drawn as the percent change in cattle numbers by county in ArcGIS 10.1 program (ESRI, Redlands, CA: Environmental Systems Research Institute) to analyze the dynamics of change in the number of animals. Latitude and Longitude geographic projection and WGS 84 Datum was from the Zonal Statistics tool based on the vector data for the counties (<https://www.nass.usda.gov/>). This tool calculates the average of the values of each variable for each county.

The animals from the previously defined breed groups (BAA, BTCE, BI) in the collection were mapped across the continental USA to determine if distribution patterns and collection gaps could be identified. Samples in the repository were spatialized within counties. Mean and standard deviations for each environmental variable by the genetic group were calculated. These variables were then overlaid on counties where four or more animals were sampled and defined as core areas. Areas with THI within 1.5 standard deviations of the core area THI were mapped by breed type. By so doing, it provides further targeting for collection development and suggests environments where the breed types might be used.

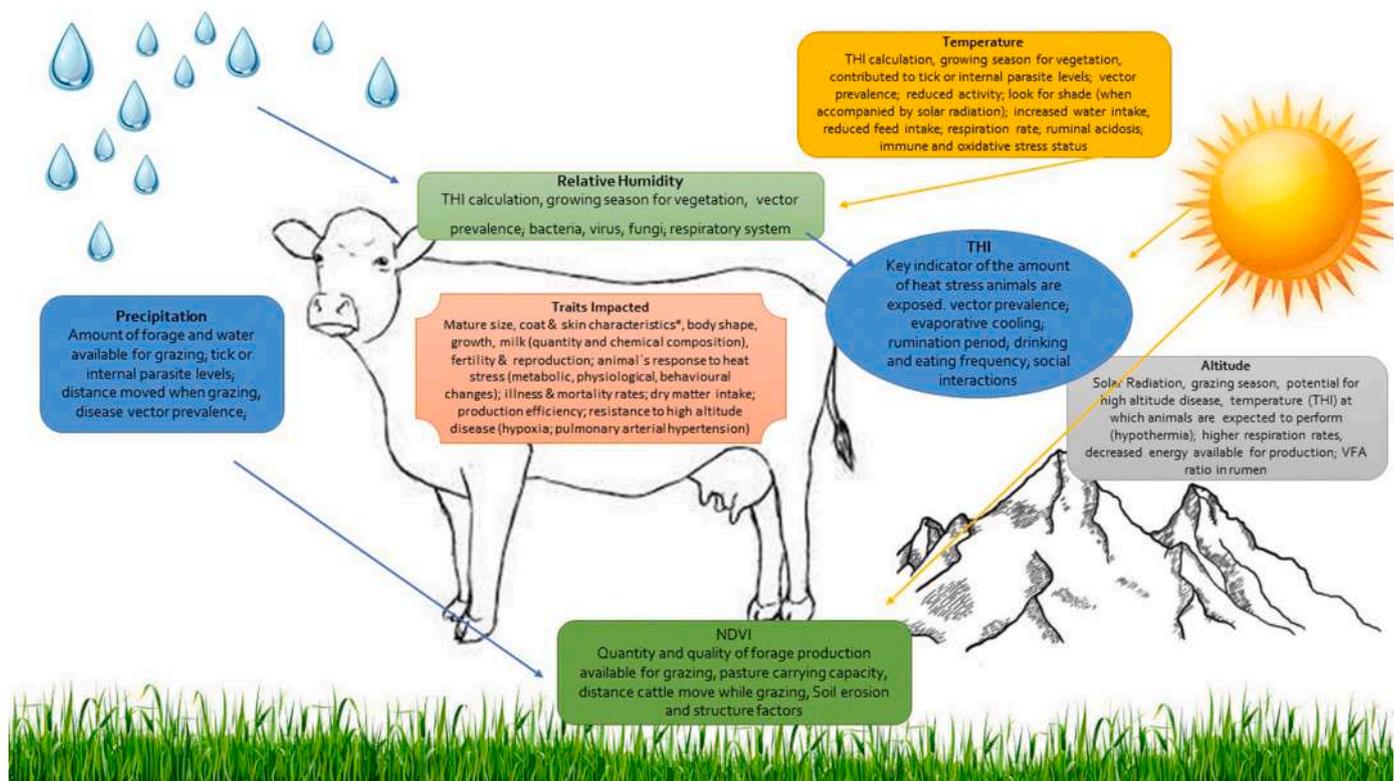


Fig. 1. Schema of how environmental conditions impact production traits in cattle.

2. Results

The gene bank has animal samples from 1891 locations. On average, there were ten animals sampled per location (Fig. 2). However, 1278 locations had less than three animals sampled, while 189 locations contributed samples from more than ten animals.

Major environmental factors: NDVI, precipitation, elevation, temperature, humidity, and THI were plotted by county and categorized into 5 zones for the country (Supplementary Fig. 1). Breed type averages for each of the environmental parameters are presented in Table 1. Vegetation cover represented by NDVI was greater in regions with higher temperatures, precipitation and lower elevation. However, these areas also have higher THI suggesting that cattle produced in high NDVI areas will be under higher environmental stress, leading to a higher prevalence of *Bos indicus* in these areas. It was apparent that altitude (meters above sea level, MASL) and THI have a negative relationship.

Fig. 3 illustrates where samples in the collection were derived compared to the distribution of the national herd. The majority of the collection was acquired from counties where the beef cattle inventory ranged from 1000 to 10,000 animals or 10,000 to 50,000 animals. Counties with these cattle densities tended to be located in the middle of the country. Across USA counties, with a category of 0 to 1000 animals were generally not sampled for the collection.

Beef cattle operations are dependent upon access to forage production, for which NDVI is a proxy (Fig. 4a). To date, the collection has samples from animals produced in all five of the mapped NDVI zones. However, there was a greater concentration of animals represented in the collection from the intermediate NDVI zones which ranged of 0.27 to 0.62. The proportion of samples from BAA decreased with increasing NDVI and THI (Fig. 4b and d, respectively), while BI increased. BTCE showed a quadratic behavior with NDVI (increasing and then decreasing above an NDVI of 0.42), but a linear decrease with increasing THI. Based upon the number of locations for each breed group 68% of BAA were sampled from NDVI areas that ranged from 0.27 to 0.52, while 37% of BTCE were sampled from the 0.27 to 0.40 zone and 33% of BI were sampled from the >0.62 zone (Table 1). Sampling locations were limited in the lowest NDVI zone (< 0.27) with only 7, 8, 4% of sampling locations for BAA, BTCE, and BI, respectively (Table 1 and Fig. 4a). Individual breed distribution maps are available from the authors on request. In addition to forage availability, access to water is critical in the western USA. In drier areas, breeding cattle operations tended to be located on or near various waterways (Supplementary Fig. 2).

THI combines humidity and temperature and is used as a heat stress indicator for livestock. Gene bank sampling has occurred among the five THI zones. As Fig. 4c illustrates, the THI zones run east to west, with THI increasing from north to south. The largest proportion of locations by THI zone for BAA and BTCE (41% and 55%, respectively), ranged in THI from 48 to 53, while 73% of BI locations were in the highest THI zone (>62). Only 6% BAA and 10% of BTCE were sampled from the highest (most stressful) THI zone.

2.1. Future additions to the collection

Given the geographic distribution of the current collection, we explored future geographic areas for sampling. Changes in cattle inventory by state (animals per year) were mapped by county over time (Fig. 5) to determine how the national cattle population had changed. Decreases were seen on the east coast and north-eastern states, which are relatively high in NDVI, precipitation, and lower THI (Supplementary Fig. 1). Increases in cattle numbers were noted in northern and southern Great Plains, and Great Basin states. All of which tend to have lower NDVI and precipitation. We note with interest increases in cattle numbers (>2.5 std dev) in the western panhandle of Texas where it has recently been reported that producers are converting crop land back in to grazing lands due to water shortages (AP News, <https://apnews.com/article/business-science-environment-and-nature-texas-aquifers-db7cc8b855ac2e0f7b184d36ac716346>, accessed 10/7/2021).

Using THI by county where (Fig. 6a and b) four or more animals from BAA, BTCE, or BI populations were sampled (denoted as Core counties) was the basis for comparing counties with or without animals being sampled for the collection. Core BAA counties, when compared to non-core counties, suggests the range for BAA is extensive (Fig. 6a). Similarly, the potential range for BTCE was expanded from core areas found in the mid-west and eastern portions of the country. But in the western half of the USA the range for BTCE was not as extensive as BAA. As Fig. 6 demonstrates, BAA and BTCE overlap substantially, particularly the states of Oklahoma, Kansas, Nebraska, Iowa, Missouri, Illinois, Indiana and to a lesser extent in North and South Dakota. Further west, these two breed groups overlapped in northern Idaho, western Washington, and western and central Oregon.

While the potential overlap among core sampling areas and other parts of the country are large for BAA and BTCE this was not the case for core BI areas and other counties (Fig. 6b). The BI sampling took place principally in the Gulf Coast region of the USA, and this is where most BI

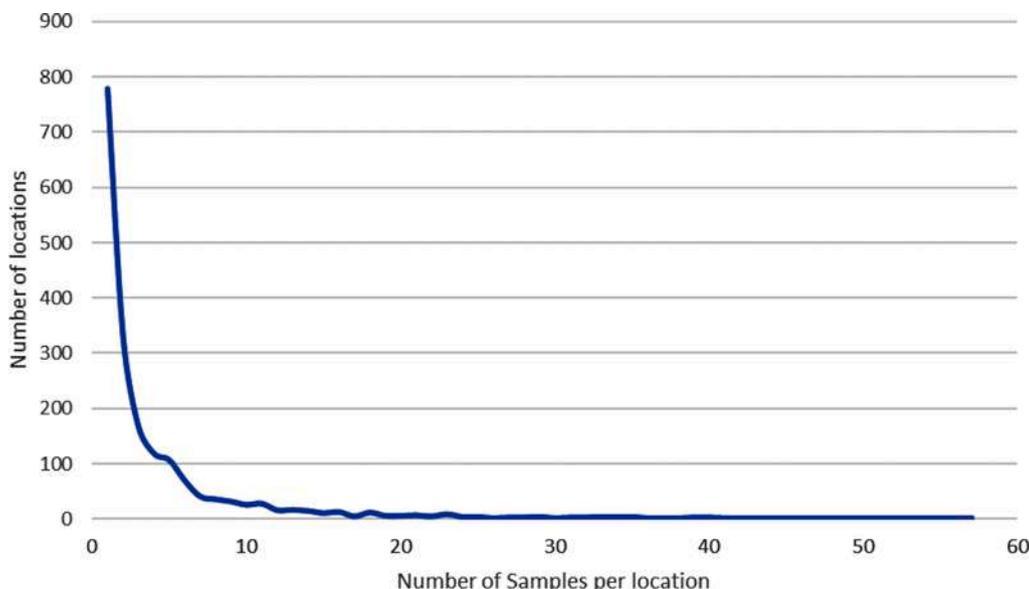


Fig. 2. Number of samples per location in the USDA-ARS Genebank.

Table 1
Number of localities (by climate type) with sample collection for each breed type (mean values).

Variable	Bos taurus		Bos taurus indicus			
	British, African, Asian Locations ³	Samples	Continental Locations ³	Samples	Locations ³	Samples
Precipitation (mm/yr)						
<585	166	8942	124	292	16	27
585–865	113	367	99	329	23	70
865–1093	135	293	88	142	26	763
1093–1345	56	341	37	57	49	284
>1345	17	69	19	23	32	77
NDVI ¹						
<0.27	34	4289	28	46	6	17
0.27–0.40	167	4823	136	423	17	60
0.40–0.52	167	432	116	240	34	65
0.52–0.62	62	150	40	60	41	817
>0.62	57	318	47	74	48	262
Altitude (masl) ²						
<233	96	436	66	88	113	1146
233–591	222	583	200	553	19	49
591–1184	84	507	49	107	10	12
1184–1979	71	276	36	69	2	11
>1979	14	8210	16	26	2	3
THI						
<48	112	8744	102	260	2	3
48–53	200	600	131	344	2	27
53–57	97	285	59	111	9	17
57–62	51	283	40	70	27	230
>62	27	100	35	58	106	944
Temperature (°C)						
<6.3	102	8562	90	231	1	1
6.3–9.7	171	596	119	225	1	2
9.7–12.8	120	410	72	237	10	36
12.8–16.4	67	344	48	87	25	234
>16.4	27	100	38	63	109	948
Relative Humidity						
<50.8	17	34	7	12	5	14
50.8–60.3	64	8366	38	73	3	4
60.3–66.3	134	670	83	169	5	6
66.3–69.8	248	864	214	551	46	294
>69.8	24	78	25	38	87	903
Total	487	10,012	367	843	146	1221

¹NDVI - Normalized Difference Vegetation Index.

²masl - meters above sea level.

³THI - Temperature Humidity Index.

³Number of collection sites > 984 as some areas had more than one cattle type.

⁴Some animals were registered only by state and so could not be included here.

are produced. The core sampling area in Nebraska denotes a research station where BI samples were derived. The Nebraska core area has probably skewed the range of similar counties further to the north than what is noted at the producer level.

In Fig. 6a and b, non-coloured areas indicate counties that lack similarity with the prescribed core locations for all three breed types. Of interest are the areas in southern Texas, Louisiana, Mississippi, Alabama, and Florida for BI, BAA, BTCE (Fig. 6b) and suggests those areas are substantially different from other locations where the breed types have been sampled. However, it is noted in Figure 3 those areas tend to have lower numbers of cattle (<10,000 animals).

3. Discussion

Beef production in the USA is nation-wide, covering a range of climates, environmental conditions, animal genotypes and phenotypes, management practices, and nutritional inputs (Bigelow and Borchers, 2017; Drouillard, 2018; USDA, 2018). It is predominately based upon 323 million hectares or 41% of the continental land area - (USDA-ERS et al., 2021 and 2021b), spanning tropical savannah to Arctic tundra, temperate plains, and mountain pastures. The vast differences in geographies and climatic conditions necessitate using a broad spectrum of breed types suited to these environments, encompassing *Bos taurus*, *Bos*

indicus breeds and their composite breeds.

These core areas, as designated, are based on sampling, and it is assumed that the presence of the breeder in the region indicates some degree of adaptation. This has been seen in Brazil, where there was significant correlation between genetic and geographic distances in sheep (McManus et al., 2021, 2020) and cattle breeds (de Souza et al., 2021). Nevertheless, the mere presence of a genetic resource may be influenced by mitigation strategies or other socioeconomic factors. Under global warming, changing environmental conditions are expected to alter breed distribution and management, under increased demands for productivity and efficiency (Boettcher et al., 2014). These authors emphasize the need for relevant information on environmental adaptation, survival and production linked to geographical information and local soil, plant and water availability.

The variability of breed types and environments where cattle are raised pose a unique challenge for gene banks. An early premise for gene bank sampling was to capture a broad sampling of breed (FAO 1998; Paiva, 2016) genetics without attention to environmental differences (FAO, 2012; 2008), despite the demonstrated genotype by environmental interactions ((Delgadillo Liberoni et al., 2020) and differences in allelic frequencies within a breed when raised in distinct environments (Blackburn et al., 2017a).

As expected, BI samples were derived from the Gulf Coast region

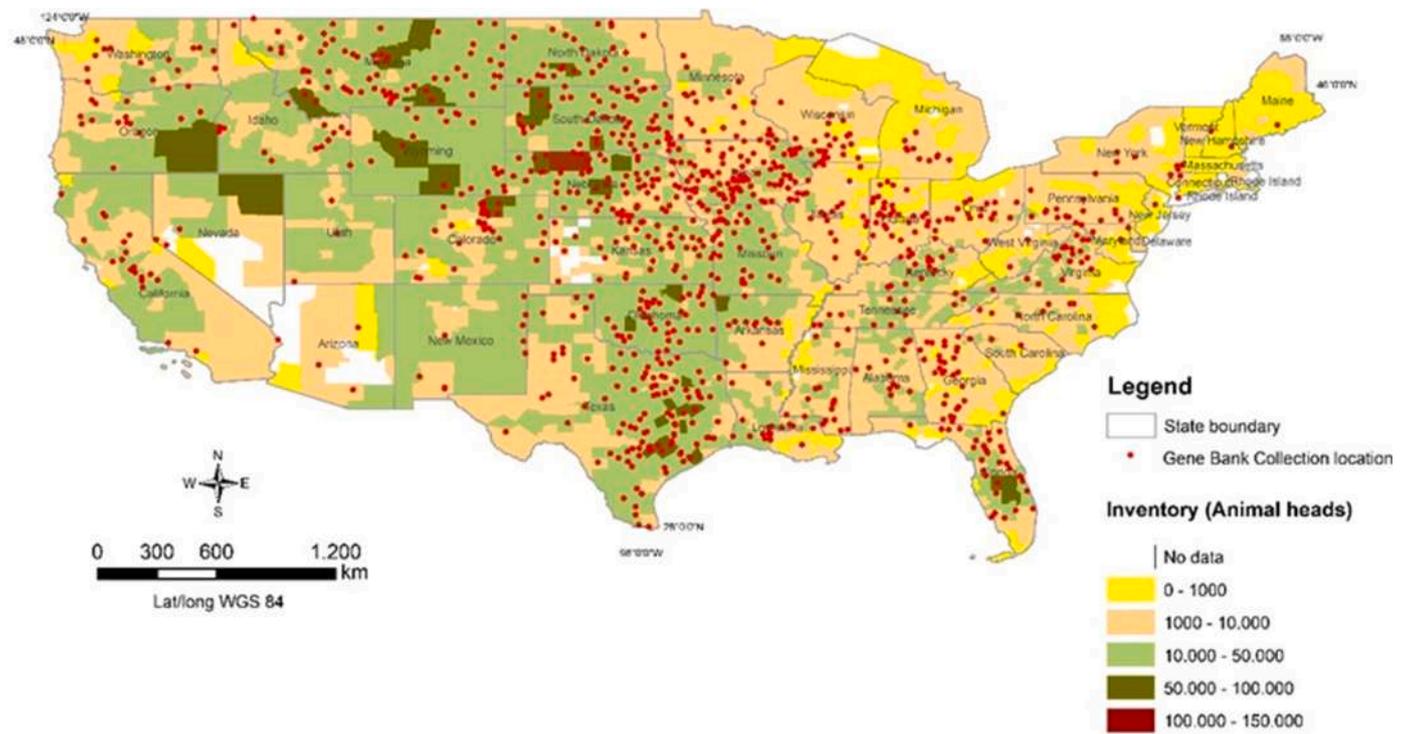


Fig. 3. USDA National genebank Collection for Beef breeds compared to NASS inventory.

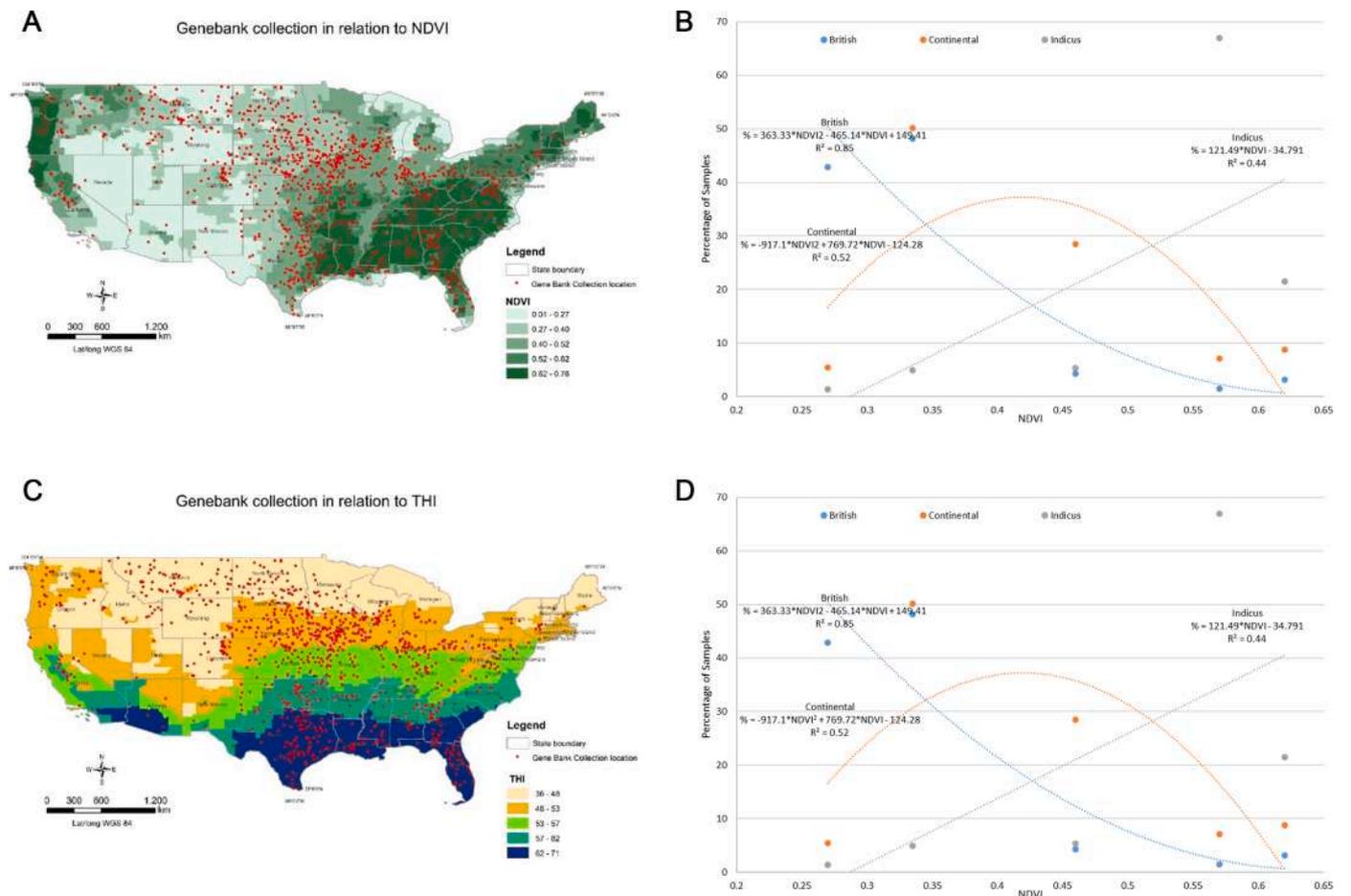


Fig. 4. Localization for USA genebank collection (A) and percentage of samples (B) relative to Normalised Difference Vegetation Index - NDVI and Temperature and Humidity Index - THI (C) and (D), respectively.

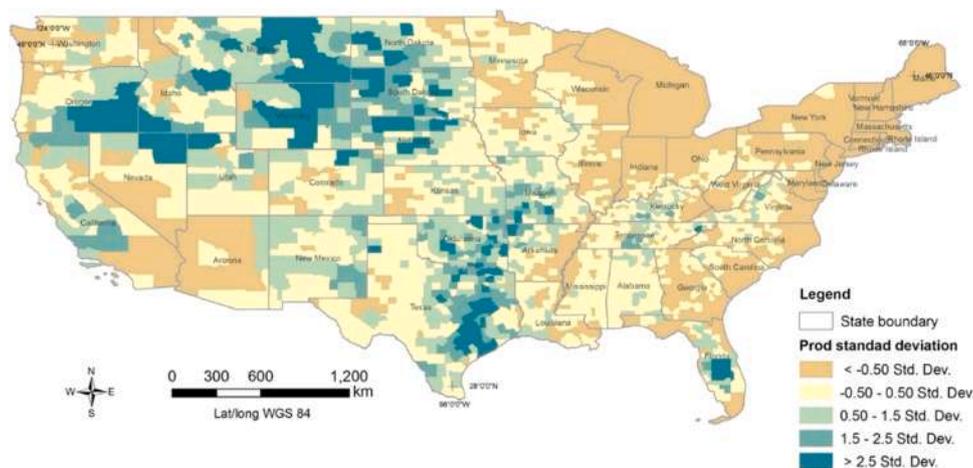


Fig. 5. Changes in beef cattle population density by US county.

while BTCE and BAA tend to be more concentrated among the Great Plains/Mid-West, with some samples being derived from the southwest and Gulf Coast areas. In the western part of the US, most *Bos taurus* animals sampled came from ranches with headquarters close to major rivers, suggesting the importance of having access to water in the country's drier regions. However, for BI this situation did not hold due to the relatively higher water and vegetation levels, as measured by NDVI, in the Gulf Coast region. Fig. 3 also indicates that gene bank sampling has predominantly occurred in the country's central portions and extending from the Canadian border to the Gulf of Mexico. Sampling also mirrors the county and states with higher concentrations of cattle, and may also indicate that producers breeding cattle for commercial customers are located in the same geographic region as their clientele. Rotz et al. (2019) state a major difference across the regions as stocking rates decrease or grazing area allotted per animal increase when moving from east to west. Figs. 3 and 4 suggest this to be the case with higher precipitation in the eastern and Midwestern regions, which enabled greater forage and feed production (NDVI) per unit of land (Fig. 4a) as well as lower THI (Fig. 4c).

Geographic areas with lower NDVI, like the southwest (New Mexico, Arizona, Nevada), are typically areas with limited numbers of breeding cattle being produced. Instead, these are areas where commercial production occurs, and producers typically purchase their bulls from other producers in the area. Also, there is a much lower use of artificial insemination among beef cattle in the south and south western regions, making sampling for the repository more problematic. Albeit more difficult, these types of areas represent targets for future collection activities.

Increases in cattle numbers tended to occur in areas with low human population density (<https://www.geogebra.org/m/jUrXhbeX>). Conversely, states with decreased cattle numbers are also associated with smaller herds and land areas, perhaps suggesting lower profitability. Understanding these changes is important (McManus et al., 2016). They can affect the adaptation of the genotypes used, socioeconomic factors and the need for new infrastructure or substitution of rural activities.

Needs for future sampling were also studied. Fig. 6a and b suggests that future sampling should be in the areas that are not coloured, it is doubtful that there are significant BI numbers raised in northern non-coloured areas. However, under a climate change scenario, the various climatic measures typically found in the Gulf Coast region will likely expand to the north. In anticipation of such a change, increased sampling from animals in the northern portions of the shaded area of Fig. 6b may be beneficial. Fig. 6b also suggests increased sampling of BI should occur along the Gulf Coast plain where THI will be the most extreme. Fig. 6a suggests collections for either BAA or BTCE should be made from

outside the coloured areas or along the fringes of those areas. Again, under a climate change scenario, further BAA and BTCE collections should focus upon sampling animals raised in the most temperature extreme parts of the Gulf Coast region and the semi-arid southwest (West Texas, New Mexico, and southern California). Sampling in the western USA should be a priority. However, as Fig. 3 indicates, the overall number of cattle in those states is lower than the mid-west. Looking to the southeast, there are areas in North and South Carolina and Georgia conducive to BTCE breeds, and collections should target those areas.

Results in Table 1 also indicate the concentration of sampling to date on BAA breeds, mainly Hereford and Angus. Under predicted climate change (Brown-Brandl, 2018) the importance and distribution of breeds may change, with substitution for those seen to be better adapted to increased temperatures and poorer quality feed. Information on available genetic resources and their production environment can therefore aid in the farmer's decision making process (Boettcher et al., 2014).

Bos indicus are seen in regions with higher precipitation and THI, while European breeds are found at higher altitudes, such as those seen in the intermountain west. *Bos indicus* samples were also derived from areas with lower NDVI and humidity but higher temperatures. That said, BI from the more arid southwest have been sampled, similar to Brazil's climatic region, where BI is more prevalent (McManus et al., 2016). While differences among BI and BTCE and BAA are distinct, there does appear to be an overlap of these genotypes among climatic parameters, suggesting genetic plasticity among the cattle types. As a result, further evaluation within and among counties with different environmental conditions are warranted.

3.1. Next steps

The variability of breed types and environments cattle are raised pose a unique challenge for gene banks. An early premise for gene bank sampling was to capture a broad sampling of breed genetics without attention to environmental differences (FAO 1998; 2008, FAO 2012) despite the demonstrated genotype by environmental interactions (Delgado-Liberona et al., 2020) and differences in allelic frequencies within a breed when raised in distinct environments (Blackburn et al., 2017a).

GIS technology for gene bank development has not been previously used. In this study, we were able to document where collections have occurred and the animals' production environment. A basic framework for collection mapping has been established, and the utilization of this tool for gene banking can be increased. Our next steps will include merging genotypes of various traits or breeds with environmental descriptors e.g., THI. Taking this approach will be useful in identifying

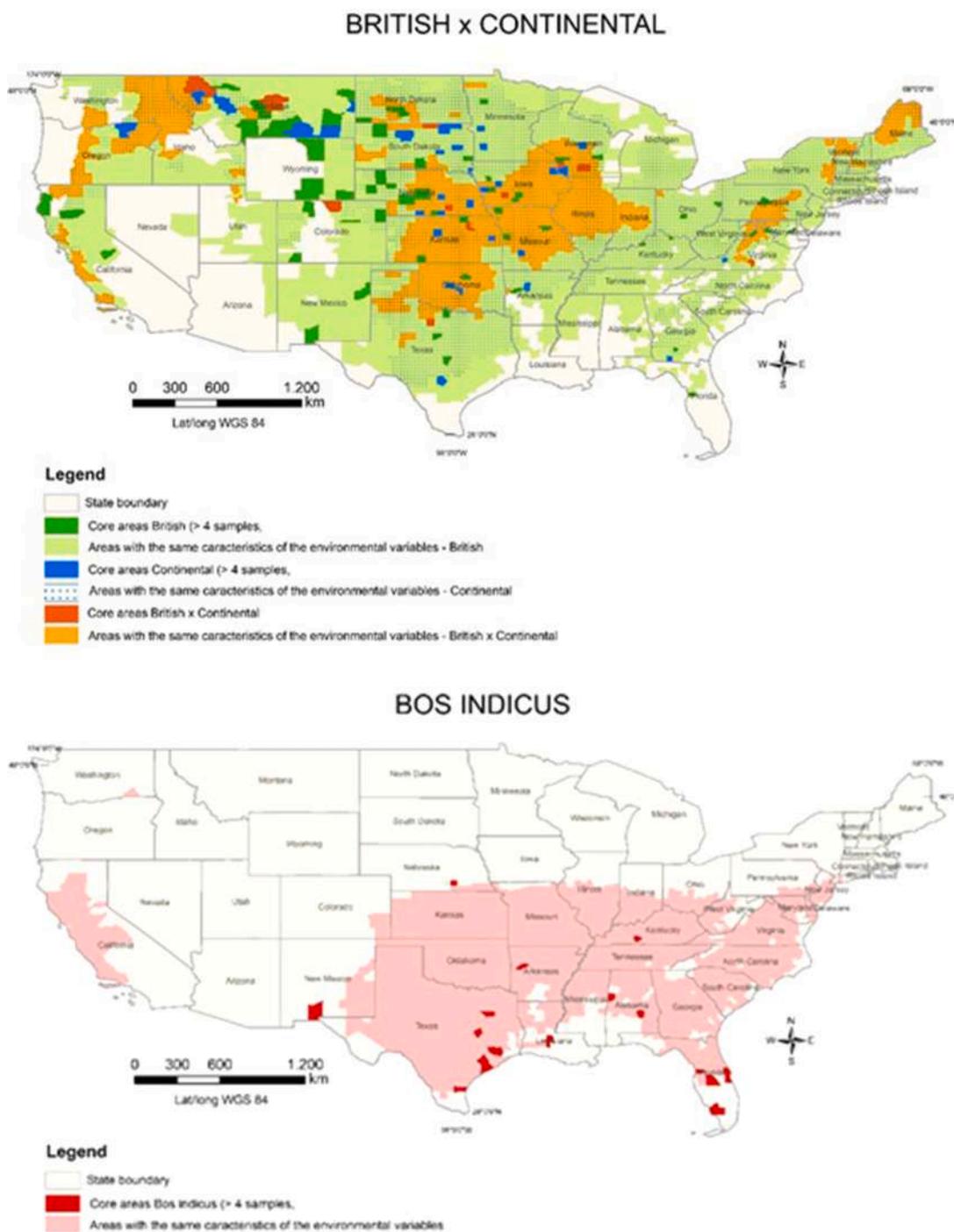


Fig. 6. Sampled and future sampling areas based upon similarities of counties for Temperature and Humidity Index - THI for (A) *Bos taurus* and (B) *Bos taurus indicus*.

gaps in the collection and may be useful in establishing which genotypes are of greater utility for a specific environment.

4. Conclusion

Based upon the environments where beef cattle are produced in the USA, the collection to date has broadly sampled those areas, particularly for BTCE and BAA. Additional sampling of BAA and BTCE is needed in the Gulf Coast region and semi-arid southwest. BI sampling should increase in the more northern states of Tennessee, Kentucky, and Arkansas to capture allele frequencies that may better enable those breeds to perform outside the Deep South and adjust to climate variability. In

addition, further sampling BI along the most southern portions of the Gulf Coast is needed. Further exploration of collections and in-situ populations across environmental situations at the molecular level will further refine the gene bank sampling process.

CRedit authorship contribution statement

Concepta McManus: Conceptualization, Methodology, Formal analysis, Investigation, Writing – original draft, Writing – review & editing, Visualization, Supervision. **Potira Meirelles Hermuche:** Methodology, Software, Formal analysis, Visualization. **Samuel Rezende Paiva:** Investigation, Writing – original draft. **Renato Fontes**

Guimarães: Methodology, Software, Visualization. **Osmar A. Carvalho Junior:** Methodology, Software, Visualization. **Harvey D. Blackburn:** Conceptualization, Methodology, Validation, Investigation, Resources, Data curation, Writing – original draft, Writing – review & editing, Supervision.

Declaration of Competing Interest

None.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:[10.1016/j.livsci.2021.104766](https://doi.org/10.1016/j.livsci.2021.104766).

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