Genetic trends of Mexican zebu cattle populations

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ABSTRACT
In Mexico, the genetic evaluations in Zebu breeds began in 2011 and there are no studies about the genetic progress achieved. Thus, this research aimed to quantify and analyze the genetic progress for growth traits in the Mexican Zebu beef cattle populations Nellore, Sardo Negro, Gyr, Indubrasil, and Guzerat. The genetic trends were obtained through weighted regression (by the number of animals) of estimated breeding values for direct birth weight, direct and maternal weaning weight, yearling weight, and weight at 540 days of age, on the year of birth. Genetic trends were also estimated by the four selection paths, groups of herds, and weighted averages of the sires’ breeding values. The results showed genetic gain as expected of genetic improvement. Nellore presented the highest positive gains for all the traits, and Gyr had the smallest gains among the breeds. Guzerat showed contrary trends for weights until weaning, and had more favorable trends for weights after weaning than the other breeds. The genetic gains obtained for the growth traits reflected the strong influence of the selection made via the maternal paths. The results between weighted and unweighted average breeding values indicate no effective strategy for disseminating genetic material with high breeding values. The genetic gains obtained in the whole populations were due to the main groups of herds. Thus, to achieve further genetic progress, it is necessary to design a cooperative breeding program with a strategy for disseminating that genetic material.

KEYWORDS
Genetic evaluation; genetic parameters; breeding values; beef cattle; tropical livestock; Bos indicus

Introduction

Beef cattle in Mexico are raised in production systems under diverse socioeconomic and agroecological conditions. About 25% of the Mexican territory has dry and humid tropical weather (INEGI 2021). In these regions, the main livestock activity is cattle production, which is carried out mainly in extensive and dual-purpose systems, using adapted genotypes based mainly on zebu breeds (Bos indicus) crossbreeding with Bos taurus breeds (Rojo-Rubio et al. 2009). The widespread use of Zebu breeds in Mexico is due to their tolerance to hot and humid weather, rusticity, ability to harness poor nutrition of forages, and resistance to a higher burden of internal and external parasites (Chan et al. 2010). The previous attributes allow Zebu cattle better adaptation to the adverse conditions of the tropical environment. The Zebu breeds are also widely used as genetic makeup of synthetic breeds, taking advantage of heterosis by crossbreeding with European breeds.
The Mexican Zebu Breeders Association (MZBA) was established in 1962 by local breeders; from 1996 then (AMCC 1996), through the ‘Ponderal Development Control Program’, this organisation oversees the recording of live weights of cattle at different ages for the Brahman, Nellore (NE), Sardo Negro (SN), Gyr (GY), Indubrasil (IB), and Guzerat (GZ) breeds (AMCC 1996). In Mexico, the genetic evaluations (GE) for growth traits in cattle populations began in 2001 as a tool to identify genetically superior individuals and implement breeding programs. However, for Zebu breeds, it was until 2005 that the MZBA published the first GE for the Brahman breed, and it was until 2011 for the other breeds.

The MZBA have the objective of maximising the genetic gain per unit of time, for the characteristics of economic importance in a genetic improvement program; with the implementation of the GE, significant genetic progress in these populations is expected. An illustration of the effectiveness of breeding programs is the case of the US Holstein population; the milk yield had a twofold increase from 1963 to 2013, and 56% of the improvement was due to genetics, according to the Council on Dairy Cattle Breeding (CDCB 2021). The genetic trend for the trait of interest is estimated to evaluate the genetic progress; the magnitude and direction of the change obtained by genetic selection over time are metrics of the effectiveness of the breeding program. The genetic trends allow the breeders to evaluate the genetic progress, and where appropriate, to redefine breeding goals to maximise genetic change, based on the use of estimated breeding values (Domínguez-Viveros et al. 2003; Malhado et al. 2008).

 Studies on genetic trends in Zebu (and synthetic breeds) populations registered for beef production in Mexico have been carried out in breeds such as Tropicarne (Domínguez-Viveros et al. 2003), Brahman (Parra-Bracamonte et al. 2007) and Brangus (Domínguez-Viveros et al. 2009). These isolated studies showed positive genetic changes for growth traits, though marginal (Domínguez-Viveros et al. 2003; Parra-Bracamonte et al. 2007). There are no recent studies about the genetic progress achieved with the implementation of GE for Zebu breeds in Mexico. Thus, the objective of this research was to quantify and analyse the genetic progress for growth traits in the Mexican Zebu beef cattle populations Nellore, Sardo Negro, Gyr, Indubrasil, and Guzerat.

**Material and methods**

The Mexican Zebu Breeders Association provided genealogical and phenotypic data for the 2018 genetic evaluations from NE, SN, GY, IB, and GZ. The pedigree consisted of 63,127, 39,264, 78,032, 141,398, and 12,340 animals for NE, SN, GY, IB, and GZ, respectively. The traits studied were birth weight (BW, kg), weaning weight (WW, kg) adjusted to 205 days of age, yearling weight (YW, kg), and weight at 540 days of age (W540). Table 1 presents the number of phenotypic records used to estimate (co)variance components, genetic parameters, and breeding values for the four traits in each breed. Genetic parameters and breeding values were estimated using the MTDFREML software (Boldman et al. 1995) and using the following univariate linear models:

\[ y = X\beta + Za + e \]  

\[ y = X\beta + Za + Mm + Wp + e \]

where \( y \) is the vector of phenotypic records for each trait; \( \beta \) is the vector of fixed effects which includes the effects of contemporary group (herd, year, season, and the combination of sex with diet and rearing condition), and the mother’s age at calving as a linear and quadratic covariate; \( a \) is the vector of direct additive genetic effects; \( m \) is the vector of maternal additive genetic effects; \( p \) is the vector of maternal permanent environmental effects; \( e \) is the vector of residual effects; and \( X, Z, M, \) and \( W \) are the incidence matrices that associate the corresponding vectors with \( y \). The model assumptions were: \( E[y] = X\beta, E[a] = 0, E[m] = 0, E[p] = 0, E[e] = 0 \), the structure of variances and covariances remained as:

| Breed  | Trait | n   | Mean ± SD | Min. | Max. | \( h^2_d \) | \( h^2_m \) | \( r_{dm} \) |
|--------|-------|-----|-----------|------|------|-------------|-------------|-------------|
| NE     | BW    | 12,426 | 31.3 ± 2.6 | 20   | 42   | 0.20        | 0.05        | -0.44       |
|        | WW    | 10,543 | 173.7 ± 36.3 | 70.6 | 290.5 | 0.22        | 0.11        | -0.38       |
|        | YW    | 9519   | 261.4 ± 61.4 | 95.8 | 497.1 | 0.28        |             |             |
|        | WS40  | 5646   | 342.7 ± 90.2 | 128.2 | 594.3 | 0.25        |             |             |
| SN     | BW    | 8625   | 32.0 ± 2.6  | 22   | 42   | 0.12        | 0.06        | -0.47       |
|        | WW    | 6004   | 188.0 ± 32.1 | 83.8 | 295.4 | 0.19        | 0.12        | -0.14       |
|        | YW    | 4912   | 286.9 ± 46.6 | 140.6 | 465.1 | 0.20        |             |             |
|        | WS40  | 2885   | 381.1 ± 50.9 | 231.1 | 532.1 | 0.21        |             |             |
| GY     | BW    | 7291   | 27.0 ± 3.3  | 17   | 37   | 0.22        | 0.07        | -0.51       |
|        | WW    | 4981   | 160.5 ± 32.7 | 62.6 | 261.1 | 0.20        | 0.11        | -0.45       |
|        | YW    | 4366   | 246.5 ± 54.2 | 93.8 | 412.3 | 0.25        |             |             |
|        | WS40  | 2984   | 327.1 ± 65.4 | 142.7 | 506.9 | 0.25        |             |             |
| IB     | BW    | 5749   | 32.5 ± 2.9  | 22   | 42   | 0.14        | 0.08        | -0.74       |
|        | WW    | 4749   | 177.4 ± 36.6 | 72.4 | 285.2 | 0.21        | 0.12        | -0.70       |
|        | YW    | 4455   | 269.1 ± 53.4 | 116.1 | 439.8 | 0.18        |             |             |
|        | WS40  | 2529   | 366.1 ± 71.4 | 171.8 | 565.2 | 0.19        |             |             |
| GZ     | BW    | 1924   | 31.9 ± 3.2  | 20   | 43   | 0.17        | 0.11        | -0.61       |
|        | WW    | 1480   | 186.9 ± 34.8 | 87.6 | 299.7 | 0.18        | 0.11        | -0.51       |
|        | YW    | 1108   | 264.1 ± 53.9 | 122.5 | 439.3 | 0.21        |             |             |
|        | WS40  | 683    | 321.4 ± 74.9 | 152.4 | 574.9 | 0.20        |             |             |

aNE (Nellore), SN (Sardo Negro), GY (Gyr), IB (Indubrasil), and GZ (Guzerat).

bBW (birth weight), WW (weaning weight), YW (yearling weight), and W540 (weight at 540 days of age).
Table 2. Descriptive statistics for estimated breeding values (EBV) and years (between parenthesis) of data included by breed*.

| Breed* | n | Mean ± SD | n | Mean ± SD |
|--------|---|-----------|---|-----------|
| BWd    | 6882 | 0.1 ± 0.3 | 13,864 | 0.1 ± 0.4 |
| WWd    | 6875 | 1.9 ± 4.7 | 13,833 | 1.4 ± 4.9 |
| WWm    | 6881 | –1.9 ± 3.2 | 13,831 | 0.6 ± 2.2 |
| YW     | 6879 | 0.6 ± 7.8 | 13,807 | 2.0 ± 8.7 |
| WS40   | 6874 | 0.3 ± 9.4 | 13,801 | 1.5 ± 10.4 |
| GZ (1999–2018) | 9585 | 0.8 ± 10.6 | 11,763 | 3.2 ± 7.4 |

*NE (Nellore), SN (Sardo Negro), GY (Gyr), IB (Indubrasil), and GZ (Guzerat).

Table 3. Genetic trends for growth traits in Zebu breeds of Mexico.

| Breed* | b ± SE* | %c | Breed* | b ± SE* |
|--------|---------|---|--------|---------|
| BWd    | 0.003 ± 0.0007*** | 0.01 | IB     | 0.07 ± 0.01*** | 0.04 |
| WWd    | 0.005 ± 0.0006*** | 0.02 | NE     | 0.16 ± 0.007*** | 0.09 |
| WWm    | 0.003 ± 0.0008ns  | 0.04 | SN     | 0.02 ± 0.005    | 0.01 |
| GZ     | 0.004 ± 0.001***  | 0.01 | GY     | 0.09 ± 0.009*** | 0.04 |
| WS40   | 0.004 ± 0.001***  | 0.01 | GZ     | 0.03 ± 0.019*** | 0.11 |

*NE (Nellore), SN (Sardo Negro), GY (Gyr), IB (Indubrasil), and GZ (Guzerat).

Results

The genetic trends for growth traits in Zebu breeds in Mexico are presented in Table 3 and Figure 1. For the direct breeding value of BW (BWd), IB and NE registered the greatest positive changes; on the other hand, SN and GY had small and null changes, respectively. The GZ presented negative changes of great magnitude. For the direct breeding value of WW (WWd), all the breeds but GZ had positive genetic trends (NE with great magnitude); GZ presented a negative and of great magnitude genetic trend. For the maternal breeding value of WW (WWm), the breeds showed an inverse performance to WWd.
except for GY, although with a low magnitude. For YW and W540, all breeds showed positive genetic trends. Although the genetic progress was larger from 2000 to 2015, it was marginal or even negative outside this time range. In relation to contrasting breeds, NE presented the highest positive gains for all the traits; GY had the smallest gains; GZ showed more negative trends for BWd and WWd, and more favourable for WY and W450.

The genetic trends estimated by selection paths are presented in Table 4. The biggest changes achieved for BWd in NE and GZ were due to the participation of the maternal selection routes (in GZ, the DC path). On the other hand, the null change in GY was due to the positive trends of the maternal and negative paternal routes (although not significant). The genetic trends in WWd for IB, NE, and GY were driven mainly due to maternal selection paths; GZ obtained its negative trend through the DB route. For YW and W540, the increases were mainly due to the maternal paths in IB, NE, SN, and GZ (p > 0.05). For GY, the positive trend was also obtained by maternal paths, despite

Figure 1. Genetic trends for growth traits for Nellore (NE), Sardo Negro (SN), Gyr (GY), Indubrasil (IB), and Guzerat (GZ) beef cattle of Mexico.
the significant negative trends in paternal routes. The genetic gains obtained for the growth traits reflected the strong influence of the selection made via the maternal paths, i.e., the cows play a significant role in the genetic progress of these populations.

The genetic trends of sires with weighted (by the number of daughters) and unweighted averages did not show clear patterns in the differences between both averages and in the frequency of use of the sires (Figure 2). Given their high variability, there are no apparent differences between the averages. The genetic trends by groups of herds are presented in Table 5. The genetic progress obtained in these breeds was due to the main groups of herds in IB, NE, and GY. The more important group in IB presented positive trends in WWd and YW; it was confirmed of a few herds with the most animals registered annually throughout the study time, and the remaining groups had non-significant and even negative trends (Table 5). For NE, positive gains in WWd and YW were obtained in the two main herd groups; the first group recorded animals over all the years of study, and the second only until 2008. For GY, positive and of low magnitude genetic trends were found in the main group of herds (with the highest number of registered animals during the whole study time) for WWd and YW; in the remaining groups, the trends were not significant.

Genetic gain with low magnitude for WWd and non-significant for YW was found in the most influential groups presented positive gains of higher magnitude (Table 5), which supported the overall genetic gains obtained for this breed. For GZ, the largest group of herds (with records from 2011 to 2018)
showed a null genetic trend for WWd, but positive and great magnitude for YW. Like the general trends, groups 2 (across all years) and 3 (until 2010) reported negative trends for WWd and positive for YW and WWm. The results showed that the general genetic gains obtained in the whole populations were due to the genetic gain attained for the groups of herds of greater importance (although not from most herds), although there were differences between herds of populations.
Discussion

The genetic trends in Mexican Zebu beef cattle populations for BW were of low magnitude, within the range reported for other populations in Mexico such as Brangus (~0.01 kg year^{-1}; Domínguez-Viveros et al. 2009), Brahman (0.0 kg year^{-1}; Parra-Bracamonte et al. 2007), and Tropicarne (0.004 kg year^{-1}; Domínguez-Viveros et al. 2003). Also, the genetic progress was similar to that published for NE (Da Silveira et al. 2019) and GZ (0.01 kg year^{-1}; Abreu et al. 2018) populations in Brazil; and for Boran beef cattle (0.0 kg year^{-1}; Abin et al. 2016) in South Africa. However, trends of much greater magnitude were estimated for the US Brangus population (0.023 kg year^{-1}; IBBA 2020) and NE in Brazil (0.073 kg year^{-1}; Chud et al. 2014). The genetic changes for BW observed in the Mexican Zebu beef cattle population are desirable. It is essential to avoid an increase of great magnitude in the BW of calves that can lead to difficulties at calving, a task that sometimes is challenging because of the positive genetic correlation between BW and WW. As WW is always under selection to increase, the challenge is to increase WW without a correlated response in BW, and selection indexes must account for the genetic correlation between these two traits to accomplish this objective.

All the breeds had low genetic trends for WW (from ~0.09 to 0.16 kg year^{-1}). These estimates were within the range of values reported for other beef cattle populations in Mexico such as Tropicarne (0.077 kg year^{-1}; Domínguez-Viveros et al. 2003); in Brazil for NE (0.05 and 0.08 kg year^{-1}; Malhado et al. 2008, 2010), GZ (0.077 kg year^{-1}; Abreu et al. 2018), GY (0.0 kg year^{-1}; Malhado et al. 2010), Tabapuá (~0.01 kg year^{-1}; Bernardes et al. 2015), and in South Africa for Boran (0.0 kg year^{-1}; Abin et al. 2016). Higher genetic gains were reported in the beef cattle Mexican populations Brangus (0.33 kg year^{-1}; Domínguez-Viveros et al. 2009) and Brahman (0.19 kg year^{-1}; Parra-Bracamonte et al. 2007), in US Brangus (0.33 kg year^{-1}; IBBA 2020), and Brazilian NE (Zuin et al. 2012; Da Silveira et al. 2019; De Oliveira et al. 2021) and Tabapuá (0.44 kg year^{-1}; Campos et al. 2016). It is worth highlighting the remarkable gains achieved in GZ (0.50 kg year^{-1}; Tramonte et al. 2019) and NE (0.85 kg year^{-1}; Chud et al. 2014) in Brazil.

Stronger negative trends for WWm than those found in this research study for SN, IB, and NE were reported in Mexican Brangus (~0.21 kg year^{-1}; Domínguez-Viveros et al. 2009) and Brazilian Tabapuá (~0.26 kg year^{-1}; Campos et al. 2016). Low or null trends, as in GY, were reported in Brazilian NE (0.005 and 0.015 kg year^{-1}; Malhado et al. 2008, 2010), Brazilian GY (0.0 kg year^{-1}; Malhado et al. 2010), and Mexican Brahman (0.0 kg year^{-1}; Parra-Bracamonte et al. 2007). On the contrary, as in GZ, positive trends of greater magnitude were estimated in US Brangus (0.031 kg year^{-1}; IBBA 2020), Brazilian NE (0.035 and 0.04 kg year^{-1}; Zuin et al. 2012; De Oliveira et al. 2021) Brazilian Tabapuá (0.03 kg year^{-1}; Bernardes et al. 2015), and South African Boran (0.282 kg yr^{-1}; Abin et al. 2016).

Genetic trends for W540 were similar to those found in other beef cattle populations; in Mexico for Tropicarne (0.21 kg year^{-1}; Domínguez-Viveros et al. 2003) and from Brazil in NE (0.14 and 0.185 kg year^{-1}; Malhado et al. 2010; Zuin et al. 2012), GZ (0.13 kg year^{-1}; Abreu et al. 2018) and Tabapuá (0.36 kg year^{-1}; Campos et al. 2016). In contrast, much higher genetic gains were reported in US Brangus (0.72 kg year^{-1}; IBBA 2020) and Brazilian GZ (0.79 kg year^{-1}; Tramonte et al. 2019), and NE (0.88 kg year^{-1}; Da Silveira et al. 2019).

The genetic trends for W540 were also within the range of values estimated in other beef cattle populations such as Mexican Tropicarne (0.26 kg year^{-1}; Domínguez-Viveros et al. 2003) and Brazilian NE (0.068 and 0.20 kg year^{-1}; Malhado et al. 2008, 2010) and GZ (0.18 kg year^{-1}; Abin et al. 2018). Although null trends were reported in beef cattle populations of Tabapuá (Campos et al. 2016) and Boran (Abin et al. 2016), greater trends of up to 0.61 kg year^{-1} were also estimated in Mexican Brahman (Parra-Bracamonte et al. 2007). The greater genetic gains achieved in other beef cattle populations for WWd indicate that there is still a possibility to increase genetic progress in the IB, GY, SN, and mainly GZ populations, even without the detriment of the maternal effect (Malhado et al. 2010; Zuin et al. 2012; IBBA 2020; De Oliveira et al. 2021).

In beef cattle populations, genetic trends by selection paths have not been reported, contrary to several dairy cattle populations. In Brazil, for Girolando herds, Canaza-Cayo et al. (2016) found the largest annual genetic changes for DB and SC paths for milk yield; and SB and SC for age at first calving after the implementation of a breeding program. Thus, the influence of maternal selection routes (DB and DC) for growth traits of Mexican Zebu breeds indicates the absence of a cooperative breeding program. The sire paths (SB and SC) are the most efficient way to achieve genetic progress due to a shorter generation interval and the higher selection intensity applied, especially for the SB path.
There were no clear differences (patterns) between weighted and unweighted averages of breeding values. In this regard, in a multibreed commercial population from Colombia, Vergara et al. (2009) obtained weighted averages of sires lower than the averages of cows (as a reference for the population). They inferred that the extensive use of bulls with breeding values for growth traits lower than the population mean negatively impacted on the genetic trends in cows and calves. In Mexico, Larios-Sarabia et al. (2020) found higher weighted averages than unweighted averages during the years of greatest genetic progress, inferring a greater frequency of use of bulls with higher genetic value for milk yield in Jersey and Brown Swiss dairy cattle populations.

In Brazil, Canaza-Cayo et al. (2016) found that comparing the weighted and unweighted selection differentials in DC was small and negative; indicating that the selection was less intense than other paths (due to the low reproductive rate). In the SB and SC pathways, the weighted and unweighted means were similar consistently for the three traits studied. However, the higher proportions (weighted to unweighted selection differentials) found in the second period indicated that, during this time, animals with higher estimated breeding values had more progeny (were used more intensively by farmers) than in the first. In the DB path, the selection differential for 305MY was greater in the second than in the first period, and it was much greater than those obtained by other selection paths indicating stronger selection through this pathway.

The general analysis of genetic trends can give limited insights into the genetic progress of populations (Parra-Bracamonte et al. 2016). Thus, the herd groups analysis helps us disentangle genetic progress within the populations. The groups of herds of greater importance (by the number of registered animals) showed genetic trends similar to the general results for the traits analysed, which indicates the common objective of those breeders (although not of the majority). However, groups of herds with different trends suggested differences in objectives or selection criteria. On this topic, Parra-Bracamonte et al. (2016) reported different genetic trends in BW and YW of four Charolais herds due to differences between breeders’ knowledge of genetic improvement tools, objectives, and selection criteria. For dairy populations in Mexico, Larios-Sarabia et al. (2020) reported large groups of herds with different selection objectives than most herds. Their participation (exclusion in Jersey and inclusion in Brown Swiss) could have contributed to the behaviour of the genetic tendencies of the populations.

Conclusions
Genetic trends for growth traits in Zebu breeds from Mexico indicate that they are in the right direction of genetic improvement. BW and WW genetic gains were of low magnitude, and results achieved in other populations for WWd indicate that there is still an opportunity to obtain greater gains. YW and W540 genetic trends are within the range of gain obtained in other beef cattle populations. Selection applied in the maternal paths was the main driving force of the genetic progress in these Mexican populations; the slight influence of paternal selection routes for growth traits indicates that breeders are not taking advantage of the most efficient way to achieve genetic progress. Moreover, the lack of patterns between weighted and unweighted average breeding values indicates no effective strategy for disseminating genetic material of animals with high breeding values among the herds. Although the genetic gains obtained were due to the main groups of herds, differences between herds of populations suggest differences in objectives and selection criteria. Thus, to achieve further genetic progress, in addition to identifying the animals with the top breeding values, it is necessary to design a strategy for the definition of breeding objectives and disseminating that genetic material using a cooperative breeding program.

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Data availability statement

The analysed database (including all the breeds) is available via communication with the corresponding author.

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