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Article

Impact of the inclusion of foreign information on Mexican genetic evaluation of Holstein sires

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Abstract:

This study aimed to evaluate the impact of including foreign information of Holstein sires on their genetic evaluation for the following traits: milk, fat, and protein production in kilograms. This was achieved by comparing breeding values (BV) and reliabilities (R), grouping of sires by number of daughters, ordering of sires, and the genetic superiority expected per year ($\Delta I_s/ys$), with different scenarios determined by the selection intensity (ip_s) of sires used in the national genetic evaluation (MEX-GE), those incorporated into the international genetic evaluation with daughters in Mexico (I-GE), and the international genetic evaluation with or without daughters in Mexico (MACE-GE). In total, was analyzed the information of 5,825 sires for MP and 3,914 for FP and PP. The foreign information has a positive impact in the MEX-GE as it improves R and the BV of the sires used in Mexico.

It also allowed to observe important differences in the BV and R between evaluations, generating an opportunity to improve the Mexican Holstein population. Therefore, it is recommended continuing participating in the Interbull program and consider using the internationally validated information in the selection process of dairy cattle and their components. These actions can significantly contribute to the increase of the productive genetic progress in Mexico.

Key words: Genetic value, Reliability, Genetic evaluation, Genetic correlation.

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Introduction

Genetic evaluation predicts the genetic merit or breeding value (BV) of an animal considering its genealogical and phenotypic information (milk production and its components, somatic cell count, conformation, among others)(1). The first genetic evaluation of Holstein cattle in Mexico was performed in 1974 by the University of Guelph (Ontario, Canada) at the request of the Asociación Holstein de México (AHM), including only conformation traits. During the following decades, other traits were included, such as milk (MP), fat (FP), and protein production (PP) in kilograms, and the scoring system for identifying highly productive and functional animals in Mexico was modified(1,2,3). Nowadays, the AHM and the Centro Nacional de Investigación Disciplinaria en Fisiología y Mejoramiento Animal (CENID-FyMA), belonging to the Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias (INIFAP), are in charge of performing genetic evaluations every four months for milk production and quality, 27 conformation traits, longevity, somatic cells, and selection indices of the Holstein cattle registered before the AHM. The methodology used to predict these BV was the Best Linear Unbiased Prediction (BLUP), which consists of a mixed model that includes simultaneous equations of fixed and random effects to estimate the variance components based on individual performance and representation of all the genetic relationships between individuals(4). The results obtained from these evaluations identify the best specimens, providing various options to the farmers for the selection process.

As the exchange of genetic material around the world increases, there is a possibility that the same animal has offspring in different countries, and thus, have more than one genetic evaluation. In Mexico, a high percentage of genetic material is imported as frozen semen;

thus, when the imported sires have information in Mexico to predict their BV, they already have a genetic evaluation in their country of origin with more information than in Mexico. To incorporate the information generated globally, Schaeffer(5) proposed a genetic evaluation methodology that integrates the information from Multiple Across Country Evaluation (MACE). To achieve this, regression equations are constructed to predict the BV of the imported sires based on the importing country, adjusting according to the origin of the information(6,7). There are numerous advantages of using the MACE system, among which are: 1) the performance of sires adjusted by the production information of their daughters from various evaluations of the participating countries and 2) the identification of existing specimens in other countries that may be good breeders under the conditions of the importing country(5,7).

This study aimed to evaluate the impact of Holstein sires foreign information on the genetic evaluation of their MP, FP, and PP traits and to predict the genetic improvement rates expected from these evaluations. By incorporating this information, it is expected to improve the precision of the BV, and therefore, the genetic improvement rates of the evaluated traits.

Material and methods

Database

The records for milk production and its components were compiled by the official production control system of the AHM and processed by the CENID-FyMA-INIFAP. To calculate the BV of the Mexican genetic evaluation (MEX-GE), was used the information of 623,207 records of MP corresponding to 355,786 animals from 527 herds and 193,236 records of FP and PP from 103,829 animals from 167 herds. The stables from which the information was obtained are distributed in 17 different Mexican states. The genealogical information corresponded to 403,817 animals, including records from up to five generations for the animals with available production. The records with productive information outside of the biological parameters observed in the production system and breed (MP adjusted to 305 days <3,500 kg or >22,000 kg per lactation, FP and PP <1.5% or >8.0%)(1) were excluded from the study.

Estimation of genetic breeding values and reliabilities

The BV of the MEX-GE was estimated using a repeatability animal model(1,8) and the BLUPF90 software with the SS-BLUPF90 package(9,10). The model used for each of the three production traits(11) was the following:

$$y = X\beta + Z_1u + Z_2p + e$$

where:

$\boldsymbol{y}$ = vector of the productive records adjusted to 305 days and maturity equivalent (milk, fat, or protein, respectively);
$\boldsymbol{\beta}$ = fixed effects vector (herd-year-season, sire-herd interaction, and age at calving);
$\boldsymbol{X}$ = incidence matrix associated with fixed effects;
$\boldsymbol{Z_1}$ = incidence matrix associated with the random effects of u;
$\boldsymbol{u}$ = random vector of additive genetic effects;
$\boldsymbol{Z_2}$ = incidence matrix associated with random effects of permanent environment;
$\boldsymbol{p}$ = vector of permanent environment effects;
$\boldsymbol{e}$ = vector of residual effects.

In addition to estimating the BV of animals, its reliability(8,12) was calculated as:

$$\left[1 - \left(\frac{PEV}{\sigma_E^2}\right)(\lambda)\right]$$

where: σ_E^2 = Environmental variance; λ = proportion of the environmental variance (σ_E^2) between the additive genetic variance (σ_A^2), which is equal to $[(1-h^2)/h^2]$; PEV = Prediction error variance, estimated as:

$$PEV = \left(1 - r_{A\hat{A}}^2\right)\sigma_A^2$$

where: $r_{A\hat{A}}^2$ = Correlation coefficient between the predicted and true values of the BV; σ_A^2 = additive variance.

During this process, was estimated the BV and R of 7,489 sires for MP and 5,148 for FP and PP. This information was provided to the International Bull Evaluation Service (Interbull) for its integration into the I-GE system.

International genetic evaluation

The BV and R information obtained from the MEX-GE (7,489 sires for MP and 5,148 for FP and PP) was processed following the guidelines established by the Interbull Data Exchange Area (IDEA) for its validation and incorporation into the international genetic evaluation (I-GE)(7). The information from each participating country is compiled and adjusted by the

Interbull with the MACE procedure based on the number, structure of contemporary groups, and international correlations(13,14). Of the total information provided by Mexico, 5,825 sires for MP and 3,914 for FP and PP had productive information on at least one daughter in more than one country; thus, they could be incorporated into the international production and pedigree base. Along the GE-I process, was performed the international genetic correlation (IGC) test, in which was only included, by participating country, the sires that met the minimum test requirements specified by Interbull(7,15). For this test, Mexico provided information from 553 sires for MP, 183 for FP, and 181 for PP.

Comparison of the breeding values and their reliabilities of the national and international genetic evaluations

Genetic trends were analyzed from the average BV obtained in the MEX-GE and the I-GE per sires birth year. To evaluate if the impact of foreign information on the MEX-GE is related to the number of daughters in Mexico, it was assigned each sire to a group (more than 50, between 10 and 50, and less than 10 daughters) and calculated the mean and standard deviation of the BV and R for each group and genetic evaluation (MEX-GE and I-GE). Additionally, to evaluate the similarity between evaluations, was calculated the Pearson correlation coefficient (ρP) for the BV and R of the three traits (MP, FP, and PP). It was also calculated the expected genetic improvement rate (β) of the use of MEX-GE and I-GE in the selection of sires through linear regression analysis.

Subsequently, sires were ordered in descending order of their BV for MEX-GE and I-GE and classified into different selection scenarios, considering the percentiles (ip_s= the best 10%, 20%, 30%, 40%, and 50%), to compare the means of the BV and R of the three traits (MP, FP, and PP) per group, the common number of sires in both evaluations during the ordering, their monotonous association using the Spearman correlation (ρS), and the calculation of the expected genetic superiority of sires per year ($\Delta I_s/ys$) using the method described by Bourdon(16) as:

$$\Delta I_s/ys = ip_s r_s \sigma_A / L_s$$

where, ip_s= selection intensity defined by the percentage of genotypically superior sires (10%, 20%, 30%, 40%, and 50%), r_s= precision of the BV of sires, σ_A=additive genetic deviation of sires, and L_s=generation interval of six years for sires parents of dams(17).

For each of the selection scenarios by percentiles, was calculated the $\Delta I_s/ys$ by considering the different ip_s, but with the results for the MEX-GE, I-GE, and complete international genetic evaluation (MACE-GE); the latter refers to all the participating sires in the international test (150,300 sires) ordered in descending order, that may or may not have daughters in Mexico.

Results and discussion

The BV obtained in the test differ on average 120 kg for MP (from -200 ± 315 kg in MEX-GE to -80.1 ± 411.5 kg for I-GE), 4.6 for FP (from -2.4 ± 8.2 kg in MEX-GE to 2.2 ± 12.5 for I-GE), and 5.8 for PP (-3.6 ± 7.9 kg in MEX-GE to 2.2 ± 12.3 kg for I-GE). On average, the R are higher in the I-GE than in the MEX-GE; they are even two times higher (from 73 to 30 for MP and from 74 to 29 for FP and PP) when considering the information from productive daughters in several of the participating countries.

In both evaluations (MEX-GE and I-GE), was observed a positive trend in the average genetic improvement per birth year; the BV of the I-GE were higher than those of the MEX-GE throughout the study period (Figure 1). It was also observed a decrease in the average R in the last years of study, which coincides with the low number of born sires in recent years (Figure 2). This decrease in R could be explained by the lower number of daughters of young sires evaluated(18,19). A previous study suggests that the decrease in the average of BV could be because initially, the evaluation only includes few offspring; once the best specimens are selected, these are frequently used to increase the average of the genetic trends within the population and the number of daughters per sire(20), which can increase the similarities of the calculated BV between the two evaluations. This is corroborated by observing the differences between the groups created based on the number of daughters they provide to the study (Table 1), where, by increasing this number, the average of BV an R in the MEX-GE and the I-GE approximate to each other, and thus, the ρP between both evaluations gradually increase. The β and their standard errors, calculated by regression analysis, show a decrease of approximately half for MP and two-thirds for FP and PP of the MEX-GE with the I-GE (from 23 ± 0.6 kg to 42 ± 0.7 kg for MP, from 0.3 ± 0.02 kg to 0.92 ± 0.03 kg for FP, and from 0.48 ± 0.02 kg to 1.1 ± 0.02 kg for PP), but the behavior of both evaluations is similar throughout the years, this may be due to the adjustment in the genetic bases. Another study concludes that the information generated in the international evaluation is a more precise indicator than the results obtained in the daughters evaluated in a single country(21), which was confirmed in this study, where was observed increased R for the I-GE in the three traits.

Figure 1: Trend of the breeding values (BV) per birth year of sires included in the Mexican (MEX) and international (MACE) evaluations for milk (MP), fat (FP), and protein (PP) production in kilograms

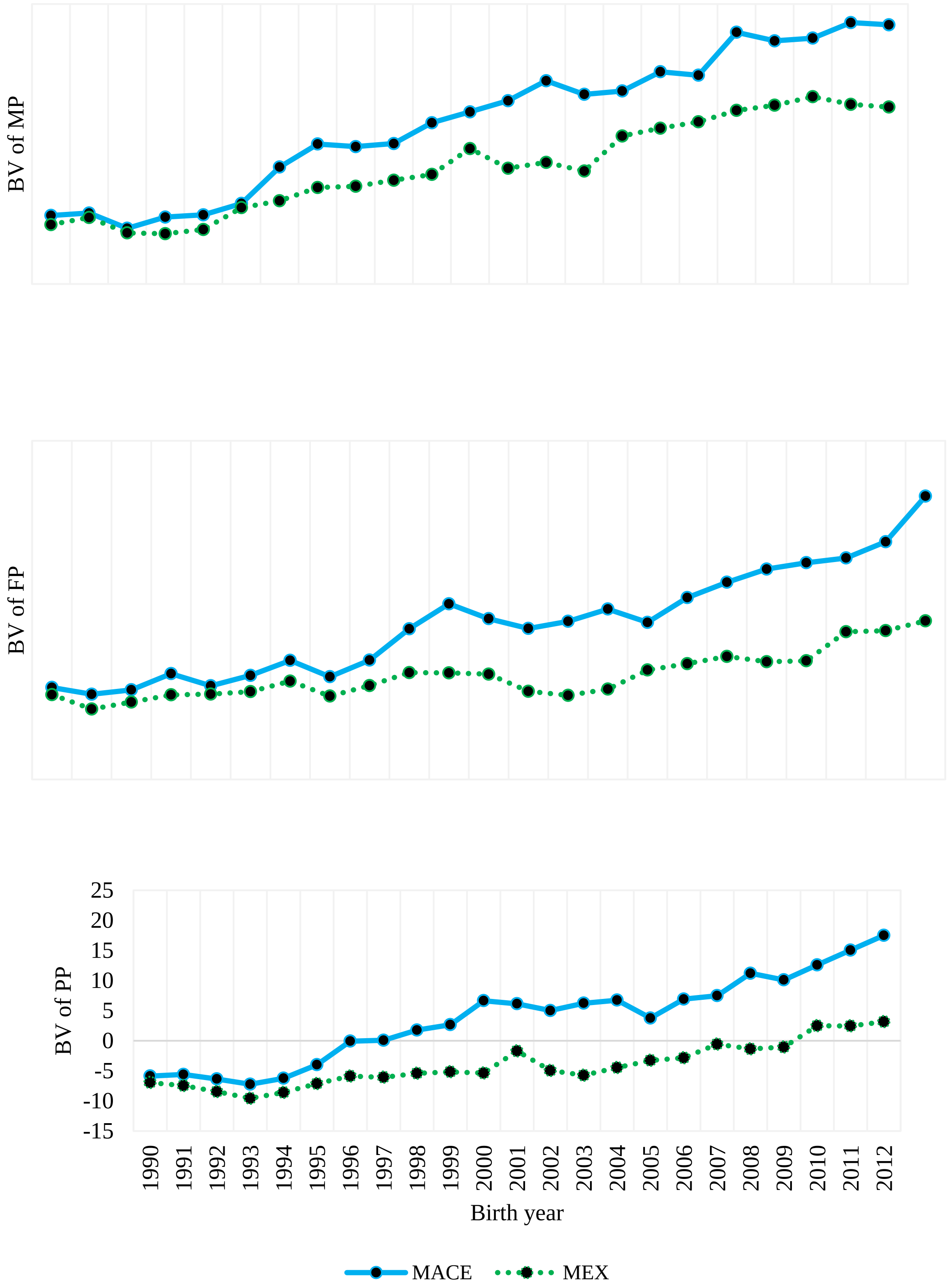

Figure 2: Trend of reliabilities (R) per birth year of sires included in the Mexican (MEX) and international (MACE) evaluations for milk (MP), fat (FP), and protein (PP) production in kilograms

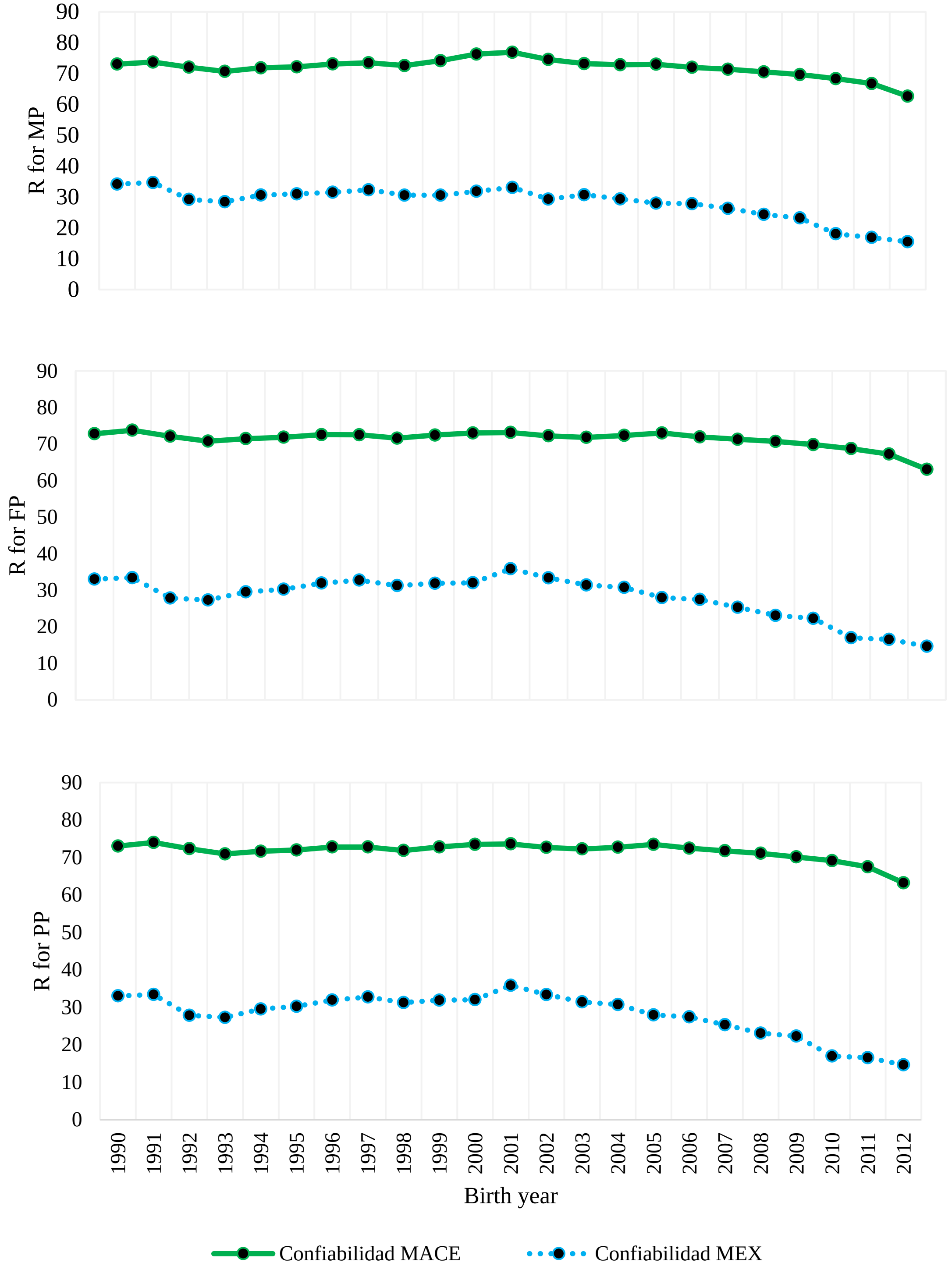

Table 1: Genetic Breeding Values (BV), reliabilities (R), and Pearson correlations (ρP) for sires classified by the number of daughters in Mexico and participating in the Mexican (MEX-GE) and international (I-GE) genetic evaluations for milk (MP), fat (FP), and protein (PP) production in kilograms (*P*<0.05)

		BV MEX-GE	**BV I-GE**	**R MEX-GE**	**R I-GE**	**ρP BV**	**ρP R**
MP	>50	-2±325	88±333	45±18	86±11	0.73	0.48
	>10 and ≤50	-137±302	44±364	31±9	74±6	0.52	0.28
	<10	-261±295	-151±420	26±7	70±5	0.61	0.19
FP	>50	0.7±11.2	4.7±12.5	56±18	84±9	0.66	0.62
	>10 and ≤50	-1.1±9.4	4.1±12.6	35±11	76±5	0.46	0.24
	<10	-3.1±7.2	1.4±12.4	24±8	71±5	0.45	0.19
PP	>50	1.5±9.1	5.9±11.2	56±18	85±8	0.64	0.62
	>10 and ≤50	-1.3±8.2	5.8±11.1	35±11	77±5	0.42	0.22
	<10	-4.7±7.4	0.9±12.4	25±8	71±6	0.53	0.17

During the first reordering analysis of sires, based on their BV (MEX-GE and I-GE), it was observed a reordering in sires, confirmed by the low calculated ρS (0.63 for MP, 0.48 for FP, and 0.55 for PP). This correlation decreases its value by increasing the ip_s, being the 10% group superior for the three traits than the other groups, which results in only 35% of sires in common. Table two shows the results of the other groups.

Table 2. Genetic Breeding values (BV), reliabilities (R), and Spearman correlations (ρS) for sires grouped by different percentiles (ip_s) and arranged in descending order by the Mexican (MEX-GE) and international (I-GE) genetic evaluations, with the percentage of sires in common in both arrangements (%Sc) for milk (MP), fat (FP), and protein (PP) production in kilograms (*P*<0.05)

			Ordered by the MEX-GE					**Ordered by the I-GE**				
	ip_s	**% Sc**	**BV MEX-GE**	**BV I-GE**	**R MEX-GE**	**R I-GE**	**ρS BV**	**BV MEX-GE**	**BV I-GE**	**R MEX-GE**	**R I-GE**	**ρS BV**
MP	10	35	356±148	364±278	37±16	79±11	0.21	149±264	654±177	28±14	73±9	*
	20	53	249±151	312±309	34±15	77±10	0.23	96±271	504±199	29±13	73±9	0.17
	30	64	176±162	252±330	32±14	76±10	0.33	52±276	402±218	29±13	74±9	0.26
	40	70	114±177	194±346	32±14	75±10	0.39	13±279	319±238	30±13	74±9	0.33
	50	74	58±195	137±359	31±13	74±9	0.48	-30±285	248±256	30±13	74±9	0.43
FP	10	26	11.4±5.2	12.6±11.1	35±17	75±8	0.18	4.1±8.4	25.5±5.7	25±14	73±7	0.14
	20	42	8.4±5	10.9±11.5	32±16	74±8	0.19	3.3±8.1	20.4±6.6	26±14	74±7	0.14
	30	53	6.8±5.1	9.8±11.7	31±15	73±7	0.21	2.3±7.9	27.1±13.9	17±7	74±7	0.21
	40	58	4.7±5.3	7.7±11.8	30±14	73±7	0.32	1.4±7.9	27.8±14.1	14±7	74±7	0.26
	50	66	3.4±5.5	6.7±11.8	30±14	73±7	0.33	0.8±7.8	28.4±14.1	12±8	74±7	0.27
PP	10	29	10.1±3.5	12.6±11.1	34±17	76±8	*	3.3±6.9	24.6±5.4	24±13	74±7	*

20	47	7.2±3.8	10.9±11.5	32±16	75±8	0.16	2.4±7.3	19.9±6.1	26±14	74±7	0.13
30	59	5.8±4.1	9.8±11.7	31±16	75±8	0.26	1.9±7.4	16.8±6.7	27±14	74±7	0.16
40	63	3.7±4.7	7.7±11.8	31±15	74±7	0.37	0.8±7.6	14.3±7.3	28±14	74±7	0.28
50	68	2.5±5.1	6.7±11.8	30±15	74±7	0.44	0.2±7.6	12.1±7.9	28±14	75±7	0.32

*=(P>0.05).

In the analysis of ΔI_s, when using the highest ip_s (which includes the highest percentile), was observed a more significant increase for the three evaluations (MEX-GE, I-GE, and MACE-GE) in the three traits, which suggests the use of these sires for the following generations (Table 3). However, it would be necessary to consider various factors within the population (rates of consanguinity, preferential treatment, adaptation to production systems, etc.) to optimize the use of these specimens. Additionally, was observed a higher ΔI_s when using the MACE-GE results due to the greater availability of animals since it represents an opportunity to increase the ΔI_s, increase the genetic variability, and provide a higher amount of selection material to the producers. However, to recommend its use, it is necessary to consider factors such as environment genotype, germplasm availability, and selection for other population interest traits.

Table 3: Expected genetic superiority per year (ΔI_s) of the sires grouped by different selection intensities (ip_s) and arranged in descending order for the Mexican genetic evaluation. Under this arrangement, was considered the estimated breeding value in Mexico (MEX), the international with daughters in Mexico (I), and all the sires that participated in the complete international test and that may or may not have daughters in Mexico (MACE)

	ip_s	ΔI_s-MEX	ΔI_s-I	ΔI_s - MACE
MP	10	18.5	24.1	28.5
	20	14.7	19.2	22.7
	30	11.9	15.6	18.5
	40	10.2	13.3	15.7
	50	8.4	10.9	12.9
FP	10	0.55	0.84	0.90
	20	0.44	0.67	0.72
	30	0.36	0.55	0.58
	40	0.30	0.46	0.50
	50	0.25	0.38	0.41
PP	10	0.54	0.83	1.83
	20	0.43	0.66	1.46
	30	0.35	0.54	1.19
	40	0.30	0.46	1.01
	50	0.25	0.38	0.83

The IGC provides a different way to evaluate the similarity between the MEX-GE and the I-GE countries. The average between the MEX-GE and the 29 participating countries was 0.79 ± 0.04 for MP, 0.80 ± 0.04 for FP, and 0.81 ± 0.04 for PP. The IGC with the countries with which Mexico has a more significant germplasm exchange and that were calculated based on more than 200 sires, such as the United States of America, Canada, the Netherlands, Germany-Austria, Great Britain, Italy, and France, reached medium levels (0.80 approximately). While the highest correlations were observed with Israel, Slovenia, Estonia, Latvia, and Lithuania (reaching IGC of 0.85, 0.86, and 0.87 for MP, FP, and PP, respectively), which could be explained by the low number of sires in common (<50 sires) and their high preference, confirmed by the significant number of daughters (>20 daughters). The lowest IGC were observed in countries with production systems different to those in Mexico, such as: New Zealand, Australia, and Ireland with values of 0.69 for MP and 0.7 for FP and PP). The observed differences between the IGC in the different countries could be because of the sire adaptation to a specific country and not to the differences in the models or preferential treatment of sires(21). Therefore, if this statement is correct, the estimation of the BV of the sires used at a national level will be closer to those obtained in countries with similar production conditions than those in Mexico. The latter could explain the results obtained with countries that contribute significantly to the number of daughters in Mexico, such as the United States of America, Canada, and the Netherlands, but that do not have the highest IGC with Mexico. These countries differ from Mexico in their production conditions, the definition of genetic bases, estimated heritability indices (h^2) for each country, and the complexity of the models used to estimate the BV and the effects applied in each model. Therefore, it is advisable to analyze the groups integrated by countries with similar evaluation conditions, thus expanding the expectations of the international market and exchanging information efficiently.

An area of opportunity for the countries that are members of Interbull is the use and exchange of genomic information, which can bring important benefits to the systems of genetic evaluation; for example, perform a more effective and faster prediction of genetic interactions(22), reduced commercialization time of the genetic material, referring to characteristics of reproductive and consanguinity importance(23), which reflects in the increased precision of the BV and their R(24).

Conclusions and implications

Foreign information has a positive effect on the MEX-GE, as it improves the R of the BV of the sires used in Mexico, mainly those with a limited number of daughters in Mexico; therefore, it is recommended to continue participating in the Interbull program. In this study, during the arrangement of sires and the verification of the genetic superiority per year, it was observed significant differences in the BV between the evaluations, generating an opportunity to improve the Mexican Holstein population. The sires not used in Mexico and with a high genetic potential for the evaluated traits represent an opportunity to improve the population. Therefore, it is important to identify, evaluate, and incorporate these sires in the Mexican Holstein population. The results obtained after incorporating the MEX-GE to the I-GE show the differences between the participating countries (explained by their diverse production systems, environmental factors, etc.). Therefore, it is essential to consider the use of the international validated information in the selection process of Mexican dairy Holstein cattle and their components, as it will contribute to the increase of the genetic, productive, and reproductive progress of the population.

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Conflicts of interest

Authors declare no conflicts of interest.

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