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Genotype × environment interaction for fertility and milk yield traits in Canadian, Mexican and US Holstein cattle

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Abstract

The objective of this study was to evaluate genotype × environment interaction (G×E) between Canada, the United States and Mexico for fertility and milk yield traits using genetic correlations between countries estimated from genetic evaluations of sires. Genetic correlation between Mexican and Canadian Holsteins for age at first calving was ≤ 0.48 and lower than the simulated value obtained accounting for data structure and selection effects. For calving interval, genetic correlation between Mexico and Canada ranged from 0.48 to 0.69. Genetic correlation between calving interval in Mexico (multiplied by -1) and daughter pregnancy rate in the United States ranged from 0.64 to 0.73, and was lower than simulated and actual Canada-United States values. Genetic correlations between Mexico and Canada and the United States for milk yield traits were ≥ 0.83 , similar to simulated genetic correlations, but lower than Canada-United States values (≥ 0.93). Heritability estimates for age at first calving, calving interval, milk yield, fat yield, protein yield, fat content, and protein content for the Mexican Holstein population were 0.06, 0.03, 0.18, 0.20, 0.19, 0.46, and 0.49, respectively. G×E interaction effects between Canada and Mexico for age at first calving were high, whereas G×E interaction effects between Canada and Mexico for calving interval and between daughter pregnancy rate in the United States and calving interval in Mexico were moderate. G×E interaction effects for milk yield traits between Canada or the United States with Mexico in registered Holsteins were low.

Additional keywords: genetic correlation; age at first calving; calving interval; daughter pregnancy rate; fat; protein

Abbreviations used: AFC (age at first calving); CI (calving interval); DPR (daughter pregnancy rate); G×E (genotype × environmental interaction); PTA (predicted transmitting ability); SD (standard deviation); US (United States).

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Introduction

Technological developments and worldwide trade of frozen semen in dairy cattle have increased since 1970, making bulls with daughters calving in different production environments more common. At the same time, this has resulted in concerns about the predictive ability of genetic evaluations of sires

obtained in different countries (Hammami *et al.*, 2009).

Genotype × environment interaction (G×E) studies may help in evaluating to what extent the predicted superiority of animals obtained under certain environmental conditions will be expressed in different environments (Mulder *et al.*, 2006). Genetic correlations between countries allow for an evaluation of the importance of

these G×E effects and help design more efficient breeding programs worldwide (Mulder *et al.*, 2006).

In this respect, studies estimating genetic correlations between Canada, the US and Western European countries for milk yield traits have shown little variation in the obtained estimates with an average estimated correlation of 0.92 (Mark, 2004). More recent estimates used by the International Bull Evaluation Service indicate lower genetic correlations for yield traits between grazing systems in New Zealand with other countries (0.75-0.76) compared to those between Canada and the US (0.92-0.94) (Interbull, 2013a).

Genetic correlations between 14 and 17 countries used in international genetic evaluations of female fertility traits for Holsteins varied from 0.51 to 0.96, with an average of 0.80 for conception traits (conception rate, non-return to estrus rate) compared to 0.60 to 0.97, with an average of 0.84 for reproductive interval traits (calving interval, days open) (Interbull, 2013c). Across-country genetic correlations involving days open, calving interval and daughter pregnancy rate are higher than those observed for non-return to estrus rate and conception rate (Jakobsen *et al.*, 2009; Nilforooshan *et al.*, 2010).

Previous studies on G×E in Mexican Holstein cattle involved the estimation of genetic correlations between countries for milk yield only (*e.g.*, Stanton *et al.*, 1991; Montaldo *et al.*, 2009), or genetic correlations between reproductive traits in Mexico with milk yield in the US (Cienfuegos-Rivas *et al.*, 2006). Estimates of genetic correlations between North America and Latin American countries are scarce for most traits. To the best of our knowledge no estimates of genetic correlations between Mexico with Canada or the US for age at first calving (AFC), calving interval (CI), fat and protein yields, and milk content traits are available. Estimates of genetic correlations between countries in dairy cattle for AFC are scarce worldwide (Cerón-Muñoz *et al.*, 2004).

The objective of this study was to estimate genetic correlations for AFC, CI, milk, fat yield, protein yield, fat content and protein content between Mexico and Canada and Mexico and the US in Holstein cattle. An

additional objective was to estimate genetic parameters for the aforementioned traits within the Mexican Holstein population.

Material and methods

Mexican genetic evaluations

Records for milk, fat and protein yields, fat and protein contents, CI, and AFC for Mexican Holstein cattle recorded from 1997 to 2008 were obtained from the Mexican Holstein Association (Querétaro, Mexico). Data for milk, fat, and protein yields were adjusted to 305 days mature equivalent by the Mexican Holstein Association (Montaldo *et al.*, 2010). Data were edited to include only records from cows with known sire, dam, and date of birth. Only records with 100 or more days in milk were included, with a minimum CI of 293 days (biological limit) and a maximum of 790 days (3 standard deviations of the mean). Age at first calving lower than 549 days (biological limit), or higher than 1,271 days (three standard deviations from the mean), were also excluded from the analyses. Contemporary groups were required to provide at least 3 records for milk yield trait analyses. For production and milk composition traits, values beyond 3 standard deviations from the mean were also excluded from the analyses. Additionally, for fat and protein contents, minimum and maximum included values were determined from their distributions and from the usual admissible values allowed for these traits (Montaldo *et al.*, 2010). Admissible values ranged from 1.9 to 5.0% for fat content, and from 2.4 to 3.8% for protein content. Values outside these ranges were considered missing values for both contents, as well as for the fat and protein yields data for the same lactation record. The number of observations per trait included in the analyses after edits is shown in Table 1. The pedigree file included 323,638 animals born between 1950 and 2007, which included 14,482 sires and 158,363 dams. Three calving seasons (or birth seasons for AFC) were defined according to

Table 1. Descriptive statistics for fertility, production and milk composition traits in Holstein cattle in Mexico. SD: standard deviation.

Trait	Records	Mean	SD	Minimum	Maximum
Age at first calving (days)	42,131	771	90	550	1,098
Calving interval (days)	55,477	423	90	294	737
Milk yield (kg)	92,981	10,955	2,901	2,000	19,320
Fat yield (kg)	65,880	380	101	62	764
Protein yield (kg)	65,880	344	83	60	618
Fat content (%)	65,880	3.41	0.49	1.91	4.90
Protein content (%)	65,880	3.09	0.23	2.40	3.80

their effect on the studied traits and to the distribution of the observations as (1) January-April, (2) May-August, and (3) September-December.

In order to estimate genetic parameters, data were analyzed using single-trait repeatability models, which included calving season by parity number, and herd-year-season of calving as fixed effects, and animal, sire by herd, and permanent environment as random effects. In order to analyze AFC, an animal model that included herd-year-birth season as a fixed effect, and the random effects of animal, and sire by herd, was used. Analyses were performed using AI-REML procedure using ASReml software (Gilmour *et al.*, 2009).

The model expressed in matrix notation was as follows:

$$y = Xb + Za + Wp + Ks + e$$

in the case of AFC it was:

$$y = Xb + Za + Ks + e$$

where y is the vector of observations for the trait; b is the vector of fixed effects; a is the vector of animal random effects; p is the vector of the random permanent environmental effects; s is the vector of sire-herd effects; e is the vector of random residual effects; and X , Z , W and K are the incidence matrices assigning observations to fixed, random animal, random permanent environmental, and sire by herd random effects, respectively.

Expectations (E) and covariance matrices (V) of random vectors are described in the following equations:

$$\begin{bmatrix} a \\ p \\ s \\ e \end{bmatrix}, E = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, V = \begin{bmatrix} A\sigma_a^2 & 0 & 0 & 0 \\ 0 & I\sigma_p^2 & 0 & 0 \\ 0 & 0 & I\sigma_s^2 & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

where σ_a^2 , σ_p^2 , σ_s^2 and σ_e^2 are scalars, A is the numerator relationship matrix and I is an identity matrix.

United States genetic evaluations

Genetic evaluations for the US were obtained directly from the USDA AIPL web site (USDA-ARS, 2009). This file contained information from 202,630 sires born from 1950 to 2001, of which 8,991 also had Mexican genetic evaluations; while only between 121 and 462 sires out of this subset (depending on the analyzed trait) had Mexican genetic evaluations with a reliability ≥ 0.5 , and also had genetic evaluations in Canada for yield and milk content traits. Insofar as the US neither generates genetic evaluations for CI nor AFC, the correlation between CI in Mexico and daughter

pregnancy rate (DPR) in the US was calculated. A total of 747 sires with DPR genetic evaluations in the US with a minimum reliability of 0.20 for the Mexican CI genetic evaluations were used.

Canadian genetic evaluations

For AFC and CI, the Canadian genetic evaluations were obtained directly from the Canadian Dairy Network (Guelph, ON, Canada), which included the genetic evaluations of 4,658 sires, of which 747 and 682 also had Mexican genetic evaluations with a reliability ≥ 0.20 for AFC and CI, respectively. The Canadian genetic evaluations for yield and milk composite traits were obtained from the Canadian Dairy Network web site (Canadian Dairy Network, 2009) which contained information from 9,084 sires born from 1969 to 2006, of which 2,575 also had Mexican genetic evaluations.

Genetic correlation estimates

Genetic correlations between countries (r_g) were obtained from the observed correlations between the predicted transmitting ability (PTA) of each bull in two countries divided by the square root of the product of their average reliabilities according to the following formula (Calo *et al.*, 1973):

$$r_g = \frac{r_o}{\sqrt{\text{arel}_i \times \text{arel}_j}} \quad [1]$$

where r_g = estimated genetic correlation, r_o = estimated correlation among PTAs, arel_i = average reliability of PTAs on country i , arel_j = average reliability of PTAs on country j .

Simulation of genetic correlations

In order to account for a possible underestimation of the genetic correlation due to selection of the sires from the country of origin, estimates of genetic correlations between PTAs in Mexico-Canada and Mexico-US obtained by [1] were compared to genetic correlations obtained from simulated PTAs in two environments assuming no G×E interaction effects and using the same number of sires and PTA reliability from the real populations (see Montaldo & Pelastre-Cruz, 2012, for more details about the simulation procedure). Thus, correlations from simulated data provide an upper limit for the estimated genetic correlation if no genotype × environment interaction effects were present. Simulated PTAs were obtained using a sire model with 10,000 replicates. The PTAs from the top 50 and 90% sires (selection intensity 0.80 and 0.20) in their country of origin for milk yield traits and fat or protein

Table 2. Parameters estimated for the studied traits for Mexican Holstein cattle.

Trait	Heritability	Repeatability	Proportion of sire-herd variance	Phenotypic variance
Age at first calving (days)	0.06 ± 0.009	–	0.051 ± 0.005	5,342 ± 40.05
Calving interval (days)	0.03 ± 0.006	0.12 ± 0.006	0.003 ± 0.002	7,716 ± 48.33
Milk yield (kg)	0.18 ± 0.009	0.35 ± 0.005	0.014 ± 0.002	5,828,000 ± 34,480
Fat yield (kg)	0.20 ± 0.011	0.39 ± 0.005	0.018 ± 0.003	7,373 ± 52.29
Protein yield (kg)	0.19 ± 0.011	0.38 ± 0.005	0.017 ± 0.003	4,952 ± 34.81
Fat content (%)	0.46 ± 0.013	0.61 ± 0.004	0.024 ± 0.003	0.199 ± 0.0023
Protein content (%)	0.49 ± 0.012	0.59 ± 0.004	0.007 ± 0.002	0.046 ± 0.0004

contents and reproductive traits (Powell *et al.*, 2003), respectively, were sampled to obtain the simulated data. Heritabilities used for simulation for Mexican Holsteins are shown in Table 2. The number of sampled sires and corresponding reliabilities are shown in Tables 3 to 5 for each trait. Heritabilities for yield traits and DPR for USA were obtained from published estimates (VanRaden *et al.*, 2004). Heritabilities for Canada were assumed as 0.43 for milk yield, 0.34 for fat yield, 0.40 for protein yield (Interbull, 2013b), 0.088 for AFC, and 0.099 for CI (Jamrozik *et al.*, 2005). Heritabilities for fat and protein contents were assumed as 0.56 both for Canada and US (Castillo-Juárez *et al.*, 2000).

Results

Descriptive statistics for the Mexican population for the studied traits are shown in Table 1. Genetic parameters estimated for the studied traits for Mexican Holstein cattle are shown in Table 2. Heritabilities for production traits were in the range of 0.18 ± 0.01 to 0.20 ± 0.01. Estimates for fat and protein content were 0.46 ± 0.01 and 0.49 ± 0.01, respectively, and those for AFC and CI were 0.06 ± 0.01 and 0.03 ± 0.01, respectively. Estimated and genetic correlations from simulated data between Mexico and Canada for AFC, using different minimum reliability levels of Mexican PTA, are shown in Table 3. The minimum reliability for Mexican PTAs considered varied from 0.20 to 0.50 which included different numbers of sires (from 61 to 747). Genetic

correlations varied from 0.33 ± 0.13 to 0.48 ± 0.16. Genetic correlations were lower than those calculated using a similar simulated data structure, which suggests the presence of G×E effects. All 1-tailed z-tests to compare if genetic correlations from actual data were smaller than the genetic correlations from simulated data for AFC were significant ($p < 0.01$).

Genetic correlations between Mexican CI and US DPR (Table 4) which are shown multiplied by -1 to facilitate interpretation, varied from 0.64 ± 0.07 to 0.73 ± 0.16. Genetic correlations for CI between Mexico and Canada (Table 4) varied between 0.48 ± 0.07 and 0.69 ± 0.13. Estimated and genetic correlations from simulated data between Canada and the US were very close to 1, irrespective of the difference in trait definition between these countries (Table 4). These results suggest the presence of moderate G×E effects for CI between Mexico-Canada and Mexico-US, but not between Canada-US. All 1-tailed z-tests to compare if genetic correlations from actual data were smaller than the genetic correlations from simulated data for CI were significant ($p < 0.01$).

Genetic correlations between Canada and the US for milk (0.97 ± 0.03), fat (0.95 ± 0.03), and protein (0.96 ± 0.03) yields (Table 5) were near unity, and were not statistically different from those obtained between Mexico and Canada (0.85 ± 0.06, 0.84 ± 0.06, and 0.92 ± 0.06) nor to those obtained between Mexico and US (0.86 ± 0.03, 0.85 ± 0.06, and 0.90 ± 0.06) for PTAs with reliabilities ≥ 75%. Correlations from simulated data for yield traits with a minimum reliability of 75%

Table 3. Genetic correlations estimated and from simulated data between Mexico and Canada for age at first calving, according to different minimum reliability levels of Mexican predicted transmitting abilities (PTAs).

Minimum reliability of Mexican PTAs (%)	Sires (n)	Average reliability		Genetic correlation	
		Canada	Mexico	Estimated	Simulated
50	61	0.95	0.62	0.48 ± 0.16	0.89 ± 0.09
40	117	0.93	0.54	0.33 ± 0.13	0.87 ± 0.08
30	224	0.91	0.44	0.40 ± 0.10	0.85 ± 0.07
20	747	0.82	0.30	0.45 ± 0.07	0.79 ± 0.06

Table 4. Genetic correlations estimated and from simulated data for calving interval in Mexico (MEX) and Canada (CAN) and daughter pregnancy rate in the United States (US), based on different minimum reliability levels of Mexican predicted transmitting abilities (PTAs).

Minimum reliability of Mexican PTAs (%)	Sires (n)	Average reliability		Genetic correlations						
		CAN	US	MEX	Estimated			Simulated		
					MEX-CAN	MEX-US	CAN-US	MEX-CAN	MEX-US	CAN-US
50	46	0.97	0.98	0.64	0.68 ± 0.16	0.73 ± 0.16	0.94 ± 0.06	0.83 ± 0.11	0.92 ± 0.10	1.00 ± 0.007
40	92	0.96	0.97	0.54	0.69 ± 0.13	0.71 ± 0.13	0.93 ± 0.05	0.77 ± 0.10	0.91 ± 0.08	1.00 ± 0.007
30	177	0.94	0.95	0.44	0.61 ± 0.11	0.66 ± 0.11	0.95 ± 0.04	0.70 ± 0.10	0.89 ± 0.08	1.00 ± 0.007
20	682	0.87	0.81	0.29	0.48 ± 0.07	0.64 ± 0.07	1.06 ± 0.02	0.57 ± 0.07	0.83 ± 0.07	1.02 ± 0.012

in Mexico and assuming a selection intensity of 0.80 for these traits, were notably similar to the estimated values. Correlations from simulated data using a minimum reliability of 50% and similar selection intensity were lower than the estimated correlations, probably because the selection intensity assumed in simulations was too high in this case. Overall, these results suggest that there are no, or very small G×E effects for these traits between the countries studied.

For fat and protein contents (Table 5) genetic correlations between Mexico-Canada (0.87 ± 0.04 to 0.89 ± 0.04) and Mexico-US (0.89 ± 0.04 to 0.91 ± 0.04) were moderately lower than those between Canada-US (0.99 ± 0.01) and to their corresponding simulated values, using a selection intensity of 0.20 (0.95 ± 0.02 to 0.97 ± 0.01). These results suggest small G×E effects for these traits between Mexico-Canada and Mexico-US. All 1-tailed z-tests to compare if genetic correlations from actual data were smaller than the genetic correlations from simulated data for fat and protein contents were significant ($p < 0.01$).

Discussion

Mean values and variability

Average AFC for Mexican heifers was 771 days (SD = 90), similar to the 778 days (SD = 89) found in US Holsteins (Cole & Null, 2010). Average CI for Mexican Holsteins was 424 days (SD = 90), which is only slightly higher than the value of 404 days (SD = 66) for US Holsteins for the period 1980-2004, but with a positive time trend (Hare *et al.*, 2006). Average AFC for Canadian Holsteins born in 2008 was 782 days (SD = 64) and average CI for primiparous Canadian Holstein cows born in 2008 was 399 days (SD = 54) (Jamrozik *et al.*, 2005).

Means for milk yield, fat yield, protein yield, and fat content were lower than the corresponding means for

registered US Holsteins for the same period (USDA-ARS, 2009). by 6, 10, 1, and 6%, respectively, while for protein content it was 3% larger. This relatively small difference is consequence of the good management in registered Holstein herds in Mexico. Breeding decisions may also have contributed to the small difference in production level between the Mexican and the Canadian and US populations. Mexican means for milk yield, fat yield, protein yield, and fat content were larger than the corresponding means for registered Canadian Holsteins for the period 2001-2008 by 13, 6, and 11%, respectively, and were 8 and 3% less for fat and protein content, respectively (ICAR, 2013), indicating that small differences exist with respect to Canada as well, albeit slightly larger compared to those for the US.

Heritabilities for the Mexican population

Heritability for AFC (0.06 ± 0.01) was close to the estimate for US (0.03) (Cole & Null, 2010) and Canadian Holsteins (0.09) (Jamrozik *et al.*, 2005). Nevertheless, it was lower than a previous estimate (0.28) for the same Mexican Holstein population (Montaldo *et al.*, 2009). as well as to estimates from the US (0.20 - 0.33) (Ruiz-Sánchez *et al.*, 2007). Differences for published AFC heritabilities may be due to within-herd confounded genetic and environmental effects (Cienfuegos *et al.*, 2006), implying that it is necessary to include the herd by sire interaction effect in the statistical models used to analyze this trait to avoid inflated heritability estimates (Mark, 2004).

Heritability for CI (0.03 ± 0.01) confirmed the low (but above zero) value previously estimated for this population (Montaldo *et al.*, 2009). This estimate is similar to estimates for CI or days open from studies from several countries in the range of 0.02 to 0.04 (Haile-Mariam *et al.*, 2003, 2008; Wall *et al.*, 2003; VanRaden *et al.*, 2004; Jorjani, 2006a), but it was smaller than an estimate from Canada (0.10) (Jamrozik *et al.*, 2005). These differences in heritability values may be related to

Table 5. Genetic correlations estimated and from simulated data for milk, fat and protein yield, and fat and protein contents between Mexico (MEX), Canada (CAN) and the United States (US) for sires evaluated in the three countries according to different minimum reliability of Mexican predicted transmitting abilities (PTAs).

Minimum reliability of Mexican PTAs (%)	Sires (n)	Average reliability			Genetic correlations						
		MEX	CAN	US	Estimated			Simulated			
					MEX-CAN	MEX-US	CAN-US	MEX-CAN	MEX-US	CAN-US	
MY	75	155	0.85	0.98	0.99	0.85 ± 0.06	0.86 ± 0.06	0.97 ± 0.03	0.80 ± 0.04	0.86 ± 0.04	0.98 ± 0.006
	50	362	0.72	0.98	0.98	0.87 ± 0.04	0.91 ± 0.04	0.97 ± 0.02	0.75 ± 0.04	0.79 ± 0.04	0.98 ± 0.004
FY	75	124	0.85	0.98	0.99	0.84 ± 0.06	0.85 ± 0.06	0.95 ± 0.03	0.83 ± 0.05	0.87 ± 0.04	0.98 ± 0.004
	50	322	0.71	0.98	0.98	0.83 ± 0.05	0.88 ± 0.05	0.96 ± 0.02	0.78 ± 0.04	0.80 ± 0.04	0.98 ± 0.007
PY	75	121	0.85	0.98	0.99	0.92 ± 0.06	0.90 ± 0.06	0.96 ± 0.03	0.82 ± 0.04	0.88 ± 0.04	0.92 ± 0.018
	50	319	0.70	0.98	0.98	0.91 ± 0.04	0.95 ± 0.04	0.96 ± 0.02	0.76 ± 0.04	0.80 ± 0.04	0.92 ± 0.011
F%	75	230	0.87	0.99	0.99	0.88 ± 0.04	0.89 ± 0.04	0.99 ± 0.01	0.97 ± 0.01	0.97 ± 0.01	0.99 ± 0.002
	50	444	0.75	0.99	0.99	0.88 ± 0.04	0.89 ± 0.04	0.99 ± 0.01	0.95 ± 0.02	0.95 ± 0.02	0.99 ± 0.001
P%	75	255	0.87	0.99	0.99	0.89 ± 0.04	0.91 ± 0.04	0.99 ± 0.01	0.96 ± 0.01	0.96 ± 0.01	1.00 ± 0.002
	50	462	0.76	0.99	0.99	0.88 ± 0.04	0.90 ± 0.03	0.99 ± 0.01	0.96 ± 0.02	0.96 ± 0.02	1.00 ± 0.001

MY = milk yield; FY = fat yield; PY = protein yield; F% = fat content; P% = protein content

differences in herd reproduction management, climate, and recording of these traits across countries.

Heritability estimates for milk, fat, and protein yields (0.18 ± 0.01 , 0.20 ± 0.01 , and 0.19 ± 0.01 , respectively) (Table 2) were close to the lower boundary of the range of published values for Interbull countries (0.19-0.59) for milk production traits (Mark, 2004). Heritabilities in the current study were similar to estimates using data from Spain (González-Recio *et al.*, 2006). Our heritability estimate for fat yield (0.20 ± 0.01) was similar to that estimated for Australian cows (0.17 to 0.22) (Calus *et al.*, 2005; Haile-Mariam *et al.*, 2008). Management and climatic effects likely modify the way Holstein cows react to these influences.

In a study using three US regions, heritability for fat content was estimated varying from 0.32 to 0.41 (Carabaño *et al.*, 1990), which was slightly lower than that observed in our study (0.46). Our estimate is within the range (0.40 to 0.52) estimated for Australian dairy cattle and different herd production levels (Calus *et al.*, 2005). In Canadian Holsteins, heritability for fat and protein contents ranged from 0.53 to 0.59 across parities (Miglior *et al.*, 2007). Heritabilities estimated for US Holstein first calving cows for fat and protein contents were both 0.56 (Castillo-Juárez *et al.*, 2000), slightly above that observed in our study of 0.46 ± 0.01 and 0.49 ± 0.01 , respectively.

Across-country genetic correlations

Fertility traits. Although relatively low PTA reliabilities were used to estimate genetic correlations

for AFC and CI, estimated genetic correlations may not be seriously underestimated, since there is no strong selection or correlated responses for these traits (Powell *et al.*, 2003; Cole & Null, 2010). Therefore, the observed values < 1 and significantly lower than correlations obtained from simulated data indicate the existence of important and moderate G×E effects for AFC, and CI, respectively. These values are also in contrast to higher estimates obtained for yield traits.

There are few estimates of the genetic correlation for AFC between countries. This correlation between Colombia and Brazil was estimated as 0.78 Cerón-Muñoz *et al.* (2004) which indicates G×E effects of moderate magnitude for AFC between these countries.

We can assume that the larger G×E effects for AFC between Mexico and Canada may be related to differences in heifer rearing systems or climatic factors between the two countries, even if averages for AFC were approximately similar in the two populations. Climatic and management differences may explain also the moderate G×E effects found between CI in Mexico and Canada and with daughter pregnancy rate in the US.

The genetic correlation between DPR in the US and CI in Canada estimated in our study (≥ 0.93), was similar to that obtained between DPR in the US and days open (multiplied by -1) in Spain (0.94) but greater than the genetic correlation between DPR in the US and first service to conception (multiplied by -1) in Canada (0.72) (Nilforooshan *et al.*, 2010). These results suggest that some genetic correlation estimates lower than 1 observed between countries for fertility traits

are likely due to different trait definitions, rather than evidence of G×E effects (Jorjani, 2005). Differences in trait definition however is unlikely a reason for the small and mostly not-significant ($p>0.10$) differences found in this paper between the estimated correlations Mexico-Canada and Mexico-US for CI or DPR.

The range of estimates of genetic correlations of reproductive interval traits (CI, days open) between 14 and 17 countries used in international genetic evaluations for Holsteins (Interbull, 2013c), varied from 0.60 to 0.97 with an average of 0.84. Specifically, the genetic correlation between days open in Canada (multiplied by -1) with DPR in US used by Interbull is 0.88, not far from the estimate of 0.94 obtained in this study. Published genetic correlation estimates across countries for CI in a range of 0.82 to 0.96 (Jorjani, 2006b) are higher, in general, than our higher values observed between Mexico and Canada (0.69 ± 0.13) and between CI in Mexico and DPR in the US (0.73 ± 0.16). Moderate G×E effects found between CI in Mexico and CI in Canada, or between CI in Mexico and DPR in the US, may be caused by differences in reproductive herd management and climatic effects in the three populations studied.

Milk yield traits. Genetic correlations were estimated as 0.88, 0.87, and 0.87 for milk, fat and protein yields, respectively, as an average for the 27 countries members of Interbull. The average correlation for the 7 core populations with information for all traits, excluding clinical mastitis and stillbirth, was 0.92 for milk, fat, and protein yields, with a range of ± 0.07 -0.08 (Mark, 2004). More recent estimates indicate lower genetic correlations for yield traits between grazing systems in New Zealand with other countries (0.75-0.76) compared to those for Canada-USA (0.92-0.94) (Interbull, 2013a). The range of genetic correlations for all countries for milk, fat and protein yields was 0.75-0.96. Interbull estimates of genetic correlations between Argentina or Uruguay and Canada, and between Argentina or Uruguay and US for yield traits are all equal to 0.85 (Interbull, 2013a).

Comparison with simulated values under the hypothesis of no G×E, indicates that G×E effects between Mexico-Canada and Mexico-US are probably small for these traits. Lack of G×E for milk yield traits may be related to the high production levels, which have increased over time (Montaldo *et al.*, 2009, 2010), making the production environment for this population gradually closer to that in the US, and the mostly temperate climate of the studied registered Mexican Holstein population in herds managed under a conventional production system (Montaldo *et al.*, 2010). Genetic correlations for

Mexico-Canada and Mexico-US for milk yield traits were greater than estimates found for New Zealand-US which support the idea that higher r_g values are associated with more similar conventional production systems between Mexico and the US for Holsteins. As most of the herds in the analyzed Mexican population are located in high plateaus with temperate climates, we may conclude that altitude above sea level (lower than 3000 m), is not associated with strong G×E effects for milk yield traits in Holsteins. Small G×E effects for fat and protein contents may be related to differences in feeding and management systems across countries.

Genetic correlation for milk traits between Canada or the US with the remaining portion of the dairy population of Mexico (grade Holsteins, crossbreeds) or for lower input production systems may be different and is a topic for future studies.

In conclusion, strong G×E interaction effects between Mexico and Canada were found for AFC, and moderate G×E interaction effects were found between Mexico and Canada for CI, and between CI in Mexico with DPR in the US. No G×E interaction effects between Mexico with Canada and the US for milk yield traits were found. There were small but significant G×E interaction effects for fat and protein contents. These findings need to be taken into account when selecting sires evaluated in Canada and the US to be used in Mexican Holstein herds.

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