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Article

Genetic selection aimed to reduce methane emissions and its effect on milk components

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Abstract:

This study aimed to estimate the response to selection through different selection indices between methane production and milk production and its components in specialized tropical, dual-purpose, and family dairy systems. Methane emissions were sampled during milking using the Guardian-NG gas monitor; milk samples were collected individually during methane sampling. DNA was extracted from the hair follicles of all the animals included in this study. The variance and covariance components were estimated using the mixed model methodology. Due to the incomplete genealogical information, molecular markers were used to build the genomic relationship matrix (Matrix G). The estimated heritability for methane emissions during milking was 0.18 and 0.32 for the univariate and bivariate analysis, respectively. The genetic correlation between the milk fat and protein percentages and methane emissions during milking was negative, -0.09 and -0.18, respectively. The response to selection, estimated through selection indices, demonstrated that it is feasible to reduce methane emissions up to 0.021 mg/L during milking in five generations without detriment to milk components.

Key words: Methane, Milk, Heritability, Genetic correlation.

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Introduction

In recent years, the Intergovernmental Panel on Climate Change (IPCC)[1] and the Food and Agriculture Organization of the United Nations (FAO)[2] declared that the agricultural sector is the principal source of short-lived greenhouse gases (GHG), such as methane (CH_4) and nitrous oxide (N_2O).

Some strategies to mitigate methane emissions from dairy cattle include reducing the herd, changing bovine diet, using supplements, immunization against methanogenic archaea, and selecting animals with lower CH_4 production[3].

The selection of low methane-producing animals requires knowledge about the genetic correlations between methane production and other characteristics of productive and economic importance[4].

A selection index is a methodology that maximizes breeding for a specific trait[5]. Selection indices have been widely used to estimate the reproduction value of dairy cattle for individual and combined characteristics for selection purposes[6].

In cattle and sheep, the variation of CH_4 emission has been demonstrated between individuals fed the same diet[7]. De Haas *et al*[8] mentioned the possibility of selecting cows with low CH_4 emissions since genetic variation suggests that the reductions would be 11-26 % in 10 yr and could be even higher in a genomic selection program. However, the available information about the opportunities to mitigate enteric CH_4 through genetic improvement is scarce. Still, the genetic selection of animals with low methane emissions could affect economically important production traits.

This study aimed to estimate the response to selection through different selection indices between methane production and milk production and components in three dairy production systems in Mexico.

Material and methods

This study was carried out in three dual-purpose (DP) production units (PUs), two specialized tropical dairy (STD) PUs, and four family dairy (FD) systems (Table 1). Milk components and methane emissions were measured in 274 cows (98, 74, and 102 in the DP, STD, and FD systems, respectively).

Table 1: Production systems sampled

Farm	System	n	Localization	Breeds
La Posta	DP	33	Veracruz	HOZ and BSZ
El Zapato	DP	16	Veracruz	HOZ
La Doña	DP	49	Puebla	HOZ, BSZ, and SMZ
Santa Elena	STD	37	Puebla	HO, BS, and HOBS
Aguacatal	STD	37	Puebla	HO, BS, and HOBS
Farm 5	FD	16	Jalisco	HO
Farm 6	FD	32	Jalisco	HO
Farm 7	FD	24	Jalisco	HO
Farm 8	FD	30	Jalisco	HO

DP= dual-purpose; STD= specialized tropical dairy; FD= family dairy.
HOZ= Holstein x Zebu, BSZ= Brown Swiss x Zebu, SMZ= Simmental x Zebu, HO= Holstein, BS= Brown Swiss, HOBS= Holstein x Brown Swiss.

Two of the three DP PUs are located in the Medellín de Bravo municipality, Veracruz, and have a tropical savanna climate, Aw(o), and an altitude of 12 m asl[9]. The annual mean

temperature and precipitation are 25 °C and 1,460 mm[9]. The third DP PU and the STD PUs are located in the Hueytamalco municipality, Puebla, at an altitude of 240 m, with a tropical wet climate (Af(c)), mean annual temperature of 23 ºC, and mean annual precipitation ranging from 2,200 to 2,500 mm[9].

The four FD PUs are located in the Tepatitlán municipality, Jalisco, at an altitude of 1,927 m. This location has a humid subtropical climate ((A)C(w1) (e)g) with an annual mean temperature and precipitation of 18 ºC and 715 mm[9].

The DP systems mainly use cross-bred *Bos taurus taurus* and *Bos taurus indicus*. The most common *Bos taurus indicus* breeds are Brahman, Gyr, and Sardo Negro; as for *Bos taurus taurus*, the most common breeds are Holstein, Brown Swiss, and Simmental[10].

One of the variants of tropical dairy systems is the STD. This system is characterized by using pure breeds, such as Holstein and Brown Swiss. Overall, STD management is similar to DP systems except for calf rearing, which is artificial, and milking, which is carried out without calf support[10].

FDs are characterized by small production units that fluctuate from 3 to 30 cows. The production units are conditioned to small areas and adjacent to the housing units, called "backyard." FDs can be intensive or semi-intensive according to the conditions of the cultivation field. Holstein is the most common breed. The technological level is considered scarce because producers do not carry out adequate feeding, reproductive, preventive, or breeding practices. This system lacks production records and has rudimentary facilities; manual milking is often performed. Feeding is based on grazing or the supply of forages and wastes from the producer's crops[11].

Methane sampling

Methane was sampled using the methodology developed by Garnsworthy *et al*[12] and the Guardian-NG gas monitor (Edinburgh Instruments, Scotland, United Kingdom); this methodology measures environmental gas concentrations every second using a non-dispersed dual-wavelength system.

The devices were installed in the feeding troughs where cows were offered feed during milking. Adaptations were made for the different types of feeding troughs to create a closed atmosphere to prevent drafts from skewing CH_4 concentrations. These adaptations aimed to

generate the least disturbance during routine milking and allow the atmospheric sampling of the trough while the animal was feeding.

An adaptation period of one week was carried out to the presence of the new troughs. CH_4 was measured for two weeks during milking; the aim was to have a minimum of 10 effective days of measurement in each PU.

Milk sampling

Milk samples were obtained from each animal during milking. Samples were at least 50 mL and were directly obtained from the weighers at the start of the measurements. After collection, samples were preserved with bronopol and identified with the PU's number and the animal's identification number.

Milk samples were analyzed in the milk quality control laboratory of the Asociación Holstein de México A.C. using the mid-infrared technique to measure protein and fat percentages.

DNA sampling and extraction

Hair follicles were collected from the hairs obtained from the tail of all the animals included in this study. Hair samples were labeled and sent to the GENESEEK laboratory (Lincoln, Nebraska). In this laboratory, DNA was extracted, and genotypes were obtained through high-density microarrays. The GGP BOVINE LD V4 array was used for the animals from FDs; with this array, it is possible to get 30,125 SNPs. As for the animals from the STD and DP systems, the GGDP BOVINE 150K array was used to identify 138,962 SNPs per animal; this is because crossed animals require a greater number of markers for the information to be valid. In this study, only the SNPs located in the 29 autosomal chromosomes were included. The quality control of the genotypes was carried out using the PLINK 1.7[13] software and consisted of 1) removing the individuals with less than 90 % of the genotypic information, 2) removing the animals with a minor allele frequency of less than 5%, and 3) removing the animals with less than 90 % of the useful markers. At the end of the quality control analysis and keeping the markers shared in both platforms, the number of available markers was 20,776 SNPs for each animal.

Statistical analysis

Estimation of the genomic relationships

Variance components were estimated using the mixed model methodology. Due to the lack of complete genealogical information needed to build the additive relationship matrix (A Matrix), molecular markers were used to construct the genomic relationship matrix between all animals (G). The G matrix was built based on the method proposed by VanRaden[14]. This method creates the M matrix using the dimensions: number of individuals (n) x number of markers (m). The matrix elements were coded as -1 (homozygous for one allele), 0 (heterozygous), and 1 (homozygous for the other allele). The $P_{(nxm)}$ matrix is subtracted from the M matrix; this subtraction results in the Z matrix (Z = M – P). The $P_{(nxm)}$ matrix contains columns with all the 2(pi-0.5) elements, where pi is the frequency of the second allele in the locus i. Finally, the G matrix was calculated as:

$$G = \frac{ZZ'}{2\sum p_i(1-p_i)}$$

Estimation of the variance components

The variance components for CH_4 emissions and the milk components (fat and protein percentages) were implemented with the ASReml-R program[15].

The model was selected based on the effects of daily milk production during measurements, lactation days, lactation period, lactation number, production system, herd number, and breed on the response variables: methane production during milking, fat percentage, protein percentage. All the logical combinations within the fixed and random effects that converged with the response variables were tested. The resulting univariate model is represented as follows:

$$y = \mu + Xb + Z_1a + W_1n + e$$

Where,

$\boldsymbol{y}$ is the vector of the response variables (CH_4 production during milking, fat and protein percentage);

$\boldsymbol{\mu}$ is the overall mean of the response variables;

$\boldsymbol{X}$ is the incidence matrix for the fixed effects of daily milk production during measurements and lactation number;

$\boldsymbol{b}$ is the solution vector for the fixed effects of daily milk production during measurements and lactation number; Z is the incidence matrix of the random effects of the animal;
$\boldsymbol{a}$ is the solution vector of the random effects of the animal $\sim N\ (0, G{\sigma^2}_a)$;
$\boldsymbol{W}$ is the incidence matrix for the random effect of the production system;
$\boldsymbol{n}$ is the solution vector for the random effect of the production system;
$\boldsymbol{e}$ is the vector of the random effects of the residuals $\sim N\ (0, I{\sigma^2}_e)$.

Estimation of the covariance components

The covariance components between CH_4 emissions during milking and milk components were calculated with the ASReml-R program[15]. The variances estimated with the univariate models were used as initial values to estimate covariances.

The bivariate model is represented in matrix terms as follows:

$$\begin{vmatrix} y_1 \\ y_2 \end{vmatrix} = \begin{vmatrix} X_1 & 0 \\ 0 & X_2 \end{vmatrix} \begin{vmatrix} b_1 \\ b_2 \end{vmatrix} + \begin{vmatrix} Z_1 & 0 \\ 0 & Z_2 \end{vmatrix} \begin{vmatrix} a_1 \\ a_2 \end{vmatrix} + \begin{vmatrix} W_1 & 0 \\ 0 & W_2 \end{vmatrix} \begin{vmatrix} n_1 \\ n_2 \end{vmatrix} + \begin{vmatrix} e_1 \\ e_2 \end{vmatrix}$$

Where, y_1 and y_2 are the vectors of the response variable (CH_4 production during milking, fat and protein percentage); X_1 and X_2 are incidence matrices for the fixed effects of daily milk production during measurements and lactation number; b_1 and b_2 are the solution vectors for the fixed effects of daily milk production during measurements and lactation number; Z_1 and Z_2 are the incidence matrices of the random effects of the animal; a and a_2 are the solution vectors of the random effects of the animal $\sim N\ (0, G{\sigma^2}_a)$; W_1 and W_2 are the incidence matrices for the random effect of the production system; n_1 and n_2 are the solution vector for the random effect of the production system; e_1 and e_2 are the random effect vectors of the residuals $\sim N\ (0, I{\sigma^2}_e)$.

Estimation of the genetic parameters

The h^2 were obtained from the variance components estimated with the univariate models. The genetic correlations (r_{xy}) were estimated from the bivariate models. The h^2 was calculated by dividing the additive variance (${\sigma^2}_a$) by the phenotypic variance (${\sigma^2}_f$)[16]:

$$h^2 = \frac{{\sigma^2}_a}{{\sigma^2}_f}$$

The r_{xy} were estimated by dividing the genetic covariance (σ_{xy}) of variables x and y between the square root of the product of the genetic variance of the variable x and y[16]:

$$r_{xy} = \frac{\sigma_{xy}}{\sqrt{\sigma^2{}_x \sigma^2{}_y}}$$

Selection index

The response to selection was estimated by different selection indices between methane production and milk production and components. A sensitivity analysis identified different scenarios in which methane emissions, fat percentage, and protein percentage could be selected. Thus, it was possible to observe the dynamics between the accuracy of the indices and their genetic gain (Table 2). The selection indices were carried out for five generations. The traits included in the indices were assigned a value based on selection importance and intensity; the sum of the values in absolute quantities must be equal to 100. CH_4 emissions were assigned values ranging from 0 to -100; fat and protein percentages were assigned values ranging from 0 to 100.

Table 2: Selection indices and selection intensity of each model trait

Index	CH_4	Fat	Protein	Index	CH_4	Fat	Protein
INDEX1	-100	0	0	INDEX34	0	10	90
INDEX2	-90	0	10	INDEX35	-40	40	20
INDEX3	-90	10	0	INDEX36	-20	20	60
INDEX4	-80	0	20	INDEX37	-30	30	40
INDEX5	-80	10	10	INDEX38	-40	50	10
INDEX6	-80	20	0	INDEX39	-10	20	70
INDEX7	-70	0	30	INDEX40	0	20	80
INDEX8	-70	10	20	INDEX41	-40	60	0
INDEX9	-60	0	40	INDEX42	-30	40	30
INDEX10	-70	20	10	INDEX43	-20	30	50
INDEX11	-70	30	0	INDEX44	-10	30	60
INDEX12	-60	10	30	INDEX45	-30	50	20
INDEX13	-50	0	50	INDEX46	-20	40	40
INDEX14	-60	20	20	INDEX47	0	30	70
INDEX15	-50	10	40	INDEX48	-30	60	10
INDEX16	-40	0	60	INDEX49	-10	40	50
INDEX17	-60	30	10	INDEX50	-30	70	0
INDEX18	-60	40	0	INDEX51	-20	50	30
INDEX19	-50	20	30	INDEX52	-20	60	20

INDEX20	-30	0	70	INDEX53	-10	50	40
INDEX21	-40	10	50	INDEX54	-20	70	10
INDEX22	-50	30	20	INDEX55	0	50	50
INDEX23	-20	0	80	INDEX56	0	40	60
INDEX24	-40	20	40	INDEX57	-20	80	0
INDEX25	-10	0	90	INDEX58	-10	60	30
INDEX26	-30	10	60	INDEX59	0	60	40
INDEX27	-50	40	10	INDEX60	-10	70	20
INDEX28	0	0	100	INDEX61	-10	80	10
INDEX29	-50	50	0	INDEX62	0	70	30
INDEX30	-20	10	70	INDEX63	-10	90	0
INDEX31	-40	30	30	INDEX64	0	80	20
INDEX32	-30	20	50	INDEX65	0	90	10
INDEX33	-10	10	80	INDEX66	0	100	0

The variance and covariance components used were those obtained with the previously described models for milk components (fat and protein percentages) and CH_4 production during milking.

The original specification of the selection index foresees the use of a correlated variable (I) based on the phenotypic performance of each animal for several traits[5]. Therefore, it is defined as:

$$I = b\,p$$

Where p is a vector of phenotypic values for the selection criteria and b corresponds to the weighting factors used in selection decision making. To maximize the correlation of I with the contribution of any candidate for the selection as a possible parent, the information is combined as:

$$Ga = Pb$$

Where G is a nxm matrix of genetic variances and covariances between all the m traits, a is a mx1 vector of values relative to the selection intensity for all traits. P is a nxn matrix of phenotypic variances and covariances between the n traits measured and available as selection criteria and b is a nx1 vector of weighting factors applied to the traits used in selection decision making. Thus, the previous equation is solved as:

$$P^{-1}\,Ga = b$$

To obtain the weighting factors contained in b, the selection candidates are classified based on the index (I).

The index precision (r_{HI}) can be described as the correlation between the index on which the selection is based and the genetic value; it is calculated as follows:

$$r_{HI} = \frac{b\ Pb}{a\ Qa}$$

Where, b is a vector of weighting factors to be applied to the traits used to decide the selection; P is a matrix of phenotypic variances and covariances between the measured traits used as selection criteria; a is a vector of relative values for all traits; Q is a matrix of the genetic variances and covariances between all the traits considered as part of the system.

The genetic gain (Δg) for each trait was estimated; it indicates the increase in performance achieved through breeding programs:

$$E\ (\Delta g) = \frac{i\mathrm{G'b}}{\sigma_I}$$

Where: i= selection intensity; G= matrix of the genetic variance-covariance of the traits; b= is a vector of weighting factors to be applied to traits used in selection decision making; $\sigma_I =$ is the standard deviation of the index.
The standard deviation of the index was calculated as follows:

$$\sigma_I = \sqrt{\mathrm{b'Pb}}$$

Where: b= vector of the weighting factors applied to the traits used in selection decision making; P= matrix of the phenotypic variances and covariances between the measured traits used as selection criteria.

Results

The CH_4 emissions in the STD system were 0.08 mg of CH_4/ L; FD and DP systems produced 0.06 mg of CH_4/ L (Table 3). The average of the three systems was 0.065 mg of CH_4/ L. As for milk components, the average fat percentage in the three systems was 4.82 %; the values per system were 3.69 % in STD, 3.72% in FD, and 6.84 % in DP. The protein percentage in the STD, FD, and DP systems was 3.20, 3.29, and 3.21 %, respectively. When combining the three systems, the average protein percentage was 3.23 %.

Table 3: Descriptive statistics of methane production and milk components in three production systems in Mexico

	Methane (mg/L)		Fat %		Protein %	
System	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**
DP (n=98)	0.06	0.039	6.84	4.938	3.21	0.405
FD (n=102)	0.06	0.014	3.72	0.632	3.29	0.315
STD (n=74)	0.08	0.016	3.69	0.492	3.20	0.417
Average	0.065	0.028	4.828	3.344	3.234	0.380

DP= dual-purpose system, FD= family dairy, STD= specialized tropical dairy, N= number of observations, SD= standard deviation.

The h^2 estimated for CH_4 emissions during milking using the univariate model was 0.19. Similarly, the h^2 for fat percentage was 0.39 and 0.18 for protein percentage.

However, the h^2 estimated using bivariate models was 0.32±0.245 for CH_4 emissions during milking and 0.46±0.278 for fat percentage. The h^2 for protein percentage was similar to the one estimated with the univariate model. However, the h^2 of CH_4 is similar to the one found in the bivariate analysis with fat percentage (0.35). The genetic correlations between milk fat and protein percentage and CH_4 emissions during milking were -0.090 ± 0.080 and -0.18 ± 0.575, respectively.

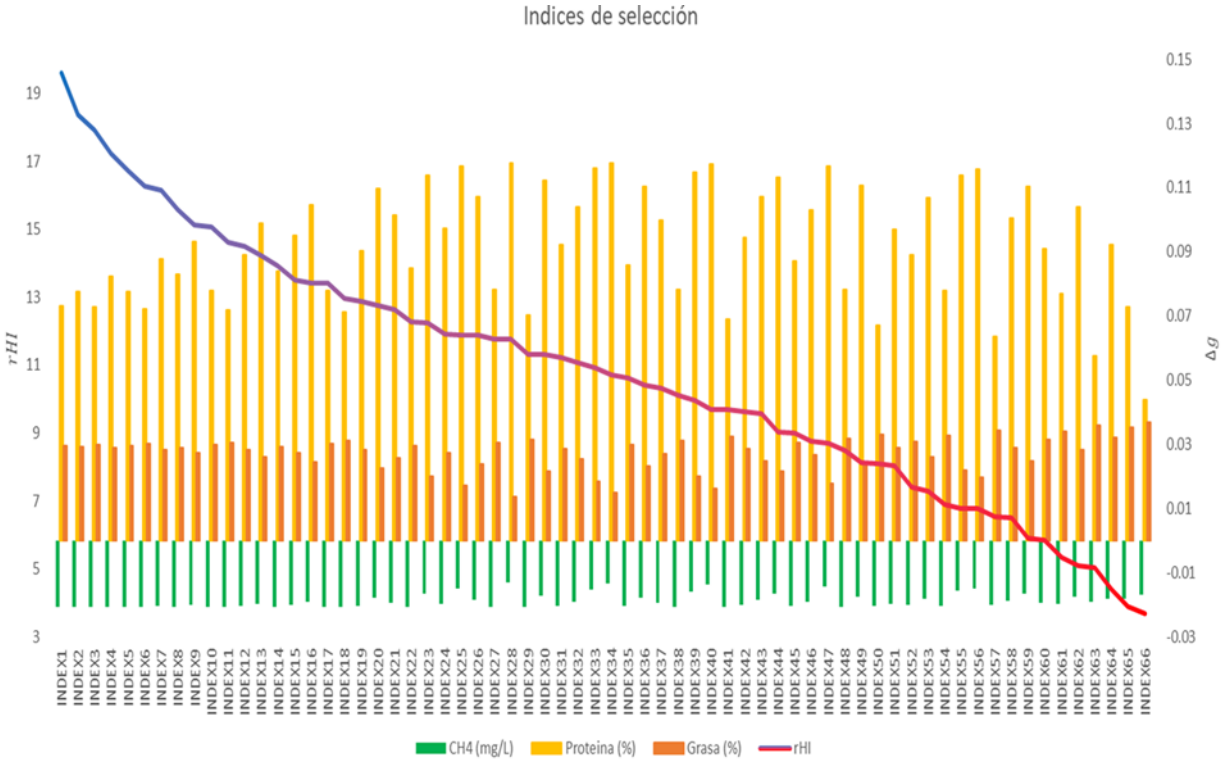
Table 4 and Figure 1 show the accuracy of the selection indices (r_{HI}) and the genetic gain (Δg). In all the selection indices, the decrease of CH_4 emissions during milking does not negatively affect milk components. Moreover, the r_{HI} of the most accurate indices are those where CH_4 emissions during milking are selected.

Table 4: Selection indices and genetic gain for CH_4 and milk components

Index	***r*HI**	**CH_4 (mg/L)**	**Fat (%)**	**Protein (%)**	**Index**	***r*HI**	**CH_4 (mg/L)**	**Fat (%)**	**Protein (%)**
INDEX1	19.58	-0.021	0.030	0.073	INDEX34	10.72	-0.013	0.015	0.117
INDEX2	18.38	-0.021	0.029	0.078	INDEX35	10.63	-0.021	0.030	0.086
INDEX3	17.92	-0.021	0.030	0.073	INDEX36	10.41	-0.018	0.023	0.110
INDEX4	17.23	-0.021	0.029	0.082	INDEX37	10.32	-0.020	0.027	0.100
INDEX5	16.72	-0.021	0.030	0.078	INDEX38	10.12	-0.021	0.031	0.078
INDEX6	16.26	-0.021	0.030	0.072	INDEX39	9.95	-0.016	0.020	0.115
INDEX7	16.14	-0.021	0.028	0.088	INDEX40	9.70	-0.014	0.016	0.117
INDEX8	15.57	-0.021	0.029	0.083	INDEX41	9.70	-0.021	0.032	0.069
INDEX9	15.13	-0.020	0.027	0.093	INDEX42	9.62	-0.020	0.029	0.094
INDEX10	15.06	-0.021	0.030	0.078	INDEX43	9.56	-0.018	0.025	0.107
INDEX11	14.61	-0.021	0.031	0.072	INDEX44	9.01	-0.017	0.022	0.113

INDEX12	14.49	-0.020	0.028	0.089	INDEX45	9.01	-0.020	0.030	0.087
INDEX13	14.21	-0.020	0.026	0.099	INDEX46	8.77	-0.019	0.027	0.103
INDEX14	13.92	-0.021	0.029	0.084	INDEX47	8.70	-0.014	0.018	0.117
INDEX15	13.50	-0.020	0.027	0.095	INDEX48	8.49	-0.021	0.032	0.078
INDEX16	13.41	-0.019	0.025	0.104	INDEX49	8.12	-0.017	0.024	0.111
INDEX17	13.40	-0.021	0.030	0.078	INDEX50	8.09	-0.020	0.033	0.067
INDEX18	12.96	-0.021	0.031	0.071	INDEX51	8.05	-0.020	0.029	0.097
INDEX19	12.86	-0.020	0.028	0.090	INDEX52	7.41	-0.020	0.031	0.089
INDEX20	12.74	-0.018	0.023	0.110	INDEX53	7.28	-0.018	0.026	0.107
INDEX21	12.63	-0.019	0.026	0.101	INDEX54	6.90	-0.020	0.033	0.078
INDEX22	12.27	-0.021	0.030	0.085	INDEX55	6.78	-0.016	0.022	0.114
INDEX23	12.23	-0.017	0.020	0.114	INDEX56	6.78	-0.015	0.020	0.116
INDEX24	11.90	-0.020	0.027	0.097	INDEX57	6.52	-0.020	0.034	0.064
INDEX25	11.89	-0.015	0.017	0.117	INDEX58	6.52	-0.019	0.029	0.100
INDEX26	11.89	-0.018	0.024	0.107	INDEX59	5.89	-0.017	0.025	0.110
INDEX27	11.76	-0.021	0.031	0.078	INDEX60	5.86	-0.020	0.032	0.091
INDEX28	11.75	-0.013	0.014	0.118	INDEX61	5.35	-0.020	0.034	0.077
INDEX29	11.32	-0.021	0.032	0.070	INDEX62	5.08	-0.017	0.028	0.104
INDEX30	11.30	-0.017	0.021	0.112	INDEX63	5.02	-0.019	0.036	0.057
INDEX31	11.23	-0.020	0.029	0.092	INDEX64	4.40	-0.018	0.032	0.092
INDEX32	11.08	-0.019	0.025	0.104	INDEX65	3.90	-0.018	0.035	0.073
INDEX33	10.91	-0.015	0.018	0.116	INDEX66	3.67	-0.017	0.037	0.044

Figure 1: Precision of the selection indices and genetic gain for CH_4 and milk components



In the indices with greater r_{HI}, indices from 1 to 10, this variates from 15.06 to 19.58 in five generations; this would result in CH_4 reductions ranging from 0.021 to 0.020 mg/L, fat percentage increases ranging from 0.027 to 0.030 and from 0.072 to 0.093 for protein percentage. These results indicate that milk production decreases when CH_4 emissions decrease. For the remaining indices, the changes in CH_4 emissions during milking, fat percentage, and protein percentage were not significant; however, the r_{HI} is lower.

Discussion

The CH_4 emissions during milking estimated in this study are lower than those reported by Bell *et al*[17]; this is possibly due to diet heterogeneity. In the farms analyzed in this study, animals are fed by grazing; in the specialized systems, animals are fed a concentrate-based diet. The h^2 of CH_4 production during milking estimated in this study are similar to those reported by other authors with metabolic chambers[18,19] or even with prediction equations[8]. These results coincide with those reported by other authors using similar CH_4 measuring methodologies[20]; this suggests that CH_4 during milking is a trait that could be potentially

used in breeding programs because it can be easily incorporated into production control programs and requires unsophisticated equipment compared to respiratory chambers; additionally, this equipment can be mobilized to places of difficult access. The fat percentage h^2 estimated in this study is higher than those observed in other studies[21-22]. The protein percentage h^2 is lower than the 0.23 reported by Othmane *et al*[23]; this may be due to the inherent heterogeneity in dairy production units depending on the herd's diet and race.

The genetic correlations between CH_4 emissions and milk components suggest genetic antagonism. However, the estimates in this study were not different from zero. The CH_4 and grams of milk fat correlation observed by Pszczola *et al*[4] is higher (0.21) than that reported in this study; the correlation between CH_4 and grams of milk protein in this study was similar to the one reported by Lassen *et al*[24] (0.39). In both cases, the opposite sign. It is important to mention that this difference is due to the units of measurement since milk production and the percentages of milk components have a negative correlation. In contrast, milk production and the content of its components have a positive correlation[25]. Currently, the reduction of CH_4 emissions through genetic selection has been proposed; this could reduce dairy cattle CH_4 emissions in 10 yr between 11 and 26 %[8]; 5 % in beef cattle[26].

The selection indices performed by Kandel *et al*[27] include fat and protein production, which were positively correlated with CH_4 production. Considering the units of measurement, their result is similar to the one reported in this study since the correlation between milk production and the percentage of milk components is negative. In contrast, the correlation between milk production and the content of milk components is positive[27].

Conclusions and implications

The genetic correlations between CH_4 emissions and milk components (fat and protein percentage) suggest that a breeding program aimed to simultaneously decrease CH_4 emissions and increase the percentages of milk components is feasible. In other words, these results show that it is possible to genetically select animals to reduce CH_4 emissions without negatively affecting milk composition; this is confirmed by the genetic gains per generation predicted by the selection indices. The above, with CH_4 reductions during milking in five generations ranging from 0.013 to 0.021 mg/L, without decreasing fat and protein percentages.

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Conflicts of interest

The authors declare no conflicts of interest.

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