

Association between PTA for milk from foreign Holstein sires and daughters milk yield in Brazil

Associação entre PTA para leite de reprodutores da raça Holandesa estrangeiros e produção de leite de filhas no Brasil

Asociación entre PTA para leche de toros extranjeros de la raza Holandesa y la producción de leche de progenies en Brasil

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Abstract

The genetic improvement of the Holstein breed in Brazil is supported by the use of reproductive biotechnologies, mainly due to artificial insemination. Dependent on imported cryopreserved semen, therefore, genetic material from breeders evaluated in different environments, in this way, Brazilian herds seems to be likely to not present satisfactory genetic advances, caused by the phenomenon of genotype-environment interaction. Therefore, this research aims to evaluate whether, when selecting bulls with high genetic merit for milk, they have the potential to generate progenies with superior milk yield (MY). For this, a database of Holstein heifers and cows (n=7,556) was used, containing lactation records and PTA milk data from their sire. Lactations were adjusted for environmental effects and analyzed by Spearman correlation in relation to PTA milk of their respective sire. Significant correlations ($p < 0.0001$) were found with higher coefficients for the first lactation and lower for the fifth lactation. Also, considering the PTA milk of the sires, quartiles were assembled and submitted to ANOVA demonstrating that there is a significant difference ($p < 0.0001$) between the MY of daughters between quartiles, confirming that foreign sires can be used with to generate more productive daughters in Brazil.

Keywords: Performance; Lactation; Parity; Correlation; Progeny.

Resumo

O melhoramento genético da raça Holandesa no Brasil é amparado pelo uso de biotecnologias reprodutivas, principalmente a inseminação artificial. Dependentes da importação de sêmen criopreservado, portanto, material genético de reprodutores avaliados em diferentes ambientes, desta forma, rebanhos brasileiros parecem não apresentar avanços genéticos satisfatórios, causados pelo fenômeno da interação genótipo-ambiente. Portanto, este trabalho tem como objetivo avaliar se, ao selecionar touros com alto mérito genético para leite, há o potencial de gerar progênes com produções de leite (MY) superior. Para isso, um banco de dados contendo registros de novilhas e vacas (n=7,556) contendo lactações e PTA para leite de seus respectivos pais. Lactações foram ajustadas para efeitos ambientais e analisadas para por meio de correlação de Spearman em relação aos valores de PTA para leite de seus respectivos pais. Correlações significativas ($p < 0,0001$) foram encontradas com coeficientes maiores para a primeira lactação e menores para a quinta lactação. Além disso, considerando o PTA para leite dos touros, quartis foram formados e submetidos à ANOVA demonstrando que existe uma diferença significativa ($p < 0,0001$) entre o MY das filhas entre os quartis de PTA, confirmando que touros estrangeiros podem ser usados para gerar filhas mais produtivas no Brasil.

Palavras-chave: Performance; Lactação; Paridade; Correlação; Progênie.

Resumen

El mejoramiento genético de la raza Holstein en Brasil se apoya en el uso de biotecnologías reproductivas, principalmente la inseminación artificial. Dependiente de la importación de semen criopreservado, por lo tanto, material genético de toros evaluados en diferentes ambientes, de esta forma, los rebaños brasileños no parecen presentar avances genéticos satisfactorios, causados por el fenómeno de la interacción genotipo-ambiente. Por lo tanto, este trabajo tiene como objetivo evaluar si, al seleccionar toros con alto mérito genético para producción de leche, existe el potencial de generar progenies con mayor producción de leche (MY). Para ello se contó con una base de datos que contiene registros de novillas y vacas (n=7.556) conteniendo lactancias y PTA para leche de sus respectivos padres. Las lactancias se ajustaron por efectos ambientales y se analizaron mediante la correlación de

Spearman en relación con los valores de PTA para la leche de sus respectivos padres. Se encontraron correlaciones significativas ($p < 0.0001$) con coeficientes mayores para la primera lactancia sobre la quinta relación. Además, considerando el PTA para la leche de los toros, se formaron cuartiles y se sometieron a ANOVA demostrando que existe una diferencia significativa ($p < 0.0001$) entre el MY de las hijas entre los cuartiles del PTA, lo que confirma que los toros extranjeros pueden ser utilizados para generar más hijas productivas en Brasil.

Palabras clave: Actuación; Lactancia; Paridad; Correlación; Progenie.

1. Introduction

Artificial insemination (AI) as a technology applied to reproduction has the purpose and potential of increasing genetic gain in livestock by allowing the dissemination of genetic material from sires with superior genetic merit (Moore and Hasler, 2017). Since its inception, AI remains the main vehicle for the rapid spread of genes, provided by advances in technology and the rapid acceptance of the technique by breeders (Vishwanath, 2003). Brazilian herds of Holstein cattle depend largely on semen, embryos, and imported animals, mainly from the United States of America, Canada, and Europe, with, for example, the amount exceeding one million doses of semen was imported in the first half of 2020, mainly from the United States of America (Stanton et al., 1991; ASBIA, 2022).

The globalization of dairy cattle breeding requires that bulls can be compared between countries for all interest traits (Mark et al., 2002), however, historically countries tend to evaluate sires only with data from daughters of their country (Powell et al. Norman, 1998) causing differences to be observed in progenies inserted in other environments due to the interaction between genotype-environment (Bourdon, 2014). The existence of this phenomenon implies that the best genotype in one environment does not confer the best performance in another, explained by the different physiological mechanisms required and, consequently, genotypes necessary for high performance in different environments, although there is a correlation between both (Falconer and Mackay, 1989). However, efforts have been made to develop across-country genetic evaluations that aim to improve genetic gains in other countries (Smith and Banos, 1991). Thus, this work aims to assess whether sires with genetic merit for milk evaluated in international breeding programs have the potential to conceive equally superior dairy progenies in Brazil.

2. Methodology

2.1 Data

A database containing data from Holstein heifers and cows ($n=7,556$) located in the state of Paraná, Brazil, including their respective lactations based on a period of 305 days, for females that are progenies of sires from international breeding programs there is also the predicted transmission ability for milk in pounds (PTA milk) from the sire. Animals with milk yield (MY) below 4,000 kg of milk and with less than 3 dairy controls performed, as well as animals that did not have the sire's information, or that the sire did not have the PTA milk previously calculated by the CDCD (Council on Dairy Cattle Breeding) were excluded.

2.2 Fixed effects

Daughters MY were corrected for environmental effects of herd, year of birth and times milked, if these were significant ($p < 0.0001$) in linear regression analysis in the statistical software Graphpad Prism 8, assuming the predicted values as corrected MY.

2.3 Correlation between sire PTA milk and daughters MY

To assess the degree of association between the sire's predicted transmission ability and the daughters' MY (for each

parity order), Spearman's correlation analysis was used, assuming that p-values lower than 0.0001 were significant, calculated in the Graphpad Prism 8 statistical software.

2.4 Differences between MY groups

To assess whether there is an increase in production in the daughters as a result of the selection of higher PTA milk in bulls, the animals were separated into quartiles considering the values of PTA milk, a descriptive analysis to summarize the data were performed, followed by of one-way analysis of variance (ANOVA) between quartiles of the same parity daughters MY (Chebel and Veronese, 2020; Lima et al., 2020).

3. Results and Discussion

The present study aims to determine the association between sires PTA with the MY of their daughters in Brazil. As can be seen in Table 1, the first MY is on average lower compared to others, with the highest average observed being for the third MY, similar to the patterns found by Yoon et al. (2004), Munim et al. (2006) and M'hamdi et al. (2012). Interestingly, the standard deviation of MY is larger as lactations correspond to a higher calving order.

Table 1 – Descriptive analysis of the population of Holstein females evaluated.

	PTA milk	MY 1	MY 2	MY 3	MY 4	MY 5
n	7.556	7.556	5.553	3.628	1.989	905
Mean	11	10.267	11.650	11.926	11.647	11.239
Maximum	2899	20.636	23.970	22.854	22.700	19.024
Minimum	-2451	4.036	4.052	4.009	4.018	4.057
STD	8,22	2.128	2.557	2.844	3.002	3.059

n = Number of samples; PTA milk = Predicted transmitting ability of milk in pounds of the sires; STD = Standard deviation; MY 1 = First daughters' milk yield in kg based on 305 days; MY 2 = Second daughters' milk yield in kg based on 305 days; MY 3 = Third daughters' milk yield in kg based on 305 days; MY 4 = Fourth daughters' milk yield in kg based on 305 days; MY 5 = Fifth daughters' milk yield in kg based on 305 days. Source: Authors.

The fixed effects of year and times milked per day were significant for all parity MY, while the herd effect was only significant for MY of parity 1 to 4. R2 coefficients was higher for the first lactation, decreasing as the lactation order increases as seen in Table 2.

Table 2 – Fixed effects evaluated by multiple regression for the population of Holstein females evaluated.

Milk yield	R ²	Year	Herd	TMD
MY 1	0,26	<0,0001	<0,0001	<0,0001
MY 2	0,14	<0,0001	<0,0001	<0,0001
MY 3	0,10	<0,0001	0,0466	<0,0001
MY 4	0,06	<0,0001	0,4889	<0,0001
MY 5	0,02	0,0021	0,6523	0,0013

R² = Coefficient of determination for the regression model; TMD = Times milked per day; MY 1 = First daughters' milk yield in kg based on 305 days; MY 2 = Second daughters' milk yield in kg based on 305 days; MY 3 = Third daughters' milk yield in kg based on 305 days; MY 4 = Fourth daughters' milk yield in kg based on 305 days; MY 5 = Fifth daughters' milk yield in kg based on 305 days. Source: Authors.

According to Table 3, the quartiles Q1, Q2, Q3 and Q4 based on sires PTA milk, each quartile has 1,889 animals, with PTA means of 1,091, 254, -295 and -1,004 pounds of milk, respectively. Data such as those presented demonstrate that there is great genotypic variation for the milk trait among Holstein sires in Brazil.

Table 3 – Descriptive analysis of sires predicted milk transmission ability based on pounds in the Holstein female population evaluated in each quartile.

	n	Média (lb)	Mínimo (lb)	Máximo (lb)	Desvio padrão (lb)
Q1	1.889	1.091	627	2.911	415
Q2	1.889	254	0	627	192
Q3	1.889	-295	-558	0	164
Q4	1.889	-1004	-2451	-563	347

Q1 = First quartile; Q2 = Second quartile; Q3 = Third quartile; Q4 = Fourth quartile; n = Number of animals contained in the quartile. Source: Authors.

As the MY parity increased, lower values for the correlation coefficients were obtained, such as lower numbers of pairs for comparison are observed in Spearman's correlation analysis, which proved to be significant ($p < 0.0001$) for all analyzes between milk PTA and daughters' MY, as shown in Table 4.

Table 4 – Spearman's correlation between daughter milk yield and sire predicted transmission ability for milk in the analyzed Holstein population.

	PTA milk vs. Lac 1	PTA milk vs. Lac 2	PTA milk vs. Lac 3	PTA milk vs. Lac 4	PTA milk vs. Lac 5
p value	<0,0001	<0,0001	<0,0001	<0,0001	<0,0001
r	0,1925	0,1764	0,1480	0,1396	0,1308
n pairs	7.556	5.553	3.628	1.989	905

PTA milk = Predicted transmitting ability of milk in pounds of the sires; Lac 1 = First daughters' milk yield in kg based on 305 days; Lac 2 = Second daughters' milk yield in kg based on 305 days; Lac 3 = Third daughters' milk yield in kg based on 305 days; Lac 4 = Fourth daughters' milk yield in kg based on 305 days; Lac 5 = Fifth daughters' milk yield in kg based on 305 days; p value = p value for correlation analysis; n pairs = Number of XY pairs in correlation analysis. Source: Authors.

Regarding the number of observations for each MY, MY of lower order of parity have more observations in relation to MY of higher order. Note that for all MY, quartile 1 has the highest MY averages, followed by quartiles 2, 3 and finally 4, as can be seen, for the maximum values.

Table 5 - Descriptive analysis of corrected milk yields based on kg of females from the Holstein population evaluated in each quartile.

		n	Mean (kg)	Minimum (kg)	Maximum (kg)	STD (kg)
MY 1	Q1	1.889	10.766	2.911	19.458	1.945
	Q2	1.889	10.385	3.528	15.988	1.767
	Q3	1.889	10.011	3.070	17.557	1.831
	Q4	1.889	9.906	3.388	15.234	1.640
MY 2	Q1	1.185	12.189	3.014	22.986	2.438
	Q2	1.397	11.836	3.432	18.961	2.492
	Q3	1.447	11.518	3.238	19.217	2.232
	Q4	1.524	11.184	3.761	17.842	2.244
MY 3	Q1	673	12.501	3.082	21.802	2.818
	Q2	863	12.100	3.807	22.096	2.630
	Q3	1.003	11.890	3.043	18.964	2.694
	Q4	1.089	11.464	3.921	18.443	2.606
MY 4	Q1	313	12.286	3.743	21.885	3.008
	Q2	479	11.834	3.525	18.940	2.955
	Q3	550	11.713	3.597	18.899	2.829
	Q4	647	11.142	3.433	17.700	2.837
MY 5	Q1	132	12.037	4.190	18.359	3.170
	Q2	192	11.345	3.657	16.642	2.949
	Q3	254	11.227	3.886	18.259	3.124
	Q4	327	10.863	3.864	17.234	2.862

n = Number of animals contained in the quartile; STD = Milk yield standard deviation; MY 1 = First daughters' milk yield in kg based on 305 days; MY 2 = Second daughters' milk yield in kg based on 305 days; MY 3 = Third daughters' milk yield in kg based on 305 days; MY 4 = Fourth daughters' milk yield in kg based on 305 days; MY 5 = Fifth daughters' milk yield in kg based on 305 days; Q1 = First quartile; Q2 = Second quartile; Q3 = Third quartile; Q4 = Fourth quartile; n = Number of animals contained in the quartile. Source: Authors.

In general, most quartiles differed significantly from each other, the difference being more evident in milk yields of lower parity order in relation to milk yield of higher order of parity, especially the comparison between the first and fourth quartiles, whose difference was significant for all lactations, as shown in Table 6.

Table 6 - ANOVA analysis between quartiles of milk yields corrected based on kg of females in the Holstein population.

		p value	Significative	Mean dif.
MY 1	Q1 vs Q2	<0.0001	Yes	380.9
	Q1 vs Q3	<0.0001	Yes	754.2
	Q1 vs Q4	<0.0001	Yes	860.0
	Q2 vs Q3	<0.0001	Yes	373.3
	Q2 vs Q4	<0.0001	Yes	479.1
	Q3 vs Q4	0.2703	No	105.7
MY 2	Q1 vs Q2	0.0008	Yes	353.3
	Q1 vs Q3	<0.0001	Yes	671.3
	Q1 vs Q4	<0.0001	Yes	1005.0
	Q2 vs Q3	0.0017	Yes	318.1
	Q2 vs Q4	<0.0001	Yes	652.1
	Q3 vs Q4	0.0006	Yes	334.0
MY 3	Q1 vs Q2	0.0185	Yes	401.9
	Q1 vs Q3	<0.0001	Yes	611.1
	Q1 vs Q4	<0.0001	Yes	1037.0
	Q2 vs Q3	0.3322	No	209.3
	Q2 vs Q4	<0.0001	Yes	635.1
	Q3 vs Q4	0.0016	Yes	425.9
MY 4	Q1 vs Q2	0.1369	No	452.5
	Q1 vs Q3	0.0263	Yes	573.7
	Q1 vs Q4	<0.0001	Yes	1145.0
	Q2 vs Q3	0.9082	No	121.2
	Q2 vs Q4	0.0004	Yes	692.1
	Q3 vs Q4	0.0038	Yes	570.9
MY 5	Q1 vs Q2	0.1743	No	692.1
	Q1 vs Q3	0.0581	No	810.4
	Q1 vs Q4	0.0009	Yes	1174.0
	Q2 vs Q3	0.9765	No	118.2
	Q2 vs Q4	0.2906	No	481.9
	Q3 vs Q4	0.4693	No	363.7

MY 1 = First daughters' milk yield in kg based on 305 days; MY 2 = Second daughters' milk yield in kg based on 305 days; MY 3 = Third daughters' milk yield in kg based on 305 days; MY 4 = Fourth daughters' milk yield in kg based on 305 days; MY 5 = Fifth daughters' milk yield in kg based on 305 days; Q1 = First quartile; Q2 = Second quartile; Q3 = Third quartile; Q4 = Fourth quartile; p value = p-value of ANOVA analysis; Mean dif. = Mean difference between quartiles. Source: Authors.

The major concern when using sire of foreign origin is that unfavorable interactions between genotype and environment may occur, which may reduce the potential benefits of a strategy based on potentially superior germplasm imports (Costa et al., 2000). Because the true gain depends on the genetic value of the candidate germplasm and its performance in the livestock environments in important countries and its integration with the place where the breeding is aimed (Costa et al., 2000), occurring the genotype-environment interaction, which it is when the performance between two or more genotypes changes from environment to environment (Bourdon, 2014).

Genotype-environment interactions can affect the ranking of genotypes or their magnitudes in an absolute or relative way because of the relationship of genetic, residual, and phenotypic variance between countries with different environmental conditions (Costa et al., 2000). As, also interactions between genotype and environment can be caused by the result of the interaction of heterogeneous variances (Stanton et al., 1991). However, the study of some environmental factors and their interactions with genetic effects can be considered to obtain more precision in genetic evaluations (Zwald et al., 2003).

Genetic evaluations between populations (countries, breeds and herds) allow classifying the estimated genetic merit and selecting the best sires among populations, especially when they have similar breeding objectives (Smith and Banos, 1991). The advantages of combined selections are deterministic evaluations by the simple fact of selecting the best sires for use in different populations by using a common truncation line over the estimated genetic value distributions for different populations (Smith and Banos, 1991). According to Lohuis and Dekkers (1998), the use of sires evaluated across countries can increase the response rate to genetics by up to 17%, compared to sires that are evaluated in a single country, and that this advantage can be even greater when the correlations between rating systems are low, too, when the relative size of the foreign population is large.

High genetic correlations as shown in Table 6 and in similar studies such as Stanton et al. (1991) and Costa et al. (2000) have already provided some explanations at the molecular level when analyzing single nucleotide polymorphisms (Oikonomou et al., 2009). As studies that reported comparing cows born in the United States and born in Brazil, indicating that there is a high genetic correlation for milk production between the two countries (Costa et al., 2000). According to Stanton et al. (1991), heritability for milk production based on 305 days of MY was slightly higher in the United States of America (0.25) compared to measured heritability in Latin America (0.21), because the sire variance decreases more in relation to the residual variance. In this same study, a genetic correlation of 0.91 was found between the MY equivalent of daughters born in the United States of America and in comparison, to daughters born in Latin America (Stanton et al., 1991). These values are higher than those found in this study, due to the nature of the measures, as one deals with genetic correlations and the other with phenotypic correlations, which in their nature have lower coefficients due to environmental effects (Searle, 1961).

Therefore, as sires in this study have genetic evaluation from a data collaboration program between different countries (Wiggans et al., 2011), they may indicate that evaluated females are benefited by this evaluation method, as can be observed in the production higher average for all parities of daughter females contained in the Q1 quartile, thus, the importation of germplasm from countries with well-established breeding programs is a viable option for development and genetic progress in developing countries (Costa et al., 2000), generating more productive daughters.

4. Conclusion

The genetic evaluations combined with information from several herds in different countries, together with reproductive biotechnologies revolutionized the dairy cattle breeding, especially the Holstein breed, increasing the accuracy of the genetic value estimates which consequently increased the rates of genetic gains and consequently productivity of females in Brazil, thus, the use of sires evaluated in these programs can contribute to the national genetic progress. The inclusion of information from Brazilian herds on international evaluations can improve genetic response in the future, reducing genotype-environment effects.

References

ASBIA. (2022). Dados estatísticos Index ASBIA 1º trimestre 2022: Esalq/USP. <http://www.asbia.org.br/wp-content/uploads/2022/05/Index-Asbia-1o-Trimestre-2022-Midia.pdf>.

Bourdon, R. M. (2014). *Understanding animal breeding*. Edinburgh Gate: Editora 2 Pearson. p. 518.

- Chebel, R. & Veronese, A. (2020). Associations between genomic merit for daughter pregnancy rate of Holstein cows and metabolites postpartum and estrus characteristics. *Journal of Dairy Science*, 103: 10754-68. <http://doi.org/10.3168/jds.2020-18207>.
- Costa, C. N., Blake, R. W., Pollak, E. J., & Oltenacu, P. A., Quaas, R.L., Searle, S.R. Genetic (2000). Analysis of Holstein Cattle Populations in Brazil and the United States. *Journal of Dairy Science*, 83: 2963-2974. [https://doi.org/10.3168/jds.S0022-0302\(00\)75196-4](https://doi.org/10.3168/jds.S0022-0302(00)75196-4).
- Falconer, D. S. & Mackay, T. F. C. (1989). *Introduction to quantitative genetics*. 3ª edição. Pearson, Universidade de Edinburgo. 438p. ISBN 0-470-21162-8.
- Lima, F. S., Silvestre, F. T., Peñagaricano, F., & Thatcher, W. W. (2020). Early genomics prediction of daughter pregnancy rate is associated with improved reproductive performance in Holstein dairy cows. *Journal of Dairy Science*, 103(4): 3312-3324. <https://doi.org/10.3168/jds.2019-17488>.
- Lohuis, M. M. & Dekkers, J. C. M. (1998). Merits of borderless evaluations. *Proceedings of the 6th World Congress on Genetics Applied to Livestock Production*, 26: 169-172.
- M'hamdi, N., Bouallegue, M., Frouja, S., Ressaissi, Y., Brar, S. K., & Hamouda, M. B. (2012). Effects of Environmental Factors on Milk Yield, Lactation Length and Dry Period in Tunisian Holstein Cows. *Milk Production - An Up-to-Date Overview of Animal Nutrition*. Londres: Editora IntechOpen, p. 406.
- Mark, T., Fikse, W.F., Emanuelson, U., & Philipsson, J. (2002). International Genetic Evaluations of Holstein Sires for Milk Somatic Cell and Clinical Mastitis, *Journal of Dairy Science*, 85: 2384-2392. [https://doi.org/10.3168/jds.S0022-0302\(02\)74319-1](https://doi.org/10.3168/jds.S0022-0302(02)74319-1).
- Moore, S. G. & Hasler, J. F. (2017). A 100-year review: Reproductive technologies in dairy science. *Journal of Dairy Science*, 100: 10314-10331. <https://doi.org/10.3168/jds.2017-13138>.
- Munim, T., Hussain, S.S., Hoque, M. A., & Khandoker, M. A. (2006). Genetic and non-genetic effects on productive and reproductive traits of different genetic groups of cows. *Bangladesh Journal of Animal Science*, 35(1):1-2.
- Oikonomou, G., Angelopoulou, K., Arsenos, G., Zygouianis, D., & Banos, G. (2009). The effects of polymorphisms in the DGAT1, leptin and growth hormone receptor gene loci on body energy, blood metabolic and reproductive traits of Holstein cows. *Animal Genetics*. <https://doi.org/10.1111/j.1365-2052.2008.01789.x>.
- Powell, R. L. & Norman, H. D. (1998). Use of multinational data to improve national evaluations of Holstein bulls, *Journal of Dairy Science*, 81: 2257-2263. [https://doi.org/10.3168/jds.S0022-0302\(98\)75805-9](https://doi.org/10.3168/jds.S0022-0302(98)75805-9).
- Searle, S. R. (1961). Phenotypic, Genetic and Environmental Correlations. *Biometrics*, 3: 474-480. <https://doi.org/10.2307/2527838>.
- Smith, C. & Banos, G. (1991). Selection within and across populations in livestock improvement. *Journal of Animal Science*, 69: 2387-2394. DOI: 10.2527/1991.6962387x.
- Stanton, T. L., Blake, R. W., Quaas, R. L., Van Vleck, L. D., & Carabaño, M. J. (1991). Genotype by Environment Interaction for Holstein Milk Yield in Colombia, Mexico, and Puerto Rico. *Journal of Dairy Science*, 1991, 74: 1700-1714. [https://doi.org/10.3168/jds.S0022-0302\(91\)78333-1](https://doi.org/10.3168/jds.S0022-0302(91)78333-1).
- Vishwanath, R. (2003). Artificial insemination: the state of the art. *Theriogenology*, 59: 571-584. [https://doi.org/10.1016/S0093-691X\(02\)01241-4](https://doi.org/10.1016/S0093-691X(02)01241-4).
- Wiggans, G. R., VanRaden, P. M., & Cooper, T. A. (2011). The genomic evaluation system in the United States: Past, present, future. *Journal of Dairy Science*, 94: 3202-3211. doi: 10.3168/jds.2010-3866.
- Yoon, J. T., Lee, J. H., Kim, C. K., Chung, Y. C., & Kim, C. H. (2004). Effects of Milk Production, Season, Parity, and Lactation Period on Variations of Milk Urea Nitrogen Concentration and Milk Components of Holstein Dairy Cows. *Asian-Australasian Journal of Animal Sciences*, 17(4): 479-484. <https://doi.org/10.5713/ajas.2004.479>.
- Zwald, N. R., Weigel, K. A., Fikse, W. F., & Rekaya, R. (2003). Identification of Factors That Cause Genotype by Environment Interaction Between Herds of Holstein Cattle in Seventeen Countries. *Journal of Dairy Science*, 86: 1009-1018. [https://doi.org/10.3168/jds.S0022-0302\(03\)73684-4](https://doi.org/10.3168/jds.S0022-0302(03)73684-4).