STUDY REGARDING ESTIMATION OF HERITABILITY FOR MILK PRODUCTION TRAITS IN HOLSTEIN CATTLE

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Abstract

The goal of this study is to estimate the heritability of milk, fat, and protein yields in Holstein cows from a dairy farm in Iași, Romania. The heritability of these traits during the first lactation is examined using 16 bulls and their 542 progeny and was estimated the heritability of milk, fat, and protein yields during the first lactation. Data was statistically processed with ANOVA. The findings reveal a lower heritability for milk yield (0.15 ± 0.06), a moderate heritability for fat yield (0.30 ± 0.12), and a strong heritability for protein yield (0.64 ± 0.23). These results showed that protein yield exhibits the most significant genetic influence, while milk yield demonstrates the least. The findings regarding milk yield and fat percentage should be interpreted with caution due to their proximity to the limits of the specialized data range. However, it is important to note that the observed heritability for protein percentage may be of particular difference, potentially influenced by human error or the transmission of data in an improper manner.

Key words: dairy cattle, improvement, breeding plan

A breeding program is a systematic approach used in genetics and animal husbandry to improve desired traits through controlled mating strategies. Heritability, a key parameter in breeding programs, quantifies the extent to which genetic differences contribute to the observed variation in a trait. It helps breeders identify traits that are more responsive to selection and guides the selection intensity and breeding methods employed. Higher heritability values indicate traits that can be improved more effectively through selective breeding, while lower heritability may require alternative strategies. By considering heritability, breeders can optimize their breeding programs to achieve genetic progress and targeted objectives in an objective and efficient manner. (Ivancia M., 2020).

The study of genetic parameters in animal breeding assumes a important role in comprehending the phenotypic and genotypic structure of populations. (Creangă Șt. *et al*, 2008). It provides valuable insights into heritability, repeatability, and correlations between traits, which are necessary in developing effective breeding programs. This article specifically focuses on estimating genetic parameters, particularly heritability, for milk, fat, and protein yields in Holstein cattle from a dairy farm in Romania.

The initial step in any improvement process involves a comprehensive description of the phenotypic and genotypic structure of the population under analysis. Phenotypic assessment of quantitative traits necessitates the use of statistical methods, while genotypic evaluation relies on determining genetic parameters for production traits. Among these parameters, heritability assumes significant importance as it elucidates the proportion of total variation attributed to the average effect of genes (Meuwissen T. *et al*, 2022).

Numerous researchers have estimated heritability values for milk, fat, and protein yields during the first lactation in Holstein cows. Studies conducted by Jamrozik (1997) and Strabel (2006) reported heritability estimates ranging from 0.31 to 0.36 for milk yield, 0.28 to 0.36 for fat yield, and 0.12 to 0.28 for protein yield. These estimates reflect the proportion of phenotypic variation in these traits that can be attributed to genetic factors.

This study aims to bring a contribution in animal breeding by estimating the genetic parameters, particularly heritability, associated with milk, fat, and protein yields during the first lactation in Holstein cows from Iași, Romania. These estimates will provide valuable insights into the level of genetic control and the potential for selection and improvement within these specific conditions (Djaalab I. *et al.*, 2021). The findings

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will contribute to the development of more targeted breeding strategies focused on enhancing milk production and composition in Holstein cattle from the studied dairy farm. Consequently, this research contributes in the current understanding of animal breeding by investigating the genetic parameters, specifically heritability in Holstein cows from Iași, Romania. The obtained estimates offer comprehensive insights into the underlying genetic control mechanisms that influence these important production traits. The study's results will have practical implications for dairy farmers and breeders, informing the development of more effective breeding programs and enabling the selection of superior animals with improved productivity. This investigation contributes significant findings to the scientific literature on genetic parameters and advances targeted breeding strategies aimed at enhancing the overall production potential of Holstein cattle in the specific conditions under examination.

MATERIALS AND METHODS

16 bulls of the same breed were the biological material studied and they were selected based on the criterion of having at least two daughters, totalizing a number of 542 daughters. The study ensures a diverse representation of genetic variations within the Holstein population under investigation, by including bulls with multiple daughters. The data was obtained from Holstein Ro Association. The selected bulls' daughters were obtained in 5 farms (*table 1*).

Table 1

Daughters repartition by father

Crt.	Bull code	Number of daughters
1	54031	16
2	52987	17
3	53302	17
4	53227	21
5	53743	21
6	53400	24
7	53742	24
8	52943	25
9	52505	27
10	53022	28
11	53642	42
12	53188	44
13	53349	45
14	52811	56
15	52533	60
16	52938	75
TOTAL		**542**

To assess the production traits, monthly milk samples were gathered from the farm and sent to the laboratory of the Holstein Ro Organization. The analyse of production traits, including milk, fat, and protein yields, was carried out using the Combifoss equipment that provides accurate measurements and enables the quantification of these essential production traits.

The 305-day milk, fat, and protein yields were calculated using the Test Interval Method, as recommended in the ICAR Guidelines (*ICAR Recording Guidelines*, 2022). This method considers variations in test intervals, which can commonly occur in practical dairy farming (Onaciu *et al.*, 2015). The Test Interval Method ensures precise estimation of the 305-day yields for each trait, by incorporating the appropriate coefficients from the ICAR Guidelines. This approach is preferred over other methodologies due to its ability to account for variations in test intervals, thereby providing reliable and consistent results for the estimation of milk, fat, and protein yields (Maciuc V., 2003).

To ensure data quality, cows with fewer than seven tests were excluded from the analysis. This exclusion criterion helps maintain a sufficient number of observations for robust statistical analyses and reduces the potential impact of unreliable or incomplete data on the estimation of heritability.

The heritability of the milk, fat, and protein yields was estimated based on standardized lactation records from the first lactation of cows. These standardized records enable the comparison and evaluation of production traits across different cows and lactation periods (Kim B.W. *et al*, 2009). The data were processed using ANOVA, including the genetic component that contributes to the heritability estimates.

The formula employed for estimating heritability of a trait, including milk yield, fat yield, or protein yield, is given as:

$$h^2 = (\sigma^2_a / \sigma^2_t),\text{ (Ivancia M., 2020).}$$

- h^2 represents the heritability of the trait,
- σ^2_a corresponds to the additive genetic variance specific to the trait, and
- σ^2_t denotes the total phenotypic variance including the trait's overall variation within the population.

To calculate heritability for a particular trait, such as milk yield, fat yield, or protein yield, the formula was adapted accordingly. The heritability of the interest traits was determined using:

$$h^2X = (\sigma^2_aX / \sigma^2_tX),\text{ where}$$

• X means MY, FY and PY (Ivancia M., 2020).

The additive genetic variance (σ^2_a) captures the extent of genetic influence on the trait's variation, while the total phenotypic variance (σ^2_t) accounts for the overall variation observed in the trait across the population.

Variance was calculated using the formula:

Variance = (Σ(X - μ)²) / n, where:

- Σ denotes summation,
- X represents individual observations,
- μ represents the mean of the observations, and
- n represents the total number of observations (Ivancia M., 2020)

In addition to estimating heritability, the standard deviation for each trait was calculated. The standard deviation provides an understanding of the variability within the traits and assesses the precision of the estimated heritability values (Jamrozik J., Schaeffer L.R., 1997).

The standard error (SE) is calculated as:

SE = sqrt (MSW / n), where

- MSW is the mean square error from the ANOVA, and
- n denotes the number of observations.

Justification of the chosen methodology lies in its established reliability, statistical rigor, and wide applicability in the field of animal breeding. These methods have been extensively used and validated in previous studies, ensuring accurate estimation of heritability for milk, fat, and protein yields in the Holstein breed from the Moldovian region.

RESULTS AND DISCUSSIONS

The data analysis estimates heritability for milk yield, fat yield, and protein yield. The heritability values obtained in this study were 0.15 ± 0.06 for milk yield, 0.30 ± 0.12 for fat yield, and 0.64 ± 0.23 for protein yield.

The heritability estimate for milk yield (*table* 2) indicates a lower heritability compared to the findings reported by other authors.

This suggests that the genetic contribution to milk yield variation in the studied population is relatively smaller. This observation aligns with previous studies (Creangă Şt. *et al.*, 2008; Toghiani S., 2012; Roşca N. *et al.*, 2018) that have also reported lower heritability values for milk yield in Holstein cattle populations.

The heritability estimate for fat yield (*table* 2) indicates a moderate level of heritability. This finding suggests that genetic factors play a more substantial role in the variation of fat yield compared to milk yield. The moderate heritability of fat yield is consistent with the results reported by other researchers (Jamrozik J., Schaeffer L.R., 1997; Strabel T., Jamrozik J., 2006; Stoop W. M. *et al*, 2008), indicating a consistent genetic influence on fat production in Holstein populations.

Table 2

Heritability Estimates for Milk Yield from Various Studies and Own Results

Source	h^2		
	MY	**FY**	**PY**
Own results	**0.15**	**0.30**	**0.64**
Jamrozik, 1997	0.32	0.28	0.28
Strabel, 2006	0.18	0.12	0.13
Kim, 2009	0.15	0.13	0.12
Nixon, 2009	0.14	0.26	0.20
Toghiani, 2012	0.26	0.15	0.24

The heritability estimate for protein yield (*table* 2) indicates a strong heritable character, with a value above 0.4. This finding highlights the substantial genetic contribution to the variation observed in protein yield among the Holstein cows in the studied population. The high heritability of protein yield aligns with previous research (Kim B.W. *et al.*, 2009; Wongpom B. *et al*, 2017) that has reported significant genetic effects on protein production traits in Holstein populations.

The substantial disparity observed between the heritability estimates of fat yield and protein yield in this study may be attributed to variations arising from the employed methodology when compared to existing data from the specialized literature. The ANOVA did not incorporate the complete equation of the mathematical model, including the consideration of fixed or random factors, environmental effects, and animal pedigree. This restricted information in the model equation could potentially lead to biased or even negative heritability estimates. Future studies may consider more comprehensive statistical methodologies that account for additional factors and assumptions to obtain more accurate heritability estimates for production traits.

The heritability estimates derived from this study provide significant insights into the genetic influence on milk yield, fat yield, and protein yield in Holstein cattle. This suggests that solely relying on genetic selection may not yield substantial improvements in milk production. In contrast, moderate heritability for fat yield suggests the influence of both genetic and environmental factors. Conversely, the high heritability of protein yield indicates a strong genetic influence, making genetic selection a potential key strategy for enhancing protein yield in milk.

Further research could focus on exploring environmental factors that impact milk, fat, and protein yield, including feed quality, milking practices, and living conditions. Understanding these factors could facilitate the development of a holistic breeding strategy that considers both genetic and environmental optimization. Investigating the genetic correlation between these

traits could also be beneficial in uncovering common genetic factors influencing them and informing genetic selection strategies.

Gene-mapping studies or Genome-Wide Association Studies (GWAS) could be conducted to identify specific genes or genomic regions with significant influence on these traits, enabling the development of genomic selection strategies for more efficient breeding programs. However, it is important to acknowledge that the heritability estimates in this study were limited by the methodology employed, which did not fully incorporate all relevant factors such as fixed or random effects, environmental influences, and animal pedigree. Future research should consider employing more comprehensive statistical methodologies, including mixed model approaches or machine learning algorithms, to obtain more accurate heritability estimates.

These findings contribute significantly to our understanding of the heritability of milk, fat, and protein yield in Holstein cows. However, they also underscore the need for further investigation in several areas to develop more effective and sustainable breeding strategies.

CONCLUSIONS

The study revealed that milk yield exhibited a lower heritability compared to the other production traits, indicating a relatively smaller genetic influence. Conversely, fat yield showed a moderate level of heritability, while protein yield demonstrated a strong heritable character. These findings have important implications for breeding programs, as they highlight the potential for genetic improvement in specific production traits. Further research and selection strategies should focus on enhancing the genetic potential for protein yield, while considering the limitations of ANOVA in accurately estimating heritability.

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