

GENETIC AND PHENOTYPIC TRENDS FOR UDDER TRAITS AND ANGULARITY OF HOLSTEIN FRIESIAN COWS

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ABSTRACT

The present research aimed to investigate the genetic trends for udder traits (fore udder attachment; rear udder height; udder depth; front teat placement; rear teat placement; front teat length and rear teat length) and angularity of Holstein Friesian cows in Serbia. A multi-trait animal model was used to estimate genetic parameters, through REML procedures. In the study 10403 first-lactation cows Holstein type from 12 different regions in Serbia were included. The cows were daughters of 221 Holstein Friesian sires. The age at first calving was from 19 to 44 months, and there were 10 stages of lactation. Udder type traits and angularity were classified by 24 classifiers on a linear scale of 1 to 9. Udder type traits had heritability estimates ranging from 0.03 for rear teat placement to 0.12 for fore udder attachment, and angularity had heritability 0.10. Genetic trend for angularity of Holstein Friesian cows in Serbia shows that ribs are becoming less angular and extremely rounded, while genetic trends for udder traits show that teat lengths are becoming longer and inside of quarter, and udder is shallow. The genetic trend for fore udder attachment indicates there is indirect selection for weaker udders.

Keywords: Genetic parameters, Heritability, Breeding value, Udder traits

Published first online April 30, 2022

Published final October 05. 2022

INTRODUCTION

In the cycle of dairy cattle selection, focus is put on production-related characteristics, as high-producing animals generate more income (Saowaphak *et al.*, 2017). Linear type traits are the basis of all current type classification schemes and are the cornerstone of all dairy cow identification systems (ICAR, 2018). Linear udder traits are one of the main characteristics that influence the overall efficiency and profitability of the dairy sector (Miglior *et al.*, 2005; Kern *et al.*, 2014). As a result, udder traits are increasingly of interest to producers in order to improve their herd profitability. Nevertheless, various studies suggest that selection for increased dairy cattle production has serious side effects on health and fertility characteristics due to antagonistic genetic associations between production and fertility characteristics (Kadarmideen and Wegmann, 2003; Melendez and Pinedo, 2007) and production and health characteristics (Sewalem *et al.*, 2010).

Insufficient herd reproductive performance, increased forced culling, or even both, can lead to lower milk and lower calves per cow per year, lower volunteer culling, thus increased replacement costs, and ultimately lower net returns (González-Recio *et al.*, 2006). These are the reasons behind the modern approach to the selection of dairy cattle, where focus is placed on functional, morphological traits and moreover, longevity

(Stanojević, 2017; Miglior *et al.*, 2017). Cows with a stronger, tightly attached udders are more likely to have a longer herd life, while those with rough and long teats are predicted to be culled earlier than expected (Vukasinovic *et al.*, 2002). Furthermore, Corrales *et al.*, (2011) have observed that large cows with udder depth, deep angular bodies, and good udder conformation tend to produce more milk.

Genetic selection may, therefore, create an imbalance between such significant traits (Rauw *et al.*, 1998). Nevertheless, it is important for efficient production that the breed has a morphological structure and physiological status capable of maintaining production and continuity in the herd (Saowaphak *et al.*, 2017; Fernandes *et al.*, 2019). The udder traits and the angularity of dairy cows are influenced by genetic and non-genetic factors. The knowledge of genetic correlations between traits helps to cut short the long list of traits and include the most important in selection indices (Khan and Khan, 2016). The genotype of these traits consists of a large number of genes with minor effects (minor genes). Markers associated with udder support and average teat diameter were identified; some were within genes that are involved in the development and regulation of the mammary system. Results suggest that BTA 5 is important for udder traits in cattle and are suggestive of one or a few genes or regulatory elements in the region (Tolleson *et al.*, 2017). Cole *et al.*, (2011)

found that for body conformation and udder properties, BTAX's phosphorylase kinase, alpha 2 (liver) gene (PHKA2) was highly significant. The top SNP effects in the 80 to 90 Mb regions of BTA11 predominantly affected stature, rear udder height and teat length. The same authors also stated that the most significant X chromosome SNP effects were associated with daughter pregnancy rate, dairy form, udder attachment, rear teat placement, and final score of body conformation traits.

To achieve the breeding goals, one of the essential tools in regulating the genetic selection process is to evaluate the genetic trends of certain traits with the aim of making an early adjustment to the selection process. Estimating the genetic trend of traits over a long period of time will be more reliable. But working to estimate the genetic trend in a short period of time will be more beneficial in terms of time and effort.

The purpose of this study was therefore, to determine the heritability coefficient for udder traits of Holstein Friesian cows at first calving in Serbia, as well as estimated breeding values (EBV) in order to estimate and compare genetic trends of these traits with phenotypic trends. There was also an attempt in this paper to estimate the genetic trends of the studied traits during a short period, with the intention of obtaining information on traits in order to make improvements to the selection program in a timely manner to achieve the goals of breeding.

MATERIALS AND METHODS

The research was conducted on the territory of the Autonomous Province of Vojvodina, Republic of Serbia (45.2609° N, 19.8319° E), in the period from 2011 to 2015. The data set was provided by the Main Breeding Organization (GOO) for Animal Husbandry, which is located within the Department of Animal Husbandry of the Faculty of Agriculture, University of Novi Sad. Udder type traits and angularity were classified by 24 classifiers, in accordance with the Instruction for evaluation by type ICAR (International Committee for Animal Recording), in the 12 regions, years of classification were from 2012 to 2015 on 10403 Holstein Friesian cows, which had the first calving from 2011 to 2015 in their first lactation, on a linear scale of 1 to 9. The original data records included 26,905 Holstein Friesian cows at first calving. In the following processing stages, the offspring of bulls with less than 5 daughters is excluded from the study. Furthermore, cows of no known origin and cows whose lactation was greater than 305 days when the classification was carried out were also excluded. After all these restrictions we still have records of 10403 cows. All these limitations were applied to the study in order to standardize some non-genetic factors, with the intention

of making the evaluation as accurate as possible for genetic trends in a short period. The cows are owned by 1342 breeders who participate in the implementation of the main breeding program for Holstein Friesian cattle, and they are daughters of 221 Holstein Friesian bulls.

The traits were evaluated in four seasons (winter, spring, summer and autumn), ten stages of lactation, with an interval of 30 days for every stage, 23 genetic groups were formed according to the years of birth of bulls, five calving age groups (from 19 to 44 months), and three groups of genetic compositions (I (from 75% to 87.5%), II (from 87.6% to 96.75%), III (96.75% ≥)) according to the proportion of the Holstein Friesian gene. Udder traits included fore udder attachment (FUA); rear udder height (RUH); udder depth (UD); front teat placement (FTP); rear teat placement (RTP); front teat length (FTL); rear teat length (RTL) and angularity (ANG). The fixed effects were investigated by analysis of variance PROC GLM of SAS (SAS Inst.Inc, 2012) with the following mathematical model:

$$Y_{ijklmop} = \mu + HF_i + GG_j + AFC_k + Y_l + S_m + C_o + SL_p + \text{animal} + e_{ijklmno}$$

where: μ is the overall mean, $Y_{ijklmop}$ is the observation of n^{th} cow affected by i^{th} gene ratio of Holstein Friesian cows (HF), j^{th} genetic group (genetic group formed by the year of birth of the bull), k^{th} age at first calving (AFC), l^{th} year of classification (Y), m^{th} season of classification (S), o^{th} classifier (C), p^{th} stage of lactation (SL), and we considered the effect of random additive genetic effects of animals (cow, sire and dam), in addition to the residual effect $e_{ijklmop}$. The estimation of variance components was calculated by the following model:

$$y = Xh + Zu + e$$

where: y is a vector of dependent variables; h is a vector of fixed effects; u is a vector of random additive genetic effects of animals, X and Z are incidence matrices (X for the fixed effects, Z for the additive genetic effects; and e is a vector of random residual effects. (Co)variance components were estimated using VCE6 (Groeneveld *et al.*, 2010). Univariate analyses for all combinations of traits were computed. Estimated breeding values were estimated using PEST (Groeneveld *et al.*, 1990). Genetic trend was estimated as the linear regression of average estimated breeding value of animals on the birth year from 2009 to 2013. The heritability (h^2) for udder traits were estimated as:

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}$$

where σ_a^2 and σ_e^2 are the additive genetic variance due to genetic effects and residual variance due to non-genetic effects, respectively. The pedigree file for the estimation of breeding values consisted of 10861 Holstein animals.

RESULTS

In the evaluation, the highest average score for the udder traits was 6.25 for RUH, and the lowest was 4.51 RTL, while the average score for ANG was 6.47. Most udder traits were around and above the ideal score 5 for Holstein Friesian that is defined by the ICAR. The average score for RTL was below the ideal score (4.51 vs 5), and slightly below the ideal average (4.95 vs 5) was the score for FTP. However, FUA and RUH had scores

(5.75, 6.25 respectively) below the ideal score (9). The angularity also had a score (6.47) below the ideal score (9). Descriptive statistics of the udder traits and angularity for the Holstein cows at first calving in this paper are shown in the Table 1. The greatest standard deviation SD=1.45 was for FUA and the smallest SD = 1.11 for FTL, indicates that the measured values for FTL are distributed closer to the mean, and distributed more widely for FUA.

Table 1. Means and standard deviations (SD) of udder type traits and angularity.

Trait ¹	Score		Ideal score ²	No. of records	Mean	SD	CV (%)
	1	9					
FUA	Weak and loose	Strong and tight	9	10403	5.75	1.45	25.21
FTP	Outside of quarter	Inside of quarter	5	10403	4.95	1.14	23.03
FTL	Short	Long	5	10403	5.21	1.11	21.30
UD	Below hock	Shallow	5	10403	5.99	1.21	20.20
RUH	Extremely low	High	9	10403	6.25	1.35	21.6
RTP	External	Internal	5	10403	5.71	1.34	23.46
RTL	Short	Long	5	10403	4.51	1.12	24.83
ANG	Extremely rounded	angular	9	10403	6.47	1.39	21.48

¹FUA: Fore udder attachment; RUH: Rear udder height; UD: Udder depth; FTP: Front teat placement; RTP: Rear teat placement; FTL: Front teat length; RTL: Rear teat length; ANG: Angularity. ² Ideal score: by (ICAR)

Heritability estimates of udder traits in the first lactation, shown in table 2, were in the range 0.03 \pm 0.01 for RTP to 0.12 \pm 0.02 for FUA. However, for ANG was 0.10 \pm 0.02. The results of this study reflect generally low heritability of the udder traits and ANG. This implies if there is a slight genetic change in the udder traits and ANG of Holstein Friesian cows in Serbia then one of the reasons for that is the low heritability. The values of the genetic standard deviation SD ranged from 0.21 for RTP to 0.47 for FUA. This suggests that FUA is more variable than other traits.

Table 2. Estimates of heritability (h^2) with standard errors (SE), genetic variance (σ_a^2) and standard deviation (SD) for udder type traits and angularity in (n=10403) cows.

Trait ¹	h^2	SE	σ_a^2	SD
FUA	0.12	0.02	0.219	0.47
FTP	0.06	0.01	0.079	0.28
FTL	0.05	0.01	0.052	0.23
UD	0.10	0.02	0.143	0.38
RUH	0.08	0.01	0.125	0.35
RTP	0.03	0.01	0.047	0.21
RTL	0.08	0.01	0.075	0.27
ANG	0.10	0.02	0.181	0.42

¹FUA: Fore udder attachment; RUH: Rear udder height; UD: Udder depth; FTP: Front teat placement; RTP: Rear teat placement; FTL: Front teat length; RTL: Rear teat length; ANG: Angularity.

Estimated breeding values (EBVs) for all traits are shown in Figure 1. Average EBVs for traits were relatively constant in years 2010, 2011 and 2012, after which they gradually increased until 2013 for all traits. An exception was EBVs for ANG trait, which decreased from 2009 to 2013, and also EBVs for FUA increased from 2009 to 2011 and then decreased until 2013 (Figure 1).

All udder traits and ANG showed positive and negative averages of estimated breeding values during the period 2009-2013. An exception was for FTP and RUH that had positive averages of estimated breeding values during the study period. The genetic and phenotypic trends for udder type traits and angularity are shown in Figures (2 to 9). Whereas, the phenotypic trends of the traits were assessed with the intention of comparing them with the genetic trends of the traits, but taking into account that these phenotypic trends were according to the years of classification (this means, for example, that the number of animals in 2012 when estimating the phenotypic trend is not equal to the number of animals in 2009 when estimating the genetic trend). This comparison will allow us to explain some of the environmental influences (management, nutrition, etc.), because it is known that the phenotypes are the result of genetics and the environment.

The majority of udder traits have positive genetic trends. Exceptions are FUA, and slightly negative was for RUH (Figures 2b, 3b). On the other hand, ANG has an extreme negative phenotypic and genetic trend (Figure 4) and has shown a significant linear relationship

with the year of birth ($R^2 = 0.868$). This implies that the period after 2011 Holstein heifers progressively had more loosely attached, shallower and underdeveloped udders, and ribs were closer (cows were less angular).

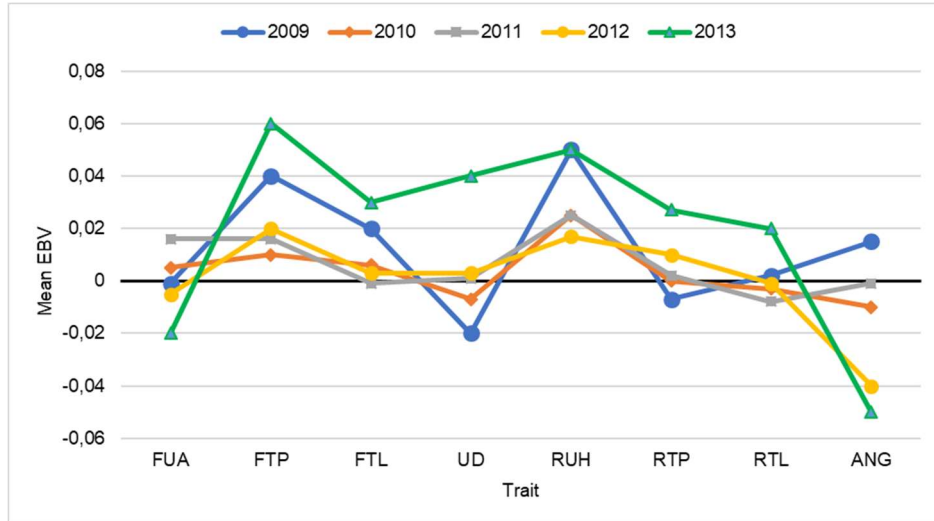
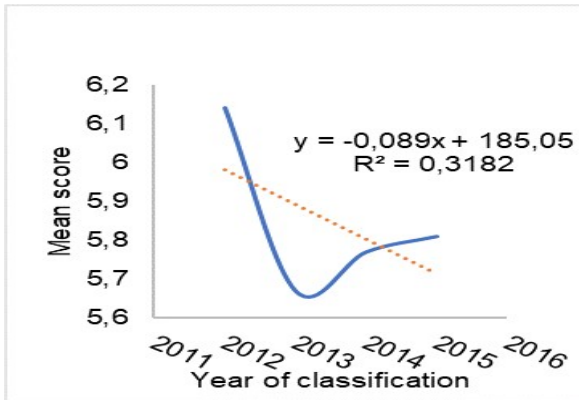
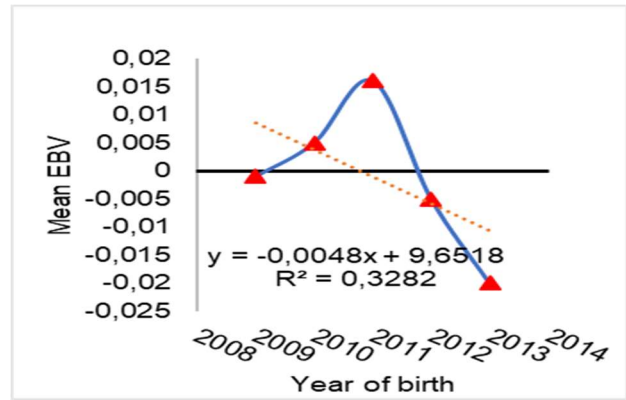


Fig. 1. Estimated breeding value (EBV) for traits in Holstein Friesian cows

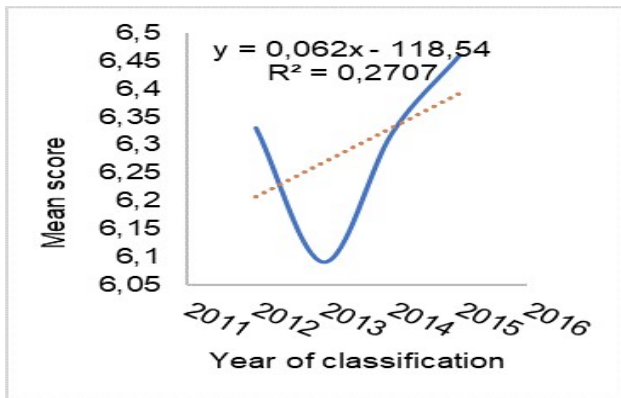


(a)

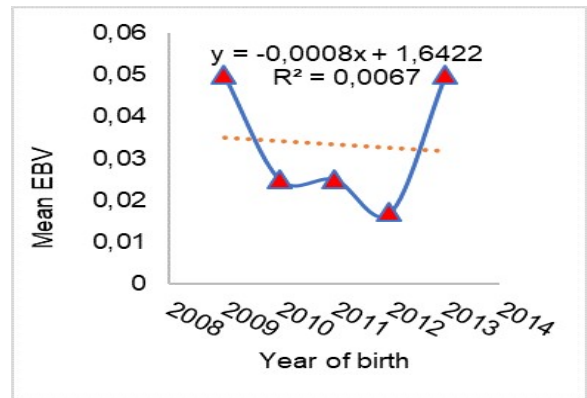


(b)

Fig. 2. (a) Phenotypic (b) genetic trend for fore udder attachment.



(a)



(b)

Fig. 3. (a) Phenotypic (b) genetic trend for rear udder height

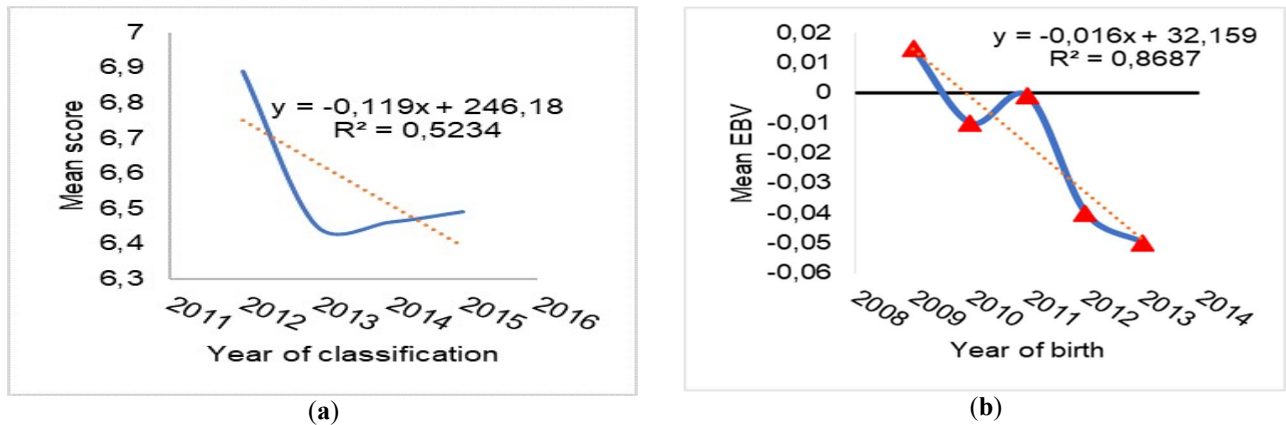


Fig. 4. (a) Phenotypic (b) genetic trend for angularity.

Genetic and phenotypic trends have been harmonious for FUA and ANG, and this reflects the appropriate environmental factors for this trait. furthermore, there is not the same slope for the genetic and phenotypic trends for RUH (Figure 3), this suggests that the environmental factors are not favorable for this trait and restrict the genetic improvement.

Average of estimated breeding values for FTL and RTL decreased from 2009 to 2011 and then increased

until 2013. Figures 5b, 6b show that the genetic trends for teat length were generally positive from 2009 to 2013. In other words, teat lengths were reduced and the breeders made a selection when they were becoming extremely short based on increasing the teat length. The genetic trend was consistent with the phenotypic trends for FTL and RTL.

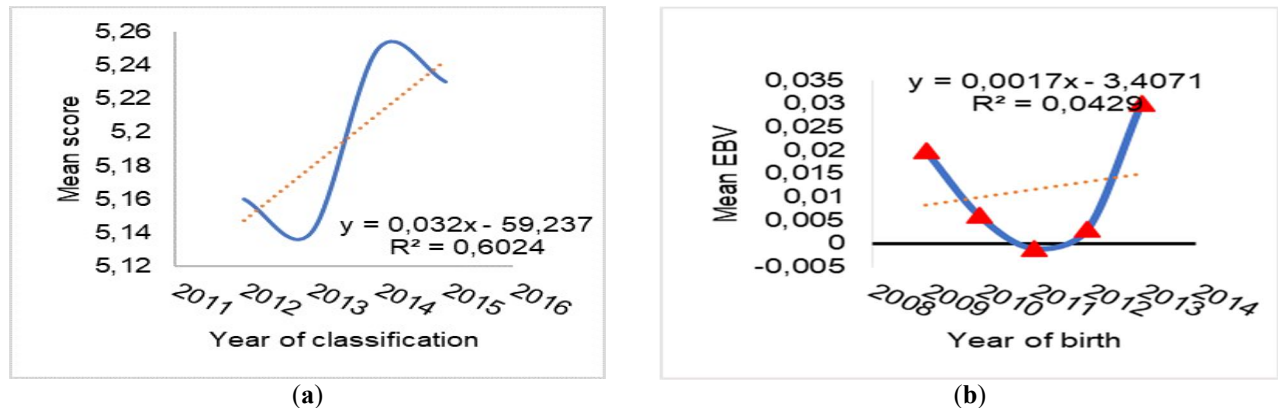


Fig. 5. (a) Phenotypic (b) genetic trend for front teat length.

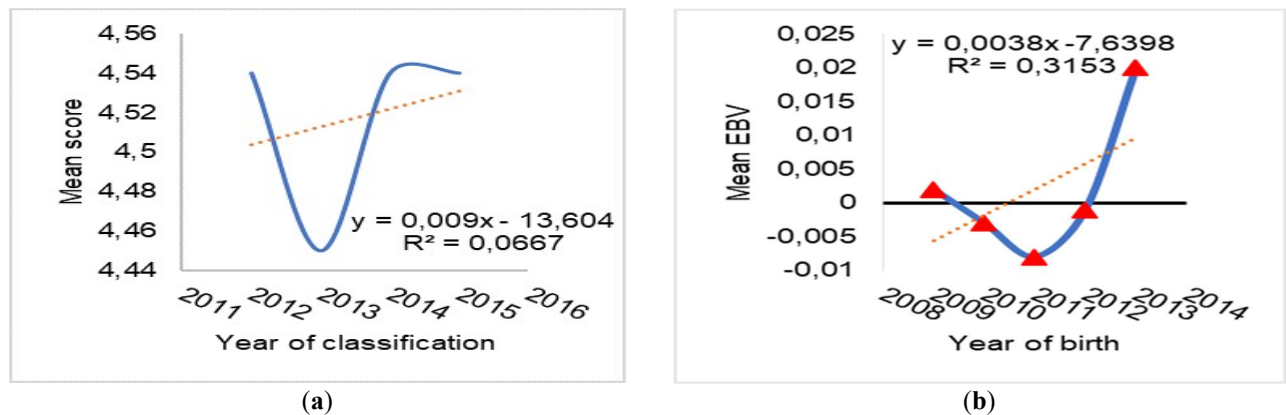
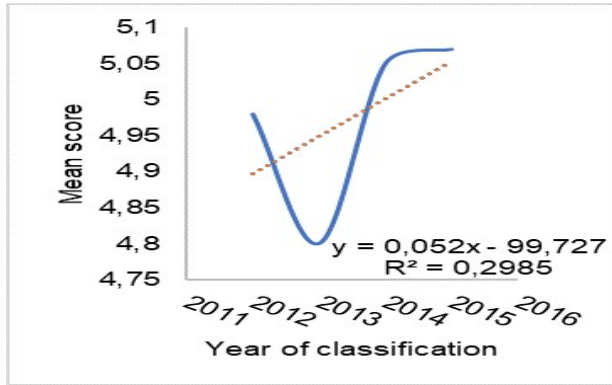


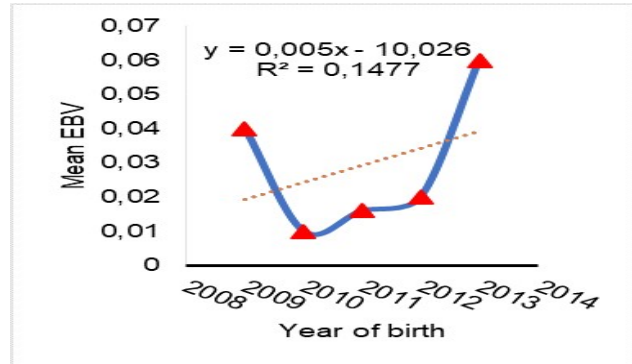
Fig. 6. (a) Phenotypic (b) genetic trend rear teat length.

Figures 7b, 8b show that FTP and RTP have a marked positive genetic trend in Holstein cattle, and it is possible that the breeders made the selection for longer and internal teats. The genetic trend for RTP showed a linear relationship with the years of birth greater than the genetic trend for FTP ($R^2 = 0.898$ vs $R^2 = 0.147$). The

phenotypic trend for FTP was positive and in accordance with the genetic trend, but the phenotypic and genetic trends for RTP were not on the same slope (Figure 8), suggesting that systemic effects (e.g., age and season at first calving, herds, etc.) did not support the genetic potential of this trait.

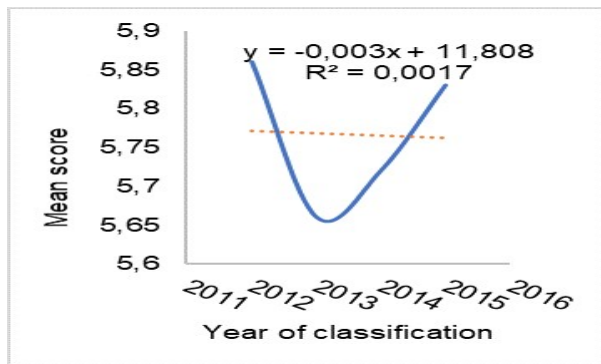


(a)

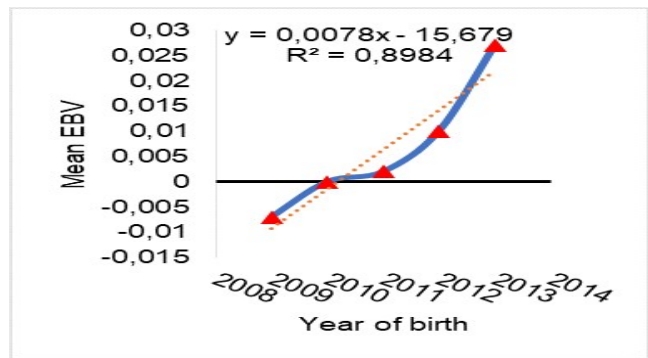


(b)

Fig. 7. (a) Phenotypic (b) genetic trend for front teat placement



(a)

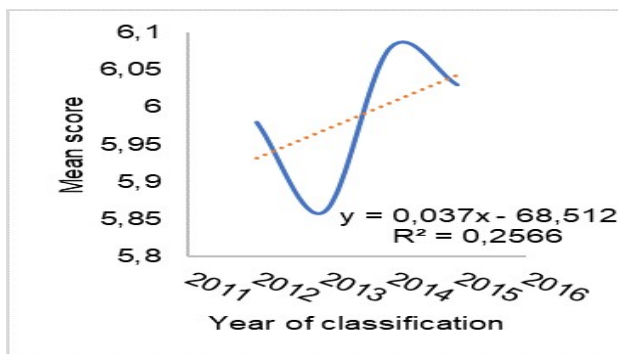


(b)

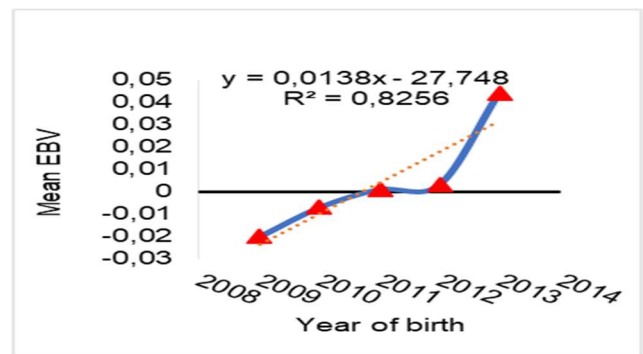
Fig. 8. (a) Phenotypic (b) genetic trend for rear teat placement

In this study, the genetic trend for UD is positive extreme optima for the entire period (Figure 9b). The coefficient of regression determination between the year of birth and the estimated breeding values (EBV) was $R^2 = 0.825$ which implies that the linear regression equation

explains 82% of the udder depth variance. The phenotypic trend for UD was consistent with the genetic trend (Figure 9a) in this study. Therefore, the environmental effects were favorable.



(a)



(b)

Fig. 9. (a) Phenotypic (b) genetic trend for udder depth.

DISCUSSION

Linear classification is based on the evaluation of traits instead of providing opinions about them (Pantelić *et al.*, 2012). In a study for the Holstein cow population in the Czech Republic reported that the average scores ranged from 4.7 for teat length to 5.2 for FUA (Zavadilová & Štápková, 2012). However, in Holstein cows of Brazil, according to research by (Campos *et al.*, 2015) average scores ranged from 4.41 for FTP to 6.69 for udder texture. The results in this study were similar to those reported by (Janković, 2017). In black and white cows in Bulgaria the average scores for FUA, RUH, RTP and UD were (5.33, 6.83, 6.58 and 3.80) respectively, and for angularity the average score was (6.53) (Marinov *et al.*, 2015) which is around the result in this study. Khan and Khan, (2015) concluded that herd, parity, stages of lactation and age of cow at classification were important sources of variation for most linear type traits.

Type traits associated with udder and angularity had lower heritabilities than estimates found in previous studies see (DeGroot *et al.*, 2002; Kadarmideen & Wegmann, 2003; Mikhchi *et al.*, 2013) for a comparison. However, slightly higher heritability value was determined by (Pantelić *et al.*, 2010) for UD (0.16). The heritability estimates for UD, FTP and FUA were 0.23, 0.52 and 0.37 respectively by (DeGroot *et al.*, 2002). However, for the same traits by (Mikhchi *et al.*, 2013) the heritability estimates were 0.32, 0.23 and 0.27 respectively, of Holstein Frisian cows in Iran. In the current study, the heritability estimations for udder traits were also lower than those reported by (Berry *et al.*, 2004; Liu *et al.*, 2014; Bohlouli *et al.*, 2015). (Janković, 2017) reported heritability estimates of 0.11 for FUA and 0.25 for RTL of Holstein Frisian cows in Serbia. In the present study, heritability estimate for angularity was found as 0.10. Slightly lower estimate (0.06 was reported by Mirza *et al.*, (2015), in Nili Ravi buffaloes of Pakistan. In contrast to these findings, very high estimates (0.54) of heritability for angularity were reported by Khan (2009) in Sahiwal cows. Heritability estimates can differ significantly depending on breed, classification system, statistical model. Therefore, comparisons should be made carefully between studies (Němcová *et al.*, 2011). Some of the possible reasons for these different values of heritability coefficients are on-farm conditions, housing, and cow nutrition, i.e. applied management (Pantelić *et al.*, 2010).

Due to the high correlation between two traits, the selection of one trait results in the other trait being genetically modified (Dube *et al.*, 2008). This change may be meaningful, and thus helps to minimize time and resources, but it may also be undesirable. According to (Theron & Mostert, 2004), in South African Holstein cattle, all udder traits have positive genetic trends, except

for teat length and slightly positive trend for UD, and this isn't in line with the results in this study where UD has positive extreme, and FUA, RUH have a negative genetic trend. On the other hand, RTP and FTP have a positive trend similar to those obtained by (Theron & Mostert, 2004; Dube *et al.*, 2008). the genetic trends of some traits may have resulted from selection for increased milk production (Dube *et al.*, 2008). Monitoring the traits of offspring in each generation, and then evaluating the udder traits and the traits of milk across multiple generations will be more reliable.

Conclusions: Genetic trends for udder type traits of Holstein Frisian cows in Serbia show that cows at first calving in the first lactation are becoming higher scores in all udder traits except for fore udder attachment, and possibly rear udder height, in addition to angularity, which generally show negative genetic trend. The phenotypic trends of all udder traits as well as angularity, on the other hand, showed agreement with the genetic trends. The fact that there is nearly the same slope of genetic and phenotypic trends suggests that factors such as management, nutrition, housing have been supportive and promote the expression of genetic change. Exceptions include the placement of rear teats and rear udder height, where the phenotypical trends are incompatible with genetic patterns. Teat lengths are getting longer, and udder teat placements are internal. This suggests that, for an unexplained cause, the concentration of breeders was to increase the teat length. It is possibly because, from the breeder's point of view, the teat length may represent an increase in milk production.

Acknowledgments: The authors are thankful to all the farmers who have collaborated and allowed access to their farms and provided data., and to people who have given their time in this research. They also thank the Ministry of Education, Science and Technological Development of the Republic of Serbia for funding the work under the contract No. 451-03-9/2021-14/200116)

Authors' contributions: HI conducted the research during his PhD studies and prepared the initial draft of the manuscript. RDj, VB and DS conceived the study idea and contributed to the preparation and editing of the manuscript. DJ, ST and TS also sourced and provided data, and collaborated in interpreting the results. All authors have read and approved the finalized manuscript.

Conflict of Interest: The authors of this paper declare that there is no conflict of interest.

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