

## GENETIC TREND OF FUNCTIONAL PRODUCTIVE LIFE IN THE POPULATION OF BLACK AND WHITE CATTLE IN SERBIA

Dragan STANOJEVIĆ<sup>1\*</sup>, Radica DJEDOVIĆ<sup>1</sup>, Vladan BOGDANOVIĆ<sup>1</sup>, Nikola RAGUŽ<sup>2</sup>,  
Denis KUČEVIĆ<sup>3</sup>, Mladen POPOVAC<sup>1</sup>, Petar STOJIĆ<sup>4</sup>, Ljiljana SAMOLOVAC<sup>5</sup>

<sup>1</sup>Department of Animal Science, Faculty of Agriculture, University of Belgrade, Serbia

<sup>2</sup>Faculty of Agriculture, Josip Juraj Strossmayer University of Osijek, Croatia

<sup>3</sup>Department of Animal Science, Faculty of Agriculture, University of Novi Sad, Serbia

<sup>4</sup>Institute PKB Agroekonomik, Serbia

<sup>5</sup>PKB Corporation Belgrade, Serbia

Stanojević D., R. Djedović, V. Bogdanović, N. Raguž, D. Kučević, M. Popovac, P. Stojić, Lj. Samolovac (2018): *Genetic trend of functional productive life in the population of black and white cattle in Serbia.*- Genetika, Vol 50, No.3, 855-862.

This research was conducted with the aim of estimating genetic trend for a functional length of productive life (FLPL) in the population of Black and White cattle in Serbia. Research and bulls genetic evaluation for functional longevity were performed on a set of data provided by Agricultural Corporation Belgrade AD (PKB) which contained data on longevity and origin of 22109 cows out of which 26% records were right-censored. Functional length of productive life (FPLP) represents a time period from the first calving to culling or censoring corrected for milk production. Breeding values were estimated using Weibull method of proportional risks within survival analysis a genetic trend for FLPL was calculated using of a regression analysis. The cows included in the analysis were on average first calved in the age of 809 days and had an average share of 81.9% genes of Holstein Friesian breed. An average length of productive life was 1267 days (41.6 months). Distribution of bull standardised breeding values did not statistically significantly differ from normal distribution. An average standardised breeding value was 99. A slightly positive genetic trend was determined, that is, the length of functional productive life was by selection increased by 0.021 day at an annual level while a reliability of estimated breeding values showed a negative trend.

*Key words:* functional longevity, genetic trend, black and white cattle

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*Corresponding author:* Dragan Stanojević, Department of Animal Science, Faculty of Agriculture, University of Belgrade, Nemanjina 6, 11080 Zemun, Serbia, phone: +38111 4413555, E-mail: [stanojevic@agrif.bg.ac.rs](mailto:stanojevic@agrif.bg.ac.rs)

## INTRODUCTION

Longevity traits represent a key segment from the aspect of an economic dairy production and are highly correlated to the profitability of dairy production (BEAUDEAU *et al.*, 2000). JAIRATH *et al.* (1994) report that the length of productive life is economically important comprising more than 50% economic value of the milk yield traits. Studying the economic value of the traits defined by breeding programme for Holstein Friesian breed in Czech Republic, WOLFOVA *et al.* (2007) observed that when productive life was prolonged by one year per cow the profit increased 74 euros per head annually on average. Longevity traits influence profitability of milk production not so much by increasing the production itself but more through reducing the production costs, primarily due to lower costs of breeding animals for replacement and larger number of animals in later, more profitable lactations as well as of reduced breeding replacement animals (RAGUŽ *et al.*, 2014).

DUCROCQ (1987) suggested two ways of studying longevity: true longevity which represents a cow's ability of not getting culled regardless the culling reasons and a functional longevity which represents cow's ability to avoid involuntary culling or culling not correlated with its own production. The only reason for culling, when considering functional longevity, seems to be low production. Functional longevity has a great effect on profitability of milk production reducing its cost and reducing also the costs of raising replacement animals (FORABOSCO *et al.*, 2006). Today functional longevity is defined as a length of productive life corrected in relation to a level of production in the herd in which the animals realised their production. In the research and genetic evaluation of the traits of longevity, longevity is most often being defined as a length of productive life (LPL). Today length of productive life (LPL) represents the most important functional trait in dairy cattle populations (NAJAFABADI *et al.*, 2016).

The aim of the research conducted is to estimate breeding values for the traits of functional longevity in bulls used for artificial insemination in the population of Black and White cattle in Serbia. On the basis of estimated breeding values a genetic trend for functional longevity was calculated.

## MATERIALS AND METHODS

The research and genetic evaluation bulls for functional longevity was carried out on the set of data provided by Agricultural Corporation Belgrade AD (PKB). Analysed dairy cattle population was developed in the early 70's by gene flow from imported Holstein-Frisian breed to Eastern-Frisian breed that was raised at PKB farms. Longevity was evaluated through functional length of productive life (FPLP). Functional length of productive life (FPLP) represents a time period from calving to culling or censoring, corrected for milk production. Breeding values were estimated using Weibull method of proportional risks within the survival analysis.

During genetic evolution of functional length of productive life a set of data which included records on production and longevity of 22109 black and white cows out of which 26% were animals with unknown values for the traits of length of productive life (censored records) was used. The animals were first calved in the period from 1987 to 2012 in the age of 600 to 1200 days and realised 8 lactations at maximum. The estimation of breeding values was performed by help of Survival Kit V6 software (DUCROCQ *et al.*, 2010) and relationship matrix created for a sire model which contributes to more precise estimation of breeding value. A

method of proportional risks was used in the analysis, while the model itself had a following form:

$\lambda(t) = \lambda_0(t) \exp(\text{year} + \text{season} + \text{rpm} + \text{farm} + \text{age} + \text{lactation} + \text{shfg} + \text{sire})$ , where:

$\lambda(t)$ - is the function of risk (immediate probability of culling) for a certain cow in the moment  $t$ ;

$\lambda_0(t)$ - Weibull primary function of risk with scalar parameter  $\lambda$  and shape parameter  $\rho$ ;

year- fixed time-dependent effect of the year of calving (1987-2012);

season- fixed time-dependent effect of the season of calving (the year is divided into 4 seasons: spring - March, April, May; summer- June, July, August; autumn- September, October, November; winter- December, January, February).

rpm- fixed time-dependent effect of relative dairy production within the herd from which the animal originates expressed in standard deviations (the effect was formed in such a way so that a total quantity of milk in given lactation was corrected to the quantity of milk which the animal realised in the first lactation and regarded as relative yield of milk in relation to the average production on farm from which the given animal originates. The differences which occurred in this way are expressed as the number of standard deviations below or above the average of the farm on which the animal was realising its production: I group  $x < -1.5$  SD, II group  $-1.5$  SD  $< x < -1$  SD, III group  $-1$  SD  $< x < -0.5$  SD, IV group  $-0.5$  SD  $< x < -0.2$  SD, V group  $-0.2$  SD  $< x < 0.2$  SD, VI group  $0.2$  SD  $< x < 0.5$  SD, VII group  $0.5$  SD  $< x < 1$  SD, VIII group  $1$  SD  $< x < 1.5$  SD, IX group  $x > 1.5$  SD)

farm- fixed time-independent effect of farm on which the animal was realising its production (1-7);

age- fixed time-independent effect of the age of the animal at first calving (I group – age at first calving less than 660 days, II group- age at first calving between 661 and 720 days, III group- age at first calving between 721 and 780 days, IV group- age at first calving between 781 and 840 days, V group- age at first calving between 841 and 900 days, VI group- age at first calving between 901 and 960 days, VII group- age at first calving between 961 and 1020 days, VIII group- age at first calving between 1021 and 1080 days, IX group- age at first calving between 1081 and 1140 days, X group- age at first calving over 1141 days);

lactation- fixed time-dependent effect of lactation (lactations from 1 to 8);

shfg- fixed time-independent effect of the share of genes of Holstein and Friesian breed (I group- animals with 0 to 50% share of genes of Holstein Friesian breed; II group- animals with 51 to 75% share of genes of Holstein Friesian breed; III group- animals with 76 to 87.5% share of genes of Holstein Friesian breed; IV group- animals with 88 to 93.75 share of genes of Holstein Friesian breed; V group- animals with more than 93.5% share of genes of Holstein Friesian breed)

sire- random time-independent effect of sire following a multivariate normal distribution.

During calculating the breeding values for the traits of longevity the variances determined by means of mentioned model within the method of proportional risks were used. Standardised breeding values were calculated by comparing the risks of the bulls with the risk and a standard deviation of bulls belonging to the base group according to the following statement:

$$EBV = \frac{(\text{estimated\_risk} - a) * (-12)}{SD} + 100, \text{ where: EBV- is a breeding value;}$$

Estimated risk- culling risk determined for a given bull on the basis of data on the traits of longevity of their daughters by means of Weibull model of proportional risks;

a- an average culling risk for the bulls of the base group;

SD- standard deviation of estimated risks of the bulls from the base group.

The base group of bulls was composed of the bulls born from 1990 to 1994.

Reliability of estimated breeding values for the traits of longevity was calculated on the basis of a following formula suggested by DUCROCQ (1999):

$$R = \frac{n}{n + \frac{4 - h^2}{h^2}}$$

where:

R- is a reliability of estimated breeding value;

n- number of non-censored daughters for each bull;

$h^2$ - estimated heritability of longevity trait.

Genetic trend for functional length of productive life was calculated using regression analysis in which the bull's year of birth was regarded as an independent variable while the culling risk for each bull was regarded as a dependent variable.

#### RESULTS AND DISCUSSION

The cows used in the analysis were first calved in the average age of 809 days (26.6 months). The cows which comprised incomplete records were calved for the first time somewhat earlier in the age of 770 days (25.3 months), while the animals whose value for the traits of longevity was known calved in the age of 823 days (27.05 months) on average. An average yield of the genes of Holstein Friesian breed in examined population was 81.9%. The share of genes of Holstein Friesian breed was larger in the set of data which contained only incomplete data accounting for 92.9%, while in complete data it accounted for 78.1%.

Table 1 shows the average value and the measures of variability of the length of productive life.

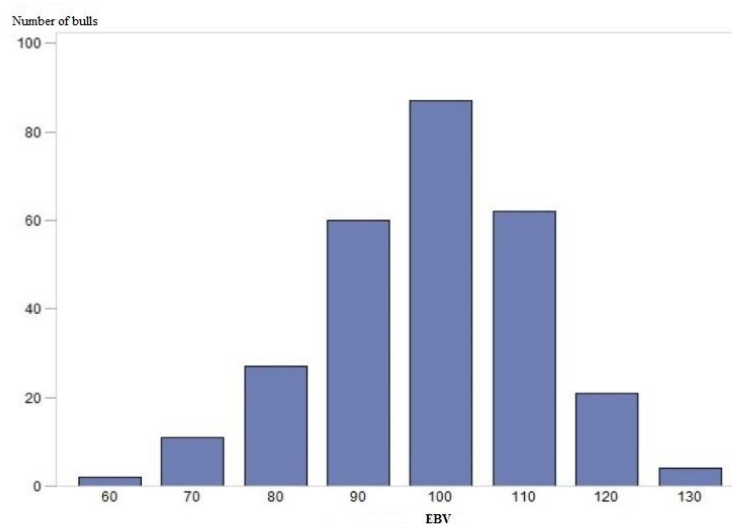
Table 1. Descriptive statistical analysis for the length of productive life (LPL)

Trait	$\bar{x}$	SD	CV (%)	min	max
LPL- all data (days)	1267	744.37	58.77	14	4271
LPL- complete data (days)	1300	763.81	58.76	14	3939
LPL- censored data (days)	1170	676.27	57.79	41	4271

Lower values of the length of productive life, both in complete and censored data were determined by RAGUŽ (2012) in the population of Holstein cows in Croatia, POTOČNIK *et al.* (2011) in the population of Holstein cows in Slovenia, as well as M'HAMDI *et al.* (2010) who analysed the same trait in the population of Holstein cows in Marocco. Similar values for the length of productive life were determined by MÉSZÁROS *et al.* (2008) in the population of Pinzgauer cow in Slovakia, while higher values for the length of analysed trait were determined

by CASSANDRO *et al.* (1999) studying the genetic parameters of the traits of longevity in the population of Brown cows in Italy.

Bulls estimated breeding values are standardised by using the average breeding values and standard deviations of bulls in the base group. Distribution of bulls standardised breeding values was statistically no significantly different from normal distribution, what was confirmed by Kolmogorov-Smirnov test ( $P>0.05$ ). A mean standardised breeding value was 99, while for the largest number of animals the breeding value (modulus) was 101. Distribution of bulls standardised breeding values is shown in graph 1.

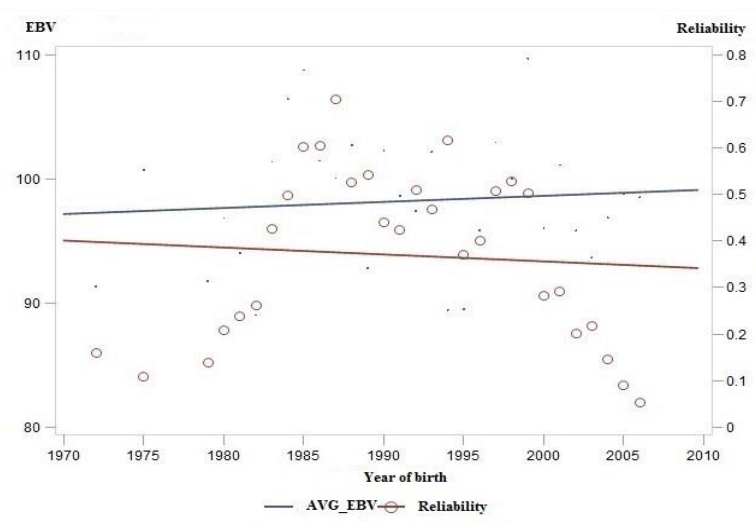


Graph 1. Distribution of standardised breeding values of bulls of Black and White breed and Holstein breed

The average reliability of estimated breeding values accounted for 0.42 with standard deviation of 0.26. Lower reliability of estimated breeding values were determined by RAGUŽ (2012) in the population of Holstein cows in Croatia, while a higher reliability of the estimated breeding values was determined by VOLLEMA *et al.* (2000). The average reliability of estimated breeding values was determined in the bulls which had 27 daughters culled. The highest reliability of estimated breeding value was determined in the bulls which had the largest number of daughters culled (more than 230 cows per bull) and those bulls were born in the period from 1985 to 1999. Reliability in this group of bulls was over 0.85. The highest reliability of estimated breeding value (0.92) was determined for the bull which had 435 daughters culled.

Genetic trend was calculated by means of a regression analysis where the year of birth of bull was regarded as an independent variable while the dependent variable was represented by the bull estimated risk of culling. A slightly positive genetic trend was determined, that is, by selection the length of productive life was increased ( $b=0.021$ ). Similarly, a slight rising trend

was observed also by RAGUŽ (2012) in the population of Holstein cows in Croatia. Genetic trend, as well as the trend which shows the reliability of the estimated breeding values is shown in graph 2.



Graph 2. Genetic trend of the bulls of Black and White and Holstein breeds for the length of productive life

Reliability of estimated breeding values had a negative trend in relation to the age of bulls, i.e. younger bulls had lower reliability of estimated breeding value. This trend is an expected one since younger bulls have smaller number of daughters culled therefore the reliability of the estimated breeding values is lower as well.

#### CONCLUSION

Notwithstanding the traits of longevity not being included in a selection programme a slightly positive genetic trend in functional length of productive life was determined in the examined population. This situation can both be a consequence of indirect selection since the traits of longevity were in positive genetic correlation with some of the traits, such as the milk yield, included in a breeding programme and a consequence of the use of semen of bulls from other populations in which the selection is performed on the traits of longevity. In a forthcoming period it will be necessary to devote greater attention to the traits of longevity and include them into breeding programmes in order to obtain more significant genetic improvement of these traits what may bring better economic results in milk production as well.

#### ACKNOWLEDGEMENTS

This research was supported by the Serbian Ministry of Education and Science, grant TR31086.

Received, September 26<sup>th</sup>, 2017

Accepted May 15<sup>th</sup>, 2018

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## GENETSKI TREND FUNKCIONALNOG PRODUKTIVNOG ŽIVOTA U POPULACIJI CRNO BELIH GOVEDA U SRBIJI

Dragan STANOJEVIĆ<sup>1</sup>, Radica DJEDOVIĆ<sup>1</sup>, Vladan BOGDANOVIĆ<sup>1</sup>, Nikola RAGUŽ<sup>2</sup>,  
Denis Kučević<sup>3</sup>, Mladen POPOVAC<sup>1</sup>, Petar STOJIC<sup>4</sup>, Ljiljana SAMOLOVAC<sup>5</sup>

<sup>1</sup>Institut za zootehniku, Poljoprivredni fakultet Zemun, Univerzitet u Beogradu, Srbija

<sup>2</sup>Poljoprivredni fakultet, Univerzitet Josip Juraj Strossmayer Osijek, Hrvatska

<sup>3</sup>Departman za stočarstvo, Poljoprivredni fakultet, Univerzitet u Novom Sadu, Srbija

<sup>4</sup>Institut PKB Agroekonomik, Srbija

<sup>5</sup>PKB, Beograd, Srbija

### Izvod

Istraživanje je sprovedeno sa ciljem da se proceni genetski trend za trajanje funkcionalnog produktivnog života (FLPL) u populaciji crno belih goveda u Srbiji. Ispitivanje i genetsko vrednovanje bikova za funkcionalnu dugovečnost izvršeno je na setu podataka koji je ustupljen od strane Poljoprivredne korporacije Beograd AD (PKB), koji je sadržao podatke o dugovečnosti i poreklu za 22109 krava, od čega su 26% činili cenzurisani zapisi. Funkcionalno trajanje produktivnog života (FPLP) predstavlja vremenski period od teljenja do izlučenja ili cenzurisanja, korigovan za proizvodnju mleka. Priplodne vrednosti procenjene su primenom Weibull-ovog metoda proporcionalnih rizika u okviru analize preživljavanja, dok je genetski trend za FLPL izračunat primenom regeresijske analize. Grla obuhvaćena analizom prvi put su se telila u prosečnom uzrastu od 809 dana i mala su prosečan udeo od 81,9 % gena holštajn frizijske rase. Prosečno trajanje produktivnog života iznosilo je 1267 dana (41,6 meseci). Distribucija standardizovanih priplodnih vrednosti bikova nije se statistički značajno razlikovala od normalne distribucije. Prosečna standarizovana priplodna vrednost iznosila je 99. Utvrđen je blago pozitivan genetski trend, odnosno selekcijom je dužina funkcionalnog produktivnog života povećana za 0,021 dan na godišnjem nivou, dok je pouzdanost procenjenih priplodnih vrednosti imala negativan trend.

Priljeno 26.IX.2017.

Odobreno 15. V. 2018.