

The effect of time elapsed from milking to scoring on udder linear scores and estimation of genetic parameters

Ante Kasap^{1*}, Dubravko Škorput¹, Dragomir Kompan², Gregor Gorjanc²,
Boro Mioč¹, and Klemen Potočnik²

¹Department of Animal Science and Technology, Faculty of Agriculture, University of Zagreb, Zagreb, Croatia

²Animal Science Department, Biotechnical Faculty, University of Ljubljana, Domžale, Slovenia

KASAP, A., D. ŠKORPUT, D. KOMPAN, G. GORJANC, B. MIOČ, K. POTOČNIK:
The effect of time elapsed from milking to scoring on udder linear scores and estimation of genetic parameters. Vet. arhiv 84, 9-18, 2014.

ABSTRACT

The study was conducted on 51,154 Holstein primiparous cows. The purpose of the study was to estimate the impact of time elapsed from last milking until scoring on the properties of udder conformation traits (fore udder attachment, rear udder height, rear udder width, udder depth, and central ligament). The purpose was also to consider the benefits of including this effect in statistical models for estimation of genetic parameters in dairy cattle. A significant ($P < 0.001$) positive linear relationship between scores of udder traits and the time of the scoring was determined. Rear udder height ($b = 0.088$) and rear udder width ($b = 0.091$) were affected the most, with the prolongation of time of scoring regarding previous milking. The investigated effect only affected the residual component of variance. Other components of variance did not change considerably when the time from milking to scoring was fitted into a basic statistical model. Estimated heritabilities ranged from 0.15 to 0.27. Slightly higher estimates of heritabilities for all traits, except for the central ligamentum, were determined when this effect was fitted into the model. Udder depth was found to be in strong negative genetic correlation with fore udder attachment ($r = -0.436$). An almost negligible negative genetic correlation between udder depth and rear udder width was determined ($r = -0.086$). Genetic correlations between all other traits were positive and low to moderate ($r = 0.15 - 0.54$). The investigated effect did not noticeably affect estimates of genetic correlations between udder conformation traits.

Key words: udder conformation traits, time interval, model, genetic evaluation

Introduction

Udder conformation traits are usually only recorded once during a cow's lifetime, which makes them relatively cheap in comparison to other traits that are routinely recorded in dairy cattle herds (DE HAAS et al., 2007).

*Corresponding author:

Dr. Ante Kasap, Young Researcher, Department of Animal Science and Technology, Faculty of Agriculture, University of Zagreb, Svetošimunska 25, 10000 Zagreb, Croatia, Phone: +385 1 239 3950; Fax: +385 1 239 3901; E-mail: akasap@agr.hr

Inconsistency in recording systems, as well as recommended statistical models, for genetic evaluation of udder conformation traits sometimes considerably hampers comparison of results from different sources. In order to overcome this problem, greater harmonization in analytical approaches has been proposed (ICAR, 2011). Succinctly, their recommendations are that the scoring scale must cover the expected biological extremes of the population in the country of assessment, classifiers should not make adjustments of scores on the field and all data should be corrected for influencing factors, such as: age, stage of lactation and season by statistical model.

Besides these effects, the shape and location of the udder considerably depend on the amounts of milk in the udder at the moment of scoring (BERRY et al., 2004; YAKUBU, 2011; DENG et al., 2012). In field conditions, we do not have this information, except immediately after milking, and therefore, we are not able to correct udder scores for this effect by a statistical model. On the other hand, daily milk yield is highly correlated with the time progression from the previous milking (FRIGGENS and RASMUSSEN, 2001). These facts imply that the information regarding time elapsed from last milking to scoring can be effectively utilized for the correction of the phenotypes for udder traits.

The purpose of this study was to highlight the importance of time elapsed from milking to scoring on the properties of udder conformation traits and to point out irregularities that may occur if udders are evaluated in different post milking periods. The purpose was also to consider the benefits of including this effect in statistical models for estimation of genetic parameters in dairy cattle.

Materials and methods

All data used in this research were provided by the Agricultural Institute of Slovenia. Cows from 2,925 herds were scored by 73 trained classifiers, using a nine-point (1 to 9) linear scoring range. The following udder linear traits were analyzed: fore udder attachment (FUA), rear udder height (RUH), rear udder width (RUW), udder depth (UD), and central ligament (CL). To be included in statistical analysis, cows were required to have scores for all investigated traits and a valid time of scoring. Time elapsed from milking to scoring (TMS) was recorded in minutes, but for the purpose of statistical analysis this information was rounded up or down to hours. Animals scored by classifiers who had less than 100 scorings were excluded from statistical analysis. In order to obtain a better distribution of records in some fixed effect classes, some adjacent classes were merged. Age at calving ranged from 18 to 43 months, but those younger than 21 months and older than 40 months were merged into a class of 21 months and 40 months, respectively. Cows scored in the first month of lactation were included in the statistical analysis as cows scored in the second month. Cows scored after seven hours from previous milking were considered to be scored exactly seven hours from the previous milking. The season was

defined as a month within a year and there were 78 seasons in total, after some adjacent seasons were merged. After data editing, a total of 50,893 records were included in the statistical analysis.

Pedigrees were created using all the available relationship information between phenotyped animals and their ancestors. After pruning of non-informative animals from the pedigree, 99,179 animals were included in the additive relationship matrix. Data editing, descriptive statistics and preliminary statistical analysis, as well as pedigree preparation, were performed using the SAS statistical package (SAS, 9.2).

Components of variance and genetic parameters were estimated with the VCE 6 program (KOVAČ et al., 2002). All calculations were first performed by a single trait animal model used in the routine genetic evaluation of primiparous cows in Slovenia. Afterwards, calculations were repeated by fitting TMS into the same model. Finally, in order to obtain genetic correlations, successive bivariate runs for all mutual combinations of traits were performed. The same model was applied for all udder traits. The scalar notation of the full model was:

$$y_{ijklmnop} = \mu + C_i * Y_j + S_k + b_r A_l + b_m L_m + b_n T_n + h_o + a_p + e_{ijklmnop}$$

where $y_{ijklmnop}$ is the udder trait score on animal p, C_i is the fixed effect of the i^{th} classifier, Y_j is the fixed effect of the j^{th} year of scoring, S_k is the fixed effect of the k^{th} season of calving, A_l is the age of first calving in months, L_m is the lactation stage in months, T_n is the time from milking to scoring in hours, b_r , b_m , and b_n are corresponding regression parameters; h_o is the random effect of the o^{th} herd, a_p is the random additive-genetic effect of the p^{th} animal, and $e_{ijklmnop}$ is random residual.

Results

A short description of linear scores, overall unadjusted means and measures of variability of the studied udder traits is presented in Table 1. The determined means for all traits exceeded 5 (expected mean of the linear scoring range). The most variable among the studied traits were fore udder attachment and central ligament.

The mean scores and measures of variability of udder traits, according to different time of scoring, are presented in Table 2. The progression of time regarding the previous milking was followed by the increase in the determined means. According to this result, stronger fore udder attachment, higher and wider rear udder, shallower udder and better expressed central ligament were expected for udders scored later, in comparison to those scored just after milking. The opposite direction of changes was determined for variability.

The results of multiple regression analysis are presented in Table 3. All predictors significantly affected the scores of udder conformation traits ($P < 0.001$). A positive linear relationship between scores and time elapsed from milking to scoring was determined.

The contribution of the TMS (b_3) in the total phenotype variability was greater compared to other covariates in the model. The determined coefficients of linear regression for this effect suggest the expected changes of the scores, if the time of the scoring is changed by one hour. Therefore, the expected difference in score for some of the investigated traits may reach almost the entire score, if the scoring time differs by 10 hours.

Table 1. Descriptive statistics for udder linear traits (n = 50 893)

Linear trait	Score description		\bar{x}	SD	CV (%)
	1	9			
FUA	week	strong	5.44	1.37	25.18
RUH	low	high	5.68	1.17	20.59
RUW	narrow	wide	5.44	1.24	22.79
UD	deep	shallow	5.81	1.22	20.99
CL	broken	strong	5.55	1.43	25.76

\bar{x} - Unadjusted mean; SD - Standard deviation; CV - Coefficient of variability FUA - fore udder attachment; RUH - rear udder height, RUW - rear udder width; UD - udder depth; CL - central ligamentum;

Table 2. Unadjusted means and standard deviations of udder scores obtained in different post milking periods

TMS	N	%	FUA	RUH	RUW	UD	CL
1	7120	14.0	5.30 ± 1.38	5.46 ± 1.19	5.20 ± 1.29	5.78 ± 1.29	5.50 ± 1.44
2	7996	15.7	5.31 ± 1.39	5.56 ± 1.17	5.24 ± 1.26	5.73 ± 1.23	5.52 ± 1.44
3	9924	19.5	5.34 ± 1.37	5.62 ± 1.17	5.33 ± 1.22	5.79 ± 1.23	5.48 ± 1.43
4	9039	17.8	5.38 ± 1.39	5.67 ± 1.15	5.42 ± 1.19	5.82 ± 1.21	5.52 ± 1.45
5	7116	14.0	5.55 ± 1.36	5.81 ± 1.16	5.59 ± 1.20	5.89 ± 1.21	5.62 ± 1.43
6	5366	10.5	5.66 ± 1.33	5.84 ± 1.14	5.69 ± 1.19	5.89 ± 1.15	5.64 ± 1.42
7	4332	8.5	5.85 ± 1.23	6.02 ± 1.06	5.89 ± 1.14	5.84 ± 1.11	5.65 ± 1.35

TMS - time from last milking to scoring (hours); FUA - fore udder attachment; RUH - rear udder height, RUW - rear udder width; UD - udder depth; CL - central ligamentum;

The impact of the studied effect was presented graphically (Fig. 1) and for this purpose, another two covariates from multiple regression analysis were treated as a constant (averages of lactation stage and the age at first calving). Rear udder height and rear udder width were found to be the most affected by scoring time.

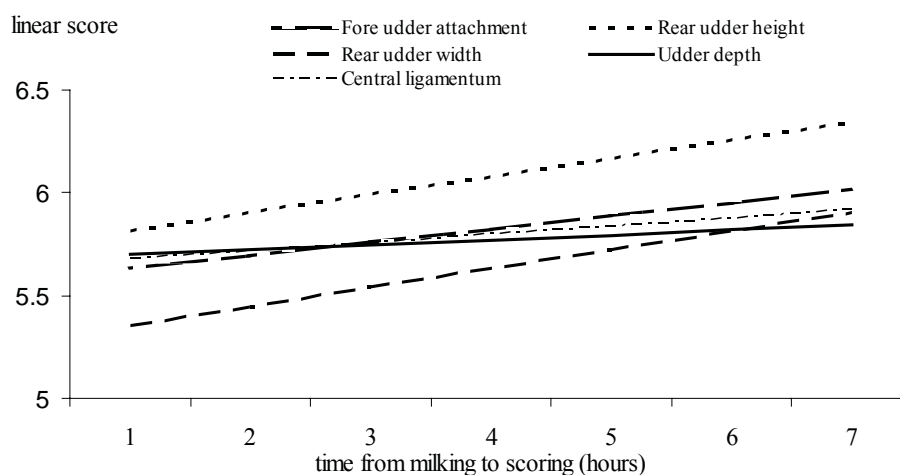


Fig. 1. Linear regression of udder scores on time from last milking to scoring

The estimated components of the variances obtained with the basic and augmented (TMS) single trait animal models are presented in Table 4. As expected, the total phenotype variance slightly decreased when the effect of period from last milking to scoring was fitted into a fixed part of the statistical model (except for central ligamentum). It was due to the reduction of the residual component of variance. The other random effects were practically unaffected by the time of scoring. Even though the additive component was not changed, including this effect in the model decreased the estimates of the heritabilities (Table 4). The estimates were low for all studied traits. The most heritable among investigated traits was found to be udder depth.

Table 3. Estimated parameters of multiple linear regression

Trait	b_0	b_1	SL	b_2	SL	b_3	SL
FUA	4.611	0.028	P<0.001	0.038	P<0.001	0.064	P<0.001
RUH	6.042	-0.001	P<0.001	-0.048	P<0.001	0.088	P<0.001
RUW	5.010	0.002	P<0.001	0.034	P<0.001	0.091	P<0.001
UD	6.400	-0.027	P<0.001	-0.004	P<0.001	0.024	P<0.001
CD	6.801	-0.042	P<0.001	-0.012	P<0.001	0.042	P<0.001

FUA - fore udder attachment; RUH - rear udder height, RUW - rear udder width; UD - udder depth; CL - central ligamentum; b_0 - intercept; b_1 , b_2 , b_3 - regression parameters for age at calving (months); stage of lactation (months); time from last milking to scoring (hours); SL - significance level.

Table 4. Variance components and heritability estimates for udder traits

Trait	M1					M1 + TMS				
	σ_a^2	σ_h^2	σ_e^2	σ_p^2	h_a^2	σ_a^2	σ_h^2	σ_e^2	σ_p^2	h_a^2
FUA	0.30	0.19	1.25	1.74	0.17	0.30	0.18	1.23	1.71	0.18
RUH	0.22	0.08	0.90	1.20	0.18	0.22	0.08	0.88	1.18	0.19
RUW	0.21	0.24	0.94	1.39	0.15	0.22	0.23	0.91	1.36	0.16
UD	0.34	0.11	0.82	1.27	0.26	0.34	0.10	0.80	1.24	0.27
CL	0.28	0.05	1.52	1.85	0.15	0.28	0.05	1.52	1.85	0.15

FUA - fore udder attachment; RUH - rear udder height, RUW - rear udder width; UD - udder depth; CL - central ligamentum; σ_a^2 ; σ_h^2 ; σ_e^2 ; σ_p^2 - variance components (additive genetic; herd; residual. total phenotype); h_a^2 - direct heritability; M1 - basic model; M1+ TMS - basic model augmented for time from milking to scoring effect.

Table 5. Genetic correlations among udder traits obtained with basic statistical model (below diagonal) and model augmented with TMS (above diagonal).

Traits	FUA	RUH	RUW	UD	CL
FUA	-	0.36	0.34	-0.44	0.15
RUH	0.35	-	0.54	0.44	0.26
RUW	0.33	0.53	-	-0.09	0.24
UD	-0.44	0.45	-0.08	-	0.29
CL	0.14	0.25	0.22	0.29	-

FUA - fore udder attachment; RUH - rear udder height, RUW - rear udder width; UD - udder depth; CL - central ligamentum.

The estimates of the genetic correlations were not considerably influenced by scoring time (Table 5). An almost negligible negative correlation was determined between udder depth and rear udder width. A considerable negative genetic correlation was determined between udder depth and fore udder attachment. Low to moderate positive genetic correlations were found between other udder traits. Rear udder width and rear udder depth were found to be the most genetically correlated among the investigated traits.

Discussion

The means and measures of variability from this study are consistent with many previous reports for primiparous Holstein cows (SCHAEFFER et al., 1985; MISZTAL et al., 1992; NĚMCOVA et al., 2011; ZAVADILOVÁ and ŠTÍPKOVÁ, 2012). The higher overall means determined in dairy herds are due to the selective choice of heifers for replacement, based upon desirable udder conformation. Also, the evaluation criteria (referent middle scores) are usually pre-determined and often do not properly follow the selection

progress. The high variability of the fore udder attachment is additionally attributed to recommendations for its assessment (DE JONG and HARBERS, 2002).

The udder conformation traits, i.e. their scores, depend on the amounts of milk produced at the time of scoring (BERRY et al., 2004; YAKUBU, 2011; DENG et al., 2012). In comparison to an empty udder, that looks like an empty hanging bag, a full or semi-full udder acquires a characteristic form and position, which make it suitable and convenient for assessment. These claims are supported by the lower variability of udder conformation traits scored later after milking. Furthermore, the linear relationship determined between udder scores and time elapsed from milking to scoring suggests a certain bias in scoring. Accordingly, the underestimation of udders can be expected that are scored earlier simply because they are empty, and an overestimation (over-score) of udders that are scored later. The results regarding rear udder width and rear udder height were consistent with our expectations, because the udder expands under milk pressure, and it is automatically scored as wider and higher. On the other hand, the results for udder depth and fore udder attachment were somewhat surprising at first. We expected a deeper udder and consequently a weaker fore udder attachment under increased amounts of milk, but the results of this study indicated a different appearance. This phenomenon may be simplistically explained and visualized by imagining a empty hanging bag in contrast to a bag completely filled with water. The tension of the udder wall increases with inflowing milk but the udder floor is not actually lowered. Furthermore, the udder is supported by strong suspensory ligaments, due to being filled with milk, and actually just expands and spreads forward, which leaves the impression that it is firmly attached to the abdominal wall.

According to our expectations, the residual component of the variance decreased while the other variance components did not change. The heritabilities estimated in our study were low and very consistent with those reported by WIGGANS et al. (2004) and MISZTAL et al. (1992), and considerably lower than those reported by DE GROOT et al. (2004). Comparisons of heritabilities derived from different sources are always tenuous, due to the different analytical approaches applied in the studies. Neglecting important sources of variation in statistical analysis seriously infringes estimates. This is usually manifested in overestimation of additive genetic effects and consequently higher heritabilities. Heritabilities from models compared within our study differed negligibly and only due to the reduced residual component of variance. Udder depth was the most heritable among the investigated traits. Estimated heritabilities indicate the rate of expected change when selection is performed for only one trait, and from that point of view udder depth is considered to be the most appropriate for efficient direct selection.

If selection is performed simultaneously for more traits, genetic correlations should always be considered in detail and selection pressure should be carefully balanced

between traits. In our study, a considerable negative genetic correlation was determined only between udder depth and fore udder attachment (-0.436). This implies that selection targeted on only one trait could considerably infringe others in a genetic sense. Besides the almost negligible negative correlation between udder depth and rear udder width, all the other udder traits were positively correlated. This indicates that it is possible to expect collateral selection progress for all traits, regardless of the choice of the trait we want to favor by selection. Estimated genetic correlations between the compared models did not differ considerably, which was somewhat expected after finding equal additive genetic variances and their ratios in single-trait analysis.

Although the results of this study clearly show that the time elapsed from milking to scoring represents a significant contribution to the total variability of udder conformation traits (scores), fitting this effect into the model for genetic evaluation of udder conformation traits did not affect the estimation of genetic parameters. It is a well known fact that predictions of breeding values are more sensitive to environmental effects, in comparison to estimates of variance components. By neglecting the effect of time elapsed from milking to scoring in the prediction of breeding values, phenotype deviations in animals scored immediately after milking could be underestimated in comparison to animals scored later. Consequently, not only the animals that are directly scored, but also those that are related to these, are given biased predictions of breeding values. One way to overcome this problem is to evaluate all the animals at the same time and preferably just before milking. However, it is hard to implement this in field conditions, which impose the necessity of including the effect of time elapsed from milking to scoring in statistical models when considering udder traits. Further studies will be conducted to investigate this in detail, by correlating breeding values from a model with and without this effect, as well as decomposing breeding values by the source of information.

Conclusions

Time from milking to scoring significantly affected scores of investigated udder traits. Greater accuracy is expected when scoring full rather than empty udders, because only full udders acquire their characteristic form and position. It would be optimal if all animals could be scored at the same time in relation to the previous milking. Since this practice is hard to implement in field conditions, correction for the effect of time elapsed from last milking to scoring is required in statistical models for the analysis of udder conformation traits.

References

- BERRY, D. P., F. BUCKLEY, P. DILLON, R. D. EVANS, R. F. VEERKAMP (2004): Genetic relationships among linear type traits, milk yield, body weight, fertility and somatic cell count in primiparous dairy cows. *Irish J. Agr. Food Res.* 43, 161-176.

A. Kasap et al.: Effect of time elapsed from milking to scoring on udder linear scores and estimation of genetic parameters

- DE GROOT, B. J., J. F. KEOWN, L. D. VAN VLECK, E. L. MAROTZ (2002): Genetic parameters and responses of linear type, yield traits, and somatic cell scores to divergent selection for predicted transmitting ability for type in Holsteins. *J. Dairy Sci.* 85, 1578-1585.
- DE HAAS, Y., L. K. G. JANSSE, H. N. KADARMIDEEN (2007): Genetic and phenotypic parameters for conformation and yield traits in three dairy cattle breed. *J. Anim. Breed. Genet.* 124, 12-19.
- DE JONG, G., A. G. F. HARBERS (2002): Determining changes in definition of conformation traits and effects on international evaluations. *Interbull Bull.* 29, 39-42.
- DENG, M. P., T. M. BADRI, M. ATTA, M. E. HAMAD (2012): Relationship between udder dimensions and milk yield of Kenana × Friesian crossbred cows. *Res. Opin. Anim. Vet. Sci.* 2, 49-54.
- FRIGGENS, N. C., M. D. RASMUSSEN (2001): Milk quality assessment in automatic milking systems: Accounting for the effects of variable intervals between milking on milk composition. *Livest. Prod. Sci.* 73, 45-54.
- ICAR (2011): Guidelines on conformation recording methods in dairy cattle. Guidelines approved by the general assembly of 37th ICAR International agreement of recording practices, 31 May - 4 June 2010, Riga, Latvia, pp. 197-219.
- KOVAČ, M., E. GROENEVELD, L. GARCIA CORTES (2002): VCE-6. a package for the estimation of dispersion parameters. Proceedings of the 7th World Congress on Genetics Applied to Livestock Production. 19-23 August, Montpellier, France, pp. 741-742.
- MISZTAL, I., T. J. LAWLOR, T. H. SHORT, P.M. VAN RADEN (1992): Multiple-trait estimation of variance components of yield and type traits using an animal model. *J. Dairy Sci.* 75, 544-551.
- NĚMCOVA, E., M. ŠTÍPKOVA, L. ZAVADILOVA (2011): Genetic parameters for linear type traits in Czech Holstein cattle. *Czech. J. Anim. Sci.* 56, 157-162.
- SAS Inst. Inc. (2009): The SAS System for Windows. Version 9.2. Cary, NC. SAS Institute.
- SCHAEFFER, G. B., W. E. VINSON, R. E. PEARSON, R. G. LONG (1985): Genetic and phenotypic relationships among type traits. *J. Dairy Sci.* 68, 2984-2988.
- WIGGANS, G. R., N. GENGLER, J. R. WRIGHT (2004): Type trait (co)variance components for five dairy breeds. *J. Dairy Sci.* 87, 2324-2330.
- YAKUBU, A. (2011): Path analysis of conformation traits and milk yield of Bunaji cows in smallholder's herds in Nigeria. *Agr. Trop. Subtrop.* 44, 152-157.
- ZAVADILOVÁ, L., M. ŠTÍPKOVÁ (2012): Genetic correlations between longevity and conformation traits in the Czech Holstein population. *Czech J. Anim. Sci.* 57, 125-136.

Received: 19 December 2012

Accepted: 10 July 2013

KASAP, A., D. ŠKORPUT, D. KOMPAN, G. GORJANC, B. MIOČ, K. POTOČNIK:
Utjecaj vremena proteklog od posljednje mužnje do ocjenjivanja na ocjene linearnih svojstava vimena i procjenu genetskih pokazatelja. Vet. arhiv 84, 9-18, 2014.

SAŽETAK

Istraživanje je provedeno na 51154 krava holštajn-frizijske pasmine. Cilj je bio istražiti utjecaj vremena proteklog od posljednje mužnje do ocjenjivanja na linearne ocjene vimena (vezanost prednjeg vimena, visinu stražnjeg vimena, širinu stražnjeg vimena, dubinu vimena i izraženost centralnog ligamenta). Cilj je također bio razmotriti prednosti uključivanja spomenutog utjecaja u statistički model za procjenu genetskih pokazatelja. Preliminarnom analizom su utvrđene veće prosječne ocjene svih svojstava koja su ocijenjena kasnije u odnosu na prethodnu mužnju. Utvrđena je statistički značajna ($P < 0,001$) linearna regresija svih ocjena vimena na vremenski interval između mužnje i ocjenjivanja. Vrijeme proteklo od mužnje do ocjenjivanja najviše je utjecalo na ocjene visine ($b = 0,088$) i širine ($b = 0,091$) vimena. Uključivanjem spomenutog učinka u statistički model za genetsko vrednovanje životinja smanjila se rezidualna varijanca dok se ostale komponente varijance nisu značajno promijenile. Procijenjeni su heritabiliteti u rasponu od 0,15 do 0,27. Heritabiliteti procijenjeni proširenim modelom bili su veći za sva istraživana svojstva osim za centralni ligament. Utvrđena je značajna negativna genetska korelacija dubine vimena s vezanošću prednjeg vimena ($r = -0,436$) te gotovo zanemariva ($r = -0,086$) negativna genetska korelacija dubine vimena sa širinom stražnjeg vimena. Ostala istraživana svojstva bila su pozitivno genetski korelirana ($r = 0,15 - 0,54$). Istraživani učinak nije značajno utjecao na procjene genetskih korelacija.

Ključne riječi: konformacijska svojstva vimena, vremenski interval, model, genetsko vrednovanje
