Estimation of Bull's Gene Effects for Milk Amount

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SUMMARY

In this paper we tried to estimate gene effects of three bulls that are mated with five populations of half-sisters by sire line for milk amount. We wanted to fortify whether the order of bull's gene effects was unchangeable or it was modified. Totally we analyzed 2824 lactation. Investigation was made on two different generations of Holstein cows (mothers and daughters). Analysis of results for milk production of mothers showed that between different populations of mothers exist significant differences ($P<0.05$ and $P<0.01$). It was fortified that order of bulls wasn't same i.e. that their breeding value (like sum of all present genes in one individual) was various on the different populations of cows.

KEY WORDS

bulls, gene effects, milk amount, half-sisters

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INTRODUCTION

Genetics and selection represent synonyms for continuous improvement of different economically important traits of domestic animals. Development of animal breeding in the world characterizes great genetic improvement of all traits in domestic animals with application of population and quantitative analysis (Lynch and Walsh, 1998) and also major application of molecular genetic and genetic engineering. Importance of artificial selection is big because by frequency modification of present and new mutated genes were created different genotype of animals' whit high production traits, which are used by people in realization of theirs economic benefits. Average value and variability of population depend of gene frequency and genotype frequency thus variation of traits in population is result of genotype variation and genes frequency variation. According to Jurić and Đikić (2001) existence of same character in population is a question of presence or absence of some genes in that specific population. Variations of gene frequency in practical selection performance provide a selection result (R). Each chosen parent has influence on modification of population with own gene effects while breeding value is represented by sum of all present gene in some individual. (Van Vleck and al., 1987; Falconer and Mackay, 1996). By investigation of bull's gene effects mated with different population of cows it will be given contribution to proficiency of estimated breeding values and also will be explored ratio between gene effects and gene interaction.

MATERIALS AND METHODS

Investigation and estimation of bull's gene effects for milk amount in standard lactation (305 days) was made on five (5) "populations" of cows which were half – sisters by sire line. Each population of half – sisters (mothers) was mated with three different sires. In this way we obtained three subpopulations of mothers and daughters in each population of half – sisters by sire line. After logical control data were accepted and total number of individuals involved in this investigation was 2824 (1412 by each generation).

In this investigation, generations were designated with G_1 (mothers) and G_2 (daughters). Population of mother was marked like M_1, M_2 and M_3, versus daughters that we marked like D_1, D_2 and D_3. Table 1 represents the ways of mating from which we produce two generation of cows (mothers – M and daughters – D).

In mentioned schemes of mating, generation G_1 (mothers) has 50 % genes from sire which made that population of half – sisters, while generation G_2 (daughters) has 25 % portion of mothers sire blood (i.e. grandfather of mother) and 50 % portion of bull's gene which is mated with population of mother.

Statistical data analyses were made by statistical procedures of SAS (SAS Institute, 1996) and SPSS (Nie and al., 1975) programs. Existence of statistical differences between means was made by GLM procedure (proc GLM). Pearson correlation coefficient was used for fortifying linearity of

Table 1. Scheme of bull's mating in population of half – sisters

Scheme of mating	Generation G_1	Mated with sire	Generation G_2	Total numbers of individuals $G_1 + G_2$
I	Mothers (M_1) – half-sisters by sire 1 (HB-74)		Daughters (D_1)	
	M_{11}	1 (HB-74)	D_{11}	78
	M_{12}	2 (HB-75)	D_{12}	142
	M_{13}	3 (HB-76)	D_{13}	32
II	Mothers (M_2) – half-sisters by sire 2 (HB-75)		Daughters (D_2)	
	M_{21}	1 (HB-74)	D_{21}	684
	M_{22}	2 (HB-75)	D_{22}	88
	M_{23}	3 (HB-76)	D_{23}	70
III	Mothers (M_3) – half-sisters by sire 3 (HB-76)		Daughters (D_3)	
	M_{31}	1(HB-74)	D_{31}	652
	M_{32}	2 (HB-75)	D_{32}	226
	M_{33}	3 (HB-76)	D_{33}	44
IV	Mothers (M_4) – half-sisters by sire 4 (HB-98)		Daughters (D_4)	
	M_{41}	1(HB-74)	D_{41}	110
	M_{42}	2 (HB-75)	D_{42}	124
	M_{43}	3 (HB-76)	D_{43}	74
V	Mothers (M_5) – half-sisters by sire 5 (HB-133)		Daughters (D_5)	
	M_{51}	1(HB-74)	D_{51}	230
	M_{52}	2 (HB-75)	D_{52}	168
	M_{53}	3 (HB-76)	D_{53}	102

Table 2. F – test, influence of environment factors on milk production for mothers and daughters

	F – test for mothers			F – test for daughters	
Source of variation	Degree of freedom	Milk (kg)	Source of variation	Degree of freedom	Milk (kg)
Herd	19	36.06***	Herd	20	28.32***
Year	19	7.59 ***	Year	14	3.09 ***
Season	3	10.11***	Season	3	11.10***
Share of interpret variance (R^2)		36.5 %	Share of interpret variance (R^2)		31.2 %

*** P < 0,001

correlation between variables while regression analysis was used for fortifying relationships between each to each variable. Differences between means of each group were tasted by t – test. Systematic influences of environment on milk production were valuated by least squares method (GLM procedure). Fixed linear model used in this investigation includes three environmental factors:

$$y_{ijkl} = \mu + F_i + G_j + S_k + e_{ijkl}$$

where: y_{ijkl} = milk production
μ = mean value of model
F_i = influence of i–th farm (i = 1…21 for daughters; i = 1…20 for mothers)
Y_j = influence of j-th year (j = 1…15 for daughters; i = 1…20 for mothers)
S_k = influence of k–th season (k = 1 (December, January, February), k = 2 (March, April, May), k = 3 (Juny, July, August), k = 4 (September, October, November)
e_{ijkl} = influence of random error

RESULTS AND DISCUSSION

Estimation of gene effects and bull's breeding value can be made correctly and precisely by elimination of systematic influence of environment on progeny productivity. Data were analysed by linear model which included three environmental factors. Theirs influence on milk production was fortified by F test and results are written in table 2.

From table 2 we can see that all systematic factors in the model have highly significant influence on milk production (P<0.001). Justification of define influence of herd, year and season in the model were proven in earlier investigation by numerous authors (Jovanovac, 1987; Jovanovac, 1989; Albuquerque and al., 1999; Dedkova and Wolf, 2001; Pribyl and Prybilova, 2001.). These systematic influences of environment represent important cause of variability in milk production. Also we can see that chosen model by mothers were clarified 36,5 % variance for milk amount while by daughters it clarified 31,2 % variance which is coincidental with results of the authors above.

Analysis of differences between groups (populations) of mothers that are half – sisters by sires line (table

3) has demonstrated highly significant difference (P < 0,01) between all groups except second and fourth. Also between third and fifth population of mothers it has not been fortified significant difference in productivity. This matches with results of major part of authors by whom sires have influence on phenotypic milk parameters of their daughters (Lazarević, 1982; Lazarević and al., 1983; citation by Petrović, 1987; Đikić, 1991; Stipić and Kapš, 1993; Đikić and Jurić, 1994.).

When we were comparing third and forth population of mothers (G_{III} : G_{IV}) we fortified no homogeneity of variances by Levene test (t – value is indicated bold) which t – value was assigned by correction degree of freedom. Analysing differences between subgroups in all schemes of mating we fortified that between subgroups of mothers weren't valid differences in milk yield. It can be seen form table 4.

At bold values (table 4) we fortified non homogeneity of variances by Levene test, whence t – value was assigned by correction degree of freedom. According to Jurić (1986) in correlation and regression analysis we have taken deviations of mothers from average of mothers and deviations of daughters from average of daughters (table 5). Regression analysis on absolute value was made for the control of regression coefficients.

Analyzing milk production of daughters whose fathers are bull 1 (HB - 074), bull 2 (HB – 075) and bull 3 (HB – 076) which were mated with different

Table 3. t – values for compared means for milk amount (kg) in 305 days of lactation between populations of mother which are half – sisters by sire line

Compared populations of mothers (G)	t - value
G_I:G_{II}	3.11**
G_I:G_{III}	5.27**
G_I:G_{IV}	2.21*
G_I:G_V	4.78**
G_{II}:G_{III}	3.35**
G_{II}:G_{IV}	0.81[NS]
G_{II}:G_V	2.37*
G_{III}:G_{IV}	**3.68****
G_{III}:G_V	0.61[NS]
G_{IV}:G_V	2.80**

** P < 0,01; * P < 0,05; [NS] = non significant

Table 4. t – test for compared means of milk amount (kg) between subpopulations of mothers in all five schemes of mating

Compared subpopulations of mothers (M)	t - value
$M_{11} : M_{12}$	**1.03**[NS]
$M_{11} : M_{13}$	0.41[NS]
$M_{12} : M_{13}$	0.99[NS]
$M_{21} : M_{22}$	0.53[NS]
$M_{21} : M_{23}$	0.71[NS]
$M_{22} : M_{23}$	0.21[NS]
$M_{31} : M_{32}$	2.05[NS]
$M_{31} : M_{33}$	**1.53**[NS]
$M_{32} : M_{33}$	**0.33**[NS]
$M_{41} : M_{42}$	1.25[NS]
$M_{41} : M_{42}$	0.20[NS]
$M_{42} : M_{43}$	2.15 [*]
$M_{51} : M_{52}$	**0.22**[NS]
$M_{51} : M_{53}$	1.31[NS]
$M_{52} : M_{53}$	1.17[NS]

[NS] = non significant: * $P < 0,05$

population of mothers, we have obtained significant regression ($b \neq 0$) for all couples of mother – daughter (table 5), except in III. scheme of matting, when we analysed bull number 3 (HB – 076) and also in IV. scheme (half – sisters by bull's 4) when we observed bull number 1 (HB – 074). In these ways of matting, regression wasn't significant ($b = 0$) although we can say that significant stream of regression was existed on 92nd % of level for bull number 1 in IV. scheme of matting. From table 5 it can be seen that all correlation coefficients were positive.

Genotypic value is also conditional with gene interaction, because parents transmit on their offspring only genes but not genotypic value, thus in animal breeding the main question is how we can change population mean from generation to generation. According to Van Vleck and al. (1987), Falconer and Mackay (1996), and Jurić and Đikić (2001) one of the main measure of change is that change which accrues if for the matting we choose one gene namely when the parent population mated with homozygous genotype A_1A_1 or A_2A_2, respectively. We can assume that some bull fertilized cow's population with only one of allelic gene A_1, while another bull fertilized another cow's population with allelic gene A_2. The difference between population mean in which equilibrium exist and population which was created by picked gene is average gene effect (Van Vleck and al., 1987; Falconer and Mackay, 1996), i.e. average gene effect it's medial value in population with unrestricted fertilization.

Practically, theory about gene effect is base of breeding value like sum of gene effects, while additive variance is rate of breeding value (Car, 1984; Hohenboken, 1985; Van Vleck and al., 1987; Falconer and Mackay, 1996; Jurić and Đikić, 2001). Table 6 represents bull's gene effects for milk amount in different population of cows and also bull's order. In table 6 we can see that order of bulls on different cow's populations wasn't the same, namely that the bull's gene effects were dissimilar on different population of cows, which bulls were matting.

Different results of production traits like milk amount, of bull's daughters in various population

Table 5: Correlation and regression coefficients for milk amount of mothers (X) and milk amount of daughters (Y) in all five schemes of matting

Ratios	N of couples mothers - daughters	Correlations analysis r	Regression analysis $Y_1 = a + bx$	$Y_2 = a + bx$	t	R^2
$M_{11} : D_{11}$	39	0.662**	- 64.19 + 0.77x	1378.99 + 0.77x	5.38**	0.439
$M_{12} : D_{12}$	71	0.811**	97.94 + 0.77x	1507.07 + 0.77x	11.51**	0.657
$M_{13} : D_{13}$	16	0.688**	107.14 + 1.18x	- 849.89 + 1.18x	3.55**	0.474
$M_{21} : D_{21}$	342	0.759**	24.23 + 0.77x	1574.55 + 0.77x	21.47**	0.575
$M_{22} : D_{22}$	44	0.374*	- 175.06 + 0.40x	3490.30 + 0.40x	2.61**	0.140
$M_{23} : D_{23}$	35	0.508**	- 66.71 + 0.51x	2933.44 + 0.51x	3.39**	0.258
$M_{31} : D_{31}$	326	0.855**	6.17 + 0.93x	659.42 + 0.93x	29.63**	0.730
$M_{32} : D_{32}$	113	0.777**	78.44 + 0.76x	1671.11 + 0.76x	13.02**	0.604
$M_{33} : D_{33}$	22	0.090[NS]	25.79 + 0.14x	4975.08 + 0.14x	0.41 [NS(31)]	0.008
$M_{41} : D_{41}$	55	0.241[NS]	122.29 + 0.24x	4581.79 + 0.24x	1.81 [NS(92)]	0.058
$M_{42} : D_{42}$	62	0.417**	21.14 + 0.46x	3277.37 + 0.46x	3.55**	0.174
$M_{43} : D_{43}$	37	0.338*	- 120.61 + 0.29x	4095.87 + 0.29x	2.12*	0.114
$M_{51} : D_{51}$	115	0.678**	68.03 + 0.67x	2290.57 + 0.67x	9.79**	0.459
$M_{52} : D_{52}$	84	0.794**	7.12 + 0.73x	1887.04 + 0.73x	11.83**	0.630
$M_{53} : D_{53}$	51	0.672**	- 59.956 + 0.64x	2359.13 + 0.64x	6.34**	0.451

** $P < 0,01$; * $P < 0,05$; [NS] = non significant; [NS (31) (92)] = significant on 31st % and 92nd % - of level

Y_1 = regression equation for mother deviation from average of mothers and daughter deviation from average of daughters

Y_2 = regression equation for mothers and daughters absolute values

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Table 6: Bull's gene effects for milk amount (kg) in 305 days of lactation and bull's order

Bull	Population of mothers (M)	Sire		Population of daughters (D)				Gene effect	Bull's order
			n	$\bar{x}$	s	VK	(D:M)*100		
074	5853.09	074	39	5772.74	694.59	12.03	98.63	- 80.35	3
	n = 126	075	71	6064.49	881.98	14.54	103.61	211.40	1
		076	16	5809.77	966.00	16.63	99.26	- 43.32	2
075	5617.23	074	342	5914.71	809.57	13.69	105.30	297.48	1
	n = 421	075	44	5685.64	690.04	12.14	101.22	68.41	3
		076	35	5770.34	728.93	12.63	102.73	153.11	2
076	5439.64	074	326	5686.60	908.04	15.97	104.54	246.96	3
	n = 461	075	113	5909.42	797.82	13.50	108.64	469.78	1
		076	22	5771.64	631.72	10.95	106.10	332.00	2
098	5671.64	074	55	5925.95	619.65	10.46	104.48	254.31	1
	n = 154	075	62	5913.64	685.02	11.58	104.27	242.00	2
		076	37	5669.3	566.72	10.00	99.96	- 2.34	3
133	5476.37	074	115	5939.5	622.65	10.48	108.46	463.13	1
	n = 250	075	84	5859.05	795.26	13.57	106.99	382.68	3
		076	51	5902.1	626.54	10.62	107.77	425.73	2

of mothers is consequent of specific combinatory capacity i.e. some non additive effect of genotype like it was pointed out by Rönningen (1975), Falconer (1977), Robertson (1977), Shested (citation by Đikić and Jurić, 1994), Gimelfarb and Willis (1994), Misztal and al. (1996), Mbaga and Hill (1997), hence on the various population of cows exanimated bulls didn't have the same order of gene effect and analogously of that these bulls didn't have the same breeding value. According to Đikić (1991) assigned differences can be imputed to object of knowledge that alone individuals in some population give subpopulations of offspring within exists various variability of production traits.

CONCLUSION

The gene effects of bulls and their breeding value weren't the same in different populations of cows, which are half – sisters by sire line. We can exemplify modification of gene effect by interaction, in explanation of non additive gene effects which gets more and more meaning today because by accepting of non additive variances we can precisely estimate genetic parameters for domestic animal production traits.

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