

DOES THE SELECTION ON SS-CASEIN AFFECT THE TRAITS IMPORTANT FOR DAIRY PRODUCTION OF SLOVENIAN BROWN SWISS CATTLE?

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ABSTRACT

The purpose of this study was to determine the impact of genomic selection on A2A2 β -casein genotype in Brown Swiss cattle on important dairy production traits – traits included in total merit index (TMI). A total of 190 Slovenian Brown Swiss cattle, 83 females and 107 males, with known direct genomic values (DGV) from InterGenomics project and known genotype for β -casein were used for estimation of the genotype effect. The determined genotype frequencies in population were 2.63 % for A1A1, 35.26 % for A1A2 and 62.11 % for A2A2 genotype. For DGV data analysis a single-trait model was used, considering genotype for β -casein as fixed effect. Analysis showed significant differences between genotypes for β -casein for three dairy production traits – TMI for dual purpose, pasterns and rear teat position. Our research indicates that selection on A2A2 β -casein genotype would not have implications for traits important for dairy production.

Key words: genomic selection, β -casein, Brown Swiss, dairy production, A2

1 INTRODUCTION

Selection of Brown Swiss cattle in recent decades was based on the polygenic traits that are especially important for dairy production. In the last few years the importance of genomic selection increased, which enabled faster genetic improvement for traits under selection. Genotyping also provided information about monogenic characteristics (traits and disorders) such as: genotype for κ - and β -casein, β -lactoglobulin, bovine polledness, etc. These monogenic characteristics can be associated with: processing and quality of dairy products, influence on human health and herd management. Their importance is increasing in both livestock and processing industry. Nowadays bull catalogues of selection companies make the information about monogenic traits available in their catalogues (Select Sires Inc., 2016; Inseme S.p.a., 2015).

One of such traits is milk protein β -casein, which is present in bovine milk in one of two genetic variants – A1 or A2. Form of this milk protein is determined by the genotype for β -casein. In cattle it exists in three different variants: A1A1, A1A2 and A2A2. Primary form of β -casein is recognized as A2, while its mutated form is recognized as A1 β -casein (Jakob, 1994; Kamiński *et al.*, 2007). Consumption of A1 β -casein in dairy products is associated with negative impact on human health. Some reports suggest that A1 β -casein is causing: formation of beta-casomorphin-7 (which is thought to induce immune response), worsened gastrointestinal physiology and digestive discomfort symptoms, type 1 diabetes mellitus, ischaemic heart disease, neurological disorders (schizophrenia, autism, postpartum psychosis) and even sudden infant death syndrome (Elitsur and Luk, 1991; Kamiński *et al.*, 2007; Clarke and Trivedi, 2014; Jianqin *et al.*, 2016).

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The frequency of the A1 allele varies in different cattle breeds. Several studies reported that Holstein Friesian breed has higher (~50 %) while Brown Swiss breed (and similar breeds) has lower A1 allele frequency (~ 25 %) (Jann *et al.*, 2002; Kamiński *et al.*, 2007). However, A2 allele prevails in Brown Swiss and this is an advantage compared to Holstein Friesian which is used as main breed for dairy production in Slovenia and Europe. For Slovenian Simmental breed, we do not have allele frequency information available.

Several studies researching associations between genetic variations of β -casein and main economically important traits for dairy production exists (milk, protein and fat yield), most of them regarding Holstein

cattle. Their general findings are confirming the association between A2A2 genotype or A2 β -casein variant and increased milk yield (Ng-Kwai-Hang *et al.*, 1984; Ng-Kwai-Hang *et al.*, 1990; Comin *et al.*, 2008; Olenski *et al.*, 2010), increased protein yield (Comin *et al.*, 2008; Olenski *et al.*, 2010) and decreased fat yield (Ng-Kwai-Hang *et al.*, 1990; Olenski *et al.*, 2010).

The aim of this study was to investigate the existence of association between selection on the A2 β -casein and traits important for dairy production (traits included in total merit index (TMI)) of Slovenian Brown Swiss due to the changes in the individual polygenic traits.

Table 1: Descriptive statistics for direct genetic values of economically important traits

	N	Mean	SD	Min	Max
Rump height	190	118.8	13.0	82.0	148.0
Rear legs-side view	190	97.6	14.7	44.1	149.8
Pasterns	190	110.9	16.1	64.5	166.3
Hoof height	190	111.6	18.9	67.2	170.9
TMI milk	190	111.3	7.5	90.9	130.8
TMI dual purpose	190	108.1	8.4	84.2	129.0
Teat length	190	88.3	13.4	43.3	122.7
Rump angle	190	99.3	13.6	53.2	139.4
Rear udder height	190	117.2	16.0	59.4	149.3
Rear udder width	190	117.2	13.8	75.9	148.3
Udder depth	190	110.5	14.6	71.0	153.5
Milking speed	190	104.9	16.2	54.9	150.6
Chest width	190	98.9	13.4	58.0	133.4
Front teat position	190	113.0	14.8	71.5	146.4
Rear teat position	190	112.1	13.7	70.6	144.8
Somatic cell score	190	104.0	6.3	92.3	126.6
Milk yield	190	113.4	9.0	84.6	137.1
Fat yield	190	113.9	9.5	87.0	142.6
Protein yield	190	115.5	9.5	87.3	144.4
Longevity	190	113.2	19.1	54.0	158.0
Body depth	190	109.7	18.9	55.8	159.6
Structural width	190	116.5	15.0	71.5	151.8
Fore udder attachment	190	114.6	17.3	65.4	170.5
Udder cleft	190	112.7	16.3	65.5	155.6
Legs overall	190	114.4	23.5	59.6	182.3
Udder overall	190	119.1	17.9	71.6	161.6
Exterior overall	190	120.4	21.3	62.9	171.6
Fat and protein index	190	115.2	9.4	87.2	143.4

N – number of animals; SD – standard deviation; Min – minimum value; Max – maximum value; TMI – total merit index

2 MATERIAL AND METHODS

The data set consisted of 190 genotyped Slovenian Brown Swiss cattle (83 females and 107 males) with direct genomic values (DGVs) for economically important traits. DNA was isolated either from animal hair samples or bull semen. The allelic variants for β -casein were obtained from genotypes using a routine procedure. Chi-square test was used to determine if population was in Hardy-Weinberg equilibrium. The effect of different variant of β -casein genotype (A1A1, A1A2, A2A2) on DGVs was analysed by GLM procedure of statistical package SAS/STAT (SAS 9.2., 2008), considering genotype for β -casein as fixed effect (Model 1). DGVs are expressed on standardised scale where mean is 100 and standard deviation is 12 points.

$$y_{ij} = \mu + G_i + e_{ij} \quad \text{Model 1}$$

where y_{ij} – DGV; G_i – β -casein genotype; $i = 1, 2, 3$; e_{ij} – residual; $j = 1, \dots, 190$

3 RESULTS AND DISCUSSION

The observed genotype frequencies were 2.63 %, 35.26 % and 62.11 % for A1A1, A1A2 and A2A2 genotypes, respectively. We are not aware of results from other Brown Swiss populations being available. However, in studied populations of Slovak Spotted cattle (Miluchová *et al.*, 2013) and Romanian Spotted cattle (Grădinaru *et al.*, 2015) which included a similar number of animals as our study, A2A2 genotype was also prevalent. In studies of Romanian and Polish Holstein Friesian cattle with numerically similar or bigger animal populations, the prevalent genotype was A1A2 (Grădinaru *et al.*, 2015; Olenski *et al.*, 2010).

Sex ratio (female : male) by genotype frequency was 40 : 60 for A1A1 genotype, 47.8 : 52.2 for A1A2 genotype and 41.5 : 58.5 for A2A2 genotype. Allele frequencies were 20.3 % for allele A1 and 79.7 % for allele A2. The β -casein genotypes in population were distrib-

uted according to Hardy-Weinberg equilibrium. The frequency of allele A2 in observed Brown Swiss population was four times higher than frequency of allele A1. These results are in agreement with prior findings of similar study where 40 animals from Slovenian Brown Swiss population were observed (Potočnik, 2015).

Mean DGV (Table 1) for TMI for dairy production was 111.3 which is almost one standard deviation (SD) higher than the average of Slovenian Brown Swiss population. For most of individual traits average DGVs were around one SD above population average. That was somehow expected because genotyped animals were preselected on parent average. For rear legs – side view, teat length, rump angle and chest width average DGVs were close to Slovenian Brown Swiss population's average.

The average value for pasterns was 110.9 while the minimum and maximum values ranged from 64.5 to 166.3. The average of investigated populations is very close to the optimum value (109 points). The average pasterns are just a little bit steeper than the optimal ones. The average for rear teat position was 112.1 while the minimum and maximum values ranged from 70.6 to 144.8. Optimum value for rear teat position is 100, while the average value of the studied population is one SD higher meaning that rear teats are placed closer to the central ligament than it is desired. The average DGV within gender for pasterns and rear teat position was higher for females (112.8 and 113.7) than males (109.4 and 110.9, respectively).

Presented results refer only to the traits with statistically significant differences among genotypes for β -casein (Table 2). Significant differences between genotypes for β -casein were recorded at two type traits (pasterns and rear teat position) and TMI for dual purpose (Table 3).

Animals with A2A2 genotype had significantly steeper pasterns (113.4 ± 1.5 points,) and higher TMI for dual purpose (109.2 ± 0.8) than animals with A1A2 genotype (106.9 ± 1.9 and 106.1 ± 1.02 , respectively). The rear teat position significantly differ between A1A1 and A2A2 genotypes – animals with A1A1 genotype

Table 2: Least square means (LSM) and standard errors (SE) of direct genomic values (DGV) for pasterns, total merit index (TMI) for dual purpose and rear teat position by β -casein genotype

	Pasterns		TMI for dual purpose		Rear teat position	
	LSM	SE	LSM	SE	LSM	SE
A1A1	104.5 ^{ab}	7.08	108.4 ^{ab}	3.7	126.7 ^b	6.06
A1A2	106.9 ^b	1.9	106.1 ^b	1.02	112.4 ^{ab}	1.7
A2A2	113.4 ^a	1.5	109.2 ^a	0.8	111.3 ^a	1.2

^{a, b} – Means within a row with different superscripts differ ($p < 0.05$)

Table 3: *P*-values of traits with estimated significant differences between β -casein genotypes

	<i>p</i> -values		
	A1A1 – A1A2	A1A1 – A2A2	A1A2 – A2A2
Pasterns	1.0000	0.6570	0.0219
TMI for dual purpose	1.0000	1.0000	0.0467
Rear teat position	0.0711	0.0412	1.0000

had rear teats placed closer to the centre of the udder quarter (126.7 ± 6.06) which is not desirable. Since the use of mechanical milking (robot) is increasing, close rear teat position indicates issues relating to the ease of milking unit attachment.

Braunschweig *et al.* (2000) found no significant effect for parental casein haplotypes on dairy production traits (milk yield, fat percentage) for Brown Swiss cattle. In comparison with our results this could indicate that genotype for β -casein is not closely linked to the expression of main polygenic traits for dairy production, considering that TMI for dual purpose includes higher economical weights for meat production traits than dairy production traits. However, in contrast to the results of Braunschweig *et al.* (2000), Boettcher *et al.* (2004) found statistically significant associations between casein gene haplotypes for milk yield and protein and fat percentages in Italian Brown Swiss population. They also came to indication that the same haplotypes were having similar effects in both Italian Brown Swiss and Holstein cattle with greater magnitude for the Brown Swiss cattle. Regarding both Slovenian Brown Swiss and Czech Fleckvieh being dual purpose breed, we can also consider the results of Kučerová *et al.*, (2006) who found significant differences among genotypes of β -casein gene locus in breeding values for milk, protein and fat yield, and fat content. Their results show tendency of allele A2 to influence milk content parameters while allele A1 tends to increase milk yield.

4 CONCLUSIONS

The analysis did not show statistically significant differences between β -casein genotypes for traits included in TMI. Inventive producers and suppliers of milk and dairy products have now an opportunity for a new niche market, which is with increasing usage of genomic selection already slowly expanding and occupying its own space in the market.

Results in literature are contradictory. Our results indicate that selection on A2A2 β -casein genotype

would not lead to the loss of variability and would not cause any major genetic changes of the most important polygenic traits in the next generations of Brown Swiss animals. There is indication of changes for three traits (TMI for dual purpose, pasterns and rear teat position) but the trend is in favour of the desired β -casein genotype. How-

ever, for more explicit results and better comparison it would be necessary to make more advanced studies regarding Brown Swiss cattle and to use larger number of animals with known genotype for β -casein and estimated breeding values.

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