

# Association between genetic polymorphism of growth-hormone-releasing hormone and the yield, chemical composition and technological parameters of cow milk (Brief Report)

## Der Zusammenhang zwischen dem genetischen Polymorphismus von Somatoliberin und der Milchleistung, Milchezusammensetzung und den technologischen Milchparametern bei Kühen (Brief Report)

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### Background

Somatoliberin or growth-hormone-releasing hormone (GHRH) belongs to a group of hypothalamic hormones. It induces an increase in the concentration of endogenous growth hormone in the blood serum of cattle (Løvendahl *et al.* 1991), increasing mean and pulsatile liberation of somatotropin and thus affecting indirectly an increase in the milk productivity of cows (Dahl *et al.* 1993). The study aimed at searching for associations between the variants of the *GHRH/HaeIII* polymorphism, described for the first time by Moody *et al.* (1995), and production traits in the examined herds and comparing the technological usefulness of milk obtained from cows with different *GHRH* genotypes. According to Szewczuk *et al.* (2008), above mentioned polymorphism is the transversion A→C located at the position A44C within initial part of intron 2 (GenBank acc. no. EF210074).

### Procedures

Examinations were carried out on 1 188 Holstein-Friesian cows of Black-and-White strain kept in two farms in the Lubusz Province (farm A) and the Western Pomeranian Province (farm B). DNA for examination was isolated from the whole peripheral blood collected to test-tubes with K3EDTA using MasterPure Genomic DNA Purification Kit provided by Epicentre Technologies. The genotypes of the *GHRH/HaeIII* polymorphism were assayed with polymerase chain reaction – restriction fragment length polymorphism (PCR-RFLP). The reaction was performed in the Biometra Tpersonal thermocycler. The following primers designed by Dybus *et al.* (2003) were applied: GHRHF 5' ttc cca agc ctc tca ggt aa 3' and GHRHR 5' gcg tac cgt gga atc cta gt 3' ( $T_a=60^\circ\text{C}$ ). The obtained DNA fragments of 297 bp were digested with 4 units of restriction enzyme *HaeIII* (gg↓cc; Fermentas). Digestion products were separated by electrophoresis in 2% agarose gel with ethidium bromide and visualized under UV light (312 nm) in a Vilber Lourmat transilluminator. The analysis of milk performance was based on the data obtained from the official milk recordings. Additionally,

milk samples from each farm ( $n=69$  for *GHRH* AA, AB, BB) were taken, in which the following was determined: chemical composition (fat, protein, lactose) using Milcos-Scan 104 device, active acidity (pH), potential acidity using titration method ( $\alpha$ SH) and flocculation time (s) using rennet method. The obtained results were analysed statistically using the Duncan multiple range test by means of Statistica 7.1 PL software.

## Results

In both herds, two alleles (*GHRH*<sup>A</sup> and *GHRH*<sup>B</sup>) and three genotypes (AA with bands of 242 bp and 55 bp; AB with bands of 242 bp, 194 bp, 55 bp and 48 bp; BB with bands of 194 bp, 55 bp and 48 bp) were identified. The BB genotype was observed most frequently (frequencies 0.631 and 0.704 for herds A and B, respectively) and the AA genotype least frequently (0.042 and 0.054, respectively). The frequencies of the heterozygous genotype were 0.327 and 0.242, respectively. The frequency of the *GHRH*<sup>A</sup> allele was higher in herd A (0.206) than in herd B (0.175). Dybus & Grzesiak (2006) found equally low frequency of the *GHRH*<sup>A</sup> allele (0.211) in the population of Polish Black-and-White cattle. In Polish Red-and-White cattle, Kmieć *et al.* (2007) estimated the frequency of the *GHRH*<sup>A</sup> allele at 0.281. Moody *et al.* (1995) reported a significantly higher frequency of the *GHRH*<sup>A</sup> allele in Angus cattle (0.700) and a lower one in Hereford cattle (0.070). In the present study, cows with the *GHRH* AA genotype were characterized by the highest milk yield in both farms. Significant differences ( $P \leq 0.05$  and  $P \leq 0.01$ ) were found within a given herd and between the analysed herds. Milk fat and milk protein contents were the highest in herd A for animals with the *GHRH* AA genotype (4.26 % and 3.43 %, respectively). Association study performed by Kmieć *et al.* (2007) revealed statistically higher values for the all analyzed milk production traits in cows with AA genotype ( $P \leq 0.05$ ). Dybus & Grzesiak (2006) also found that individuals with one or two *GHRH*<sup>A</sup> alleles might produce milk of a higher fat percentage (although not statistically significant). However, in the study performed by Szewczuk *et al.* (2008), the BB-genotype cows were characterized by a higher fat yield and percentage ( $P \leq 0.01$ ). In the present study, the milk of cows from herd A was characterized by significantly ( $P \leq 0.01$  and  $P \leq 0.05$ ) better physico-chemical and technological traits for cheese production compared to the milk of cows from herd B. The highest content of casein (2.85 %) was found in the milk of the AB heterozygotes in herd A and in the milk of the AA homozygotes in herd B (2.79 %). The milk of cows with AA and BB genotypes in farm A was characterized by the same content of whey protein (0.53 %), whereas the shortest clotting capability time (286 s) and the highest lactose content (4.92 %) were found in the milk of the AB heterozygotes. There are no other literature data concerning the association between technological usefulness of milk and the *GHRH*/*Haelll* polymorphism.

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