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Dynamics Of Dairy Production Of Heifers Of Different Genotypes Of Stearoyl-CoA Desaturase (SCD1).

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ABSTRACT

The article presents the assessment of lactation activity of heifers in terms of polymorphism of the stearoyl-coenzyme A desaturase (SCD1) gene encoding an enzyme that catalyzes the endogenous synthesis of long-chain unsaturated fatty acids in the mammary gland and other tissues that modulate the metabolic functions of the cell. Genotyping of livestock performed by PCR-RFLP showed that the studied population is polymorphic in the SCD1 gene, the allele frequency was C – 0.61, T – 0.39, and the genotype frequency was CC – 39.0% (67 animals), TC – 42.4% (74 animals), TT – 18.6% (32 animals). The analysis of lactation activity of groups of individuals is presented by indicators of average monthly milk yield by all months of lactation of the herd. Animals with the CC genotype compare favourably with individuals with other genotypes in terms of total milk yield, dynamics and lactation adequacy ratio. The significant difference for this indicator between the estimated CC and TC subpopulations was 3.7% ($P \leq 0.05$). The assessment of dairy production and lactation activity of heifers is indicative of the biological potential of animals as a whole, and can serve as an agronomic character in the preparation of breeding programs.

Keywords: gene, polymorphism, genotype, PCR-RFLP, Stearoyl-CoA Desaturase, SCD1, metabolism, lactation, milk yield, cattle, heifer

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INTRODUCTION

The main problem of dairy cattle breeding is to increase the production of animals by raising the most valuable breeds, genotypes and lines of cattle [1, 2]. The assessment of milk yield of heifers plays an important role in selective stock-breeding, as the first lactation depends on the further dairy production of livestock, its subsequent use in the economy or possible culling. Constancy of lactation (persistence) is the ability of a cow to keep milk yield at a high level after the peak of lactation [3]. It is known that the value of lactation milk production depends (among other conditions) on the maximum milk yield and the degree of its preservation during lactation. At the same maximum yield, this value of lactation will be the greater the more constant lactation curve [4]. Lactation persistency has a direct economic value, since a good consistency leads to a reduction in health and reproduction problems and, consequently, to a reduction in the cost of milk production [5, 6]. High dairy productivity causes a great tension of metabolic processes in the body and demands higher standards of feeding quality, the organization of proper nutrition.

Metabolism and energy exchange is a complex mechanical process in the body from the moment of nutrient enrichment and to the removal of metabolic products from it. Metabolic status depends on the conditions of maintenance and nutrition, the functions of individual organs and systems [7]. There is a decline after calving in the metabolic process, when the mobilization of fat reserves is necessary to provide additional energy at the beginning of lactation. This leads to a period of a negative energy balance, liveweight loss and a decrease in milk productivity [8]. Adaptation to lactation requires careful regulation and coordination of energy metabolism between key organs such as the liver and the mammary gland.

Stearoyl-coenzyme A desaturase (SCD) catalyzes the endogenous synthesis of long-chain unsaturated fatty acids in the mammary gland and other tissues that modulate the metabolic functions of the cell. The SCD enzyme deficiency in animals causes the decrease of the fat content in tissues, the increase in insulin sensitivity and, as a result, the metabolism acceleration [9]. The stearoyl-CoA Desaturase (SCD1) gene is localized on chromosome BTA 26. It consists of 6 exons and 5 introns and contains 17 088 bp; SNP (T878C) in exon 5 causes a substitution of valine by alanine (V→A) [10, 11].

The aim of the work was to assess the dynamics of dairy productivity of heifers with different genotypes of stearoyl-CoA desaturase.

MATERIALS AND METHODS

The study was conducted under the conditions of Integrated Agricultural Production Centre "Stud farm named after Lenin" of Atninsky district of the Republic of Tatarstan on 172 Holstein heifers. Genotyping of DNA samples of blood specimens of experimental animals was carried out by PCR-RFLP according to the predeveloped protocol [12].

The composition of the reaction mixture with a total volume of 20 µl included oligonucleotide primers (Eurogen, Russia) with the following sequence:



Amplifcons yielded from the polymerase chain reaction were hydrolyzed for 16 hours at the temperature of 37 °C in the presence of endonuclease *Fsp4HI* (SibEnzyme, Russia). RFLP products have undergone the electrophoretic separation in agarose 2.6% gel with subsequent visualization in a UV transilluminator and documentation in the Gel&Doc system (BIO Rad, USA).

In addition to genetic analyses in the study, we performed statistical calculations using data on productivity for 305 days and average monthly milk yield on first lactation of the official electronic filing system containing information about the herd, "SELEX". Processing of experimental data is performed using the formulae of biometric analysis by applying the MS Office program. To check the significance level of the obtained data, Student t-test was used for independent samples.

RESULTS AND DISCUSSION

As a result of the study, all possible allelic variants and genotypes of the SCD1 gene were identified. The variability of the C and T alleles was 0.61 and 0.39. The genotypes showed the following distribution: CC – 39.0% (67 animals), TC – 42.4% (74 animals), TT – 18.6% (32 animals). Following the results of the first lactation, it has been established that the highest milk yield and concentration of the protein mass fraction differ in individuals with the CC genotype of 7052,8 kg and 3.40% ($P \leq 0.05$), and the mass fraction of milk fat reliably prevail in animals with the TT genotype of 4.10% ($P \leq 0.01$) [14].

Lactation curves were built according to the average monthly milk yield (Fig. 1) for a comprehensive picture of dynamics of milk production. The graphs show that the highest milk yield was recorded in 4th month in heifers with the genotype of stearyl-CoA desaturase CC, differing generally in the maximum milk yield for the first lactation.

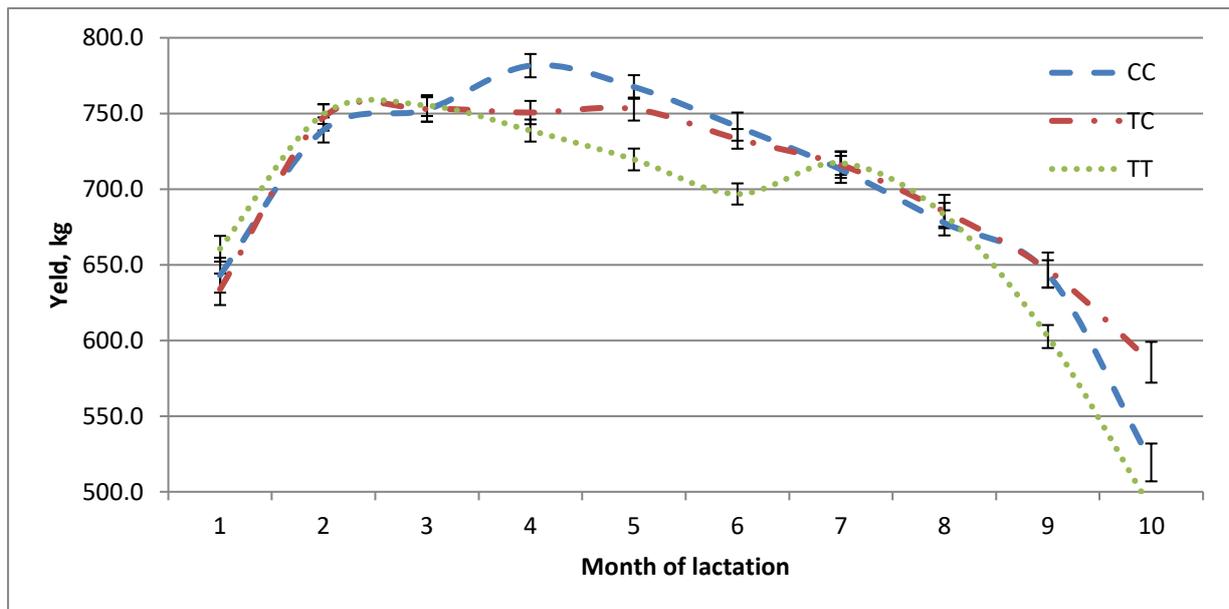


Figure 1: Lactation curves of the milk productivity of heifers with different SCD1 genotypes

Throughout the first lactation individuals with heterozygous genotype TC demonstrate consistency of lactation activity, stable average monthly milk yield, in comparison with herdmates of other groups (CC and TT). Animals with the TT genotype having a bimodal lactation curve are characterized by unstable dairy productivity and low persistence. It is likely that this is indicative of the weak mobilization of fat reserves due to the inability to stabilize metabolic processes and coordinate energy metabolism.

Based on the data on the highest daily milk yield for each month of lactation, the adequacy ratio of lactation for each of the identified genotypes was calculated: CC – 78.4%, TC – 74.7% and TT – 75.9%. The significant difference for this indicator between the estimated CC and TC subpopulations was 3.7% ($P \leq 0.05$). The data obtained indicate that the heifers carrying the homozygous CC genotype according to the SCD1 - *Fsp4HI* gene locus generally outperform individuals with other genotypes in total milk yield, the dynamics of lactation activity and lactation adequacy ratio.

CONCLUSION

The distribution of alleles and genotypes of the SCD1 gene established in the course of genotyping testifies to the biological diversity of the studied cattle population. Animals with the CC genotype compare favourably with individuals with other genotypes in terms of total milk yield, the dynamics of lactation activity and lactation adequacy ratio. The assessment of dairy productivity and lactation activity of heifers is indicative of the biological potential of animals as a whole, and can serve as an agronomic character in the preparation of breeding programs.

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