

ABSTRACT

The low level of reproduction traits and other reproductive disorders of cows are one of the most important problems of dairy farmers. The reasons for this phenomenon, which is one of the functional cattle traits, are multifactorial and include both environmental and genetic aspects. Their elucidation in terms of the relationship with reproductive potential may in the future improve the profitability of the production system; therefore, it is expedient to search for genes, whose protein products may condition the variability of the discussed traits, as well as molecular mechanisms that can explain this variability. In this context, the analysis of polymorphic variants of *IGF-1*, *JY-1* and *ER-1* genes in connection with cow's reproductive traits should be considered fully justified; firstly, because of their biological role in the regulation of reproductive processes in females, and secondly, due to the nature of the molecular mechanism, hypothetically indicating the determination of the quantity and variability of encoded proteins.

The aim of the study. The aim of the research conducted in Jersey cows and Polish Holstein-Friesian black-and-white varieties, is the analysis of the possible relationship between polymorphic variants in the regulatory regions of the *IGF-1*, *JY-1* and *ER-1* genes and selected reproductive traits, such as the age of the first calving, period between calving and the first insemination, calving interval, interpregnancy period, length of pregnancy, fertilization efficiency, calf birth weight.

Research hypotheses:

1. The occurrence of polymorphism in the regulatory region of the *IGF-1* gene (GenBank: AF017143) can create or abolish potential binding sites for transcription factors, translating into the level of IGF-1 expression. Given the biological role of this protein in the regulation of reproductive functions, it seems reasonable to hypothesize that this will be related to the level of cows' reproductive traits.
2. Sequence variation in the 3'UTR region of the *JY-1* gene (GenBank: JF262042.2) can potentially affect the stability of JY-1 mRNA, its binding to proteins supporting its transport to the cytoplasm, and translation efficiency. It can therefore be assumed that the above processes may be related to the expression of the JY-1 protein and the reproductive functions of cows.



3. Sequence changes in the promoter region of the *ER1* gene (GenBank AY340597) may be related to the level of estrogen receptor expression, thereby shaping the level of cows' reproductive traits

Material and methods. The study covered a total of 991 individuals, including: 758 Polish Holstein-Friesian black-and-white cows (West Pomeranian Voivodeship) and 233 Jersey cows (Greater Poland Voivodeship). Peripheral blood collected to a tube containing tripotassium edetate (K3EDTA) was the material used in the study. The commercial MasterPure™ DNA Purification Kit for Blood was used to isolate genomic DNA from peripheral blood. PCR-RFLP and ACRS-RFLP were used for the genotyping of selected genes. Statistical analysis of the results was carried out using the Statistica 10.0 software (StatSoft) under the academic license. Reproductive traits for individual breeds were analyzed according to a specific linear model.

Results. The obtained frequencies of the polymorphic variants of the analyzed genes have shown that there is polymorphism in the *IGF-1/SnaBI*, *ER-1/BglII* regions and to a lesser extent in *JY-1/BsrI*, because Jersey cows showed monomorphism in relation to the latter polymorphism.

Conclusions. Demonstration of variability within the analyzed genes allowed to elucidate the causes of interbreed differences in the context of the occurrence of a specific level of reproductive traits, as well as to broaden the knowledge on the genetic control mechanisms of cattle reproductive traits.

17.09.2019, Sara Tabor-Osowska