

## ABSTRACT

Among the group of cationic peptides, we can distinguish cathelicidins, which are antimicrobial peptides (AMPs). They are found in many vertebrates, where they play a significant role in the immune system. In cattle, there are seven cathelicidins encoded by seven different genes. The cathelicidins, due to their antimicrobial, antiviral and antifungal properties and the fact that they are found, among others, in the mammary gland, may represent a group of peptides that are important for both preventing and supporting the immune system during mastitis. The occurrence of differences at the DNA level is referred to as polymorphism, and these changes are the result of molecular processes, including mutations, which can become fixed or disappear in the course of evolution and adaptation to a changing environment. The search for polymorphisms that can shape performance traits and be used to improve marker-assisted animal selection programmes is an issue worth continuing.

The main aim of this study was to analyze polymorphisms occurring within the *CATHL2*, *CATHL3*, *CATHL5*, *CATHL6*, and *CATHL7* genes in Polish Holstein-Friesian Black and White dairy cattle and to establish potential relationships between genotypes of analyzed gene fragments and performance traits in dairy cattle.

The study included Holstein-Friesian Black and White cows from which peripheral blood was collected for DNA isolation. Experiments were designed for 13 polymorphic sites and, in the case of the determination of 12 polymorphisms, the ACRS method was used during the design of the primers in order to create a cut site for the restriction enzyme. Assays were carried out using the PCR-RFLP method, by which polymorphisms located within the genes encoding cathelicidins were analyzed. The obtained products were digested with restriction enzymes. The obtained results were examined by statistical analysis, which revealed associations between the genotypes and selected parameters of milk performance, such as milk yield, protein, fat and lactose content in milk and somatic cell count. In addition for the *CATHL2/MseI* polymorphism, a correlation was made between the obtained genotypes and selected reproductive indices: interbreeding period, inter-pregnancy period, length of pregnancy, length of drying period, postpartum rest period, insemination service period and insemination index.

The results confirmed the presence of three genotypes in all polymorphisms tested and statistically significant differences between polymorphisms and selected parameters ( $P \leq 0.01$ ,  $P \leq 0.05$ ).