Abstract

Introduction: *Mastitis* is an inflammation of the mammary gland, which can occur either in the form of easily visible clinical symptoms or in a subclinical form diagnosed on the basis of indirect indicators such as somatic cell count in milk. The disease is caused by microorganisms (bacteria, viruses, fungi), whose presence in the cow's udder tissues triggers inflammation. It has been found that there are genetic differences in susceptibility/resistance to udder inflammation in dairy cattle. Susceptibility or resistance to *mastitis* is a multi-gene trait, whose inheritance mechanism is difficult to trace due to non-additive interactions between genes and interactions between genes and environment. Cow breeding programmes aimed at reducing the incidence of *mastitis* use genetic differences in susceptibility/resistance to the disease to search for genetic markers associated with udder inflammation.

In this dissertation, I analyse polymorphic variants of genes whose products are associated with the autophagy process (*CTSD*, *PRKCQ*, *SH3GLB1*, *BCL2* and *ATG14*). Autophagy is essential for the regulation of the immune response (both specific and non-specific) to infection and it can therefore be hypothesised that polymorphisms located in the genes whose products are involved in this process may be associated with resistance or susceptibility to *mastitis*. In addition, during my study I estimated the non-additive effects of the analysed genes and examined the effects of the individual genes whose expression levels may depend on the physiological condition of the animal.

Aim: The aim of this study was to search for associations between the polymorphic variants of the *CTSD*, *PRKCQ*, *SH3GLB1*, *BCL2* and *ATG14* genes and resistance to *mastitis* in Black-and-White Holstein-Friesian dairy cows, and to estimate possible non-additive effects between the genes under study and the variability of the gene effects in relation to environmental factors.

Material and methods: The material for the study was peripheral blood collected from 745 cows, from which DNA was isolated and analysed by PCR. The animals were kept under identical environmental conditions and subjected to milk performance testing using the A4 method. The results of the study were analysed statistically for individual lactation stages (I, II, III), subsequent lactations (I, II, III, IV, V and VI) and all lactations combined, and according to the health class of the cow (clinical, subclinical *mastitis*). Additionally, cows suffering from clinical *mastitis* were included in the study. Clinical cases were documented by an experienced veterinarian, who recorded data on the incidence of *mastitis acuta* and