Inflammatory state of the mammary gland (mastitis) is mainly caused by bacteria. Mastitis is characterized by physical, chemical and microbiological changes in the milk composition. Both clinical and subclinical mastitis causes economic losses. Commonly two groups of staphylococci, important agents of mastitis, are distinguished: coagulase-positive (CoPS) and coagulase-negative (CoNS). CoPS cause predominantly chronic subclinical mastitis while CoNS are considered as minor pathogens causing mild clinical disease. The study was performed to measure differences in the level of expression of genes CXCL5, ITGAL and CCR1 in udder secretion tissue taken from cattle infected with CoPS and CoNS and from healthy animals. The study was conducted on 40 Polish Holstein-Friesian cows of Black-and-White variety. The animals were suffering from chronic and recurrent mastitis. Altogether, 51 parenchyma samples from udder quarters were collected: CoPS-infected (N=25), CoNS-infected (N=13) and non-infected (N=13). Total RNA was isolated using RNeasy Mini Kit (Qiagen), then cDNA templates were prepared and gene expression was determined using qPCR (LightCycler 480, Roche). The GAPDH gene was used as a reference. The expression level of the CXCL5 gene was higher in samples of animals infected with CoPS and CoNS than in non-infected ones. There were differences in the ITGAL gene expression between all three studied groups: higher mRNA level was in the CoPS-infected than in the CoNS-infected samples, and higher mRNA levels in the CoPS-infected and CoNS-infected samples than in non-infected ones. However, no differences in the expression of the CCR1 gene between studied groups were observed. Increased expression of studied genes in both CoPS-infected and CoNS-infected animals proves that CoNS also trigger the immunity of udder secretory tissue, although, they are considered as less pathogenic bacteria.