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EXPRESSION ANALYSIS OF *CCL20* IN CELLS FROM THE MILK OF GYR COWS BEFORE AND 24 HOURS AFTER ARTIFICIAL INFECTION WITH *STREPTOCOCCUS AGALACTIAE*

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Dairy cattle breeds of European origin are recognized as being more productive and also more demanding in terms of management and nutrition than are Zebu breeds. Therefore, the expected higher production is not always borne out in tropical regions in dairy farms that are less technically advanced. Among the zebuine breeds, the Gyr breed is particularly well adapted to Brazilian environmental conditions. For this reason, it has been intensely used in crosses, and is the preferred breed for the formation of crossbred dairy herds in Brazil. Several factors affect dairy production, among animal health problems, infecto-contagious diseases stand out the most, and mastitis is the main such disease afflicting dairy cattle from an economic standpoint. Mastitis is an inflammatory response of the mammary gland caused frequently by pathogenic microorganisms. The genes involved in the immune response have been indicated as likely candidates for understanding resistance and susceptibility to this disease. The identification of factors that contribute to the predisposition of the mammary gland to mastitis will facilitate the development of new strategies to control this disease, such as identification of genes that can be used as markers in animal breeding programs. Therefore, by means of real time PCR technique it was evaluated the profile for the expression of *CCL20* (*chemokine C-C motif ligand 20*) gene in milk cells of 17 Gyr cows artificially inoculated with a strain of *Streptococcus agalactiae*. Milk samples were collected before inoculation (hour 0) and 24 hours after inoculation. Total RNA was extracted from milk and the first strand of the cDNA was synthesized. Primers used to analyze *CCL20* gene expression and both endogenous references (*RPLP0* - ribosomal protein large P0 - and *Ubiquitin*) were designed using *Primer Express* software (Applied Biosystem) based on sequences from *GenBank* database. Statistical analysis were performed using REST©2009 software, developed by M. Pfaffl (Technical University Munich) and Qiagen. Comparisons between gene expression levels indicated that on time 24, animals expressed 13.2 times more *CCL20* than on time 0 ($p < 0.001$). CCL20 is a chemokine that interacts with the CCR6 receptor and the CCL20-CCR6 pair is responsible for the chemoattraction of immature dendritic cells, T effector cells and B cells. The recruitment of these cell types provides the link to the humoral immune response. During bacterial infection of the bovine mammary gland, a large number of leukocytes migrate to the udder to establish the response against the pathogen. However, the population of leukocytes is not yet well defined, therefore studies of gene expression related to the immune response can help to better characterize this population and to understand how the host responds to a determined pathogenic microorganism. Financial Support: CNPq, CAPES, FAPEMIG and EMBRAPA/AGROFUTURO