Resumos do 57º Congresso Brasileiro de Genética • 30 de agosto a 2 de setembro de 2011
Centro de Convenções do Hotel Monte Real Resort • Águas de Lindóia • SP • Brasil
www.sbg.org.br - ISBN 978-85-89109-06-2

Relative expression of *IL-12* gene on milk cells from Dairy Gyr cows infected with *Streptococcus agalactiae*

Fonseca, I[1]; Pinto, ISB[2]; Rettore, JVP[3]; Ferreira, MBD[4]; Brito, MAVP[2]; Brandão, HM[2]; Guimarães, SEF[1]; Martins, MF[2]
[1]Universidade Federal de Viçosa, UFV, Viçosa, MG, [2]Embrapa Gado de Leite, Juiz de Fora, MG, [3]Universidade Federal de Juiz de Fora, MG, [4]Fazenda Experimental Getúlio Vargas, Centro Tecnológico do Triângulo e Alto Paranaíba, EPAMIG
isabela.f.fonseca@ufv.br

Keywords: Immune response, Mastitis, qPCR

Dairy cattle farming is one of the most important activities of the Brazilian agricultural industry, however such factors as weather, infrastructure, labor, zootechnical and genetic potential, public politics and animal health cause the activity to be expensive and of low yield for many breeders. Mastitis is characterized by the presence of an inflammatory response in the mammary gland caused by metabolic and physiological alterations, injuries or, more frequently, pathogenic microorganisms, being speed and efficiency of the host's immune response a crucial factor for establishment, persistence and severity of the infection. Associated with sanitary care, the selection of animals that are resistant to the disease and the incorporation of this trait into the herds seem to be a promising way to reduce problems caused by this disease. Many genes are involved on the determination of mastitis resistance or susceptibility, and so the present work aim was to characterize the expression of *interleukin 12 (IL-12)* gene in milk cells from dairy Gyr cows, infected with *Streptococcus agalactiae*, one of the main pathogens that causes mastitis, before (time 0) and 10 hours after the inoculation with the pathogen (time 10), in order to better understand the mechanism of immune response. Total RNA was extracted from milk cells of 17 animals raised by Getulio Vargas Experimental Farm-EPAMIG, located in Uberaba, State of Minas Gerais, Brazil. Milk was collected immediately before inoculation with the pathogen and 10 hours after. First strand of the cDNA was synthesized and gene expression was analyzed using Real Time PCR technique. Primers used to analyze *IL-12* gene expression and both endogenous references (*RPLP0* and *Ubiquitin*).were designed using *Primer Express* software (Applied Biosystem) based on sequences from *GenBank* database (http://www.ncbi.nlm.nih.gov). Statiscal analysis were performed using REST©2009 software, developed by M. Pfaffl (Technical University Munich) and Qiagen, available at http://www.gene-quantification.de/rest-2009.html. Comparisons between gene expression levels indicated that on time 10, animals expressed 2.4 times more *IL-12* than on time 0 ($p < 0.05$). IL-12 is a cytokine synthesized by T-lymphocytes and dendritic cells, acting as a mediator between innate and acquired immune response. This protein regulates differentiation of T-lymphocytes and recruits neutrophils, which arriving on infection site phagocyte infecting bacteria and release antibacterial peptides, among other compounds. Due to the functions redeemed by this cytokine, gene expression levels were expected to raise on time 10, when compared with time 0. The identification and characterization of gene expression on animals with mastitis is essential on the search for genes that could be tested and validated as markers for such physiological conditions.
Financial Support: CNPq, FAPEMIG, CAPES and EMBRAPA/AGROFUTURO