SP 5304 P. 167
2011
SP-PP-5304

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

Expression analysis of *IL-1β* in cells from the milk of Gyr cows before and after artificial infection with *Streptococcus agalactiae*

Martins, MF[1]; Fonseca, I[2]; Pinto, ISB[1,5]; Pereira, WP[3]; Guimarães, SEF[2]; Ferreira, MBD[4]; Brito, MAVP[1]; Brandão, HM[1]
1Embrapa Gado de Leite, Juiz de Fora, MG, 2Universidade Federal de Viçosa, UFV, Viçosa, MG, 3Centro de Ensino Superior de Juiz de Fora, Juiz de Fora, MG, 4Fazenda Experimental Getúlio Vargas, Centro Tecnológico do Triângulo e Alto Paranaíba, EPAMIG, 5Bolsista de Apoio Técnico II - FAPEMIG
mmartins@cnpgl.embrapa.br

Keywords: Gene expression, Mastitis, Real Time PCR

Among the sanitary problems in animal production, infectious diseases are the most distinctive, with mastitis being one of the main diseases in the economics aspect of dairy cattle. This disease is characterized by an inflammatory response in the mammary gland, often caused by pathogenic microorganisms, whose speed and effectiveness of host immune response is crucial for the establishment, persistence and severity of infection. However, not always the phenotype of resistance/susceptibility is associated with mutations in the gene responsible for the characteristic, sometimes this phenotype can be made by simple changes in the level of expression or, alternatively, by the late expression of given gene, when compared with other phenotypes. This information can be used later in animal breeding, providing an effective approach to increase the genetic resistance to disease. Thus, in order to better understand the mechanisms involved in immune response in phenotype resistance/susceptibility to mastitis, the relative quantification expression of the *IL-1β* gene (interleukin 1β) was performed on milk cells from Dairy Gyr cows infected artificially with *Streptococcus agalactiae*, one of the most important pathogens causing mastitis. Milk samples were collected (200 mL) from 17 cows, immediately before the inoculation of pathogen (time 0) and 10 h after the inoculation (time 10). Total RNA was extracted from cells present in the milk, the first strand of cDNA was synthesized and the analysis of gene expression was performed using the methodology of Real-Time PCR. The primers used to evaluate the expression of *IL-1β* gene and the two endogenous controls (*RPLPO* and *Ubiquitin*) were designed using Primer Express (Applied Biosystems) software from sequences obtained from GenBank database (http://www.ncbi.nlm.nih.gov). Statistical analysis was performed by REST©2009 software, developed by M. Pfaffl (Technical University Munich) and Qiagen, available at http://www.gene-quantification.de/rest-2009.html. Comparison of gene expression level of the animals at different times when milk was collected showed that in time 10 there was an increase of 12 times in the expression of the *IL-1β* gene in relation to time 0 ($p<0.001$). IL-1β is a key component of the innate immune response accelerating the inflammatory response. IL-1β is responsible for recruiting neutrophil during the infection on the mammary gland, when the macrophages recognize invading bacteria, they release IL-1β, stimulating the bactericidal activity of neutrophils and also producing prostaglandins and leukotrienes, which increase the local inflammatory reaction. The significant difference in the expression of *IL-1β* gene suggests that it plays an important role in the mechanisms of resistance to cattle mastitis.
Financial Support: CNPq, FAPEMIG, CAPES and EMBRAPA/AGROFUTURO

SP 5304
P-167