EuroSciCon

June 21-22, 2018
Paris, France

EuroSciCon Conference on
Microbiology & Virology

Arch Clin Microbiol 2018 Voulume: 9
DOI: 10.4172/1989-8436-C3-012

BIOINFORMATICS: DETERMINATION OF GENE EXPRESSION PROFILE FOR SOME HUMAN IMMUNE GENES AFTER INFECTION WITH EBOLA VIRUS

Abdulrhem T Al-Ghazal
University of Mosul, Iraq

Objectives: Ebola virus (EBOV), a member of the Filoviridae family, causes severe and often lethal hemorrhagic fever in humans and nonhuman primates. The infection with EBOV causes the release of proinflammatory cytokines and chemokines which may represent factors of the severity of the hemorrhagic shock. Determining the level of human mRNAs of immune inflammatory cytokines after EBOV infection is regarded as important aspect to understand the relationship between EBOV and its host at molecular level.

Methods: Sixteen immune genes were subjected to this study using analysis of Real-time-reverse transcription PCR-array (RT-PCR-array, SABioscience). Control genes were taken from previous studies to get the fold change of gene expression.

Results: The results showed that all subjected genes were up regulated with different fold change (FC) (CCL20 CCL23,CCL3, CCL4, CCL5, CCL8, CCR2, CCR7, CXCL2, CXCL3, CXCL6, IFNA2, IL10, IL1A, IL1B and TNF) ranged between 52.1797 FC for CCL20 and 4.3032 FC for TNF. These results revealed that EBOV has severe impact on specific human immune inflammatory genes.

bakurius@yahoo.com