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Investigation of long noncoding RNA (lncRNA) in Crimean-Congo Hemorrhagic Fever patients

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Statement of the Problem: Crimean–Congo Hemorrhagic Fever (CCHF) is a fatal disease caused by the CCHF virus. Viral infections cause significant changes in cell transcriptomy including long non-coding RNA (lncRNA). Some lncRNAs expressed in infected cells are used to regulate the expression of viral and host genes. Expression of cellular lncRNAs can lead to altering the antiviral response. The aim of this study is to investigate of lncRNA gene expression profiles in CCHF patients at first time of the world.

Methodology & Theoretical Orientation: The lncRNAs expression levels were compared between case and control populations. Total RNA extraction from blood was performed according to protocol with PAX gene blood RNA kit. RIN values of samples were determined using 2100 Bioanalyzer (Agilent Technologies). For microarray, lncRNA gene expression was determined using Sure Print G3 Human gene expression v3 (Agilent Technologies). Results of lncRNAs expression were analyzed by GeneSpring (Ver 3.0) bioinformatics program. Microarray results of some important lncRNAs were validated using RT-PCR.

Findings: As a result of bioinformatics analysis of microarray data in CCHF patient and control group, 36 lncRNA was found statistically significant. Five of these lncRNAs were down-regulated, while 31 lncRNA were up-regulated according to the control group. Among the significant lncRNAs, the highest down regulation was lnc-SAMD11-2 (fold change: 40.37; p: 0.03); the highest up

regulated FER1L4 (fold change: 17.67; p <0.01).

Conclusion & Significance: In this study, lncRNAs, which are important in the pathogenesis of CCHF, were first detected in the world. This results obtained from the study will contribute to explain the role of lncRNAs in pathogenesis of CCHF.

Recent Publication

1. Bayburt B, Arslan S, Özbilüm N, Engin A and Bakir M (2018) HULC and 7SL RNA expression levels in patients with Crimean-Congo hemorrhagic fever. *Journal of Medical Virology* 90(12):1822-1826.
2. Kızıldağ S, Arslan S, Özbilüm N, Engin A and Bakir M (2018) Effect of TLR10 (2322A/G, 720A/C and 992T/A) polymorphisms on the pathogenesis of Crimean Congo hemorrhagic Fever Disease. *Journal of Medical Virology* 90(1):19-25.
3. Arslan S, Berkan O, Lalem T, Özbilüm N, Goksel S, Korkmaz O, Çetin N and Devaux Y (2017) Long non-coding RNAs in the atherosclerotic plaque. *Atherosclerosis* 266:176-181.
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5. Bakır M, Gözel M G, Köksal I, Aşık Z, Günel Ö, Yılmaz H, But A, Yılmaz G and Engin A (2014) **Validation of a severity grading score (SGS) system for predicting the course of disease and mortality in patients with Crimean-Congo hemorrhagic fever (CCHF). Eur J Clin. Microbiol. Infect. Dis. 34(2):325-30.**

Biography

Serdal Arslan works as an Associate Professor at Department of Medical Biology, Faculty of Medicine, Sivas Cumhuriyet University (Turkey). He has a PhD Degree of Molecular Biology. His expertise is molecular medicine. He has been working on noncoding RNAs in different diseases especially infectious diseases. He has been conducting molecular genetic studies in Crimean–Congo Hemorrhagic Fever disease in recent years.

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