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PCR array profiling of antiviral genes in human embryonic kidney cells expressing *Human coronavirus OC43* structural and accessory proteins

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Background & Objective: *Human coronavirus OC43* (*HCoV-OC43*) causes common cold and is associated with severe respiratory symptoms in infants, elderly and immunocompromised patients. *HCoV-OC43* is a member of *Betacoronavirus* genus that also includes the Severe Acute Respiratory Syndrome (SARS) and the Middle East Respiratory Syndrome (MERS) coronaviruses. Both *SARS-CoV* and *MERS-CoV* were shown to express proteins with the potential to evade early innate immune responses. However, the ability of *HCoV-OC43* to antagonize the intracellular antiviral defense has not yet been investigated. The objective of this study was to investigate the role of *HCoV-OC43* structural (membrane and nucleocapsid) and accessory (ns5a and ns2a) proteins in the modulation of antiviral gene expression profile in human embryonic kidney 293 (HEK-293) cells using PCR array analysis.

Method: *HCoV-OC43* membrane (M), nucleocapsid (N), ns5a and ns2a mRNA were amplified and cloned into the pAcGFP1-N expression vector (Clontech), followed by transfection in HEK-293 cells. Expressions of M, N, ns5a and ns2a proteins were confirmed by indirect immunofluorescence test. Three days post-transfection, the cells were challenged by Sendai virus. The human antiviral response PCR array system (Qiagen) was used to profile the antiviral gene expression in HEK-293 cells, using the fold regulation comparison and the manual normalization methods.

Result: Around 50-60 genes were down-regulated by *HCoV-OC43* proteins, the most prominent genes being those critical for the activation of transcription factors involved in the antiviral response like interferon regulatory factors (IRFs) and activator protein-1 (AP-1). Among the most important down-regulated genes were those coding for interferons (IFNs) mitogen-activated protein kinases (MAPKs), pro-apoptotic and pyroptotic proteins (Caspases, cathepsins, tumor necrosis factor), pro-inflammatory cytokines (interleukins), pattern recognition receptors (PRRs; toll-like receptors and NOD-like receptors) and their signaling transduction proteins (TICAM1, MAVS).

Conclusion: This study shows for the first time that similarly to *SARS-CoV* and *MERS-CoV, HCoV-OC43* has the ability to down-regulate the transcription of genes critical for the activation of different antiviral signaling pathways.

Biography

Meshal Beidas has completed his MSc from the University of Leeds. He is currently pursuing PhD in Medical Microbiology at Kuwait University, Kuwait.

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