CHLAMYDIA TRACHOMATIS INFECTION AND DEVELOPMENT OF EPITHELIAL MESENCHYMAL TRANSITION IN CONJUNCTIVA: POSSIBLE EPIGENETIC MECHANISMS UNVEILED

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Introduction: Trachoma is the most common cause of infectious blindness worldwide, initiated by repeated infection of the conjunctiva with *Chlamydia trachomatis* (*Ct*). The resulting chronic inflammation and formation of fibrotic tissue eventually lead to corneal damage. Based on the facts that epithelial to mesenchymal transition (EMT) plays an important role in the development of fibrosis and that EMT is epigenetically regulated process, the aims of this study were to reveal the capacity of *Ct* to induce EMT *in vitro* and to unveil potential underlying epigenetic mechanisms.
Methods: Human conjunctival epithelial (HCjE) cells were infected with 10^7 IFU of *Ct* for 72 h. EMT-inducing signaling pathways, as well as mRNA and protein expression of EMT markers (E-cadherin, fibronectin and a-SMA) were evaluated by RT-qPCR, Immunoblotting and Immunocytochemistry. DNA methylation patterns of selected regions of E-cadherin, fibronectin and a-SMA genes were examined by Methylation-Specific PCR, High Resolution Melting analysis and Bisulfite Sequencing.
Results: Infection with *Ct* was accompanied with the activation of EMT-inducing signaling pathways, downregulation of epithelial marker E-cadherin and upregulation of mesenchymal markers fibronectin and a-SMA. While DNA methylation status of E-cadherin gene promoter correlated with its expression, methylation status of fibronectin and a-SMA genes couldn't be related to their expression levels.
Conclusion: *Ct* infection of HCjE cells triggers EMT that goes along with changes in the methylation profile of the E-cadherin promoter. Sequence of events described herein could contribute to scarring process in trachoma and open up possibilities for development of new therapeutic strategies in trachoma treatment.

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