Differential regulation of the transcriptomic and secretomic landscape of sensor and effector functions of human airway epithelial cells.

Lehmann R, Müller MM, Klassert TE, Driesch D, Stock M, Conrad T, Moore C, Schier U, Guthke R, Slevogt H (2018) Differential regulation of the transcriptomic and secretomic landscape of sensor and effector functions of human airway epithelial cells. *Mucosal Immunol* 11(3), 627-642.

Abstract

Protein secretion upon TLR, TNFR1, and IFNGR ligation in the human airways is considered to be central for the orchestration of pulmonary inflammatory and immune responses. In this study, we compared the gene expression and protein secretion profiles in response to specific stimulation of all expressed TLRs and in further comparison to TNFR1 and IFNGR in primary human airway epithelial cells. In addition to 22 cytokines, we observed the receptor-induced regulation of 571 genes and 1,012 secreted proteins. Further analysis revealed high similarities between the transcriptional TLR sensor and TNFR1 effector responses. However, secretome to transcriptome comparisons showed a broad receptor stimulation-dependent release of proteins that were not transcriptionally regulated. Many of these proteins are annotated to exosomes with associations to, for example, antigen presentation and wound-healing, or were identified as secretable proteins

related to immune responses. Thus, we show a hitherto unrecognized scope of receptor-induced responses in airway epithelium, involving several additional functions for the immune response, exosomal communication and tissue homeostasis.

Involved units

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Leibniz-HKI-Authors

Theresia Conrad

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Reinhard Guthke

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doi: 10.1038/mi.2017.100

PMID: 29297499