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## Alterations of the proteome and transcriptome in induced sputum samples from smokers and early-stage COPD subjects

Thomas Schneider, Bjoern Titz, Alain Sewer, Ashraf Elamin, Florian Martin, Sophie Dijon, Emmanuel Guedj, Gregory Vuillaume, Marja Talikka, Michael J Peck, Nveed I Chaudhary, Nikolai V Ivanov, Julia Hoeng and Manuel C Peitsch  
Philip Morris International, Switzerland

Chronic Obstructive Pulmonary Disease (COPD) is one of the most prevalent lung diseases characterized by poorly reversible airflow limitation and incorporating both emphysema and chronic bronchitis. Cigarette smoking has been identified as a key risk factor for disease development and progression. In a basic model of COPD the disease is initiated when the physiologic response mechanisms to cigarette smoke exposure are compromised, example because of long-term exposure effects combined with aging-related changes. In this parallel-group, case-controlled clinical study we asked to which extent the biological effects in this chronic-exposure-to-disease model are reflected in the proteome and cellular transcriptome of induced sputum samples. For this, 60 age and gender-matched individuals for each of four study groups were selected: Current asymptomatic smokers, current-smoker COPD patients, former smokers and never smokers (total of 240 subjects). Induced sputum was collected, the cell-free supernatant was analyzed by quantitative proteomics (isobaric-tag based) and the cellular mRNA fraction was analyzed by microarray-based expression profiling. The sputum proteome of current smokers (asymptomatic or COPD patients) clearly reflected the common physiological responses to smoke exposure including alterations in mucin/trefoil proteins, peptidase regulators and a prominent xenobiotic/oxidative stress response. The latter also induced the sputum transcriptome perturbations which additionally revealed an immune-related polarization change. The (long-term) former smoker group showed minor observable effects when compared to never smokers. In summary, our study demonstrates that sputum proteomics/transcriptomics analyses can capture the complex physiological response to cigarette smoke exposure which appears to be only slightly modulated in early-stage COPD patients.

### Biography

Thomas Schneider has completed his PhD from University of Zurich and Post-doctoral studies in microbiology and molecular plant physiology at the University of Zurich with a focus on quantitative analyses of complex proteomes from different origins. Since 2012 he is working as a Scientist at the Philip Morris International Research & Development Center in Neuchatel, Switzerland. He has published more than 20 papers in the field of quantitative proteomics in reputed journals.

[Thomas.Schneider@pmi.com](mailto:Thomas.Schneider@pmi.com)

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