Systems Toxicology of Wood Smoke

M. Dilger, Eggenstein-Leopoldshafen/DE, L. Ramme, Eggenstein-Leopoldshafen/DE, S.C. Sapcariu, Esch-Belval/LU, S. Mülhopt, Eggenstein-Leopoldshafen/DE, C. Schlager, Eggenstein-Leopoldshafen/DE, A. Reda, Munich/DE, J. Orasche, Munich/DE, O. Armant, Eggenstein-Leopoldshafen/DE, E. Maser, Karlsruhe/DE, A. Hartwig, Karlsruhe/DE, R. Zimmermann, Munich/DE, K. Hiller, Esch-Belval/LU, S. Diabaté, Eggenstein-Leopoldshafen/DE, H.-R. Paur, Eggenstein-Leopoldshafen/DE, C. Weiss, Eggenstein-Leopoldshafen/DE

PD Dr. Carsten Weiss, Karlsruhe Institute of Technology (KIT), Institute of Toxicology and Genetics (ITG), Hermann-von-Helmholtz-Platz 1 76344 Eggenstein-Leopoldshafen

Air pollution is one of the prime causes for premature death. A growing number of epidemiological studies have linked air pollution to adverse health effects like respiratory and cardiovascular symptoms or lung cancer. Nevertheless, the relevant constituents of air pollution, which are responsible for different adverse effects and the underlying toxicity pathways have yet to be identified. Here, we address this knowledge gap by focusing on wood combustion, an important source for air pollution.

In order to identify the toxic constituents of wood smoke aerosol, we exposed human A549 and BEAS-2B cells to 1:10 diluted wood smoke using a recently developed air-liquid-interface exposure system. We first characterized the effects of wood smoke by transcriptional profiling using genome-wide mRNA-sequencing. The disturbance of affected cellular pathways identified by bioinformatic approaches was verified by targeted analysis of selective markers by established assays. To determine the responsible aerosol constituents initiating the molecular actions of wood smoke, we hypothesized that the transcriptional signatures can be used to query toxicogenomic databases and discover compounds triggering similar gene expression profiles thus providing potential lead candidates.