

More effective approach to show changes in human metabolism with molecular maps

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By applying multi-platform metabolomics, wide range of metabolites were detected and quantified in both human plasma and lung lavage fluid. Metabolites showed different trends in response to interventions such as different meal and biodiesel exhaust exposure. Masoumeh Karimpour defends her dissertation on Wednesday 15 June at Umeå University.

The word metabolism originates from the Greek word "μεταβολισμός" (metabolismós), which means "change". Input from the environment and lifestyle can affect human metabolic pathways. Hence, the study of metabolism and its constituents, the metabolites, is a powerful way to elucidate factors behind the influence of the environment on humans. Metabolomics is used to track changes and perturbations in the human body by investigating metabolite profiles indicating the change of metabolite levels over time and in response to different challenges.

In Masoumeh Karimpour's dissertation work, the main focus was on applying multiplatform-metabolomics (mass spectrometry and nuclear magnetic resonance) to study the human metabolome following exposure to perturbations, such as diet (in the form of a challenge meal) and exhaust emissions (air pollution exposure in a controlled setting).

For the initial pilot postprandial study, the aim was to investigate the plasma metabolome response after a well-defined meal during the postprandial stage for two types of diet (vegan and vegetarian). It was found that independent of the background diet type, levels of

metabolites returned to their baseline levels after three hours.

In air pollution study, considerable number of metabolites were detected and identified in lung lavage fluid after biodiesel exhaust exposure compared to filtered air exposure. A number of metabolites in bronchial wash, bronchoalveolar lavage, and plasma were shown to be responsive to biodiesel exhaust exposure.

The use of multiplatform-metabolomics was found to enhance the metabolome coverage and to provide complementary findings that enabled a better understanding of the biochemical processes reflected by the metabolite profiles. In summary, the new analytical methods developed to investigate the responsiveness of the human plasma and lung lavage metabolome proved to be useful in an analytical perspective, and provided important biological findings.

Extension of metabolomics strategies and analysis methods to detect and identify more [metabolites](#) and at lower levels will help to elucidate the mechanisms behind the effects of interventions and environmental influences on the [human](#) body. Specifically, exposure-related effects on cardiorespiratory or other similar diseases could facilitate the identification of disease specific biomarkers, drug development and illness treatment.

More information: Read the dissertation:
[urn.kb.se/resolve?urn=urn:nbn:se:umu:diva-120591](https://nbn-resolving.org/urn:nbn:se:umu:diva-120591)

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