

Strategies for suspect and non-targeted screening of new emerging chemicals in human biomonitoring **Martin Krauss & Carolin Huber**



General concepts

Target analysis/ target screening



Quantify 10s-100s of *known* compounds

• Suspect screening of expected contaminants



Detect & confirm 100s (1000s?) of *known* compounds

• Non-target screening (NTS) for fingerprinting of mixtures and discovery of new chemicals

Detect **"ALL"** known & *unknown* compounds





Screening methods & compound domains





Non-target screening: workflow



Modified from Hollender, Schymanski, Singer & Ferguson, 2018, ES&T Feature, 51:20, 11505



Non-target screening: workflow



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Non-target screening: workflow



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NTS of water samples



Small river *upstream* of wastewater treatment plant

Small river *downstream* of wastewater treatment plant

Large peaks are (mainly) anthropogenic contaminants



Challenges in NTS of biological samples



Urine samples (1 batch), direct injection after filtration

>180'000 peaks

- Xenobiotic compounds are typically small peaks against the biological background
- Severe matrix effects
- MS¹ and MS² spectra have a high background noise



Challenges in NTS of biological samples



Search for halogenated compounds based on isotopologue pattern (e.g., HaloSeeker) *Léon et al., Anal. Chem. 91:3500*

Search for compounds with time trends in time-series samples *Plassmann et al., Anal. Bioanal. Chem.* 408, 4203

Compound-class specific analysis (diagnostic fragments/neutral losses)

Comparison of exposure and control groups

Massive (metabolome) annotation and expanding MS² libraries



Current activities at UFZ

- Automated high throughput suspect screening for heterocyclic and aromatic amines and their conjugates in direct injected urine samples based on tandem MS information
- High throughput screening strategy for biomarkers of pesticide exposure using in-vitro generation of metabolites





Suspect screening workflow at UFZ

Identifying Small Molecules via High Resolution Mass Spectrometry: Communicating Confidence

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Computational processing of HRMS data

- Development of workflows based
- on open source software packages
- Use of high performance computing Linux (centOS7) based calculation cluster 2564 cores / 25.8 TB RAM
- Example:
 - ~ 20 000 detected features per sample
 - >100 000 aligned features per batch (25 samples + QC)

Galaxy

Obtaining metabolite information for possible biomarkers

• Strategy I:

Literature Search => registration dossiers of pesticides

~130 parent compounds => List of ~800 suspects

 \Rightarrow only a few of them are commercially available at reasonable prices

• Strategy II:

S9 human liver experiments with parent compounds

⇒ Will also facilitate identification (RT and MSMS data generation of statistically relevant features)

Getting higher confidence for candidates

Human S9 liver experiments

Current activities within work package 16

• LC/GC-HRMS profiling of a exchange of existing EU cohort studies

 \Rightarrow Review of results 20-21/05/19

- Expanding HBM-relevant capabilities MS/MS libraries
- Curation of a suspect list of emerging contaminants for HBM (including metabolites)
- Comparison of existing/developed methods for
- quality assessment of screening procedures

Upcoming activities in WP 16

• WP 15-16 interaction: Joint survey on pesticide exposure in hotspots and control areas

Need to share work among four groups \Rightarrow Harmonisation

Thank you very much for the attention!

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