NORMAN Collaborative Non-target Screening Trial Workshop

Eawag, September 15-16, 2014

Background:

The NORMAN Collaborative Trial on Non-target Screening was part of the NORMAN Joint Plan of Action for 2013, following up from the NORMAN-JRC workshop in Stresa (2010) identifying the need for comparison and harmonisation of non-target screening methods in Europe. The organization, scientific and technical preparation, collection and evaluation of the results, preparation of the evaluation report, organisation of the related discussion workshop and dissemination of the results was conducted by EI, Eawag, UFZ, UMEA and LfU. The trail itself was connected to the International Joint Danube Survey 3 organised by the International Commission for the Protection of the Danube River (ICPDR; August/September 2013) and the samples for the trial were sampled within the survey.

Objectives:

Main objective:
To draft recommendations by the NORMAN Association on the use of non-target and suspect screening for the identification of emerging and river basin specific pollutants
Specific objectives:
(1) The analysis of samples using MS techniques established in each of the participating laboratories and declaration of:
    (a) how many substances are present in the sample, and
    (b) how many of them can be provisionally identified by suspect and non-target screening.
(2) Training dataset for storage and re-processing of raw mass spectral data
(3) Scientific publication(s)

Core Team:

The non-target screening trial, workshop and evaluation was organised by a core team consisting of Jaroslav Slobodnik, Ildi Ipolyi, Peter Oswald (Environmental Institute (EI), Slovak Republic), Juliane Hollender, Heinz Singer and Emma Schymanski (Eawag, Switzerland), Tobias Schulze and Martin Krauss (UFZ – Helmholtz Centre for Environmental Research, Germany) and Peter Haglund (University of Umeå (UmU), Sweden). Thomas Letzel (Technical University of Munich, TUM), provided retention index standards and the evaluation of those results.

The minutes of the collaborative trial were compiled by E. Schymanski based on the presentations, own notes, those of J. Schollee (Eawag) from the workshop and feedback from the core team.

Expectations of the Workshop:

The main aims and expectations of the workshop included an agreement on harmonized terminology, workflows and reporting formats, as well as a message to the subsequent NORMAN-SOLUTIONS workshop on non-target screening. Discussion also aimed to assess the basis for two publications (general and mass spectrometry) and potential follow-ups to the trial.

Timeline:

Collaborative Trial		*Results Evaluation*	
Application deadline	15 October 2013	Core team meeting	26 June 2014
Sample distribution	December 2013	Workshop with participants	15-16 Sept. 2014
Result submission	15 March 2014	Report and publication	December 2014

Sampling and Analysis

Sampling: The sample was collected from JDS57, downstream of Ruse/Giurgiu (RO/BG; rkm 488), 18th of September 2013 (see Figure 1). Preparation included a large volume solid-phase extraction of 1000 litres of water sample by UFZ (see Figure 2). A freeze dried aliquot equivalent to 1.5 L water was sent to each participant, along with a fabrication blank. Samples were dispatched from UFZ to EI and from EI to participants along with two retention index mixtures: LC-MS from TUM; GC-MS from EI. Sample reconstitution was to be performed according to the given instructions, but based on the needs of the analytical method.

Participants were requested to analyse with LC-HR-MS(MS) and/or GC-MS within two days from sample arrival and submit results within two months of the sample dispatch. The results and evaluation was discussed by the core team before the workshop.

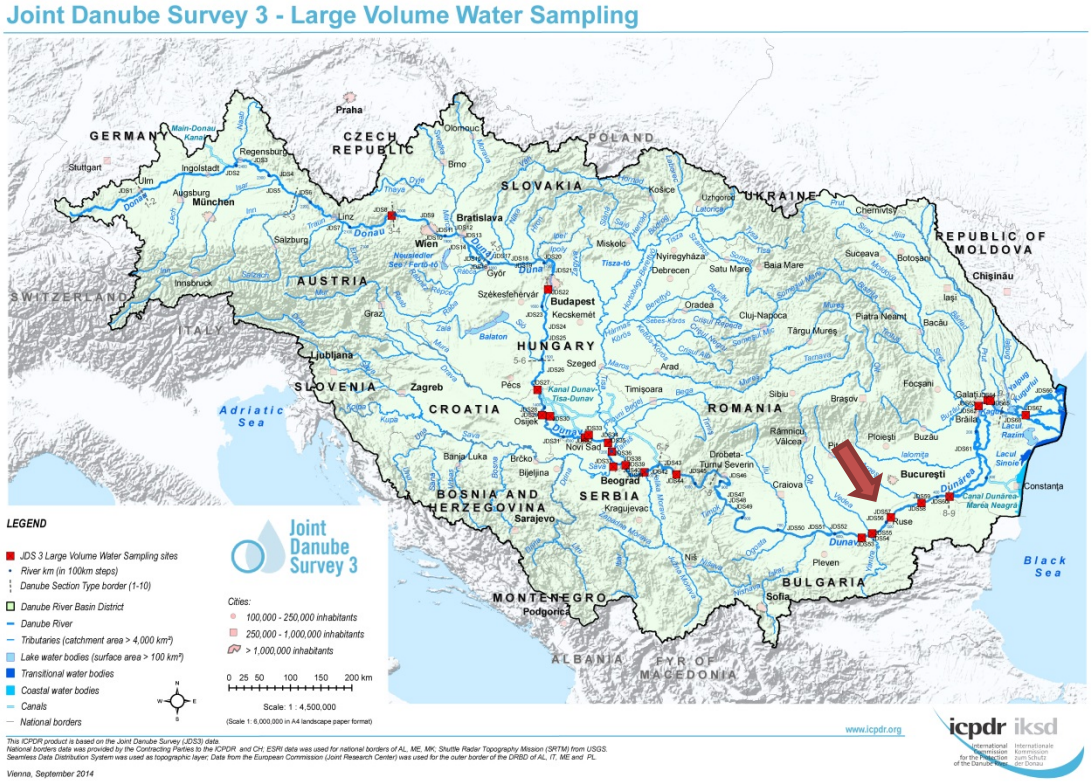

Figure 1: Overview map of the Joint Danube Survey. Map modified from the original provided by the International Commission for the Protection of the Danube River (ICPDR).

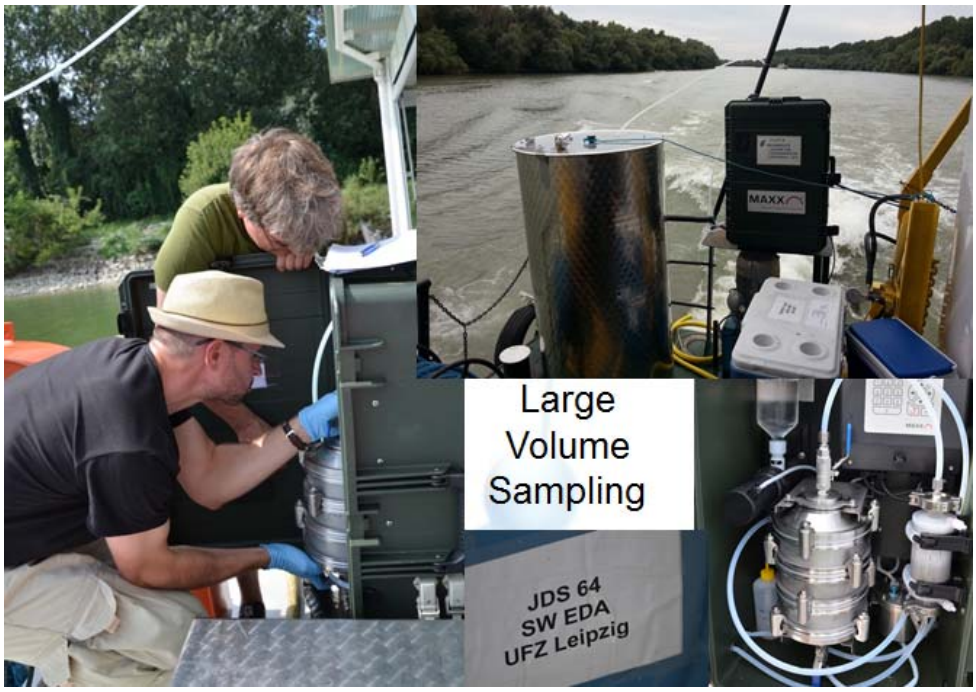

Figure 2: Large volume sampling on the Joint Danube survey. Collage source: Jaroslav Slobodnik.

Reporting Requirements

Mass spectrometry: Full scan chromatograms were to be provided along with the results and:

- the resolving power (with referenced *m/z*),
- collision energies used for generation of product ion spectra (e.g. MS/MS) and
- a parent mass lists including:
    - (a) the masses of all detected target compounds;
    - (b) all masses assigned to a suspect detected in the chromatogram;
    - (c) all masses of peaks picked for identification in non-target screening;
    - (d) retention times of all masses (not just targets); and
    - (e) intensities of all detected masses.

Data evaluation for the workflow concentrated on:

- Target screening – software
- Confirmation of identity of detected targets – procedure
- Suspect and non-target screening – software, procedures and databases used
- Retention time prediction method using standard mixture or own method (if applicable)
- Fragmentation prediction method (if applicable)

The definitions for participants to use in the reporting were given as follows:

- TARGET – substance ***WITH a standard available*** in the laboratory, ability to report provisional (semi)quantitative results;
- SUSPECT – substance ***WITHOUT a standard available*** in the laboratory, suspected to be present in the sample, searched based on the availability of a mass spectrum in mass spectral libraries or prior knowledge;
- NON-TARGET – substance not foreseen to be in the sample and identified using mass spectral elucidation tools;
- UNKNOWN – substances present in the sample remaining unknown.

Participants

A total of 26 institutes from 15 countries signed up for the collaborative trial and received samples. Seven institutes from 6 countries delivered GC-MS results (SUEZ Environment, University Jaume I (UJI), Rijkswaterstaat (RWS), University of Athens (UoA), VEOLIA, EI, UmU. Sixteen institutes from 10 countries delivered LC-MS results: NIVA, SUEZ Environment, University of Antwerp (UoA_TC), TUM, UJI, Eawag, RWS, UoA, VEOLIA, IRSTEA, UFZ, University of Padua (UoP), German Federal Institute of Hydrology (BfG), Langenau Water Supply (LW), Croatian Waters (CW) and University of Tübingen (UoT). Germany (6) and France (3) both had multiple representatives in the LC-MS category, while two French representatives also participated in the GC-MS category. The participants ranged from institutes experienced in non-target screening and those using the trial to perform non-target screening for the first time. Eight institutes did not deliver any results; the reasons for non-submission generally included instrumentation issues and lack of time.

Sample Stability and Homogeneity Testing (I. Ipolyi)

GC-MS (20 substances, EI) and LC-MS (50 substances, UFZ) methods were used to evaluate the sample stability. Three to five time-points were collected over 1 month under refrigerated conditions for stability, while the homogeneity was tested on three replicates. The conclusion was that the sample exhibited sufficient homogeneity and stability for the purpose of the collaborative trial.

Results Collection (via DCTs) and Data Evaluation

The data collection templates (DCTs) were modified from the NORMAN DCTs and structured in a way to ensure the necessary minimum information was available for a sound evaluation. These proved very demanding to fill in properly and ***will need to be revised for future trials***. The participants felt that these were complex and time-consuming to fill in, while the definitions and fields were confusing. From the evaluator perspective, the information provided was very varied and it was challenging to find a common point for the evaluation due to inhomogeneity in the datasets received. The following points were reassessed during pre-treatment:

- Method reporting: it was not clear to all participants that the “method” entry was generic as LOQs and LODs were requested, which are substance specific (high reporting demand).
- Re-categorisation of the data:
    - Some institutes separated based on the analytical method (target vs non-targeted acquisition) rather than *how* the substance was identified
    - Due to confusion with the definitions, “targets”, “suspects” and “non-targets” and “unknowns” were re-categorized to be consistent with agreed definitions. As agreed during the workshop, “non-targets” and “unknowns” were merged into one category.
- Generation of comparable substance identifiers (SMILES ⇔ CAS ⇔ InChI Keys)
    - Some institutes only provided CAS (non-unique, no structure), some SMILES (non-unique but structure) and some only gave formulas and names (non-unique, no structure).
- Harmonisation of concentration calculations (extract vs water concentrations)
- The evaluation was split into GC-MS and LC-MS, sorted by method (instrumentation), the identification procedure and category and whether quantified.
- The information provided in the DCTs is priceless for retrospective analysis –“harmonized DCTs” needed (question: *does it make sense to harmonize between GC-MS and LC-MS?*)

Results of the GC-MS measurements

In general, few substances were reported per participant (especially when compared with LC-MS), due in part to the sample preparation and also different concepts of data evaluation. A total of 348 "target + suspects" were reported over all institutes, compared with 116 "non-targets + unknowns". Generally DB-5MS columns were used and half the participants used large volume injections (LVI) compared with the other half (pulsed) splitless. Most participants used Agilent instruments, 2 Agilent-LECO, 2 Agilent-Waters and one Thermo. Solvents varied (acetonitrile (1), dichloromethane (3), toluene, (3), hexane (2)) and while most participants used electron impact ionisation (EI), two also used Atmospheric Pressure Chemical Ionisation (APCI) or Positive/Negative Chemical Ionisation (PCI, NCI). Vendor software was used by all to perform target identification, while suspect/unknown identification was generally performed using AMDIS and the NIST library; xcms and ChromaLynx was also used. While caffeine was the only quantified substance to overlap between the GC and LC lists, many substances overlapped in the suspect/unknown lists and ***this substance overlap needs more evaluation***. The approaches remain complementary.

Retention Index- GC-MS (P. Oswald)

The retention information (see Figure 3) helps add confidence to the identification by adding chromatographic information to the mass spectrometry. A *retention time* is reproducible under constant chromatographic conditions. A *relative retention time* $r=t_{r1}/t_{r2}$ *for any two peaks* is comparable between different systems but different temperature programs cannot be compensated. The *Kovats Retention Index* gives the retention time of a certain compound normalised to the retention time of adjacently eluting *n*-alkanes. Derived for *isothermal conditions and a non-polar system*, this has error ± 10 units. A *Retention Index* (RI) normalises the retention time of a certain compound (e.g. using the *n*-alkanes) for temperature-programmed chromatography with an error of ± 100 units. Generally, carrier gas pressure and flow rates, pre-columns, column length, diameter, stationary film thickness or different isothermal temperatures/temperature ramps all have little-no influence on RI.

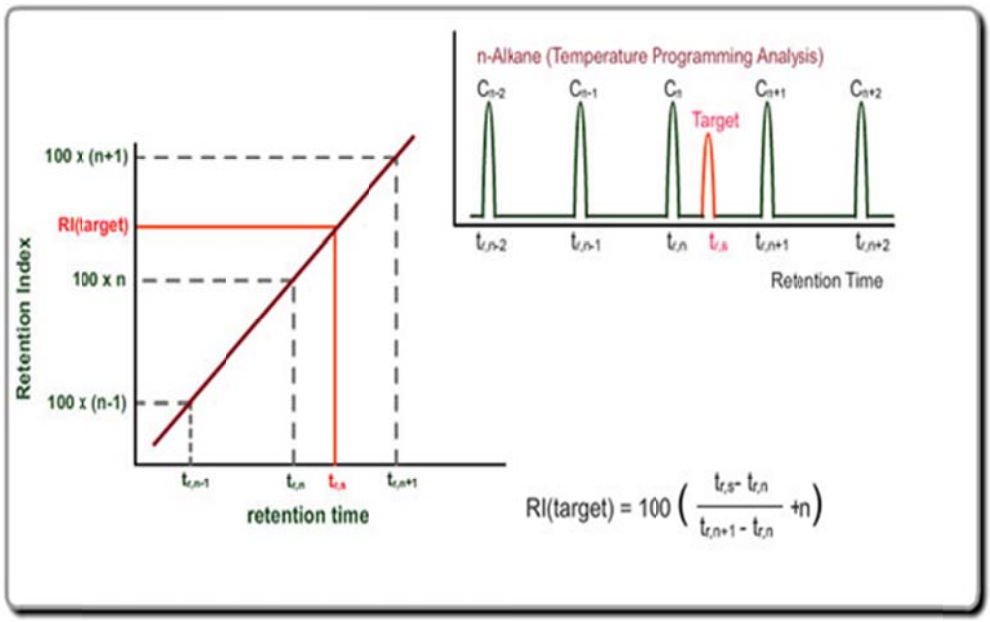

Figure 3: Calculation of linear retention index. Source: Peter Oswald.

The reproducibility of the RI is (excluding overloading, column activity or reactive compounds):

- On the same system: ± 10 units
- Between identical systems: ± 15 units
- 100% polydimethylsiloxane column: ± 15-50 units
- 95% polydimethylsiloxane-5% polydiphenylsiloxane: ± 20-100 units (depending on the polarity of compounds)

For participants in the trial, most RIs were ± 100 of the NIST values, where available. One participant deviated strongly from this, due to very polar columns used - non-polar columns give best comparability. The results showed that the RI is valuable to *enhance the confidence of identification in GC-MS analysis* also in combination with other information such as soft ionisation to confirm molecular mass. For the collaborative trial, this enabled normalisation and comparison of the datasets while the combination of EI/PCI and RI is powerful for retrospective analysis.

Summary of Participant Feedback and Discussion

- ***Sample enrichment and preparation was not good for GC– should be changed in a future trial***
  - Challenge: sending samples in solvents is more difficult than dry (regulatory reasons)
  - Filtering (more particulate matter => more apolar compounds), evaporation (loss of volatiles), greater enrichment needed?
  - Deconvolution did not work well for the trace levels observed
  - Either LVI or 10x pre-concentration or similar was needed to see anything at all
- ***Insufficient time for non-target identification***
  - Need more time and better timing of sample delivery for better results
- The chromatography is generally not optimised for non-target identification
  - Perform instead a long run with low temperature and e.g. 40 min run time.
  - Optimized chromatography => optimized peaks => better for deconvolution software
- In-house databases with retention information first choice database, with NIST as back-up
  - NIST generally used with match/reverse match values of 80 or 85 % as a cut-off
  - There may be greater uncertainty using Kovat's index for GCxGC methods, as 1-D RTs are reconstructed from the 2-D RTs, but this depends on the primary column used. If the primary column is non-polar, the difference from reference values should be negligible.
  - NIST not specific enough for APCI – more specific libraries, use of exact mass required.
- ***Better software is desirable, especially using exact mass, HR-MS, soft ionisation techniques***
- Soft Ionisation:
  - Combination of soft and hard ionisation provides valuable additional information but better software needed; can use RT to correct for results and adducts to confirm mass.
  - Requires a change of source (time-consuming); more stability needed for CI.
  - Only see ~50 % of substances seen in EI-MS, but limited in injection amounts.
  - Will become routine eventually
- All participants agreed that ***both exact mass and RI are important*** – RI provides complementary information, while exact mass provides additional information to help EI identification (but won't help with e.g. isobaric pesticides)
  - Best combination exact mass, NIST match and RI

- ***APCI-GC would have a similar workflow to LC-APCI-MS/MS***
    - No libraries, but can do a wide screening as for LC approaches due to the usual presence of the molecular ion. However, generally little fragmentation is observed.
    - With respect to sensitivity, one participant commented that APCI is maybe 10x more sensitive than EI_QTOF, but also a newer machine
    - Both M+ and M+H+ occur in APCI-MS and have to be checked for suspect screening. For non-target one can perform two injections, one in dry conditions and one with extra H_2O added to force adduct formation and subsequently assign the molecular ion.
    - Perfect machine for screening: but then don't have the EI-MS libraries to compare
- ***Low resolution instrument would have GC-MS workflow: AMDIS => NIST => Match or unknown***
    - Concept of suspect doesn't make sense in this workflow
    - Non-target screening is database matching with NIST, if no convincing candidate is in the library, generally remains "unknown".

Results of the LC-MS measurements

The participants in the LC-MS measurements were a mix of experienced laboratories through to others performing non-target screening for the first time. In general, many more substances were reported for the LC-MS measurements. Over all 16 participants, a total of 1072 "target + suspects" were reported, compared with 21380 "non-targets + unknowns", contrasting with the GC-MS results where fewer unknowns were present than targets. Of these, 500 compounds had reported concentrations and after adjusting the reported concentrations to represent the final concentration in the water, these were generally within 1-2 orders of magnitude (there was some debate here about whether this deviation is acceptable or whether the corrections made were sufficient). No substance was found by all participants, while sulfamethoxazole, carbamazepine and atrazine were the most quantified substances.

With respect to the analytical methods and instrumentation, generally C18 columns used, with only one participant using tandem LC also with a HILIC column. Narrow bore columns were used (2-3 mm ID) but no nano or micro-LC methods and while most (10) participants used HPLC, 5 used UHPLC. The solvents were more evenly distributed, with 7 laboratories choosing acetonitrile/water versus 8 choosing methanol/water. The injection volumes ranged from 2-20 µL, with two participants injecting 100 µL. A range of vendors were represented (note: one participant used two instruments), including ABSciex (2), Agilent (5), Bruker (1), Thermo (6), Waters (3). More coarsely, 11 instruments belonged to the ToF family, while 6 belong to the Orbitrap family. Despite this, only three participants ran their samples above a resolution of 70,000. All participants used electrospray ionisation (ESI), while the mass scan range varied between *m/z*=50-2000 (Orbitrap users generally 100-1000, ToF users with a wider range). MS/MS acquisition was generally data dependent.

The data analysis was extremely varied, with a wide range of vendor and non-vendor approaches used and many different databases. Target identification and quantification was generally dominated by vendor software (e.g. ChromaLynx, MassHunterQuant, MassLynx, Target Analysis, Trace Finder, Unifi), while this was quite different for suspects/non-targets (e.g. DAIOS, ExactFinder 2.0, Data Analysis, ForensicTox, MassBank, MasterView, MetFusion, internal lists, Metlin database (pesticide, forensic), PeakView, Profinder, StoffIdent, Xcalibur and so on).

Retention Comparison – LC-MS (T. Letzel)

The retention comparison in LC-MS was termed RTI (retention time index) to distinguish between the RI (retention index, GC) and LC methods. While a standard mix was given, in principle any mix could be used as long as it consists of neutral compounds with a wide distribution of log P (= log Kow) from e.g. -1 to 5. For this assessment, logD is now used instead of logP to account for charged compounds, while ChemAxon is used for the calculations.

For the target compounds, of the 26 found over 3 times, the root square deviation (RSD) was <3% for 11, 3-6% for 11 and > 6% for 4 of the 26. With respect to StoffIdent, the logD matching is ± 0.5 log units, while the correction for negatively charged substances is ±1 log unit. Neutral molecules are corrected by subtracting 1 log unit if logD is < 0.35 and by adding 1 log unit if logD is > 4. Neutral molecules in the logD range of 0.35 to 4 are not corrected. No adjustment is made for positively charged molecules, due to a lack of data evaluation. The correction and the matching is based on empirical experience and is performed automatically in StoffIdent. For example, for Eawag, of 105 targets; 96 of these are in StoffIdent, while 81 (77%) were within the calculated logD range. Similarly for Langenau: of 70 targets detected, 60 were in StoffIdent and 50 (83%) were within the logD range.

Retention Time Information Discussion, LC-MS

- Question from participants: are these logD limits too harsh? Outside the errors of the prediction?
- Connecting StoffIdent and MassBank would be ideal to perform spectral search on suspects.
- Search StoffIdent with your own formats – contact Thomas Letzel with example format.
- Retention time prediction – everyone says it is useful, but few used it, why?
    - Approaches used included Letzel index, QSAR approach, “conversion” of database retention times to own system
    - Other participants had insufficient time to use e.g. CHI or logP/logD approaches
    - Too much uncertainty to use this as confirmation/rejection of a target identity
    - But, useful as a filtering criteria for non-target identification (which hardly any participant managed); e.g. for Level 3.
    - Not useful for substances where the prediction is known to be poor
    - Errors: narrow range can lead to false exclusion; large errors means too inaccurate.
    - QSAR approach promising; logP often better than logD because the latter also includes errors in pKa prediction
    - No best approach yet – more investigations required.
    - In general: ***retention time information (not index) is a useful term*** as it is more flexible

Summary of Participant Feedback and Discussion for LC-MS: Analysis

- Universal choice of reverse phase (RP) LC and only one with tandem RP & HILIC
    - ***RP separation is good generic method for screening***; HILIC (and other phases) are too specialised but complementary and useful for specific cases
    - HILIC and alternative columns could help measure substances in the dead volume
    - Solvent issues with HILIC: high water content is problematic and polar compounds are difficult to pre-concentrate. Solvent exchange may be necessary.

- Generally narrow bore columns used (1-3 mm), no nano- or micro-LC
    - Theory: less matrix suppression and higher sensitivity with nano-LC but no one tried
    - Some experience with chips, but preconcentration results in losses that may be avoided with direct injection.
- HPLC (10 participants) versus UHPLC (5 participants)
    - HPLC needed in many cases to give sufficient time for MS/MS experiments desired.
        - HPLC "all in one" experiment vs UPLC requiring several injections
    - 5 minute UHPLC run time gives all ion suppression and matrix squeezed into the smaller time, so longer runs better for non-target screening
    - => ***recommendation for HPLC or long UHPLC runs***
- Solvent: ACN vs MeOH
    - Different selectivity, different adducts (more with ACN?), purity/supplier plays a role
    - Solvent choice shouldn't affect the RTI calculation (***more data on this wanted***)
    - MeOH better from a green chemistry point of view, but ***no recommendation on solvent***
- Injection volume: most had 2-20 µL, some up to 50-100 µL
    - Better sensitivity with large volume – how to avoid overloading and chromatographic problems with pre-concentrated samples? ***More discussion required***
- Resolution: how high do you need to go?
    - Hard to give definite answer, many compounds resolve well at 30,000, some require >60,000 (see e.g. Kellmann et al, 2009, J Am Soc Mass Spectro, 20, 1464–1476).
    - ***Recommendation to go for the highest resolution possible on your machine that suits the acquisition speed required for analysis***
    - Unit resolution QqQ could be used under certain circumstances for suspect screening but impossible for non-target => ***QqQ should be excluded from subsequent NT Trials***
- Ionisation: all participants used ESI: why not APCI / APPI?
    - Complementary technique: gives more information but insufficient time to use it here
    - As for other analytical methods: analysis time is short compared to slow data processing. ESI positive and negative minimum needed for non-target.
    - ***Data processing is the clear bottleneck – need software to merge information***
- Mass scan range: Lowest m/z ≤ 80 (9) or 100 (6). Highest m/z 1000 (8) or ≥ 1200 (7)
    - What is the appropriate range? NDMA 75 g/mol vs Vancomycin 1450 g/mol. Large scan range can limit the sensitivity of some instruments
    - ***Recommend minimum m/z = 100-1000, optimum 50-2000***
- MS/MS acquisition
    - Data-dependent MS/MS offers greater sensitivity but often requires reanalysis – most participants used this.
    - Data-independent MS/MS (SWATH, MSe, bbCID, all-ion, …) delivers fragments of all parent ions and also enables quantitation over fragments but not trivial to associate fragments with parents. No software available yet.

Summary of Participant Feedback and Discussion for LC-MS: Data Evaluation

- Very few true "non-target" results
  - Many experienced a lack of time => did not get to non-targets
  - ***"Real" non-target screening is too time consuming for the trial***
  - Few "promising" non-targets if extensive target and suspect screening performed
  - Many experienced insufficient intensity to obtain good MS/MS
- Suspect screening better performed "smart" not broad
  - StoffIdent has ~9,000 compounds – the bigger the better; smaller databases possible e.g. "DuftStoffIdent" – for fragrances; "StoffIdent for other regions"; REACH, …
  - ***Desire to have consolidated suspect platforms, not so many different ones***
  - Debate: screen big or screen smart? Screen big but with functionality?
    - Suspect list depends a lot on the question you are trying to answer
    - Could be restricted to ionisable compounds, to specific exposure routes (e.g. wastewater versus agriculture), …
  - A common list of suspects, e.g. NORMAN, StoffIdent, ChemSpider
  - High abundance peaks one way to eliminate false positives
  - "Peak detection", "deconvolution": nice peak does not necessarily mean nice identification (or rather, nice identification does not necessarily mean nice peak)
  - Better results achieved with multiple measurements, as suspects /non-targets require re-measurement e.g. data dependent (dd) versus data independent analysis (DIA), Eawag or 5-fold injection to distinguish sample from noise (Langenau)
  - ***General agreement to "share" suspects, but no agreement on how***.
  - ***New NORMAN task to develop suspect list with categorisation***
- Software needs
  - Soft ionisation: exact mass & specific ESI libraries needed (especially ESI negative)
  - Insufficient elucidation tools for non-target identification
  - Retention prediction tools needed
  - Better software required for suspect screening approaches – workflow still time consuming and need too many different platforms
  - ***Dream of a "fully automated workflow" and "batch searchable accurate MS/MS"***
- Libraries used:
  - Agilent "PCDLs" e.g. Broecker, Herre and Pragst PCDL/toxic-forensics Library (7509 compounds), 1664 pesticides, 16,000 synthetic substances (latter crashed the system for one participant).
  - NIST MS/MS (NIST11 ~4500 compounds, NIST14 ~8200 compounds).
  - In-house libraries – e.g. 2000 compounds, 1500 compounds, 500 compounds, 2200 compounds (with RT & fragments for 800).
  - Waters database with 730 compounds but different RTs
  - Bruker Pesticide Screener (700 pesticides with RT & fragments)
  - Thermo EFS (~1000 compounds), forensics & toxicology.

Definitions:

- Proposal to merge the confidence level with terminology (see Figure 4).

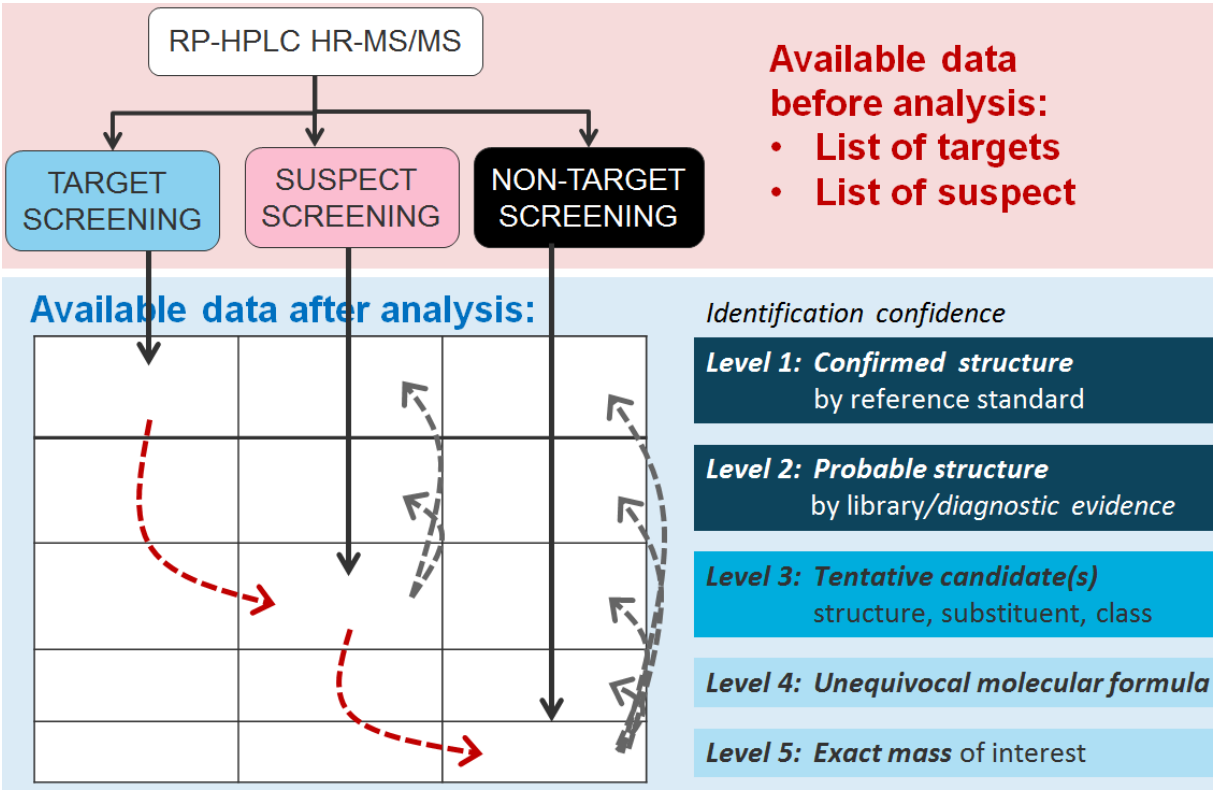

Figure 4: Workflow nomenclature and evolution of targets, suspects and non-targets with confidence levels. The grey arrows indicate how suspects and non-targets can increase in confidence according to the evidence, while the red arrows show what happens to targets and suspects where the evidence does not confirm the identity. Source: H. Singer.

- Definition: Target Screening vs. Target Analysis
  - Quantification is a lot of extra work – ***do not require quantification for future trials***
  - Target always has the reference standard – to distinguish if quantification is present, add this to the name, e.g. Quantitative Target Screening or Quantitative Target Analysis
  - Authorities require high certainty and quantification (most agree, not all) with calibration curves, IS, etc. Typically skip "screening" and go straight to "analysis", i.e. quantification.
  - Also add the score (ID points) to the level to reflect uncertainty, e.g. if no MS/MS but still Level 1 with reference standard
  - ***Requirement: MS, RT and MS/MS (latter where available).***
- Definition: Suspect Screening
  - General definition: ***no reference standard available, but exact mass and a structure***
- Definition of non-target: effectively not a target and not a suspect
  - General agreement to remove confusing distinction between "non-target" and "unknown".
- General agreement that this terminology doesn't apply to GC
  - Concept of "suspect" doesn't apply to EI-MS

Workshop Wrap-up

- In general the trial was a good experience and a lot was learnt.
    - First trial ever – collaborative trial, with a very ambitious scope.
    - More concrete aims needed for next trial.
    - A benchmark dataset would be good for next time, e.g. spiked sample or spiked blank
    - The use of two different samples for GC-MS and LC-MS methods should be considered, with the option to analyse both if the laboratory methods/instrumentation allows. This would give a better understanding of the overlap between LC and GC.
    - Timing: the trial was much more work than expected, improve timing & buffers
- Some recommendations for parameters agreed on (see above in bold)
- GC-MS and LC-MS approaches are complementary; target and suspects dominate LC-MS results.
- ***Agreement to use the dataset as a test to explore retrospective screening approaches***
- Generally, the MS method seems reasonably harmonized – data processing far from harmonized!
- General agreement to share suspects: new NORMAN task to investigate how.
- Paper summarizing the mass spectrometric aspects of trial for a special issue in Analytical and Bioanalytical Chemistry: core team + Nikos Thomaidis & Christian Zwiener, one co-author from the other labs and remaining persons involved in the acknowledgements.
- General agreement to repeat trial; timing agreed in 2016, but not at the end of the year!
    - In the meantime, would be possible to do more with the non-target data in this trial
    - Several participants seemed keen to do more with the non-target data
- Good feedback on the workshop;
    - Some would have appreciated more opportunities to exchange ideas with those more experienced – i.e. discussions in smaller groups.