Ivan Rusyn

Institution or company: Texas A&M University

Ivan Rusyn is University Professor in the Department of Veterinary Physiology and Pharmacology in the School of Veterinary Medicine & Biomedical Sciences at Texas A&M University in College Station. He is also Chair of the Interdisciplinary Faculty of Toxicology, Director of a NIEHS T32 training program in "Regulatory Science in Environmental Health and Toxicology," and Director of the Superfund Research Center. His studies on health effects of chemical agents resulted in over 320 peer-reviewed publications which were cited over 32,000 times (h-index=85). He has served on and chaired several US National Academies committees, and World Health Organization/International Agency for Research on Cancer Monographs working groups. He is serving on the advisory board for Texas Department of Public Health. He served on the Board of Environmental Studies and Toxicology for the National Academies, the Board of the Scientific Councilors of the United States National Institute of Environmental Health Sciences and the Research Committee of the Health Effects Institute. Dr. Rusyn received a doctor of medicine degree from Ukrainian State Medical University in Kyiv and a Ph.D. in toxicology from the University of North Carolina at Chapel Hill. He conducted postdoctoral research at the Massachusetts Institute of Technology and Heinrich-Heine University in Dusseldorf. Dr. Rusyn's laboratory is funded by grants and cooperative research agreements from the National Institutes of Health and US Environmental Protection Agency, institutional funding from Texas A&M University, the industry, and other sources.

Method Name in non-abbreviated full form.

Method description in brief.

See below

Applicability of method.

m/z Range for Agilent 6500 series QTOF:

These mass ranges are discussed in this document:
- Standard 3200 m/z range
- 1700 m/z range (with transmission tune options)
- Extended mass range (10,000 m/z, 20,000 m/z, 30,000 m/z)" (Agilent 6500 Series Q-TOF LC/MS Tuning Guide)

Molecular Weight Range:

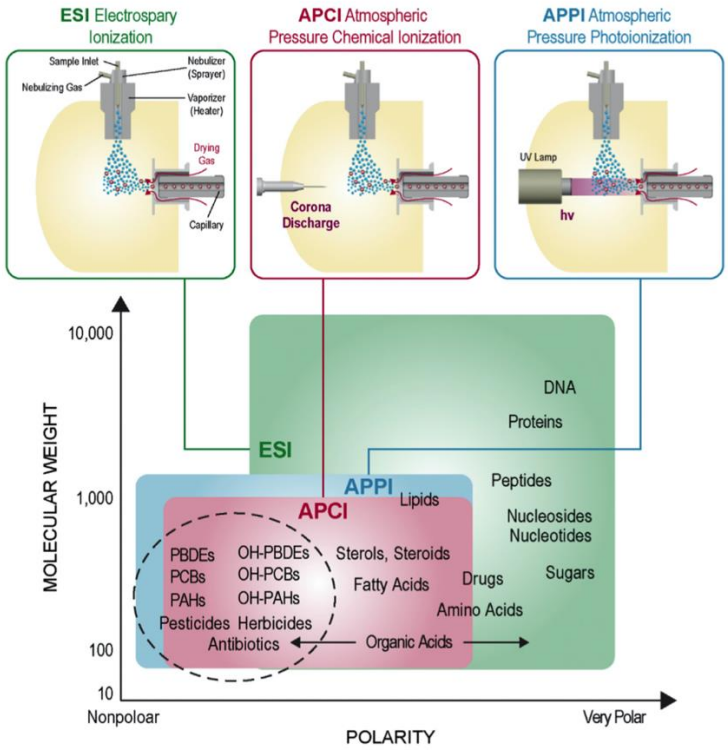
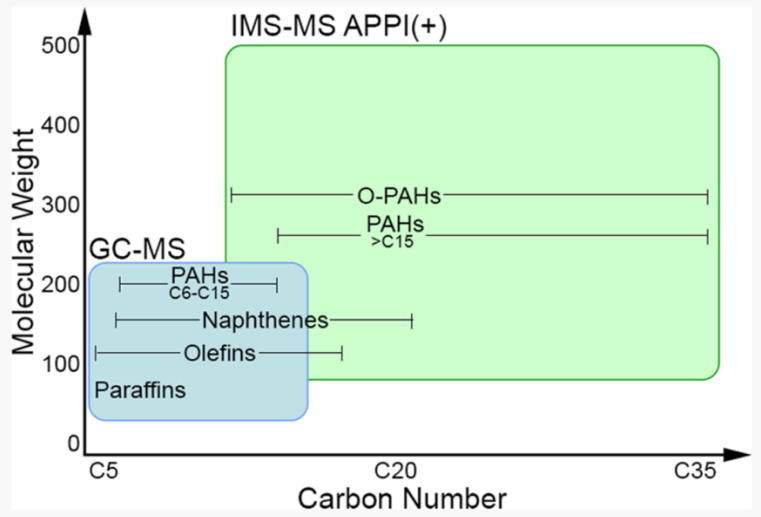


Fig. 2. Different ionization techniques for polar and nonpolar molecules. Electrospray ionization (ESI) is mainly used for polar compounds, while atmospheric pressure chemical ionization (APCI) and atmospheric pressure photoionization (APPI) are needed for molecules of lower polarity. PAHs: polycyclic aromatic hydrocarbons; OH-PAHs: hydroxylated PAHs; PCBs: polychlorinated biphenyls; OH-PCBs: hydroxylated PCBs; PBDEs: polybrominated biphenyl ethers; OH-PBDEs: hydroxylated PBDEs.

(Zheng et al. 2018)

Carbon Number Range:



(Roman-Hubers et al. 2021)

Resolution:

"A 6560A ion mobility (resolving power (RP)≈25 000) Q-TOF-MS (RP≈60) drift tube instrument with nitrogen gas (Agilent Technologies, Santa Clara, CA) was used for sample analysis." (Roman-Hubers et al. 2021)

*Note: The same instrument model was used for all other publications mentioned herein.

Sample preparation required.

Crude Oils:
"For IMS–MS analysis, each crude oil sample was diluted to 500 µg oil in 1 mL of 1:1 v/v methanol:toluene." (Cordova et al. 2023)

"For GC-MS analyses, all oil samples were weighed and dissolved in dichloromethane (no precipitate was visible and it is assumed that the samples dissolved completely) to a final dilution of 1 mg of oil per 1 mL of dichloromethane. For the IMS-MS analyses, the same dichloromethane-diluted oil samples were used, but they were solvent exchanged from dichloromethane to 1:1 v/v toluene:methanol (Purcell et al. 2007a; Grimm et al. 2017)." (Roman-Hubers et al. 2020)

Refined Products:
"Neat and extracted samples were prepared for IMS-MS analysis as follows. A glass syringe was first used to add 100 µL of each sample to a glass vial. Substances were then diluted 3× by adding 200 µL of 50:50 acetonitrile/toluene buffer and vortexing. The glass syringe was rinsed in triplicate with acetone, hexane, and methanol between the preparation of each sample." (Cordova et al. 2023)

"In accordance with published standard procedures,8,23 all petroleum substances were diluted prior to IM-MS analysis to a final concentration of 1 mg/mL using 1:1 (v/v) methanol:toluene containing 0.5% (v/v) formic acid to increase protonation efficiency and [M + H]+ ion generation from basic compounds for IM-MS analysis in positive ion mode." (Grimm et al. 2017)

Oil-Exposed Water Samples:
"Water samples (1.5 mL) were centrifuged for 5 min, and the top clear layer (1 mL) was added to 1 mL of methanol (CAS no. 67- 56-1, Sigma-Aldrich, St. Louis, MO) containing 0.05 % acetic acid (CAS no. 64-19-7, Sigma-Aldrich). Samples were thoroughly vortexed and 200 µL of each sample (n = 42) was infused (50 µL min− 1) directly into the APPI source." (Roman-Hubers et al. 2022)

Weathered Oil Slicks:
"Representative oil samples were analyzed using ion mobility spectrometry-mass spectrometry (IMS-MS). Each sample wasdiluted to a concentration of 1.5 mg mL−1with a 50:50 (v/v)mixture of HPLC-grade toluene and methanol." (Aeppli et al. 2022)

DMSO Extracts:
"Neat and extracted samples were prepared for IMS-MS analysis as follows. A glass syringe was first used to add 100 µL of each sample to a glass vial. Substances were then diluted 3× by adding 200 µL of 50:50 acetonitrile/toluene buffer and vortexing. The glass syringe was rinsed in triplicate with acetone, hexane, and methanol between the preparation of each sample." (Cordova et al. 2023)

Method strengths.

Fast analysis and wide C# range

Estimated time for analysis.

For Petroleum-Derived Products (Crude & Refined):
Sample Preparation: "For IMS–MS analysis, each crude oil sample [for 195 crude oils] was diluted to 500 µg oil in 1mL of 1:1 v/v methanol:toluene." (Cordova et al. 2023) – i.e., time per samples is < 1 minute

Data Acquisition via IMS: "For the present study, nontarget analysis was conducted using IMS coupled to a quadrupole time-of-flight (QTOF) MS instrument (model G6560A; serial# SG1711C002; Agilent Technologies). Atmospheric pressure photoionization (APPI)was operated in positive mode, and samples underwent direct injection into the instrument at a rate of 50µL/min for a total run time of 1.5 min. … Agilent's MassHunter Acquisition software was used to acquire raw data files for each sample run. Agilent's IM–MS Browser 10.0was then used to calibrate raw files and calculate CCS for the individual features in all files." (Cordova et al. 2023)

Data Processing & Interpretation: "After calibration, Agilent's MassProfiler software (Ver.B08.00) was used to align features across samples and generate a single data matrix for analysis. … Raw sample files used for data processing included the appropriate calibrant file taken before sample runs, all blanks, and individual files for sample replicates. These filtering criteria yielded a data matrix of 68 232 features aligned for 195 crude oil samples (Supporting Information, Table S3). … The raw, aligned data matrix was then filtered and processed to obtain a dataset for molecular formula assignment. First, features were filtered to include only those with abundances (Abd)>7000 in 2 of 3 replicates in any of the samples. This threshold was arbitrarily determined by the consistent presence of 13C isotopic partners and historical petroleum biomarkers (identified by compound matching to a $^{DT}CCS_{N2}$ library) for features with abundance>7000. The average abundance of each remaining feature was then calculated across triplicates of each sample. Next, the average abundances of features present in two blanks were calculated to minimize batch differences in blank abundance by using: 1) the blank acquired prior to all sample runs, and 2) the most recent blank acquired prior to running a given sample. Averaged blank feature abundances ($AvgAbd_{Blanks}$)were then subtracted from corresponding averaged sample feature abundances ($AvgAbd_{SampleReps}$). Features for which $AvgAbd_{Blanks}$>$AvgAbd_{SampleReps}$ or $AvgAbd_{SampleReps}$=0 across all samples were excluded from further analysis. In total, 3528 features remained for further analyses (Supporting Information, Table S4). A schematic diagram detailing the IMS–MS data analysis workflow can be found in the Supporting Information, Figure S1. Next, KMD computational workflow was utilized to assign molecular formulas to individual features, as detailed elsewhere (Roman-Hubers et al., 2021a). Briefly, KMD based on CH2 (KMD-CH2; exact mass=14.01565) was calculated for filtered features (n=3528) in parts per thousand (ppt; Equations 1 and 2). … Features were then plotted as KMD-CH2 versus m/z to determine homologous series, appearing as horizontal rows of features and defined as those with the same KMD-CH2 (y) and differing by multiples of 14 Da (x). Anchor features were identified by compound matching to a $^{DT}CCS_{N2}$ library (Baker, 2021) with an m/z tolerance of ± 5 ppm and ± 2 mDa and a $^{DT}CCS_{N2}$ tolerance of ± 1%, enabling molecular formula assignment for the remaining members of the anchor series. After characterization of the anchor series, other series were characterized using elemental mass defects to navigate the KMD-CH2 scale and assign molecular formulas to constituents. Plotting KMD-CH2 versus CCS facilitated isomeric discrimination, and KMD calculated in terms of hydrogen (KMD-H) was then used to organize compounds into homologous series by carbon number, providing increased confidence in molecular formula assignments." (Cordova et al. 2023, processing methods described in more depth in Roman-Hubers et al. 2021)

***Note: These are the most recent methods for data processing and were used for the following studies:**

Method weaknesses.

This is a non-targeted analysis. See Roman-Hubers et al 2023 (DOI: 10.1016/j.yrtph.2022.105310) for additional details on strengths and weaknesses of this and other methods.

Result interpretation / visualisation / presentation.

Please see publications above and Roman-Hubers et al 2023 (DOI: 10.1016/j.yrtph.2022.105310) for visualization examples.

Relevant Papers

Cordova, A. C., Dodds, J. N., Tsai, H. H. D., Lloyd, D. T., Roman-Hubers, A. T., Wright, F. A., ... & Rusyn, I. (2023). Application of Ion Mobility Spectrometry-Mass Spectrometry for Compositional Characterization and Fingerprinting of a Library of Diverse Crude Oil Samples. *Environmental Toxicology and Chemistry*.

Cordova, A. C., Klaren, W. D., Ford, L. C., Grimm, F. A., Baker, E. S., Zhou, Y. H., ... & Rusyn, I. (2023). Integrative Chemical–Biological Grouping of Complex High Production Volume Substances from Lower Olefin Manufacturing Streams. *Toxics*, *11*(7), 586.

Roman-Hubers, A. T., Aeppli, C., Dodds, J. N., Baker, E. S., McFarlin, K. M., Letinski, D. J., ... & Rusyn, I. (2022). Temporal chemical composition changes in water below a crude oil slick irradiated with natural sunlight. *Marine Pollution Bulletin*, 185, 114360.

Roman-Hubers, A. T., Cordova, A. C., Rohde, A. M., Chiu, W. A., Donald, T.J., Wright, F. A., ... & Rusyn, I. (2022). Characterization of compositional variability in petroleum substances. *Fuel*, 317, 123547.

Roman-Hubers, A. T., Cordova, A. C., Aly, N. A., McDonald, T. J., Lloyd, D. T., Wright, F. A., ... & Rusyn, I. (2021). Data Processing Workflow to Identify Structurally Related Compounds in Petroleum Substances Using Ion Mobility Spectrometry–Mass Spectrometry. *Energy & Fuels*, 35(13), 10529-10539.