

Supplementary Material for

Linking Micropollutants to Trait Syndromes across Freshwater Diatom, Macroinvertebrate, and Fish Assemblages

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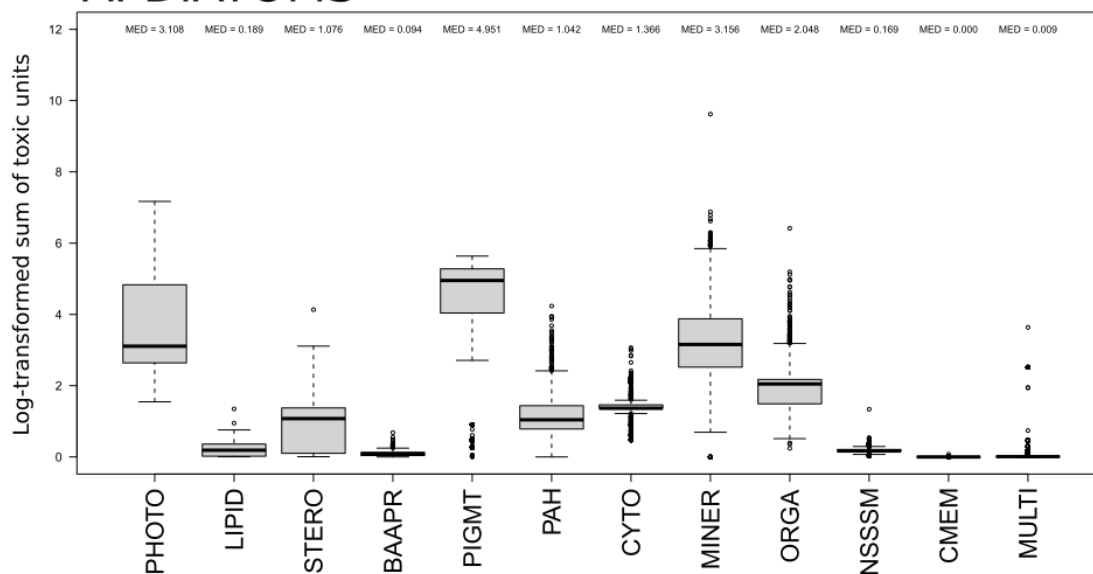
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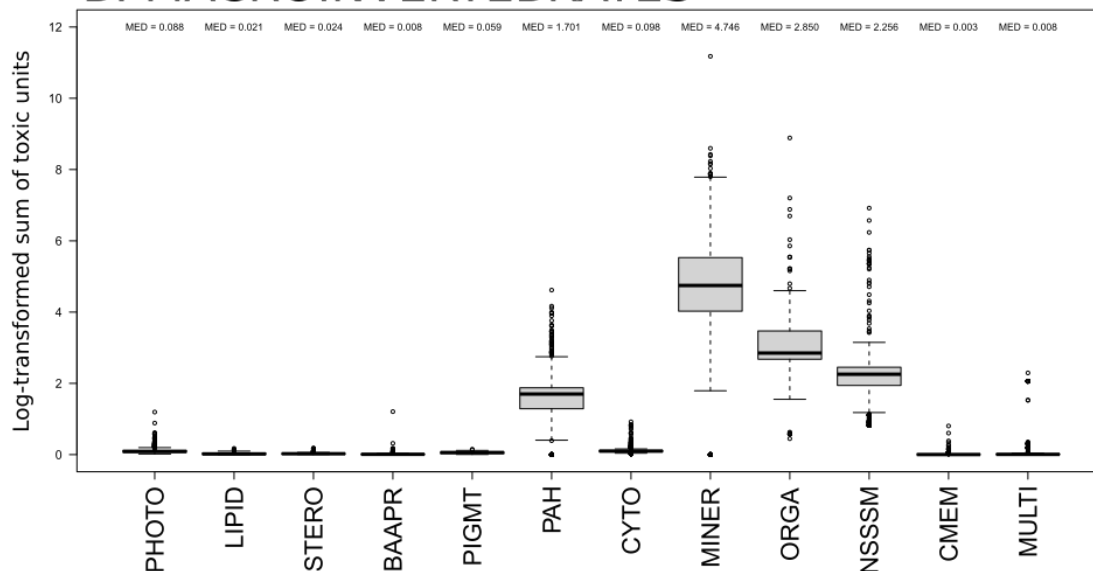
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Supporting material includes one figure and the legend of supplementary tables.

A. DIATOMS



B. MACROINVERTEBRATES



C. FISHES

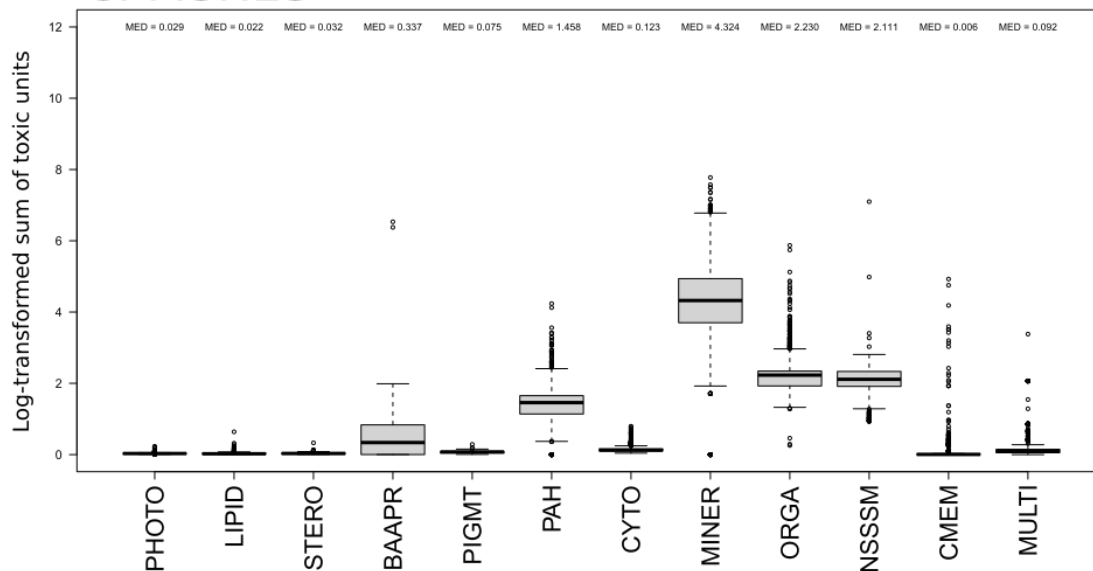


Figure S1. Box-plots (Min/Q25/Median/Q75/Max) describing the distribution of the $\log(x+1)$ -transformed sum of toxic units of the broad categories of micropollutants or modes of action for benthic diatom (A), benthic macroinvertebrate (B) and fish (C) assemblages. Median values are given at the top of each sub-figure. Please refer to Table 1 of the main manuscript for the full names of the broad categories of micropollutants and modes of action. N = 2,007. Legends of supplementary tables found in the Excel file

Table S1. List and description of diatom traits and trait categories. Please refer to Larras et al. (2017) for further details about the dataset.

Table S2. List and description of macroinvertebrate traits and trait categories. Please refer to Tachet et al. (2010), Mondy & Usseglio-Polatera (2013) and Beck et al. (2021) for further details about the dataset.

Table S3. List and description of fish traits and trait categories. Please refer to Dézerald et al. (2020) for further details about the dataset.

Table S4. List of the studied micropollutants, including their categories or mode of action (MoA; based on the target functions or systems). The median effective concentrations (EC_{50}) used for the calculation of the toxicity level of micropollutants (expressed as sums of toxic units) are included in this table. For fishes, when appropriate, the median lethal concentration (LC_{50}) was used as equivalent to EC_{50} . The column “Sources” informs about the source(s) of the EC_{50} , respectively for diatoms (d), macroinvertebrates (m) and fishes (f). Toxicity values were retrieved from three open databases: the Pesticide Properties DataBase (PPDB; <http://sitem.herts.ac.uk/aeru/ppdb/>), Malaj et al. (2014) and the INERIS database (<https://substances.ineris.fr/fr/search>). Modes of action were retrieved using the R4P database (R4P, 2019). Please refer to Table 1 of the main manuscript for the full name and description of the broad categories of micropollutants or modes of action.

Table S5. List of the individual trait categories, which exhibited a non-significantly different ability to predict the effect of micropollutant than that of the whole trait syndrome by using generalized additive models (GAM). For a given mode of action (MoA), generalized likelihood ratio (GLRT) tests were done to compare models based on individual trait categories (i.e., the toxic effect of a MoA modeled as a function of an individual trait category constitutive of a trait syndrome and significantly correlated with the considered MoA; e.g., Figures 2, 3 and 4) and global models based on the whole set of trait categories from the same syndrome (i.e., the toxic effect of a MoA modeled as a function of the trait syndrome; see Figures 2, 3 and 4). For each combination “trait syndrome x MoA”, the trait categories listed in the table correspond to those for which the individual and global models have been considered as non-significantly different based on the GLRT test ($p.value \geq 0.05$) after Bonferroni's correction. An empty cell indicates that the trait syndrome provided a better model performance than each individual trait category of the syndrome. Conversely, a cell with the code “ALL” indicates that all the individual trait categories of a syndrome explained a similar proportion of the total variance than the trait syndrome model.

Table S6. Explained variance (adjusted R^2) of the generalized additive models (GAM) based on each of the trait syndromes and each of the trait categories for the benthic diatom assemblages. The $\log(x+1)$ -transformed sum of toxic units of each mode of action (MoA) was

modeled as a function of (i) individual trait categories or (ii) all the trait categories belonging to a given syndrome. Results are only given for the trait categories, which were significantly correlated with the considered MoA (see Figure 2).

Table S7. Explained variance (adjusted R^2) of the generalized additive models (GAM) based on each of the trait syndromes and each of the trait categories for the benthic macroinvertebrate assemblages. See the legend of Table S6 and Figure 3 for further details.

Table S8. Explained variance (adjusted R^2) of the generalized additive models (GAM) based on each of the trait syndromes and each of the trait categories for the fish assemblages. See the legend of Table S6 and Figure 4 for further details.

Table S9. List of the model taxa, which could be considered as the best theoretical representatives of trait syndromes for diatom assemblages. For further details about the identification of these model taxa, please refer to sections 2.3 and 3.3 of the main manuscript.

Table S10. List of the model taxa, which could be considered as the best theoretical representatives of trait syndromes for benthic macroinvertebrate assemblages. For further details about the identification of these model taxa, please refer to sections 2.3 and 3.3 of the main manuscript.

Table S11. List of the model taxa, which could be considered as the best theoretical representatives of trait syndromes for fish assemblages. For further details about the identification of these model taxa, please refer to sections 2.3 and 3.3 of the main manuscript.