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Combining predictive and analytical methods to elucidate pharmaceutical biotransformation in activated sludge†

Leo Trostel,^{‡a} Claudia Coll,^{‡a} Kathrin Fenner^{‡*ab} and Jasmin Hafner^{‡ab}

While man-made chemicals in the environment are ubiquitous and a potential threat to human health and ecosystem integrity, the environmental fate of chemical contaminants such as pharmaceuticals is often poorly understood. Biodegradation processes driven by microbial communities convert chemicals into transformation products (TPs) that may themselves have adverse ecological effects. The detection of TPs formed during biodegradation has been continuously improved thanks to the development of TP prediction algorithms and analytical workflows. Here, we contribute to this advance by (i) reviewing past applications of TP identification workflows, (ii) applying an updated workflow for TP prediction to 42 pharmaceuticals in biodegradation experiments with activated sludge, and (iii) benchmarking 5 different pathway prediction models, comprising 4 prediction models trained on different datasets provided by *enviPath*, and the state-of-the-art EAWAG pathway prediction system. Using the updated workflow, we could tentatively identify 79 transformation products for 31 pharmaceutical compounds. Compared to previous works, we have further automatized several steps that were previously performed by hand. By benchmarking the *enviPath* prediction system on experimental data, we demonstrate the usefulness of the pathway prediction tool to generate suspect lists for screening, and we propose new avenues to improve their accuracy. Moreover, we provide a well-documented workflow that can be (i) readily applied to detect transformation products in activated sludge and (ii) potentially extended to other environmental studies.

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Environmental significance

Transformation products (TPs) of micropollutants in the environment are, like their parent compounds, a potential threat to human and ecosystem health, but their environmental impact is generally not well understood. Identification and characterization of TPs are crucial to understand their fate in the environment, in particular for pharmaceuticals for which no TP study is required for market approval. Here, we propose an updated workflow for TP identification using computational prediction of suspect TPs followed by HRMS screening in activated sludge experiments. By applying our workflow to 31 pharmaceuticals, we tentatively identified 79 TPs. We compare our results to previously published workflows to highlight recent advances in analytical and computational method development and to provide guidance for future TP identification efforts.

Introduction

The fate of an anthropogenic chemical in the environment is to a large extent determined by its intrinsic capability to be biotransformed by microorganisms. Biodegradation leads to the transient or permanent presence of transformation products (TPs), which can, like their parent compounds, be characterized by their behavior in the environment in terms of persistence,

mobility, toxicity, and their ability to bioaccumulate. In certain cases, TPs have been found to be more persistent, mobile and/or toxic than their parent compound,^{1–3} which further highlights the importance of considering TPs in the environmental risk assessment of chemicals. Biodegradation studies identifying half-lives and biotransformation products are mandatory for certain classes of chemicals, *i.e.*, pesticides.^{4,5} For pharmaceuticals, in contrast, only the characterization of human metabolites is required by regulation in the European Union,⁶ leading to a knowledge gap regarding the fate of active pharmaceutical ingredients (APIs) in the environment. As most APIs reach wastewater treatment plants (WWTP), understanding their fate in activated sludge is primordial. However, the identification of TPs is challenging because (i) the TP structures are

^aDepartment of Environmental Chemistry, Swiss Federal Institute of Aquatic Science and Technology (Eawag), Dübendorf, 8600, Zürich, Switzerland. E-mail: kathrin.fenner@eawag.ch; Fax: +41 58 765 5802; Tel: +41 58 765 5085

^bDepartment of Chemistry, University of Zürich, 8057 Zürich, Switzerland

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‡ These authors contributed equally: Leo Trostel, Claudia Coll.



not known in advance, and (ii) often no analytical standards are available to confirm the exact structure.

Helbling *et al.* (2010) first addressed systematically the issue of TP identification.⁷ To detect previously unknown degradation products of micropollutants in activated sludge, the authors presented a workflow combining computational and analytical approaches: (i) automatic generation of a suspect list of potential TPs for each compound, (ii) spiking activated sludge reactors with parent compounds, and (iii) screening the sludge samples for suspected TPs using liquid chromatography coupled to high-resolution tandem mass spectrometry (LC-HR-MS/MS). In the first step (i), expert-curated biochemical transformation rules were iteratively applied to a chemical structure of interest to predict biodegradation pathways involving potential TPs. Typical pathway prediction tools are PathPred,⁸ BNICE,⁹ RetroPathRL¹⁰ or the University of Minnesota Pathway Prediction System (UM-PPS).¹¹ The UM-PPS, which was used in Helbling *et al.*,⁷ is specifically designed for biodegradation studies and can prioritize likely over less likely biotransformations using prioritization rules (also called relative reasoning rules) to yield biochemically plausible biotransformation pathways and corresponding TPs.¹² In the third step (iii), the generated suspect list was then used to extract single ion chromatograms for matching masses, which were further analyzed for peak formation over time, isotopic fit and shared fragments between parent compound and TPs.¹³ Still today, the main challenges of this approach are the high number of false positives in the suspect list leading to a low prediction precision, *i.e.*, a low number of correctly predicted TPs per total number of predicted TPs, and the need for individual inspection of the extracted ion chromatogram (XIC), and MS and MS/MS spectra for each candidate. Without reference standards, considerable efforts are still needed for the resolution of TPs' isomeric structures and TP quantification, such as the development of advanced identification workflows and even the development of novel approaches (*e.g.*, machine learning models) to predict ionization efficiencies that can improve the detection of more candidate TPs and the estimation of their concentration.¹⁴

In the past years, this workflow was applied and modified by different research groups to identify TPs in samples from biotransformation experiments. In particular, the prediction methods and underlying biodegradation databases have evolved to yield more accurate TP predictions: in 2012, the University of Minnesota Biodegradation/Biocatalysis Database and Pathway Prediction System (UM-BBD/PPS)¹⁵ was moved to Eawag and renamed to EAWAG-BBD/PPS, while keeping its original pathway prediction tool (PPS) and biodegradation data obtained from pure or enrichment cultures (BBD). In 2015, Wicker *et al.* re-implemented the EAWAG-BBD/PPS platform as enviPath, and the original BBD database was transferred to the new platform as EAWAG-BBD data package.¹⁶ In 2017, Latino *et al.* collected soil biodegradation data for 317 pesticides from regulatory reports and compiled them into the EAWAG-SOIL data package.¹⁷ The latest data addition to enviPath is EAWAG-SLUDGE, which contains biodegradation data for 91 micropollutants in activated sludge collected from scientific

literature (<https://envipath.org/package/7932e576-03c7-4106-819d-fe80dc605b8a>). Compared to its predecessors, enviPath not only holds more data, but also provides an improved pathway prediction system where the expert-curated reaction prioritization rules were replaced with a machine-learning algorithm that learns the relative reasoning rules directly from the data.^{18,19}

On the analytical side, new solutions emerged that facilitate the identification of TPs, in particular to decrease the workload of manually investigating mass matches for long suspect lists: different automated tools (*Sieve*, *Compound Discoverer*TM by Thermo Fisher ScientificTM, among others) now address this issue by peak prioritization based on intensity, isotopic pattern, mass defect, time course of peak formation and predicted retention time (RT) by quantitative structure retention relationships (QSRR).^{20,21} Furthermore, the interpretation of MS spectra is facilitated by spectral library search (*e.g.*, MassBank,²² NIST,²³ mzCloud²⁴) and *in silico* fragmentation tools (*e.g.*, Mass Frontier, SIRIUS,²⁵ CFM,²⁶ MetFrag²⁷).

These recent developments require a systematic analysis of previous studies to form an accurate picture of the current state-of-the-art in TP identification in biodegradation experiments, and to benchmark the performance of newly available tools against the original methods. To address this need, we (i) provide an overview of previous publications on TP identification in activated sludge or wastewater, (ii) present an updated, partially automated workflow for TP identification (Fig. 1), (iii) apply it to elucidate biotransformation processes of 42 pharmaceuticals, for many of which no TPs have been reported before, in a batch experiment with activated sludge, and (iv) evaluate the accuracy of five different TP prediction algorithms to guide future applications.

Methods

Literature search

The objective of the literature search was to collect all publications on TP identification experiments in activated sludge or samples from wastewater treatment plants (WWTP) that used pathway prediction to generate suspect lists. The search terms “biotransformation”, “sludge” or “waste water”, “pathway prediction system” or “*in silico* metabolism prediction” or the name of a prediction system (*e.g.*, “Pathpred”) or “suspect screening” were used in Reaxys (<https://www.reaxys.com>, last accessed 29/08/2022) and Clarivate Web of Science (<https://www.webofscience.com>, last accessed 01/09/2022). Furthermore, a Scopus (<https://www.scopus.com>, last accessed 02/09/2022) search for citation of the articles by Helbling *et al.* (2010)⁷ or Wicker *et al.* (2015)¹⁶ was performed. For each relevant article presenting results on TP identification, we extracted (i) the number of predicted and identified TPs, (ii) the substance class, (iii) the initially spiked concentration of test chemicals (if applicable), (iv) the pathway prediction method, (v) the experimental setup, (vi) the analytical method, and (vii) whether the TP identification was solely based on a suspect list (suspect screening) or whether additional TPs were identified by comparing full-scan MS data from different time points to



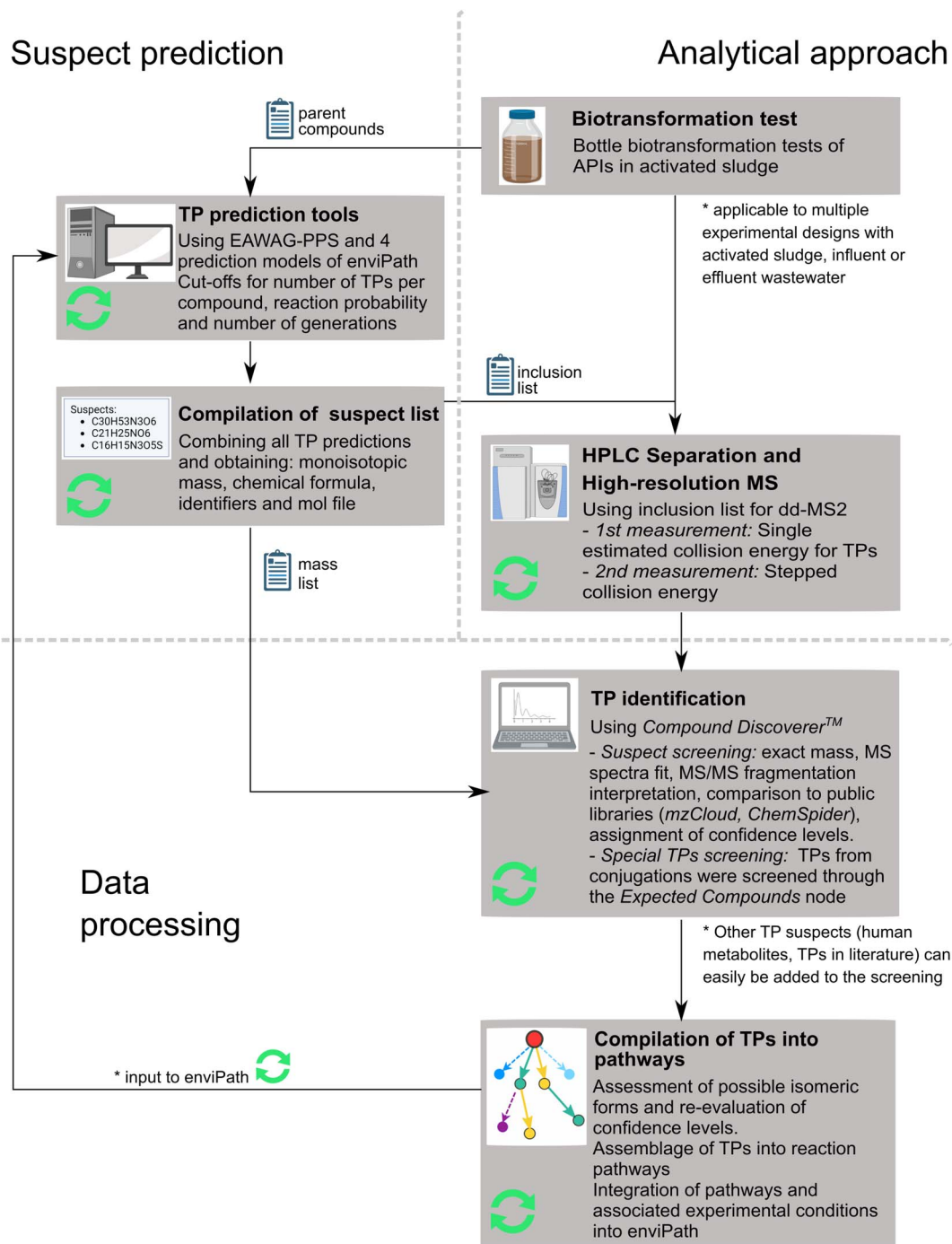


Fig. 1 Workflow for TP identification in a biotransformation experiment starting from a suspect list (icons from BioRender). Main steps of the workflow are in bold text followed by the specific procedure applied in this study. Green circular arrows indicate updates from the workflow of Helbling *et al.*

detect emerging metabolites (non-target screening). Reviews were analyzed separately to identify general trends in analytical and computational methodologies.

TP identification workflow

The overall workflow for suspect TP identification included six steps (Fig. 1): (i) predicting TPs using pathway prediction tools,

(ii) compiling a suspect list and annotating structures with MS-relevant information, (iii) performing biotransformation experiments, (iv) analyzing samples using liquid chromatography coupled to high-resolution tandem mass spectrometry, (v) identifying TPs from HR-MS data (including suspect screening and assignment of confidence levels), (vi) compiling identified TPs into pathways. Each step is described in detail in the next subsections. Compared to the original workflow



proposed by Helbling *et al.*,⁷ the following steps were updated (Fig. 1, see green circular arrows): (i) suspect and mass list generation, (ii) second LC-MS measurement with stepped collision energy, (iii) spectral library search within *Compound Discoverer*, (iv) assignment of confidence levels according to Schymanski *et al.*,²⁸ (v) prediction of conjugation reactions using *Compound Discoverer*, (vi) feedback of curated TP pathways into enviPath.

TP prediction tools

Suspect lists were obtained from EAWAG-PPS and enviPath. For enviPath, 4 pathway prediction models were trained on different combinations of the publicly available enviPath data packages EAWAG-BBD, EAWAG-SOIL, and EAWAG-SLUDGE to study the effect of adding different training data sets on the prediction performance. The following machine-learning models were trained using the respective data packages from EAWAG for provide different purposes: (i) ML-ECC-BBD was trained on pathway data in EAWAG-BBD and considered the standard, reference model. (ii) ML-ECC-BBD + SOIL was trained on pathway data from both EAWAG-BBD and EAWAG-SOIL to study the effect of biasing the model towards biodegradation in soil. (iii) ML-ECC-BBD + SLUDGE was trained on EAWAG-BBD and EAWAG-SLUDGE to study the effect of biasing the model towards biodegradation in activated sludge. (iv) ML-ECC-BBD + SOIL + SLUDGE was trained on all three data packages to see if including a maximum number of training pathways increases model performance. Table 1 shows the size and composition of the training sets used for the different models. All models used MACCS fingerprints as molecular descriptors and were trained using multi-label Ensemble Classifier Chains (ECC). Further details on the training of relative reasoning models can be found elsewhere.¹⁶

For the TP prediction, EAWAG-PPS was run in batch mode using relative reasoning for three iterations with a neutral aerobic likelihood cut-off. The enviPath TP prediction was also run in batch mode (for details, see Methods section on “Data availability”), with a cut-off at 50 TPs per parent compound. The search algorithm employed a greedy pathway search in a weighted network, where the nodes are compounds and the edges are biotransformation reactions weighted with the predicted probability of the reaction to happen, given available data and competing reactions. The reaction probability p_{edge} is obtained from the ML-based relative reasoning algorithm. For a child node n generated during the pathway search, the probability $p_{\text{node},n}$ is calculated as the product of $p_{\text{edge},n-1 \rightarrow n}$ of the

reaction producing the TPs with the probability of its direct parent node ($p_{\text{node},n-1}$). During the search, the nodes are expanded in order of decreasing combined probability until the maximum of 50 TPs is reached, or no more TPs with a combined probability greater than zero are available for further expansion. The node and reaction probabilities are reported for each predicted TP, indicating their probability to be observed experimentally given the underlying relative reasoning model. The pathway search algorithms used by EAWAG-PPS and enviPath are illustrated in Fig. S1 (ESI-I).[†]

Compilation of suspect list

Python (version 3.6.13) scripting was used to combine the TPs predicted by the five different models into one suspect list, and to determine their monoisotopic mass, chemical formula, InChIKey, CAS number and structure as mol file using the Python libraries RDKit (version 2020.09) and PubChemPy (version 1.0.4). Some TPs were predicted for several parent compounds, in which case they were merged in the suspect list used for screening but counted separately in the method evaluation and comparison. From the suspect list, we extracted the charged masses for HRMS measurements (inclusion list), and the formulae and Molfiles for TP identification in *Compound Discoverer* (mass list).

Experimental setup of sludge reactors

The experimental setup of the sludge reactors was adapted from Gulde *et al.*²⁹ In short, sludge-seeded and aerated bottle reactors were spiked with the mixture of 46 selected compounds at an initial concentration of $8 \mu\text{g L}^{-1}$ (details in ESI-I Table S3[†]). The APIs were selected based on commercial availability, expected measurability using HPLC-HRMS/MS, and predictability of the corresponding TPs. The selected substances show a wide range of structural moieties and diversity in their functional groups. Only irbesartan,³⁰ valsartan,^{7,31–34} metformin³⁵ and hydrochlorothiazide³⁴ were previously investigated in biotransformation experiments in activated sludge or wastewater samples. Further, olanzapine, mirtazapine, rivastigmine, aliskiren, atazanavir, efavirenz and rosuvastatin were screened for in waste water samples.^{36–38} The environmental fate of the remaining 35 APIs has not been investigated to the best of our knowledge. Control experiments were used to reveal abiotic degradation, sorption processes, and matrix background (ESI-I Table S4[†]). The airflow of half of the reactors was augmented with CO_2 to assess biotransformation at pH 6 in addition to the native pH of

Table 1 Training sets used to build relative reasoning models for pathway prediction in enviPath

Model	Number of reactions (pathways) in training data			Total
	EAWAG-BBD	EAWAG-SOIL	EAWAG-SLUDGE	
ML-ECC-BBD	1480 (220)	—	—	1480 (220)
ML-ECC-BBD + SOIL	1480 (220)	2447 (317)	—	3927 (537)
ML-ECC-BBD + SLUDGE	1480 (220)	—	355 (91)	1835 (311)
ML-ECC-BBD + SOIL + SLUDGE	1480 (220)	2447 (317)	355 (91)	4282 (628)



approximately 7.5. Additionally, reactors were run at two levels of total suspended solids (TSS): dilute (DB, TSS = 0.6 g L⁻¹) and high biomass (HB, TSS = 7.1 g L⁻¹). Samples were taken from biotransformation reactors at time points 0 (triplicate), 2 h, 4 h, 9 h, 24 h, 30 h (triplicate), 48 h, 54 h and 72 h and were centrifuged. The aqueous phase was transferred to an LC-MS amber vial and stored at -20 °C until analysis. Two calibration curves were used, one in nanopure water and one in sludge matrix, at concentrations of 0.05, 0.1, 0.2, 0.5, 1, 2, 5 and 8 µg L⁻¹. A more detailed description of the experimental setup of the sludge reactors can be found in the ESI-I, Section S3.†

HPLC-HRMS/MS analysis

The samples of the biotransformation experiments were measured using an HPLC-HRMS/MS (QExactivePlus, Thermo Fisher Scientific, Waltham, MA, USA) approach. For the HPLC separation, a standard method adopted from Achermann *et al.* was used.³⁴ More details can be found in the ESI-I (Section S4).† In a first measurement, mass spectra were acquired in full-scan in positive and negative ionization modes and then a data-dependent top 5 analysis (ddMS2-top5) was used. The [M + H]⁺ and [M - H]⁻ masses of parent APIs and predicted TPs were included in the inclusion list. A single normalized collision energy (NCE) for each compound in the inclusion list was calculated by an empirical formula (eqn (1)).³⁹ In a second measurement, samples from four time points (0 h, 2 h, 24 h and 72 h) were re-measured with a stepped NCE approach where fragments from 3 different collision energies (15, 35 and 60) were simultaneously collected, thus improving the chances of obtaining relevant MS² spectra for structure elucidation of suspect TPs. For the second measurement, TPs arising from conjugation reactions predicted by *Compound Discoverer*TM during the analysis of the first measurement were added to the inclusion list. The HRMS settings are further detailed in the ESI-I (Section S4.2).†

$$\text{Normalized collision energy [NCE]} = \text{mass}[u] \times (-0.41) + 160 \quad (1)$$

TP identification

The *Compound Discoverer*TM software (Thermo ScientificTM, Version 3.2) was used for TP suspect screening. The procedure included compound detection, comparison to suspect mass list, *in silico* prediction of fragments and (spectral) library search (*mzCloud*, *ChemSpider*), described in more detail in the ESI-I (Section S5†). The entries of plausible candidates were reviewed manually based on peak shape, isotopic pattern and chromatographic area evolution over time and comparison to controls. Confidence levels were reported according to Schymanski *et al.*:²⁸ 1 (confirmed structure by reference standard), 2a (probable structure by spectral library match), 2b (probable structure by diagnostic evidence), 3 (tentative candidate with reasonable MS²), 4 (unequivocal molecular formula found), 5 (exact mass found). Finally, molecular structures were drawn based on structural evidence.

*Compound Discoverer*TM was further used to identify TPs resulting from conjugation reactions. *N*-Acetylation and *N*-succinylation were shown to be highly relevant for primary and secondary amines,⁴⁰ but their prediction is beyond the scope of biodegradation tools, which focus on the breakage (and not formation) of molecular bonds. Conjugation reactions (acetylation, formylation, fumarylation, malonylation and succinylation) were therefore predicted using the *Expected Compounds* nodes of *Compound Discoverer*. In addition, we also screened literature to find TPs reported in previous studies. While we did not include TPs arising from conjugation reactions and TPs reported in literature in the suspect list, we still searched for their presence in the LC-HRMS measurements. These TPs were analyzed separately to avoid interfering with our evaluation of TP prediction methods and are therefore discussed separately as *manual suspects*.

Comparison of prediction methods

To evaluate and compare the performance of the different TP prediction methods, we calculated how many TPs we would have found by applying each method separately. For each method, we determined the precision according to eqn (2). Next, we wanted to know if we could have obtained a better performance in terms of precision if we had stopped the prediction algorithm earlier. To answer this question, we generated smaller suspect lists by only keeping TPs that would have been obtained with a given cut-off threshold, and we evaluated the number of correctly predicted TPs and the precision of these reduced suspect list. By varying the cut-off threshold for the number of generations for all methods, we obtained the prediction performance for TPs generated in 1, 2 and 3 generations. We further varied the cut-off threshold for the maximum number of TPs to predict from 1 to 50. As EAWAG-PPS does not support setting a threshold for the maximum number of TPs, the analysis of TP ranks was performed for *enviPath* methods only. The analysis was implemented in Python (see Data availability section for details).

$$\text{Prediction precision [\%]} = \frac{\text{number of predicted and found TPs}}{\text{number of predicted TPs}} \times 100\% \quad (2)$$

Results and discussion

EAWAG-PPS is the most popular TP prediction tool

To assess the current state-of-the-art in suspect screening of TPs in wastewater or activated sludge systems, we performed a literature search for the timespan between 2010 and 2022, and we found 27 publications that used predicted TPs to screen samples (Table 2 and ESI-I Table S1†). The most widely used tools for generating suspect lists were UM-PPS and EAWAG-PPS, which were applied in 7 and 12 studies, respectively. *PathPred*⁸ (2 studies, both in combination with EAWAG-PPS) and *MetabolitePredict*⁴¹ (2 studies, one in combination with EAWAG-PPS) were also applied, even though these tools are not specific to



maintained. Out of these, only UM-PPS/EAWAG-PPS/enviPath are specific to microbial biodegradation prediction. As these tools are also the most widely applied methods for TP prediction in the context of environmental chemistry, they are the focus of our study.

Thousands of potential TPs predicted by EAWAG-PPS and enviPath

Based on the results from the literature search, we focused on EAWAG-PPS and its successor platform enviPath to generate suspect lists and to evaluate their respective performances in correctly predicting TPs. We chose EAWAG-PPS as a benchmark and compared it to the four enviPath models trained on different data packages. The enviPath models were trained on four different combinations of the following data packages: EAWAG-BBD containing 220 pathways, EAWAG-SOIL containing 317 pathways, and EAWAG-SLUDGE containing 91 pathways. Models were trained on BBD only, BBD + SOIL, BBD + SLUDGE, and BBD + SOIL + SLUDGE packages (Table 1).

To obtain a suspect list, we applied the five pathway prediction models to the 46 pharmaceuticals. All the prediction systems combined generated a total of 5570 TPs, out of which 348 (6.25%) TPs were predicted by all methods. The EAWAG-PPS predicted an average of 47 TPs per compound, ranging from four to 441 TPs. For example, fingolimod only has two hydroxyl moieties acting as reactive sites, resulting in four predicted TPs. In contrast, naloxegol features a long polyethylene glycol chain that can be cleaved at alternative reactive sites according to reaction rules, leading to 441 predicted TPs. The four enviPath models were limited to a maximum of 50 TP per compound, which was reached for almost all compounds. One of the exceptions is metformin, for which the enviPath pathway expansion converged at three TPs, meaning that no more reactions occurred according to the available biotransformation and relative reasoning rules. However, metformin may be a special case, as this small molecule only has a few reactive sites and a particular structure that may not be well represented in the training data.

Biodegradation behavior observed for 34 compounds

A total of 42 out of the 46 spiked compounds were detected in the bottle reactors using the *Compound Discoverer* workflow. Acalabrutinib, ceritinib and orlistat were filtered out by the *Compound Discoverer* workflow due to low intensity of *m/z* ions and could only be found by manual exploration of the chromatograms and mass spectra in the raw files of sludge samples or in freshly spiked calibration samples. Ridaforolimus was detected only in pure aqueous standards at 1 mg L⁻¹. This behaviour could be explained by low ionization efficiencies, instability of the API or rapid losses such as volatilization or sorption to glass and/or plastic materials. We therefore excluded these four APIs from further analysis.

Six other APIs, atovaquone, clotrimazol, efavirenz, mometasone, nilotinib and regorafenib were detected in the samples from the sludge reactors; however, in the biotransformation reactors no clear degradation trend was observed over the time

course of the experiment, and in the sorption control reactors these APIs show a decrease in the area by at least one order of magnitude from time-point 0 h to 24 h (ESI-II, Sections S4.2, S4.3, S4.5, S4.7, S4.9 and S4.10†). All these six compounds have a (predicted) soil adsorption coefficient log *K*_{oc} between 3 and 5.5 (ESI-I Table S3†), which would be consistent with noticeable losses by sorption to sludge. Substantial sorption to soil organic material hinders microbial biotransformation, and hence the formation of TPs, due to low bioavailability.⁶⁷ Mometasone and nilotinib were also dissipated abiotically in the high pH abiotic controls (ESI-II, Sections S4.7 and S4.9). Finally, atomoxetine, duloxetine, mirtazapine, rivastigmine and terbinafine, all APIs with amine moieties, show non-linear kinetics in the biotransformation reactors at high pH (ESI-II, Sections S3.4, S3.11, S3.19, S3.26 and S3.29†), which could indicate that some level of ion-trapping occurred in parallel to biotransformation.⁶⁸ For the remaining 31 pharmaceuticals, we obtained clear trends of decreasing concentration over time (for details, see ESI-II†). However, we proceeded with TP identification for all APIs, independently of their biotransformation behavior.

Suspect screening identifies 67 TPs

A total of 79 TPs were tentatively identified, out of which 67 were found with the help of the suspect list and twelve additional TPs were tentatively identified using the list of manual suspects (see Methods section for details). TPs were found for 31 parent compounds. Confidence levels were assigned to the TPs according to Schymanski *et al.* during the screening process (Fig. 2).²⁸ The structures of only seven TPs (9%) were confirmed with a reference standard (level 1) and one additional TPs (1.3%) showed a good match with the spectral library *mzCloud* (level 2a). Diagnostic evidence (level 2b) was found for the structures of eleven TPs (14%). Most TPs (56, 71%) were reported with tentative structures (level 3) and for four (5%) the MS² spectra were not conclusive (level 4). Levels 3 and 4 include TPs for which several possible isomeric structures were considered possible. For example, Clp_TP_3 is the oxidation product of clopidogrel. Hydroxylation, *N*-oxidation, *S*-oxidation or oxidative *N*-dealkylation are plausible reaction mechanisms for the observed modification to the chemical formula, but not enough structural evidence was found to determine a specific structure and its corresponding reaction mechanism (Fig. 2). Three TPs (Val_TP_5, level 4; Val_TP_7, level 1; and Val_TP_12, level 3) were assigned to both valsartan and irbesartan, since they could originate from both parents and the experimental setup did not allow for distinguishing their origin. These three TPs were counted double in the results, as they could originate from both parent compounds. The confidence levels depend on the availability of reference standards and database spectra, as well as on the quality of reported and measured MS² data. For 34 TPs, the best fragmentation was achieved using a stepped collision energy approach, where the analyte is exposed to three different collision energies for each data-dependent scan.

In a next step, tentatively identified TPs were manually assembled into pathways with the help of the suspect lists, which contain information on the biotransformation that is



Table 3 Predicted and found TPs for each of the 42 parent compounds

Parent compound	Abbreviation	Total predicted TPs	TPs found from suspect list	TPs found from manual suspects ^a	Overall Precision
Aliskiren fumarate	Ali	231	1	0	0.43%
Amlodipine besylate	Aml	78	1	3	1.28%
Atazanavir sulfate	Ata	144	0	0	0.00%
Atomoxetine	Atm	100	1	1	1.00%
Atovaquone	Ato	84	0	0	0.00%
Budesonide	Bud	85	0	1	0.00%
Canagliflozin hydrate	Can	124	1	0	0.81%
Clopidogrel bisulfate	Clp	110	5	0	4.55%
Clotrimazol	Clo	68	0	0	0.00%
Dapagliflozin	Dap	144	1	0	0.69%
Dasatinib	Das	156	1	0	0.64%
Dienogest	Die	94	0	0	0.00%
Dolutegravir sodium	Dol	147	1	0	0.68%
Duloxetine	Dul	89	0	1	0.00%
Efavirenz	Efa	64	0	0	0.00%
Ezetimibe	Eze	85	2	0	2.35%
Fexofenadine	Fex	111	4	0	3.60%
Fingolimod hydrochloride	Fin	84	0	0	0.00%
Hydrochlorothiazide	Hyd	118	0	1	0.00%
Irbesartan	Irb	129	4	0	3.10%
Keto-desogestrel	Ket	108	1	0	0.93%
Lumiracoxib	Lum	94	1	0	1.06%
Metformin hydrochloride	Met	3	0	1	0.00%
Mirtazapine	Mir	149	3	0	2.01%
Mometasone furoate	Mom	148	0	0	0.00%
Naloxegol	Nal	472	0	0	0.00%
Nilotinib	Nil	174	0	0	0.00%
Olanzapine	Ola	137	2	0	1.46%
Omeprazole	Ome	117	1	0	0.85%
Panobinostat lactate	Pan	80	3	0	3.75%
Pemetrexed	Pem	160	3	0	1.88%
Pioglitazone hydrochloride	Pio	109	4	1	3.67%
Quetiapine fumarate	Que	141	7	0	4.96%
Regorafenib	Reg	74	0	0	0.00%
Rivastigmine hydrochloride	Riv	87	3	1	3.45%
Rosuvastatin calcium	Ros	130	4	0	3.08%
Tadalafil	Tad	95	1	0	1.05%
Terbinafine hydrochloride	Ter	138	6	2	4.35%
Ticagrelor	Tic	136	2	0	1.47%
Valsartan	Val	120	3	0	2.50%
Vildagliptin	Vil	88	1	0	1.14%
Vorinostat	Vor	59	0	0	0.00%
Total		5064	67 (64 ^b)	12	1.35%

^a TPs that were not predicted by any of the evaluated prediction methods but found in literature or using *Compound Discoverer's* conjugation reaction prediction are here called manual suspects. ^b TP count without duplicate TPs from irbesartan and valsartan.

It should be noted that these low values for precision represent a worst-case scenario, as the suspect list can be further filtered to increase the precision. For example, removing compounds with a mass below the quantification limit of the analytical method (100 g mol^{-1}) slightly increases the prediction precision of the suspect list from 1.35 to 1.37%. If a small suspect list is required, the precision can be further increased by adapting the parameters of the pathway search: In EAWAG-BBD, the generation threshold can be set to 1, 2 or 3, and in enviPath the maximum number of TPs to predict can be defined. However, limiting the number of generations or TPs to predict comes at the cost of losing

correctly predicted TPs. To characterize this trade-off, we analyzed the effect of different thresholds for these two parameters on the precision and the number of correctly predicted TPs. For the number of generations, the threshold analysis showed that the precision peaks at the first generation for all methods (5.4–7.3%), where EAWAG-PPS correctly predicts 19 TPs and the enviPath models between 26 and 29 TPs (Fig. 3). Regarding the threshold of the maximum numbers of TPs to predict, the precision peaks between 10.9 and 13.0% if only the top 2 TPs are predicted. The number of correctly predicted TPs reaches a plateau at a threshold of 30 predicted TPs, beyond which the workload increases but not





Fig. 4 Comparison of biotransformation rules leading either to well-defined or ambiguous structures. The rules were categorized into monooxygenation (+O, white), hydrolysis and hydration (+H₂O, light gray) and desaturation (–H₂, dark gray).

reaction sites or characteristic cleavage moieties. Desaturation-type reactions (–H₂) were only predicted and found for the oxidation of primary (bt0001) and secondary alcohols (bt0002). The type of reaction could be determined through the atomic modifications relative to the precursor molecule, but the site of transformation was only identifiable in 62% of the cases. The beta-oxidation process (bt0337) was observed once and was not considered in Fig. 4, because it does not fit into any of the proposed categories.

Complementary approaches reveal and fill knowledge gaps in TP prediction models

Careful analysis of the time trends in chromatogram areas revealed TP-like behavior for several unidentified compounds, indicating that not all formed TPs were predicted by the employed pathway prediction methods. To identify the structures of analytes with TP behavior, we searched literature for known TPs, and we predicted conjugation reactions. APIs are particularly prone to undergo conjugation, as they often contain primary and secondary amines. However, this type of transformation is not covered by any of the TP prediction methods analyzed here, because they all focus exclusively on catabolic reactions. As a result, we tentatively identified four TPs that underwent either *N*-acetylation or *N*-succinylation. For conjugation reactions, the MS² spectra are closely related to those of the parent because they share the same molecular backbone, thus facilitating TP identification. Therefore, screening for conjugates can help identify additional TPs by considering reaction classes that are beyond the scope of the TP prediction tools.

Another eight TPs were either previously reported in literature or derived by expert logic (e.g., suspected hydroxylation

when observing corresponding mass signature and TP-like behavior over time). Three of them were previously reported in literature and reference standards were available to the authors, but they were neither predicted nor part of any of the used databases. For example, the TP guanlylurea of metformin was not predicted, even though it is known to literature.⁷² These cases highlight the importance of expanding the databases towards more diversity in terms of chemical structure, application class, and biodegradation environment. In the particular case of pharmaceuticals, it could be helpful to also consider metabolites produced by human metabolism or human microbiomes, because of the potential overlap of degradation mechanisms present in human and wastewater systems. For example, the only detected TP of aliskiren was not predicted by any TP prediction model but reported to also occur in human metabolism.⁵² Computational tools for drug metabolite prediction could therefore be applied to complement environmental TP prediction with prediction tools for human drug metabolism (e.g., Metabolitepredict,⁴¹ NICEdrug.ch,⁷³ Biotransformer 3.0 (ref. 74)).

Conclusion

We present an updated workflow to identify TPs in activated sludge biodegradation experiments using suspect screening. We applied the workflow to 46 pharmaceutical substances and tentatively identified 79 TPs for 31 parent compounds. Of these, 66 (83%) are TPs reported for the first time in activated sludge, and only 13 TPs have previously been reported in similar or wastewater studies. We further compared our workflow with a comprehensive list of similar studies, and we discussed limitations of the analytical and computational methodology.

This workflow was applied to a specific biotransformation experiment and achieved a good ratio of found TPs per parent despite having an initial spiked concentration of 8 µg L⁻¹ only, which is more than an order of magnitude lower than the concentrations of the original experiment conducted by Helbling *et al.*⁷ and the majority of studies reviewed here. Regarding the analytical methods, 15 out of the 27 analyzed studies complemented suspect screening with non-target screening to detect more TPs. Since conjugation reactions are not currently predicted by the EAWAG-PPS or enviPath, we suggest to complement the suspect list with TPs formed by acetylation, formylation, fumarylation, malonylation and/or succinylation. Another approach to detect more TPs would be to perform a systematic literature review on each parent compound to expand the suspect list towards TPs found in environmental biodegradation studies or mammalian metabolism.

Although our prediction precision is comparable to the precision reported by other studies and sufficient to perform a successful suspect screening, a higher precision would decrease the manual effort required to verify mass spectra. A systematic approach to improve the precision of the TP prediction methods would involve the collection of more high-quality biodegradation data to better cover the chemical diversity of organic micropollutants, and hence to increase the



prediction accuracy of the machine learning models. However, if resources are limited, predicting 30 TPs per parent compound with the currently available models will achieve reasonable predictions without any significant loss in sensitivity. Currently, the training data sets for BBD, SOIL and SLUDGE together contain 623 degradation pathways, which only represents a small fraction of the chemical compound space. The combination of all these and the incorporation of the EAWAG-PPS led to the most comprehensive suspect list.

To share our results with the scientific community in a computer readable format, we enriched the EAWAG-SLUDGE data package with the newly obtained biodegradation pathways for 34 pharmaceuticals in activated sludge, thus feeding our learnings back into the design-build-test-learn cycle to evolve towards robust biotransformation prediction tools adapted to different environmental situations. As data acquisition is crucial to develop better models, future work will focus on improving the integration of the prediction platform enviPath with MS screening tools and on facilitating systematic and standardized data upload to enviPath. We hope that our work can guide TP identification efforts in the future and encourage researchers to share biodegradation data openly to improve prediction models.

Disclaimer

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Data availability

The biotransformation pathways were uploaded to the enviPath database and integrated into the publicly accessible EAWAG-SLUDGE package available at <https://envipath.org/package/7932e576-03c7-4106-819d-fe80dc605b8a>. Results are further detailed in the ESI-I and II (Supplementary_Information_I.docx and Supplementary_Information_II-TP_data.docx).[†] Raw MS output can be obtained from the authors upon reasonable request. All scripts used to predict TPs, create suspect lists, and analyze data are publicly available at https://github.com/FennerLabs/TP_predict. The TP prediction uses the enviPath platform and therefore requires the installation of the enviPath python API (enviPath-python version 0.2.0, <https://github.com/enviPath/enviPath-python>). Detailed instructions can be found in the README file of the git repository. This resource also provides the code to convert the output of the enviPath pathway prediction and EAWAG-PPS into suspect lists that are compatible with the *Compound Discoverer* software.

Author contributions

CC, KF and JH designed the study. CC and LT performed sludge experiments, LC-MS measurements and analysis in *Compound Discoverer*. LT and JH performed data conversion and analysis. JH predicted transformation products. LT, CC, KF and JH wrote

the manuscript. KF reviewed all the TP structural assignments and acquired the funding.

Conflicts of interest

There are no conflicts of interest to declare.

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