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Per- and polyfluoralkyl substances (PFAS) in drinking water system: Target and non-target screening and removal assessment

Yu-Qing Wang, Li-Xin Hu *, Ting Liu, Jia-Hui Zhao, Yuan-Yuan Yang, You-Sheng Liu, Guang-Guo Ying *

SCNU Environmental Research Institute, Guangdong Provincial Key Laboratory of Chemical Pollution and Environmental Safety & MOE Key Laboratory of Theoretical Chemistry of Environment, South China Normal University, Guangzhou 510006, China
School of Environment, South China Normal University, University Town, Guangzhou 510006, China

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ABSTRACT

The massive use and the persistence of per- and polyfluoroalkyl substances (PFAS) have led to their frequent detection in aquatic environments, which may further threaten drinking water safety. So far, our knowledge about the occurrence of PFAS in drinking water system is still very limited. Here we investigated the occurrence and removal of PFAS in a drinking water system using non-target, suspect and target screening strategies. Sampling was performed in three seasons in the drinking water system including a water source, two drinking water treatment plants, and tap water in five households. The results showed detection of 17 homologous series with 51 homologues in non-target screening and 50 potential PFAS detected in suspect screening. Probable structures were proposed for 15 PFAS with high confidence levels (the first three of the five levels), with seven of them being reported for the first time in drinking water system. Semi-quantification was performed on seven homologous series based on target PFAS, the estimated total concentrations for non-target PFAS ranged between 4.10 and 17.6 ng/L. Nine out of 50 target PFAS were found and precisely quantified (<LOQ-13.4 ng/L) with predominance of perfluorocarboxylic acids (PFCA) and perfluorosulfonic acids (PFSA). All target and non-target PFAS were detected in tap water with similar concentrations in all three seasons. Removal efficiency for the detected PFAS in each processing unit was almost zero, indicating the recalcitrance of these chemicals to the conventional treatment process. The findings from this study clearly show the wide presence of PFAS in the whole drinking water treatment process, and suggest an urgent need for effective removal technology for this group of chemicals.

1. Introduction

Per- and polyfluoroalkyl substances (PFAS) are synthetic organic chemicals in which the hydrogen atoms are partially or completely substituted by fluorine atoms (Buck et al., 2011). Due to their hydrophobic, lipophobic and thermostable properties (Lindstrom et al., 2011), PFAS are widely used in industrial and commercial products such as non-stick coating (Trier et al., 2011), surfactants (Chu et al., 2016), food-packaging materials (Schaider et al., 2017) and aqueous film-forming foams (Place and Field, 2012) since the 1950s, leading to numerous emissions into the environment (Wang et al., 2017).

The stability of the carbon-fluorine bond determines that PFAS are highly persistent and can be hardly degraded once they are released into the environment (Pan et al., 2016; Podder et al., 2021). With the increasing usage of PFAS, the widespread presence of PFAS has been reported in different kinds of environmental matrixes, including air (Yu et al., 2018), surface water (Podder et al., 2021; Sharma et al., 2016), drinking water (Chow et al., 2021; Jin et al., 2009), sediments (Bai and Son, 2021), fish (Liu et al., 2018), marine mammals (beluga whale, dolphin and finless porpoise) (Barrett et al., 2021; Sciancalepore et al., 2021; Stockin et al., 2021; Wang et al., 2021) and even human samples (paired maternal and cord sera, breast milk and blood) (Li et al., 2020; Olsen et al., 2017; Zheng et al., 2021). Besides, numerous studies have proved that PFAS are toxic to multiple organs throughout the body and can be bio-accumulated in humans and organisms (Houck et al., 2021; Lindstrom et al., 2011; Pan et al., 2014b; Podder et al., 2021; Roth et al., 2021).

The major sources of PFAS in the aquatic environment include

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* Corresponding authors at: School of Environment, South China Normal University, University Town, Guangzhou 510006, China.
E-mail addresses: lixin.hu@m.scnu.edu.cn (L.-X. Hu), guangguo.ying@m.scnu.edu.cn (G.-G. Ying).

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discharge from wastewater treatment plants (Lenka et al., 2021; Pan et al., 2016), emission of manufacturing facilities (Jacob et al., 2021; Wang et al., 2018), industrial factories and landfill leachate (Fuertes et al., 2017). The insufficient removal of PFAS in wastewater treatment plants and the direct discharge from surface runoff affect drinking water sources and further threaten drinking water safety (Lenka et al., 2021). Drinking water is a primary PFAS exposure route (Sunderland et al., 2019), and the PFAS in human serum have been closely associated with their occurrence in the drinking water (Daly et al., 2018; McDonough et al., 2021). Meanwhile, the occurrence of PFAS in drinking water has been reported with the predominance of perfluorooctane sulfonic acid (PFOS) and perfluorooctanoic acid (PFOA) (Domingo and Nadal, 2019) at various concentrations all over the world, such as 0.17–18.9 ng/L in the U.S. (Chow et al., 2021), <0.10–45.9 ng/L in China (Jin et al., 2009; Pan et al., 2016), 89.0–1200 ng/L in Colorado, U.S. (McDonough et al., 2021), and 0.56–47.0 ng/L in the Netherlands (Gebbink et al., 2017). Due to awareness of PFAS toxicity, legacy PFAS such as PFOA and PFOS have been phased out while novel PFAS alternatives have recently been produced and used, which results in more complex chemical composition profiles in the environment. However, the production cut of legacy PFAS has not resulted in a reduction of their residues in the environment due to their persistence. The increasing number of novel PFAS, along with their precursors and degradation products puts a certain pressure on environmental monitoring based on traditional target analysis. Therefore, it is urgently needed to have a comprehensive understanding of PFAS in the drinking water system.

Meanwhile, target analysis using high-performance liquid chromatography coupled with mass spectrometry (HPLC-MS) can achieve the quantification of known chemicals with the reference standards. This characteristic provides concentration accuracy for target analysis while ignoring many unknown chemicals. Fortunately, a recently developed analytical technique known as non-target screening using high-resolution mass spectrometry (HRMS) makes it possible to identify the novel chemicals without the available reference standards (Hollender et al., 2017). Dozens of studies have employed non-target analysis to implement the identification of the unknowns and broaden the number of cognitive chemicals (Krauss et al., 2010). As for PFAS, benefits from their unique structure, characteristic fragment ion searching and homologous series detection along with Kendrick Mass Defect analysis are utilized to identify unknown PFAS (Liu et al., 2015; Roach et al., 2011). Until now, few studies are focusing on PFAS in full-scale drinking water treatment systems (Pan et al., 2016; Takagi et al., 2011).

The objectives of this study are to investigate the occurrence of PFAS in a drinking water system with two conventional drinking water treatment plants (DWTPs), and to explore their removal efficiency in DWTPs and their variations in tap water. To accomplish this, target analysis was applied to accurately quantify the known PFAS in water samples collected from the drinking water system; suspect and non-target screening were employed to screen more unknown PFAS; and precise concentrations of target PFAS and their responses in non-target screening were utilized to achieve the semi-quantitation of the unknowns. To the best of our knowledge, this is the first research that focus on both legacy and novel PFAS in the entire drinking water supply system using target and non-target analysis. The results from this study fill the gap of the variation of PFAS in drinking water supply system. It can facilitate better understanding of what PFAS in our drinking water and also provide scientific basis for further control.

2. Materials and methods

2.1. Chemicals and reagents

Authentic standards of 50 target PFAS along with their 19 corresponding internal standards were purchased for target analysis, and detailed information of these PFAS is provided in the Supporting Information (Table S1). The mixed standard solution and the mixed internal standard solution were prepared separately in methanol at 100 ng/L and stored at −20 °C. The ultrapure water was generated by a Milli-Q system (Veolia, UK) and HPLC grade methanol and acetonitrile were purchased from Merck (Darmstadt, Germany). Besides, all the other reagents (e.g. ammonia, acetic acid and ammonium acetate) were purchased with HPLC grade from reliable suppliers.

2.2. Sample collection

A drinking water system with two conventional drinking water treatment plants (DWTPs) in Guangzhou, South China was selected for this study. The two DWTPs are less than 100 m apart, share the same water source, employ the same treatment processes and jointly supply drinking water to the service area. The water source belongs to the Pearl River system, which has effluent discharges from domestic and industrial sources including cement factories, leather factories, paper factories and metal, and plastic packaging factories in the upper reaches. The two DWTPs have the following treatment units: biological pretreatment (suspended filler biological contact oxidation), coagulation, horizontal sedimentation, and V-type filter. Fig. S1 illustrates the treatment processing flow of the DWTPs and the 18 sampling points from water source to tap water, including one water source, six treatment units in each DWTP and five households within 3–5 km for tap water.

Samples were separately collected in three seasons i.e. August 2020, December 2020 and March 2021. At each sampling point, three replicate water samples (0.5 L each) were collected in high-density polyethylene bottles, which had rinsed with Milli-Q water, methanol and sampling point in-situ water for three times beforehand. All collected water samples were transported to the laboratory in coolers and stored at 4 °C in the dark and were extracted within 48 h. It is worth noting that the sampling points B-P2 and TW2 were not accessible in August 2020. At last, a total of 156 samples were collected to achieve the goals of this study.

2.3. Sample extraction

All replicate samples were simultaneously filtered using glass fiber filters (GF/F, 70 mm, 0.7 μm, Whatman) and spiked with the internal standard solutions (50 μL of 100 μg/L each) before solid-phase extraction (SPE). The extraction of water samples was performed by Oasis WAX Cartridges (500 mg, 6 mL, Waters) based on our previously reported method (Chen et al., 2021; Pan et al., 2014a). Briefly, the cartridges were preconditioned by 0.1% NH_4OH in methanol, 4 mL of methanol and 4 mL of Milli-Q water in sequence, then the water samples were passed through the cartridges at a flow rate of approximately 5–10 mL/min. Then, the cartridges were dried for about 2 h under vacuum and hereafter eluted by 4 mL of methanol and 4 mL of 0.1% NH_4OH in methanol in succession. The eluents were nearly dried under a gentle stream of nitrogen and re-dissolved with 0.5 mL methanol. After the vortex for 30 s, the extracts were filtered using 0.22 μm membrane filters (organic phase, nylon) into 1 mL polypropylene (PP) vial with polyethylene (PE) cap, and then stored in −20 °C before analysis.

2.4. Instrumental analysis

2.4.1. Target analysis

Quantitative analysis of 50 target PFAS and their 19 corresponding internal standards in the extracts was performed according to our previous method (Chen et al., 2021). The determination was conducted using ultra-performance liquid chromatography equipped with Xevo TQ-S triple quadrupole mass spectrometer (Waters, Milford, MA, USA) with an electrospray ionization source (UPLC-ESI-MS/MS). Briefly, 2 μL samples were injected into an ACQUITY UPLC BEH C18 analytical column (2.1 × 50 mm, 1.7 μm) at a column oven temperature of 40 °C with a pump delivering 0.4 mL/L of the mobile phase (A: 2 mM ammonium acetate in Milli-Q; B: acetonitrile). The gradient elution procedure was as follows: 0–0.5 min, 98 %A; 6 min, 20 %A; 8 min, 0 %A. The negative mode was applied based on characteristics of PFAS in the multiple-reaction monitoring (MRM) mode. The MS/MS parameters for the instrument were optimized for individual chemicals and detailed information and instrumental parameters are given in the Supporting Information (Table S2).

2.4.2. Non-target and suspect screening

The non-target and suspect screening were performed according to our previous method through an Agilent 1290 Infinity II LC system coupled with an Agilent 6545 quadrupole-time-of-flight mass spectrometer (QTOF-MS) with electrospray ionization (ESI) source (Wang et al., 2022; Zhao et al., 2022). Replicative samples were injected at 3 μL into an Agilent EclipsePlus C18 analytical column (3.0 × 150 mm, 1.8 μm) at a column oven temperature of 40 °C with a pump delivering 0.3 mL/L of the mobile phase. Full scan (50–1700 Da) and MS^2 scan (20–1700 Da) in both positive and negative ionization modes were acquired in separate sample runs. The data acquisition was under dependent acquisition mode (DDA), and five eligible precursors with the highest response were fragmented. Accurate mass spectra were collected in 2 GHz high-resolution mode with two collision energy (10 V and 40 V). Meanwhile, a further iterative injection aiming at maximum feature acquisition was employed to alleviate the demerits of DDA, the other five features were fragmented while the high-response features were shielded. The mobile phase composition, gradient elution process of chromatography and mass spectrometry parameters are described in the Supporting Information (Text S1).

2.5. HRMS data processing

The acquisition data from the HRMS were processed by a non-target workflow conducted according to previous studies (Feng et al., 2021; Jacob et al., 2021). R software (version 4.0.5) and the Agilent Qualitative Analysis 10.0 were applied. The raw data were transformed to mzXML format using MSConvert software and the converted files were imported into the R software for peak picking by the "xcms" package. Features with intensity over 2000 in the solvent blank and procedural blank were eliminated from the dataset. For suspect screening, an *in-house database* including 50 PFAS and an online database (Massbank of North America (MoNA), 145,799 MS^2 spectra, https://mona.fiehnlab.ucdavis.edu/) were applied. In addition, a suspect list that recorded 8163 PFAS (Norman, https://www.norman-network.com/) without MS^2 spectra was applied to accomplish the supplement of chemicals. The *in-house database* was set up by the reference standards mentioned above. Spectral data of the mixed standard (1 mg/L) was acquired by HRMS and the peak list was imported into R (version 4.0.5) matching to MS^2 fragments by the "metID" package (constructing database function)

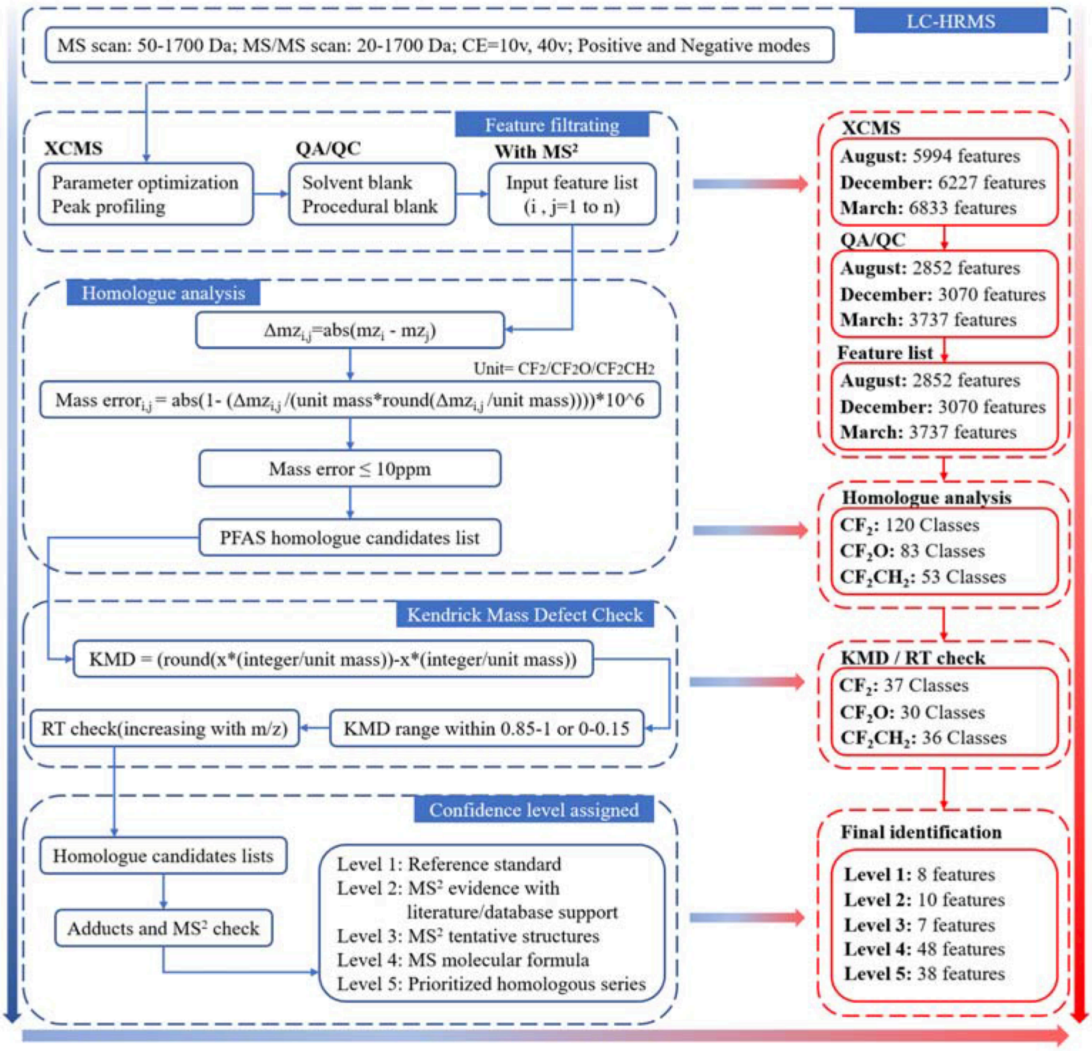


Fig. 1. The workflow of the nontarget screening and the variation of features number during feature detection, elimination and confirmation process.

(Shen et al., 2019). The data downloaded from the internet were also recorded to databases in the same way. The dataset of suspects was matched to databases with a mass error of 5 parts per million (ppm) and a retention time tolerance of 30 s (when match to the in-house database with retention time record). Meanwhile, except for protonated ions or deprotonated ions, other additive forms had been eliminated to avoid false-positive as much as possible.

For non-target screening, homologous series detection along with Kendrick Mass Defect analysis were utilized to detect possible homologues (Hensema et al., 2021; Jacob et al., 2021). Workflow performed in R software was conducted, and the detailed process can be found in Fig. 1 (Li et al., 2020; Yu et al., 2018). Briefly, repeating units (CF_2, CF_2O and CF_2CH_2) were searched to prove the evidence of the existence of potential homologous series with a *m/z* window of 10 ppm among the homologous series. Then the peak shape and MS^2 fragments were extracted in Agilent Qualitative Analysis 10.0 to prelude noise. Meanwhile, regular fragment distribution must be observed among a homologous series, such as the increasing trend of retention time with increasing *m/z*. Besides, Kendrick Mass Defect was considered, and only the features within the range of 0.85–1 or 0–0.15 were refined. In addition, characteristic fragments of common PFAS ions were searched using R software. Constraints are set that only features with characteristic fragments ($[FSO_3]^-$, $[C_nF_{2n+1}SO_3]^-$, $[CF_2O]$-, etc.) and at least one of $[C_nF_{2n+1}]^-$ would be recorded in the suspect list. The mass of interest was first compared with results reported in previous studies, and then assigned by Metfrag (https://msbi.ipb-halle.de/MetFrag/) and Agilent Qualitative Analysis 10.0. Chemical formula was set to contain up to 50C, 100H, 50F, 5 N, 15O, 2S. Potential formulas were proposed based on observed *m/z* and MS^2 spectra for each homologous series. Five confidence levels were assigned to proposed structures referring to criteria established in the previous study (Schymanski et al., 2014). Substantially, features that could be confirmed with authentic standards (Retention time confirmation, provided in Supporting Information, Table S8) were confirmed to be Level 1; probable structures with MS and MS^2 evidence along with studies or database support were assigned with Level 2; those structures with MS and MS^2 evidence but no studies or database support stayed at Level 3; Level 4 indicated tentatively identified compounds with MS evidence and MS^2 fragments available, but a further confirmation for the only structure was needed; the prioritized homologous series which at least one of the homologues has MS^2 evidence were defined as Level 5.

2.6. Quality control/quality assurance

Procedural blank samples and quality control samples (0.5 L Milli-Q water each in HDPE bottles) were processed along with every batch of water samples in triplicates, respectively. The internal standard method was employed in the target analysis and R values of the target standard curve for individual analytes were all over 0.99. The method limit of detection (LOD) was defined as the concentration giving a signal-to-noise ratio of three while the method limit of quantification (LOQ) was defined as ten times signal to noise ratio. The performance of PFAS extraction was evaluated by recoveries of quality control samples (spiked with 20 ng/L mixed standard solution). The method LOD and LOQ values and recoveries for the individual analytes are displayed in the Supporting Information (Table S3). Besides, standard mixture solution and methanol were injected in turn after every six samples during instrumental analysis to ensure the mass and quantification accuracy and precision of the instrument. The mixed solution of reference masses (Agilent, USA) was continuously injected into the mass spectrometer during Q-TOF analysis process to have real-time correction of the mass axis (positive: 121.0509 and 922.0098; negative: 112.0509 and 1033.0098).

2.7. Statistical analysis

The proposed structures of identified PFAS were drawn by Chemdraw 19.0. The boxplots were performed by Origin 2021b and the T-test was conducted by IBM SPSS statistics 21, and the statistical significance was accepted at $p < 0.05$.

3. Results and discussion

3.1. Target analysis

50 target PFAS are consisted of 12 classes (legacy and alternative PFAS), e.g. 13 perfluorocarboxylic acids (PFCA), and eight perfluorosulfonic acids (PFSA) (Table S1). The complete results of target analysis are summarized in Tables S4–S6 and displayed in Fig. 2. All target PFAS detected at each sampling point exceeded the limit of detection (LOD), and the concentration value exceeded the limit of quantification (LOQ). The concentration values were the average of triplicate samples of each sampling site and standard deviations was calculated to ensure the accuracy of the results (Tables S4–S6).

There were six, six, and nine PFAS out of 50 target PFAS detected in the drinking water system in August, December and March, respectively. As seen in Fig. 2, the composition of detected target PFAS in August and December were the same, all of them subordinate to PFCA (PFBA, PFHxA, PFHpA and PFOA) and PFSA (PFBS and PFOS). The exact six PFAS were also detected in March with three extra PFCA compounds (PFPeA, PFNA and PFDA). Most of them were short-chain PFAS ($C \leq 8$). With pK_a estimated to be near zero for PFCA and −1 for PFSA, the mobility of PFCA and PFSA are relatively strong in the environment compared with others (Bai and Son, 2021), which makes them ubiquitous. Substantially, PFCA and PFSA are also the most produced and used categories of PFAS since their production (Flores et al., 2013), resulting in significant residues in surface water and the surrounding environment. As the most common and most frequently detected PFAS, some previous studies have linked them to drinking water sources, even drinking water and bottled water (Chow et al., 2021; Jin et al., 2009; Pan et al., 2016). A previous study has determined the highest concentrations of PFOS and PFOA (over 10 ng/L each) in the drinking water samples of Shenzhen and Guangzhou over other 19 cities from various Chinese regions (Jin et al., 2009). Also in Guangzhou, the analogous composition of PFAS was observed (seven PFCA and three PFSA) in two local DWTPs and the average of total 10 PFAS concentrations ranged from 4.74 to 14.3 ng/L in the influent and 3.34 to13.9 ng/L in the effluent (Pan et al., 2016). Chow et al. (2021) found the existence of 32 PFAS in U.S. bottled water, consisting primarily of PFCA (0.17–16.46 ng/L) and PFSA (0.17–18.9 ng/L).

It is worth mentioning that all detected target PFAS in this study were observed in all 18 sampling sites with negligible fluctuation, indicating the low removal efficiency of conventional drinking water treatment for these PFAS. PFBA was the predominant compound (4.98–13.4 ng/L) detected in three sampling seasons with different concentration ranges and the highest concentration range occurred in March (8.57–13.4 ng/L). Other target PFAS were below 5 ng/L in December (0.38–3.56 ng/L) and March (0.10–4.40 ng/L) and 2 ng/L in August (<LOQ-1.90 ng/L). T-test was carried out between every two adjacent units in DWTPs, between SW and P1 and between P6 and TWs based on the exact concentrations of target PFAS as statistical support (Table S7). The variation trends of target PFAS among process units in the two plants were similar. Except for the concentrations for P3 and P4 in December (Tables S4-S7, $p < 0.05$), every other two adjacent units showed not much significant difference ($p > 0.05$). Meanwhile, T-test results between SW and P1 and between P6 and TWs ($p > 0.05$) also proved that the pipeline transportation of drinking water from source to the taps did not significantly affect the concentrations of target PFAS. The exact PFAS in P6 with a similar concentration were detected in tap water (0.24–12.2 ng/L), however, none of the tap monitoring sites

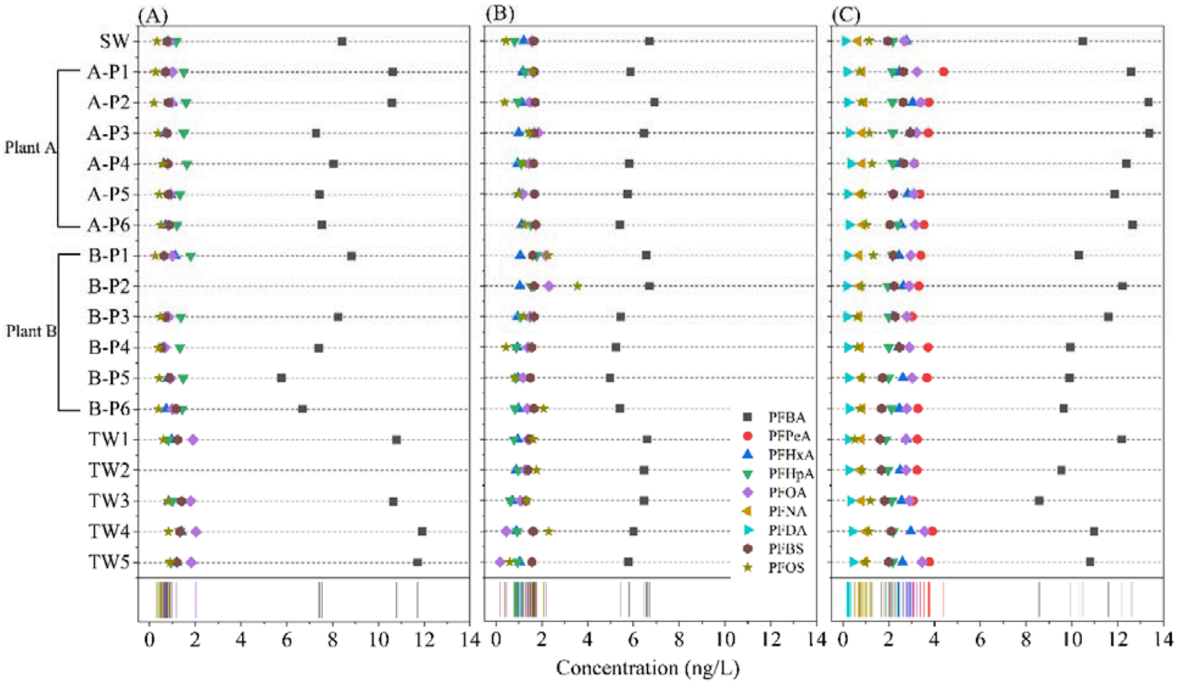


Fig. 2. Concentrations (ng/L) of detected PFAS based on target analysis of 50 target PFAS in drinking water supply system of three seasons. (A): August 2020; (B): December 2020; (C): March 2021. The rugs below illustrate the density of concentration distribution of individual PFAS in the whole system. Note: samples from B-P2 and TW2 were not available due to accessibility problem in August.

exceed the limits of the European drinking water directive (0.1 μg/L for sum concentration of 20 PFAS) or the health advisory level (70 ng/L) set by the U.S. Environmental Protection Agency (Chow et al., 2021). Even so, PFAS consumed by residents through drinking water would still pose a threat to human health as these compounds may accumulate in human body (Domingo and Nadal, 2019). Besides, most of the target PFAS were elevated to a small degree during transfer from the water source to DWTPs while slight variations were observed between the effluents and the tap water. No obvious change in PFAS with increasing service distance was observed in tap water.

3.2. Non-target and suspect screening

Limited by available reference standards, target analysis could not provide insight into the presence of all species of PFAS in the drinking water system. Thus, non-target workflow (Fig. 1) was developed to identify potential PFAS existing in the drinking water system as much as possible. The peak picking of water extracts was performed by the “xcms” package using R software based on conversed HRMS acquired data. A total of 5994, 6227 and 6833 features were extracted in August, December and March in negative mode, respectively. The triplicate blank samples extracted along with the water sample were considered as procedural blank, and the features present in the triplicates were eliminated. After the blank subtraction, 2852, 3070 and 3737 features were retained in the suspect dataset. It had to be clear that the feature detected in the positive mode was much more than those in the negative mode, however, neither non-target nor suspect screening traced potential PFAS in positive mode. Therefore, the subsequent discussion of the screening results only focuses on the negative mode.

For non-target screening, homologue analysis was carried out by workflow we established in R software. The list of suspicious features was input into the workflow, and homologous sequences containing repeat units (CF_2, CF_2O and CF_2CH_2) were scanned, and 120, 83 and 53 candidate sequences were captured for further confirmation, respectively. Subsequent inspection of Kendrick Mass Defect (KMD, within the range of 0.85–1 or 0–0.15) and RT (positively correlated between *m/z* and RT) helped us narrow the candidates to 37 series with CF_2 unit, 30 series with CF_2O unit, and 36 series with CF_2CH_2 unit. Fig. 3 illustrates an example of the analytical evidence for identification. The accurate mass of this feature was 512.9598 in full scan with the retention time of 18.32 min, as can be seen in Fig. 3A. And the feature was selected by the homologues analysis workflow as a homologue of Class 1. The accurate mass and isotope peak distribution (Fig. 3B), along with the other homologues in Class 1 contributed to the certain ion formula of $[C_{10}F_{19}O_2]^-$. When it came to further structure identification, the MS^2 spectra under 10 V and 40 V (Fig. 3C) of this feature were extracted, respectively. MS^2 fragments of 168.9884, 218.9864, 268.9834, 318.9806 and 468.9697 were observed under collision energy of 10 V while 68.9951, 118.9917 and 168.9886 were found under 40 V. Besides, we further matched the retention time of this feature to an authentic reference in suspecting screening and the RT error was within 30 s (RT error = 19 s).

Through these identified evidences (MS, isotope peak distribution, MS^2 fragments, RT and *in-house database* support) and later vetting for all homologues of this homologous series, the proposed structure for Class 1 was accepted with the confidence of level 1. Meanwhile, the following structure identification of homologous series provided reliable MS^2 evidence for five homologous series with 12 homologues available. The necessary information of these seven homologous series is summarized in Table 1 while detailed identified information is displayed in Table S8. After searching and comparing, four of these five classes with 11 PFAS were determined to have literature and database support, and were upgraded to confidence level 2 according to the level criterion mentioned above. The Metfrag online prediction website was applied for further verification of proposed structures. Correspondingly, the other classes with 2 homologues were assigned to confidence level 3. The remaining series lacked sufficient MS^2 fragments evidence and were later excluded from the candidate series. In the five classes, Class 1 and Class 2 were identified to be PFCA and PFSA with four homologues each, five of them were also detected in target analysis and one of the PFSA was speculated by MS^2 fragments and homologous patterns. Mass tolerance of the PFCA and PFSA homologues ranged from −0.2–1.2

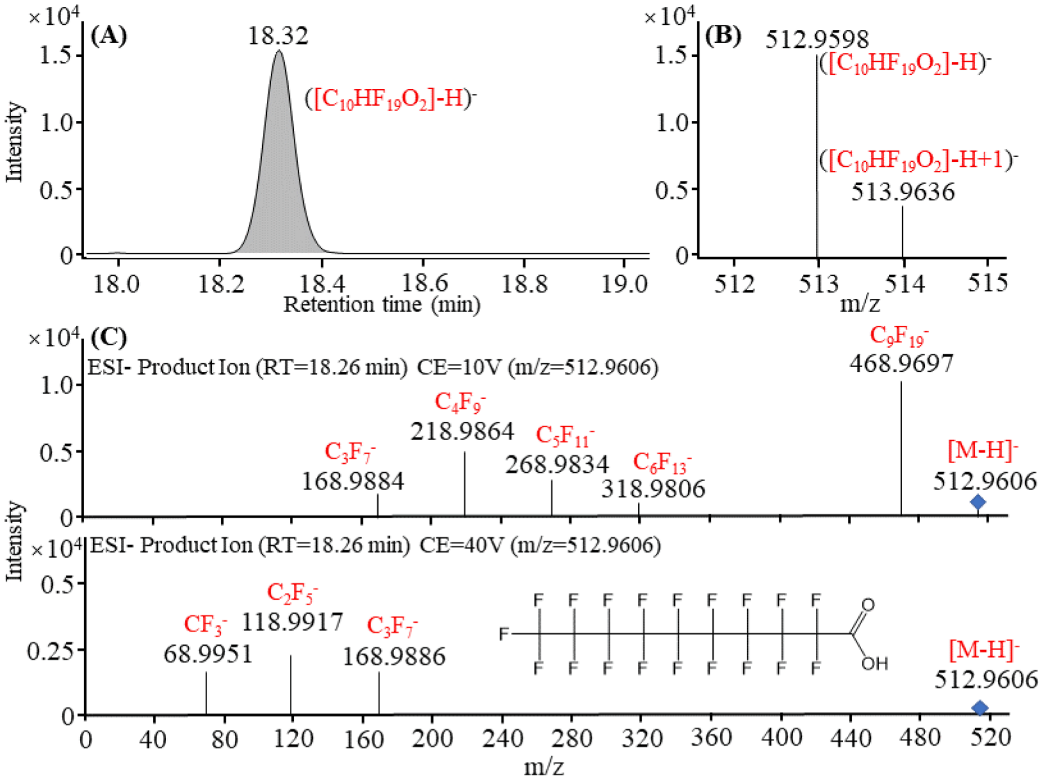
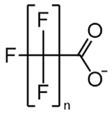
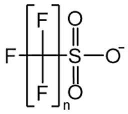
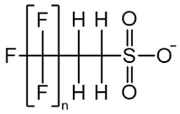
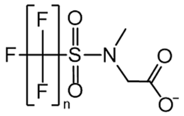
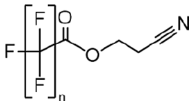


Fig. 3. Illustration on the structural elucidation of a non-target PFAS example. The feature (512.9598) is one homologue extracted from homologous Class 1 in the negative mode. (A) The chromatogram of this feature is extracted from water samples at a retention time of 18.32 min, and the ion formula $[C_{10}HF_{19}O_2]^-$ is generated based on mass and (B) isotope peaks distribution. (C) MS^2 spectra were performed under CE = 10 V, 40 V with major fragments of 68.99, 118.99, 168.99, 218.99, 268.98, 318.98 and 468.97. The proposed structure is displayed, and later confirmed by its authentic standard.

Table 1

Summary of homologous series identified with a confidence level above 3 in drinking water supply system, including structures, theoretical masses, observed masses, retention time (RT) and confidence levels (CLs).

Class	Structure	n	Ion Formula	Theoretical Mass	Observed Mass	Error (ppm)	RT (min)	CLs
1		6 7 9	$C_7O_2F_{13}^-$ $C_8O_2F_{15}^-$ $C_{10}O_2F_{19}^-$	362.9696 412.9664 512.9600	362.9695 412.9665 512.9606	−0.3 0.2 1.2	11.74 15.60 18.26	1 1 1
2		3 4 6 8	$C_3O_3F_7S^-$ $C_4O_3F_9S^-$ $C_6O_3F_{13}S^-$ $C_8O_3F_{17}S^-$	248.9462 298.9430 398.9366 498.9302	248.9519 298.9428 398.9365 498.9301	1.2 −0.7 −0.3 −0.2	5.86 13.54 16.79 19.40	2 1 1 1
3		2	$C_4H_4O_3F_5S^-$	226.9807	226.9787	−8.8	10.11	2
4		6 10	$C_9H_5F_{13}NO_4S^-$ $C_{13}H_5F_{21}NO_4S^-$	469.9737 669.9609	469.9745 669.9637	1.7 4.2	18.04 22.76	2 2
5		1 7	$C_6F_5H_3NO_2^-$ $C_{12}F_{17}H_3NO_2^-$	216.0089 515.9898	216.0075 515.9905	−6.5 1.4	13.16 20.10	3 3

ppm, and the RT errors compared to authentic standards were all within 30 s. Identification of PFCA and PFSA series coincident with target analysis directly verifies the feasibility and accuracy of our homologous screening workflow. In addition, 12 extra classes of homologous series based on full scan data were remained as prioritized homologous of interests, for at least one of them had the potential characteristic MS^2 fragments for PFAS while the MS^2 fragments of other homologues were not available. To the best of our knowledge, class 5 is reported for the first time here while class 4 and 5 are first discovered in drinking water.

Characteristic fragments screening mainly focused on the compounds identified in previous literature. Features with characteristic fragments ($[FSO_3]^-$, $[C_nF_{2n+1}SO_3]^-$, $[CF_2O]$-, etc.) were selected and further structure elucidation were based on the proposed structures reported in previous literature. Homologous series of Class 1, 2 and 4 were also detected in this section, which cross confirmed the feasibility of the non-target method we applied. However, only one potential PFAS identified as sodium *p*-perfluorous nonenoxybenzene sulfonate (OBS) was finally verified to exist in the drinking water system and retained as confidence level 2. Analytical details are provided in the Supporting Information (Table S9).

For suspect screening, the suspect data set were matched to the *in-house database*, the MONA database and the 8613 PFAS mass list download from Norman with a mass tolerance of 5 ppm and/or RT error of 30 s. As a result, four features, 248 features and 297 features were separately matched to three databases. However, since the MONA database contains MS^2 spectra more than just of PFAS, most of the features were eliminated after checking the formula. Then, the MS and MS^2 spectra of the remaining features were extracted by software Agilent Qualitative Analysis 10.0, and we examined the chromatographic peak shape and MS^2 fragment of every feature manually. After the false-positive elimination, three features were assigned as confidence level 1 with in-house reference standard validated, two features were assigned as confidence level 2 (Table S9), and 48 out of 297 features matched to 8613 PFAS mass list with accurate mass, formula and available MS^2 spectra were later assigned as confidence level 4 (Table S10).

To sum up, we eventually summarized five homologous series with 12 homologues and three additional individuals with high confidence levels (7 chemicals as level 1, 5 as level 2 and 4 as level 3). In addition, 48 features were tentatively confirmed with level 4 and 12 classes of 38 potential homologues were retained as level 5 (Table S11). And the specific formula and structure are needed in future studies on chemicals of levels 4 and 5.

3.3. Semi-quantification of non-target PFAS

To gain a better understanding of the distribution of non-target PFAS in the drinking water system, a semi-quantification method based on previous studies (Jacob et al., 2021; Li et al., 2020) were performed. Five target PFAS (three PFCA and two PFSA) that were also detected in non-target screening with credible responses were employed. The ratios of the peak area of the target PFAS and the concentrations of individual chemicals precisely quantified by TQS were considered as a pivot for conversion. Besides, the target PFAS corresponding to even individual non-target PFAS were selected based on structures (function groups and perfluorinated chain length), retention time and masses of that non-target PFAS. The selected references for each non-target PFAS are all provided in the Supporting Information (Table S12) and the linear correlations of selected target PFAS were evaluated as support (Fig. S10). The estimated concentration was considered as the product of the peak area of a non-target PFAS and the ratio of its corresponding target PFAS. However, it has to be aware that the features detected in characteristic fragments searching and suspect screening were distinct to select target PFAS, and the complex structures and functional groups truly add obstacles to semi-quantitation performed this way. Thus, subsequent concentration estimation was carried out mainly around the homologous series detected in non-target screening.

The results of semi-quantification are displayed in Fig. 4, and the complete concentration values of all PFAS in every sampling site among three seasons are provided in the Supporting Information (Tables S13–S15). The display of the water treatment process is based on the average value of two DWTPs with their standard deviations available. Fig. 4A-C illustrates the estimated concentrations of individual non-target PFAS without target precise quantification. The case was found that nearly all non-target PFAS were below 5 ng/L in August and March while relatively greater concentrations of some PFAS were discovered in December. The dominant PFAS found in non-target analysis was 669.9637 of Class 4, reaching up to 10.3 ng/L in December and approximately 3 ng/L in the other two sampling seasons. The total residual levels of non-target PFAS ranged from 4.10 ng/L to 17.6 ng/L, however, it will change when more potential structures are proposed in the future.

The slight float in concentration from the water source to the influent of DWTPs was reflected in all three seasons, which coincided with the results of the target analysis. During the treatment process, these PFAS showed a stable presence during the treatment process in August and December without significant fluctuations, while the concentrations of compounds tended to decrease in March. Besides, compared with the effluents of DWTPs, non-target PFAS extracted from tap water had a

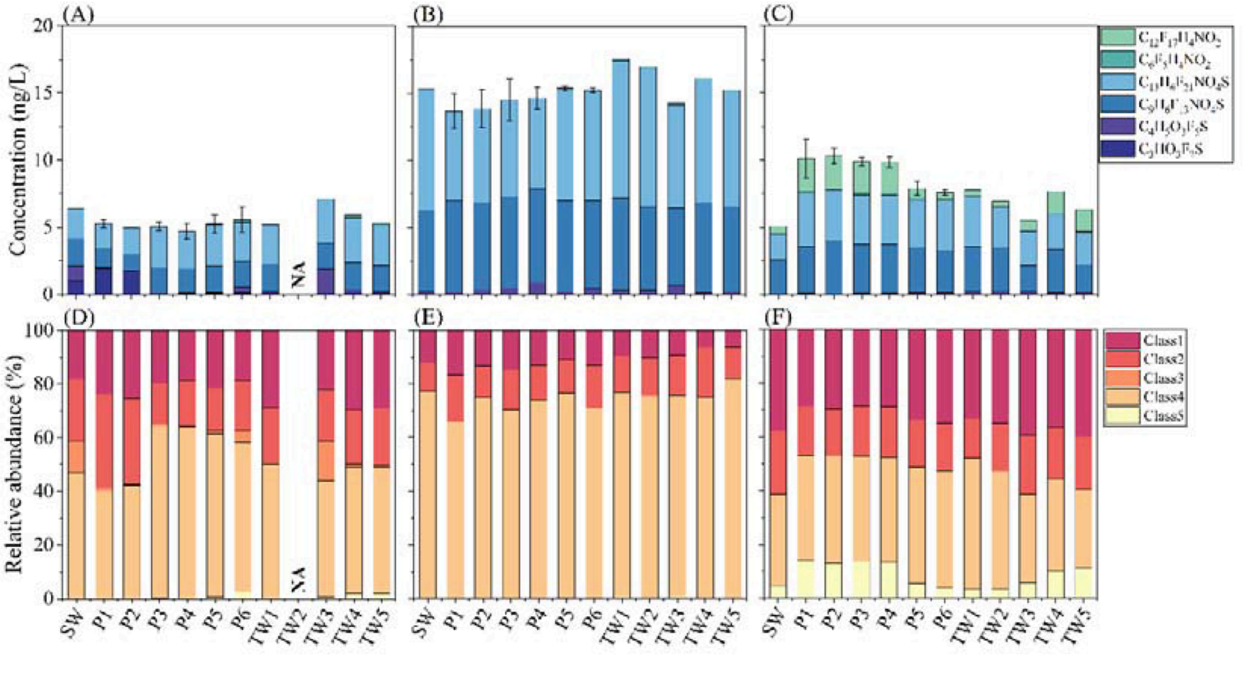


Fig. 4. Estimated concentrations of each homologue and relative abundance of homologous series detected in non-target screening based on semi-quantification. Estimated concentrations of individual non-target PFAS without target precise quantification are displayed for (A) August 2020; (B) December 2020; and (C) March 2021. The values of processing units are based on the combination of two DWTPs, the error bars represent the deviation between two DWTPs. Relative abundance of each homologous series in (D) August 2020; (E) December 2020; and (F) March 2021 are also summarized.

slight increase, and the PFAS in the tap water of three sampling seasons had a similar distribution with no clear variation trend with distance. The results of different homologous series are demonstrated in Fig. 4D-F. Class 1, 2 and 4 were major homologous series, accounting for more than 80% in all three sampling seasons. Meanwhile, the proportion of classes 4 decreased significantly by at least 10–30% in March, while Class 1 and 5 increased.

3.4. *Removal efficiency of target and non-target PFAS*

To understand PFAS removal in each treatment unit of the two DWTPs, the boxplots are employed to reflect removal efficiency of all target and non-target PFAS (Fig. 5) and the statistical results based on T-test are displayed in Table S16. Each box is the integration of the removal rate of all detected PFAS in that treatment unit. The respective removal efficiencies of the two DWTPs are provided separately as a parallel verification. However, it is noted that with the unavailable concentration at the sampling site B-P2 in August, the statistics of P2 and P3 in Plant B of that sampling season could not be performed. Previous studies have shown that the conventional water treatment process based on coagulation and sedimentation could not degrade PFAS effectively while biological treatment would increase the PFAS in the finished water with a high probability (Rahman et al., 2014; Takagi et al., 2011). This is because biological treatment can only break the C-C bond but not the C-F bond (Gagliano et al., 2020), leading to the increase of short-chain PFAS. This phenomenon was also observed in this study as a considerable number of PFAS had negative removal rates at P2 (biological treatment). In general, the average and median removal rate values for each treatment process were around zero with different range distributions, supported by T-test (Table S16). Similar results about removal efficiencies of individual units were reported in a previous study (Eschauzier et al., 2012). Meanwhile, the most variable removal rate distribution appeared at P3 (coagulation), and it could be seen that the removal efficiency of Plant B in this treatment unit was much better than that of Plant A. Besides, it is worth noting that sodium hypochlorite was added for disinfection at the end of the process showed a negative removal rate on the detected target and non-target PFAS instead. Based on the results from the present and previous studies, PFAS showed persistence in conventional water treatment processes with limited or no removals. Although the concentration levels of PFAS in tap water are relatively low, the exposure risks to human health should not be neglected.

In addition to conventional process, advanced oxidation processes (AOPs), powdered activated carbon (PAC) and granular activated carbon (GAC) adsorption, and membrane filtration such as reverse osmosis (RO) are employed in advanced DWTPs. Currently applied AOPs has also been proved to have limited removals on PFAS (Takagi et al., 2011; Thompson et al., 2011). The existence of C-F bond makes them resistant to oxidation (Rahman et al., 2014) and short-chain PFAS can be produced as the long-chain precursors being broken down (Pan et al., 2016). In recent years some progresses had made to indicate an effective decomposition of PFAS based on AOPs, but no practical applications have been reported yet in DWTPs (Trojanowicz et al., 2018). GAC has showed higher removals of PFAS than PAC in conventional DWTPs (Eschauzier et al., 2012; Kim et al., 2020; McCleaf et al., 2017; Pan et al., 2016). However, after GAC treatment, there still exist PFAS residues (mostly short-chain PFAS) in the finished water as it depends on the chemical structures and charcoal particle size (Kim et al., 2020; Rahman et al., 2014). With benefit from the low molecular weight cut-off (MWCO) of RO, almost complete removal ($\geq$99%) for PFAS could be observed in DWTPs including RO units (Flores et al., 2013; Glover et al., 2018; Thompson et al., 2011). This suggests that reverse osmosis membrane process would be a good choice for removing PFAS in drinking water system.

4. Conclusion

The combined target analysis and non-target screening showed the presence of a variety of PFAS in drinking water system. 15 PFAS with high confidence levels (L1, L2 and L3) were proposed based on MS^2 fragments in suspect and non-target screening, while only nine PFCA and PFSA were detected in target analysis. Almost no removals were observed for the detected PFAS in two conventional DWTPs. Although there is no immediate health risk, long term exposure risks should not be neglected. This suggests a need to better and effective treatment technologies (e.g. GAC and RO) in order to protect human health. The results from this study fills the data gap on the occurrence of 19 highly potential PFAS (nine in target analysis and 15 in suspect and non-target screening) in Guangzhou, and provide basis for future monitoring of PFAS in drinking water system. Moreover, PFAS confirmed with lower confidence levels need in-depth structural analysis. Future work should focus on the existence of more PFAS and the transformation and toxicity of these PFAS. Retrospective analysis can be performed for deeper analysis when better identification tools are available.

CRediT authorship contribution statement

Yu-Qing Wang: Investigation, Writing – original draft. **Li-Xin Hu:**

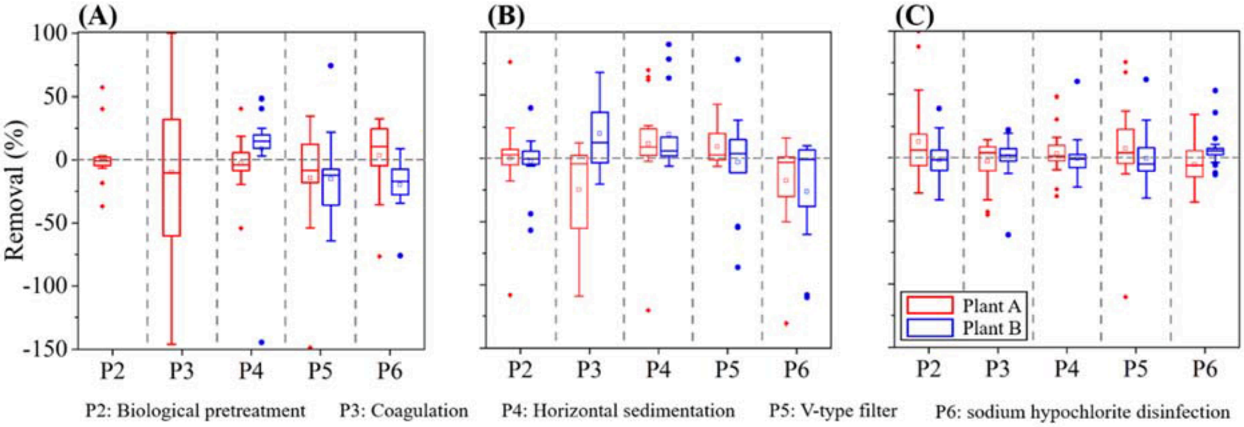


Fig. 5. Boxplots for removal efficiencies of PFAS in different processing units of two full-scale DWTPs. The data in boxplots combined both target and non-target results. Attention was paid to the parallelism of the treatment of two DWTPs in (A) August 2020; (B) December 2020; and (C) March 2021. P2-P6 in turn represent the five treatments (biological pretreatment, coagulation, horizontal sedimentation, V-type filter and sodium hypochlorite disinfection) applied in two DWTPs. The removal rate of each processing unit equals to the ratio of the difference between the influent and effluent of that unit to the influent. The upper, lower edges and median of every data set are reflected in the corresponding position in the boxes, and the small square in each box represents the average of that data set.

Methodology, Software, Writing – review & editing. **Ting Liu:** Data curation. **Jia-Hui Zhao:** Data curation. **Yuan-Yuan Yang:** Validation. **You-Sheng Liu:** Writing – review & editing. **Guang-Guo Ying:** Funding acquisition, Supervision, Writing – review & editing.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.envint.2022.107219.

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