Supporting Information

Bioconcentration of cedarwood oil in rainbow trout

Roxana Sühring [1], Chang'er L. Chen[1,2], Michael S. McLachlan[1], Matthew MacLeod[1]

[1]Department of Environmental Science and Analytical Chemistry (ACES), Stockholm University, Stockholm, Sweden

[2]Environmental Research Institute (ERI)/School of Environment, Guangdong Provincial Key Laboratory of Chemical Pollution and Environmental Safety & MOE Key Laboratory of Environmental Theoretical Chemistry, South China Normal University, Guangzhou, 510006, China

*corresponding author: Roxana Suehring; current affiliation: Ryerson University, 350 Victoria St, Toronto, ON M5B 2K3; email: Roxana.suehring@ryerson.ca

Summary:

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1. The bioconcentration factor

The bioconcentration factor (BCF) describes the ratio of chemical concentration in an organism's body (usually fish) (C_B) [mol kg^{-1}] and the concentration of freely dissolved chemical in water (C_{WD}) [mol L^{-1}] at steady state (OECD, 2012). Kinetically the BCF can be expressed as the ratio of the uptake rate constant (k_1) [L kg^{-1} d^{-1}] and the total elimination or depuration rate constant (k_T) [d^{-1}].

The BCF [L kg^{-1}] is calculated as

$$BCF = \frac{C_B}{C_{WD}} = \frac{k_1}{k_T} \quad (1)$$

The total depuration rate constant (k_T) [d^{-1}] is a sum parameter of the different elimination processes that can occur in a fish, i.e. excretion (k_E) [d^{-1}], elimination through respiration (k_2) [d^{-1}], metabolic biotransformation (k_M) [d^{-1}], and growth dilution (k_G) [d^{-1}].

$$k_T = k_E + k_2 + k_M + k_G \quad (2)$$

In a BCF experiment in which the concentrations of the target analytes (C_X) are measured at different time points (t) throughout the elimination process, the total depuration rate constant can be calculated as follows (Arnot and Gobas, 2004):

$$k_T = \frac{lnC_{X,t2} - lnC_{X,t1}}{t2 - t1} \quad (3)$$

In the presented study, we used an abbreviated dietary exposure experiment with internal benchmarking to determine the depuration rate constant and derive the BCF for cedarwood oil constituents in rainbow trout. Using a single feeding event meant that the duration of the experiment and number of test animals could be reduced compared to a standard OECD 305 test because the time and testing during the uptake phase were eliminated. On the other hand, the uptake rate constant (k1) could not be measured in this test set up and had, instead, to be estimated.

2. Estimating the uptake rate constant (k_1)

The OECD 305 recommends a model proposed by Arnot and Gobas (2004) as one of the suitable methods to estimate k_1. In previous studies we also found that the Arnot and Gobas (2004) k_1 model results in a good agreement of derived BCFs for neutral hydrophobic substances with respective BCFs measured in standard regulatory test set ups reported in the literature (Chen et al. 2018).

The uptake rate k_1 [L kg^{-1} d^{-1}] based on the Arnot and Gobas (2004) model is calculated with

$$k_1 = \frac{E_W \times G_V}{W} \quad (4)$$

where E_W is the chemical transfer efficiency at the gill [unit less], G_V is the gill ventilation rate [l d^{-1}], and W is the wet weight of the fish [kg].

According to Gobas and Mackay (1987), E_W is calculated as

$$E_W = \left(R_{WW} + \frac{R_{LW}}{K_{OW}}\right)^{-1} \quad (5)$$

Where R_{WW} is the diffusive resistance in the water phase (approx. 1.88), R_{LW} is the diffusive resistance in the lipid phase (approx. 155) and K_{OW} is the octanol-water partitioning coefficient of the test substance.

The gill ventilation rate G_V can be calculated as

$$G_V = \frac{M}{E_{OX} \times C_{OX}} \quad (6)$$

Where M is the metabolic oxygen requirement of the fish [mg d^{-1}], C_{OX} is the dissolved oxygen concentration in water [mg l^{-1}] (7 mg l^{-1} in this experiment), and E_{OX} is oxygen transfer efficiency across the gills (approx. 0.65, according to Arnot et al. 2008).

M can be calculated as

$$\log_{10} M = 2.8 + 0.786 \log_{10} W + 0.017\, T \quad (7)$$

With W: fish weight [kg] and T: Temperature [°C] (10 °C in this study).

Based on equations 4-7 k_1 can be calculated as

$$k_1 = \frac{10^{2.8 + 0.786 \log_{10} W + 0.017\, T}}{0.65\, W \left(1.85 + \frac{155}{K_{OW}}\right) C_{OX}} \quad (8)$$

For hydrophobic substances (K_{OW} > 1000) the term $1.85 + \frac{155}{K_{OW}}$ approaches 1.85.

Therefore,

$$k_1 = \frac{10^{2.8 + 0.786 \log_{10} W + 0.017\, T}}{0.65\, W * 1.85\, C_{OX}} \quad (9)$$

For a specific experiment, $C_{OX,}$ W and T are the same for all test chemicals. Therefore, k_1 can be approximated as a constant for high K_{OW} substances analysed in the same experiment (Chen et al., 2018).

The OECD 305 (2012) advises against the use of a bioavailability correction factor for the estimated k_1 in dietary exposure studies on hydrophobic substances. In accordance with these recommendations, no correction factor was applied in the k_1 estimates.

2.1 Validity and uncertainty of k_1 estimates

An important assumption for the estimation of k_1 is that k_1 is equal for all test and benchmark substances. Therefore, an additional important assumption is that the uncertainty of k_1 is equal for all test substances and benchmark substances as well. The reasoning for this assumption is that the parameters that determine the uncertainty of k_1 are independent of the differences in physical-chemical properties for the chosen test and benchmark substances.

These assumptions are valid for test substances and benchmark substances that are hydrophobic with K_{OW} > 1000. For high K_{OW} substances the term $1.85 + \frac{155}{K_{OW}}$ in equation 8 approaches 1.85. The other determinants of k_1, fish weight (W), water temperature (T) and the dissolved oxygen concentration (C_{OX}), are independent of the properties of the test chemicals. The uncertainty associated with these parameters affects all test and benchmark chemicals equally and can be minimized by controlling the growth rate, water temperature and dissolved oxygen concentration in the water. Because the uncertainty is the same for all test and benchmark chemicals, it does not impact the relative magnitude of the derived BCFs between chemicals, even if the absolute values of the BCFs are subject to the uncertainty introduced by estimating k_1. To address the uncertainty in the absolute value of the BCF, threshold benchmarking (discussed in section 3.1. below) as well as the literature comparison were used.

3. Using internal benchmarking in an abbreviated in-vivo dietary exposure BCF study

The dietary exposure approach outlined in the updated OECD 305 test guideline has been criticised for the variability in the quality of the proposed approaches to estimate k_1 which can lead to significant differences in the derived BCFs (Crookes and Brooke, 2011). For the presented abbreviated test set up with a single dietary exposure event, inter-individual variability presents another challenge, because of differences in e.g. feeding behaviour of the fish on the day of exposure which could lead to considerable differences in the exposure of each individual fish.

Both the inter-individual variability in dietary exposure BCF studies and the correct choice of a model to estimate k_1 can be addressed through internal benchmarking.

Benchmarking in BCF experiments is similar to the use of so-called internal standards in analytical chemistry: concentrations of target analytes are measured relative to the concentrations of a well-characterized standard with a known behaviour in the test system. I.e. the depuration rate k_T of a target analyte (change in concentration (dC) over time (dt)) is measured relative to the change of the concentration of the benchmark substance (dC_{BM}) over time resulting in a benchmarked depuration rate constant k_{TBM}*:*

$$\frac{dC}{dt} \Rightarrow \frac{d(\frac{C}{C_{BM}})}{dt} = k_{TBM} \quad (10)$$

In the presented study, we use this benchmarking concept in two ways: 1. **conservative benchmarking** and 2. **threshold benchmarking**.

3.1 Conservative benchmarking

Conservative benchmarking is used to control for the inter-individual variability of target analyte concentrations in fish, due to e.g. differences in feeding behaviour and growth rate during the BCF experiment.

The target analytes and benchmark substances were fed to the fish at the same time to ensure the respective concentrations would be subject to the same sources of inter-individual variability. Analogue to the calculation of the depuration rate constant for the target analytes (equation 3), the depuration rate constants of the conservative benchmarking substances (k_G) can be calculated as:

$$k_{TCBM} = k_G = \frac{lnC_{CBM,\,t2} - lnC_{CBM,t1}}{t2 - t1} \quad (11)$$

where C_{CBM} is the measured concentration of the conservative benchmarking substance (CBM) at time *t*.

Only substances that are not be eliminated by exhalation (k_2), metabolism (k_M), or excretion (k_E) within the timeframe of the experiment were selected as conservative benchmark substances. Therefore, the depuration rate constant for the conservative benchmarking substances (k_{TCBM}) is assumed to be equal to the depuration rate constant for growth dilution of the fish used in the experiment (k_G).

The inter-individual variability and growth-corrected depuration rate constant k_{TG} of target analytes in an experiment with conservative benchmarking substances can then be calculated as (Chen et al., 2018):

$$k_{TG} = k_T - k_G = \frac{\ln\left(\frac{C_{X,t2}}{C_{CBM,t2}}\right) - \ln\left(\frac{C_{X,t1}}{C_{CBM,t1}}\right)}{t2 - t1} \quad (12)$$

where C_X is the measured concentration of the test substance X at time *t*. Since the experiment has multiple sampling time points, k_{TG} is obtained from a linear regression of the natural logarithm of the benchmarked test substance concentration against time.

Using an estimated uptake rate constant (k_1) (equation 9) the conservative benchmarked BCF (BCF_{CBM}) can be calculated as:

$$BCF_{CBM} = \frac{k_1}{k_{TG}} \quad (13)$$

The OECD 305 test guideline recommends the use of growth correction in the calculation of a dietary exposure BCF. The BCF_{CBM} presented here corrects for growth-dilution as well as additional sources of inter-individual variability due to e.g. differences in feeding behaviour. It is a growth-corrected dietary exposure BCF as defined by the OECD 305 test guideline.

3.2 Threshold benchmarking

Threshold benchmarking is used to screen a dataset for substances that likely meet or do not meet the B or vB criteria. In threshold benchmarking, the depuration rate constant of the target analytes is calculated relatively to the depuration rate constant of a known B or vB threshold benchmarking substance. The threshold benchmarked depuration rate constant (k_{TBM}) is calculated as:

$$k_{TBM} = \frac{\ln\left(\frac{C_{X,t2}}{C_{TBM,t2}}\right) - \ln\left(\frac{C_{X,t1}}{C_{TBM,t1}}\right)}{t2 - t1} \quad (14)$$

where C_X and C_{TBM} are the measured concentrations of test substance X and threshold benchmark substance (TBM) at time *t*, respectively. Analogous to the calculation of k_{TG}, k_{TBM} is obtained from a linear regression of the natural logarithm of the threshold benchmarked test substance concentration against time for experiments with multiple sampling time points.

If k_{TBM} > 0, the target analyte is eliminated slower from the organism than the threshold benchmarking substance, if k_{TBM} < 0 the target analyte is eliminated faster from the organism than the threshold benchmarking substance.

Threshold benchmarking has the advantage that the potential transgression of a regulatory threshold for bioaccumulation potential can be assessed based on the measured depuration rate constants alone- without the need to estimate k_1- as well as based on derived BCFs.

3.3 Standard error and confidence intervals

The standard error of the mean depuration rate constant (k_T) and benchmarked depuration rate constant (k_{TG}) were calculated with

$$SE = \frac{\sigma}{\sqrt{n}} \quad (15)$$

with σ being the sample standard deviation and n being the number of samples.

The 90 % confidence interval was calculated by calculating the 5th and 95th confidence level as

5^{th} = Mean – *SE* x 1.96 (16)

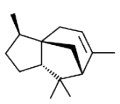
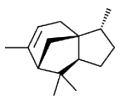
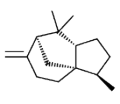
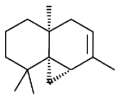
and

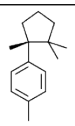
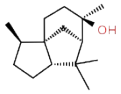
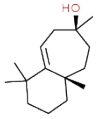
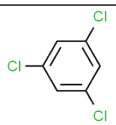
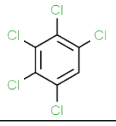
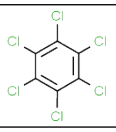
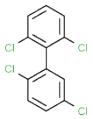
95^{th} = Mean + *SE* x 1.96 (17)

where "Mean" refers to the mean k_T or k_{TG}, respectively.

Confidence intervals for the bioconcentration factor (BCF) and benchmarked bioconcentration factor (BCF_{BM}) were calculated from the 5th and 95th confidence level of k_T and k_{TG}, respectively using equation (1). It should be noted that depuration rate constants with a slope of 0 result in an undeterminable BCF. In this case, the BCF has been reported as > the median value.

Table S1. CAS, molecular weight (MW) [g mol^{-1}], logK_{OW}, quantification ion (Quant ion), confirmation ions (Conf Ions), retention time (RT) [min], and used isotope-labelled standard for GC-MS analysis of target analytes and benchmark substances

Target	CAS	MW	logK_{OW}*	Quant Ion	Conf Ions	RT	IS	Structure
α-Funebrene	50894-66-1	204.35	5.74	119	105, 93	14.86	AC-d4	
α-Cedrene	469-61-4	204.35	5.74	119	105, 93	15.34	AC-d4	
β-Cedrene	546-28-1	204.35	5.82	93	105, 91	15.44	AC-d4	
Thujopsene	470-40-6	204.35	6.12	119	105, 133	15.57	AC-d4	

Cuparene	16982-00-6	202.34	6.19	132	119, 91	16.47	AC-d4	
Cedrol	77-53-2	222.37	4.33	95	150, 81	17.75	AC-d4	
Widdrol	6892-80-4	222.37	4.84	95	151	17.75	AC-d4	
Benchmark								
Trichlorobenzene	108-70-3	181.45	4.02	180	145	11.85	13C-HCB	
Pentachlorobenzene	608-93-5	250.33	5.17	250	108, 215	16.52	13C-HCB	
Hexachlorobenzene	118-74-1	284.80	5.73	284	286	18.76	13C-HCB	
Isotope-labelled standard								
d4-Acetyl-cedrene	n.a.	250.40	n.a.	250	252	19.44	n.a.	
13C-HCB	n.a.	290.00	n.a.	290	292	18.80	n.a.	
Injection standard								
2,2',5,6'-PCB	41464-41-9	291.99	6.09	220	292	20.74	n.a.	

*predicted by EPISuite v.4.11

Table S2. Characterisation of Cedarwood oil batch AS00254371 (compounds with ~1% or more contribution to the total chromatogram area (% Total))

Constituent	**CAS #**	**% Total**	**Normalised on 100%**	**Notes**
α-Cedrene	469-61-4	26	32	
Cedrol/Widdrol	77-53-2/ 6892-80-4	22	28	
Thujopsene	470-40-6	19	24	
β-Cedrene	546-28-1	3.9	4.8	
Cuparene	16982-00-6	3.0	3.8	
β-Himachalene	1461-03-6	1.9	2.4	Could not be detected in the fish samples
Sesquiterpene		1.5	1.9	
β-Chamigrene	18431-82-8	1.4	1.7	Could not be detected in the fish samples
Sesquiterpene		0.94	1.2	

β-Funebrene	79120-98-2	0.75	0.94	Could not be detected in the fish samples
α-Funebrene	50894-66-1	0.68	0.85	

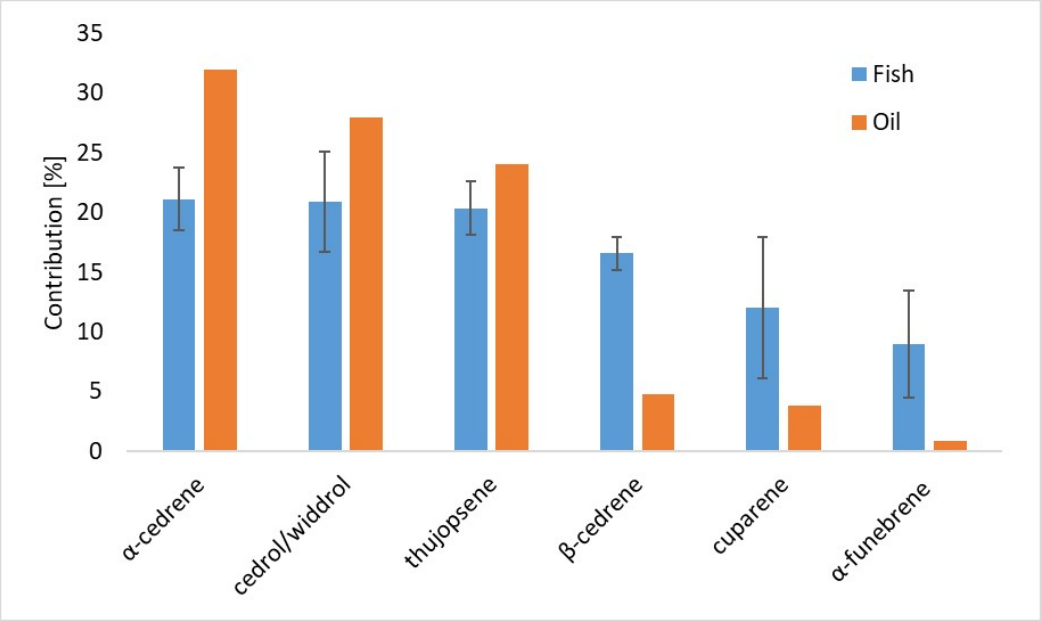


Figure S1. Contribution [%] of individual Cedarwood oil constituents in the pure oil sample (orange) and exposed rainbow trout sampled at day 1 of the experiment (blue).

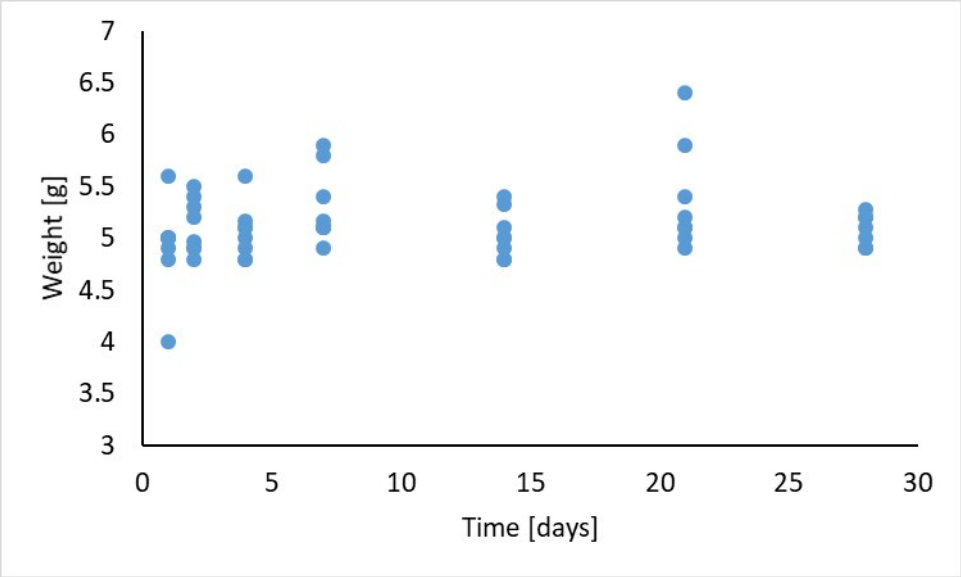


Figure S2. Weight [g] of the tested fish.

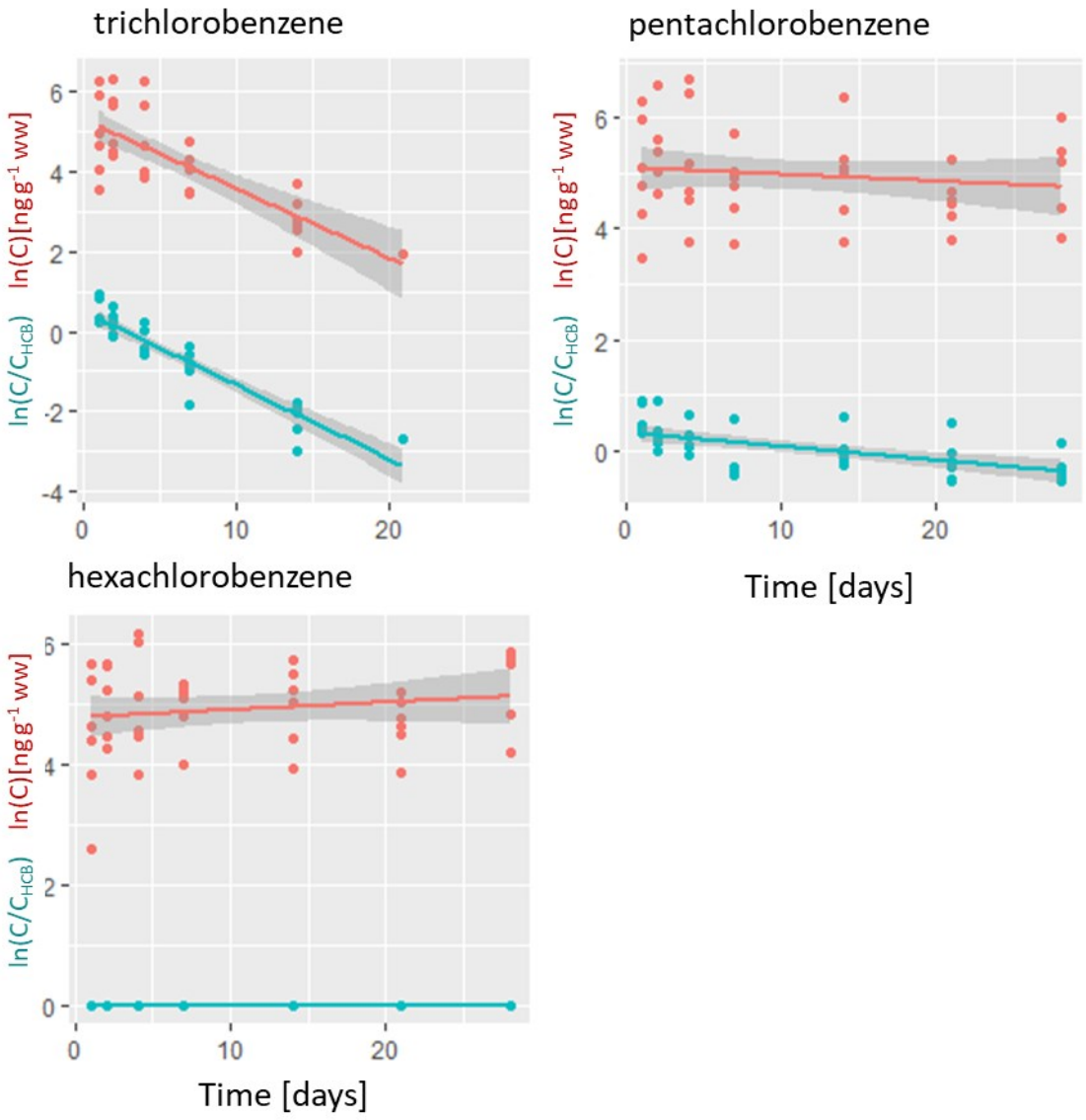


Figure S3. Depuration kinetics for the benchmark substances plotted as the natural logarithm (ln) of the measured concentrations for TrCB, PeCB, and HCB, respectively [ng g^{-1} ww] (orange) and the ln target analyte concentrations benchmarked with HCB (blue) against the time [days].

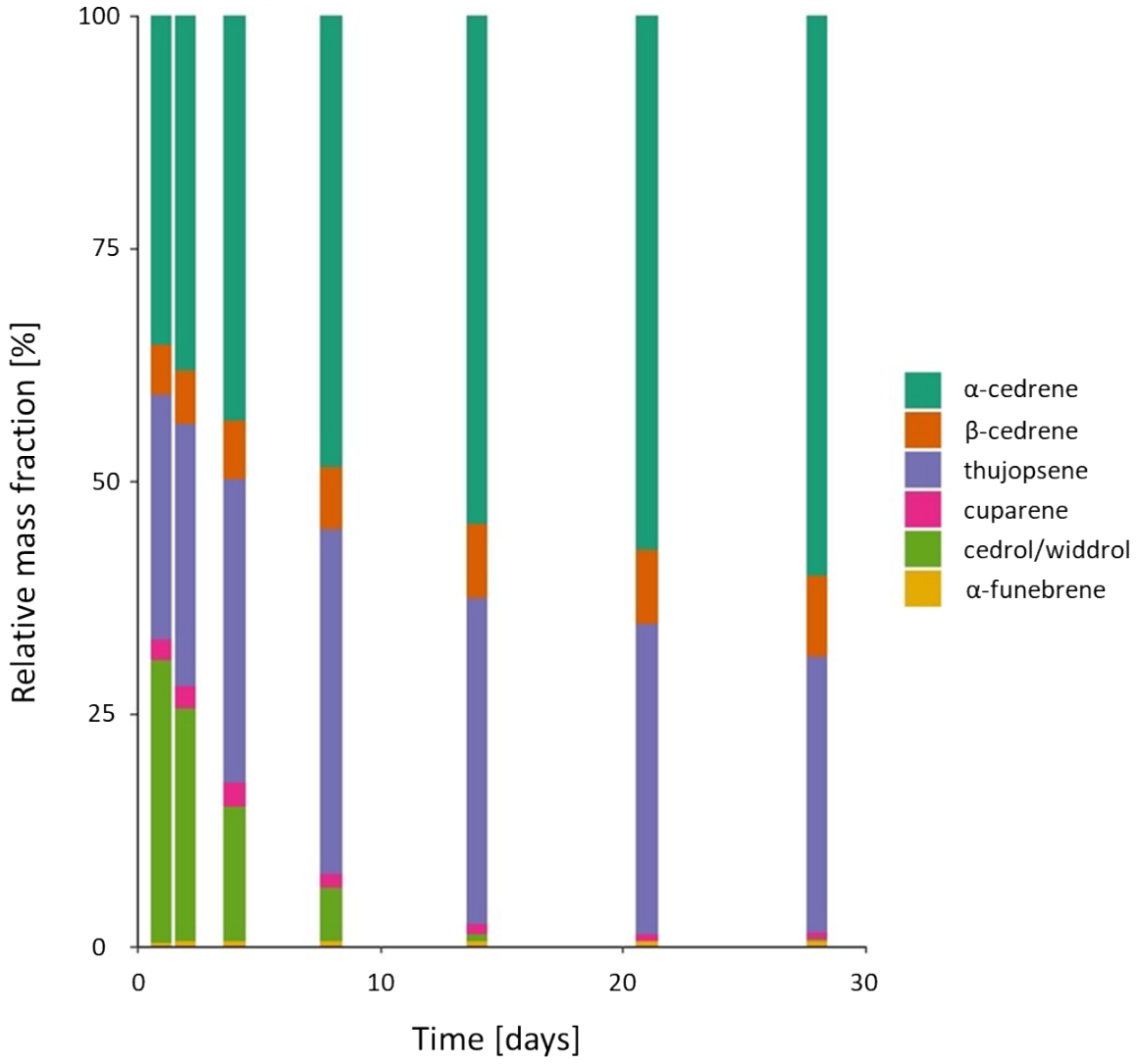


Figure S4. Contribution of the main Cedarwood oil constituents at different sampling days.

Table S3. Concentrations [µg g^{-1} ww] of target analytes and benchmarks substances in individual fish

Fish No	Day	Fish weight [g]	α-Cedrene	β-Cedrene	Thujopsene	Cuparene	Cedrol/ Widdrol	α-Funebrene	TrCB	PeCB	HCB
1	1	83	4.7	0.67	3.1	<LOQ	2.4	<LOQ	0.058	0.070	0.045
2	1	101	0.82	0.14	0.56	<LOD	1.8	<LOD	0.035	0.033	0.014
3	1	104	7.2	1.1	5.7	0.40	5.7	<LOQ	0.10	0.12	0.082
4	1	124	10	1.5	7.5	0.79	7.8	0.15	0.14	0.16	0.10
5	1	95	28	4.3	20	2.8	26	0.42	0.36	0.40	0.29
5-2	1	95	36	5.3	29	2.7	16	0.47	0.51	0.54	0.22
1	2	79	7.3	1.1	5.2	0.39	3.9	<LOQ	0.080	0.10	0.087
2	2	66	23	3.7	18	2.5	22	0.31	0.31	0.27	0.27
3	2	98	5.2	0.77	3.8	<LOQ	4.0	<LOQ	0.087	0.10	0.071
4	2	36	15	2.3	11	0.82	14	0.17	0.28	0.22	0.19
5	2	42	11	1.6	7.9	0.67	5.7	0.13	0.11	0.15	0.12
2-2	2	66	44	6.4	32	2.6	15	0.65	0.54	0.72	0.29
1	4	164	37	5.7	29	2.3	14	0.66	0.29	0.63	0.47
2	4	72	7.5	1.1	5.5	<LOQ	1.9	<LOQ	0.055	0.092	0.085
3	4	108	13	1.9	11	0.86	4.2	0.17	0.10	0.18	0.17
4	4	120	3.4	0.48	2.6	<LOQ	1.8	<LOD	0.048	0.042	0.046
5	4	103	6.4	0.87	3.9	<LOQ	1.8	<LOQ	0.054	0.11	0.095
1-2	4	164	51	7.6	43	3.6	14	0.84	0.51	0.80	0.41
1	7	206	15	2.2	11	0.42	0.53	0.16	0.033	0.15	0.21
2	7	168	4.2	0.56	2.8	<LOD	0.60	<LOQ	0.031	0.041	0.054
3	7	65	7.7	1.1	6.0	<LOQ	1.3	<LOQ	0.056	0.079	0.12
4	7	108	13	1.8	10	0.56	1.4	0.16	0.061	0.12	0.16
5	7	113	16	2.1	13	0.64	1.9	0.19	0.075	0.13	0.18
1-2	7	206	14	2.0	11	0.61	1.8	0.22	0.12	0.31	0.17
1	14	73	15	2.2	10	0.43	<LOQ	0.17	0.016	0.15	0.18
2	14	52	4.8	0.71	3.1	<LOD	<LOQ	<LOQ	0.014	0.077	0.083
3	14	98	16	2.4	9.3	<LOQ	<LOQ	0.16	0.012	0.19	0.24
4	14	93	10	1.4	4.8	<LOQ	<LOQ	<LOQ	0.024	0.16	0.15
5	14	52	2.6	0.37	2.1	<LOD	<LOQ	<LOD	<LOQ	0.043	0.050
3-2	14	98	30	4.3	20	0.80	0.21	0.42	0.041	0.58	0.31
1	21	97	10	1.4	5.1	<LOQ	<LOD	<LOQ	<LOD	0.091	0.15
2	21	115	12	1.7	5.3	<LOQ	<LOD	0.13	<LOD	0.11	0.18
3	21	107	6.4	0.91	3.8	<LOD	<LOD	<LOQ	<LOQ	0.086	0.10
4	21	138	5.9	0.83	4.3	<LOD	<LOD	<LOQ	<LOD	0.068	0.090
5	21	186	2.4	0.35	1.5	<LOD	<LOD	<LOD	<LOD	0.045	0.047
3-2	21	115	8.7	1.2	5.1	<LOQ	<LOD	0.13	0.012	0.19	0.12
1	28	99	17	2.6	8.2	<LOQ	<LOQ	0.18	<LOD	0.22	0.30
2	28	30	21	3.2	8.5	<LOQ	<LOQ	0.17	<LOD	0.22	0.29
3	28	66	27	3.9	15	<LOQ	<LOQ	0.33	<LOD	0.18	0.31
4	28	185	3.2	0.45	1.2	<LOD	<LOD	<LOD	<LOD	0.046	0.07
5	28	118	8.0	1.1	5.1	<LOQ	<LOD	<LOQ	<LOD	0.079	0.13
3-3	28	66	36	5.1	19	0.39	<LOQ	0.45	<LOD	0.41	0.35

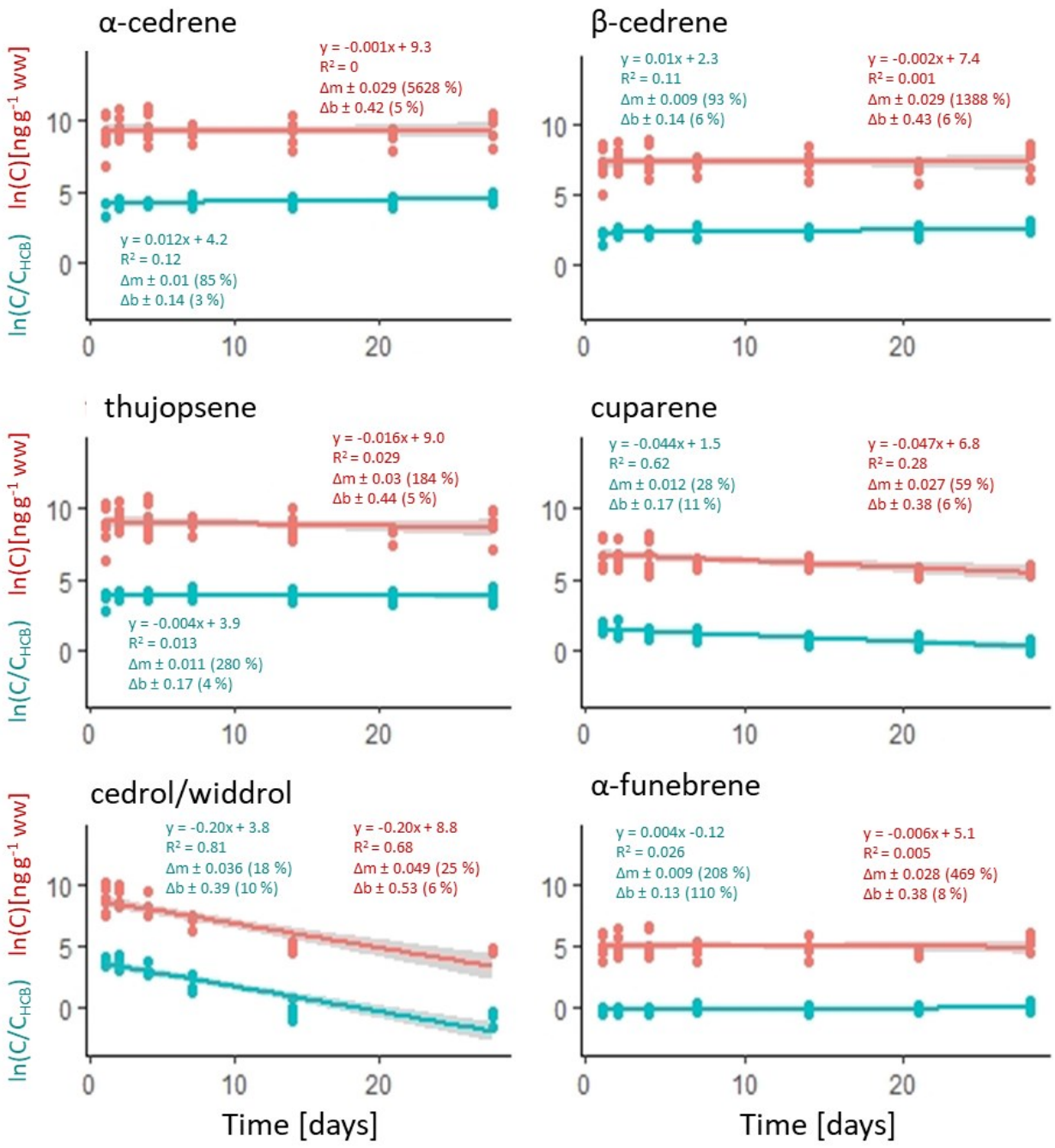


Figure S5. Threshold benchmarked depuration kinetics for the main Cedarwood oil constituents plotted as the natural logarithm (ln) of the measured target analyte concentrations [ng g^{-1} ww] (orange) and the ln target analyte concentrations threshold benchmarked with PeCB (blue) against the time [days].

Table S4. k_T [d^{-1}] and k_{TG} [d^{-1}] ± 1.96 x SE (5th and 95th percentile) benchmarked with HCB for the main Cedarwood oil components and BMs.

Name	k_T	k_{TG}
α-Cedrene	0.001 ± 0.029	0.013 ± 0.007
β-Cedrene	0.002 ± 0.029	0.015 ± 0.008
Thujopsene	0.016 ± 0.030	0.029 ± 0.009
Cuparene	0.047 ± 0.027	0.067 ± 0.013
Cedrol/Widdrol	0.20 ± 0.049	0.23 ± 0.036
α-Funebrene	0.006 ± 0.028	0.02 ± 0.011
BMs		
TrCB	0.17 ± 0.053	0.19 ± 0.053
PeCB	0.012 ± 0.028	0.025 ± 0.012
HCB	-0.013 ± 0.024	n.a.

4. k_M prediction in R

4.1 Input data

Data on k_{TG} and $logK_{OW}$ for the target Cedarwood oil constituents as well as benchmark substances were loaded as two seperate data frames called “df” and “ref”, respectively.

```
df <- as.data.frame(CWO_ktg)
ref <- as.data.frame(referenceCWO_ktg)
```

4.2 Linear regression

The chosen benchmark substances are assumed to be eliminated via gills (k_2) and growth-dilution (k_G) only. The growth-corrected ($k_{TG(BM)}$) of the benchmark substances therefore equals (k_2) of the benchmark substances.

k_2 is defined as $$k_2 = \frac{E_w * G_v}{L_B * W_B * K_{OW}} = k_{TG(BM)}$$

where E_W is the chemical transfer efficiency at the gill [unitless], G_V is the gill ventilation rate [$l\ d^{-1}$], W_B is the wet weight of the fish [kg], L_B is the lipid content of the fish [kg lipid/kg fish], and K_{OW} is the octanol-water partitioning coefficient of the target analyte (Gobas & Morrison, 2000).

$E_W * G_V\ and\ L_B * W_B \ll K_{OW}$.

Therefore, $k_{TG(BM)} \rightarrow \frac{1}{K_{OW}}$, or $Logk_{TG(BM)} \sim LogK_{OW}$.

The linear regression model for $Logk_{TG(BM)} \sim LogK_{OW}$ can be fitted with

```
pred_logkTG = lm(logkTG ~ logKOW, data = ref)
```

with

```
summary(pred_logkTG)
```

```
##
## Call:
## lm(formula = logkTG ~ logKOW, data = ref)
##
## Residuals:
##         1         2         3         4
##  0.142556  0.002634  0.073779 -0.218969
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.6740     0.7429   2.253   0.1530
## logKOW       -0.6342     0.1509  -4.203   0.0522 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.192 on 2 degrees of freedom
## Multiple R-squared:  0.8983, Adjusted R-squared:  0.8475
## F-statistic: 17.67 on 1 and 2 DF, p-value: 0.05221
```

4.3 Predicting the diffusion based (gill) elimination rate of the target analytes

The fitted linear relationship between $Logk_{TG(BM)}$ and $LogK_{OW}$ can be used to calculate the diffusion based (gill) elimination rate (k_2) for the target analytes at a 95% confidence level:

```
kx_log <- predict(pred_logkTG, df, interval = "prediction", level = 0.95)
```

The predicted k_2 for the target analytes can then be used to calculate k_M for the respective target analytes, based on

$k_M = k_{TG} - k_2$

```
pred_log <- as.data.frame(kx_log) # transforming the predicted k2 into a
dataframe to be able to merge it with the kTG dataset

all_log <- cbind(df, pred_log) # add the predicted logarithmic k2 values
(median, 5th and 95th percentile) as a new column to the kTG dataset

trans_kx <- as.data.frame(10^all_log$fit) # transform to non-logarithmic

colnames(trans_kx) <- "predicted kx" #set the column names

all_trans <- cbind(all_log, trans_kx) # add median k2 column to the
all_log dataframe
```

```
calc_trans <- as.data.frame(all_trans$kTG - all_trans$`predicted kx`) #
calculate kM
```

The resulting k_M of the target analytes are

```
kM_trans <- cbind(all_log$Chemical, calc_trans) # create a new dataframe
with the chemical names and kM values
colnames(kM_trans) <- c("Chemical", "kM") # set the column names
kM_trans # display the dataframe
```

```
##   Chemical         kM
## 1     aCed 0.00219009
## 2     bCed 0.00538194
## 3      Thu 0.02279370
## 4      Cup 0.06139675
## 5      CDL 0.14527350
## 6     aFun 0.00919009
```

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OECD, Test No. 305: Bioaccumulation in Fish: Aqueous and Dietary Exposure; OECD Publishing: Paris, 2012; p 72.

Images of chemical structures were obtained from the Chemspider website:

α-Funebrene: CSID:21170410, http://www.chemspider.com/Chemical-Structure.21170410.html (accessed 12:12, May 26, 2020)

α-Cedrene: CSID:4936353, http://www.chemspider.com/Chemical-Structure.4936353.html (accessed 12:03, May 26, 2020)

β-Cedrene: CSID:9281621, http://www.chemspider.com/Chemical-Structure.9281621.html (accessed 12:09, May 26, 2020)

Thujopsene: CSID:390845, http://www.chemspider.com/Chemical-Structure.390845.html (accessed 12:14, May 26, 2020)

Cuparene: CSID:78392, http://www.chemspider.com/Chemical-Structure.78392.html (accessed 12:16, May 26, 2020)

Cedrol: CSID:59018, http://www.chemspider.com/Chemical-Structure.59018.html (accessed 12:17, May 26, 2020)

Widdrol: CSID:85136, http://www.chemspider.com/Chemical-Structure.85136.html (accessed 12:19, May 26, 2020)

Trichlorobenzene: CSID:7662, http://www.chemspider.com/Chemical-Structure.7662.html (accessed 12:23, May 26, 2020)

Pentachlorobenzene: CSID:21106570, http://www.chemspider.com/Chemical-Structure.21106570.html (accessed 12:27, May 26, 2020)

Hexachlorobenzene: CSID:8067, http://www.chemspider.com/Chemical-Structure.8067.html (accessed 12:28, May 26, 2020)

2,2',5,6'-PCB: CSID:35581, http://www.chemspider.com/Chemical-Structure.35581.html (accessed 12:29, May 26, 2020)