Transfer of PCBs from sediment to biota in the Rhône river: contamination pathways and trophic transfer in a risk assessment perspective

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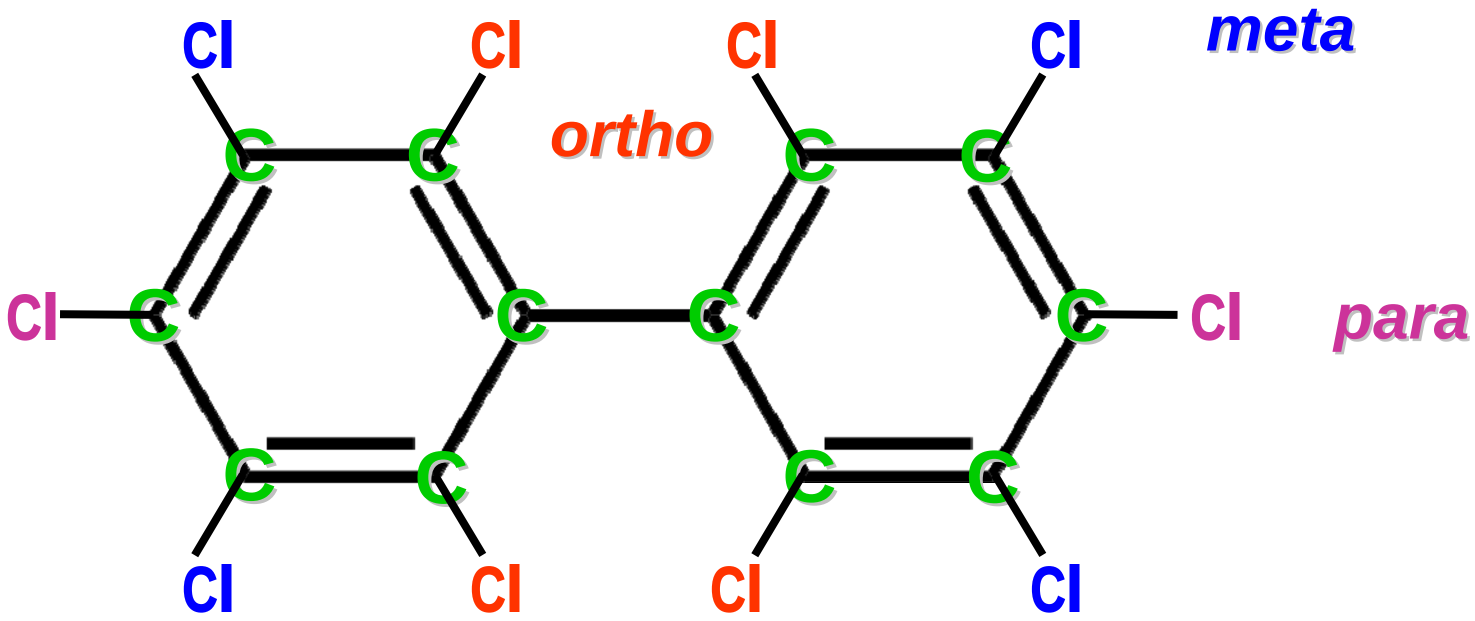
ZABR
ZONE ATELIER BASSIN DU RHONE
RHONE BASIN LONG TERM ENVIRONMENTAL RESEARCH

SeMoVi, 7 September 2010

What are PCBs?



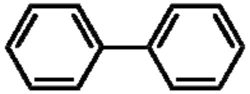
209 combinations = 209 congeners

- 7 indicators (PCBi) very common and persistent in trophic chains : #28 (3), #52 (4), #101 (5), #118 (5), #138 (6), #153 (6) et #180 (7)
- 12 coplanars, more toxic, effects similar to dioxins (PCB-DL) : #77 (4), #81 (4), #105 (5), #114 (5), #118 (5), #123 (5), #126 (5), #156 (6), #157 (6), #167 (6), #169 (6) et #189 (7)

Factors influencing fish PCB contamination

- ➢ Nature of the main known factors:

Chemical (Kow)

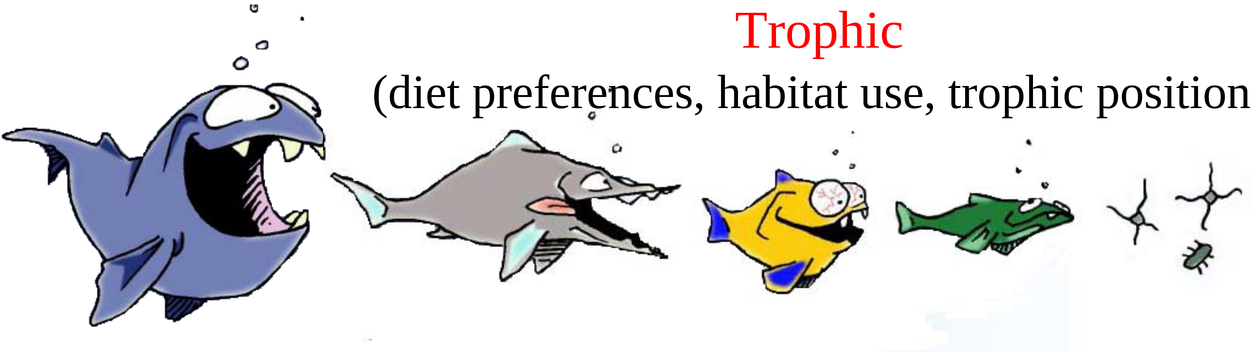


Trophic

(diet preferences, habitat use, trophic position)

Physiological

(lipid content, body size, sex)



- ➢ Factors likely to influence both between- and within-species variability in PCB concentrations

- ➢ Generally studied independently, while it seems essential to understand their relative contributions

Critical to understand the primary factors influencing bioaccumulation of PCB in fishes for predicting and assessing risks to upper-trophic levels consumers including humans

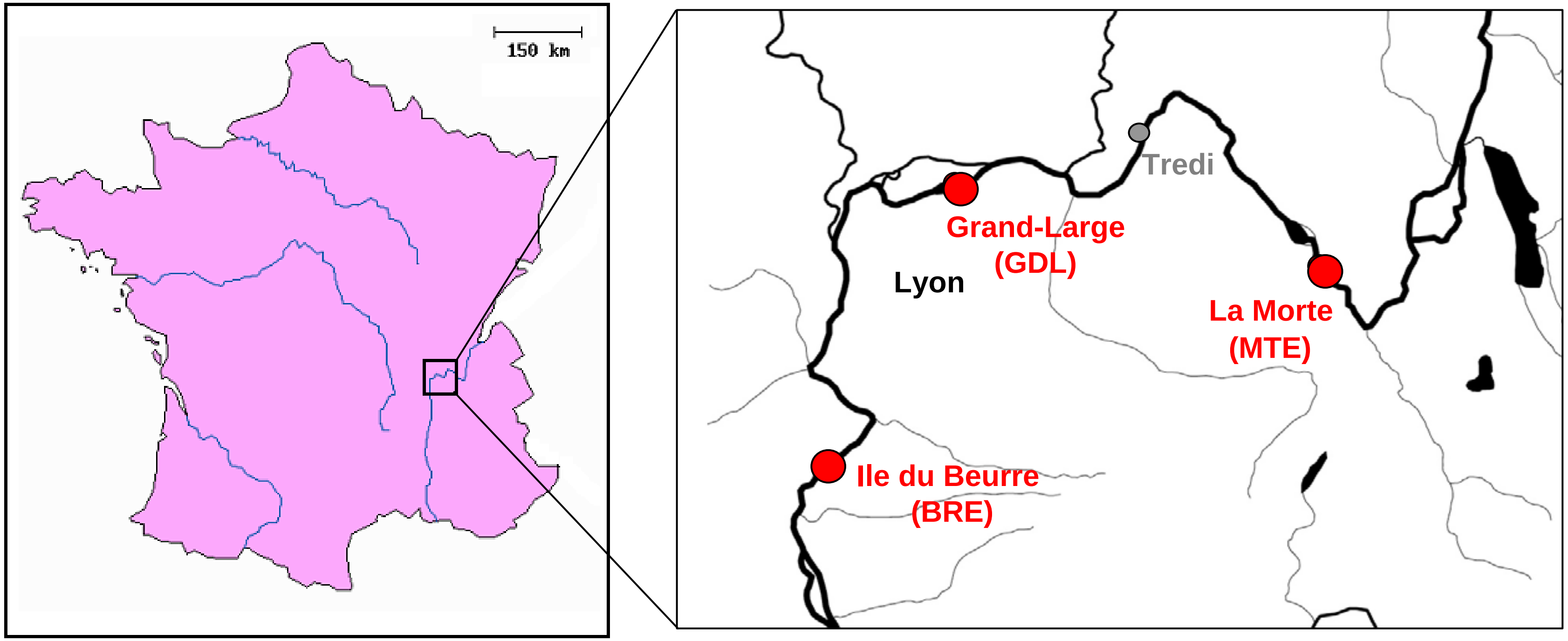
Objectives of the project

- Determine the history of the contamination of the Rhône river in the vicinity of Lyon (sediment cores)
- Identify PCB contamination pathways that could explain between and within species variability in fish concentration levels
- Describe PCB transfer along fish trophic chain

Determine a PCB level in the sediment in agreement with the European regulatory threshold for fish consumption of 8 pg TEQ_{tot} (dioxin, furan, PCB-DL) /g wet weight → $\Sigma PCB_i \approx 153$ ng/g wet weight

Data

Study sites



DECINES

CONTAMINATION DU RHÔNE EN PCB

RAPPEL

Par Arrêtés Préfectoraux
du 14 septembre 2005 et du 6 avril 2006,
la consommation de poissons pêchés dans
le Rhône est interdite.

Fish species

3 large and long-living cyprinids prone to accumulate PCB over many years, having different diets and exploiting different habitats

- **Bream** (*Abramis brama*):
  Live in standing waters and feed at the bottom and the water column

- **Chub** (*Squalius cephalus*):
  More often in standing and running waters and feed at the bottom as in the water column or at the surface

- **Barbel** (*Barbus barbus*):
  Bottom feeders and live in running rather than deep waters

Data and analyses

- <u>Sampling</u> (August 2008 to January 2009)

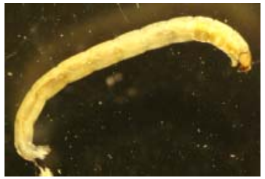
Sites	Bream	Chub	Barbel
La Morte (MTE)	7 (3♀ + 4♂)	20 (13♀ + 7♂)	11 (11♀ + 0♂)
Grand-Large (GDL)	15 (9♀ + 6♂)	15 (6♀ + 9♂)	15 (8♀ + 7♂)
Île du Beurre (BRE)	17 (10♀ + 7♂)	17 (12♀ + 5♂)	5 (3♀ + 2♂)

- <u>Analyses</u>
  - Weight, size, sex
  - Age (scalimetry)
  - Stable isotopes: Carbon ($\delta^{13}C$) and Nitrogen ($\delta^{15}N$)
  - PCB$_i$ (7 congeners)
  - Lipid content
  - Gut content

Invertebrates species

Known to be in these fish species diet

- **Chironimids (diptera)**



- **Gammarids (crustacea)**

- **Ephemeroptera**

- **Corbicula and *Pisidium* (mollusc)**
  - ***Corbicula***: large one only (> 2cm), fed deeply in sediment → detrital carbon sources
  - ***Pisidium***: fed at the sediment surface → more autochtonous carbon sources

Data and analyses

- Sampling (July 2008 and April 2009)

Sites	Chironomids	Gammarids	Ephemeroptera	Corbicula	Pisidium
MTE	25	260	94	15	140
GDL	200	170	21	13	160
BRE	400	130	_	24	130

- Analyses
  - Weight, number of individuals
  - Stable isotopes: Carbon ($\delta^{13}C$) and Nitrogen ($\delta^{15}N$)
  - PCBi (7 congeners) + PCB-DL (12 congeners)
  - Lipid content

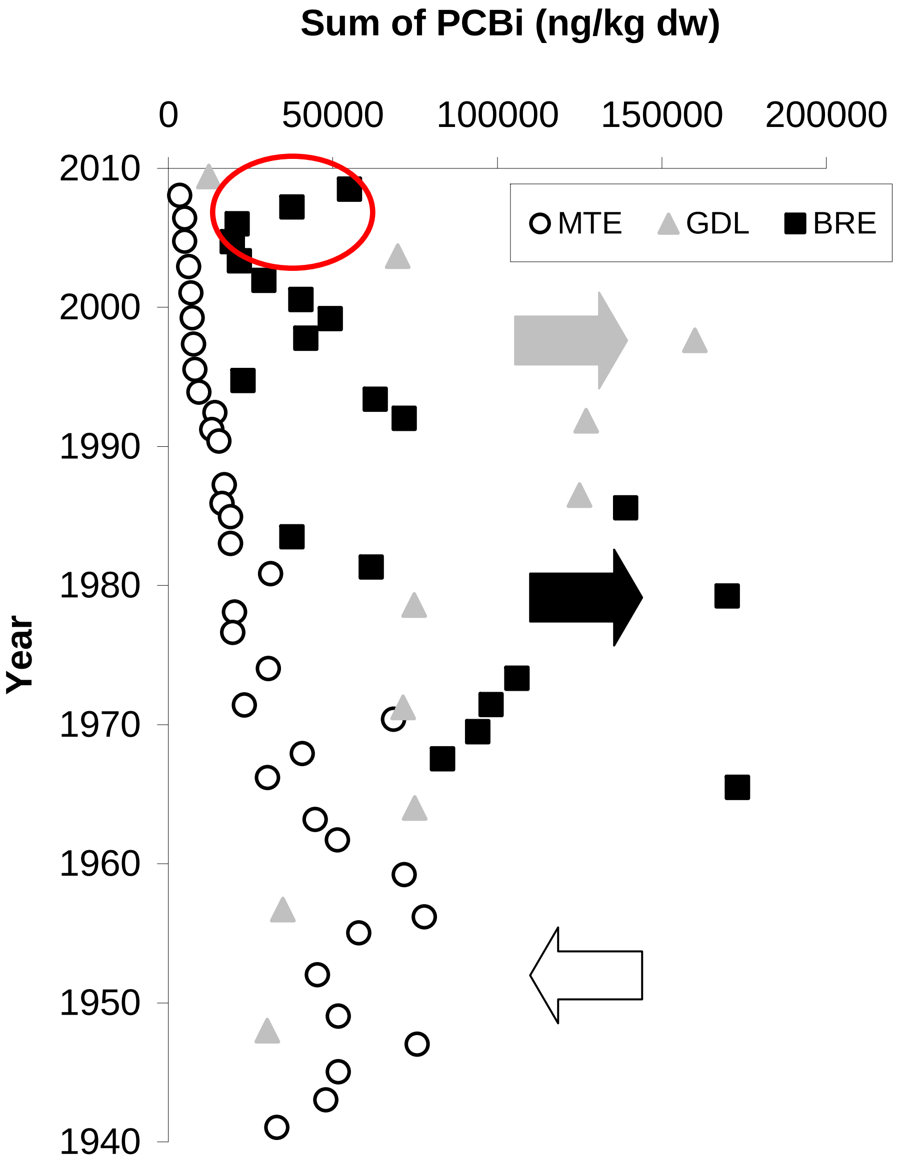
Sediment cores

- Radionuclide (^{238}U, ^{226}Ra, ^{210}Pb, ^{137}Cs, ^{7}B, ^{60}Co) measurement used to age the successive layers in each core.

- PCB analysis

Results of contamination data

Sediment contamination

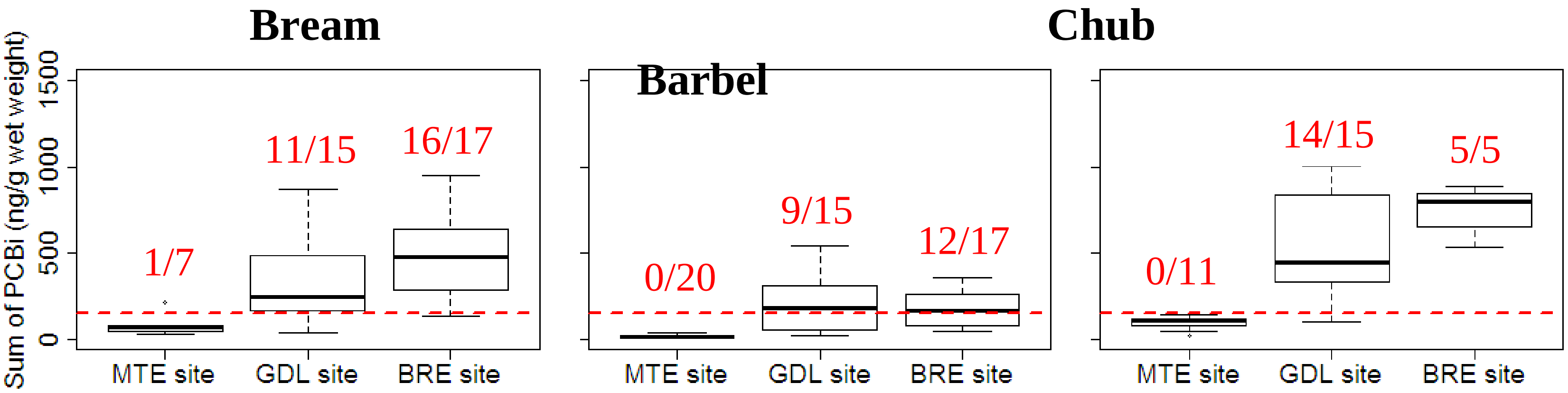


MTE : old contamination, decrease from 80th

GDL: more recent contamination

BRE : high contamination in 1980, then decrease until 2006 (new sources or modification of deposition patterns?)

Fish contamination



- Contamination < European regulatory threshold at MTE, High contamination at GDL and BRE (levels = 2005)
- High variability within and between species: chub < bream < barbel
- No difference between males and females

PCB contamination pathways

Stable Isotope Analyses

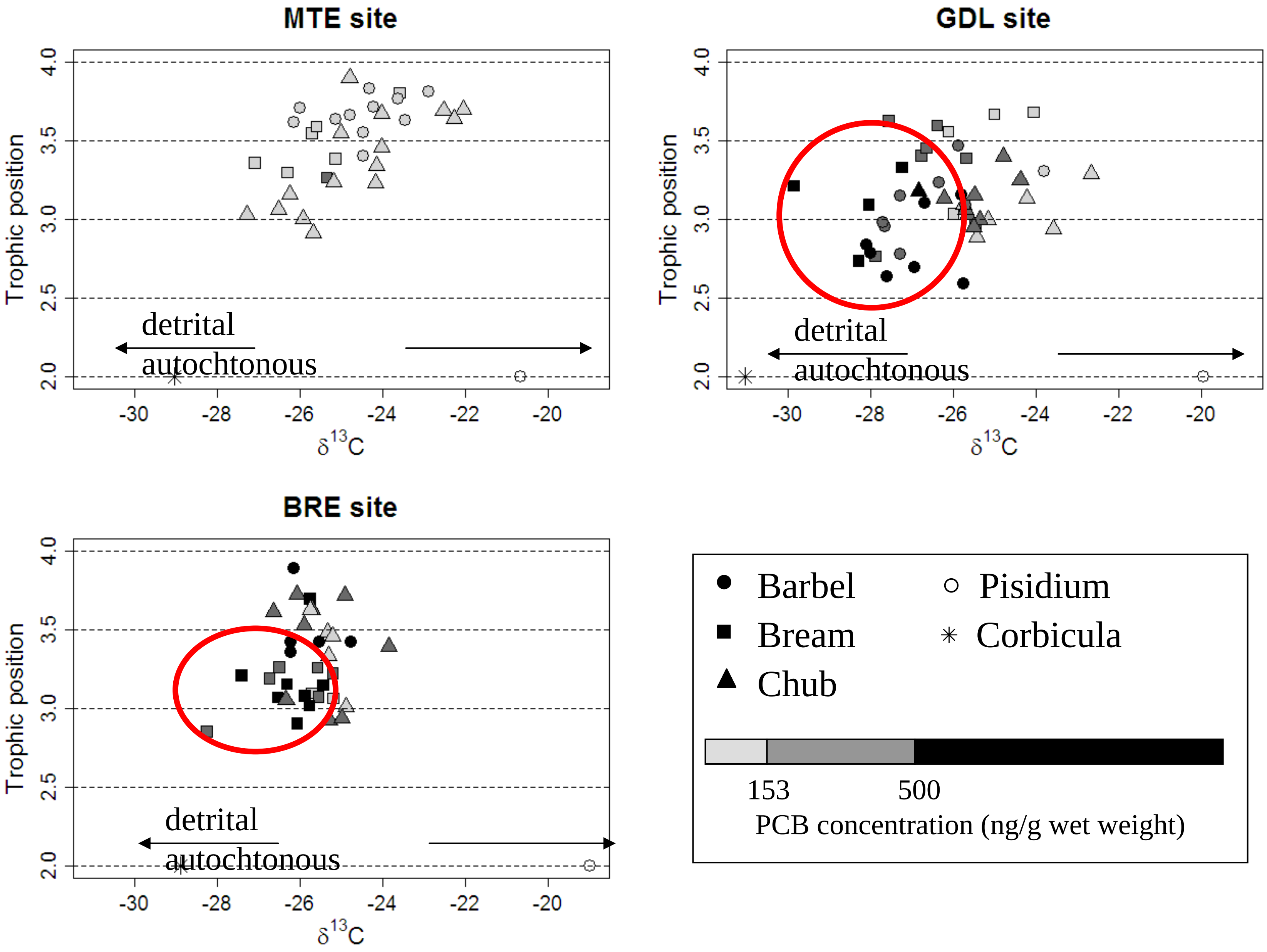
- Rely PCB concentrations to trophic position (from $\delta^{15}N$ values) and carbon pathways (from $\delta^{13}C$ values)

- Until now, trophic position deterministically estimated from $\delta^{15}N$ values (Post, 2002)

- Here, Bayesian inference used to estimate species TP, by considering $\delta^{15}N$ and $\delta^{13}C$ data variability and uncertainty around the parameters (prior information)

  ↳ Marginal posterior distribution for each parameter and joint posterior distribution (correlation between parameters)

Results


MTE site
GDL site
BRE site
Trophic position
2.0
2.5
3.0
3.5
4.0
-30
-28
-26
-24
-22
-20
$\delta^{13}C$
detrital
autochtonous
● Barbel
■ Bream
▲ Chub
○ Pisidium
✳ Corbicula
153
500
PCB concentration (ng/g wet weight)

Stable Isotope Mixing Models

- To determine the contribution of eah baseline on the isotopic signature of each fish species → type of habitat exploited

- Data: 2 origins of carbon (detrital/ autochtonous) et 2 stable isotopes (C and N)

$$\begin{cases} \delta^{13}C_E = F_d * \delta^{13}C_d + F_a * \delta^{13}C_a \\ \delta^{15}N_E = F_d * \delta^{15}N_d + F_a * \delta^{15}N_a \\ F_d + F_a = 1 \end{cases}$$

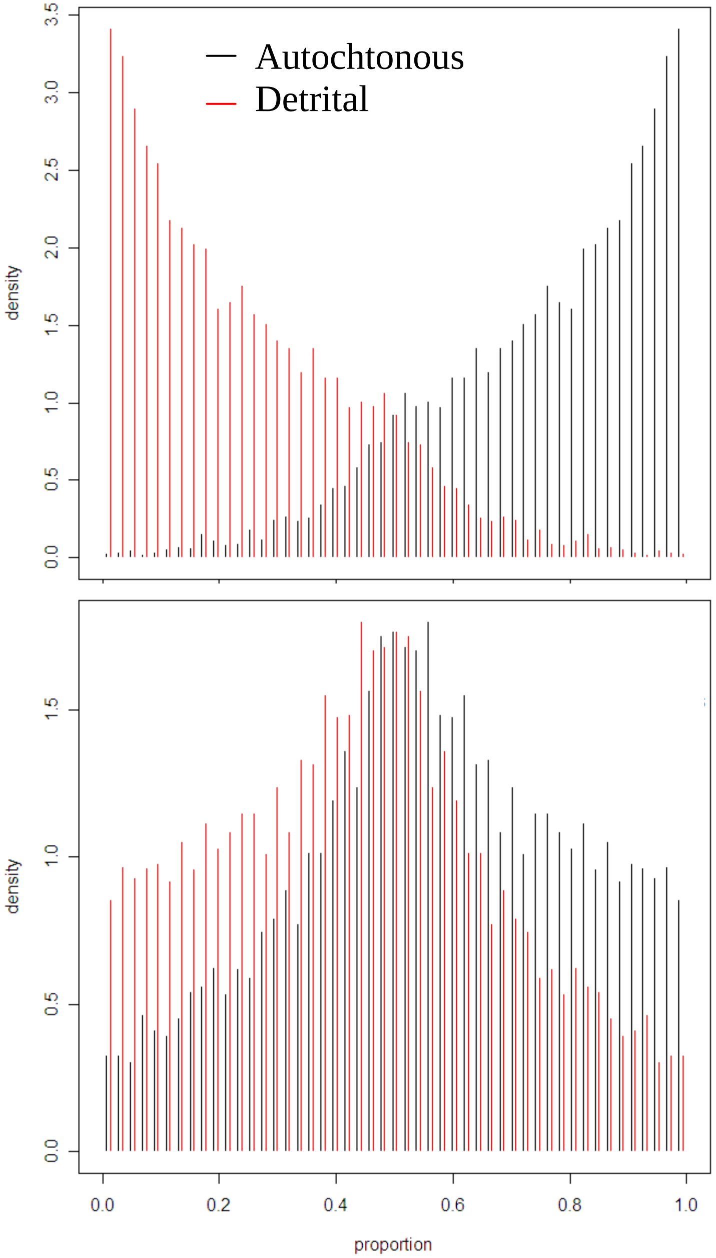
F_d : contribution of detrital carbon (*Corbicula*)
F_a : contribution of more autochtonous carbon (*Pisidium*)

- Goal : find the best combination of the 2 contributions to obtain the best fit to the data → Bayesian Inference

- Package SIAR in R

- Application for each species in each site

Results : 2 different profils

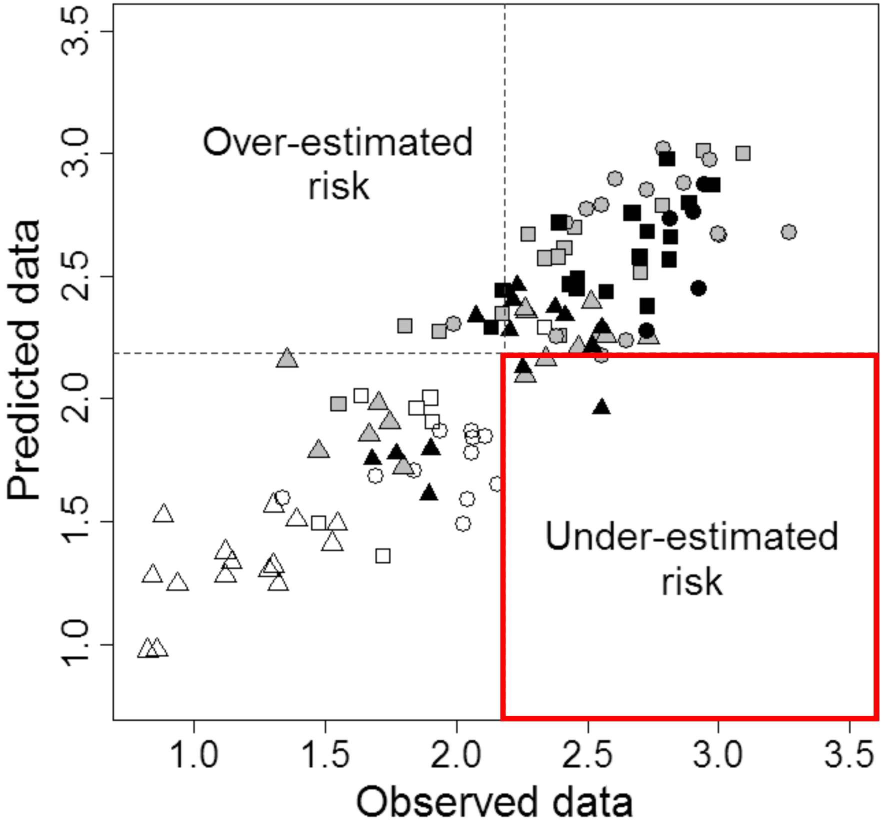


- Trophic chains mainly supported by autochtonous carbon:
  - At GDL for the 3 species (high prey availability)
  - For the chub at the 3 sites (opportunistic species)
- Trophic chains supported by the two carbon origins: exploitation of the 2 habitat types for the bream and the barbel at BRE and MTE

Predictive statistical model

- ➢ Backward stepwise regression on a log-linear model to explain fish PCB concentration according to: size, TP, % of detrital carbon, lipid content, sex and site (maximal PCB concentration in the sediment at which fishes were exposed during their life)

78% of the total variability explained by 3 variables: size, % of detrital carbon and concentration in the sediment

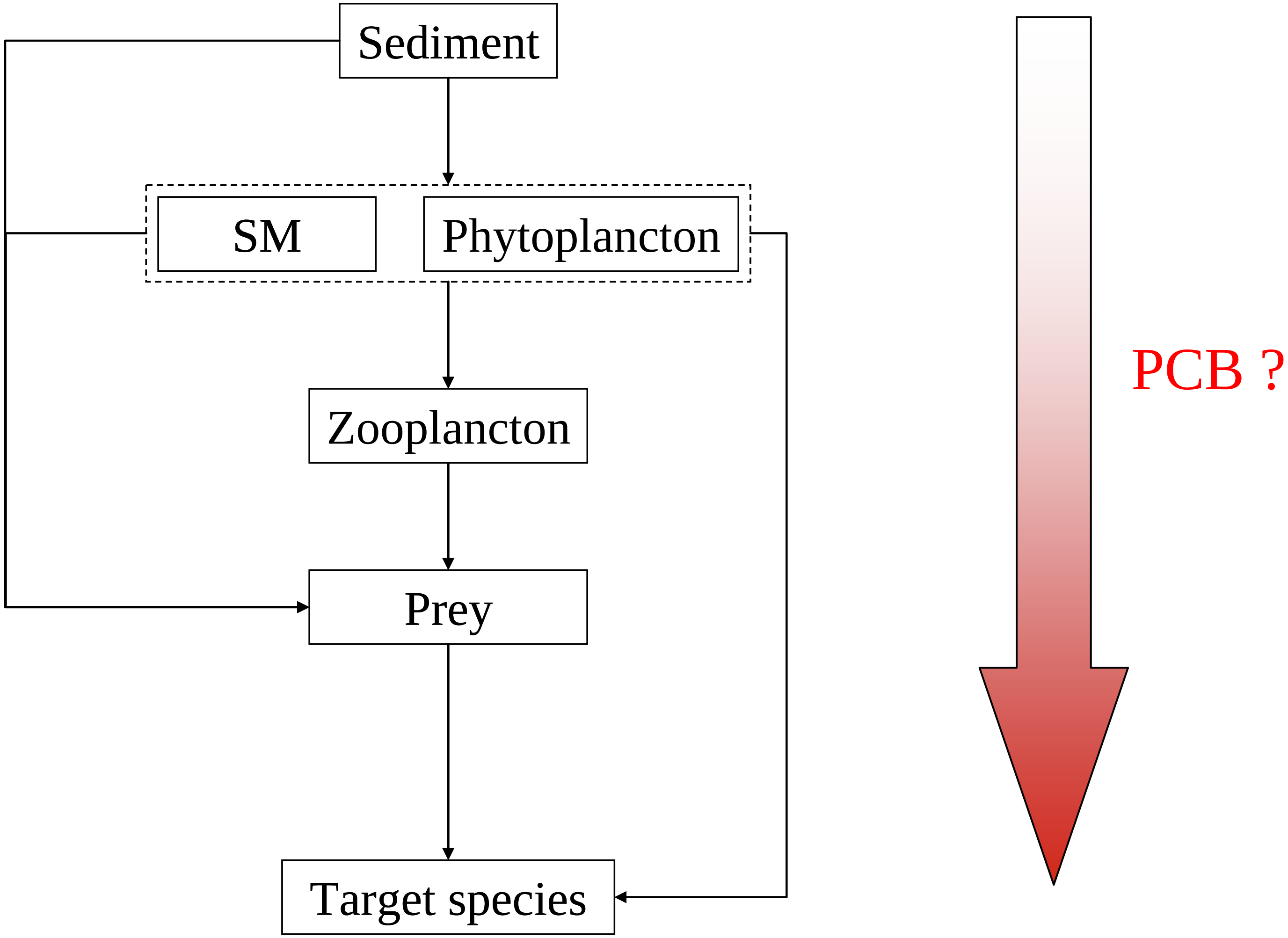


□ Bream ○ Barbel △ Chub

☐ MTE ▨ GDL ■ BRE

Efficient in a risk assessment perspective for fish consumption but not easy to use for environmental manager

Transfer of PCB along trophic chain



Sediment

SM

Phytoplancton

Zooplancton

Prey

Target species

PCB ?

Gut Content Analyses

- Determination of ingested preys

Bioaccumulation model

- Principles: kinetic bioaccumulation model physiologically based, describing PCB concentrations for the congener *c*

Fish:

$$\frac{dC_c(t)}{dt} = \overbrace{\boxed{U}\,\boxed{\alpha_c}\,Cw_c(t)}^{\text{Respiratory way}} + \overbrace{\sum_j \boxed{\beta_c}\,\boxed{Q_j}\,\boxed{F}\,C_j(t)}^{\text{Trophic way}} - \overbrace{\left(\boxed{E_c} + \boxed{G}\right)C_c(t)}^{\text{Metabolic way}}$$

U : Water filtration rate → $U(W,T)$

α_c : assimilation efficiency of the dissolved congener c → $\alpha(K_{ow})$

β_c : assimilation efficiency of ingested particles → $\beta(K_{ow})$

Q_j : diet preference for the prey j

F : Ingestion rate → $F(W,T)$

E_c : Excretion rate → $E(W)$

G : Growth rate → $G(L,W,t)$

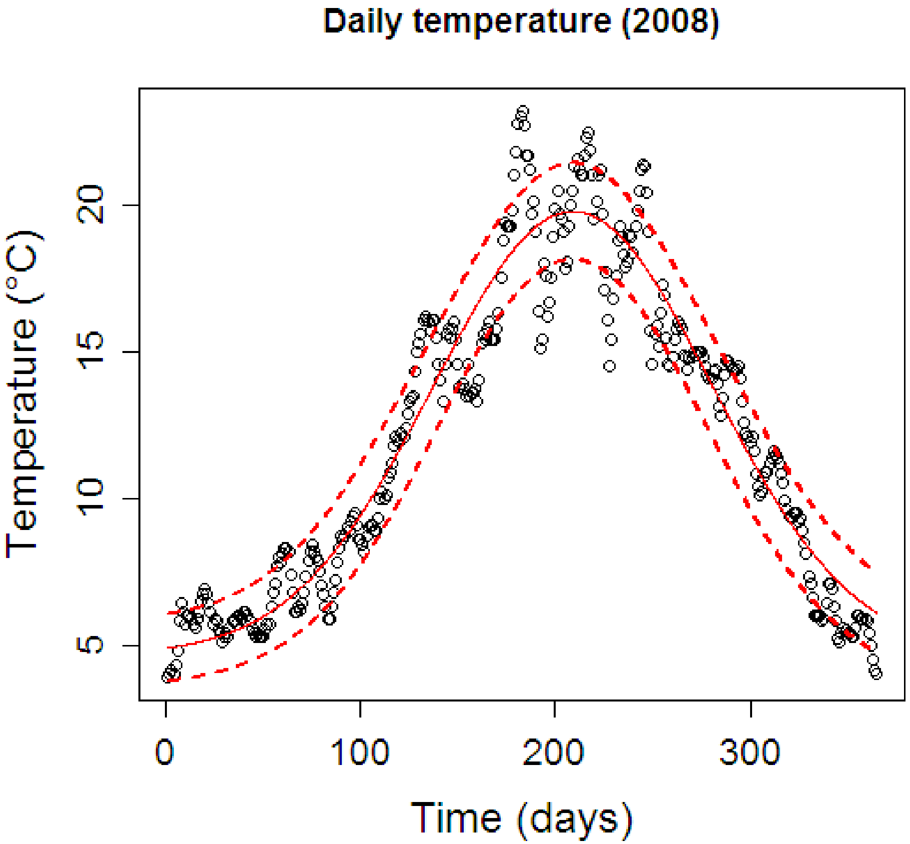
↳ Bayesian inference to estimate parameters involved in each function

Annual variation of water temperature (near GDL)

- Model of annual variation

$$T = \delta + \alpha * \exp\left(-\mathbf{0.5} * \frac{(t-\beta)^2}{\sigma^2} \right)$$

Bayesian inference



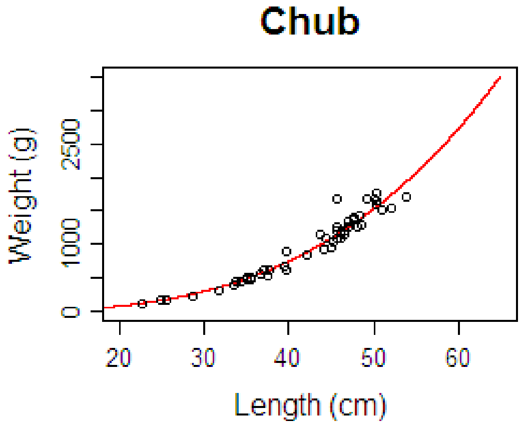
Temperature estimated by randomly drawing in the credibility interval for each day

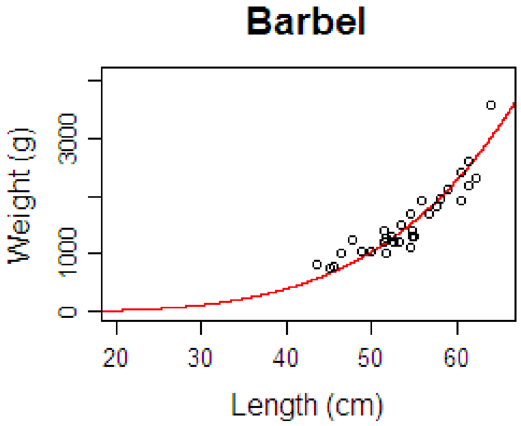
Growth rate estimation (1)

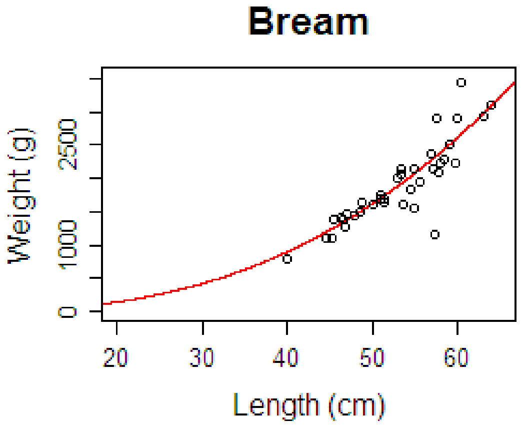
- Length / Weight relation for each species

$$\log(W) = a * \log(L) - b$$

Bayesian inference





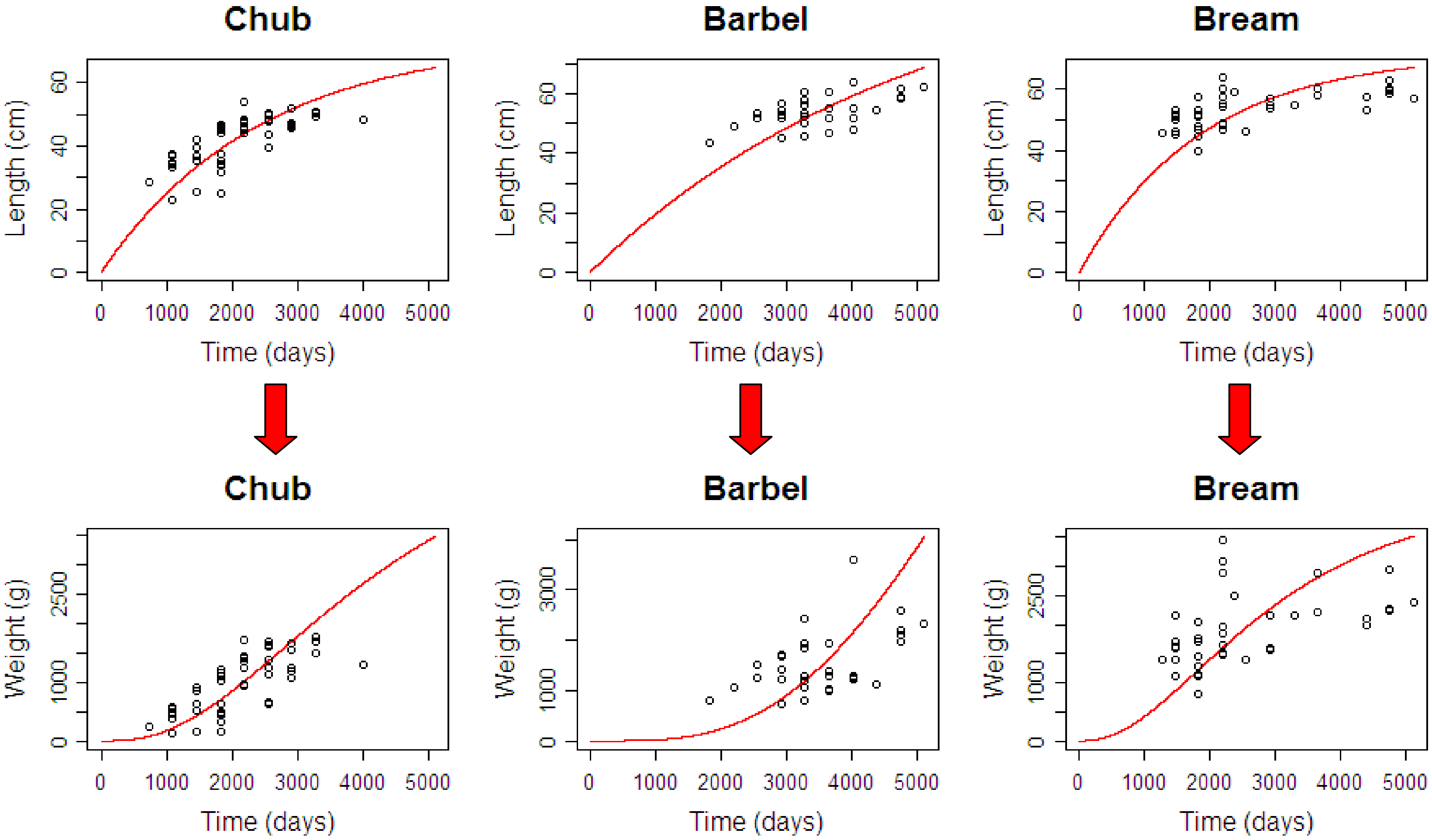


Growth rate estimation (2)

- Von Bertalanffy growth model

$$\frac{dL(t)}{dt} = r\left(L_\infty - L\right)$$

Bayesian inference for each species



Growth rate estimation (3)

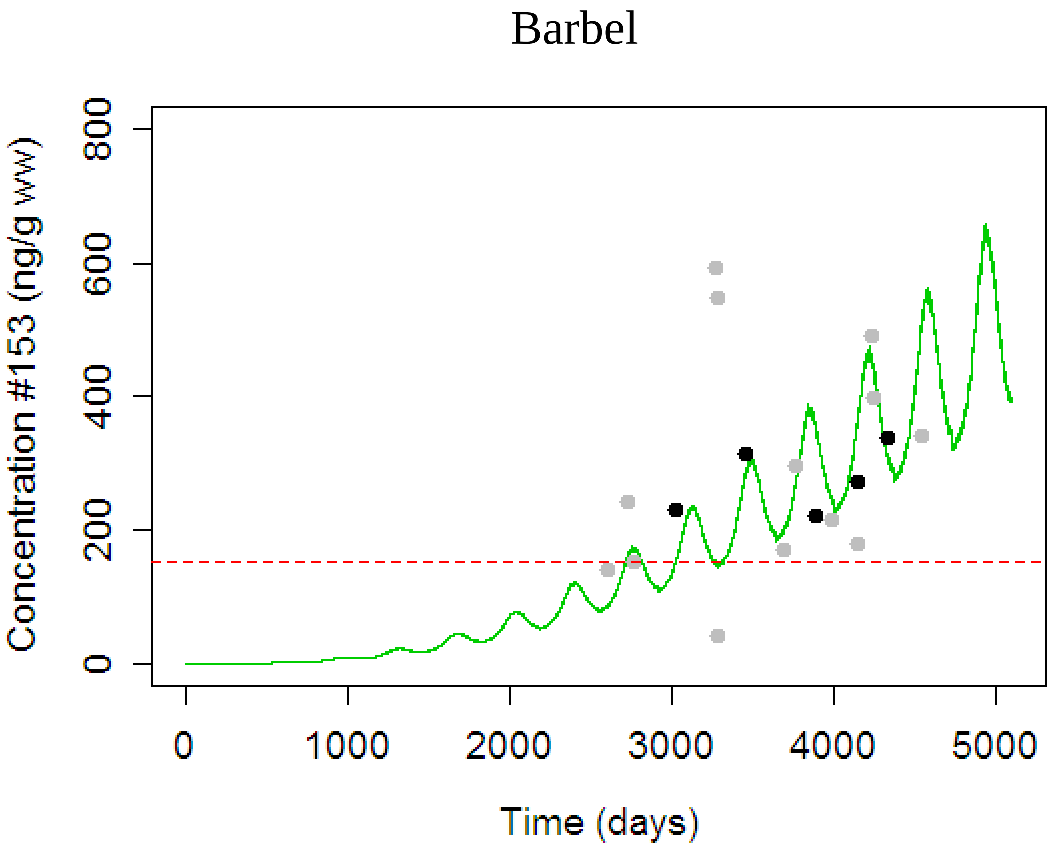
- Method 1:

$$g = \ln\left(\frac{W_{t+\mathbf{1}}}{W_t}\right) \quad \Rightarrow \quad G = \exp(g) - \mathbf{1}$$

- Method 2: Population dynamic model (in development)

Preliminary results on #153

- Respiratory way neglected, β, F and E estimated by equations of Loizeau (2001) for sea bass, fixed concentrations in invertebrates (GDL)



Perspectives

Model currently in progress so many aspects should be improved:

- Each function clearly specified and associated parameters estimated.
- Couple the bioaccumulation model to a dynamic population model for fishes
- Develop a bioaccumulation model for invertebrates that link fishes to sediment (detrital / autochtonous carbon use)
- Test the model sensitivity and credibility

Île du Beurre

Thank you

La Morte

Stable Isotope Analyses

- Rely PCB concentrations to trophic position (from $\delta^{15}N$ values) and carbon pathways (from $\delta^{13}C$ values)

- Until now, trophic position deterministically estimated from $\delta^{15}N$ values (Post, 2002):

$$TP_f = \lambda + \frac{\delta^{15}N_f - \left(\alpha\,\delta^{15}N_{b1} + (1-\alpha)\delta^{15}N_{b2}\right)}{\Delta N} \quad \text{with} \quad \alpha = \frac{\delta^{13}C_f - \delta^{13}C_{b2}}{\delta^{13}C_{b1} - \delta^{13}C_{b2}}$$

λ : Trophic position of the 2 baselines (usually primary consumers, $\lambda = 2$)

α: Proportion of nitrogen in the consumer ultimately derived from the base of the first food-web

$\delta^{15}N_{bi}$ and $\delta^{13}C_{bi}$: $\delta^{15}N$ and $\delta^{13}C$ values for the baseline i

ΔN : Enrichment in $\delta^{15}N$ per trophic level (3.4 ‰ in average)

- Here, Bayesian inference used to estimate species TP, by considering $\delta^{15}N$ and $\delta^{13}C$ data variability and uncertainty around the parameters

Bayesian inference

- Principles:

Prior distribution on parameters and data

Marginal posterior distribution for each parameter

Joint posterior distribution (correlation between parameters)

- Computation:
  - Prior distributions on data and parameters:

$\delta^{15}N \sim \mathrm{N}\left(\overline{\delta^{15}N}, \sigma_N\right)$

$\delta^{13}C \sim$ $\mathrm{N}\left(\overline{\delta^{13}C}, \sigma_C\right)$

$\sigma_N \sim \mathrm{G}(0.001,0.001)$

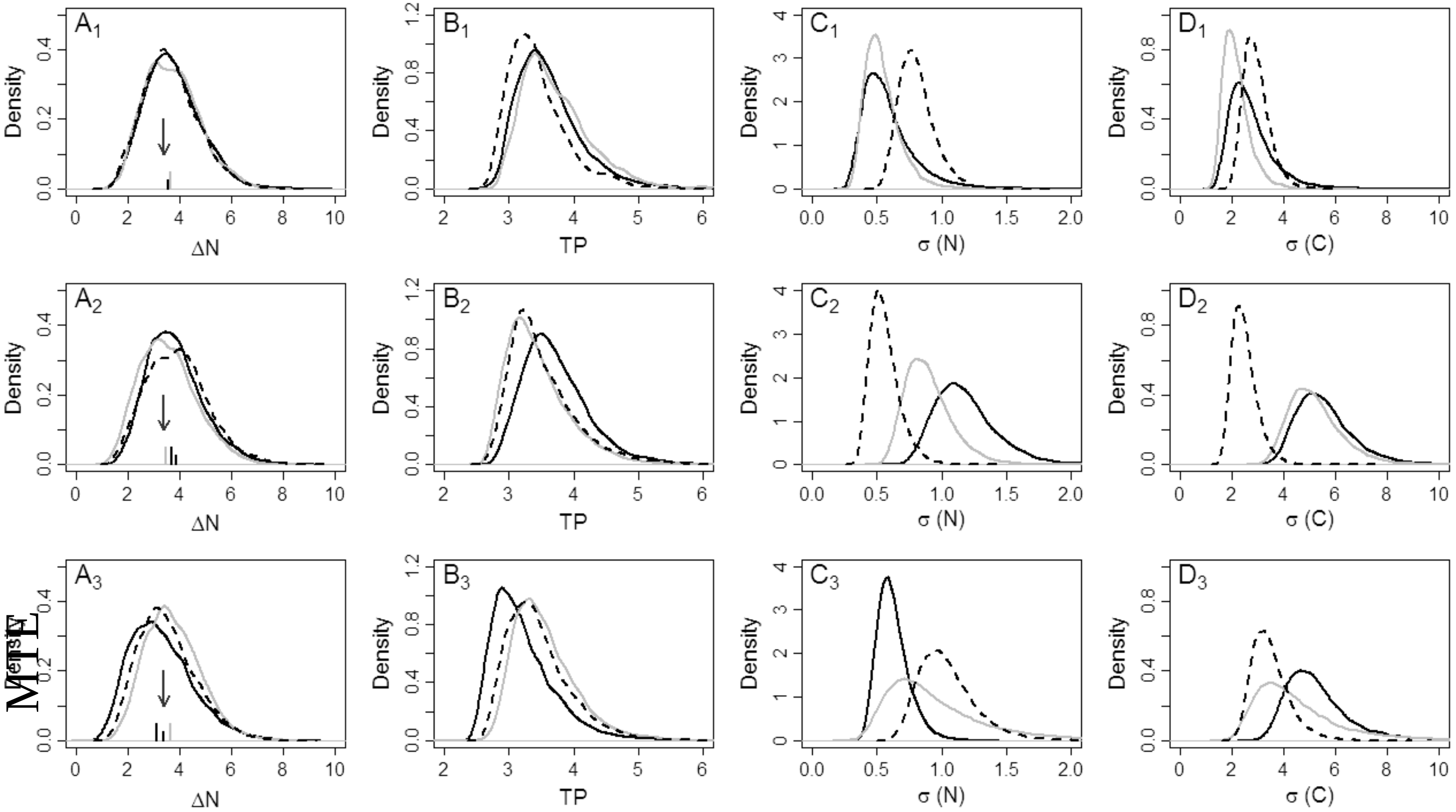
$\mathrm{N}(\mathbf{3.4}, \mathbf{1.5})$

$\sigma_C \sim \mathrm{G}(0.001,0.001)$

$\Delta N \sim$ (Post, 2002) TP ~ U(2,5)

  - Complex models: Monte-Carlo Markov Chain (MCMC) with Winbugs and WBDiff

Marginal posterior distributions



GDL

BRE MTE

— Bream

- - - Chub

— Barbel

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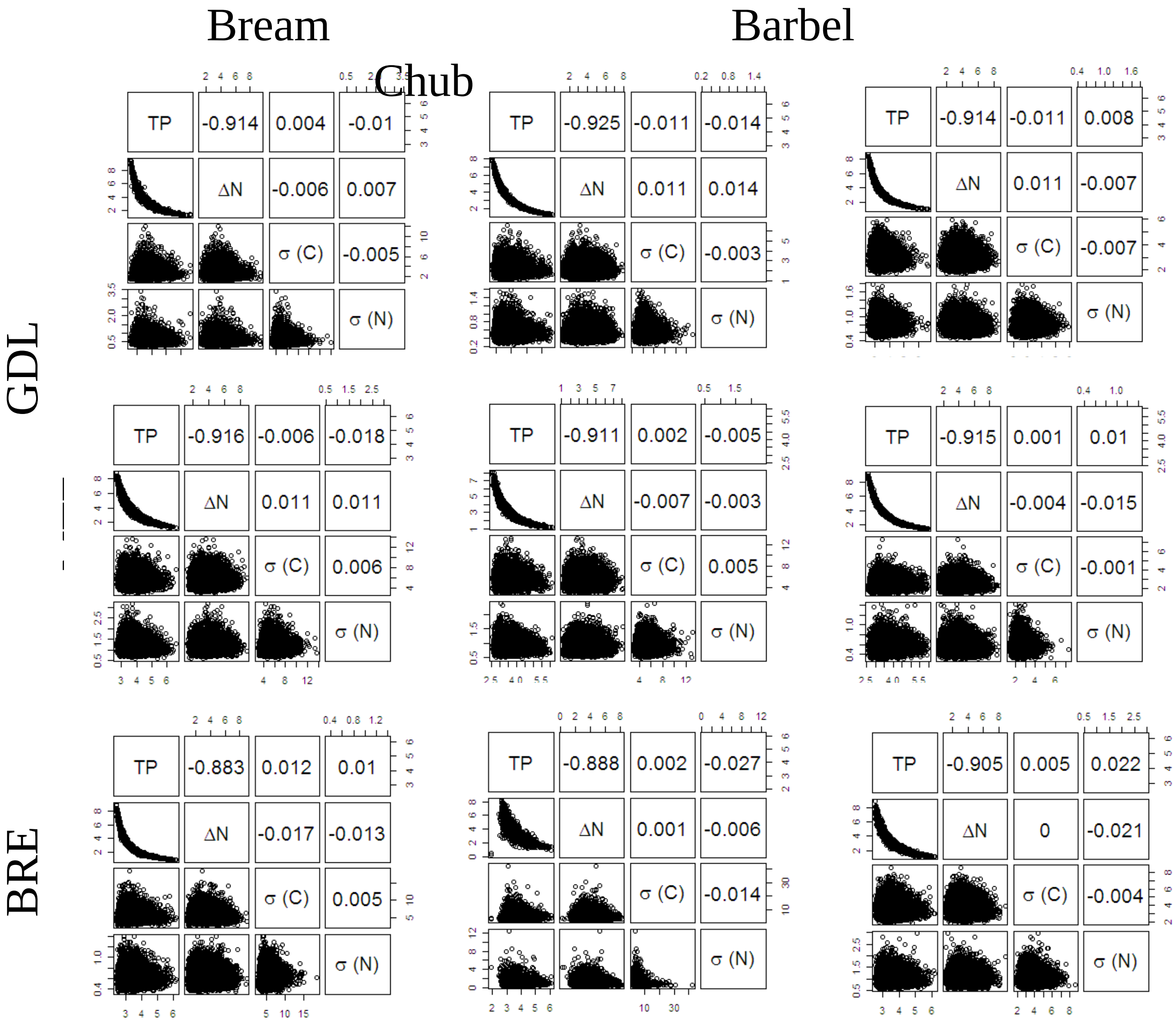
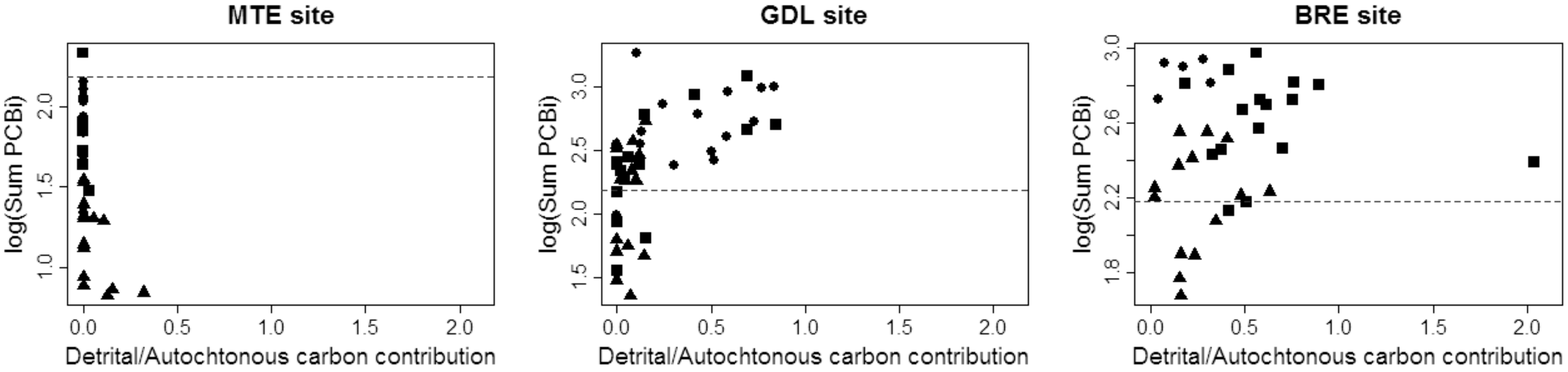
Joint posterior distributions

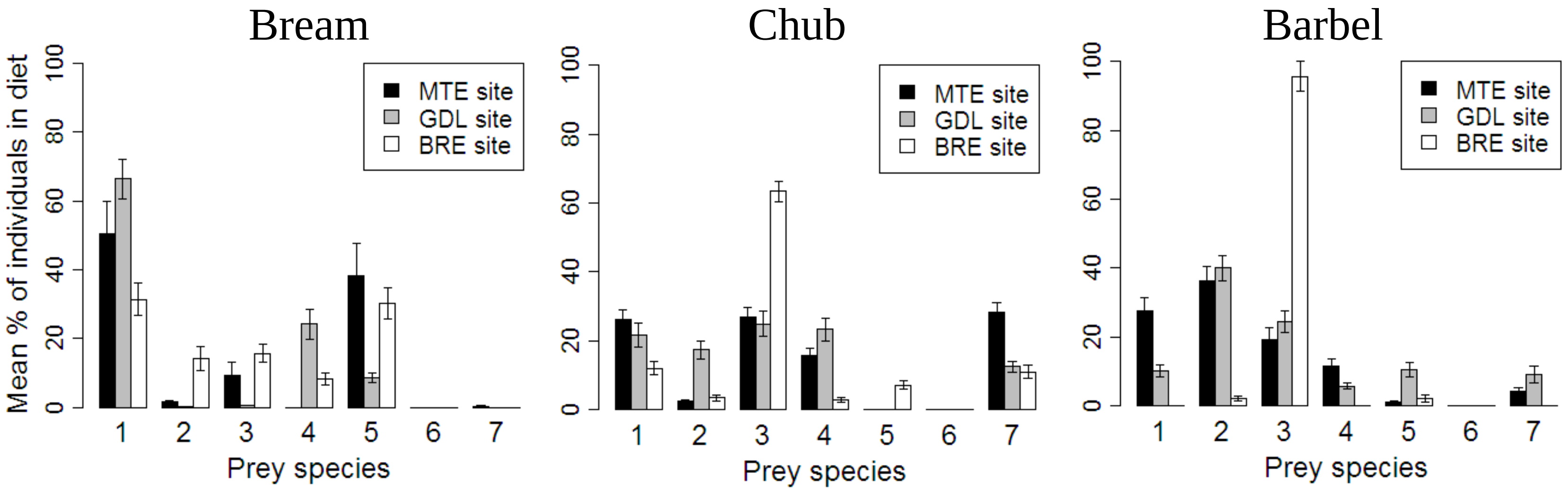


Contribution of detrital and autochtonous carbon source on individual contamination levels



Gut Content Analyses

- Determination of ingested preys



1- Dipterans; 2- Other aquatic insects; 3- Crustaceans; 4- Gastéropoda; 5- Bivalves; 6- Macrophytes; 7- Other preys (algae, terrestrial or aerial insects, oligochaetes, fish, litter)

- Low individual variability (only adults)
- Differences in diet preference between species and between sites
- No sex and size effect on diet