Quantification of BDOC of different water masses in East China Sea

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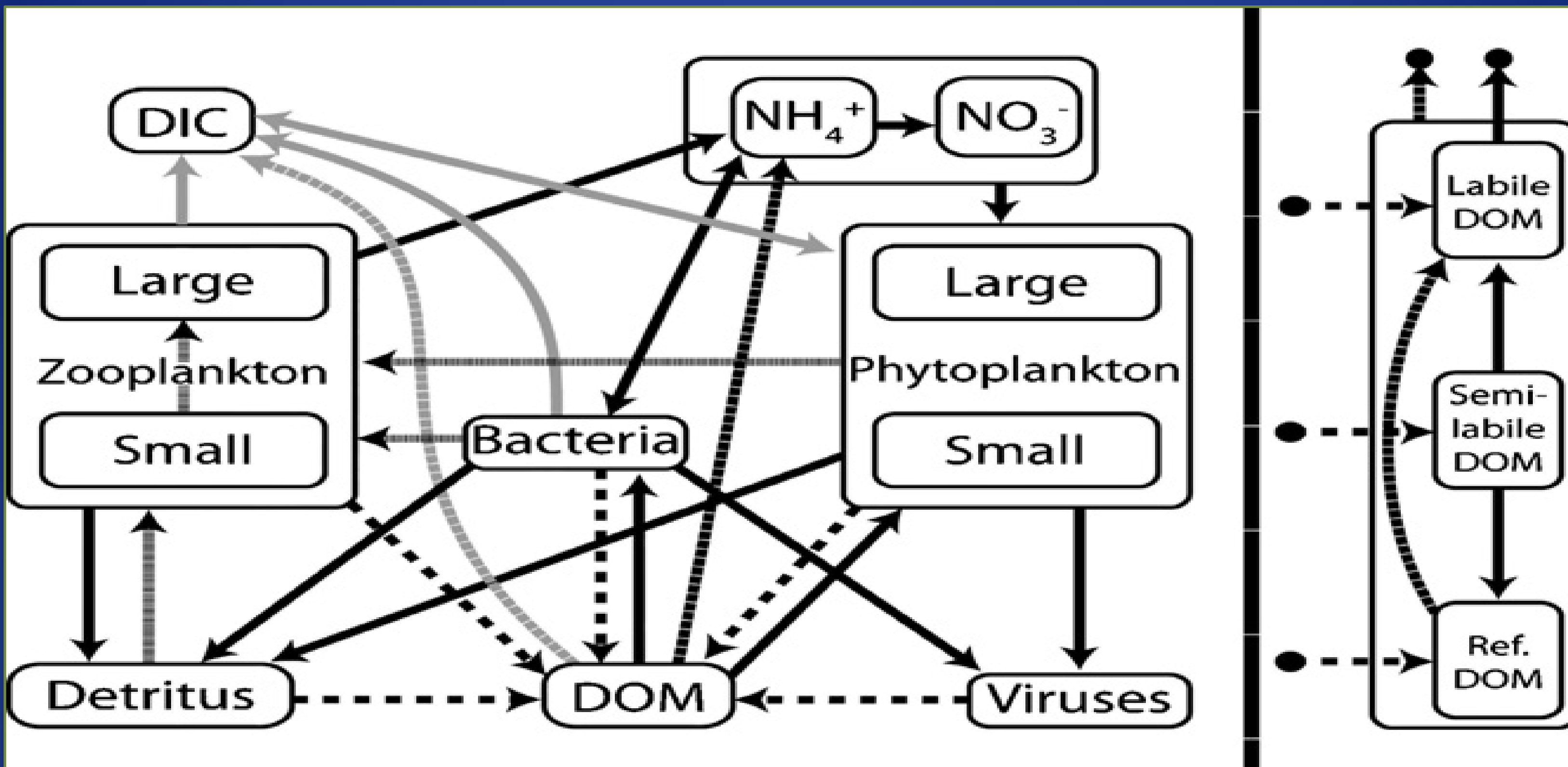
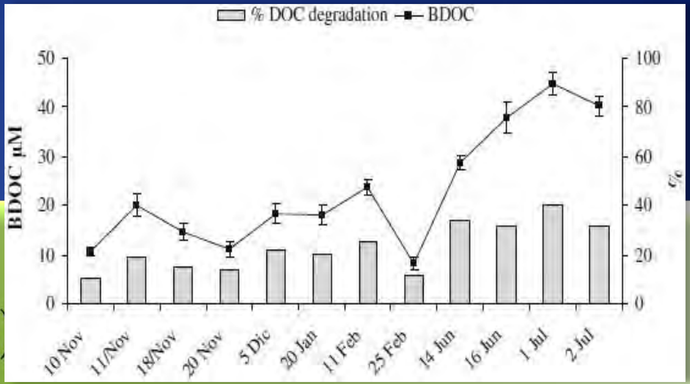
Introduction



DOC: Dissolved organic carbon, largest carbon pool of ocean, 700Pg *vs* 750Pg CO2 atmo 1% *vs* 1 yr fossil fuel

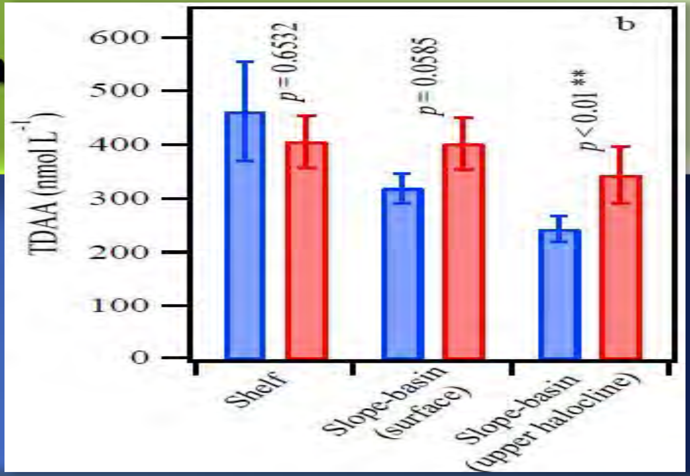
Microorganism: Major consumer of DOC(bacteria)

BDOC



Latest research

Sea water(Vittor et al., 2009—**BDOC difference**)
Sea ice(Fasching et al., 2012—**DIC output**)
Amazon river(Benner et al., 2012—**Composition**
…



Shelf?

DOC

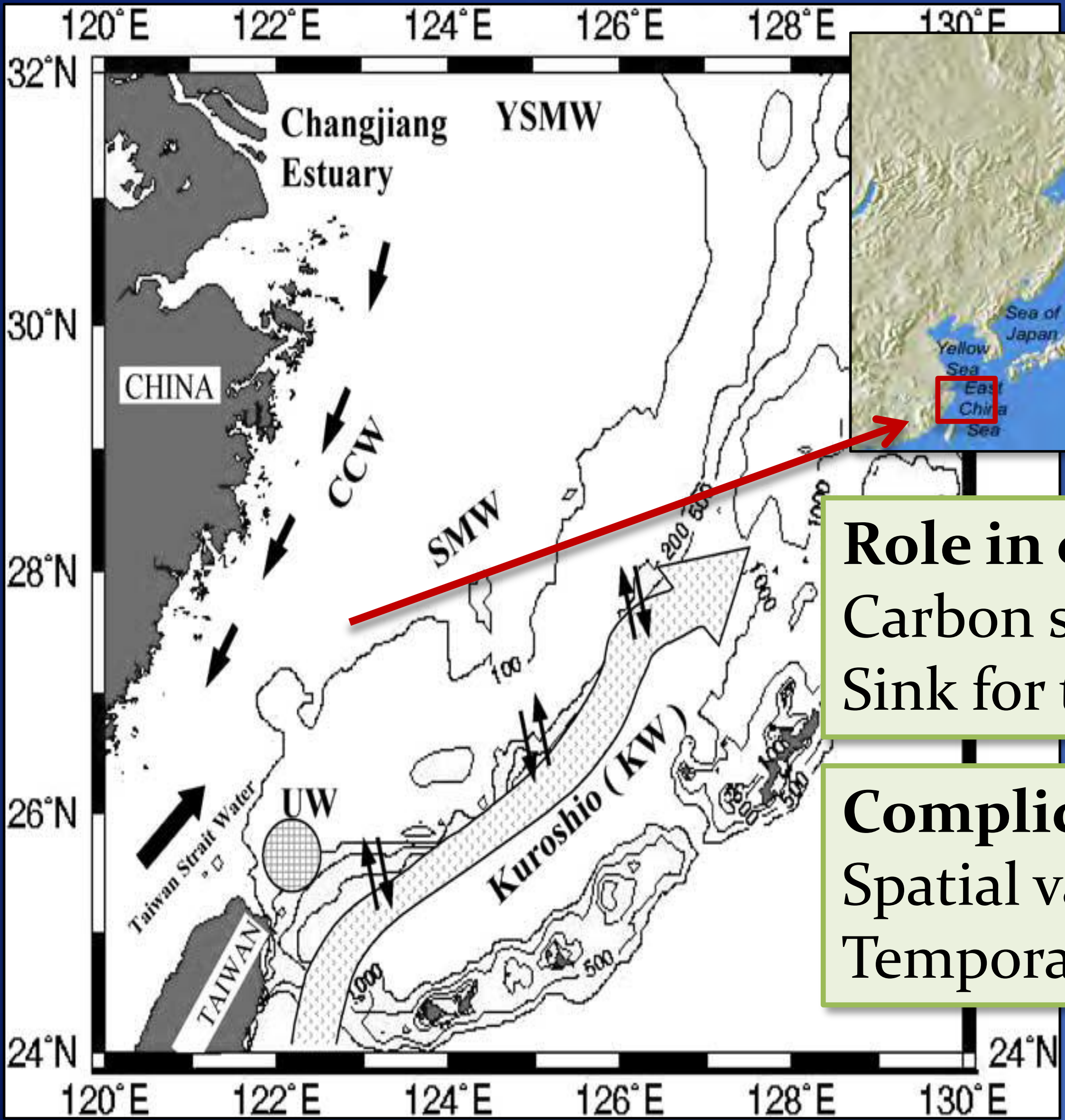
RDOC

BDOC

Refractory, the major part of DOC

Bio-available, **minor and dynamic!**
BP+BR, a major carbon flux in the ocean(Kirchman, 2008)

East China Sea(ECS)



Role in carbon cycle

Carbon source of the Pacific

Sink for the atmospheric CO_2

Complicated and puzzled

Spatial variation: Water masses?

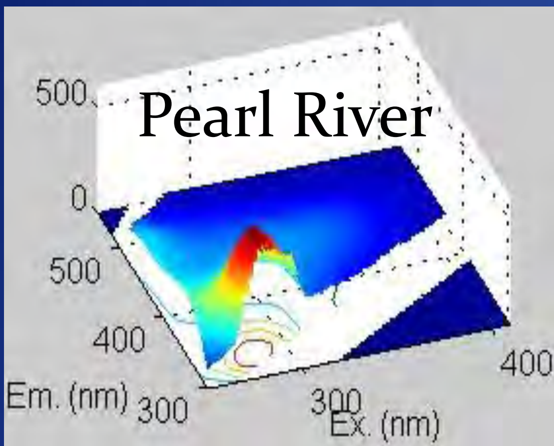
Temporal variation: Dynamic?

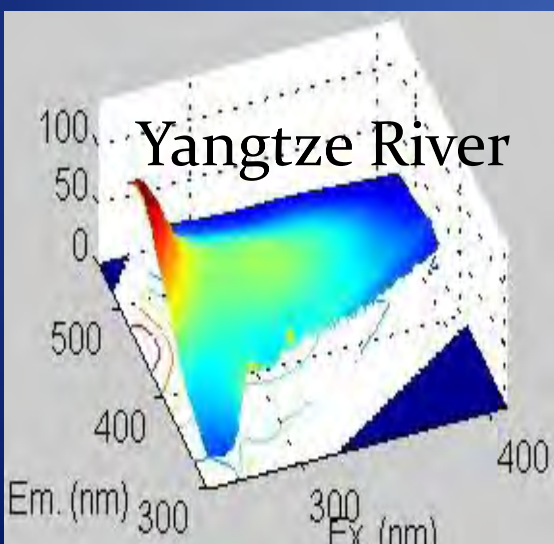
Hypothesis

- Bio-available DOC among various water masses in ECS are different;
- There is a link between bio-available DOC with their chemical structure.

Method

3-D Fluorescence spectra (EEMs)

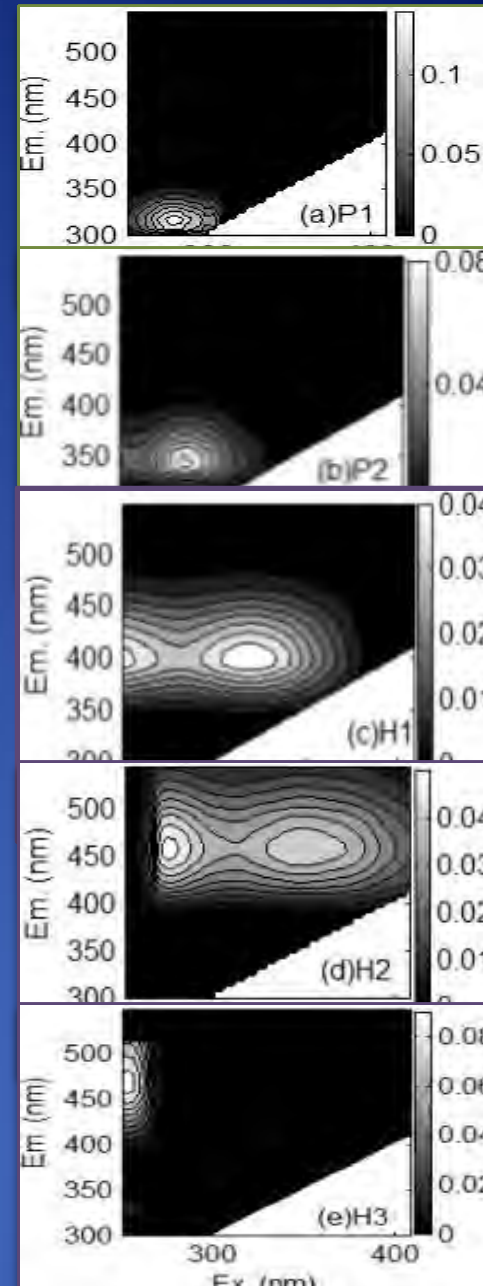




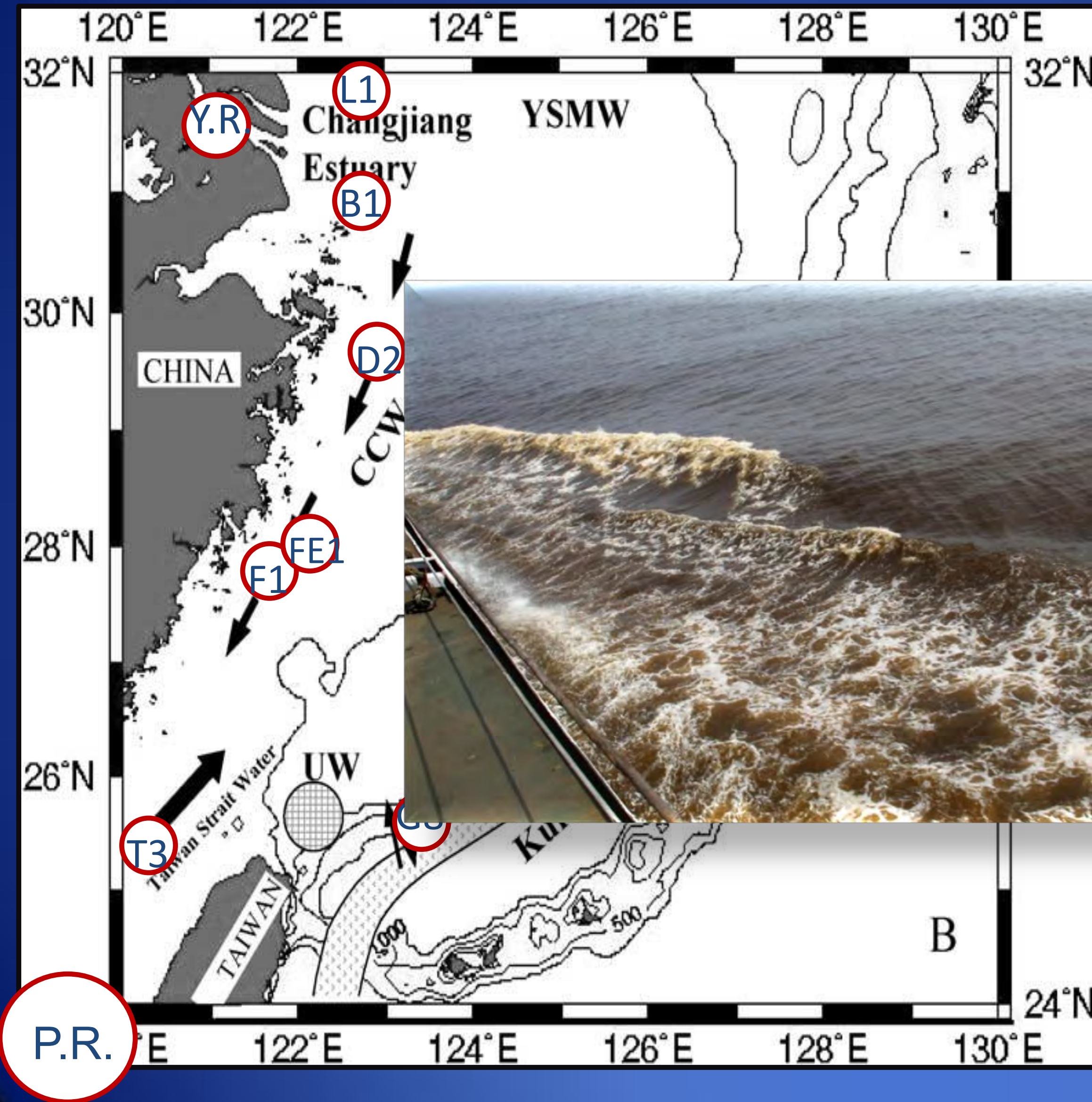
PARAFAC analysis

Coble, 2007
Stedmon and Bro, 2008

name	type	property
P1	Protein	B, labile
P2		T, labile
H1	Humic	M, less labile
H2		C, refractory
H3		A, refractory



Sampling Sites

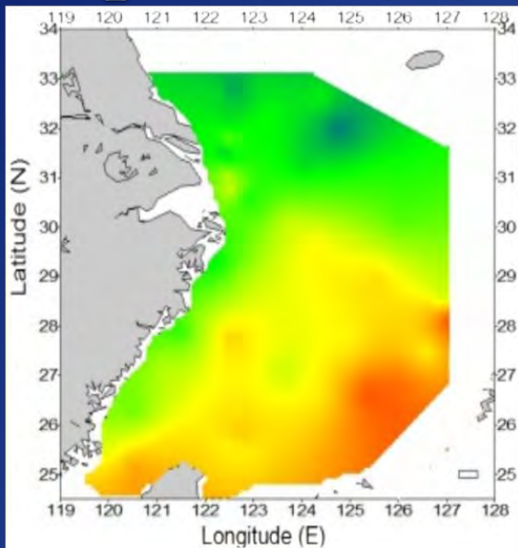


Cruise:
2011/5/10-2011/6/5

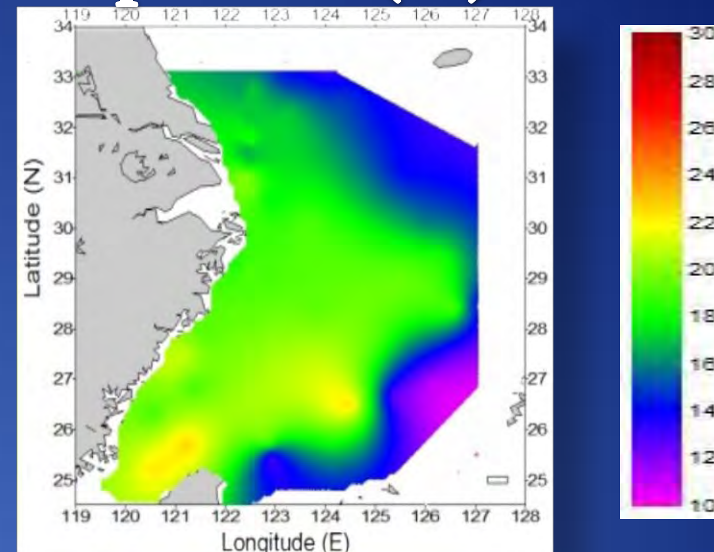
St.	sal	water mass
Y.R	0.1	Yangtze River(Y.R.)
	23.4 30.9	Plume of Y.R.
	0.1	Pearl River(P.R.)
	30.3	Bloom
	31.2	Red tide
T3	34.5	Taiwan C.
G8	34.5	Kuroshio C.
D2	31.9	Coast

Background

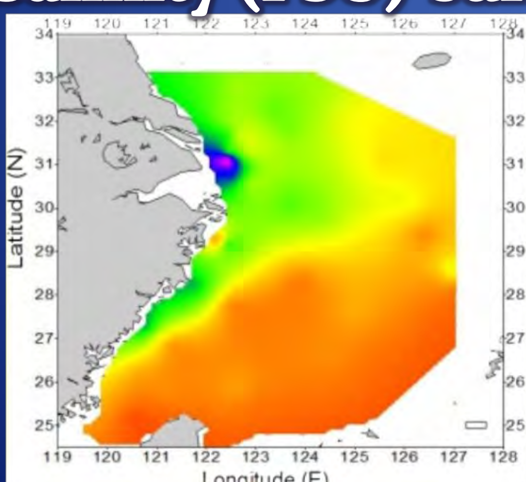
Temperature(℃)-surface



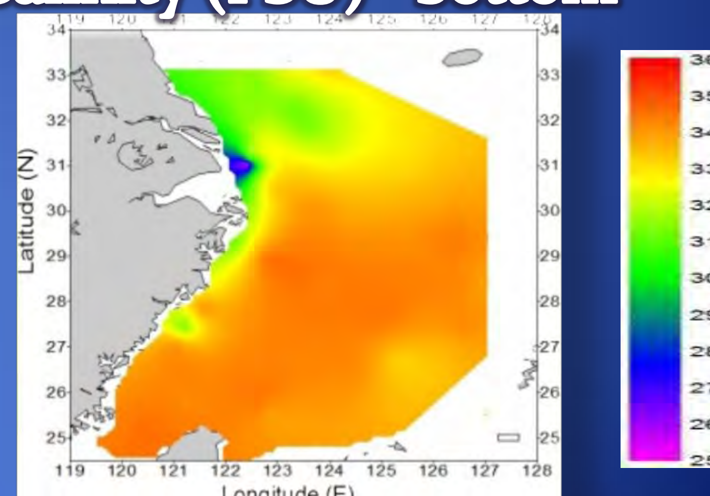
Temperature(℃)-bottom



Salinity (PSU)-surface

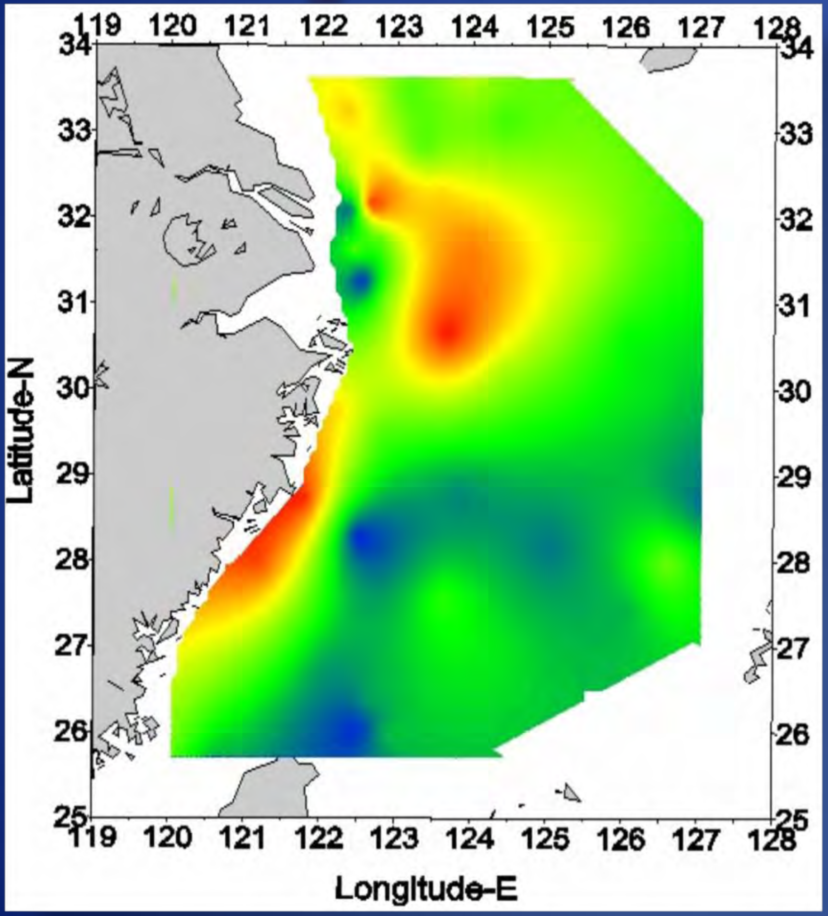


Salinity (PSU)--bottom

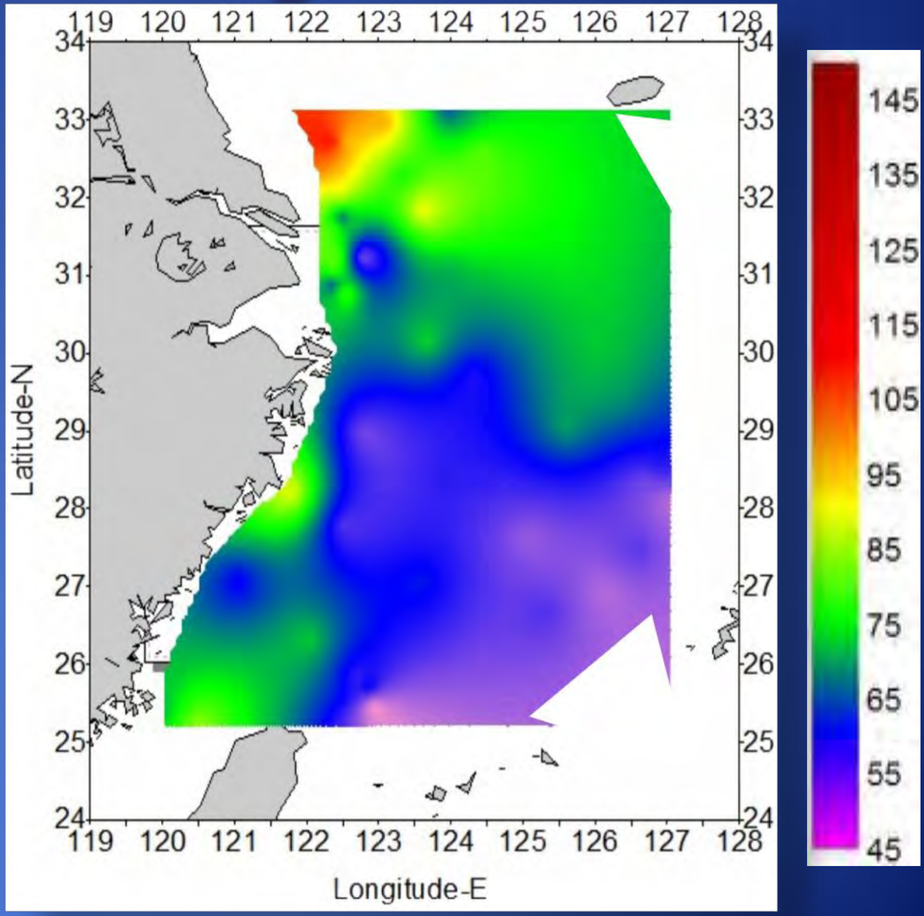


Distribution of DOC in ECS

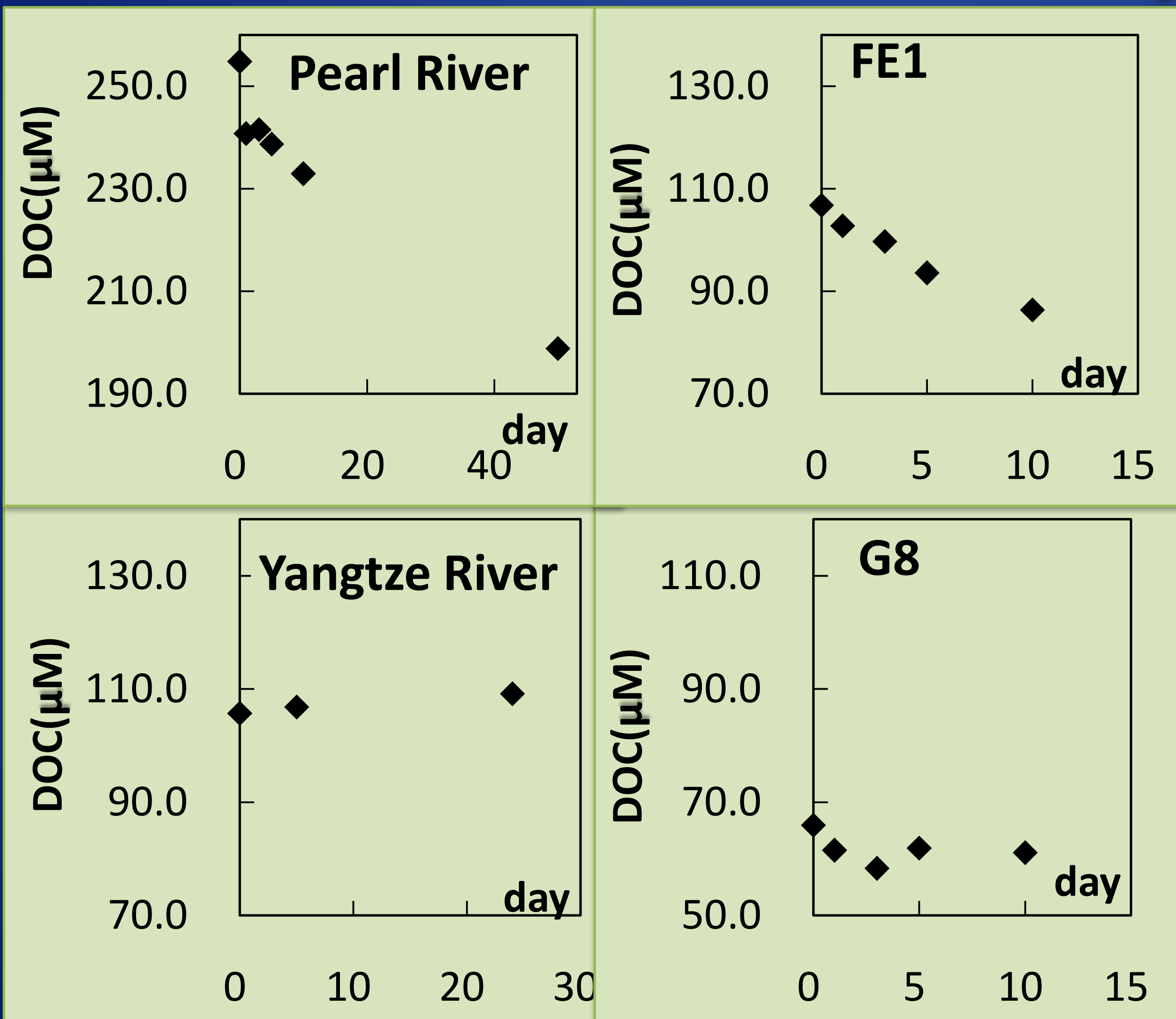
DOC- μM-bottom



DOC- μM-surface



Degradation of DOC



→ Difference K(d^{-1})

$C=C_o e^{-kt}$(Hung et al，2003)

- Taiwan C.T3: Shelf water, bio-available
- Kuroshio C.G8: Oceanic water, less bio-available
- Bloom FE1: Highly bio-available
- Estuary of Y.R. inconsistency

BDOC

Spatial and Temporal variation

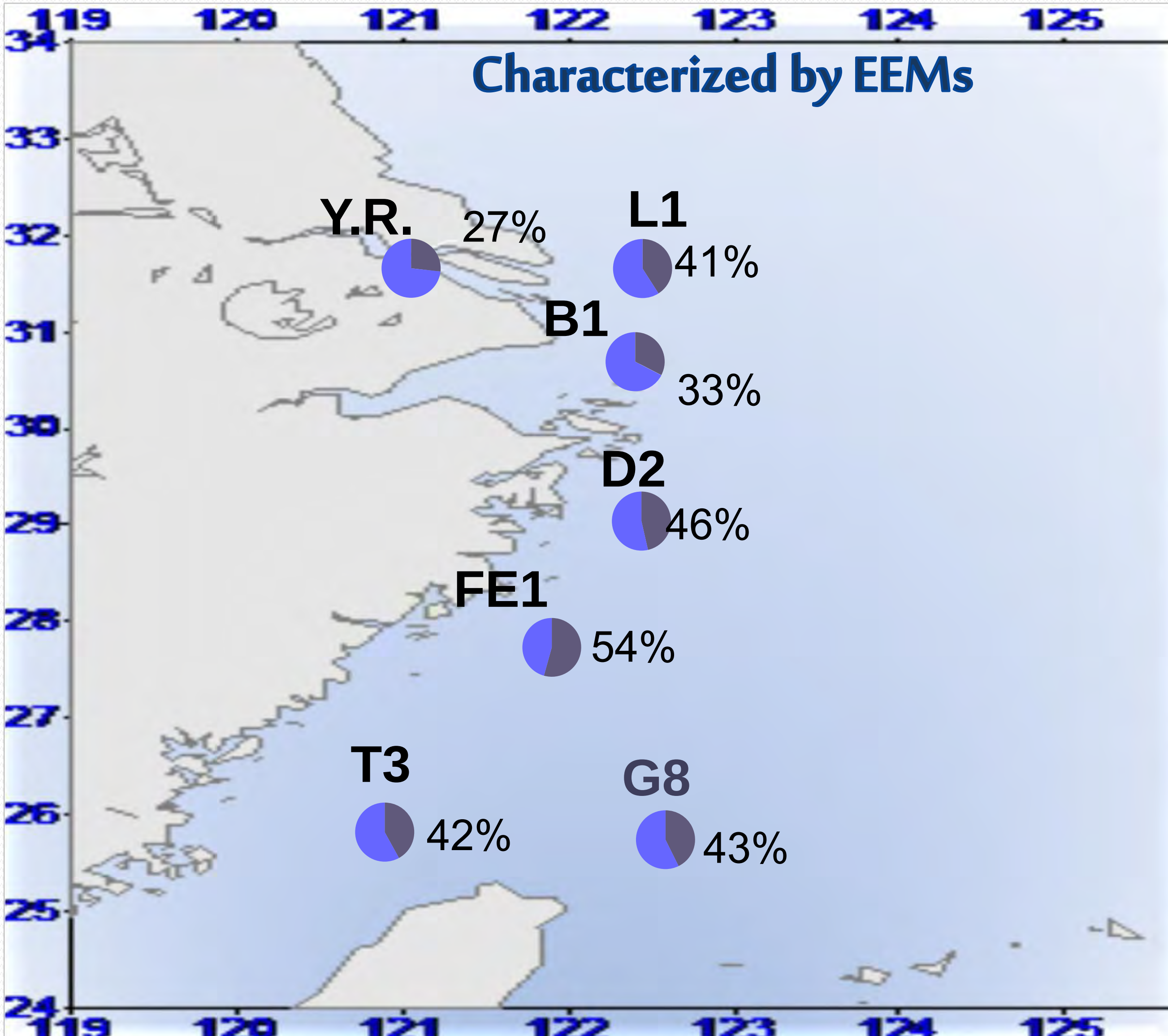
Source	Taiwan C.	Kuroshio C.	Mix shelf water	Coastal water	Bloom	Y.R. plume	Y. R.	P.R.
BDOC (μM)	26. [illegible]	6.8	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
K (d^{-1}) (This study)	0.0 [illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
K (d^{-1}) (Literature)	0.0 [illegible] (W [illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

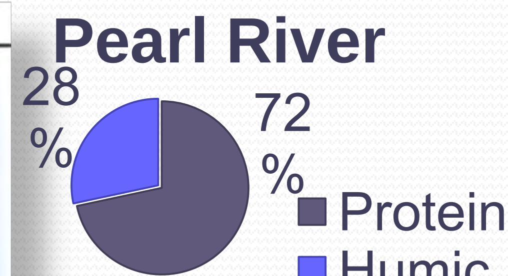
Region comparison	Water masses	DOC (μM)	K (d^{-1})
North Atlantic	Shelf water		0-0.4
Georges Bank slope	Shelf deep water	50	0
North Pacific	ocean		0.005
Satilla River	terrestrial water	333	0.0012

K: degradation rate constant
'W'for winter,'S'for summer.

Hung et al.,2003; Kirchman et al., 1991; Hopkinson et al., 1997; Moran et al., 1999; Lin,2006

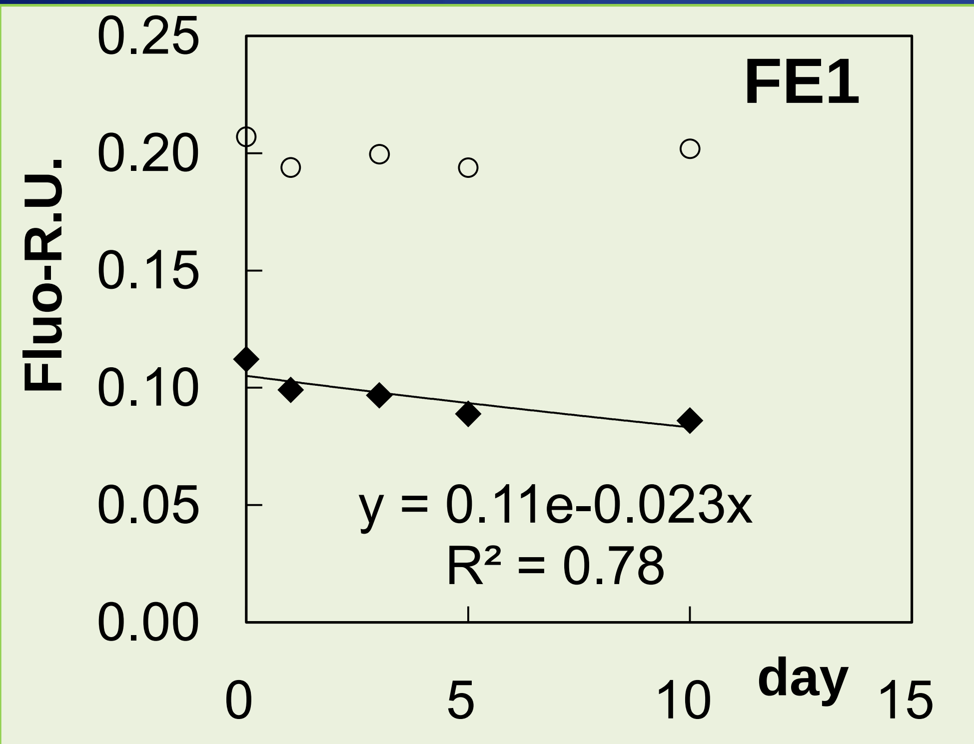
Spatial variation of DOM

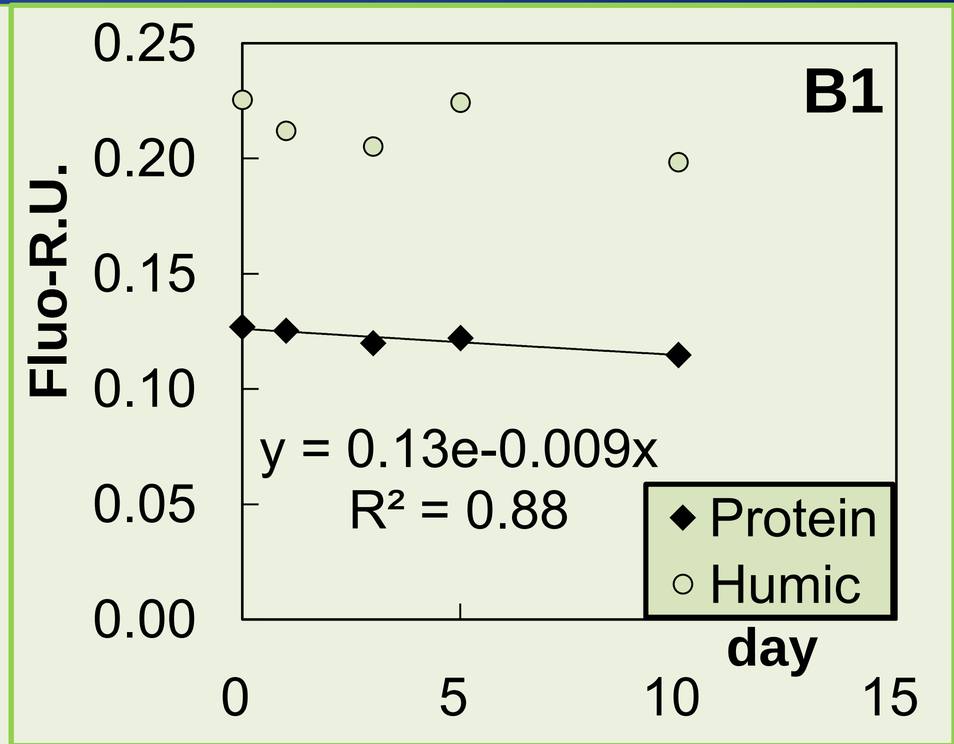




ST.	∑P %
Y.R.	27
B1	32
L1	41
ZJ	72
FE1	54
F1	50
T3	42
D2	46
G8	43

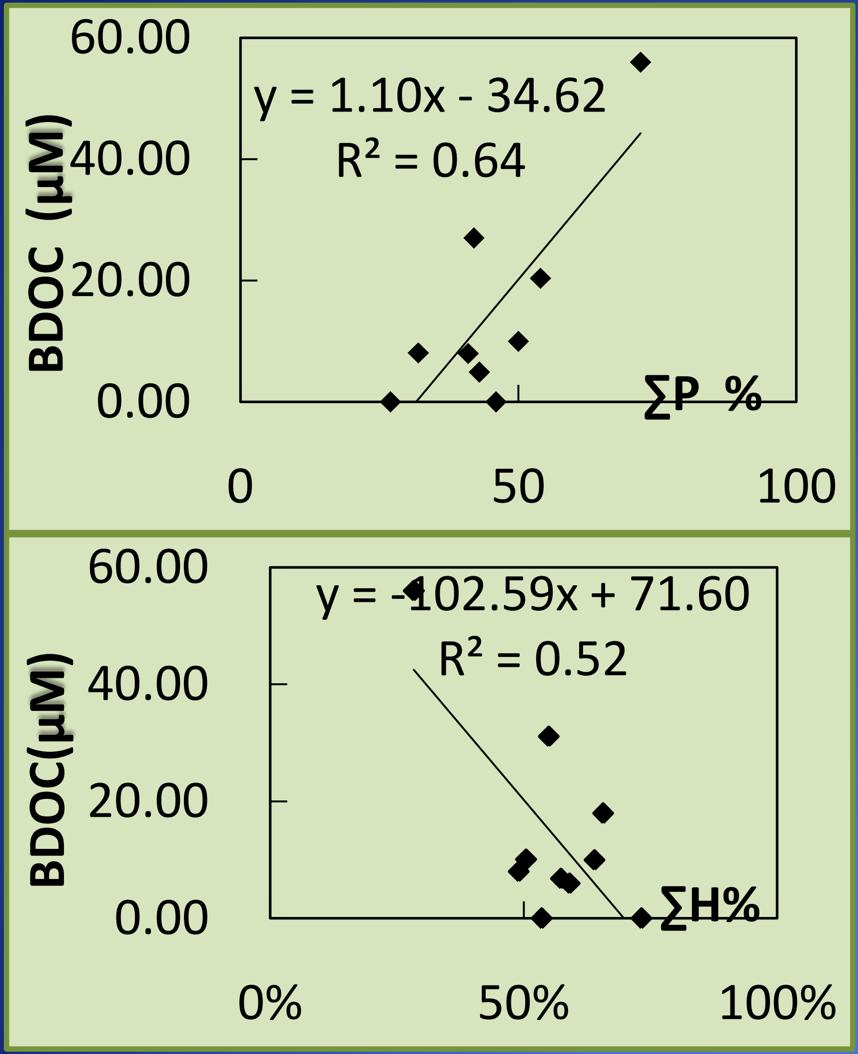
Degradation of Protein(P)





Bloom (d^{-1})	Y.R. plume (d^{-1})
0.021-0.018 *vs* 0.023	0.0055 *vs* 0.009

□ Protein:
Labile component



- **Protein:**

Labile

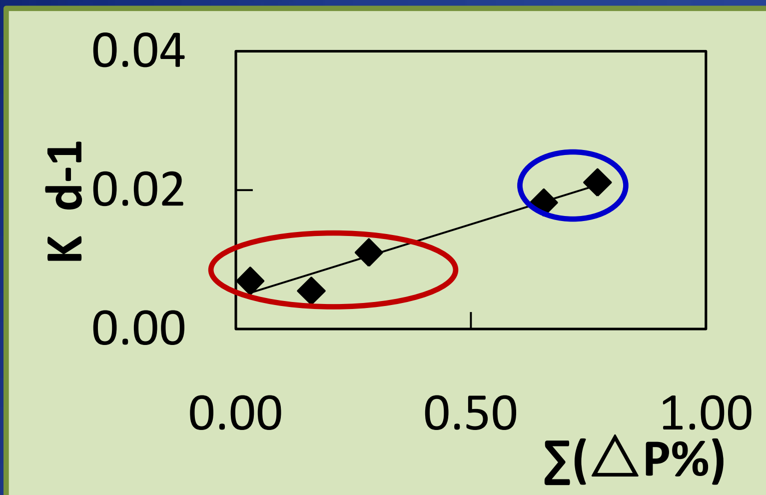
Exponential function degradation

- **Humic:**

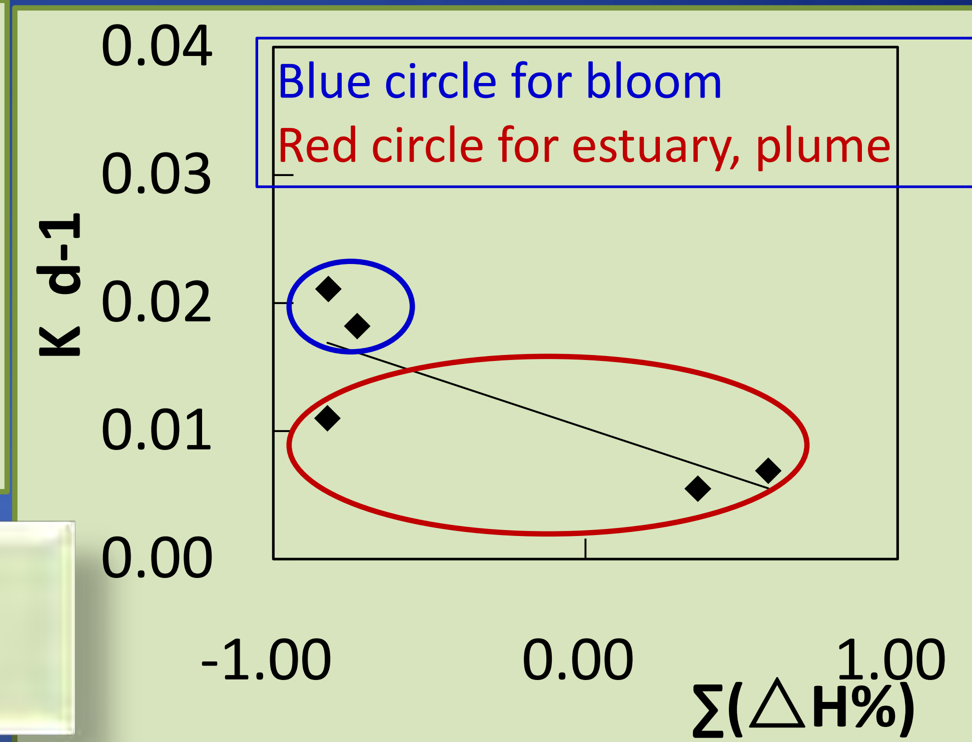
Less labile/refractory

? Different from Protein

Degradation of Humic(H)



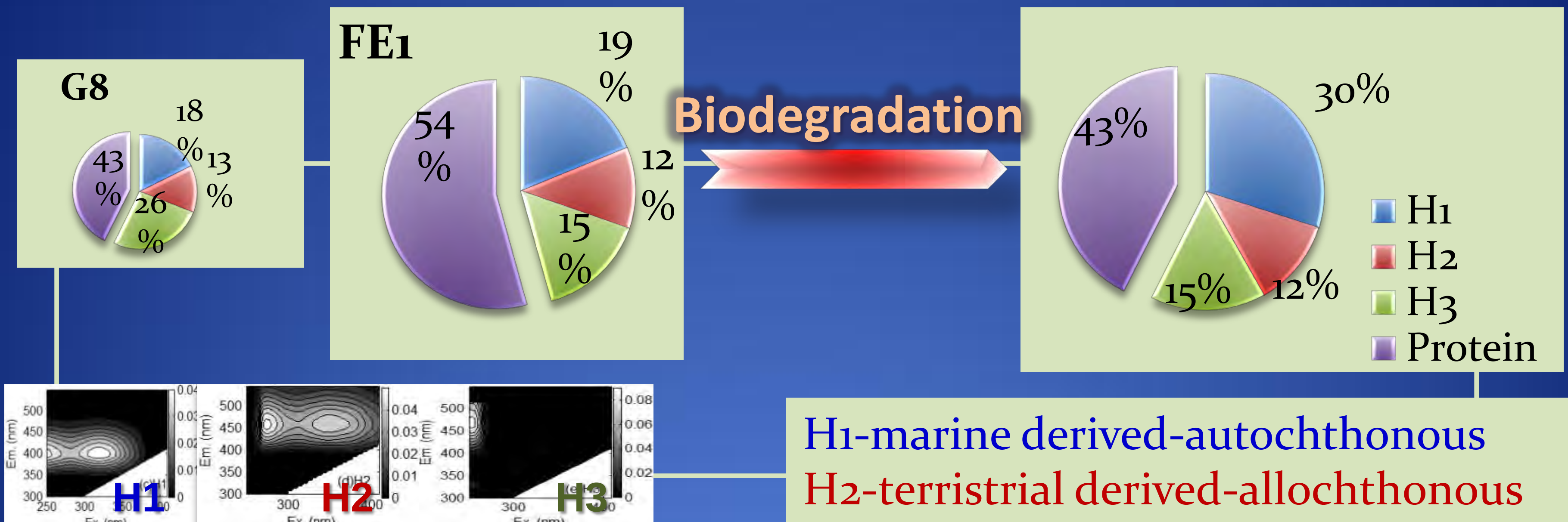
∑(△H%):
sum of [H (first day)-H(last day)]
<0: Produced; >0: Degraded.



Bloom: autochthonous DOM
Estuary: allochthonous DOM

Degradation of H

Autochthonous DOM

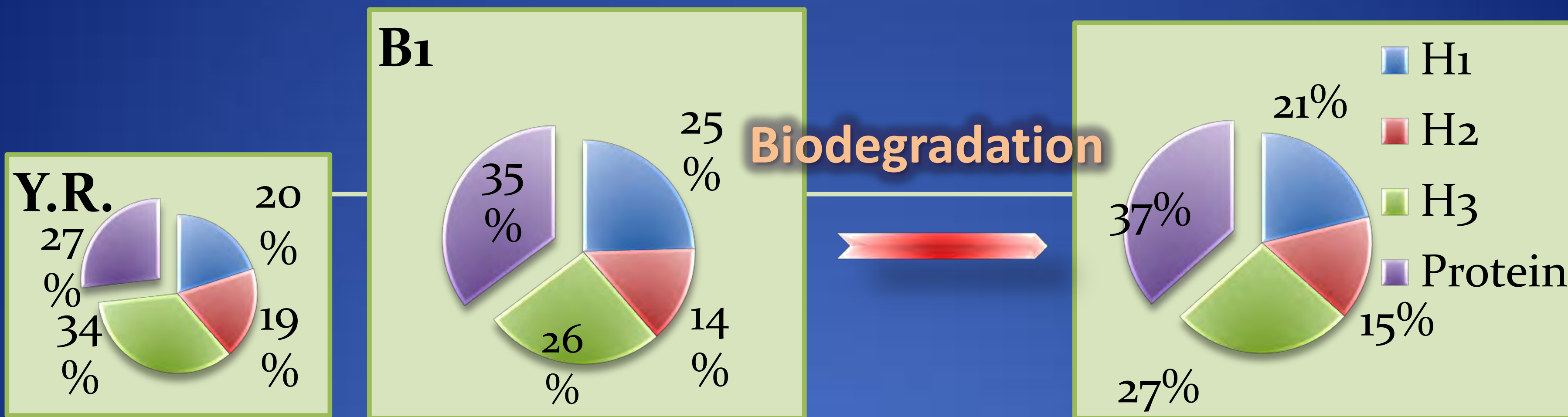


Bloom water: FE1, F1

- **Phytoplankton derived DOM**
- **BDOC:10-18uM *vs* 6.1μM (shelf water)**

Degradation of H

Allochthonous DOM



H1-marine derived/human activity ?

H2-terristrial derived-allochthonous; H3-terristrial derived/other…

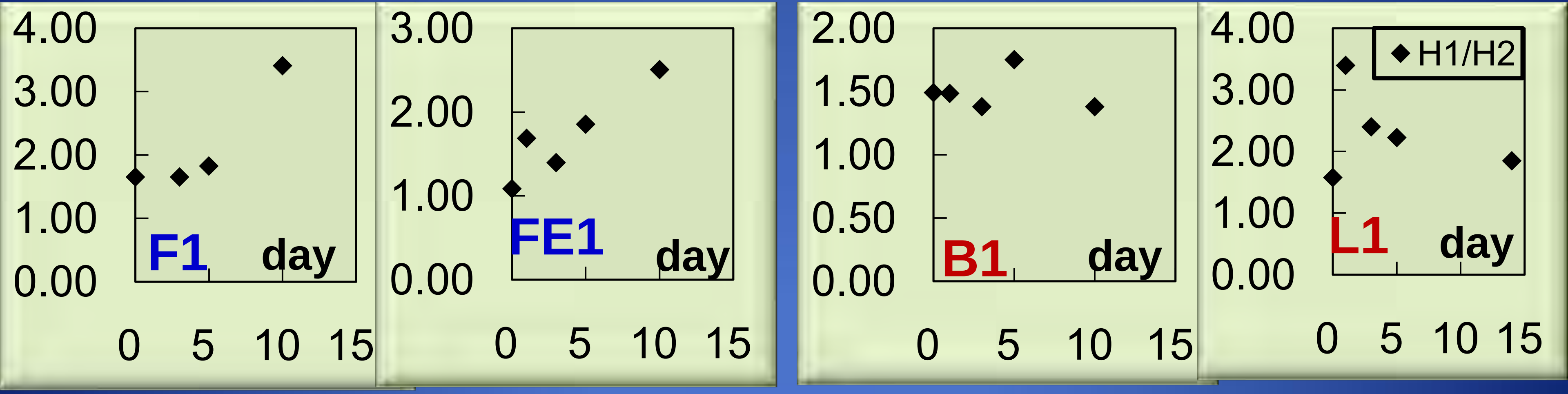
Y.R. Plume water: ***Y.R. Sal=0.1, B1 Sal=23.4,***

BDOC: 0-7.9μM *vs* 6.9μM (ocean water)

Selective Degradation of H

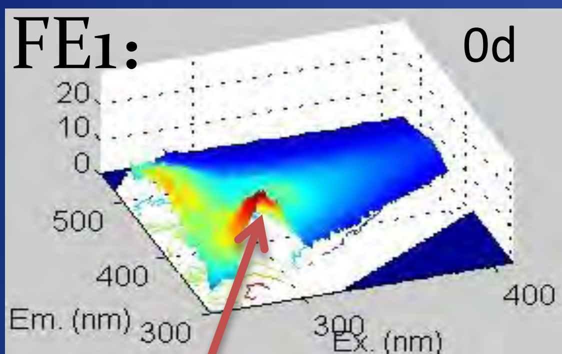
Source of Humic

Different biodegradation, production



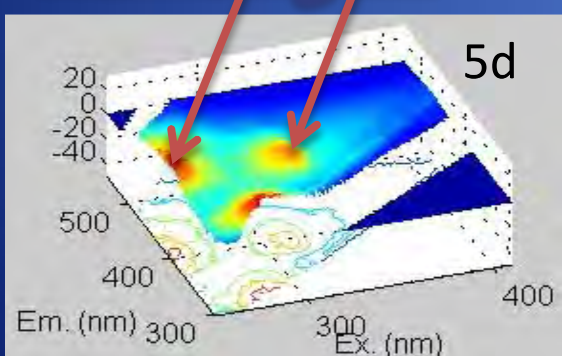
Production of RDOM

Transformation from protein to humic



Protein

Humic-H3 H1



Bacteria

DOM transformation

Bio-sequestration /biodegradation

Carbon cycle

Conclusion

▫BDOC of water masses is quite different from each other.

- DOC degradation rate varied from 0 to 0.027(d-1), lowest in Y.R., higher in bloom and shelf water(Taiwan current).

▫BDOC is influenced by the composition of DOM.

- BDOC higher protein peak, RDOC with higher humic peak.
- Biodegradation process is influenced by percent of bioavailable component.
- Production of RDOM by microorganism may contribute to inactive carbon pool.

The future research

Labile DOC

Bacteria

Respiration-DIC(CO_2)

1.Seasonal variation

50%?

2.Bacteria production

Limnol. Oceanogr., 40(2), 1995, 436–441

Quantifying the role of heterotrophic bacteria in the carbon cycle: A need for respiration rate measurements[1]

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PICES

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Thanks for your attention !