Hydrographic controls on marine organic matter fate and sedimentary microbial diversity in the western Irish Sea

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INFOMAR
Integrated Mapping for the Sustainable Development of Ireland's Marine Resource

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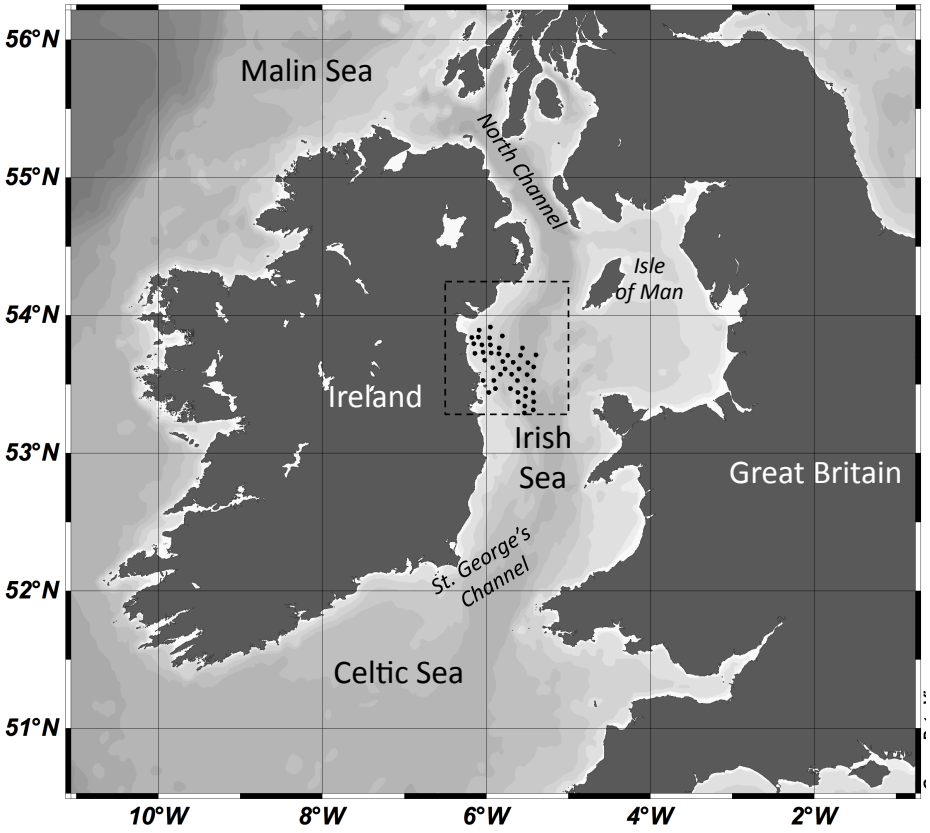
Introduction

- Coastal ocean - disproportionately important in global carbon cycle & biological productivity
- Human use – Shipping, ports, fishing, energy
- Complex & dynamic physical, chemical, biological processes
- Shallow semi-enclosed basin
- Oceanography & plankton ecology quite well studied
- Little known about organic matter (OM) and prokaryote ecology

Irish Sea



- **OM cycling – the key biological process in the marine environment**
- **Key role of prokaryotes recognised in recent years**

Western Irish Sea hydrographic zonation

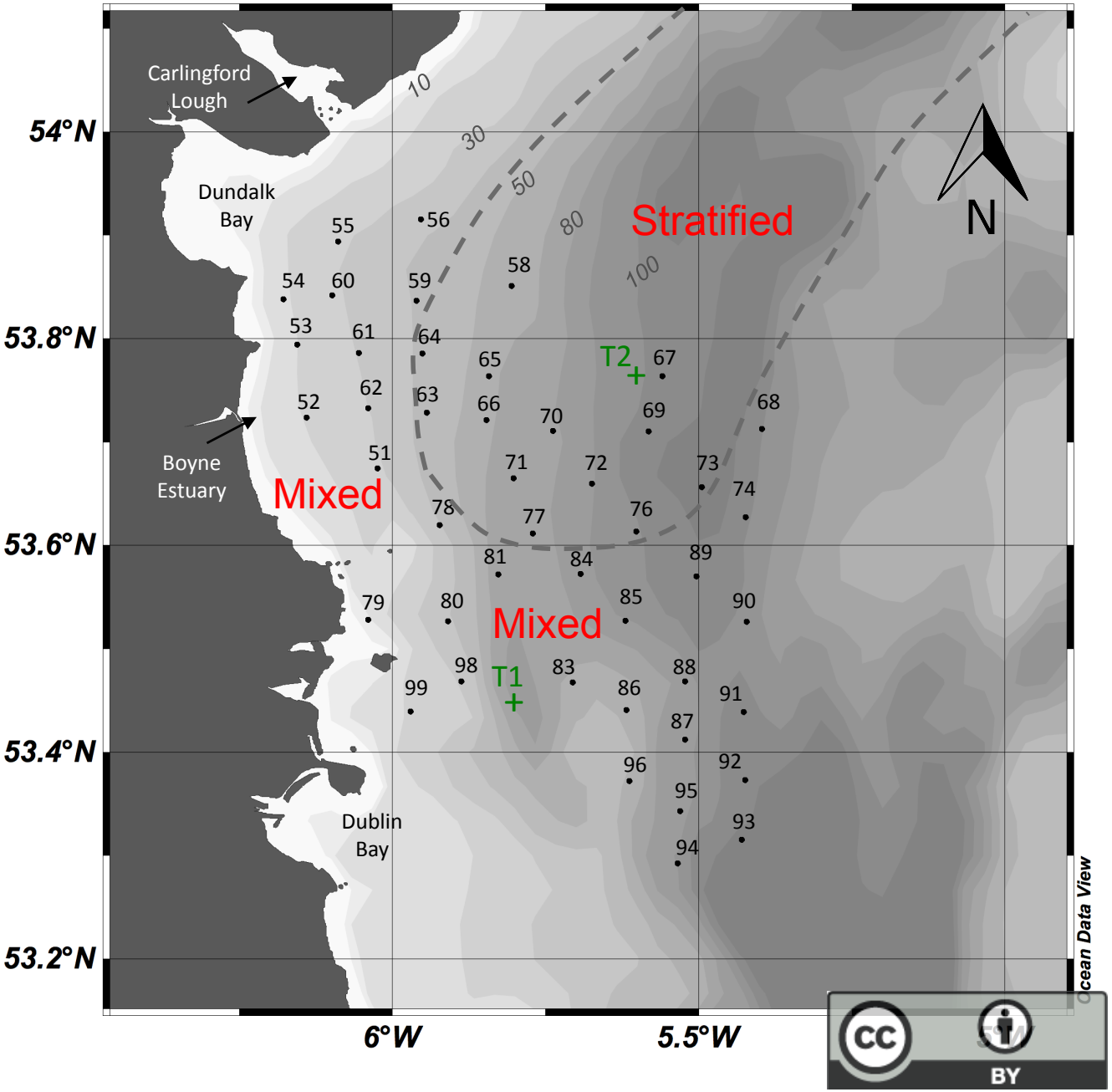
<u>Nearshore/south</u> =
dynamic, high-energy, vertically mixed

<u>Offshore</u>= deeper water, weaker tidal flow

Thermal stratification offshore causes ***annual gyre system***

- impacts Seasonal bloom & primary productivity
- April – Aug
- mixed > stratified

(Hill 1994,1996,1997; Gowen 1995; Dickey-Collas 1996,1997; Kennington 2006)



Questions & Objectives

- Composition & sources of sedimentary organic matter (SOM) in the Irish Sea
  - plankton detrital input
  - terrestrial input
- Sedimentary bacterial biomass abundance and community composition, roles in OM cycling
- Relationship between hydrographic regime and SOM and sedimentary bacterial communities

Approach

Bulk parameters

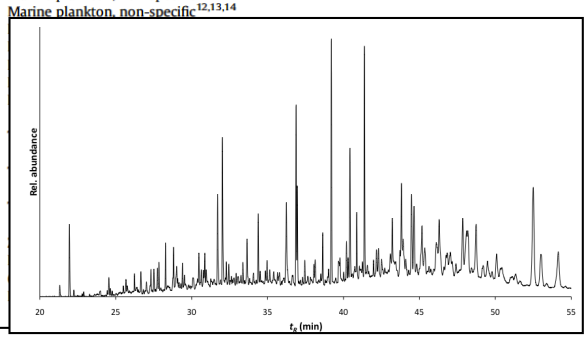
- Particle size, % sand, silt, clay,

  TOC, TN

Lipid biomarkers

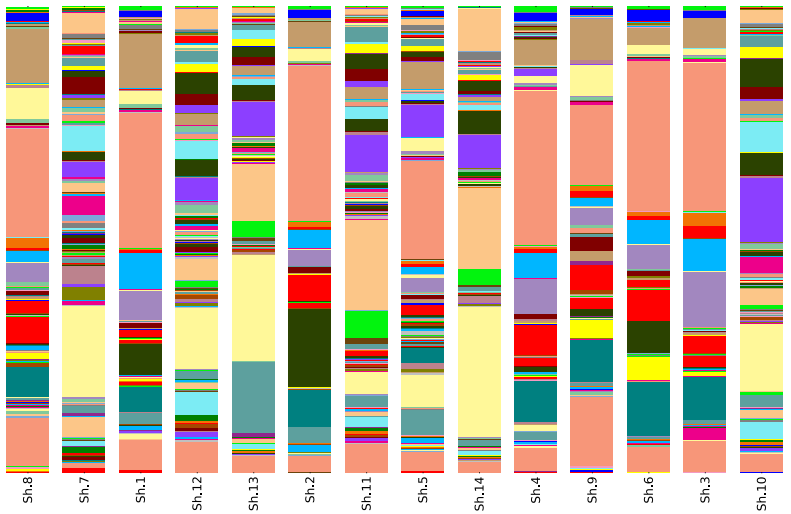
- marine input – phytoplankon, zooplankton sterols, fatty acids, wax esters, highly branched isoprenoids
- terrestrial input – vascular plant waxes lipids e.g. long chain *n*-alkanes and *n*-alkanols, plant sterols

Biomarker	Likely source
Sterols	
24-norcholesta-5, 22-dien-3β-ol	Zooplankton, degradation of phytoplankton sterols[1]
24-norcholesta-22-en-3β-ol	
22-trans-cholesta-5,22-dien-3β-ol	Zooplankton detritus[2]
trans-27-nor-24-methyl-cholest-22-en-3β-ol	Dinoflagellates[3], benthic invertebrates[4]
cholest-5-en-3β-ol	Macrofauna, zooplankton biomass/detritus[5]
5-α(H)-cholestan-3β-ol	Bacterial reduction of C_{27} stenols[6]
cholesta-5,24-dien-3β-ol	Marine phytoplankton, diatoms[5]
24-methylcholesta-5,22-dien-3β-ol	Marine phytoplankton, diatoms[1,7]
24-methylcholesta-22-en-3β-ol	Marine invertebrates (sponges)[8], phytoplankton[9]
24-methylcholesta-5-en-3β-ol	Higher plants[10], green algae[1]
24-methyl-5-α(H)-cholestan-3β-ol	Bacterial reduction of C_{28} stenols[6]
24-methylcholesta-5-24(28)-dien-3β-ol	Diatoms, marine phytoplankton[1,7]
24-ethylcholesta-5,22-dien-3β-ol	Terrestrial higher plants[10], some marine algae[11]
24-ethylcholesta-5-en-3β-ol	Terrestrial higher plants[10], some marine algae[11]
24-ethylcholesta-5,24(28)-dien-3β-ol	Green microalgae[1]
4α,23,24-trimethyl-5α-cholesta-22-en-3β-ol	Dinoflagellates[1,5]
Phospholipid fatty acid	
Saturated straight chain fatty acids	Marine plankton, non-specific[12,13,14]
Monounsaturated straight chain fatty acids	Marine plankton, non-specific[12,13,14]
Polyunsaturated fatty acids	
Branched (and cyclic fatty acids)	
Eicosapentaenoic acid	
Docosahexaenoic acid	
9-cis-hexadecenoic acid	
11-cis-octadecenoic acid	
Long chain odd carbon *n*-alkanes (C_{25} to C_{33})	
Long chain even carbon *n*-alcohols (C_{26} to C_{32})	
n-alkane carbon preference index	
n-alkanol carbon preference index	
Friedelan-3-one	
Urs-12-en-3β-ol	
Wax esters (C_{28} to C_{34})	
C_{25} Highly branched isoprenoids	
3,7,11,15-tetramethyl-2-hexadecen-1-ol	
2, 6, 10, 14-trimethylpentadecane	
2,6,10,14-tetramethylhexadecane	

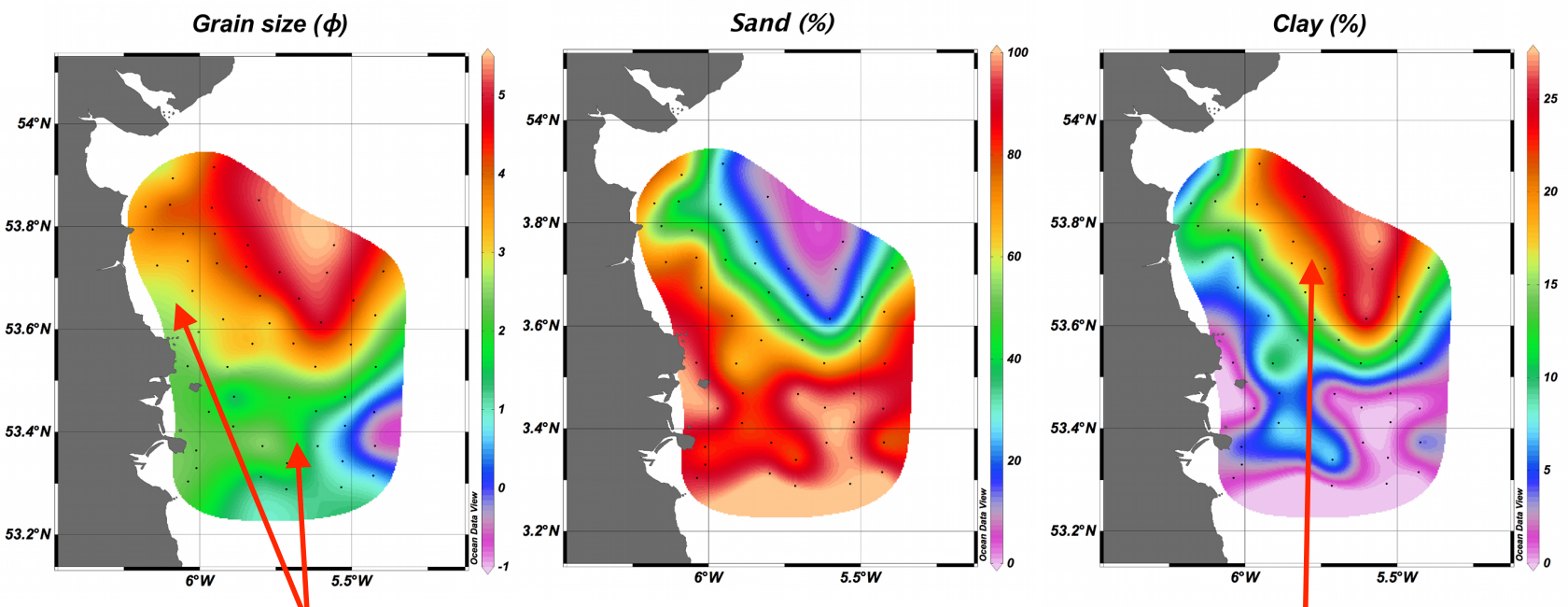


Bacterial biomarkers &16S rRNA community analysis

- bacterial phospholipid fatty acids
- DGGE and pyrosequencing

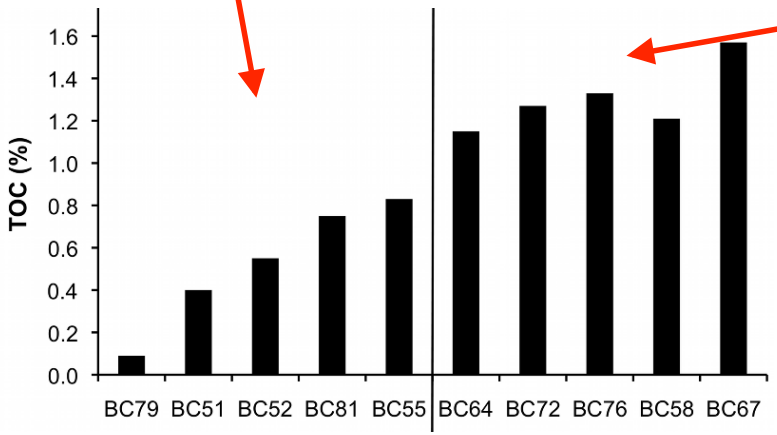


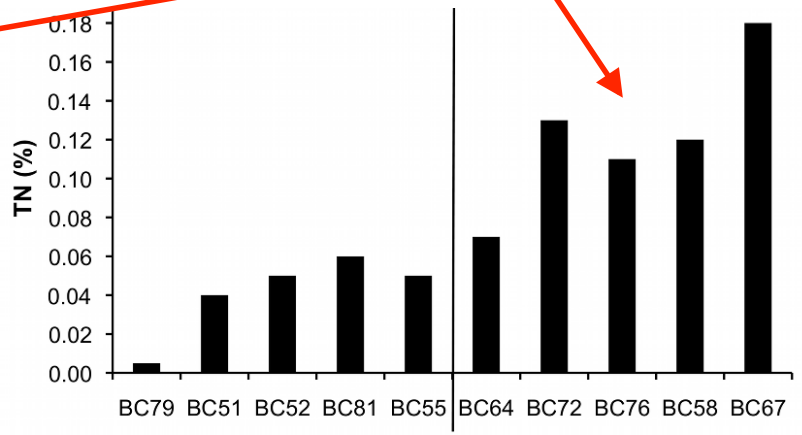
The sedimentary setting



Dynamic, non-depositional, sand

Depositional, mud





Phytodetritus input to sediments

- $C_{28}\Delta^{5,22}$, $C_{28}\Delta^{5,24(28)}$ sterols, C_{25} HBIs - → **Diatoms**

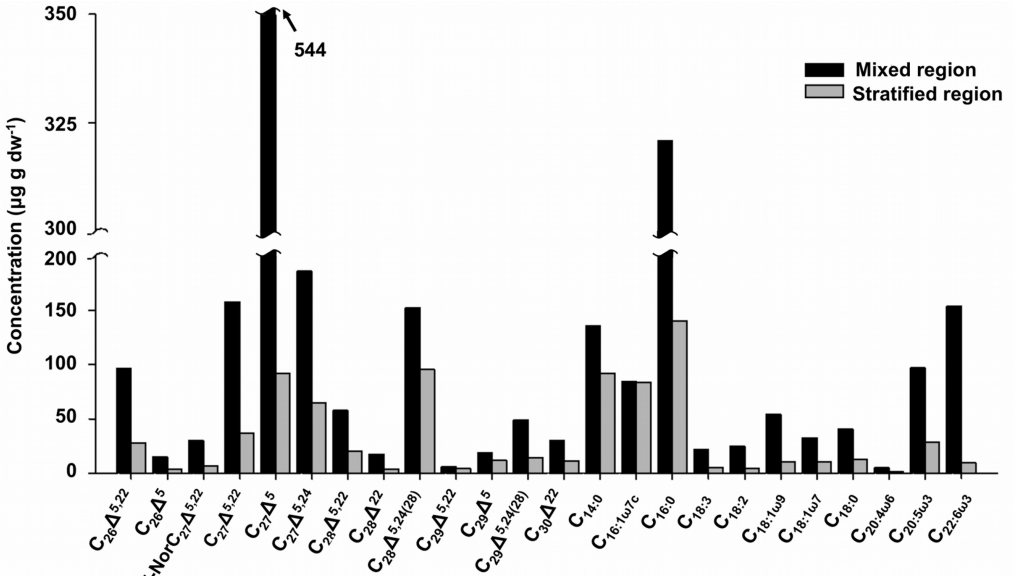
$C_{30}\Delta^{22}$ → **Dinoflagellates**

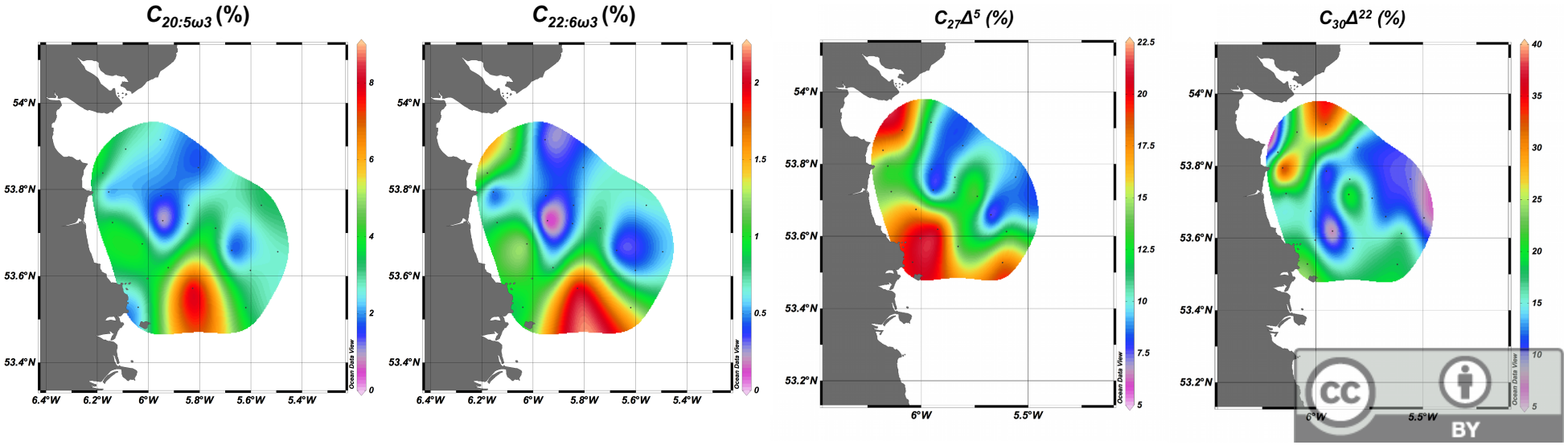
$C_{26}\Delta^{22}$, $C_{26}\Delta^{5,22}$ $C_{27}\Delta^{5}$, wax esters – → **copepod zooplankton**

↑ algal biomass in mixed waters

  - copepod zooplankton

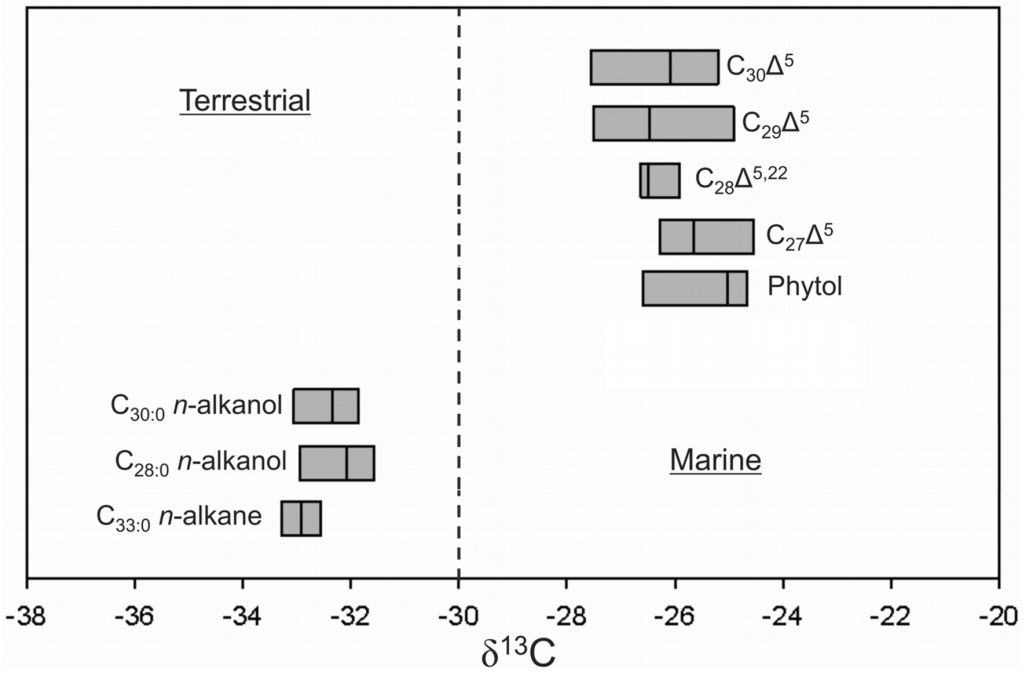
↑ relative fresh detrital input in mixed region

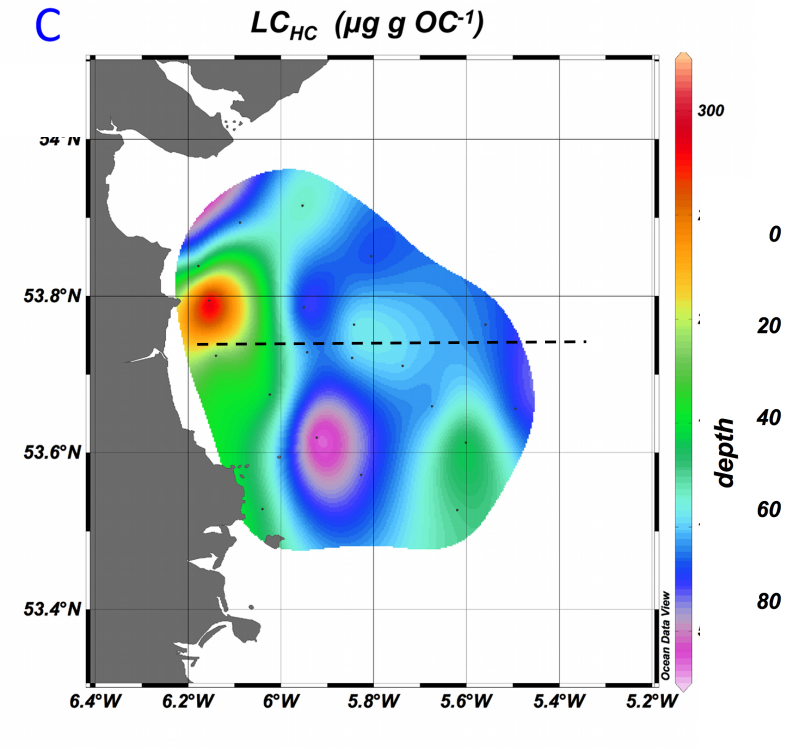


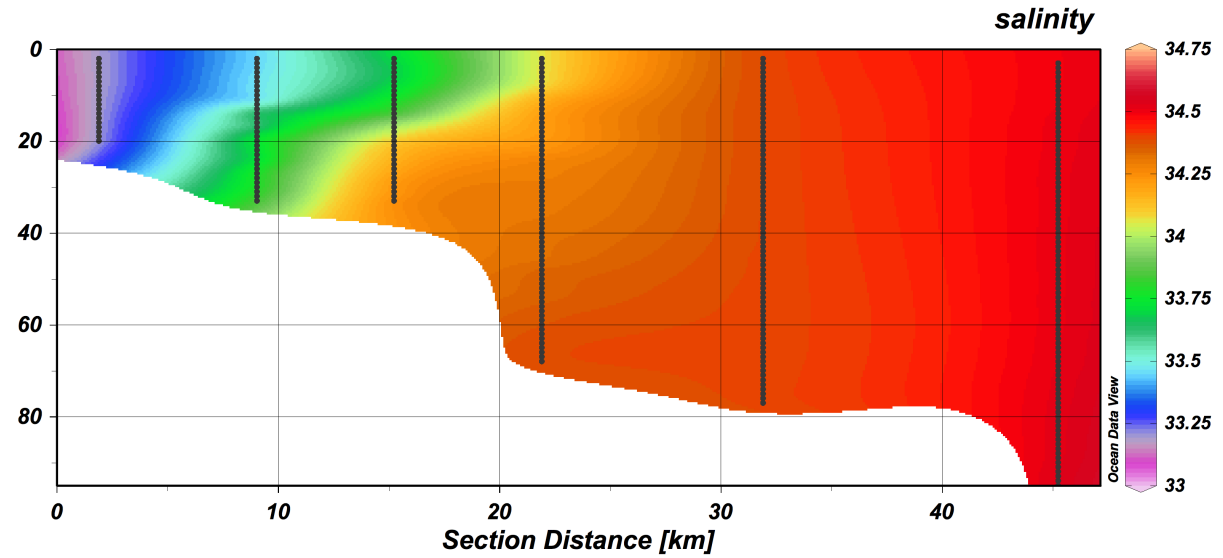


Terrestrial input

- Plant wax alkanes/alkanols abundant
- Terrestrial $\delta^{13}C$ signature
- Riverine input - Boyne Estuary
- Preferential deposition in nearshore sandy muds, less terrestrial influence offshore

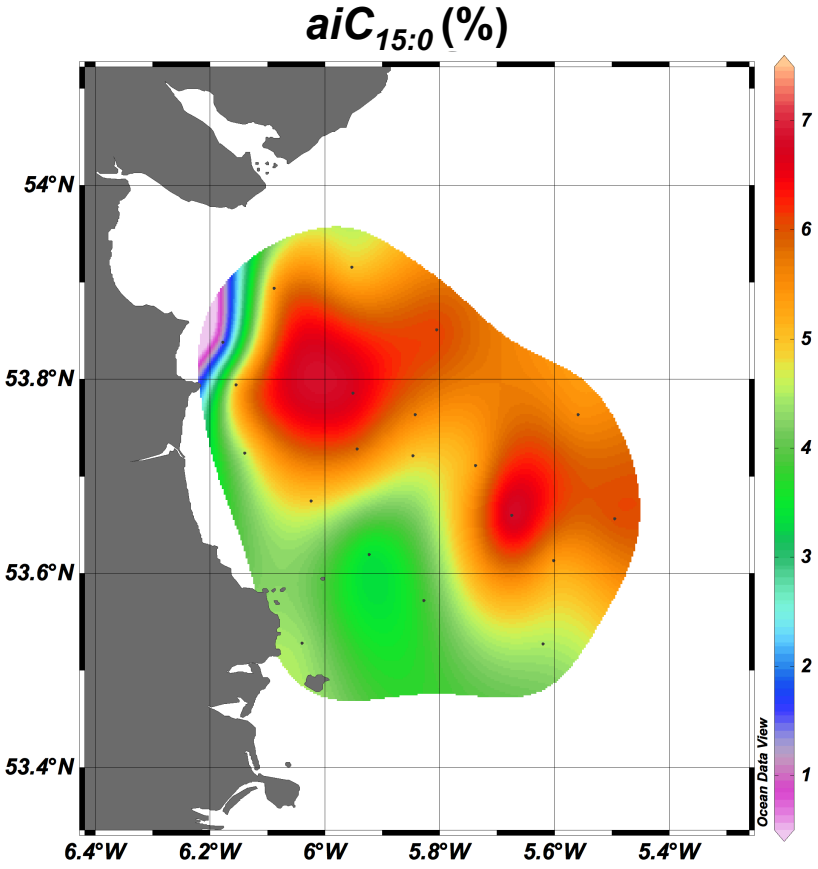


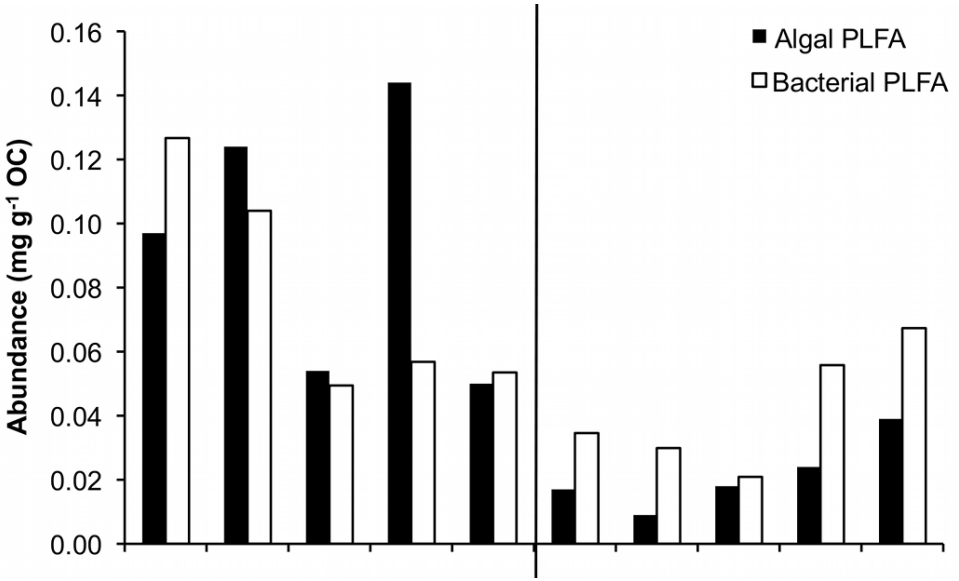




Bacterial biomass distribution

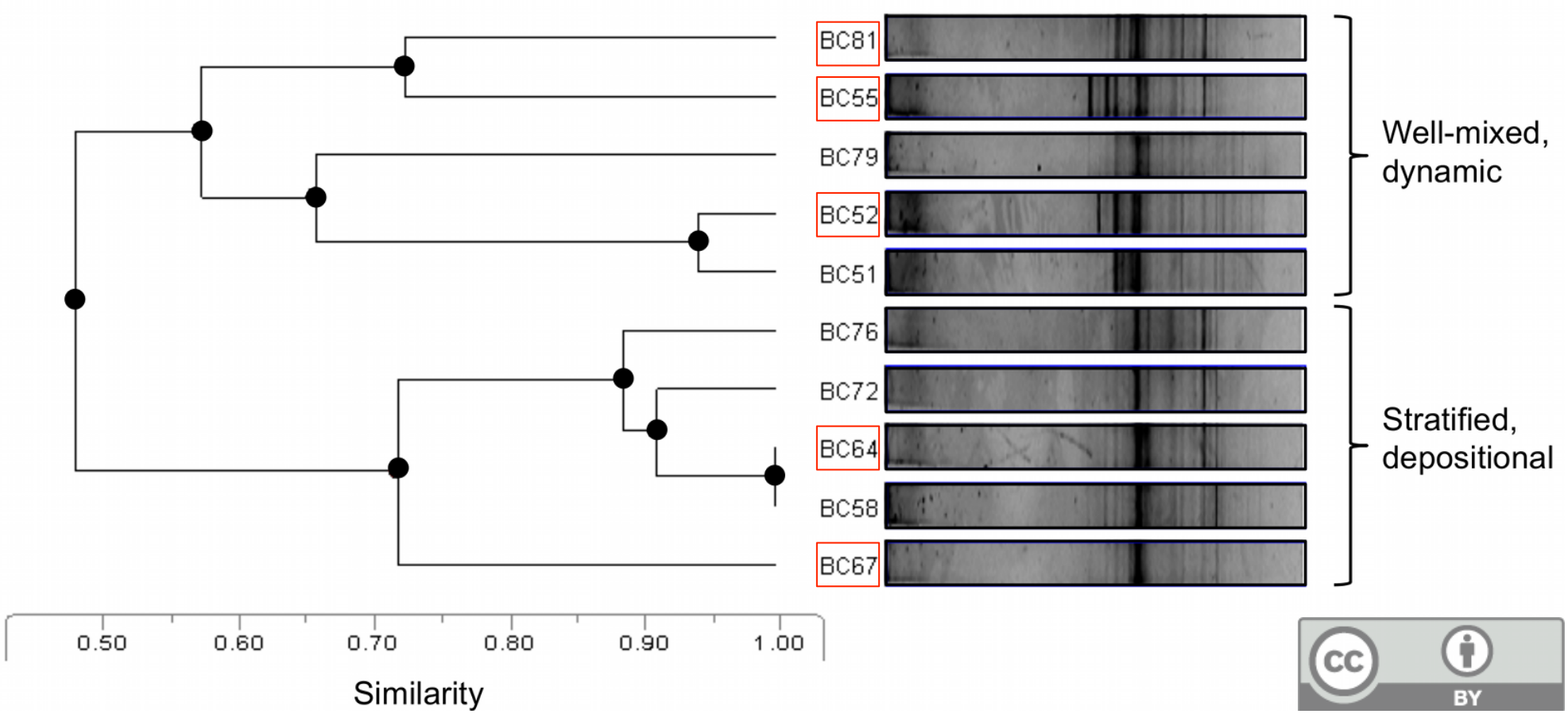
- Higher abundance in muddy sediments offshore
- Per g OC, greater contribution of bacteria in mixed region, as with phytodetritus input





Sedimentary bacterial communities

- Distinct bacterial communities
- Higher community similarity offshore
- Higher heterogeneity in mixed setting
    - due to dynamic environmental conditions?



Bacterial community composition

53% Flavobacteria, Clostridia, γ-proteobacteria

(δ-proteobacteria = 23%)

Clostridia: *Tepidibacter*

Flavobacteria: *Lutimonas*

γ-proteobacteria: Marinicellales

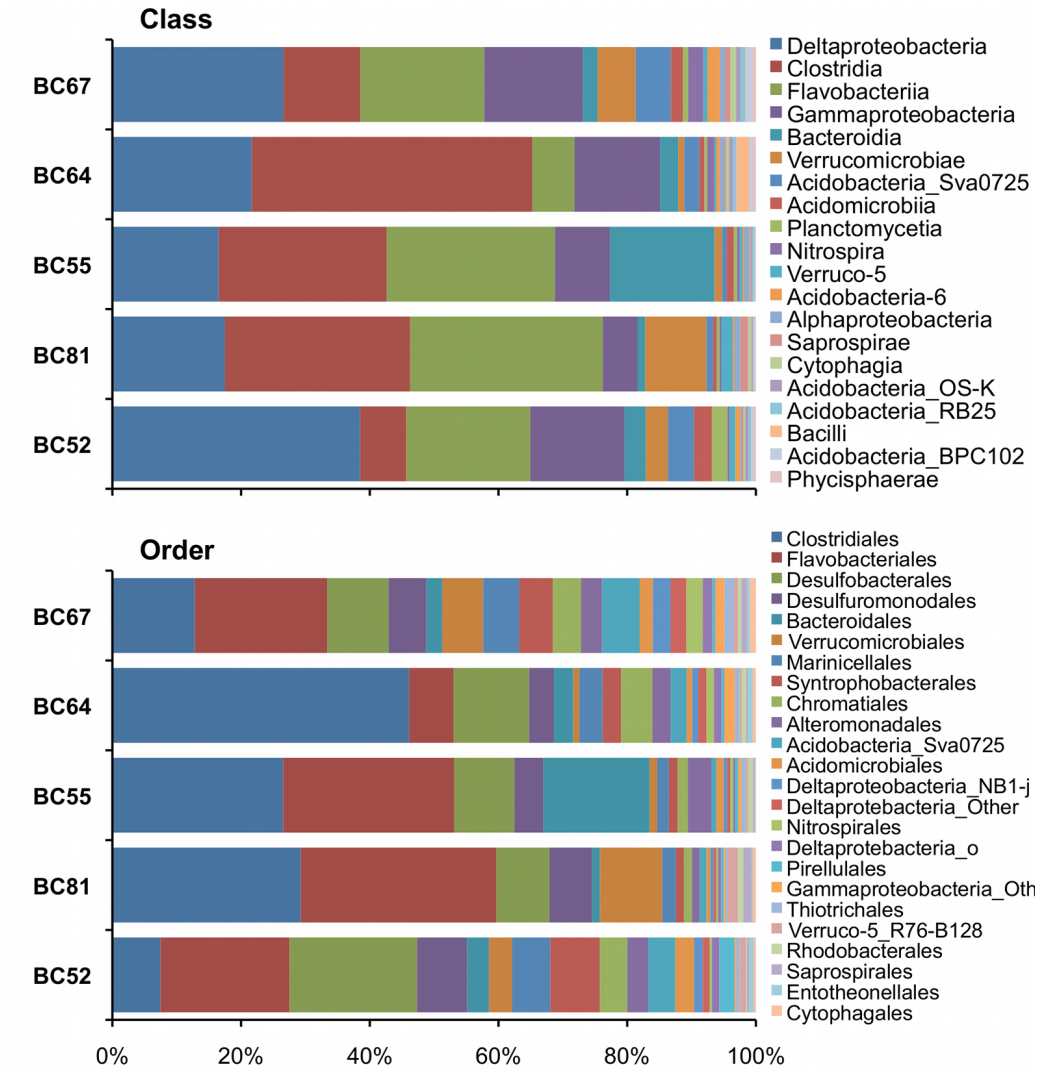
Psychromonadaceae

- Organoheterotrophs

- High productivity coastal settings

- Degradation of phytodetritus

(Kirchman 2002; Zinger 2011)



Summary

1. Plankton bloom is a major OM source to surface sediments

   - OM sourced from by diatoms, dinoflagellates & copepods

2. Significant riverine input of terrestrial OM, concentrated in nearshore muddy sediments

3. Hydrographic regime impacts

   - sedimentary OM composition and abundance
   - bacterial community abundance and diversity

4. Bacterial community specialised in fresh phytodetritus mineralisation

5. Coupling between water column productivity and sedimentary productivity/activity

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