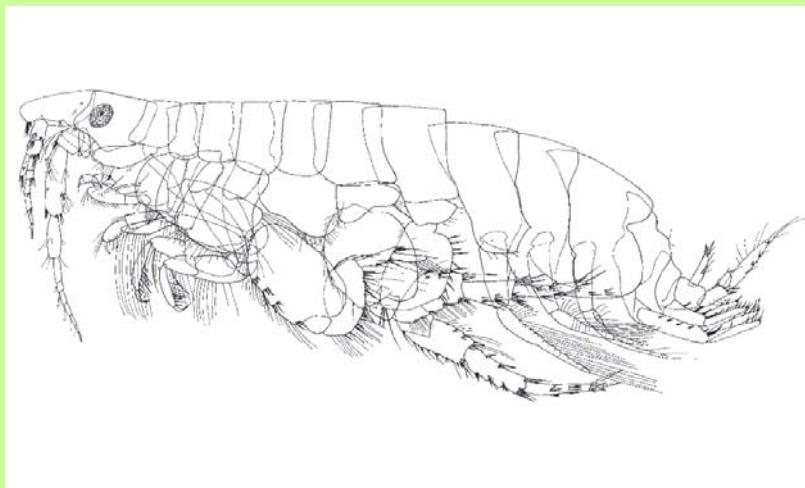


# Research into the distribution of the genus *Bathyporeia* (Crustacea, Amphipoda) by means of molecular markers.

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From d'Udekem d'Acoz, 2004

# **Bathyporeia: classification**

Ordo Amphipoda

Subordo Gammaridae

Superfamily Gammaroidea (16 families)

Family Bathyporeiidae BOUSFIELD & SHIH 1994

Genus Bathyporeia LINDSTRÖM 1855

- B. borgi* d'Udekem d'Acoz & Vader, 2005
- B. chevreuxi* d'Udekem d'Acoz & Vader, 2005
- B. cunctator* d'Udekem d'Acoz & Vader, 2005
- B. elegans* Watkin, 1938**
- B. elkaimi* d'Udekem d'Acoz & Menioui, 2004
- B. gladiura* d'Udekem d'Acoz & Vader, 2005
- B. gracilis* G. O. Sars, 1891
- B. griffithsi* d'Udekem d'Acoz & Vader, 2005
- B. guilliamsoniana* Bate, 1857**
- B. ledoyerii* d'Udekem d'Acoz & Menioui, 2004
- B. lindstromi* Stebbing, 1906
- B. microceras* d'Udekem d'Acoz & Menioui, 2004
- B. nana* Toulmond, 1966
- B. parkeri* Bousfield, 1973
- B. pelagica* Bate, 1857**
- B. phaiophtalma* Bellan-Santini, 1973
- B. pilosa* Lindström, 1855**
- B. quoddyensis* Shoemaker, 1949
- B. sarsi* Watkin, 1938**
- B. tenuipes* Meinert, 1877
- B. watkini* d'Udekem d'Acoz, Echchaoui & Menioui, 2005

Genus Amphiporeia SHOEMAKER 1929

Family Pontoporeiidae DANA 1853

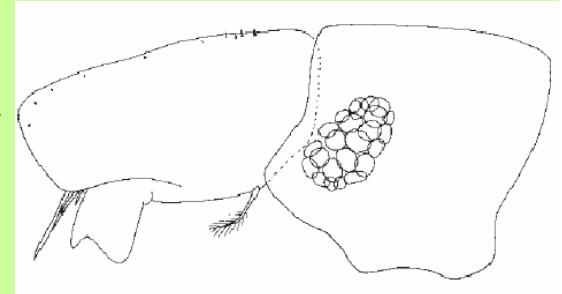
Genus Diporeia BOUSFIELD 1979

Monoporeia BOUSFIELD 1979

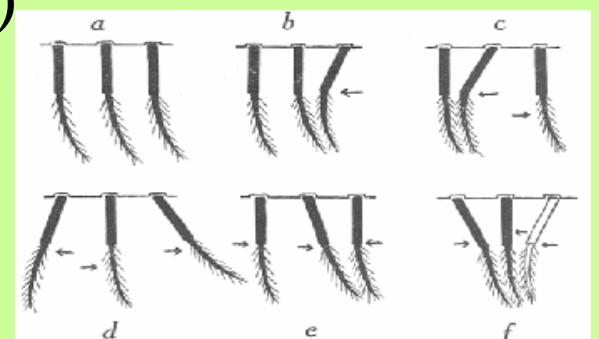
Pontoporeia KROYER 1842

# Introduction (1)

- Macrofauna species
- Pseudorostrum
  - basal part of the peduncle of the first antenna
  - extended along vertical axis
  - geniculate articulation with second article
- Digging species, restricted to sandy bottoms
  - Very fine well-sorted sands
  - < 5-10% silt (except for *B. pilosa*)
  - 90% in first 5 cm, not deeper than 12 cm
- Swimming and digging (Watkin, 1939)
  - pleopods (metachronal rhythm)

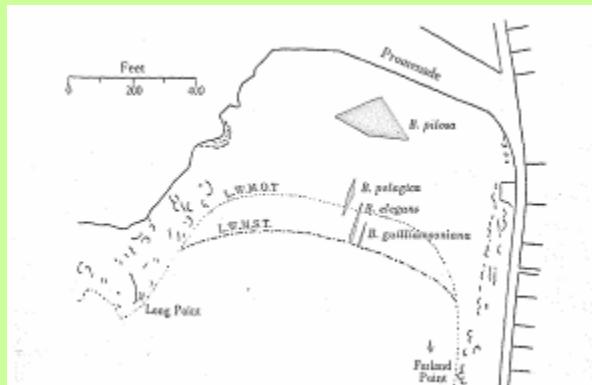


From d'Udekem d'Acoz, 2004

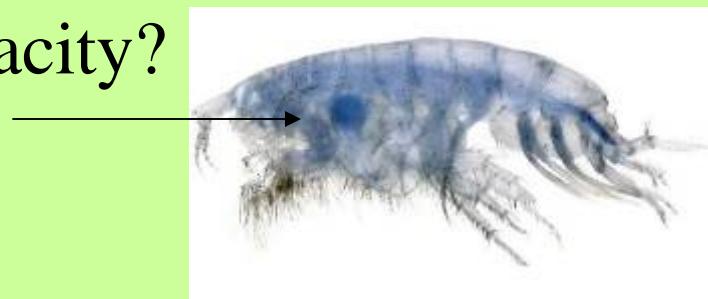


# Introduction (1)

- Atlantic species, not in tropical and south part of West Atlantic
- Selective depositfeeders: micro-organisms, detritus
- Zonation (Watkin, 1939)
  - Not all species present on every shore



- breeders: limited dispersal capacity?



[http://en.wikipedia.org/wiki/Brood\\_pouch\\_%28Peracarida%29](http://en.wikipedia.org/wiki/Brood_pouch_%28Peracarida%29)

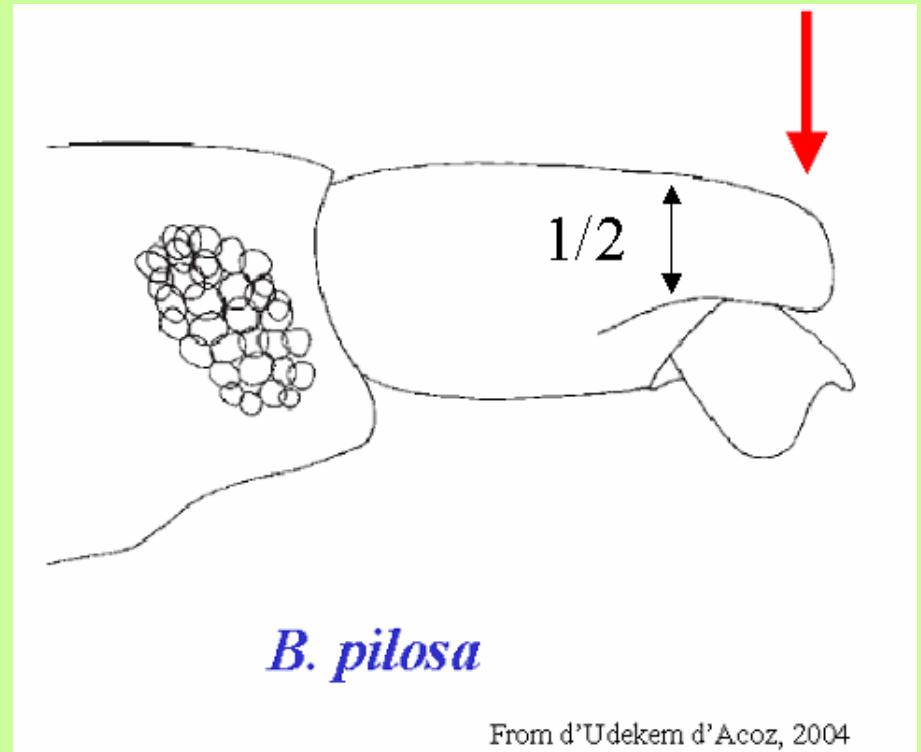
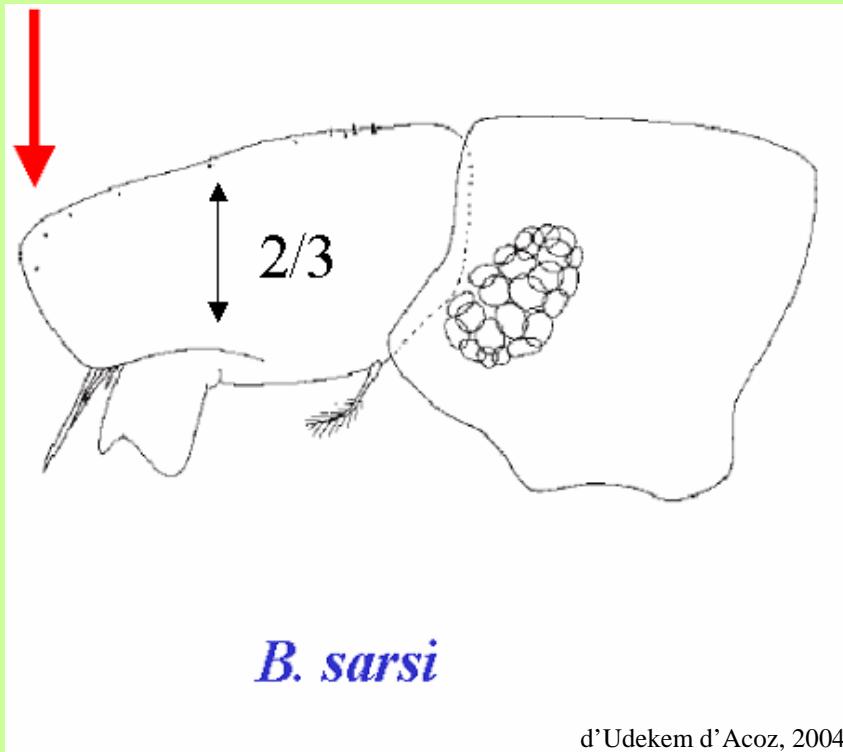
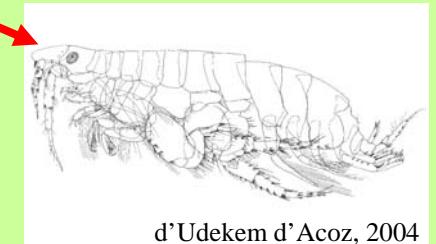
# Introduction (2)

- problems concerning **correct taxonomic identification**
  - taxonomic identification of amphipods is complex, great expertise is needed for a correct species identification (Costa *et al.*, 2004)
    - genus *Bathyporeia*: one of the most problematic taxa concerning species identification (d'Udekem d'Acoz, 2004)

# Introduction (2)

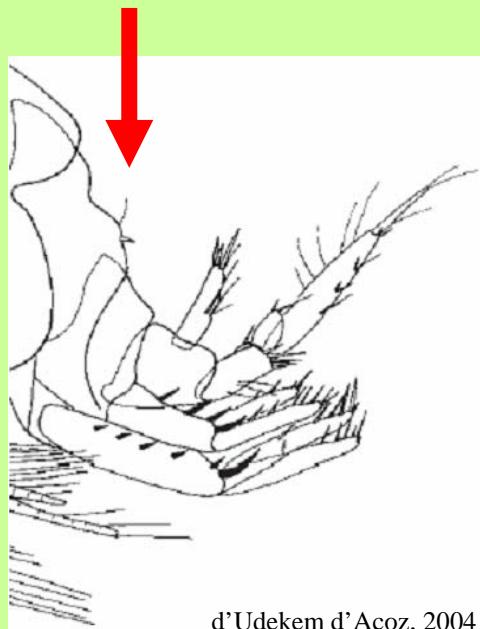
Distinction between intertidal species:

- shape of pseudorostrum
- implantation first antenna

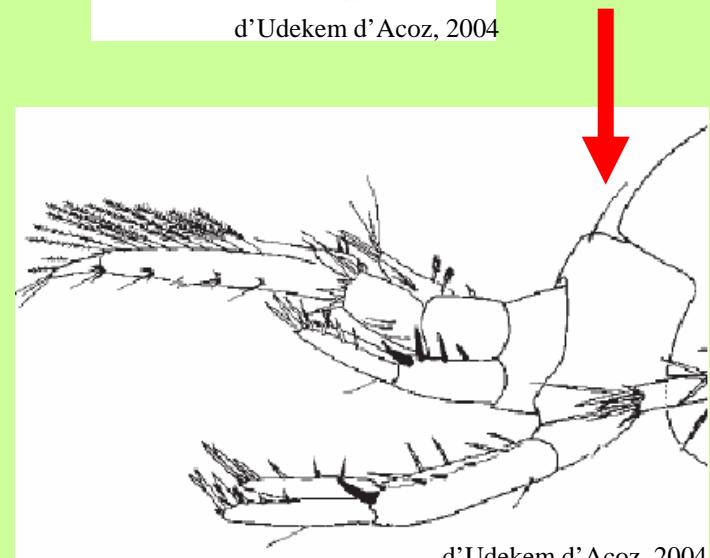
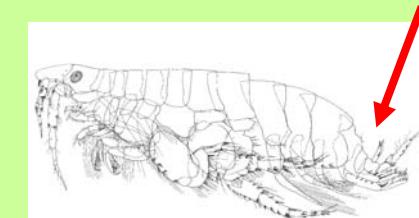


# Introduction (2)

Distinction subtidal – intertidal species:  
posteriorly directed spines on first urosomite



*B. elegans*



*B. sarsi*

From d'Udekem d'Acoz, 2004

# Introduction (3)

- problems concerning **correct taxonomic identification**
  - presence of **cryptic species?** (d'Udekem d'Acoz & Vader, 2005)  
→ *B. tenuipes* complex: *B. tenuipes*, *B. chevreuxi*, *B. cunctator* & *B. lindstromi*

# Introduction (3)

## CRYPTIC SPECIES

= “*two or more distinct species that are erroneously classified (and hidden) under one species name*”  
(Bickford *et al.*, 2007)

- several reasons:
  - non-visual mating signals: differences in mating pheromones or mating calls
  - morphological stasis: stabilizing selection on morphology due to extreme environmental conditions
- Can be identified using **molecular tools** because they are genetically different

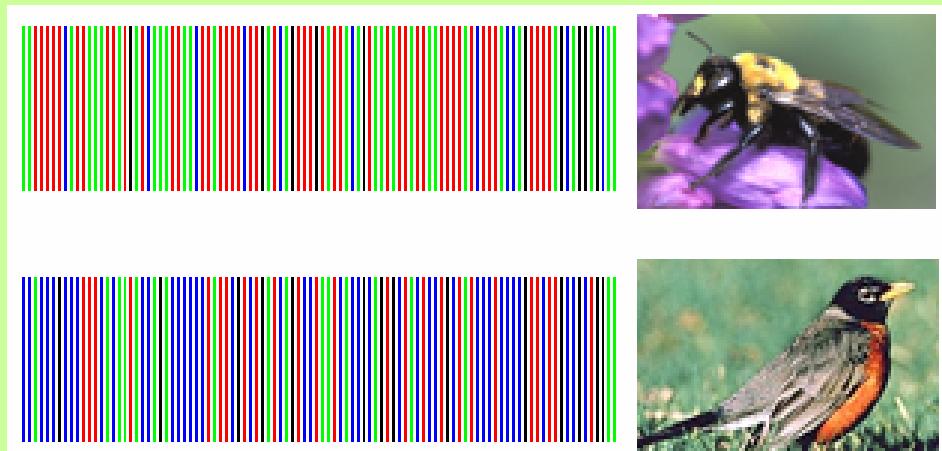
# Introduction (3)

Use of molecular data to:

- identify species within the genus using DNA: **DNA-barcoding**
- distinguish morphologically identical species or cryptic species

# Introduction (3)

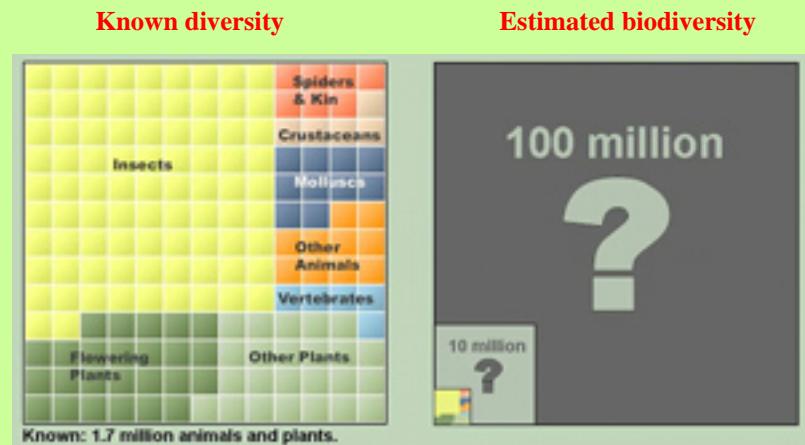
- **DNA-barcoding:** standardized approach to identify plants and animals using minimal DNA sequences, called DNA-barcodes
- **DNA-barcode:** short DNA-sequence, from a uniform locality on the genome, used for identifying species



# Introduction (3)

## Why use DNA-barcoding?

- quickly and cheaply recognize known species
- discovery of not yet known species
- new tools for appreciating and managing Earth's biodiversity

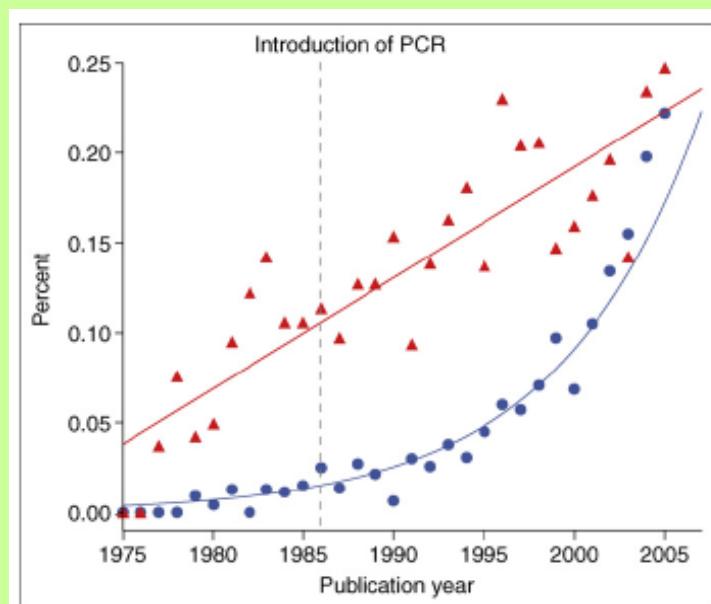


identify quickly and accurately the species of a specimen whatever its condition (egg, larva..)

<http://phe.rockefeller.edu/barcode/>

# Introduction (3)

- Molecular techniques highlighted that biodiversity can be strongly underestimated based only on morphological identification
- Increased recognition of cryptic species since mid 1980s (Bickford *et al.*, 2007; 'Trends in Ecology & Evolution')

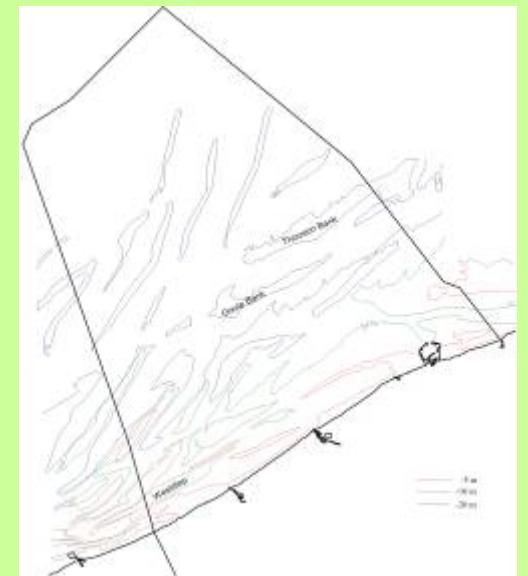


# General Objectives

- (1) Can molecular tools be used to identify the different species and eventually discover cryptic species within this genus?
- (2) Get insight in the degree of genetic variability within the genus
- (3) Get insight in the degree of genetic structuring between and within the intertidal species of the *Bathyporeia* genus.
  - Differences in population genetic structure?
  - Exchange of genetic material limited by absence of a pelagic larva?
  - Cap Griz Nez, harbour of Zeebrugge: barriers?

# Materials & Methods (1)

- Collecting intertidal samples along the French-Belgian-Dutch coast and subtidal samples on three sandbanks: Westdiep, Thornton bank, Goote bank
  - Intertidal: digging and sieving
  - Subtidal: Belgica – van Veen grab



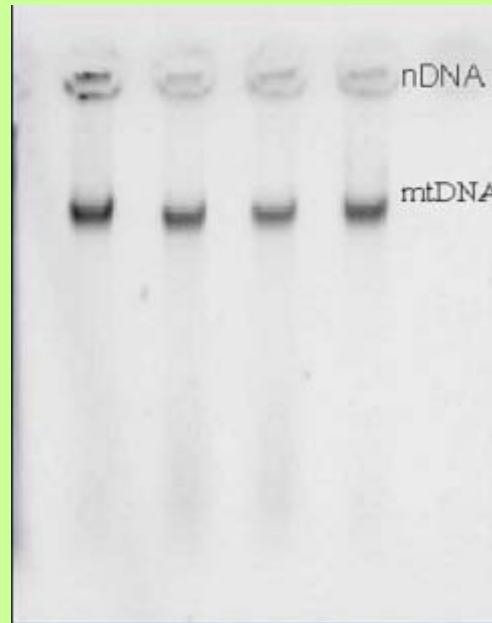
# Materials & Methods (2)

Morphological identification of the collected samples: *B. pilosa*, *B. sarsi*, *B. pelagica*, *B. elegans* & *B. guilliamsoniana*

Molecular analysis:

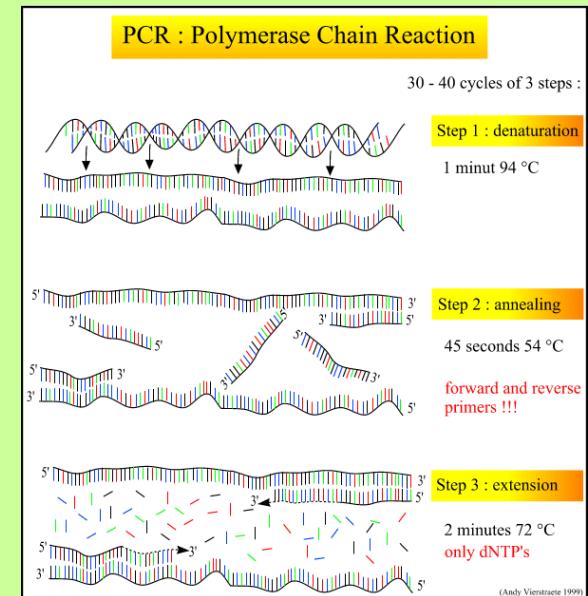
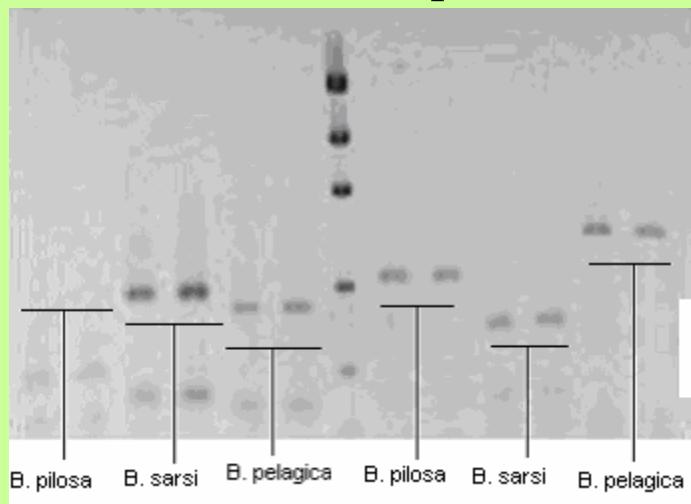
-DNA extraction

\*CTAB extraction using phenol  
\*Qiagen Dneasy kit  
\* Bionobile QuickPick SML gDNA



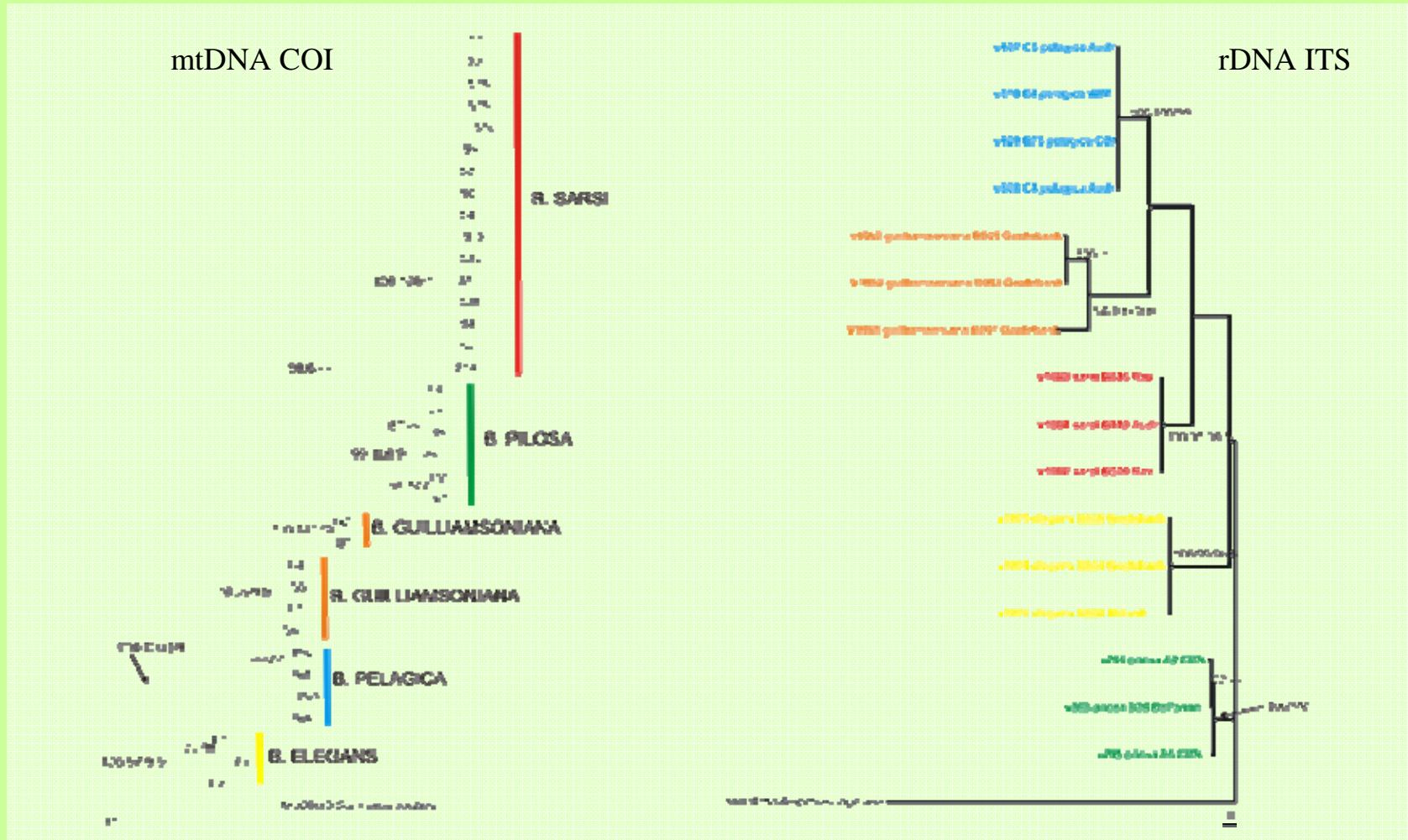
# Materials & Methods

- Molecular analysis:
  - DNA amplification: mitochondrial COI gene (“barcoding marker”) and nuclear ITS
  - DNA sequencing
  - RFLP analysis
    - Restriction enzymes MboI and AluI
    - Distinction between intertidal species



# Results & Discussion (1)

- Phylogenetic patterns within the genus



# Results & Discussion (1)

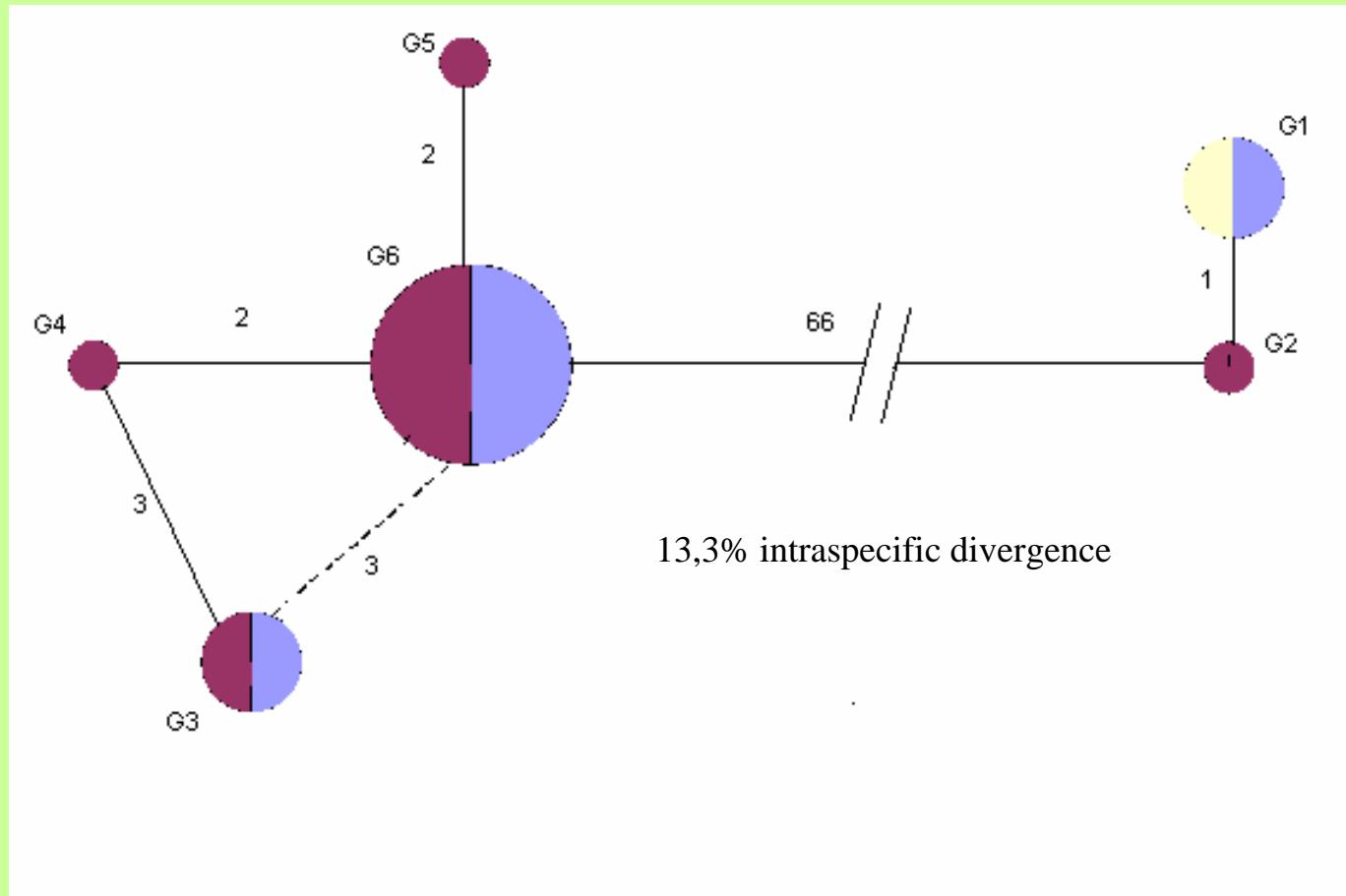
- Phylogenetic patterns within the genus
  - COI and ITS: at least 5 divergent clades → COI useful for DNA barcoding
  - Genetic divergence between different species varying between 12,4 and 20%

	<i>B. pelagica</i>	<i>B. sarsi</i>	<i>B. pilosa</i>	<i>B. guilliamsoniana</i>	<i>B. elegans</i>
<i>B. pelagica</i>	<b>0,7</b>	<b>19,3</b>	<b>17,3</b>	<b>14,3</b>	<b>20</b>
<i>B. sarsi</i>	20	<b>0,8</b>	<b>13,1</b>	<b>13,6</b>	<b>12,4</b>
<i>B. pilosa</i>	18,6	14,5	<b>2</b>	<b>12,4</b>	<b>18,3</b>
<i>B. guilliamsoniana</i>	18,9	18,2	17,6	<b>8,4</b>	<b>15</b>
<i>B. elegans</i>	21,1	19,2	20	20	<b>1,5</b>

# Results & Discussion (1)

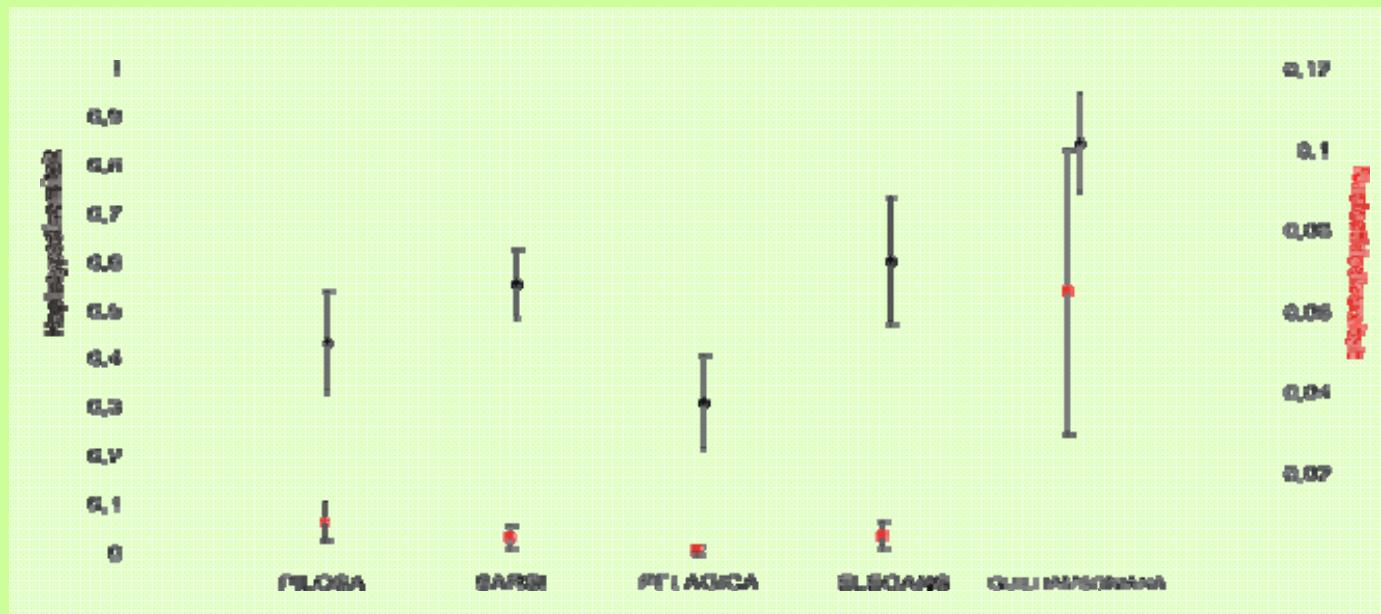
- Phylogenetic patterns within the genus
  - COI and ITS: at least 5 divergent clades → COI useful for DNA barcoding
  - Large diversity within *B. guilliamsoniana*
    - \*Morphologically: one species
    - \*Two distinct groups supported by high bootstrap values
    - \*High sequence divergence within the ‘species’

	<i>B. pelagica</i>	<i>B. sarsi</i>	<i>B. pilosa</i>	<i>B. guilliamsoniana</i>	<i>B. elegans</i>
<i>B. pelagica</i>	<b>0,7</b>	19,3	17,3	14,3	20
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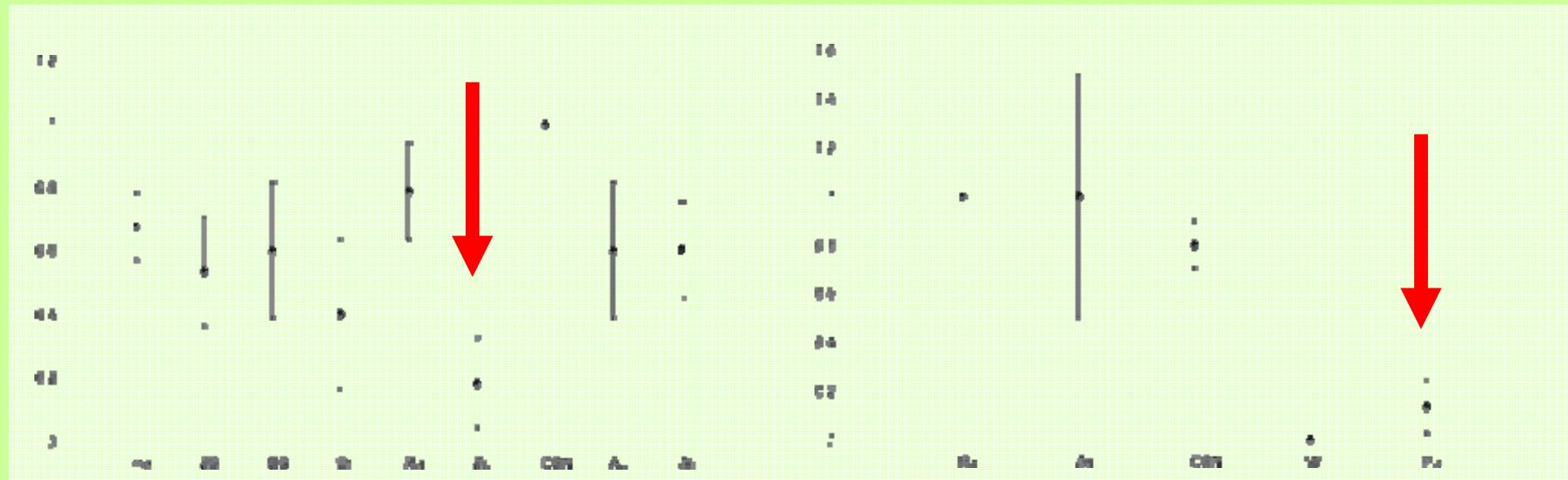
# Results & Discussion (2)

- Patterns of genetic diversity:
  - Intertidal species: higher diversity for *B. sarsi* than for *B. pilosa* → zonation on the beach?
  - Higher diversity within subtidal species than within intertidal species → habitat stability?



# Results & Discussion (3)

- Population-genetic structure *B. pilosa* – *B. sarsi*
  - Lower haplotype diversity in De Panne & Zuydcoote  
→ bottleneck or selective sweep?



# Results & Discussion (3)

- **Analysis of Molecular Variance (AMOVA):** variation mainly explained through differences **within** populations
- ***B. pilosa*:** 18,7% variation observed between populations
  - subtle spatial structure present
- ***B. sarsi*:** <7% of variation between populations, **no significant spatial structuring.**
- **Link between zonation on the beach and dispersal capacity?**

# Conclusions

- Using molecular markers, the different species can be distinguished → COI can be used as a DNA-barcode within this genus
- Genetic diversity within *B. guilliamsoniana* → cryptic species?
- Link between distribution and genetic diversity.
- Link between zonation on the beach and dispersal capacity.