Vegetación marina alrededor del mundo: Patrones, importancia y evolución

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Macroalgae / Seaweeds
Patrones


Antarctic Marine Flora

Small forms of *Fucus* from the European coasts
Sampling area
Updated checklist of Deception Island

76 species

- 39 Rhodophyta
- 19 Phaeophyceae
- 18 Chlorophyta

63.3% of the known Antarctic flora

New cites for the Deception marine flora

1. *Austropugetia crassa* R. L. Moe
2. *Delisea pulchra* (Greville) Montagne
3. *Leniea lubrica* R. L. Moe
4. *Pantoneura plocamioides* Kylin
5. *Porphyra plocamiestris* R. W. Ricker
6. *Chordaria linearis* (J. D. Hooker & Harvey) A. D. Cotton

BCN-Phyc Herbarium
(Plant Biodiversity Resource Centre of the University of Barcelona).

Antibiotic properties of macroalgae from Antarctica

Methodology
## Antibiotic properties of macroalgae from Antarctica

### Methodology

<table>
<thead>
<tr>
<th>Microorganisms used in the antibiotic assay</th>
<th>Antarctic</th>
<th>Microorganism Type</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Psychrobacter</em> sp.</td>
<td>Gram -</td>
<td></td>
</tr>
<tr>
<td><em>Paracoccus</em> sp.</td>
<td>Gram -</td>
<td></td>
</tr>
<tr>
<td><em>Arthrobacter</em> sp. (A)</td>
<td>Gram +</td>
<td></td>
</tr>
<tr>
<td><em>Arthrobacter</em> sp. (B)</td>
<td>Gram +</td>
<td></td>
</tr>
<tr>
<td><em>Oceanobacillus</em> sp.</td>
<td>Gram +</td>
<td></td>
</tr>
<tr>
<td><em>Bacillus aquamaris</em></td>
<td>Gram +</td>
<td></td>
</tr>
<tr>
<td><em>Micrococcus</em> sp.</td>
<td>Gram +</td>
<td></td>
</tr>
</tbody>
</table>

### Pathogens

<table>
<thead>
<tr>
<th>Microorganisms used in the antibiotic assay</th>
<th>Antarctic</th>
<th>Microorganism Type</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Vibrio cholerae</em> CECT-657</td>
<td>Gram -</td>
<td></td>
</tr>
<tr>
<td><em>Escherichia coli</em> O157:H7, ATCC 43888</td>
<td>Gram -</td>
<td></td>
</tr>
<tr>
<td><em>Pseudomonas aeruginosa</em> NCTC 10332T</td>
<td>Gram -</td>
<td></td>
</tr>
<tr>
<td><em>Escherichia coli</em> CECT515</td>
<td>Gram -</td>
<td></td>
</tr>
<tr>
<td><em>Bacillus cereus</em> CECT 4014</td>
<td>Gram +</td>
<td></td>
</tr>
<tr>
<td><em>Staphylococcus aureus</em> CECT 59</td>
<td>Gram +</td>
<td></td>
</tr>
<tr>
<td><em>Candida albicans</em> CECT 1001</td>
<td>Fungus Saccharomycetes</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Activity depending on Inhibition area radius</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>No effect</td>
<td>0 (-)</td>
</tr>
<tr>
<td>Weak inhibition</td>
<td>0-1mm (+)</td>
</tr>
<tr>
<td>Moderate Inhibition</td>
<td>&gt;1-3mm (++)</td>
</tr>
<tr>
<td>Strong Inhibition</td>
<td>&gt;3-7mm (+++)</td>
</tr>
<tr>
<td>Very Strong Inhibition</td>
<td>&gt;7-15mm (++++)</td>
</tr>
</tbody>
</table>

Lippert et al. (2003)

Acar (1980)
Antibiotic properties of macroalgae from Antarctica

22 Antarctic macroalgae tested

- 14 Rhodophyta (8 showed activity)
- 8 Phaeophyceae (4 showed activity)

Tested microorganisms

- Antarctic bacteria were inhibited for most algae
- Gram- were more resistant
- *Escherichia coli, Pseudomonas aeruginosa* & *Candida albicans* were the most resistant

Source: Camacho (2017)

Source: Carcedo (2018)
Chemical activity in different climate change scenarios

- Does Temperature changes affect to the chemical defences expression on macroalgae?
- Compare 3 different temperature scenarios in 3 different biomes (Antarctica, Mediterranean, Tropic)
- *Cystosphaera jacquinotii, Cystoseira compressa, Sargassum sp.*
Genus *Plocamium* J.V. Lamouroux in Antarctica

- **P. cartilagineum** (Linnaeus) P.S. Dixon
- **P. hookery** Harvey
- **P. secundatum** (Kützing) Kützing
Genus *Plocamium* J.V. Lamouroux

in Antarctica


Small forms of *Fucus* from the European coasts

*Fucus vesiculosus* Linnaeus
*Source*: aphotomarine

*Fucus serratus* Linnaeus
*Source*: wikipedia
The genus *Fucus*

*Fucus* Linnaeus, 1753

About 9 accepted species
- *F. chalonii*
- *F. cottonii*
- *F. vesiculosus*
- *F. spiralis*
- *F. serratus*
- *F. radicans*
- *F. distichus*
- *F. virsoides*
- *F. ceranoides*

Source: *Algaebase* (11-07-2018)

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Bayesian phylogenetic tree based on mtDNA 23S sequences. Numbers above and below the line are Bayesian posterior probability and MP bootstrap values (1000 replications), respectively. Source: Coyer et al. (2006)
Fucus chalonii Feldmann

F. spiralis var. nanus (Stackhouse) Batters

Fucus cottonii M.J.Wynne & Magne

F. spiralis var. limitaneus (Montagne) I.M. Pérez-Ruzafa
Ecology

*Fucus chaloni*i Feldmann

*Fucus spiralis var. nanus* (Stackhouse) Batters

*F. spiralis var. limitaneus* (Montagne) I.M. Pérez-Ruzafa
Ecology

Fucus cottonii M.J.Wynne & Magne
Distribution
1. What is the position of those small *Fucus* forms in the phylogenetic tree? Are they true species? How was their evolution?

2. How different are populations? Are those differences related to ecology?

3. Is the distribution changing? Is there any pattern?
Methodologies

• **Phycological analysis:** classical study of morphology and anatomy.

• **Genetic analyses:** DNA-Barcoding & analysis of repetitive elements from the genome (microsatellites)

• **Measures of the DNA nuclear content (C-values):** current methodology by fluorimetry. Application of flux cytometry.

• **Karyotype analyses:** chromosome staining and Image analysis.

• **Species distribution analyses and niche comparison:** by maximum entropy algorithms and niche definition algorithms.
Sampling
Results

Conceptacle structure and germling growth. Fig. 6. Mature oogonium containing egg cells ready to be released; Figs 7–8. Antheridia (Fig. 7) and germlings (Fig. 8) after 6 days in culture from Locality 1 (Ilulunnginga) (possible damage to the attachment rhizoids due to transfer to microscope slide). Fig. 9. Immature oogonia from Locality 2 (Clifden). Fig. 10. Immature oogonia. Fig. 11. Antheridia both from Locality 3 (Achill Sound). Scale bar is 50 μm.

**Table 2.** Calculated $F_{IS}$, $H_{exp}$ and allelic richness ($\hat{A}$) for $n$ individuals from populations of *Fucus spiralis* (Fs), *F. vesiculosus* (Fv) and small salt marsh *Fucus* (ssmF) from Locality 2 (Clifden) and Locality 3 (Achill Sound).

<table>
<thead>
<tr>
<th>Locality-taxon</th>
<th>$n$</th>
<th>$F_{IS}$</th>
<th>$H_{exp}$</th>
<th>$\hat{A}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>2-Fs</td>
<td>6</td>
<td>0.590*</td>
<td>0.327</td>
<td>1.400</td>
</tr>
<tr>
<td>2-ssmF</td>
<td>5</td>
<td>0.271</td>
<td>0.513</td>
<td>2.800</td>
</tr>
<tr>
<td>2-Fv</td>
<td>6</td>
<td>0.102</td>
<td>0.570</td>
<td>2.726</td>
</tr>
<tr>
<td>3-Fs</td>
<td>15</td>
<td>0.618</td>
<td>0.295</td>
<td>1.472</td>
</tr>
<tr>
<td>3-ssmF</td>
<td>6</td>
<td>0.510*</td>
<td>0.374</td>
<td>2.600</td>
</tr>
<tr>
<td>3-Fv</td>
<td>14</td>
<td>0.504*</td>
<td>0.813*</td>
<td>4.266</td>
</tr>
</tbody>
</table>

Significant $F_{IS}$ values are marked with an asterisk. Allelic richness ($\hat{A}$) is standardized to $n = 5$.

**Table 3.** Pairwise $F_{ST}$ values comparing populations of *Fucus spiralis* (Fs), *F. vesiculosus* (Fv) and small salt marsh *Fucus* (ssmF) from Locality 2 (Clifden) and Locality 3 (Achill Sound).

<table>
<thead>
<tr>
<th>Locality-taxon</th>
<th>2-ssmF</th>
<th>2-Fv</th>
<th>3-Fs</th>
<th>3-ssmF</th>
<th>3-Fv</th>
</tr>
</thead>
<tbody>
<tr>
<td>2-Fs</td>
<td>0.408</td>
<td>0.447</td>
<td>0.059</td>
<td>0.469</td>
<td>0.238</td>
</tr>
<tr>
<td>2-ssmF</td>
<td>0.073</td>
<td>0.492</td>
<td>0.349</td>
<td>0.474</td>
<td>0.064</td>
</tr>
<tr>
<td>2-Fv</td>
<td>0.526</td>
<td>0.464</td>
<td>0.078</td>
<td>0.327</td>
<td>0.182</td>
</tr>
<tr>
<td>3-Fs</td>
<td>0.497</td>
<td>0.327</td>
<td>0.182</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3-ssmF</td>
<td></td>
<td></td>
<td></td>
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<td></td>
</tr>
</tbody>
</table>

Results from STRUCTURE (A) and INSTRUCT (B) analyses with $K = 2$; and from INSTRUCT analysis with $K = 3$ (C). Localities 2 and 3 consist of individuals sampled as Fucus spiralis (Fs), F. vesiculosus (Fv) and small salt marsh Fucus (ssmF). Each individual is represented by a bar and colours represent the proportional assignment to the STRUCTURE/INSTRUCT groups.

The two first principal components (PC) of a Principal Component Analysis showing genetic affiliation of haplotype composition of ssmF (blue), F. vesiculosus (ves) (green) and F. spiralis (spi) (orange-red) from Locality 2 (Loc2) and Locality 3 (Loc3). The circles represent 95% inertia ellipses for the populations, which characterizes the dispersion of each population around its centre of gravity. Percentages along axes indicate the proportion of overall variability explained by the principal components.

Average nuclear DNA content (2C; pg) in *Fucus vesiculosus* (Fv, black circles), *F. spiralis* (Fs, grey circles) and small salt marsh *Fucus* (ssmF, white circles). Data from Illaunnginga (Locality 1), Clifden (Locality 2) and Achill Sound (Locality 3) are shown, together with unpublished data from Norway (**) and earlier published data (*) from Spain (Gómez Garreta *et al*., 2010), USA (Kapraun, 2005) and France (Phillips *et al*., 2011, recalculation from Peters *et al*., 2004).

**Source:** Sjøtun *et al.* (2017)
Bayesian tree of COI region for the studied species of Fucus plus several other species from the genus from GenBank

Results
Discussion

• The ssmF showed high variation with respect to reproduction mode, genetic affiliation and nuclear DNA content.

• ssmF can originate from different Fucus taxa (Coyer et al., 2006; Neiva et al., 2012). This is supported by our microsatellite study (in ex.: locality 2 ssmF derived mainly from F. vesiculosus, Locality 3 ssmF higher degree of hybridization/introgression)

• Kapraun, 2005; Gómez Garreta et al., 2010; Phillips et al., 2011 reported variable genome size for some brown algae, ¿autopolyploids?, ¿allopolyploids?
Near Future...

• Keep studying the composition of Antarctic flora quantitatively (Second BLUEBIO expedition)

• Finish the current Antarctic experiments and start new collaborations (role of seaweed in cloud formation & Passengers)

• Apply the methodologies showed to all the small *Fucus* forms and compare the results to understand the underlying processes of their evolution
Thank You!