Versatilidade e importância da metagenômica

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Environmental Pollution

journal homepage: www.elsevier.com/locate/envpol

Bacteria-invertebrate interactions as an asset in developing new antifouling coatings for man-made aquatic surfaces☆

Vanessa Ochi Agostini, PhD [a, f, 1], Erik Muxagata, PhD [b], Grasiela Lopes Leães Pinho, PhD [a], Igor Stelmach Pessi, PhD [c, d], Alexandre José Macedo, PhD [e, *]

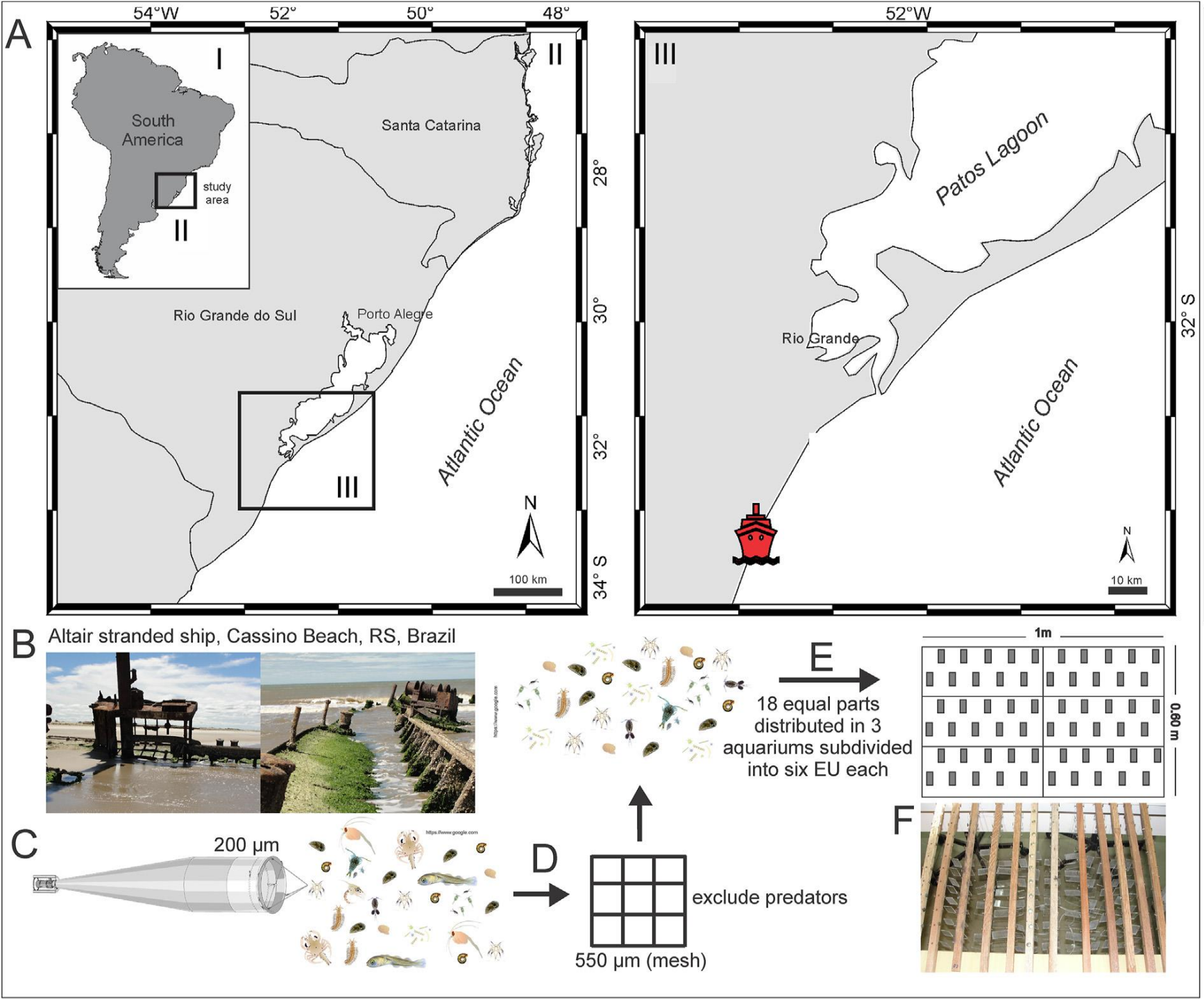
Breve contextualização do problema e relevância do tema

Indústria: incrustração

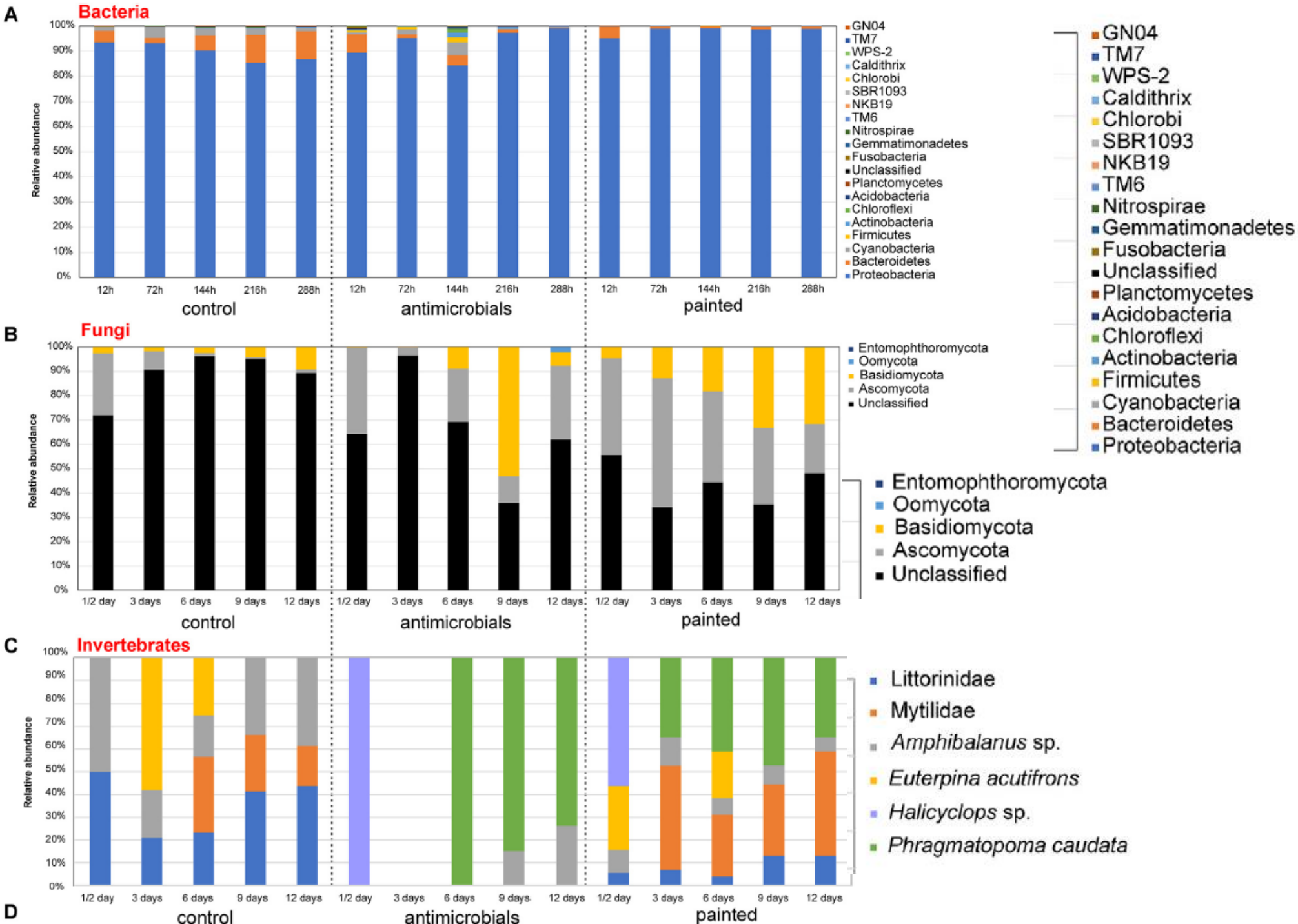
2017: porto de Rio Grande teve uma movimentação de **2.834 embarcações**, totalizando o transporte de mais 37 milhões toneladas em carga.

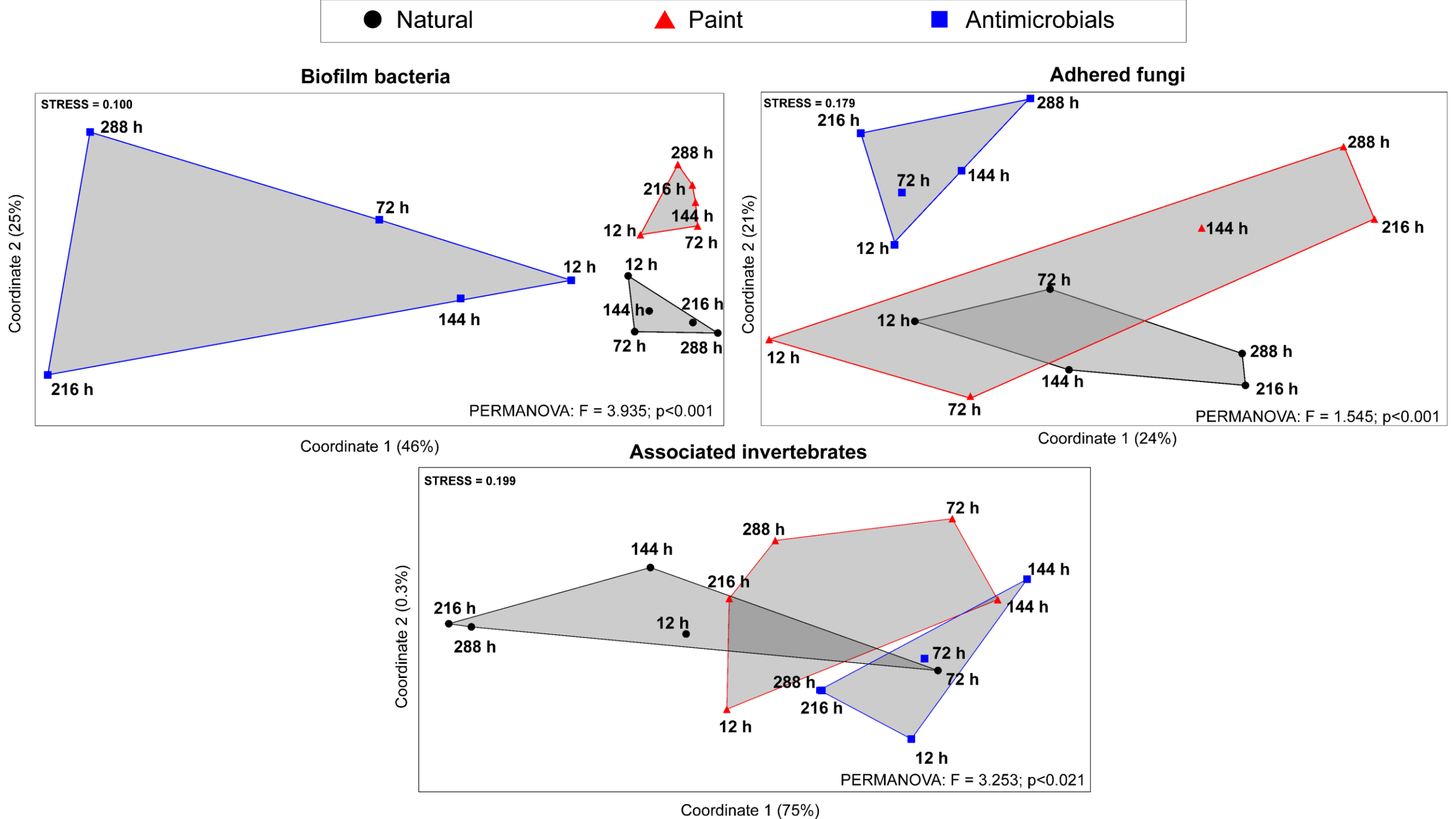
Marinha amaericana: **U$ 180 – 260 milhões** por ano para manutenção. Mais de **US$ 2 bilhões** em 10 anos (*Schultz MP et al., Biofoiuling, 2011*).

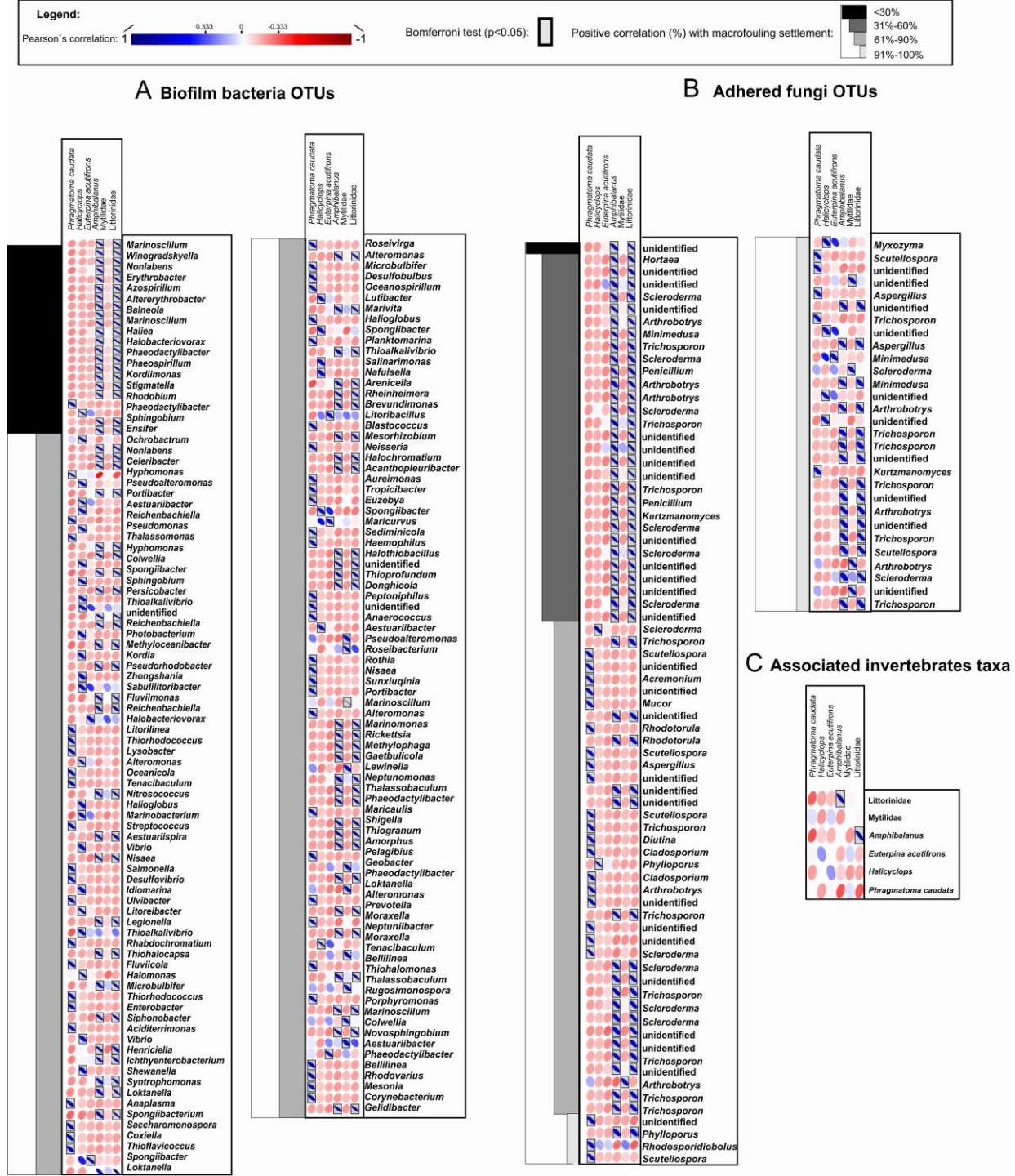
Metodologia

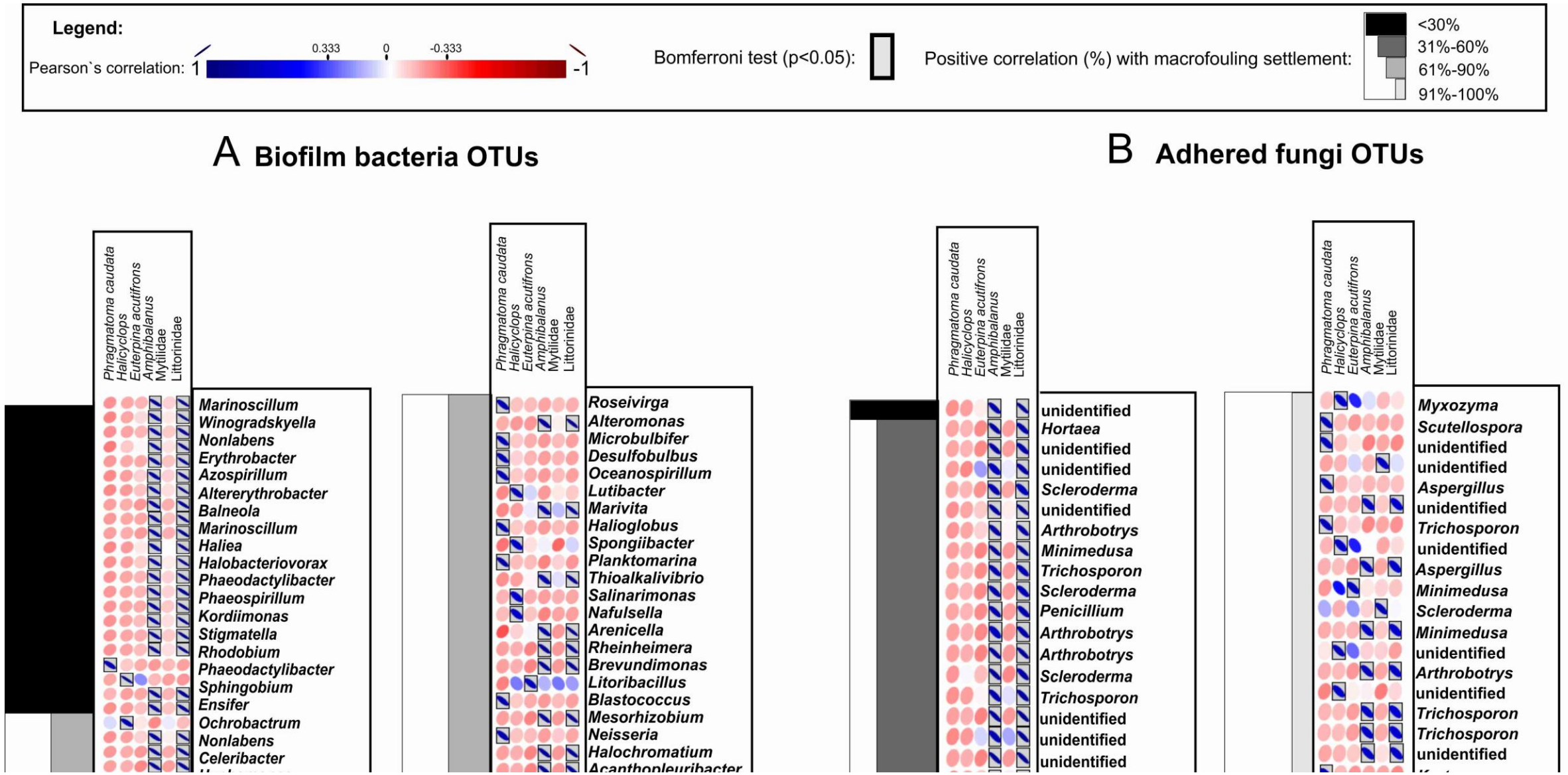


Resultados


A
Bacteria
Relative abundance
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
12h
72h
144h
216h
288h
control
antimicrobials
painted
GN04
TM7
WPS-2
Caldithrix
Chlorobi
SBR1093
NKB19
TM6
Nitrospirae
Gemmatimonadetes
Fusobacteria
Unclassified
Planctomycetes
Acidobacteria
Chloroflexi
Actinobacteria
Firmicutes
Cyanobacteria
Bacteroidetes
Proteobacteria
B
Fungi
1/2 day
3 days
6 days
9 days
12 days
Entomophthoromycota
Oomycota
Basidiomycota
Ascomycota
Unclassified
C
Invertebrates
Littorinidae
Mytilidae
Amphibalanus sp.
Euterpina acutifrons
Halicyclops sp.
Phragmatopoma caudata
D


Natural
Paint
Antimicrobials
Biofilm bacteria
STRESS = 0.100
288 h
72 h
12 h
144 h
216 h
288 h
216 h
144 h
72 h
12 h
12 h
144 h
216 h
72 h
288 h
PERMANOVA: F = 3.935; p<0.001
Coordinate 2 (25%)
Coordinate 1 (46%)
Adhered fungi
STRESS = 0.179
288 h
216 h
72 h
144 h
12 h
288 h
144 h
216 h
72 h
12 h
12 h
288 h
144 h
216 h
72 h
PERMANOVA: F = 1.545; p<0.001
Coordinate 2 (21%)
Coordinate 1 (24%)
Associated invertebrates
STRESS = 0.199
72 h
288 h
144 h
216 h
144 h
216 h
12 h
144 h
288 h
72 h
72 h
288 h
216 h
12 h
12 h
PERMANOVA: F = 3.253; p<0.021
Coordinate 2 (0.3%)
Coordinate 1 (75%)


Legend:
Pearson´s correlation: 1 0.333 0 -0.333 -1
Bomferroni test (p<0.05):
Positive correlation (%) with macrofouling settlement:
<30%
31%-60%
61%-90%
91%-100%
A Biofilm bacteria OTUs
Phragmatoma caudata
Halicyclops
Euterpina acutifrons
Amphibalanus
Mytilidae
Littorinidae
Marinoscillum
Winogradskyella
Nonlabens
Erythrobacter
Azospirillum
Altererythrobacter
Balneola
Marinoscillum
Haliea
Halobacteriovorax
Phaeodactylibacter
Phaeospirillum
Kordiimonas
Stigmatella
Rhodobium
Phaeodactylibacter
Sphingobium
Ensifer
Ochrobactrum
Nonlabens
Celeribacter
Hyphomonas
Pseudoalteromonas
Portibacter
Aestuariibacter
Reichenbachiella
Pseudomonas
Thalassomonas
Hyphomonas
Colwellia
Spongiibacter
Sphingobium
Persicobacter
Thioalkalivibrio
unidentified
Reichenbachiella
Photobacterium
Methyloceanibacter
Kordia
Pseudorhodobacter
Zhongshania
Sabulilitoribacter
Fluviimonas
Reichenbachiella
Halobacteriovorax
Litorilinea
Thiorhodococcus
Lysobacter
Alteromonas
Oceanicola
Tenacibaculum
Nitrosococcus
Halioglobus
Marinobacterium
Streptococcus
Aestuariispira
Vibrio
Nisaea
Salmonella
Desulfovibrio
Idiomarina
Ulvibacter
Litoreibacter
Legionella
Thioalkalivibrio
Rhabdochromatium
Thiohalocapsa
Fluviicola
Halomonas
Microbulbifer
Thiorhodococcus
Enterobacter
Siphonobacter
Acidiferrimonas
Vibrio
Henriciella
Ichthyenterobacterium
Shewanella
Syntrophomonas
Loktanella
Anaplasma
Spongiibacterium
Saccharomonospora
Coxiella
Thioflavicoccus
Spongiibacter
Loktanella
Roseivirga
Alteromonas
Microbulbifer
Desulfobulbus
Oceanospirillum
Lutibacter
Marivita
Halioglobus
Spongiibacter
Planktomarina
Thioalkalivibrio
Salinarimonas
Nafulsella
Arenicella
Rheinheimera
Brevundimonas
Litoribacillus
Blastococcus
Mesorhizobium
Neisseria
Halochromatium
Acanthopleuribacter
Aureimonas
Tropicibacter
Euzebya
Spongiibacter
Maricurvus
Sediminicola
Haemophilus
Halothiobacillus
unidentified
Thioprofundum
Donghicola
Peptoniphilus
unidentified
Anaerococcus
Aestuariibacter
Pseudoalteromonas
Roseibacterium
Rothia
Nisaea
Sunxiuqinia
Portibacter
Marinoscillum
Alteromonas
Marinomonas
Rickettsia
Methylophaga
Gaetbulicola
Lewinella
Neptunomonas
Thalassobaculum
Phaeodactylibacter
Maricaulis
Shigella
Thiogranum
Amorphus
Pelagibius
Geobacter
Phaeodactylibacter
Loktanella
Alteromonas
Prevotella
Moraxella
Neptuniibacter
Moraxella
Tenacibaculum
Bellilinea
Thiohalomonas
Thalassobaculum
Rugosimonospora
Porphyromonas
Marinoscillum
Colwellia
Novosphingobium
Aestuariibacter
Phaeodactylibacter
Bellilinea
Rhodovarius
Mesonia
Corynebacterium
Gelidibacter
B Adhered fungi OTUs
unidentified
Hortaea
unidentified
unidentified
Scleroderma
unidentified
Arthrobotrys
Minimedusa
Trichosporon
Scleroderma
Penicillium
Arthrobotrys
Arthrobotrys
Scleroderma
Trichosporon
unidentified
unidentified
unidentified
unidentified
Trichosporon
Penicillium
Kurtzmanomyces
Scleroderma
unidentified
Scleroderma
unidentified
unidentified
unidentified
Scleroderma
unidentified
Scleroderma
Trichosporon
Scutellospora
unidentified
Acremonium
unidentified
Mucor
unidentified
Rhodotorula
Rhodotorula
Scutellospora
Aspergillus
unidentified
unidentified
unidentified
Scutellospora
Trichosporon
Diutina
Cladosporium
Phylloporus
Cladosporium
Arthrobotrys
unidentified
Trichosporon
unidentified
unidentified
Scleroderma
Scleroderma
unidentified
Trichosporon
Scleroderma
Scleroderma
unidentified
unidentified
Trichosporon
unidentified
Arthrobotrys
Trichosporon
Trichosporon
unidentified
Phylloporus
Rhodosporidiobolus
Scutellospora
Myxozyma
Scutellospora
unidentified
unidentified
Aspergillus
unidentified
Trichosporon
unidentified
Aspergillus
Minimedusa
Scleroderma
Minimedusa
unidentified
Arthrobotrys
unidentified
Trichosporon
Trichosporon
unidentified
Kurtzmanomyces
Trichosporon
unidentified
Arthrobotrys
unidentified
Trichosporon
Scutellospora
Arthrobotrys
Scleroderma
unidentified
Trichosporon
C Associated invertebrates taxa
Littorinidae
Mytilidae
Amphibalanus
Euterpina acutifrons
Halicyclops
Phragmatoma caudata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0
-0.333
-1
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Haliea
Halobacteriovorax
Phaeodactylibacter
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Kordiimonas
Stigmatella
Rhodobium
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Sphingobium
Ensifer
Ochrobactrum
Nonlabens
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Roseivirga
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Arenicella
Rheinheimera
Brevundimonas
Litoribacillus
Blastococcus
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unidentified
Hortaea
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unidentified
Scleroderma
unidentified
Arthrobotrys
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Trichosporon
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Arthrobotrys
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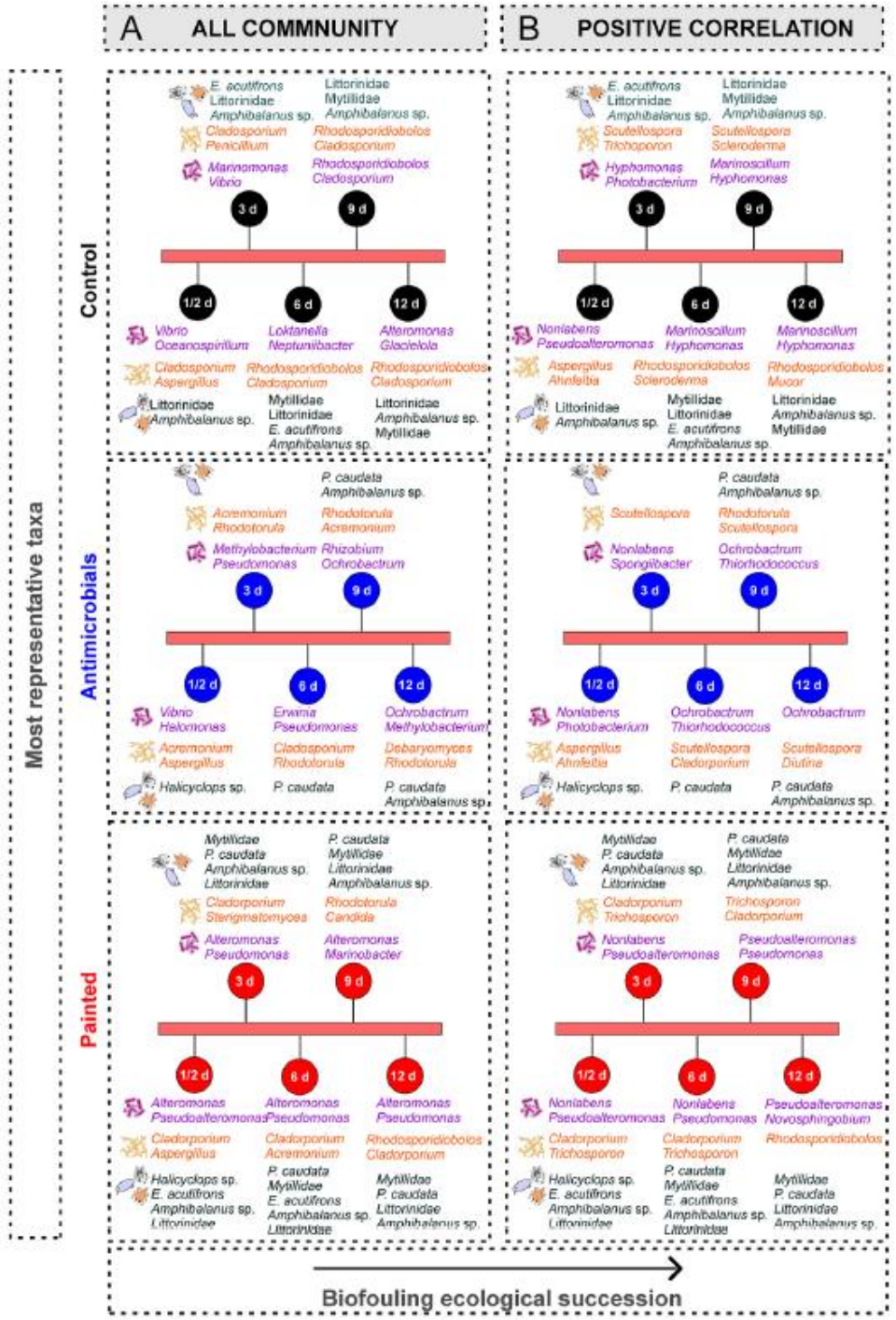
Scleroderma
Trichosporon
unidentified
unidentified
unidentified
Myxozyma
Scutellospora
unidentified
unidentified
Aspergillus
unidentified
Trichosporon
unidentified
Aspergillus
Minimedusa
Scleroderma
Minimedusa
unidentified
Arthrobotrys
unidentified
Trichosporon
Trichosporon
unidentified

Conclusões



IV. Macrofouling (fouling, sedentary, and vagile) establishment on hard substrates is strongly correlated with the composition of an existing Gram-negative heterotrophic bacterial biofilm (mainly Proteobacteria and Bacteroidetes). Each macrofouling species showed strong positive correlation with a specific biofilm bacterial composition, however other factor also affecting the biofouling community as the condition of the substrate;

V. From both ecological and economical points of view, the information provided here on the inter-kingdom interactions between micro- and macrofouling can be used to develop successful and safe control strategies to prevent biofouling development on aquatic man-made structures.

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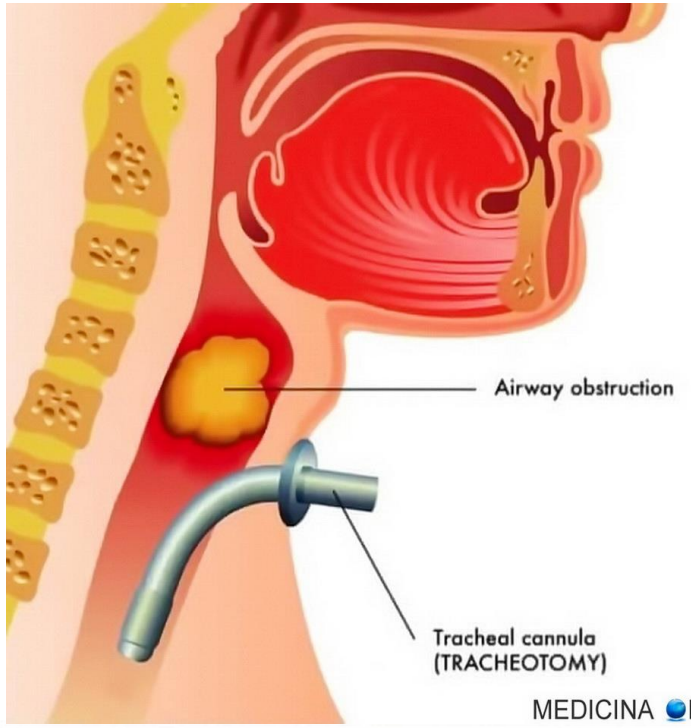
ORIGINAL ARTICLE

High microbiome variability in pediatric tracheostomy cannulas in patients with similar clinical characteristics

Leonardo Palma Kuhl [a,b,*], Paulo José Cauduro Marostica [b,c], Alexandre José Macedo [d], Gabriel Kuhl [a], Marina Siebert [e,f,g], Denise Manica [a,b], Leo Sekine [h], Cláudia Schweiger [a,b]

Breve contextualização do problema e relevância do tema



Tracheostomy is a surgical procedure that creates a shortcut for the air to reach the lungs.

It establishes a communication (or tunnel) between the cervical skin and the trachea, which is maintained pervious by a cannula.

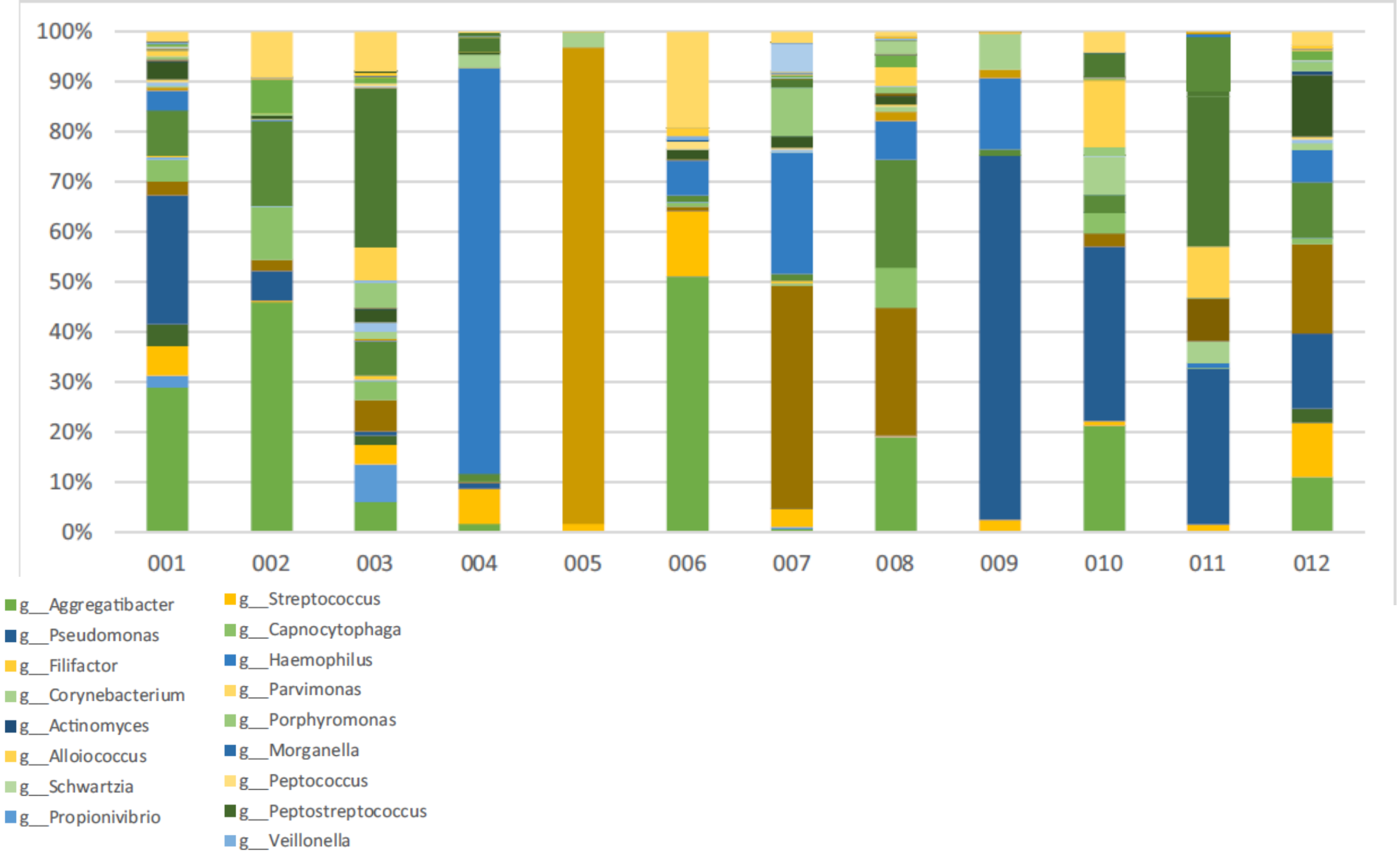
Indications for tracheostomy in children nowadays are mainly related to chronic obstruction of upper airways (e.g., laryngeal stenosis or vocal fold paralysis), management of mechanical ventilation, and treatment of bronchopulmonary aspiration.[1–3] Another obstructive airway pathology with potential necessity for tracheostomy is glossoptosis. Glossoptosis is defined as the posterior collapse of the base of the tongue resulting in varying degrees of respiratory obstruction. It may occur as a consequence of mandibular hypoplasia (Robin Sequence), but it also occurs in patients with neurological disorders related to hypotonia.[4–6]

Pacientes

Table 1 Clinical characteristics of the 12 patients.

Sample	Age (years)	Time from tracheostomy (years)	Feeding route	Syndrome	Comorbidities	Recurrent LRI	Time from last cannula change (days)	Cannula size	Peristomal granuloma	ATB (day of sampling)	ATB (last 3-months)
001	8.2	8.1	Oral	Facio-auricular-vertebral	Yes	No	98	5	No	No	No
002	5.4	5.2	G-tube	None	Yes	No	98	4.5	Yes	No	Yes
003	7.7	7.5	Oral/G-tube	Richieri-Costa-Pereira	Yes	No	98	4.5	No	No	No
004	2.1	1.9	NG-tube	None	Yes	No	98	3.5	No	No	Yes
005	9.2	9	Oral	Stickler	No	No	91	4.5	No	No	No
006	2.2	2.1	Oral	None	Yes	No	91	3.5	Yes	No	No
007	4	1.4	NG-tube	None	Yes	Yes	138	4	No	No	Yes
008	7.2	3.9	Oral	None	Yes	No	80	5	No	No	No
009	11.7	8.3	Oral	Picnodisostosis	No	No	98	4	No	No	Yes
010	5.4	5.2	G-tube	Apert	Yes	No	119	4.5	No	No	Yes
011	9.1	9	Oral	Treacher-Collins	Yes	No	98	4	No	No	No
012	2.2	2.1	NG-tube	None	Yes	No	91	3.5	Yes	Yes	No

LRI, Lower Respiratory Infection; ATB, Antibiotics; G-tube, Gastrostomy; NG-tube, Nasogastric Tube.


100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
001
002
003
004
005
006
007
008
009
010
011
012
g__Aggregatibacter
g__Pseudomonas
g__Filifactor
g__Corynebacterium
g__Actinomyces
g__Alloiococcus
g__Schwartzia
g__Propionivibrio
g__Streptococcus
g__Capnocytophaga
g__Haemophilus
g__Parvimonas
g__Porphyromonas
g__Morganella
g__Peptococcus
g__Peptostreptococcus
g__Veillonella

Resultados

Table 3 Genera proportion per sample.

001		002		003	
Genus	%	Genus	%	Genus	%
Aggregatibacter	29.48	*Aggregatibacter*	50.67	*Moraxella*	34.42
Pseudomonas	26.33	*Fusobacterium*	18.69	*Treponema*	8.30
Fusobacterium	9.21	*Capnocytophaga*	11.62	*Fusobacterium*	7.49
Streptococcus	6.07	*Eikenella*	7.33	*Alloiococcus*	7.15
Capnocytophaga	4.36	*Pseudomonas*	6.69	*Neisseria*	6.75
Mycoplasma	4.32	*Neisseria*	2.44	*Aggregatibacter*	6.42
Haemophilus	4.05	*Prevotella*	0.72	*Porphyromonas*	5.55
Neisseria	2.87	*Porphyromonas*	0.59	*Streptococcus*	4.11
Prevotella	2.81	*Haemophilus*	0.40	*Capnocytophaga*	4.08
Treponema	2.43	*Leptotrichia*	0.31	*Mycoplasma*	2.19
Others	8.07	Others	0.54	Others	13.54

Conclusões

Table 2 Prevalence of total reads per genus on metagenomics.

Genus	%
Aggregatibacter	17%
Pseudomonas	15.9%
Heamophilus	12.4%
Neisseria	8.8%
Staphyloccus	8.3%
Fusobacterium	6.5%
Moraxella	5.8%
Streptococcus	4.6%
Alloiococcus	3.0%
Capnocytophaga	2.9%
Corynebacterium	2.5%
Prevotella	2.5%
Porphyromonas	1.8%
Eikenella	1.2%
Treponema	0.9%
Elizabethkingia	0.9%
Stenotrophomonas	0.8%
Mycoplasma	0.8%
Achromobacter	0.5%
Acinetobacter	0.5%
Others	2.4%
Total	100%

Our study describes the use of 16s RNA metagenomics for bacterial microbiome identification present on tracheostomy cannulas of a specific group of children.

Although some bacterial genera demonstrated greater abundance (e.g., *Aggregatibacter*, *Pseudomonas*, *Haemophilus*, *Neissera*, *Staphylococcus*, *Fusobacterium* and *Moraxella*), composition of patients' individual microbiome showed high variability, even with similar clinical characteristics.

Despite the descriptive nature of this study, we hope to create foundations for more complex questions regarding microbiology interactions of these patients.

Obrigado!

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