



Marine Biology / Bacteriology

Marine Biotechnology in the Caribbean: Study of <i>Codakia orbicularis</i> Gill Proteins	155
<i>J.P.F. Gourdine</i> and E.J. Smith-Ravin	
The Post Larval Settlement of Fishes on a Coral Reef of Guadeloupe (FWI)	157
<i>Y. Frejaville</i> , Y. Bouchon-Navaro, M. Louis and C. Bouchon	
Antimicrobial Substances from Marine Bacteria	159
<i>C. Walters</i>	
The CHALOUBE Project: Global Change, Dynamics of Exploited Marine Diversity, and Viability of Fisheries	161
<i>F. Blanchard</i> and O. Thèbaud	
A Spatial and Temporal Study of the Benthic Communities in the Coral Reefs of the Bay Islands, Honduras	163
<i>P. Portillo</i> , Y. Bouchon-Navaro, M. Louis and C. Bouchon	
Significance of Environmental Variables for the Structure of Fish Assemblages in the Lagoon of the Grand Cul-De-Sac Marin (Guadeloupe – FWI)	165
<i>A. Vaslet</i> , C. Bouchon, Y. Bouchon-Navarro and M. Louis	
Seagrass Beds as Important Habitats for Juvenile Fishes in the Bay of the Grand Cul-De-Sac Marin (Guadeloupe, F.W.I.)	167
<i>D. Kopp</i> , Y. Bouchon-Navarro, C. Bouchon and M. Louis	
Colonization of Sunken Wood in the Caribbean Area: Influence of the Environment	169
<i>M.C.Z. Laurent</i> and O. Gros	
Bacterial Symbiosis in Wood Fall Bivalves	169
<i>M.C.Z. Laurent</i> and O. Gros	
Description of the Extracellular Bacterial Interactions in Marine Nematodes From <i>thalassia testudinum</i> Environment	170
<i>L.C. Maurin</i> and O. Gros	
Observation of Marine Nematodes Along a Transect Beach-Seagrass Beds of <i>thalassia testudinum</i>: a SEM Analysis	170
<i>L.C. Maurin</i> , C. Grateloup, M. Delannay and O. Gros	

Marine Biotechnology In The Caribbean: Study Of *Codakia orbicularis* Gill Proteins

Jean-Philippe F. GOURDINE, Emilie Juliette SMITH-RAVIN

Université Antilles Guyane, Pointe à Pitre, 97159 GUADELOUPE - jsmithra@univ-ag.fr**Abstract**

The white clam, *Codakia orbicularis* (Linné, 1758), a tropical bivalve widely consumed in the Caribbean, inhabits the sulphur-containing sediments inherent to phanerogam seagrass beds. It possesses sulfur-oxidizing endosymbiotic bacteria localized in specialized cells in its gills. We presumed the existence of gill proteins of interest which would be required for adaptation to the stressful environmental conditions, particularly to the presence of sulphur and of sulfo-oxidizing bacteria. The full-length cDNA of its major gill protein had been successfully recovered using molecular biology techniques. This protein, named Codakine, is a dimeric mannose binding C-type lectin which might be involved in symbiosis process and immune defense. Future prospective work will involve the use of codakine against pathogenic organisms and symbiotic bacteria. These results reinforce the interest which should be put in marine biotechnology research in the Caribbean.

Introduction

The Caribbean islands and Brazil are the fourth biodiversity hotspot in the world concerning terrestrial or marine fauna and flora. Marine environments present a great genetic diversity and a number of ecosystems scarcely known (Myers *et al.* 2000). This important biodiversity and the potential activities of isolated compounds should aim to the development of fundamental and practical research in marine biotechnology. This development is necessary in order to value the potential applications of the isolated products in health and environmental areas. Consequently our studies were carried out on the white clam *Codakia orbicularis* (Linné, 1758). This bivalve lives in sandy sulfured sediments of phanerogam-based ecosystems (*Thalassia testudinum*). Considering the stressful conditions of its habitat, presence of hydrogen sulfide and the symbiotic sulfo-oxidizing bacteria living in its gills, we might expect to isolate compounds of biotechnological interest (Berg and Alatalo 1984). Studies on gill proteins of *C. orbicularis* on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) in presence of DTT and lectin blotting assay, show a prominent weakly glycosylated protein of about 14 kDa on which we decided to focus our attention (Gourdine and Smith-Ravin 2002).

Materials & Methods

From the 14kDa band, a partial peptide sequence were deduced using matrix assisted laser ionisation/desorption time of flight mass spectrometry (MALDI-TOF MS/MS). Polymerase chain reaction (PCR) was used on clones derived from a cDNA library of *C. orbicularis* and degenerate oligonucleotides in order to isolate the corresponding gene (Gourdine and Smith-Ravin 2006). Bioinformatics softwares (BLAST, CLUSTALW, Rosetta software, etc.) were used to establish first, second and tertiary structures of the 14 kDa protein. According to bioinformatics analysis, we have decided to purify the protein, to perform chromatography on mannose-agarose column. (Gourdine and Smith-Ravin 2006).

Results & Discussion

Electrophoretic profile of total gills protein of *C. orbicularis* is presented in figure 1. All the extraction buffers used show the presence of the major 14 kDa protein. The cDNA sequence of the major protein named codakine (Genbank AAX19697) is of 447 base pairs corresponding to 135 aminoacids (Fig.2).

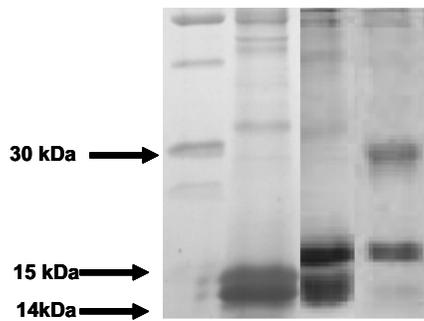


Fig. 1 : 18 % SDS-PAGE of total gill proteins of *C. orbicularis* ;

Lane 1 standard molecular weight markers.
Lane 2 CHAPS extraction buffer plus DTT ;
Lane 3 : Tris-HCl extraction buffer plus DTT ;
Lane 4 : Tris-HCl extraction buffer minus DTT

```

ac
tgaattcggcttgtagattgaattgttcaactgtggttgactgtagtctttctgtgcaaa
atgagattctcgttcagctcttctgtgtttgtcgttagtggaaacagcagcagcgggc
M K I L V A V F L V L V V V G T A A A G
tgtccgacggctggaaccagttcctcgtatctatgtttatctaccagtcagccaaagcc
C P D G W T Q F L D L C Y I Y Q S A K A
tcatgggctcagcacagagcagctgcaagctttaggtggtattcttgcgaaaccggac
S W A S A Q S S C Q A L G G I L A E P D
actgcatgogagaacgaggtgctaatacctatgtgtagagaaaatggagatgctggtagc
T A C E N E V L I H M C R E N G D A G S
tttggaccctggttggaggtcaaaaagtccgcccgggctggcaatggtcttcatccggg
F G P W L G G Q K V G G A W Q W S S S G
gcagcttttgattacttacgttggggccaaacgaaccaaataacagcggaggtaacgaa
A A F D Y L R W G P N E P H N S G G N E
gactgcctacactacaactgcttccatggaatgacctacgatgcbattatcaagcttcc
D C L H Y N W L S W N D L R C H Y Q A S
tacttatgccaagagagccgctgagaaaaagttttctccagtaaacacgcaagtaaca
Y L C Q R A A E *
gcaacgtggttttaacgtcttgaagcataaacagcaagttgcatcgaagttgaaacatgt
tcttgcaaaattatgctgttaabtagaagaacactctgtgcgaatttttaagatctaaac
atcctctatctatgaaccattcttaaatacaactcaagatcaaaa

```

Fig.2 : cDNA derived aminoacid sequence of Codakine (Genbank AAX19697). Initial aminoacid sequence found by MALDI-TOF MS/MS is indicated in bold. The initiator and stop codons are shaded in black, and a potential polyadenylation signal is shown in bold and shaded in grey.

Theoretical isoelectric point and molecular weight confirmed the previous work (16.087 kDa, pI 4.72) peptide (Gourdine and Smith-Ravin 2006). Bioinformatics analysis of cDNA sequence showed Codakine as a mannose-binding C-type lectin. Affinity chromatography on mannose-agarose column confirmed that Codakine is a homodimeric calcium-dependant mannose-binding lectin

(14 kDa for each monomer) which contains a 2 kDa signal peptide (Gourdine et al. 2006a). Codakine presents homologies with vertebrates and invertebrate lectins involved in immune system, cellular mediation and sulphur-oxidizing bacterial symbiont mediation (Gourdine et al. 2006b). Research works are underway to define the role and action of codakine *in vivo* and *in vitro* experiments.

Acknowledgements

We are grateful to Dr Nick TOTTY from Cancer Research Council (United Kingdom), Dr P. GREENWELL, Dr M. DWEK, Dr S. RUGOOPUTH and A. MARKIV (University of Westminster, London) for their supports.

References:

- Berg, C.J., and Alatalo, P. 1984. Potential of chemosynthesis in molluscan mariculture. *Aquaculture* **39**: 165-179.
- Gourdine, J.-P., Markiv, A., Rugooputh, S., Greenwell, P., Dwek, M.V., and Smith-Ravin, E.J. 2006a. Characterization of Codakine, a new Mannose-Binding Lectin from the gills of the tropical clam *Codakia orbicularis* in preparation.
- Gourdine, J.-P., Markiv, A., and Smith-Ravin, E.J. 2006b. Computational analysis of Codakine and marine related homologues, reveals a common C-Type lectin folding *unpublished data*.
- Gourdine, J.-P., and Smith-Ravin, E.J. 2002. Electrophoretic separation of gill proteins of the clam *Codakia orbicularis*. *Prep. Biochem. Biotechnol.* **32**: 341-353.
- Gourdine, J.-P., and Smith-Ravin, E.J. 2006. Analysis of a cDNA-derived sequence of a novel mannose-binding lectin, codakine, from the tropical clam *Codakia orbicularis*. *Fish and Shellfish Immunology*, submitted.
- Myers, N., Mittermeier, R.A., Mittermeier, C.G., da Fonseca, G.A., and Kent, J. 2000. Biodiversity hotspots for conservation priorities. *Nature* **403**: 853-858.

The Post-Larval Settlement Of Fishes On a Coral Reef Of Guadeloupe (FWI)

Y. FREJAVILLE, Y. BOUCHON-NAVARO, M. LOUIS, C. BOUCHON

Laboratoire de Biologie Marine – DYNECAR, Université des Antilles et de la Guyane
Campus de Fouillolè, B.P. 592, 97159 Pointe-à-Pitre, Guadeloupe - Yann.Frejaille@univ-ag.fr

Abstract

In order to study qualitatively and quantitatively the specific phase of settlement of coral reef fishes, 18 monthly samplings of 24h were carried out on a coral reef located in the southeast coast of Guadeloupe. A total of 3 867 fishes representing 50 families were sampled. Redundancy analysis showed that settlement occurred almost only at night, preferably during the new moon phase; strong winds pushing the large pelagic patches of post larvae in direction of the coast, associated with high swells and current speeds carrying them on the reef were also very favourable to settlement.

Introduction

The early life of most coral reef fishes is pelagic, from the egg to the post larval stage. At the end of this stage that can last from 2 to 12 weeks, the fishes must find a coral reef to settle (Doherty, 1982). Then the fishes will quickly loose their pelagic adaptations to become juveniles, very similar to the adult form and begin their demersal life on the reef.

The interannual variations of the size of exploitable coral fish stocks is mainly governed by the quantity of fishes settling on the reefs each year, then by the mortality rate affecting them after their settlement (Shima, 1999).

The coral reef fishes represent an extremely important food resource for the countries of the intertropical zone. However, this crucial phase of the life cycle of reef fishes, conditioning the dynamics of exploited stocks, has never been studied in the Lesser Antilles. It thus seemed important to carry out a study of the flow of post-larvae settling on the reefs of Guadeloupe in order to know better their abundance, taxonomy and the environmental factors influencing their settlement.

Materials & Methods

From October 2003 to December 2004, 18 monthly samplings of fish post-larvae were conducted at different moon phases, on the coral reef of a small islet (îlet Gosier) located in southeast coast of Guadeloupe. During each field trip, fishes were sampled every 2 hours during 24 hours.

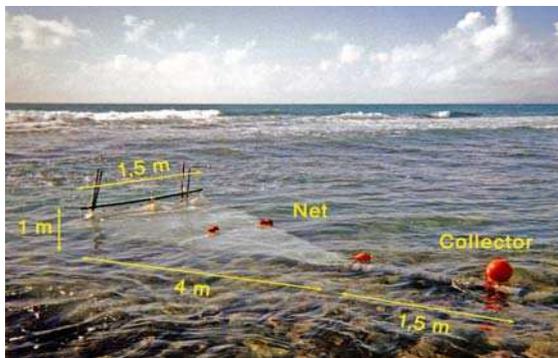


Fig. 1 : the sampling device.

The sampling device used was a crest net of pyramidal shape (fig. 1) fixed on the reef flat, facing the surge at approximately 50m of the reef crest. The drifting vegetal material (leaves of marine Phanerogams mostly) and the post larval fishes (Fig. 2) trapped by the net were retained in a tubular collector. Every 2 hours, the sample was collected and fixed with a 5% formalin solution for later identification and treatment.



Fig. 2 : Post-larval specimens of Gerreidae, Monacanthidae, Diodontidae and Apogonidae.

In the same time, several environmental factors were measured: current speed, swell, nebulosity, rainfalls, speed and direction of the wind, state of the tide, state of the nycthemeral cycle, presence of the moon and moon phase, weight of drifted vegetal material, physicochemical parameters of the sea water.

In order to relate the characteristics of the incoming flow of settling post-larvae (numerical abundance, number of families, species diversity and equitability) with the environmental factors measured, the redundancy analysis (RDA) was used (software: CANOCO).

Results & Discussion

A total of 3 867 fishes representing 50 families were sampled. The most abundant families were represented by Gobidae (over 50% of the total captures), Clinidae, Scaridae, Clupeidae, Labridae and Gerreidae (Fig. 3). The most frequently captured families are the Gobidae (present in 43% of the samples), Scaridae (24,5%), Gerreidae (23,6%), Labridae (16,6%) and Clinidae (16,2%).

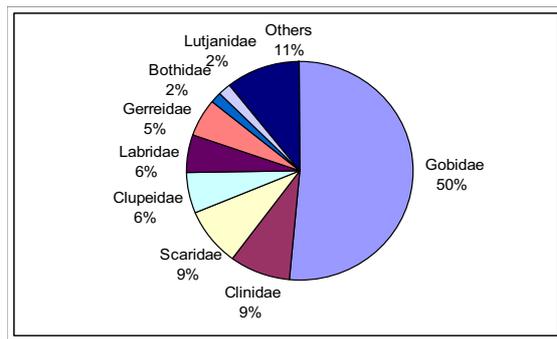


Fig. 3 : relative taxonomic composition of the settlers.

As it was observed in similar studies carried out in the Pacific (Dufour and Galzin, 1992), the post-larval settlement occurred almost exclusively at night (88,5% of the total captures). The intensity of settlement (expressed in individual per thousand cubic meter of filtered water) increased after dusk (fig. 4), then showed a peak during the second part of the night, and decreased at dawn. On the other hand, between 10 a.m. and 2 p.m., when sunlight is maximal, the settlement rate was very low (0.9% of the total captures).

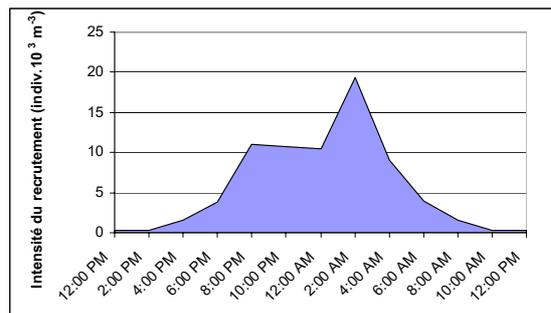


Fig. 4 : nycthemeral variations of the settlement intensity.

Among the 23 environmental variables introduced in the RDA, five had a significant statistical influence on the fish settlement (fig. 5), two were quantitative and three qualitative. They explained 38.6% of the total variance. Axis 1 was correlated to the variable "swell" ($r = 0.75$), "daylight" ($r = 0.58$) and "current" ($r = 0.59$). Numerical abundance, family richness, diversity and equitability of the settlers were positively related to swell and current and negatively related to daylight on this axis. Axis 2 was correlated to the variable "south wind" ($r = 0.68$), which was opposed to the variable "full moon". Abundance of the fishes was positively correlated to "south wind" and negatively related to the "full moon" on axis 2. But, the canonical coefficients are very low on this axis.

The predominant nocturnal settlement and the negative effects of sunlight and full moon on the abundance of post-larvae traduce an important negative phototropism of the settlers. This is probably intended to reduce their vulnerability to the predators hunting by sight that abound on the reefs.

The results of the RDA also showed that strong south winds played an important role in settlement by pushing the large pelagic patches of post-larvae in direction of the

coast, when they come back to the surface during the night.

Moreover, high swells and currents carrying the settlers on the reef are also important factors explaining the variability of settlement. Strong hydrodynamic conditions, unfavourable to predation, may provide additive protection to the settlers.

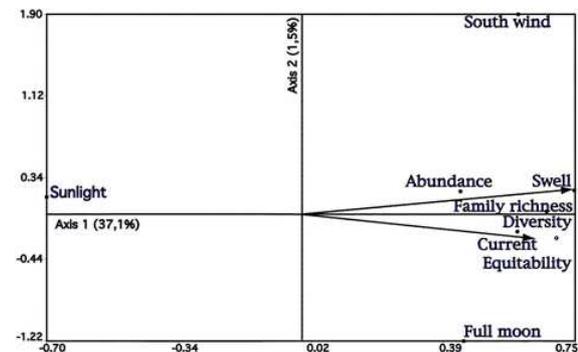


Fig. 5 : projection (biplot) of the redundancy analysis.

The average settlement rate calculated for the studied reef was 9 fishes per linear meter of reef front and per hour, representing around 80 000 settlers per meter and per year. However, in order to extrapolate those results to the whole island of Guadeloupe and thus to estimate the recruitment of fish in exploitable stocks, it would be necessary to undergo similar studies on various coasts of the island, under various influences of the trade winds and during several years (Robertson and Kaufmann, 1998) because of the importance of inter-annual variability in settlement rates.

References:

- Doherty, P.J., (1982). Some effects of density of the juveniles of two species of tropical territorial damselfishes. *J. Exp. Mar. Biol. Ecol.* 65, 249-261
- Shima, J., (1999). Variability in relative importance of determinants of reef fish recruitment. *Ecol. Lett.* 2, 304-310.
- Dufour, V., Galzin, R., (1992). Le recrutement des poissons récifaux de Polynésie française, impact sur la dynamique des peuplements et conséquences sur la gestion des stocks. *Cybius* 16 (4), 267-277.
- Robertson, D., Kaufmann, K. (1998) Assessing early recruitment dynamics and its demographic consequences among tropical reef fishes: Accommodating variation in recruitment seasonality and longevity. *Australian Journal of ecology* 23, 226-233.



Marine Biology / Bacteriology

Antimicrobial Substances From Marine Bacteria

CARL WALTERS, MARILAINE MOTA-MEIRA AND MARC LAVOIE

*Department of Biological and Chemical Sciences, The University of the West Indies, Cave Hill**Campus P. O. Box 64, Bridgetown BB 11000 Barbados**cwalters582@yahoo.com, motameira@yahoo.com, mlavoie@uwichill.edu.bb***Abstract**

The arsenal of effective antibiotics used in clinical medicine is decreasing in the face of emerging antimicrobial resistance mechanisms. Thus, there is increasing need to find new sources of inhibitory substances. One such source is the marine environment, with its abundance of organisms that would undoubtedly have developed unique metabolic and physiological capabilities that ensure survival in diverse habitats. These capabilities offer the potential to produce metabolites that would not be observed from terrestrial microorganisms. A total of 373 isolates obtained from marine samples (sea weed, sea water, coral and sponge) were screened and of these isolates, 55 (15%) produce an inhibitory substance active against at least one indicator microorganism (*Micrococcus luteus*, *Staphylococcus aureus*, *Escherichia coli*, *Salmonella enteritidis*, *Enterococcus faecalis* and *Candida albicans*). However, only 5 (9%) isolates produce their inhibitory substance in liquid medium. These results clearly show the marine environment to be a source worth investigating for potentially novel inhibitory substances.

Introduction

The most important medicines and antibiotics in use today were obtained from terrestrial microorganisms. However, the arsenal of effective antibiotics used in clinical medicine is decreasing with the increased antimicrobial resistance among microorganisms. Thus, there is a need to find new sources of inhibitory substances. One such source is the marine environment. Work carried out by Rosenfeld and Zobell in 1947, showed that marine microorganisms are capable of producing antibacterial substances. More recent work include bacterial isolates that show fungicidal activity (1,6). Further more, marine invertebrates have also been shown to produce substances that are antagonistic towards clinically isolated antibiotic-resistant bacteria (3) as well as terrestrial bacteria (8).

The aims of this study are to *i*) to detect bacterial antagonistic substances among marine isolates, *ii*) to assess the activity spectra of these substances against different bacterial pathogens, *iii*) to optimize the production of these antibacterial agents in liquid media, *iv*) to purify them and *v*) to determine their chemical nature.

Materials and Methods

Marine samples were collected and screened for presence of bacterial isolates. Afterwards, the deferred antagonism assay was carried out to determine whether they produce an antimicrobial substance. Isolates producing inhibitory substances were preliminary identified and stocked in the isolation medium with 20 % glycerol at -20°C and -80°C. Subsequently, the production of the antimicrobial substance in broth culture was carried out.

Results and Discussion

The marine environment and the bacteria therein is becoming an important source for microbial products due to the likelihood that they would possess a greater molecular diversity than do their terrestrial counterparts (2). Thus the high number of antimicrobial substance producing strains observed (15%) is of particular importance (Table 1).



Marine Biology / Bacteriology

Table 1: Number of producing isolates from different sources.

Source	# of isolates obtained	# of isolates producing an inhibition zone	% of isolates producing an inhibition zone
Sea weed	134	17	13
Sea water	65	6	9
Coral	34	0	0
Sponge	141	32	23
Total	373	55	15

The inhibitory isolates were more active against *M. luteus* and two were active against yeasts (Table 2).

Table 2: Inhibition of indicator strains by marine isolates.

Indicator Strain	# of isolates producing an inhibition zone
Gram positive bacteria	
<i>M. luteus</i>	45
<i>S. aureus</i>	1
<i>M. luteus</i> and <i>S. aureus</i>	4
<i>M. luteus</i> , <i>S. aureus</i> and <i>E. faecalis</i>	2
Gram negative bacteria:	1
<i>E. coli</i> and <i>S. enteritidis</i>	
Yeast: <i>C. albicans</i>	2

Most of these producing isolates were from sponges (Table 1). Metabolites previously ascribed to sponges have been recently demonstrated to be synthesised by microbial symbionts of sponges (5). Sponges are also one of the richest sources of both biologically active secondary metabolites and chemical diversity (4, 7). The high percentage of isolates producing their inhibitors in liquid medium (9%) will permit an easier purification.

Of the isolates producing in liquid medium, only one gave clear inhibition zones. This isolate was identified as being a member of the genus *Staphylococcus*. Two other isolates (an *Actinomycete* and a *Bacillus*) produced their antagonistic substance in liquid medium. Bacteria from these genera are known to produce clinically important medicines.

Conclusion

There is a high rate of marine bacteria (especially from sponges) that are capable of producing microbial inhibitors. Also, an important proportion of these inhibitors are produced in liquid cultures and further work is needed to characterise these inhibitory substances.

Acknowledgements

Thanks to the Caribbean Health Research Council for funding the project, the Department of Biological and Chemical Sciences of the University of the West Indies, Cave Hill Campus and Renata Goodridge for collecting the samples used in this project.

References

- Buck, J. D. *et al.* 1962. Inhibition of Yeast by a Marine Bacterium. *J. Bacteriol.* 85: 1132-1135
- Belarbi, E. H. *et al.* 2003. Producing Drugs from Marine Sponges. *Biotechnology Advances.* 21: 585-598
- Jang, W. S. *et al.* 2003. Biological Activities of Synthetic Analogs of Halocidin, an Antimicrobial Peptide from the Tunicate *Halocynthia aurantium*. *Antimicrobial Agents and Chemotherapy.* 47: 2481-2486
- Kijjoo, A and P. Sawangwong. 2004. Drugs and Cosmetics from the Sea. *Mar. Drugs.* 2: 73-82
- Lee, Y. K. *et al.* 2001. Microbial Symbiosis in Marine Sponges. *The Journal of Microbiology.* 39: 254-264
- Oleinikova, G. K. *et al.* 2001. Cyclic lipopeptides with fungicidal activity from the sea isolate of the bacterium *Bacillus subtilis*. *Russ. Chem. Bull., Int. Ed.,* 50: 2231-2235
- Proksch, P. *et al.* 2003. Drugs from the Sea - Opportunities and Obstacles. *Mar. Drugs.* 1: 5-17
- Zheng, L. *et al.* 2005. Antimicrobial screening and active compound isolation from marine bacterium NJ6-3-1 associated with the sponge *Hymeniacidon perleve*. *World Journal of Microbiology and Biotechnology.* 21: 201-206



Marine Biology / Bacteriology

**The CHALOUPÉ project:
global change, dynamics of exploited marine biodiversity, and viability of fisheries.**

Fabian Blanchard and Olivier Thébaud

1 Ifremer, Fisheries Resources laboratory of French Guyana, BP 477, 97331 Cayenne, French Guyana.

2 Ifremer, Marine Economy Department, BP 70, 29280 Plouzane Cedex, France.

Fabian.Blanchard@ifremer.fr

Abstract

The CHALOUPÉ project, global change, dynamics of exploited marine biodiversity, and viability of fisheries, is a multidisciplinary research programme which objective is to provide a diagnostic on the bio-economic factors that lead major changes observed in the fisheries in three different types of ecosystems at the scale of the last decades.

Three case studies are the basis of the study : the up-welling system of south Morocco, the open temperate continental shelf of the Bay of Biscay (France) and the tropical continental shelf of French Guyana under Amazonian influence. The main factors driving changes differed among ecosystems : climate change (or variability), overexploitation and impact of fishing on biodiversity, globalisation of the seafood market, incentives.

In French Guyana, the objectives will focus on the impact of trawling shrimp fisheries and of climate change on the biological communities, the effects of the "El Niño"/"La Niña" events on shrimp recruitment and the economic consequences of measures to mitigate biodiversity impact through bio-economic modelling.

Introduction

Major changes are currently being observed in marine ecosystems and in the human activities, particularly fishing, that depend upon them. If the ecosystems are sustainable naturally, the observed changes raise growing concerns, both in terms of the loss of biodiversity of marine populations, and in the capacity of the communities to absorb these changes without being radically transformed. These worries apply to the sustainability of fisheries.

The effects of fishing and of climate change have by now been identified as key factors in the evolution of marine populations and communities. The effect of this evolution on fisheries specifically has been that its development operates in a context of failed regulations on access to resources. The extent of these changes and the relative weight of different factors on a regional scale have yet to be quantified. This is the principal objective of the CHALOUPÉ Project.

The anticipated output of the project is an assessment of the observed changes, evolutionary factors, and the sustainability of communities/ fisheries systems in three types of regional ecosystem : the temperate continental shelf of the Bay of Biscay, the tropical shelf of French Guyana, and the up-welling ecosystem of Morocco. The Chaloupe projet will be presented here focusing on the French Guyana case study.

The output is dependent upon the compilation and combined analysis of chronological series data related to environmental conditions, characteristics of populations and fisheries, fisheries economics, and the evolution of governance, as well as system modelling.

The project, which will last three years (2006-8), benefits from financing by the National Research Agency (France), obtained under the framework of the 'Biodiversity 2005' call for appeals, and put together by teams working on fisheries ecology, economy, and modelling. It is coordinated by Ifremer (F. Blanchard and O. Thébaud), the French research institute for the exploitation of the sea.

Material and Methods

Two complementary approach are developed within Chaloupe : statistical analyses of biological and economic data sets and modelling of the bio-economic systems. Hence four work-packages (WP) were designed :

- WP1) ecological dynamics : analyses of the temporal variations of environmental factors (sea surface temperatures, bottom temperatures, salinity, up-welling index...), analyses of the community changes from trawling sampling survey data
- WP2) economic dynamics : description of the institutional and management context of fisheries, analyses of the temporal changes of the fisheries landings in biomass and monetary value, analyses of the changes in price of the seafood products...
- WP3) integrated sets of multi-disciplinary indicators for state diagnostic of the ecosystem and fisheries: implement a

Marine Biology / Bacteriology

methodology of economic and bio-ecological indicator boards that summarized the knowledge on the state diagnostic as short reports

WP4) modelling of the functioning of the biological community/exploited resource/fishery taking into account driving factors (such as climate change and/or market changes for example)

WP4) The bio-economic model of the shrimp fishery developed by C. Chaboud (IRD-France) in Madagascar will be modified and adapted to the Guianese case. Data from field get by Ifremer since three decades will be used to the parameterisation and build environmental scenarios as well as mitigation measures to avoid biodiversity impacts (turtle excluding device, by-catch reducing device, interaction with frigatebirds feeding on discards).

Preliminary results in the French Guyana case study

WP1) Environmental data analysed were mainly SST (sea surface temperatures) collected from the ICOADS data set available from internet. The data showed a significant increase of the SST occurring from 1994-1995 of about 0.6°C (Figure 1). This increase can be locally greater than 1°C.

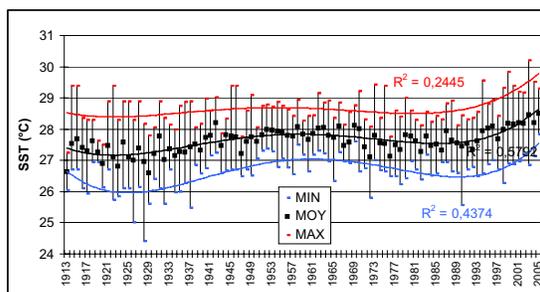


Figure 1. Temporal variations of the yearly averaged sea surface temperatures (SST in °C) in black squares, the minimal and maximal monthly value observed in the year and polynomial fit of these 3 variables with the r-squared value.

According to low seasonal variability, this could have impact on the fish community composition as compared to the situation of the Bay of Biscay where the most sub-tropical species became dominant (Blanchard and Vandermeirsch, 2005; Poulard and Blanchard, 2005). The analyses of community changes will be carried out using data from demersal trawling surveys carried out during the wet and dry season in 1992, 1993 and 1994 in French Guyana. Three new surveys will be then carried out according to the same sampling scheme.

WP2) The economic analyses will be focused on the shrimp fishery. Surveys will be made by inquiring the directors of the companies. Decrease of the shrimp price since 2000-2001 due to the arrival of shrimps from farming on the market as well as the increase of oil seems to be the most important factors.

WP3) Bio-economic indicators will then be choose to characterise the state of the system.

Discussion

These works will contribute to a more holistic approach of the fishery management. It is usually call the ecosystem approach to fisheries and is in fact the applying of the principle of sustainable development : social equity and welfare, environment friendly and economic efficiency. However, according to this principle the human aspect remain here poorly known and studied; one more next step (among other possible) would be to integrate social sciences to be able to get also a diagnostic on the fishermen communities.

References

- Poulard, J-C., and Blanchard, F. (2005). The impact of climate change on the fish community structure of the eastern continental shelf of the Bay of Biscay. *ICES Journal of Marine Science* **62**, 1436-1443.
- Blanchard, F., and Vandermeirsch, F. (2005). Warming and exponential abundance increase of the subtropical fish *Capros aper* in the Bay of Biscay (1973-2002). *Comptes-Rendus Académie des Sciences, série Biologies* **328**, 505-509.

Marine Biology / Bacteriology

A Spatial and Temporal Study of the Benthic Communities in the Coral Reefs of the Bay Islands, Honduras

PEDRO PORTILLO, YOLANDE BOUCHON-NAVARO, MAX LOUIS, CLAUDE BOUCHON

Laboratoire de Biologie Marine-DYNECAR, Université des Antilles et de la Guyane,
BP 592, 97159 Pointe-à-Pitre, Guadeloupe, France
pportill@univ-ag.fr

Abstract

A study was conducted on the benthic communities of the coral reefs of the Bay Islands of Honduras (Utila, Roatán and Guanaja) with the objectives to describe in what way coral communities are organized and to identify the factors that influence the coral distribution around the Bay Islands. A total of 92 sites was surveyed qualitatively on the reefs according to different depths, reef geomorphological units, geographical location and different sectors of local pollution pressure. Data were analyzed by a canonical correspondence analysis in which species composition surveys were correlated to geomorphological, geographical and pollution factors used as ecological and anthropogenic explanatory variables. Three different coral communities were identified. Their distribution is explained in 21 % by reef geomorphological factors, 7 % by bacterial and chemical pollution pressure and 4 % by a latitudinal gradient. A total of 50 coral species was found. No differences were found for coral species richness and community distribution between the three islands. Species richness varied from 10 to 34 species according to the stations and increased from the reef flats toward the fore reefs with a maximum of species richness between 10 to 25 m. The average number of species was 17.5 (± 0.9) on the reef flats, 20.8 (± 1.8) on the upper part of the fore reefs and 23.9 (± 1.6) on the lower part between 10 to 25 m.

Introduction

The Bay Islands of Honduras are located in the south western part of the Caribbean Sea 40 to 50 kilometers off the Honduran north coast by 16° to 16° 30' N and 85° 50' to 87° W extended within a southwest-northeast axis. It is an archipelago composed of three major reef islands (Utila, Roatán and Guanaja), three minor islands and about 65 coral cays (Fig. 1).

The Bay Islands have a highly developed coral reef system composed of fringing reefs around the island of Utila and on the south coast of Roatán and Guanaja. Barrier reefs are found mostly on the north coasts of Roatán and Guanaja. Extended reef flats characterize the windward side of the islands in contrast to the leeward side where the reef flats are narrower and where the outer reef slope drop abruptly to a depth of 30 m.

Due to their close distance from the continent, the Bay Islands are influenced by direct discharges from the major rivers located in the north coast of Honduras. These islands are also submitted to different local pollution pressures due to the discharge of non-treated sewage and industrial wastewaters to the ocean. This is enhanced by the improper disposal of solid wastes and increasing deforestation as well as by the modification of littoral zones due to a rapid touristic development.

The present study describes in what way coral communities are organized and identifies the different factors that influence the coral distribution in the Bay Islands.

Materials and Methods

Underwater qualitative reef surveys were carried out according to different depths, reef geomorphological units, geographical location and different sectors under local pollution pressure.

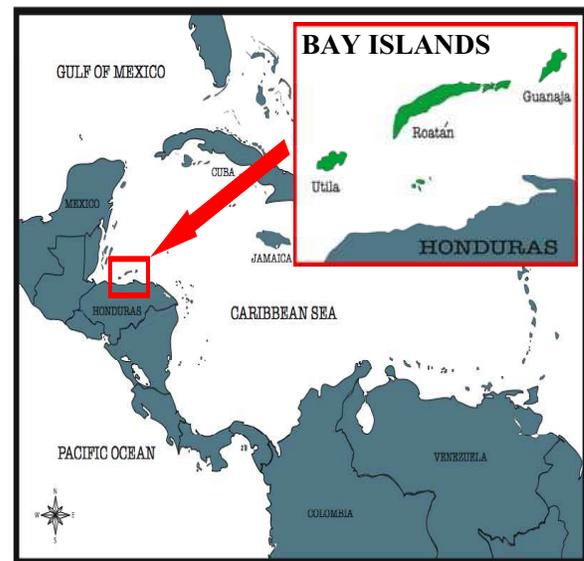


Figure 1: Location of the Bay Islands of Honduras in the Caribbean.

A total of 92 stations were studied: 24 in Utila, 50 in Roatán and 18 in Guanaja. Around the islands, different sectors corresponding to various local pollution pressure were delimited from a study on the quality of the coastal waters done by Lafforgue *et al.* (2001), in parallel to the present study.

Presence-absence data from the 92 sites were analyzed by a canonical correspondence analysis (ter Braak, 1988). Six pollution indices and a latitudinal and a longitudinal gradient constituted the quantitative variables. Qualitative descriptors corresponding to two main geographical locations (windward and leeward side of the islands) and 12 reef geomorphological units were also used as explanatory variables in the analysis.

Marine Biology / Bacteriology

Results and Discussion

A total of 50 coral species including three species of hydrocorals were identified. This can be compared to the latest species revision in the Caribbean done by Cairns (1999), in which 73 coral species were observed. It shows that the Bay Islands have very high coral species diversity.

No differences were found for coral species richness and community distribution between the three islands. Species richness varied from 10 to 34 species according to the stations and increased from the reef flats towards the fore reefs with a maximum of biodiversity between 10 to 25 m. This has been already observed in the Caribbean (Bouchon and Laborel, 1986,1990) and in the Indo-pacific region (Bouchon, 1996). The average number of species was 17.5 (± 0.9) on the reef flats, 20,8 ($\pm 1,8$) on the upper part of the fore reefs and 23.9 (± 1.6) on the lower part between 10 to 25 m.

The canonical correspondence analysis revealed that the corals species in the Bay Islands are distributed in three major groups: corals of the reef flats, corals of the shallow outer reef slopes from 1 to 5 m and corals from the deeper outer reef slopes from 5 to 25 m (Fig.2).

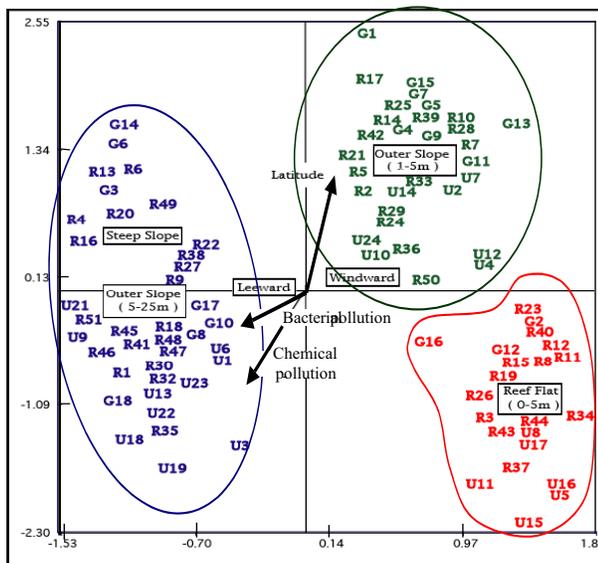


Figure 2: Canonical correspondence analysis biplot of sampling stations and ecological and anthropogenic descriptors.

Variance partitioning showed that 9 variables out of the 24 variables tested explained 32 % the coral distribution around the islands: 21 % is explained by geomorphological factors, 7 % by bacterial and chemical pollution pressure and 4 % by a latitudinal gradient. Among these factors coral communities are mainly controlled by depth. In fact, depth gathers two major ecological factors, which are light and water agitation. Water agitation is stronger in the shallow water areas and moderate in the outer slopes from 5 to 25 m. Both

indices influence the development of corals and the species composition of the zone.

Corals from the deeper outer slopes from 5 to 25 m are the group mostly affected by bacterial and chemical pollution. The bacterial pollution index consisted simultaneously of total coliforms and fecal coliforms counts strictly referring to *Escherichia coli* as a direct indicator of human fecal pollution. Fecal pollution can be related to various coral diseases and the presence of organic matter and nutrient discharges that enhance the eutrophication of the coastal waters and increase the competition for space between corals and macro algae. The chemical pollution index concerned mainly heavy metals such as copper, zinc, cadmium and lead associated with anticorrosive or antifouling paints and additives in the gasoline. Other compounds found in pesticides also composed this index. Chemical pollution threatens the corals reproductive physiology, which limits its population dynamics.

The existence of a significant impact of the latitudinal position of the stations confirms that there is a continental influence over the coral community. The river plumes originated from the continent that reach the Bay Islands carries organic matter, nutrients and particles in suspension. This also participates to the eutrophication of the island coastal waters and limits the penetration of light.

Coral communities in the Bay Islands are organized according to depth and reef morphological zones. Moreover, the distribution of coral species is influenced by a latitudinal gradient, which highlights a continental influence and is also sensitive to local bacterial and chemical pressure.

References:

1. Bouchon C., 1996. Recherches sur des peuplements de Sclératiniaires Indo-Pacifiques (mer Rouge, océan Indien, océan Pacifique). Thèse doctorat ès Sciences, Univ. Aix-Marseille II : 338 pp.
2. Bouchon C., Laborel J., 1986. Les peuplements coralliens des côtes de la Martinique. *Ann. Inst. Oceanogr.* Paris, 62 (1) : 251-289.
3. Bouchon C., Laborel J., 1990. Les peuplements coralliens du Grand Cul-de-Sac Marin de Guadeloupe (Antilles Françaises). *Ann. Inst. Oceanogr.* Paris, 66 (1-2) : 19-36.
4. Cairns S.D., 1999. Species richness on recent Scleratinia. *Atoll Res. Bull.*, 459: 1-46.
5. Lafforgue M., Pateron C., Ricard M., 2001. Informe complementario al diagnóstico de la calidad de las aguas de las Islas de la Bahía. Informe técnico No. CAC 04. Subprograma Manejo Integral de los Recursos Naturales. Proyecto de Manejo Ambiental de las Islas de la Bahía, Honduras: 194 pp.
6. ter Braak C.J.F., 1988. A FORTRAN program for canonical community ordination by (partial) (extended) (canonical) correspondence analysis, principal components analysis (version 2.1) Agricultural Mathematics Group, report LWA-88-02, Wageningen.

Significance of environmental variables for the structure of fish assemblages in the lagoon of the Grand Cul-de-Sac Marin (Guadeloupe, F.W.I.)

Amandine VASLET, Yolande BOUCHON-NAVARO, Claude BOUCHON and Max LOUIS

Laboratoire de biologie marine - DYNECAR

Campus de Fouillole, Université des Antilles et de la Guyane, 97167 Pointe à Pitre, Guadeloupe, France
amandine.vaslet@univ-ag.fr

Abstract

The aim of the study is to describe the spatial patterns of the mangrove shoreline fish assemblages in the lagoon of the Grand Cul-de-Sac Marin of Guadeloupe and to try to understand the processes affecting this distribution. For that, fishes were collected at 32 stations and 18 environmental variables were simultaneously measured. Canonical correspondence analyses and hierarchical clusterings revealed the existence of two geographical gradients controlling the fish distribution. The first one is a “coast-seawards” gradient which opposes stations located near river mouths to stations under coral reef influence. The second gradient corresponds to an “east-west” axis in the lagoon which could be interpreted as an enrichment of coral formations in the western part of the lagoon.

Introduction

Mangrove ecosystems are known to play an important ecological role for fish communities. They provide a shelter, a source of food and a nursery ground for numerous fish species (Ley, et al., 1999; Sheridan, Hays, 2003; Hindell, Jenkins, 2004). The mangroves of Guadeloupe have been studied since 1974 (Louis et Lasserre, 1982; Louis et Baelde, 1987; François-Lubin, 2005; Vaslet, 2005). Louis (1983) identified three systems which composed the mangrove ecosystem: the channel system, the mangrove lagoon system and the mangrove shoreline system. This research is undertaken in order to study the relationships between fish spatial distribution and environmental variables in this last system.

Materials and Methods

The Grand Cul-de-Sac Marin is a lagoon of 11 000 hectares limited along the coast by a mangrove fringe and seawards by a barrier reef. A total of 32 stations were sampled along the mangrove fringe of the lagoon and around several islets. The sampling area spread from Sainte Rose on the west to the Rotour's channel on the east including Carénage, Fajou and Macou's islets (Fig. 1).

Fish were sampled using a hoop net called “capéchade” which was settled during 24 hours at

fence net (35 m long, 2 cm mesh size) which deviated fish migrating along the shore into three hoop nets. The sampling period took place from February to April 2005, during the dry season. The fish were brought back to the laboratory where they were identified, counted, measured and weighed.

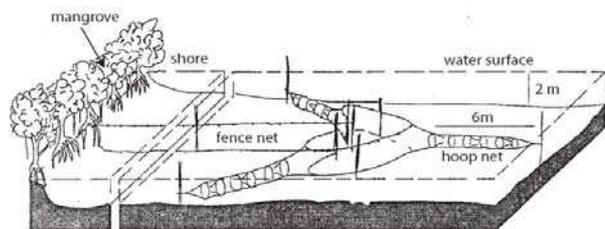


Figure 2: The fish hoop net called “capéchade” used to sample in the mangrove.

At each station, 16 quantitative environmental descriptors were measured: latitude, longitude, temperature, salinity, pH, dissolved oxygen, nitrate and phosphate concentrations, turbidity, depth, chlorophyll a, pheophytin a, suspended materials, organic materials present in sediment, reef and river proximity. Two qualitative variables were also

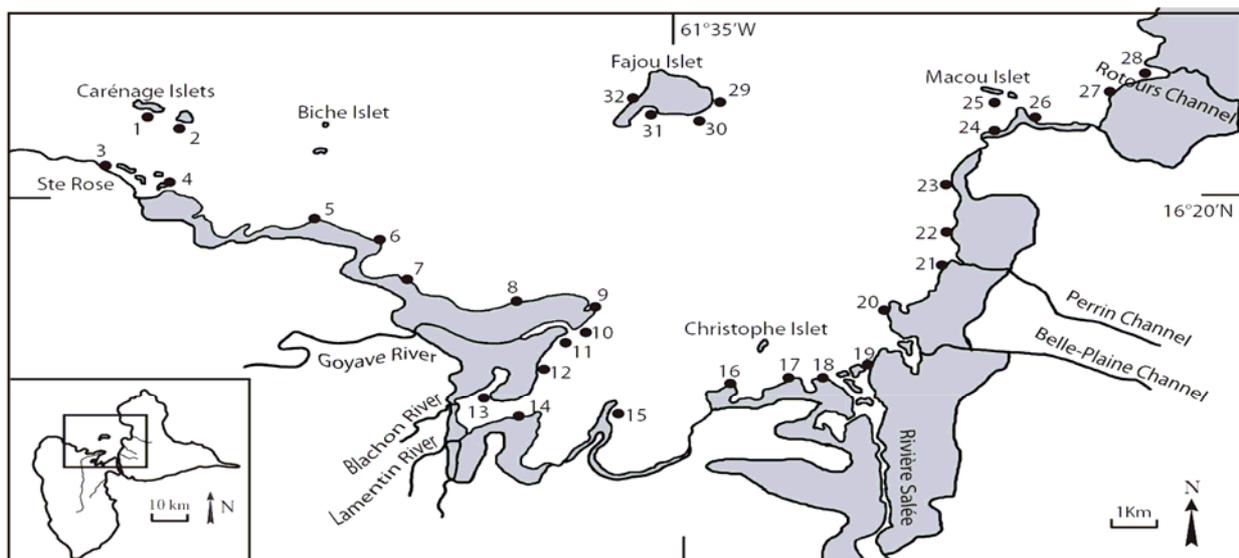


Figure 1: Location of sampling stations in the lagoon of the Grand Cul-de-Sac Marin in Guadeloupe.

indicated such as the water motion (calm or turbulent) and the presence or absence of seagrass beds.

Statistical analyses like canonical correspondence analyses (ter Braak, 1994) and hierarchical clusterings were performed on the data calculated from fish abundance, biomass and presence-absence.

Results and Discussion

A total of, 89 fish species belonging to 37 families were identified. Rare species (only one specimen per species) were not included in the analyses. Statistical analyses were performed on fish abundance, fish biomass and fish presence-absence data and gave similar results. Thus, only those obtained with fish abundance are described.

CCA analyses revealed and explained relationships between environmental descriptors and fish abundance. The biplot built with axis 1 and axis 2 showed a Guttman effect due to a quadratic relation between the two axes (Legendre et Legendre, 1998). Thus, the final factorial plan was plotted using axes 1 and 3. This projection reveals higher canonical correlations with environmental descriptors (Fig.3). Hierarchical classification was performed on fish abundance and divided the stations into four groups. Those groups are also represented on the plan and revealed the existence of several assemblages in the fish community (Fig.3).

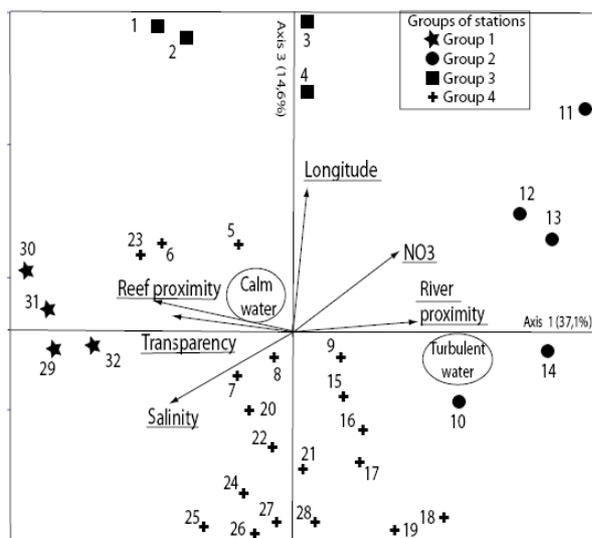


Figure 3: Canonical correspondence analyse biplot of sampling stations and environmental descriptors.

On the CCA biplot (Fig.3), only statistical significant descriptors are indicated. The two axes explained 51,7% of the canonical analysis (axis 1: 37,1%; axis 3: 14,6%). On axis 1, the first group of stations is correlated to water transparency, salinity, reef proximity and calm water (Fig.3). On the other side of this axis, stations of group 2 are linked to nitrate concentrations, river proximity and rough water. Thus, those stations are opposed along a “coast-seawards” gradient. On the third axis of the CCA biplot, a correlation was found with the factor “Longitude” which could be linked to an “east-west” separation of the lagoon fish assemblages. On the west part of the lagoon, the seagrass beds include coral heads whereas these are absent in the eastern

part. This second gradient separates the stations of groups 3 and 4.

Statistical analyses have demonstrated the existence of two geographical gradients controlling the fish distribution. The first gradient is a “coast-seawards” gradient which opposed stations under coral reef influence to stations located near river’s mouth. This gradient is characterized by six environmental descriptors: salinity, reef proximity, river proximity, nitrate concentrations, water transparency and water motion. The second gradient was correlated to the variables “Longitude” corresponding to an “east-west” separation in the lagoon. This gradient could be also interpreted as a westward decreasing terrestrial influence revealed by an enrichment of the western part of the lagoon with coral formations. That explains the presence of reef fish species mixed to the typical mangrove fish community. To complete the present study, further investigations have been undertaken concerning the temporal variation of the fish assemblages of the mangrove shoreline system.

Acknowledgements

Thanks are expressed to the Parc National de la Guadeloupe for the support of this study.

References

- François-Lubin V., 2005. Les peuplements de poissons des canaux et des rivières: “Le cas du canal Belle-Plaine” (Guadeloupe). Thèse de doctorat. Université des Antilles et de la Guyane: 350 pp.
- Hindell J. S., Jenkins G. P., 2004. Spatial and temporal variability in the assemblage structure of fishes associated with mangroves (*Avicennia marina*) and intertidal mudflats in temperate Australian embayments. *Marine Biology*. 144: 385-395.
- Legendre L., Legendre P., 1998. Numerical ecology. 2nd English edition. Elsevier Science BV, Amsterdam: vx + 853 pp.
- Ley J. A., McIvor C. C., Montague C. L., 1999. Fishes in mangrove prop-root habitats of northeastern Florida Bay: distinct assemblages across an estuarine gradient. *Estuarine, Coastal and Shelf Science*. 48: 701-723.
- Louis M., 1983. Biologie, écologie et dynamique des populations de poissons dans les mangroves de Guadeloupe (Antilles Françaises). Thèse de doctorat, Université de Montpellier II: 275 pp.
- Louis M., Baelde P., 1987. Fish communities in Guadeloupe mangroves. *Proc. V Congr. europ. Ichtyol. Stockholm* 1985. 175-180.
- Louis M., Lasserre G., 1982. Etude du peuplement de poissons dans les lagunes des mangroves de Guadeloupe (Antilles Françaises). *Symposium International sur les lagunes côtières, Bordeaux (France)*. *Oceanologica Acta*. N° SP Septembre. 333-338.
- Sheridan P., Hays C., 2003. Are mangroves nursery habitat for transient fishes and decapods? *Wetlands*. 23: 449-458.
- ter Braak C. J. F., 1994. Canonical community ordination. Part I: Basic theory and linear methods. *Ecoscience*. 1: 127-140.
- Vaslet A., 2005. Dynamique spatiale des peuplements ichthyologiques de la bordure lagunaire du Grand Cul-de-Sac Marin en Guadeloupe (Antilles Françaises). Rapport de stage de DEA, Université des Antilles et de la Guyane : 40 pp.

Seagrass Beds As Important Habitats For Juvenile Fishes In The Bay Of The Grand Cul-De-Sac Marin (Guadeloupe, F.W.I.)

Dorothee Kopp, Yolande Bouchon-Navaro, Claude Bouchon, Max Louis
Laboratoire de Biologie Marine, DYNECAR, Université Antilles-Guyane, Campus de Fouillol
97159 Pointe-à-Pitre Cedex, Guadeloupe - France - dkopp@univ-ag.fr

Abstract

In Guadeloupe, seagrass beds of *Thalassia testudinum* occupy important areas in the lagoon of the bay of the Grand Cul-de-Sac Marin. To examine the influence of adjacent shallow water habitats like coral reefs and mangroves on the seagrass juvenile fish assemblages, two seagrass beds were studied: one located near a coral reef, and one near coastal mangroves. Both habitats were sampled using a seine-net and a trap net.

The examination of minimal and maximum lengths for each species of the two sites revealed that the majority of the fishes caught in the samplings are of small size. The mean size of a fish was found to be 7.9 ± 0.2 cm in the coastal seagrass beds and 7.5 ± 0.2 cm in the seaward ones. Individuals less than 8 cm represented 70% of the fish population near the reef and 59% close to mangroves. Both types of seagrass beds function as an important nursery habitat for juveniles since an equivalent number of fishes with a size inferior to 6 cm was found in both sites. The examination of the faunistic list revealed that near the reef, the recruitment of juveniles was due to coral-reef fishes in addition to the typical seagrass species. Near mangroves, seagrass beds represent a good recruitment area for species from different origins (mangrove, seagrass and reefs).

Introduction

The role of seagrass beds as nursery and feeding grounds for fishes is widely recognized (Parrish 1989, Yañez-Arancibia et al. 1994, Jackson et al. 2001). In tropical areas, the seagrass beds are often adjacent to coral reefs and mangroves and offer an opportunity to study the ecological interactions between these ecosystems. In the Grand Cul-de-Sac Marin bay in Guadeloupe, the ichthyofauna has already been studied in mangroves (Louis and Guyard 1982), in seagrass beds (Bouchon-Navaro et al. 2004) and in coral reefs (Bouchon-Navaro 1997) but the linkage of fishes between these biotopes remain largely unknown. The aim of this study was to examine if two seagrass beds, either associated with mangroves or coral reefs, were used as equivalent nursery grounds for juvenile fishes.

Materials and Methods

Two sampling sites were chosen in the Grand Cul-de-Sac Marin bay (Figure 1), one located near the fringing mangroves (seagrass-mangrove) and one located close to the reef crest (seagrass-reef). Both seagrass beds consist of *Thalassia testudinum* intermingled with sparse *Syringodium filiforme*.

Two fishing gears were used: a seine-net (Figure 2) and a trap net called "capéchade" (Figure 3).

To determine if the fishes were on juvenile stage, we decided to consider as juvenile all the fishes which are smaller than the minimum maturation size L_m determined with the equation of Froese and Binohlan (2000).

Results and Discussion

A total of 98 fish species belonging to 36 families were collected in the two seagrass beds. 71 were observed in the seagrass - reef, 50 species in the seagrass - mangrove and 23 species were observed at both sites.



Figure 1: The Grand Cul-de-Sac Marin bay

According to the calculated L_m , 74 species were represented only by juvenile fishes, 20 species present juvenile and adult fishes and four species were represented only by adult fishes.

A total of 21 442 fish was collected in the two sites. In the seagrass-reef, 9 555 fishes were collected and 87.7% of the fishes were juveniles. In the seagrass-mangrove, a total of 11 887 fishes were captured and 98.3% of the fishes collected were under the size of maturity. Concerning biomass, the data showed that in the seagrass-reef the juveniles represented respectively 73.6% and 97.4% of the total biomass collected in the seagrass-reef (44.4 kg) and in the seagrass-mangrove (65 kg).

Marine Biology / Bacteriology

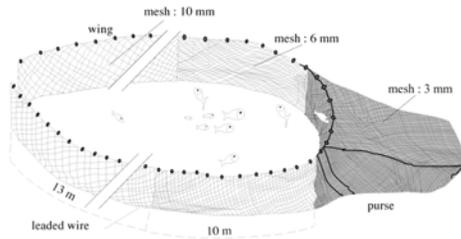


Figure 2: The seine-net

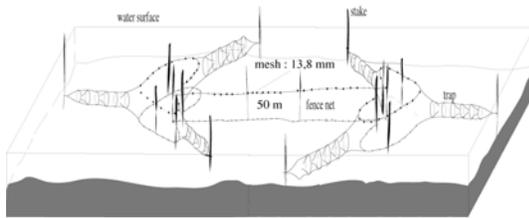


Figure 3: The "capéchade"

The examination of minimal and maximum lengths for each species of the 2 sites reveals that the majority of the species captured in the samplings are of small size. The mean size of a fish in the seagrass meadows was found to be 7.7 ± 0.12 cm (7.9 ± 0.16 cm in the coastal seagrass beds and 7.5 ± 0.20 cm in the seaward ones). Examination of the distribution of size-classes for all the collected fishes shows that small-sized individuals formed the majority of the fish community. Individuals less than 8 cm represent 70% of the fish population near the reef and 59% close to mangroves. Figure 4 shows that both seagrass beds function as important nursery habitats for juvenile fishes since an equivalent number of individuals between 0 and 6 cm was found in the 2 sites. Seagrass beds close to mangroves shelter more medium-sized fishes (6 to 14 cm) than those close to the reef. A Kolmogorov-Smirnov test shows that there is no significant difference between the two size distributions ($p > 0.99$). The modal class for the two distributions is 4-6 cm.

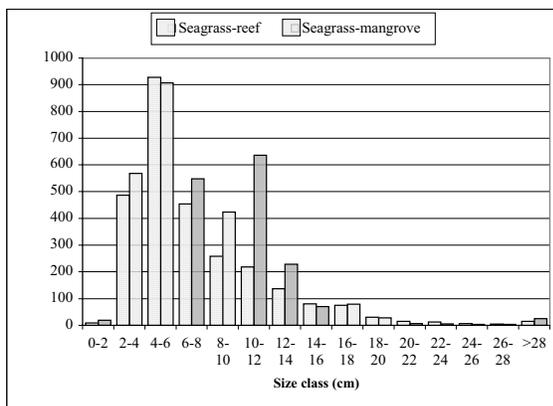


Figure 4: Distributions of size classes for seagrass fish communities

After considering all the individuals, the distribution of size classes was analysed for some species for which enough data were available. Examination of the histograms for the common species shows that juvenile fishes seem to be more abundant near the coast than near the reef. The fishes of big size are mainly observed in the seagrass-reef while the small-sized fishes of the same species are mainly found in the seagrass-mangrove. The histograms concerning mangrove species reflect the tendency observed on Figure 4. A first peak is observed between 2 and 4 cm and a second one between 12 and 14 cm. This higher abundance of medium sized fishes is only observed for the fish populations near mangroves.

The results of the present study highlight the fundamental role of *Thalassia testudinum* seagrass beds for the juvenile fish assemblages and the importance of the location of the seagrass beds, either near the reefs or near mangroves. This study confirms with quantitative data the role of these seagrass beds as nurseries and recruitment areas in Guadeloupe as it has already been reported in the Caribbean region. Moreover, seagrass beds harbour a lot of juveniles of commercially valuable species and their protection will be necessary for a sustainable management of resources for coastal fisheries. They must be included in the marine protected areas as coral reefs and mangroves.

References:

1. Bouchon-Navaro Y. (1997). Les peuplements ichtyologiques récifaux des Antilles. Distribution spatiale et dynamique temporelle. *PhD Thesis*, Université Antilles-Guyane, 242 pp.
2. Bouchon-Navaro Y., Bouchon C., and Louis M. (2004). L'ichtyofaune des herbiers de Phanérogames marines des Antilles françaises: intérêt de leur protection. *Revue Ecologie (Terre Vie)* 5, 253-272.
3. Froese R. and Binohlan C. (2000). Empirical relationships to estimate asymptotic length, length at first maturity and length at maximum yield per recruit in fishes, with a simple method to evaluate length frequency data. *Journal of Fish Biology* 56, 758-773.
4. Jackson E., Rowden A., Attrill M., Bossey S., and Jones M. (2001). The importance of seagrass beds as habitat for fishery species. *Oceanography and Marine Biology Annual Review* 39, 269-303.
5. Louis M. and Guyard A. (1982). Contribution à l'étude des peuplements ichtyologiques dans les mangroves de Guadeloupe (Antilles françaises). *Bulletin Ecologie* 13, 9-24.
6. Parrish J. (1989). Fish communities of interacting shallow-water habitats in a tropical oceanic region. *Marine Ecology Progress Series* 58, 143-160.
7. Yañez-Arancibia A., Lara-Dominguez A. and Pauly D. (1994). Coastal lagoons as fish habitats. In: Kjerfve, B. (Ed.), *Coastal Lagoon Processes* 12. Elsevier Science Publishers, Amsterdam, 363-376.



Marine Biology / Bacteriology

Colonization of Sunken Wood in the Caribbean Area: Influence of the Environment

M. Laurent and O. Gros

UMR-CNRS 7138, Systématique-Adaptation-Evolution, Equipe « Symbiose ». Université des Antilles et de la Guyane. UFR des Sciences Exactes et Naturelles, Département de Biologie. B.P. 592. 97159 Pointe-à-Pitre Cedex, Guadeloupe. France. olivier.gros@univ-ag.fr

Abstract

The work proposed here will focus on the question of the biodiversity, establishment, and function of organisms associated with marine wood falls, in the Caribbean area. This program relies on conducting both field studies on natural systems and experiments in various environments, particularly around Guadeloupe (16°N 61.5W) West Indies where some densities of wood falls could occur. Wood degradation and organisms establishment will be followed by regular field observations.

As an experimental strategy, we propose the deployment of wood parcels experimentally immersed between 600m and 2000m via anchors of Fish Aggregating Devices (FADs) and/or in shallow water environment (mangrove swamp and seagrass). Moreover, miniature in situ sensors will be deployed with the woods in order to monitor in situ physical and chemical parameters characterizing the wood interface during its decomposition in relation with the process of colonization by symbiotic organisms as mussels. Thus, we will be able to investigate the colonization process in relation to the environmental changes induced by wood decomposition and colonisation.

First results obtained using SEM and FISH observations are presented here showing that some of the organisms colonizing such woods possessed bacterial symbionts as observed in some protozoans and metazoans as nematodes.

Bacterial Symbiosis in Wood Fall Bivalves

M.C.Z. Laurent and O. Gros

UMR-CNRS 7138, Systématique-Adaptation-Evolution, Equipe « Symbiose ». Université des Antilles et de la Guyane. UFR des Sciences Exactes et Naturelles, Département de Biologie. B.P. 592. 97159 Pointe-à-Pitre Cedex, Guadeloupe. France - olivier.gros@univ-ag.fr

Abstract

During the Panglao cruise in the Bohol sea (Philippines) in May 2005, various bivalves associated with sunken wood were collected between 300 and 1800 meter depths.

Results from our study demonstrated the existence of bacterial symbionts in the lateral zone of the gill filaments. These bacteria are extracellular in the mytilids collected and intracellular in the lucinid species examined. Extracellular bacteria are located between microvilli at the apical surface of the cells all along the lateral zone of gill filaments while endocellular bacteria observed are envacuolated in large cells called bacteriocytes. Based on TEM observations, these gram negative bacteria are not methanotrophic due to the lack of concentric stacking of intracellular membranes in their cytoplasm. Based on FISH experiments, these bacteria are γ -Proteobacteria excepted in one sample where positive hybridizations were observed with β -Proteobacteria probes.

These results underline the diversity of organisms associated with sunken wood and the importance of chemosynthetic symbiosis in this kind of "ecosystems". Comparative studies on experimentally sunken wood are in progress in the Caribbean area in various kinds of environments (mangrove swamp, seagrass and deep sea) in order to provide more data about biogeography and establishment and biodiversity of fauna associated with sunken wood.



Marine Biology / Bacteriology

Description Of The Extracellular Bacterial Interactions In Marine Nematodes From *Thalassia testudinum* Environment.

L. C. Maurin and O. Gros

UMR-CNRS 7138, Systématique-Adaptation-Evolution, Equipe « Symbiose ». Université des Antilles et de la Guyane. UFR des Sciences Exactes et Naturelles, Département de Biologie. B.P. 592. 97159 Pointe-à-Pitre Cedex, Guadeloupe. France. - olivier.gros@univ-ag.fr

Abstract

The marine free-living nematodes and particularly those belonging to the family of Stilbonematinae are usually found in the microoxic zone of the sulfidic sediments (Shiomer et al., 1990). In this study, we have investigated the nematodes living in the seagrass bed of *T. testudinum* known to possess sulfur-oxidizing organisms such as the lucinid clams.

The results presented here demonstrate the existence of extracellular bacteria located on the body surface of these nematodes by SEM and FISH analyses. At least four morphotypes of nematodes were identified harbouring bacteria on their cuticle. Based on SEM observations, each symbiotic nematode possesses a particular bacterial coat constituted by a typical bacterial morphotype characterized by its shape and size. Moreover, *in situ* hybridization (FISH) with oligonucleotide probes have shown that these extracellular symbionts are eubacteria. Experiments are in progress to identify the group of membership of these bacteria (α , β , γ or δ -Proteobacteria) by using other specific probes.

Such ectosymbionts may represent thioautotrophic bacteria as already described in various nematodes from other sulfidic environments. No phylogenetic analysis was done in this study to compare their DNA sequence to that of other marine invertebrate symbionts described to date.

Reference: Schiomer F., Novak R., and Ott J. 1990. Metabolic studies on thiobiotic free-living nematodes and their symbiotic microorganisms. *Marine Biology* 106: 129-137.

Observation of Marine Nematodes Along a Transect Beach-Seagrass Beds of *Thalassia testudinum*: a SEM Analysis

L.C. Maurin, C. Grateloup, M. Delannay and O. Gros

UMR-CNRS 7138, Systématique-Adaptation-Evolution, Equipe « Symbiose ». Université des Antilles et de la Guyane. UFR des Sciences Exactes et Naturelles, Département de Biologie. B.P. 592. 97159 Pointe-à-Pitre Cedex, Guadeloupe. France. olivier.gros@univ-ag.fr

Abstract

In the marine sediments, the most important taxon of the meiofauna is represented by free-living nematodes, which account for 60% to 90% of the total fauna (Coull, 1999). Some of them belonging to the family of Stilbonematinae present strong interactions with symbiotic bacteria (Polz et al., 1992).

The marine nematodes collected along a transect beach - marine seagrass bed in Guadeloupe were observed by Scanning Electron Microscope (SEM) in order to determine the presence of bacterial ectosymbionts on their cuticle.

The preliminary results obtained show a nematofaunal composition slightly different along the transect with 5 ectosymbiotic species of nematodes associated with *T. testudinum* sediment against 2 species collected in sand between the seagrass bed and the beach. Non-symbiotic nematodes were also observed : 4 species were frequently found in the sediment of the seagrass against 2 species outside *T. testudinum* environment. While non-symbiotic nematodes are characterized by a high abundance compared to the symbiotic ones, their specific diversity appeared lower.

These observations describe (i) the distribution of the ectosymbiotic and non-ectosymbiotic nematodes in shallow water *T. testudinum* beds and (ii) the diversity of the extracellular symbiotic interactions of the marine nematodes in sediment.

Further studies would be necessary to account for the whole of meiofauna in such ecosystem and evaluate all symbiotic organisms colonizing *T. testudinum* environment.

References:

Coull B.C. 1999. role of meiofauna in estuarine soft-bottom habitats. *Australian Journal of Ecology* 24: 327-343.
Polz M., Felbeck H., Novak R., Nebelsick M., Ott J. 1992. Chemoautotrophic, sulfur-oxidizing symbiotic bacteria on marine nematodes: morphological and biochemical characterization. *Microbial Ecology* 24: 313-329.