

MICROFOULING COMMUNITY IN BAY OF CARTHAGE (NORTHERN TUNISIA) : PRELIMINARY IDENTIFICATION AND BIOACTIVE PROPERTIES

Wafa Cherif¹, Leila Ktari^{1*}, Ons Dali Yahya - Kefi² and Monia El Bour¹
¹ INSTM: 28, Rue 2 mars 1934 Salammbô 2025 Tunisie - leila.ktari@instm.nrnt.tn
² INAT: 43, Avenue Charles Nicolle 1082 Cité Mahrajène Tunisie

Abstract

Marine bio-fouling concerns any immersed structure. In order to specify fouling mechanism, we studied microbial communities and bioactive interactions for biofilms obtained from an experimental disposal.

Keywords: Fouling, Bacteria, Diatoms, Biodiversity

Introduction

In seawater, immersed structures rapidly accumulate colonising organisms that may range from microscopic bacteria to larger larvae or invertebrates. The first stage of this biofouling consists on a biofilm formed by unicellular organisms specially bacteria and microalgae [1]. Thus, we focused on these microfouling communities formed on an immersed experimental system to analyse biodiversity and potential biological activities.

Methods

Bacteria and microalgae were isolated from immersed steel and glass plates disposed in a shallow marine site (Bay of Carthage – northern coast of Tunisia) [2]. *Identification*: Bacteria strains were specified basically on cultural, morphological and biochemical identification while morphological identification of fouling microalgae was realised on the basis of microscopic observations. *Antagonism test*: Disc diffusion method [3] was used to detect the potential antagonistic effect of all isolates against 15 sensitive bacteria including fish and human pathogens.

Results and discussion

A group of thirty one bacterial strains were isolated with predominance of Gram negative (58%) mainly *Aeromonas hydrophila* and *Pseudomonas vesicularis* (Table1).

Tab. 1. Isolated microorganism from steel and glass plates.

Identified bacteria	Identified microalgae
<i>Weeksella virosa</i> ;	<i>Licmophora sp.</i> ; <i>L.</i>
<i>Shezarella putrefaciens</i> ;	<i>dalmatica</i> ; <i>L. anglica</i> ;
<i>Chryseobacterium</i>	<i>Nitzschia sp.</i> ; <i>N.</i>
<i>marinosepticum</i> ;	<i>frustulum</i> ; <i>N. palea</i> ; <i>N.</i>
<i>Brevundimonas</i>	<i>dissipata</i> ; <i>N.</i>
<i>vesicularis</i> ;	<i>longissima</i> ; <i>N.</i>
<i>Staphylococcus</i>	<i>angularis</i> ;
<i>Epidermidis</i> ;	<i>Synedra sp.</i> ; <i>S.</i>
<i>Aeromonas hydrophila</i> ;	<i>barbatula</i> ; <i>S. pulchella</i> ;
<i>Staphylococcus xylosum</i> ;	<i>Grammatophora sp.</i> ; <i>G.</i>
<i>Pantoea spp.</i> ;	<i>oceanica</i> ;
<i>Pseudomonas putida</i> ;	<i>Pevonia erinacea</i> ;
<i>Chryseobacterium</i>	<i>Swirella sp.</i> ;
<i>indologenes</i> ;	<i>Pleurosigma sp.</i> ;
	<i>Fragilaria sp.</i> ;
	<i>Navicula sp</i>

Besides, 19 different species of microalgae, all diatoms, were identified with dominance of: *Licmophora* and *Nitzschia*.

Antagonism test revealed interesting activities for one specie: *Chryseobacterium indologenes* with large spectrum of activity mainly against *Staphylococcus aureus* (Table 2).

Tab. 2. Antagonistic activity of fouling bacteria *Chryseobacterium indologenes* against pathogenic strains.

Test strains	Inhibition zone (mm)
<i>Escherichia coli O126B16</i>	12
<i>Staphylococcus aureus</i>	35
<i>ATCC 25923</i>	
<i>Salmonella typhylum</i>	10
<i>E. coli ATCC25922</i>	7
<i>Enterococcus faecalis ATCC 29212</i>	traces

Results obtained were in accordance with previous studies, particularly for the predominance of *Pseudomonas sp.* [4] in the bacterial community and *Licmophora sp.* for microalgae [5].

Further experimentations are in progress for molecular speciation of producers.

References

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