

Molecular structure of bacterial biofilms involved in iron biocorrosion

Florence Mercier-Bion, Catherine Berthomieu-Hiene, Virginie Chapon, Jean-Paul Gallien, Laurent Urios, Delphine Neff, Philippe Dillmann

► **To cite this version:**

Florence Mercier-Bion, Catherine Berthomieu-Hiene, Virginie Chapon, Jean-Paul Gallien, Laurent Urios, et al.. Molecular structure of bacterial biofilms involved in iron biocorrosion. EuroCorr 2019, Sep 2019, Seville, Spain. cea-02327914

HAL Id: cea-02327914

<https://hal-cea.archives-ouvertes.fr/cea-02327914>

Submitted on 23 Oct 2019

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Molecular structure of bacterial biofilms involved in iron biocorrosion

Florence MERCIER-BION⁽¹⁾, Catherine BERTHOMIEU-HIENE⁽²⁾, Virginie CHAPON⁽²⁾, Jean-Paul GALLIEN⁽¹⁾, Laurent URIOS⁽³⁾, Delphine NEFF⁽¹⁾, Philippe DILLMANN⁽¹⁾

- (1) Laboratoire Archéomatériaux et Prévision de l'Altération, NIMBE, CEA-CNRS, Université Paris-Saclay, CEA Saclay, 91191 Gif-sur-Yvette, France
- (2) Laboratoire Interactions Protéine Métal, CEA Cadarache, 13307 Saint-Paul-les-Durance, France
- (3) IPREM, Université de Pau et des Pays de l'Adour, 64000 Pau, France

To a better knowledge of iron biocorrosion mechanisms occurring in different applications (nuclear context, petroleum industry, cultural heritage,...), it is crucial to define which bacteria are active and their role. Despite a wide literature on the influence of bacteria on iron corrosion rates, most often considering a single metabolic group (Iron-Reducing Bacteria IRB, Sulfate-Reducing Bacteria SRB), the role of each species in a population involving various metabolisms possibly affecting corrosion remains unknown. At the same time, it is also essential to identify the corrosion products and to be able to link them to a possible bacterial activity. Our study is then devoted to the local diagnostic of the action of bacterial strains in iron corrosion. An innovative methodology for diagnosing the active bacterial strains in iron corrosion at the micrometric scale was developed by using vibrational techniques such as Attenuated Total Reflection Infra-Red ATR-IR and μ Raman spectroscopies. The first step was the set-up of a preparation protocol and its optimization for the characterization of bacteria by ATR-IR to obtain the vibrational fingerprint of bacterial strains performing metabolisms already identified in the nuclear context (IRB, SRB and sulfate-oxidizing bacteria SOB). The spectral fingerprint was also determined for iron coupons corroded in the presence of each strain. The question of the ability to discriminate the strains, whether planktonic or in biofilm, by their vibrational fingerprint was resolved. Indeed, the discrimination of the three bacterial strains was possible in the spectral region around 1000 cm^{-1} . Furthermore, the strains evidenced spectra differences according to their growth mode: for strains in planktonic form, the most intense bands of the IR spectrum were those of amide I and II while for the ones in biofilm form, these were the bands of exopolysaccharides (compounds excreted by bacteria when they form biofilms) in the region around 1000 cm^{-1} . These results allow discrimination by the ATR-IR spectrum of different bacterial strains in planktonic or in biofilm form. Since both the three strains but also their form (planktonic or biofilm) were distinguishable by their IR spectrum, experiments were conducted on iron coupons corroded with the bacterial consortium. The objective was to determine the active strains and to couple this information with the nature of the corrosion products. This diagnostic tool for bacterial signature determination can be transposed to a variety of corrosion problems providing significant benefits.