



**HAL**  
open science

## Labelling strategy and membrane characterization of marine bacteria *Vibrio splendidus* by in vivo <sup>2</sup>H NMR

Zeineb Bouhleb, Alexandre A Arnold, Dror E. Warschawski, Karine Lemarchand, Rejean Tremblay, Isabelle Marcotte

### ► To cite this version:

Zeineb Bouhleb, Alexandre A Arnold, Dror E. Warschawski, Karine Lemarchand, Rejean Tremblay, et al.. Labelling strategy and membrane characterization of marine bacteria *Vibrio splendidus* by in vivo <sup>2</sup>H NMR. *Biochimica et Biophysica Acta: Biomembranes*, 2019, 1861 (4), pp.871-878. 10.1016/j.bbamem.2019.01.018 . hal-02567658

**HAL Id: hal-02567658**

**<https://hal.science/hal-02567658>**

Submitted on 30 Nov 2020

**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.

# Labelling strategy and membrane characterization of marine bacteria *Vibrio splendidus* by *in vivo* $^2\text{H}$ NMR

*Zeineb Bouhlef*<sup>1,2</sup>, *Alexandre A. Arnold*<sup>1</sup>, *Dror E. Warschawski*<sup>1,3</sup>, *Karine Lemarchand*<sup>2</sup>, *Réjean Tremblay*<sup>2</sup> and *Isabelle Marcotte*<sup>1\*</sup>

<sup>1</sup> Department of Chemistry, Université du Québec à Montréal, P.O. Box 8888, Downtown Station, Montreal, Canada, H3C 3P8

<sup>2</sup> Institut des Sciences de la Mer de Rimouski, Université du Québec à Rimouski, 310 allée des Ursulines, Rimouski, Canada G5L 3A1

<sup>3</sup>UMR 7099, CNRS - Université Paris Diderot, IBPC, 13 rue Pierre et Marie Curie, F-75005 Paris, France

\*Corresponding author

Tel: 1-514-987-3000 #5015

Fax: 1-514-987-4054

*E-mail: [marcotte.isabelle@uqam.ca](mailto:marcotte.isabelle@uqam.ca)*

## ABSTRACT

*Vibrio splendidus* is a marine bacterium often considered as a threat in aquaculture hatcheries where it is responsible of mass mortality events, notably of bivalves larvae. This bacterium is highly adapted to dynamic salty ecosystems where it has become an opportunistic and resistant species. In an attempt to characterize their membranes as a first and necessary step toward studying bacterial interactions with diverse molecules, we establish a labelling protocol for *in vivo*  $^2\text{H}$  solid-state nuclear magnetic resonance (SS-NMR) analysis of *V. splendidus*.  $^2\text{H}$  SS-NMR is a useful tool to study the organization and dynamics of phospholipids at the molecular level, and its application to intact bacteria is further advantageous as it allows probing acyl chains in their natural environment and study membrane interactions. However, due to the complexity of metabolic pathways and biological systems, isotopic labelling can be challenging. In this study, we show that *V. splendidus* can be labelled using deuterated palmitic acid, and demonstrate the importance of surfactant choice in the labelling protocol. Moreover, we assess the impact of lipid deuteration on the general fitness of the bacteria, as well as the ratio of saturated-to-unsaturated fatty acid chains and its impact on the membrane properties. We further characterize the evolution of *V. splendidus* membrane fluidity during different growth stages and relate it to fatty acid chain composition. Our results show a superior membrane fluidity during the stationary growth phase compared to the exponential growth phase under labelling conditions - an information to take into account for future *in vivo* SS-NMR studies. Our lipid deuteration protocol optimized for *V. splendidus* is likely applicable other microorganisms for *in vivo* NMR studies.

## KEYWORDS

In-cell NMR, deuterium, isotopic labelling, membrane fluidity, fatty acids, magic-angle spinning

## ABBREVIATIONS

CHAPS, 3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulfonate hydrate; cyC17:0, cyclopropaneoctanoic acid-2-hydroxyl acid; cyC19:0, cyclopropaneoctanoic acid-2-octyl acid; CMC, critical micelle concentration; d<sub>31</sub>-PA, deuterated palmitic acid; DF, degree of freedom; DPC, dodecylphosphocholine; F, F-statistic; FA, fatty acid; FAME, fatty acid methyl ester; GC-MS, gas chromatography-mass spectrometry; M<sub>2</sub>, second spectral moment; MTT, 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide; OA, oleic acid; OD, optical density; OG, octylglucopyranoside; LB, Lysogeny broth; P, probability value; PA, palmitic acid; SFA, saturated fatty acid; SS-NMR, solid-state nuclear magnetic resonance; MAS, magic angle spinning; UFA, unsaturated fatty acid.

## 1. INTRODUCTION

*Vibrio* species are Gram-negative bacteria widely spread in coastal marine and estuarine waters and sediments [1-4]. They might also be found in aquatic animal tissues, causing serious pathologies leading in some cases to economic loss in aquaculture industry [5-8]. To date, most research on marine *Vibrio* species concerned their effects on aquatic organisms acting on immunological process [8-14]. As a matter of fact, a common trait of all members of the *Vibrio* genus is their opportunistic nature, which allows them to benefit from the collapse of the immune system of cultured organisms in specific conditions to become virulent [14, 15]. Investigating the virulence/response of these species requires considering numerous biotic and abiotic factors where the physiological responses can remain elusive. For instance, *V. splendidus* are different from their *Vibrio* congeners by their high genetic variability between strains, where each strain can have a different opportunistic and/or virulence pattern [8, 15, 16].

Very few researches have so far focused on the membranes of environmental bacteria compared to human pathogens, albeit the importance of the external cell envelopes in biological events. Marine bacteria are of great interest for membrane properties investigation considering their high resistance phenotypes and high adaptability to a large scale of salinity and temperature, attributable to their permanent exposure to changing ecosystems [1, 3, 4, 11, 17-21]. Moreover, marine and coastal environments constitute a dynamic platform for water mixing, thus containing a plethora of molecules such as pollutants, aquatic bioactive components, organic or chemical toxins and industrial antibiotics [22-27]. The cell envelope of indigenous bacteria in such environments represents the first barrier encountered by external molecules which could either cross the membrane and ultimately intracellular sites, or directly affect their structural components [28, 29]. Acquiring knowledge on *Vibrio* membrane structure and fluidity would help tackling physiological processes inside the cell and gain a better understanding of the interaction mechanisms of these marine bacteria with molecules in their environment. This should contribute to improve investigations of larval infections and therapeutic treatments in aquaculture.

The objective of this work was to establish a protocol to deuterate the lipid acyl chains in *V. splendidus* membranes, to enable the *in vivo*  $^2\text{H}$  solid-state nuclear magnetic resonance (SS-NMR) study of this marine bacterium. More specifically we used the indigenous 7SHRW strain isolated from the St. Lawrence Gulf sediments (Canada) which can cause significant mortalities to blue mussels and scallops at larval stages [30, 31], and has the advantage to be easily cultured in laboratory conditions. Like other marine bacteria, very few research on membrane phospholipids of *Vibrio sp.* are available [32-36] and studies on *V. splendidus* in this regard are even more sparse. To the best of our knowledge, only one study describes membrane phospholipids of *V. splendidus*, using a strain living in deep anoxic sediments [37].

Deuterium SS-NMR is an excellent tool to investigate the structure and dynamics of membrane lipids at the molecular level [38-40]. Traditionally applied to model systems, the emerging field of *in vivo* SS-NMR now enables the study of intact living organisms such as bacteria, microalgae, and small invertebrates [41-45]. Warnet et al. showed that magic-angle spinning (MAS) can be used in  $^2\text{H}$  in-cell SS-NMR studies to shorten the acquisition time by a factor of 10 while simultaneously maintaining spectral sensitivity, thus favoring the *in vivo* character of the experiment [46]. However,  $^2\text{H}$  NMR requires isotopic labelling which can be challenging in biological organisms such as *V. splendidus*. Notably, deuteration labelling protocols of bacteria phospholipids require the use of surfactants [45, 47, 48] to micellize deuterated fatty acids prior to their uptake by the bacteria and use in the phospholipids biosynthesis. These surfactants can possibly affect the membrane. Moreover, the natural saturated/unsaturated lipid ratio in the bacterial membrane should be preserved. A careful optimization of the deuteration protocol is thus necessary to ensure genuine *in vivo* characterization of these microorganisms.

In this work we propose for the first time a protocol for the deuteration of lipids in a model marine bacterium, *V. splendidus*. To do so, we assessed the effect of different surfactants on the cell growth. We also studied the effect of palmitic and oleic acid on the lipid profile and membrane fluidity by *in vivo*  $^2\text{H}$  SS-NMR as a function of cell growth stage. The labelling strategy developed here has the potential to be amenable to the *in vivo* NMR investigations of a variety of marine and terrestrial bacteria.

## 2. MATERIALS AND METHODS

### 2.1 Materials

Triton X-100 and 3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulfonate hydrate (CHAPS), Brij35, oleic (OA) and deuterated palmitic ( $d_{31}$ -PA) acids, deuterium-depleted water, as well as 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT), and fatty acid methyl ester (FAME) mix C4-C24 were all purchased from Sigma Aldrich (Oakville, Canada). Dodecylphosphocholine (DPC) and octylglucopyranoside (OG) were obtained from Avanti Polar Lipids (Alabaster, AL). Polyethylene glycol sorbitan monolaurate (Tween® 20) was purchased from BioShop Canada Inc. (Burlington, Canada), whereas LB (Lysogeny broth) Broth Miller was obtained from BioBasic Inc. (Markham, Canada).

### 2.2 Bacterial growth and $^2H$ labelling protocol

*Vibrio splendidus* strain 7SHRW were isolated from sediments of Hillsborough River, Prince Edward Island (Gulf of St. Lawrence, Canada) [30]. Cell culture was initiated by adding 100  $\mu$ l of a frozen cell stock solution (in 40% glycerol at  $-80^{\circ}\text{C}$  in 10 mL LB medium (NaCl 10g/L, tryptone 10 g/L, yeast extracts 5 g/L), and incubated at  $24.5^{\circ}\text{C}$  ( $\pm 0.5^{\circ}\text{C}$ ) on a rotary shaker (INFORS HT Multitron Pro, USA) operating at 100 rpm. After 3 days of growth, bacteria were transferred into 250 mL Erlenmeyer flasks containing 100 mL of LB 1X (initial  $\text{OD}_{600\text{nm}}$  adjusted to  $\approx 0.02$ ) and 1 mL was transferred into a 24-well plate to monitor the growth kinetic with a multiple plate reader (Infinite M200 TECAN, Männedorf, Switzerland). Plates were conditioned to  $24.5^{\circ}\text{C}$  ( $\pm 0.5^{\circ}\text{C}$ ) and to an agitation of 87 rpm before measuring the absorbance at 600 nm every 30 min during 48 hours. For each treatment, 3 to 4 wells were used. For isotopic labelling, *V. splendidus* were grown in the same conditions as described above but in an LB medium enriched with deuterated palmitic acid ( $d_{31}$ -PA). Prior to each use, the *Vibrio* strain was grown for two days and its purity was verified on LB-agar. The initial bacteria concentration was adjusted to be the same between replicates, *i.e.*, an optical density ( $\text{OD}_{600\text{nm}}$ ) of 0.02 at 600 nm wavelengths.

Initially, different commonly used surfactants were tested to micellize palmitic acid (0.3 mM) in culture media, and bacterial growths were monitored. Surfactants were used above their critical micelle concentration (CMC): Brij35 (0.1 mM), Tween20 (0.06 mM), Triton-X (0.4 mM), OG (20 mM), CHAPS (6 mM), and DPC (1.5 mM). The lipid deuteration procedure was optimized as follows: LB culture medium was supplemented with a mixture of  $d_{31}$ -PA (0.3 mM) and Tween-20 (0.14 mM), heated at 85°C, and the corresponding solution was flash-frozen and heated again several times until the complete dissolution of  $d_{31}$ -PA crystals. Protonated OA was added in the same proportions (0.3 mM) during bacteria inoculation, to mitigate potential unbalance of the saturated/unsaturated fatty acid (SFA/UFA) ratio within the membrane [46]. Potential effect of the  $^2\text{H}$  labelling was verified by comparing the growth of bacteria in deuterated and non-deuterated media. The specific growth rate ( $\mu$ ) was estimated from the slope regression of  $\ln(\text{OD}_{600\text{nm}})$  as a function of elapsed time [49]

### *2.3 Fatty acid profile analysis*

Fatty acid (FA) profiles were analyzed using gas chromatography combined to mass spectrometry (GC-MS) to obtain the proportion of each FA (deuterated or protonated) in  $\text{ng}\cdot\text{mg}^{-1}$ , and were expressed as relative concentration (weight % relative to total FA contents) as described by Tardy-Laporte et al. [48]. Briefly, starting from three pools of 30 to 60 mg of dry-frozen bacteria, total lipids were extracted using dichloromethane/methanol (2:1  $\text{CH}_2\text{Cl}_2/\text{MeOH}$  v/v) and 0.88% KCl solution in a Potter glass homogenizer. Neutral and polar lipids were separated by elution through a silica gel column (30×5 mm) hydrated with 6% water. Polar lipids were transesterified using 2 mL of  $\text{H}_2\text{SO}_4$  (2% in MeOH) and 0.8 mL of toluene. Final extracts were diluted in hexane solution and adjusted to a volume of 0.5 mL before GC-MS analysis (Agilent technology-7890A, Santa Clara, CA, USA). FA analyses were performed in parallel on a FAME mix which was used as a standard.

### *2.4 Sample preparation for $^2\text{H}$ SS-NMR analysis and viability assays*

Freshly collected bacterial cells were centrifuged at 4000 rpm for 10 min to remove the culture medium. Pellets were then suspended in a saline sterile rinsing solution (9‰ NaCl) to remove

any residual FAs and detergent molecules, and centrifuged again at 3800 rpm for 5 min. Rinsing was carried out at least 3 times, twice with saline solution prepared with nanopure water, and a final wash with saline solution prepared with deuterium-depleted water. The final pellet was used to fill a 4-mm zirconium oxide rotor, which corresponds to approximately 90 mg of hydrated bacteria. NMR experiments were performed on deuterated bacteria harvested at three different growth times (mid-log, early stationary phase and late stationary phase) and prepared in triplicate.

Following NMR experiments *V. splendidus* viability was determined using MTT reduction assays [50]. Cell suspensions from NMR samples were diluted in 5 replicates to a final OD<sub>600nm</sub> of 0.1 each, and were mixed with MTT solution (5mg/ml) to a ratio of MTT/cell suspension of 1:10 (v/v). The mixture was incubated in Eppendorf tubes for 20 minutes at 25°C with open caps until the formation of formazan crystals. Preparations were centrifuged (10.000g × 1min.) and the crystal pellets were dissolved in dimethylsulfoxide and incubated at room temperature for 15 minutes. Optical density was measured at 550 nm and cell viability of bacteria was expressed in relative percentage compared to freshly harvested bacteria before rinse. MTT assays were performed on triplicates of cultures corresponding to the NMR samples.

### 2.5 *In vivo* <sup>2</sup>H SS-NMR experiments and moment analysis

All <sup>2</sup>H solid-state NMR experiments were performed at 25°C on a Bruker Avance HD III wide Bore 600 MHz spectrometer (Billerica, MA, USA) using a double-resonance magic angle spinning (MAS) probe tuned to 92.1 MHz. Sample spinning frequency was set to 10 kHz. Typically, spectra were acquired using a Hahn Echo pulse sequence with the following operating conditions: 5 μs 90° pulses separated by an echo delay of 100 μs and a recycle time of 0.5 s. Each spectrum was obtained in approximately 43 min of acquisition time, corresponding to 4096 scans. A total of 32k points were acquired for a spectral width of 500 kHz. Spectra were Fourier transformed after application of a 50 Hz exponential line broadening and zero filling to 64k points.

Spectral moment analysis was performed using MestRenova software V6.0 (Mestrelab Research, Santiago de Compostela, Spain) and a macro developed by Pierre Audet (Université Laval). The second moment ( $M_2$ ) was calculated as described in equation 1 [46]:

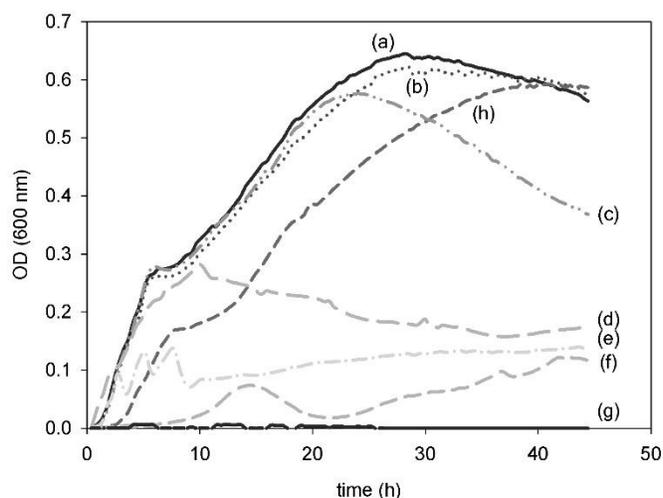
$$M_2 = \omega_r^2 \frac{\sum_{N=0}^{\infty} N^2 A_N}{\sum_{N=0}^{\infty} A_N} = \frac{4\pi^2 \nu_Q^2}{5} \langle S_{CD}^2 \rangle \quad (1)$$

where  $\omega_r$  is the spinning frequency,  $N$  the side band number, and  $A_N$  the area of each sideband obtained by spectral integration,  $S_{CD}^2$  is the mean square order parameter, and  $\nu_Q$  is the quadrupolar splitting constant equal to 168 kHz for a C-D bond in acyl chains [51].

### 3. RESULTS

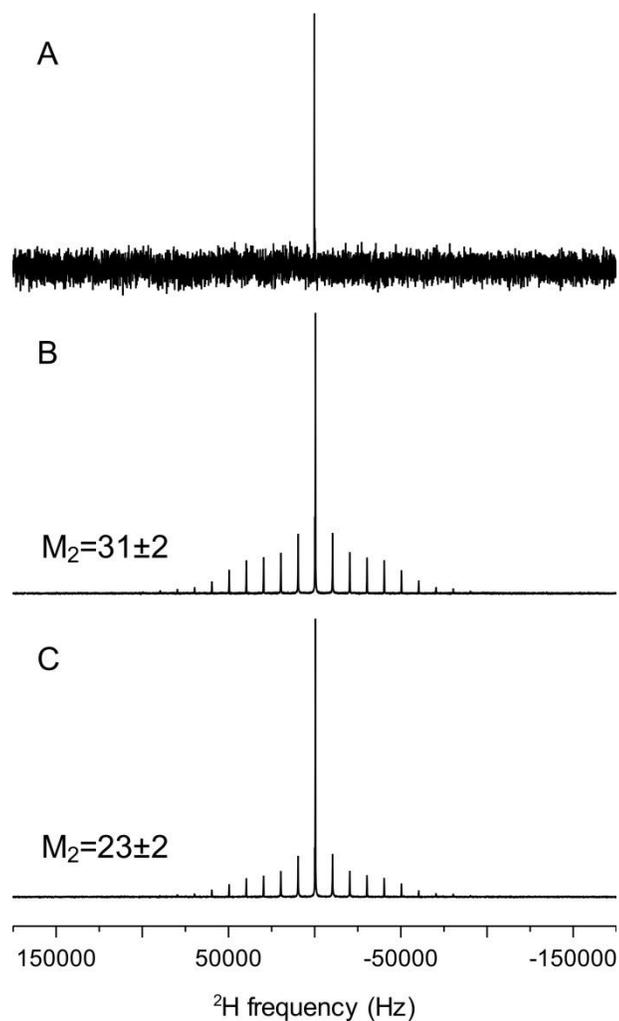
#### 3.1 Optimized $^2\text{H}$ labelling of *V. splendidus* for *in vivo* SS-NMR

The enzymatic machinery of bacteria energetically favours the incorporation of exogenous FAs into phospholipids [52], thus enabling the incorporation of deuterated PA chains exclusively in the membranes. We based our  $^2\text{H}$  labelling procedure of *V. splendidus* on a previously published protocol for another Gram(-) bacterium, *Escherichia coli*, which involved micellization of FAs by DPC in the growth medium to facilitate the FA uptake. However, since the presence of surfactants could be harmful to bacteria, and since another surfactant (Brij-58) we tested a series of detergents to identify the best suited for optimal bacterial lipid deuteration. Therefore, Tween-20, Brij-35, DPC, Triton-X, CHAPS and OG were assessed. To do so, we first monitored bacterial growth in different culture media when mixing protonated palmitic acid (PA) with these non-anionic surfactants above their CMC. Figure 1 shows that Tween-20 is the less harmful detergent for the lipid deuteration of *V. splendidus*, and that a high concentration of bacteria is measured even at a detergent concentration of 0.25 mM, *i.e.*, well above Tween-20's CMC (0.06 mM). A concentration of 0.14 mM of Tween-20 was thus employed for the rest of the study because it allows complete solubilization of PA (concentration of 0.3 mM) without affecting the bacterial culture.



**Figure 1:** Effect of different surfactants on *V. splendidus* growth. Control (a) experiment using the growth medium, and was compared to the following detergents at their CMC: Tween-20 (b), Brij-35 (c), DPC (d), Triton-X (e), CHAPS (f) and OG (g). Tween-20 was also tested at 0.25 mM (h).

The deuteration of *V. splendidus* membrane lipids was then verified by  $^2\text{H}$  SS-NMR. The second spectral moment  $M_2$  was calculated to assess the membrane fluidity. When specific quadrupolar splittings cannot be measured,  $M_2$  values are good reporter of the spectral distribution which reflects the lipid phases - the greater the  $M_2$  value, the greater the lipid ordering. Figure 2B-C shows that the deuteration protocol used herein was successful as a good signal-to-noise ratio is observed *in vivo* by  $^2\text{H}$  SS-NMR when bacteria are sampled in the exponential growth phase. The importance of the surfactant-mediated micellization step can be seen in Figure 2A which shows that when  $d_{31}$ -PA is used without Tween-20, no side bands can be detected (*i.e.*, there is no labelling). Figure 2C also shows that supplementing the culture medium with oleic acid (OA) in addition to  $d_{31}$ -PA leads to a reduction in side bands intensities, indicating an increase in membrane fluidity further demonstrated by the decrease in  $M_2$  value. These findings suggest that both unsaturated (OA) and saturated ( $d_{31}$ -PA) FAs were integrated by the cell. The *in vivo* NMR conditions during *V. splendidus* analysis were confirmed by estimating the bacterial viability, which was  $95 \pm 5 \%$ .



**Figure 2 :** *In vivo*  $^2\text{H}$  MAS (10 kHz) SS-NMR spectra of *V. splendidus* harvested in the mid-log phase. Control experiment corresponding to bacteria labelled with  $\text{d}_{31}$ -PA without detergent (A), bacteria labelled with  $\text{d}_{31}$ -PA in the presence of Tween-20 (0.14 mM) without (B), and with (C) OA (1:1). Spectra are normalized according to the central peak. Average second spectral moments  $M_2$  are indicated ( $10^9 \text{ s}^{-2}$ ).

### 3.2 Fatty acid composition as a function of cell growth and labelling conditions

Since the labelling protocol was successful, the membrane FA profile was monitored in order to quantify the assimilation of exogenous FAs at different growth stages and assess the potential impact of  $^2\text{H}$  labelling on the membrane. Lipid analyses were thus performed on labelled and

non-labelled bacteria and comparisons established between growth media enriched with d<sub>31</sub>-PA, with and without OA. Cell growth data are presented in the “*Supplementary material*” section. Figure 3 shows that the incorporation of d<sub>31</sub>-PA is indeed successful and that 77% of the PA acyl chains in the membrane are deuterated during the mid-log phase for *V. splendidus* grown in the presence of d<sub>31</sub>-PA (amounting to 44% of all FAs). The deuteration level of PA was maintained as high as 69% (31% of all fatty acids, numerical values are reported in *Supplementary material*, Table SI1) when OA was added in the growth medium, in spite of the high incorporation of OA into the membranes lipids.

Depending on the growth regimes, *V. splendidus* FA profile reveals more than 15 different FA chains with three major and recurring components: palmitoleic acid (C16:1), PA (C16), and OA (C18:1) (Fig.3). Our results (Fig. 3A) indicate that deuteration with d<sub>31</sub>-PA respects the native composition of *V. splendidus*. In addition, exogenous OA was highly incorporated during the exponential phase, at the expense of palmitoleic acid - the most naturally abundant UFA in *V. splendidus* membranes. The choice to enrich the culture with OA as an UFA was to balance as much as possible the incorporation of saturated d<sub>31</sub>-PA and to allow comparison with previously published deuteration protocols for other bacteria such as *E. coli* [45-47]. It also enabled exploring the adaptability of *V. splendidus* to integrate exogenous FAs and to modulate its FA chain fluidity accordingly.

Indeed bacteria responded to the enrichment with both exogenous FAs by including them in their lipid profile, more strikingly during the exponential phase, without affecting much the proportions of the other FAs (Fig. 3B). Permutational multivariate analysis of variance (Permanova) on Bray-Curtis matrices (Primer 7.0.13) of FAs composition of cell culture from different treatments and growth phases reveal significant interaction between both factors (DF = 2 and 22, Pseudo-F = 4.05, p = 0.005). Pair-wise Permanova comparison test indicates more specifically where differences were observed. Interestingly, the FA compositions were similar to that of the native bacteria membranes during the plateau phase (Fig. 3A), suggesting an adaptation of the bacteria to the growth medium (p = 0.089). In contrast, growing bacteria with only d<sub>31</sub>-PA leads to a more altered FA profile (p = 0.002). For instance, the major FA chains for

*V. splendidus*, i.e., palmitoleic acid, was reduced by more than half, and other UFAs such as cyclopropane FAs (cyC17:0 and cyC19:0) were highly synthesized under this regime (see *Supplementary material*).

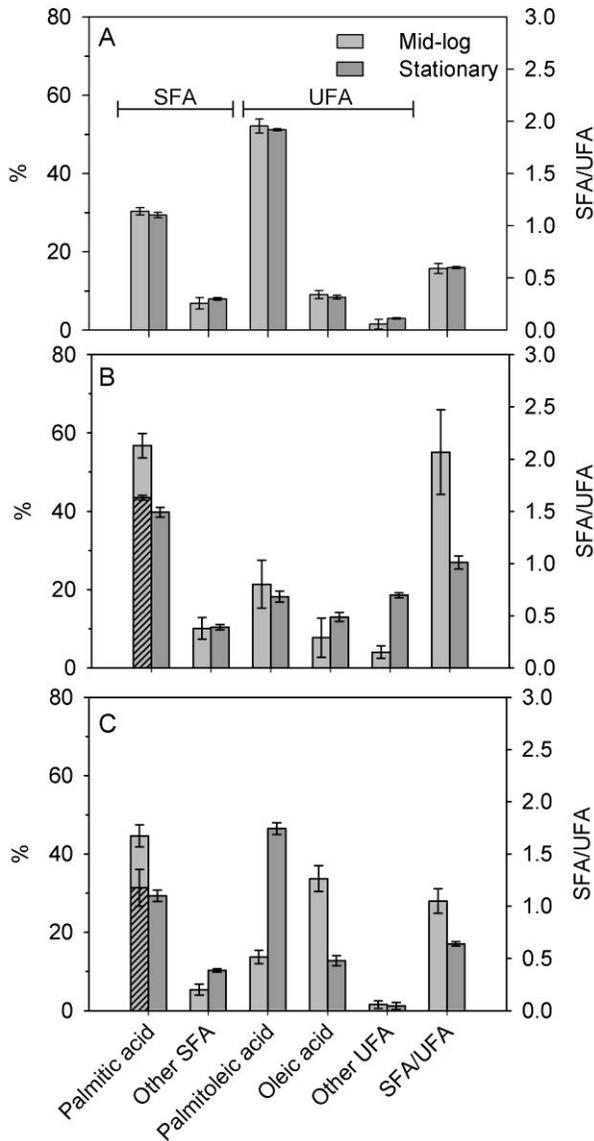


Figure 3: Fatty acid composition and corresponding SFA/UFA ratio at exponential (mid-log) and early stationary growth phases of *V. splendidus* in the presence of exogenous FAs. (A) Control sample in LB medium, (B) in presence of d<sub>31</sub>-PA (1:1), and (C) in presence of d<sub>31</sub>-PA and OA. Other SFAs includes lauric, myristic, pentadecanoic, heptadecanoic, stearic, arachidic and capric acids. Other UFAs include myristoleic, eicosenoic, lionelic, ricinoleic, stearidonic, pentamethyl heptane, pentadecanoic, cyclopropaneocatanoic (cy17:0), and cyclopropaneocatanoic (cyC19:0) acids and other cyclic FAs (See complete table in SI). Hatched histograms indicate the relative proportion of d<sub>31</sub>-PA per total palmitic acid. Saturated/unsaturated fatty acid ratios were calculated from FA content expressed in mol% per total FA (See S.I). Growth temperature was 25°C for all cultures.

Under labelling conditions, both with and without OA, the SFA/UFA ratios were higher in the exponential phase. However, the ratio was reversed in the plateau phase due to increased

biosynthesis of UFAs such as palmitoleic acid (C16:1) or cyclopropane FAs (cyC17:0 and cyC19:0). It should also be noted that the SFA/UFA ratio of bacteria labelled in the presence of OA and during early stationary phase (SFA/UFA =  $0.66 \pm 0.05$ ) was close to that of unlabelled cultures which was about  $0.59 \pm 0.05$  and  $0.60 \pm 0.01$  during mid-log and early stationary phases, respectively.

### *3.3 Membrane fluidity characterization by SS-NMR*

The  $^2\text{H}$  SS-NMR spectra obtained for the labelled bacteria (Figure 4) show that membrane rigidity varies with cell division. Under the same growth conditions ( $d_{31}$ -PA with OA) and in a timeframe of 5 hours, a reduction was observed in the sideband intensity and number. Accordingly, the  $M_2$  values dropped by half going from the mid-log to the stationary phase. These results are consistent with the decreased SFA/UFA ratio which reveal an increase in membrane fluidity as a function of growth time under the same growth conditions.

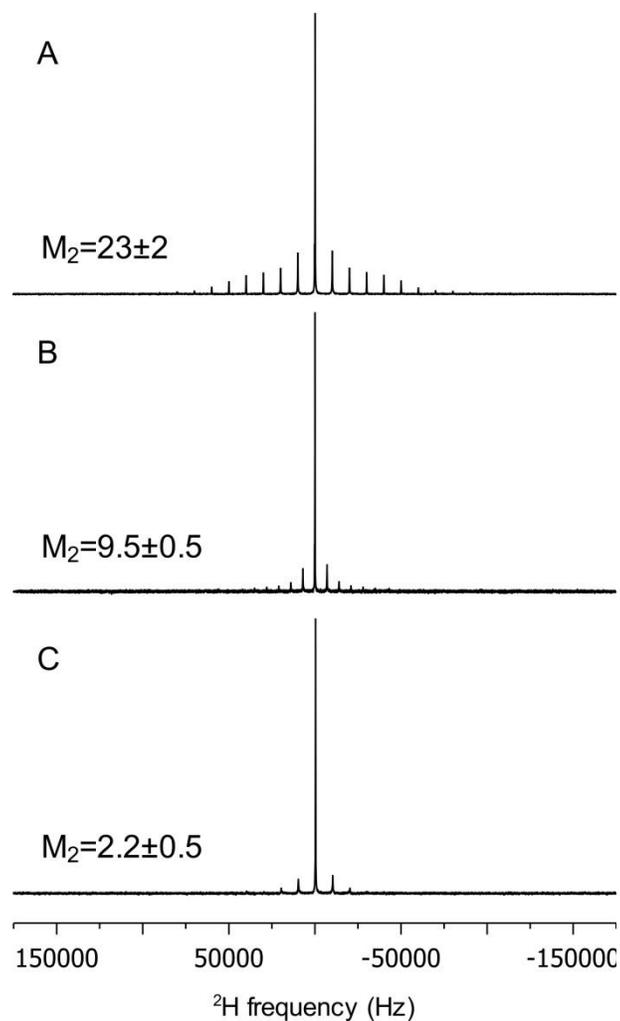


Figure 4:  $^2\text{H}$  MAS (10 kHz) SS-NMR spectra of intact *V. splendidus* harvested at three different cell growth times: (A) after 15 h in the mid-log phase ( $\text{OD}_{600\text{nm}} \approx 0.3$ ), (B) after 22 h ( $\pm 2\text{h}$ ) at the beginning of the stationary stage ( $\text{OD}_{600\text{nm}} \approx 0.5$ ), and (C) after 30 h at advanced stationary phase ( $\text{OD}_{600\text{nm}} \approx 0.5$ ). Bacteria were labelled with  $\text{d}_{31}\text{-PA}$  in presence of OA. Average second spectral moments  $M_2$  are indicated ( $10^9 \text{ s}^{-2}$ ).

## 4. DISCUSSION

### 4.1 $^2\text{H}$ labelling optimization for in vivo study of membranes by $^2\text{H}$ SS-NMR

Deuterium labelling of lipid chains is a useful approach to explore changes occurring in biological membranes using SS-NMR. However, when studying living organisms, the

deuteration protocol could be a disturbing factor to physiological pathways, or induce stress. Previously published work has established the feasibility and pertinence of bacterial membrane deuteration on human pathogens *E. coli* and *B. subtilis* [45-48, 53]. Here, a marine bacterium, *V. splendidus*, is deuterated for the first time while minimizing disturbances on the microorganism. Although *V. splendidus* and previously characterized *E. coli* [45, 46] are both Gram(-) bacteria, differences in  $^2\text{H}$  SS-NMR spectra between these two species were expected, as they may be related to species-specific biological requirements [54, 55].

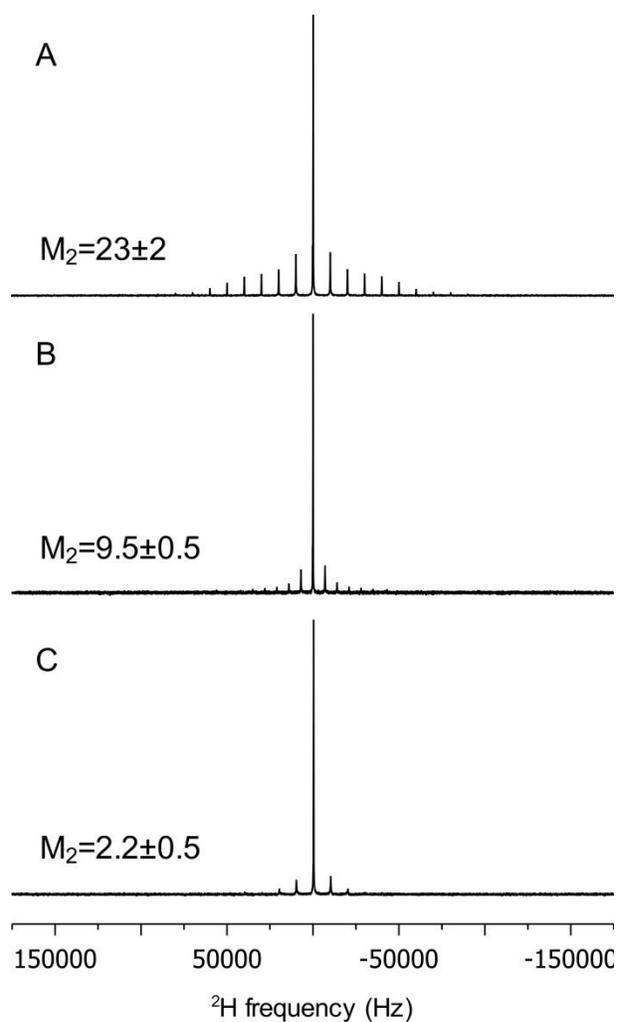


Figure 4:  $^2\text{H}$  MAS (10 kHz) SS-NMR spectra of intact *V. splendidus* harvested at three different cell growth times: (A) after 15 h in the mid-log phase ( $\text{OD}_{600\text{nm}} \approx 0.3$ ), (B) after 22 h ( $\pm 2\text{h}$ ) at the beginning of the stationary stage ( $\text{OD}_{600\text{nm}} \approx 0.5$ ), and (C) after 30 h at advanced stationary phase ( $\text{OD}_{600\text{nm}} \approx 0.5$ ). Bacteria were labelled with  $\text{d}_{31}\text{-PA}$  in presence of OA. Average second spectral moments  $M_2$  are indicated ( $10^9 \text{ s}^{-2}$ ).

The capacity of the bacteria to grow under our labelling conditions was first verified. While deuteration of molecules such as FAs does not affect their structure and thermodynamical

stability, surfactants used to facilitate the deuterated FA incorporation into the bacteria [56], could have a detrimental effect since detergents are commonly used for biochemical applications such as extraction of membrane proteins. Therefore, the physiological state of the bacteria during labelling procedure was monitored using growth kinetics, and our results showed that Tween-20 had the lowest impact. This result is in agreement with Schuck et al. who compared sensitivities of diverse cells toward a set of detergents and showed that Tween-20 was always the least effective in provoking membrane resistance, and the best at preserving membrane integrity [57]. Tween-20 has a low CMC, does not affect protein activity, and is rarely used for cell lysis or protein extraction, but rather as a gentle washing agent. [57, 58]. On the other hand, although harmless for the first 10 hours of culture, the zwitterionic detergent DPC used to deuterate *E. coli* and *B. subtilis* lipids showed a hampering action on *V. splendidus* at longer exposure time, which could be explained by its ability to break protein-lipid and lipid-lipid associations [58, 59].

*De novo* synthesis of FAs is the most energetically expensive mechanism in phospholipid synthesis for bacteria membrane [36]. Because they do not have specialized functional cellular compartments, prokaryotic organisms rely on multiple regulation tools to control their phospholipid composition according to the niche in which they live [34, 36, 37, 60, 61]. Overall, bacteria tend to sustain their membrane homeostasis through adaptation mechanisms by maintaining zwitterionic/anionic, protein/lipid [60] or FA chain ratios [62]. The SFA/UFA ratio is one of the most used reporters of membrane fluidity [63-65] as well as bacterial adaptive strategies [63-67]. Our results showed that when PA was added in the growth medium of *V. splendidus* without OA, bacteria adapted by synthesizing more cyclic fatty acids (cyC17:0 and cyC19:0) that restored membrane fluidity. Similarly, when OA was also added and despite the fact that OA is not the major UFA in *V. splendidus*, this FA was highly integrated in the exponential phase, resulting in a FA profile similar to that of unlabelled bacteria. The SFA/UFA ratios determined here confirm the need to enrich the medium with UFAs during labelling with  $d_{31}$ -PA in order to avoid extreme shifts from the natural lipid composition (Fig. 3), in agreement with previous work carried out on *E. coli* [45-47].

In short, our lipid deuteration protocol on *V. splendidus* allowed a similar or better labelling rate as compared to previous work on bacteria. Lipid profile analyses showed 77% deuteration of C16:0 acyl chains at mid-log when d<sub>31</sub>-PA was added to the growth medium, while a 69% labelling was determined when equal proportions of d<sub>31</sub>-PA and OA were employed. For both protocols (with and without OA), the deuteration level is thus higher than what was reported for *E. coli*, *i.e.*, 60-69% for bacteria grown in the presence of d<sub>31</sub>-PA [45, 46]. Except for minor differences in the FA incorporation process [34] and a different culture time lapse, the lipid metabolism of *Vibrio* species is very similar to *E. coli*'s since they are both Gram(-) bacteria with similar transcriptional regulatory genes for FA metabolism and phospholipid composition [34, 36, 62, 66].

#### 4.2 Membrane evolution during bacterial growth

Our results showed that the membrane fluidity varied with bacterial growth during the labelling process. Indeed bacteria experience the fastest growth rate in the exponential phase during which they produce membrane lipids [61]. Once lipids are synthesized, the lipid profile remains the same until the stationary phase is reached, *i.e.*, when nutrients become limited, DNA replication, protein synthesis and respiration are reduced, and cell lysis begins [68]. Previous *in vivo* NMR studies have been carried out on bacteria sampled at the mid-log growth stage [45-48] which provides good NMR signal-to-noise ratio. However, our results revealed that samples obtained at later stages, especially the late exponential stage, provide additional advantages.

Indeed GC-MS analyses showed that exogenous PA and OA were highly integrated in the membrane at mid-log phase during which they become the most abundant FA chains in the membrane (Figure 3). In subsequent growth stages, PA and OA diminished to reach more “native” proportions (*i.e.*, those measured in the control samples), either by being converted into other lipid chains or by triggering the biosynthesis of other FAs. This is consistent with other investigations on *Vibrio* species, showing that exogenous FAs are incorporated by direct trans-acylation or after incorporation into the biosynthesis pool [34]. Additionally the SFA/UFA ratio, which decreased as a function of growth time, reaching that of unlabelled bacteria (especially when both PA and OA were added to the culture medium), validate the evolution of the FA

profile. The  $^2\text{H}$  SS-NMR spectra also reveal a decrease in membrane fluidity as a function of *V. splendidus* growth stages when  $\text{d}_{31}\text{-PA}$ , and to a lesser extent when equal proportions of OA and  $\text{d}_{31}\text{-PA}$ , are added to the growth medium (Figure 4). In the exponential phase, a more rigid membrane was observed, close to a gel phase ( $M_2$  above  $20 \times 10^9 \text{ s}^{-2}$ ), whereas in later stages the  $M_2$  value was closer to that of a fluid phase membrane ( $M_2$  below  $10 \times 10^9 \text{ s}^{-2}$ ) [46]. Since the FA composition and SFA/UFA ratio were closer to their “native” values in the late exponential phase, the lower  $M_2$  values would thus report with biological membranes in the fluid phase [69].

The contribution of signal from free  $\text{d}_{31}\text{-PA}$  cannot explain the change in lipid profile during cell growth. Indeed Figure 2A shows no  $^2\text{H}$  SS-NMR signal after rinsing. Additionally, free  $\text{d}_{31}\text{-PA}$  is insoluble in water and would lead to a very broad  $^2\text{H}$  SS-NMR spectrum with  $M_2$  above  $70 \times 10^9 \text{ s}^{-2}$  (data not shown), which is incompatible with our results. Moreover, the  $^2\text{H}$  SS-NMR spectrum of  $\text{d}_{31}\text{-PA}$  crystals would not vary with growth time. In light of these results, the increase in membrane fluidity with cell growth time would be explained by a gradual adaptation of the microorganism metabolism upon isotopic labelling to cope with possible stress and disturbance of metabolic pathways [63-65] due to chemical isotopic labelling. In most cases, stress is known to lead to an increase in membrane rigidity, although the opposite pattern could happen in the case of marine prokaryotic organisms, and specifically for *Vibrio* species [33, 65]. The increased fluidity due to increased UFA proportions, and notably cyclopropanes FAs observed when PA was added in the growth medium, seems to prove such environmental stress [65, 70]. However, when both PA and OA were present in the medium, cyclopropane FA proportions were inverted (Table SI1), suggesting that stress was reduced [70]. Similarly, the superimposed growth curves (see Fig. SI1) indicate that *V. splendidus* metabolism kinetics under isotopic labelling was not affected by labelling stress. Therefore, the FAs turnover would be fast and all exogenous  $\text{d}_{31}\text{-PA}$  transferred into the membrane lipids at the mid-log phase. Yet, being long and saturated, they would induce large  $M_2$  values. In the late exponential phase, bacteria would have had enough time to regulate their metabolism to the presence of exogenous FAs in the growth medium, generally through adapting their enzymatic machinery [61], and have either converted into or synthesized new UFAs in order to reduce the membrane rigidity, and reach their initial membrane state, as observed by the reduced  $M_2$  values.

## 5. CONCLUSION AND PERSPECTIVES

Setting out labelling procedures is an important step towards developing effective and reliable tools for *in vivo* NMR studies. Here, membranes of intact *V. splendidus* were characterized for the first time by SS-NMR, as a model of marine Gram(-) bacteria. This work provides a better understanding of changes in bacterial membrane properties as a function of growth time and conditions that have never been studied so far on any biological system by *in vivo* NMR. Overall, the present study should help in the design of efficient labelling protocols of bacteria, which takes into account not only the technical spectroscopy requirements for analyses (such as signal-to-noise ratio) but also biological considerations. This  $^2\text{H}$  labelling protocol is useful for  $^2\text{H}$  SS-NMR, but it could be useful for neutron diffraction, and could also be transposed to the labelling of cell membranes by other isotopes such as  $^{13}\text{C}$ . Additionally, by characterizing the membrane of *V. splendidus*, a potential virulent bacterium for marine organisms, this work paves the way towards studying the interactions of its membrane with exogenous molecules in the aquatic environment.

## ACKNOWLEDGMENTS

This work was supported by the Natural Sciences and Engineering Research Council (NSERC) of Canada (grant 326750-2013 to I.M. and grant 299100 to R.T.) and the Centre National de la Recherche Scientifique (UMR 7099 to D.E.W.). Z.B. would like to acknowledge the Ressources Aquatiques Québec (RAQ) research network (RS-171172) for the award of scholarships and Pierre Audet for sharing the MestRenova macro. I.M. and R.T. are members of the RAQ.

## COMPETING INTERESTS

No competing interests declared.

## AUTHOR CONTRIBUTIONS

Z.B. designed and conducted all sampling, data collection and analysis, and wrote the first draft of the manuscript. D.E.W. and A.A. contributed to the data analysis and writing of the manuscript. K.L. provided the initial *Vibrio* strain culture and participated to the revision of the manuscript. R.T. and I.M. designed and supervised the research, contributed to the data analysis and writing of the manuscript.

## REFERENCES

1. Urakawa, H. and I.N.G. Rivera, Aquatic environment, in *The biology of vibrios*. 2006, *American Society of Microbiology*. p. 175-189.
2. Thompson, F.L., T. Iida, and J. Swings, Biodiversity of *vibrios*. *Microbiology and molecular biology reviews*, 2004. 68(3): p. 403-431.
3. Cavallo, R.A. and L. Stabili, Presence of *vibrios* in seawater and *Mytilus galloprovincialis* (Lam.) from the Mar Piccolo of Taranto (Ionian Sea). *Water Research*, 2002. 36(15): p. 3719-3726.
4. McDougald, D. and S. Kjelleberg, Adaptive responses of *Vibrios*, in *The biology of vibrios*. 2006, *American Society of Microbiology*. p. 133-155.
5. DiSalvo, L., J. Blecka, and R. Zebal, *Vibrio anguillarum* and larval mortality in a California coastal shellfish hatchery. *Applied and Environmental Microbiology*, 1978. 35(1): p. 219-221.
6. Crab, R., A. Lambert, T. Defoirdt, P. Bossier, and W. Verstraete, The application of bioflocs technology to protect brine shrimp (*Artemia franciscana*) from pathogenic *Vibrio harveyi*. *Journal of applied microbiology*, 2010. 109(5): p. 1643-1649.
7. Frans, I., C.W. Michiels, P. Bossier, K. Willems, B. Lievens, and H. Rediers, *Vibrio anguillarum* as a fish pathogen: virulence factors, diagnosis and prevention. *Journal of fish diseases*, 2011. 34(9): p. 643-661.

8. Travers, M.-A., K.B. Miller, A. Roque, and C.S. Friedman, Bacterial diseases in marine bivalves. *Journal of invertebrate pathology*, 2015. 131: p. 11-31.
9. Velji, M., L. Albright, and T. Evelyn, Immunogenicity of various *Vibrio ordalii* lipopolysaccharide fractions in coho salmon *Oncorhynchus kisutch*. *Diseases of aquatic organisms*, 1992. 12(2): p. 97-101.
10. Paillard, C., F. Le Roux, and J.J. Borrego, Bacterial disease in marine bivalves, a review of recent studies: trends and evolution. *Aquatic Living Resources*, 2004. 17(4): p. 477-498.
11. Pruzzo, C., G. Gallo, and L. Canesi, Persistence of *vibrios* in marine bivalves: the role of interactions with haemolymph components. *Environmental microbiology*, 2005. 7(6): p. 761-772.
12. Beaz-Hidalgo, R., S. Balboa, J.L. Romalde, and M.J. Figueras, Diversity and pathogenicity of *Vibrio* species in cultured bivalve molluscs. *Environmental microbiology reports*, 2010. 2(1): p. 34-43.
13. De Decker, S. and D. Saulnier, *Vibriosis* induced by experimental cohabitation in *Crassostrea gigas*: Evidence of early infection and down-expression of immune-related genes. *Fish & shellfish immunology*, 2011. 30(2): p. 691-699.
14. Liu, X., C. Ji, J. Zhao, and H. Wu, Differential metabolic responses of clam *Ruditapes philippinarum* to *Vibrio anguillarum* and *Vibrio splendidus* challenges. *Fish & shellfish immunology*, 2013. 35(6): p. 2001-2007.
15. Gay, M., T. Renault, A.-M. Pons, and F. Le Roux, Two *Vibrio splendidus* related strains collaborate to kill *Crassostrea gigas*: taxonomy and host alterations. *Diseases of aquatic organisms*, 2004. 62(1-2): p. 65-74.
16. Liu, R., L. Qiu, Z. Yu, J. Zi, F. Yue, L. Wang, H. Zhang, W. Teng, X. Liu, and L. Song, Identification and characterisation of pathogenic *Vibrio splendidus* from Yesso scallop (*Patinopecten yessoensis*) cultured in a low temperature environment. *Journal of invertebrate pathology*, 2013. 114(2): p. 144-150.

17. Kogut, M. and N.J. Russell, The growth and phospholipid composition of a moderately halophilic bacterium during adaptation to changes in salinity. *Current Microbiology*, 1984. 10(2): p. 95-98.
18. Eguchi, M., E. Fujiwara, and N. Miyamoto, Survival of *Vibrio anguillarum* in freshwater environments: adaptation or debilitation? *Journal of Infection and Chemotherapy*, 2000. 6(2): p. 126-129.
19. Sarita, G.B., Multiple antibiotic resistances of *Vibrio* isolates from coastal and brackish water areas. *American Journal of Biochemistry and Biotechnology* 2005.
20. Masini, L., G. De Grandis, F. Principi, C. Mengarelli, and D. Ottaviani, Research and characterization of pathogenic *vibrios* from bathing water along the Conero Riviera (Central Italy). *Water research*, 2007. 41(18): p. 4031-4040.

#### References

1. Urakawa, H. and I.N.G. Rivera, Aquatic environment, in *The biology of vibrios*. 2006, *American Society of Microbiology*. p. 175-189.
2. Thompson, F.L., T. Iida, and J. Swings, Biodiversity of *vibrios*. *Microbiology and molecular biology reviews*, 2004. 68(3): p. 403-431.
3. Cavallo, R.A. and L. Stabili, Presence of *vibrios* in seawater and *Mytilus galloprovincialis* (Lam.) from the Mar Piccolo of Taranto (Ionian Sea). *Water Research*, 2002. 36(15): p. 3719-3726.
4. McDougald, D. and S. Kjelleberg, Adaptive responses of *Vibrios*, in *The biology of vibrios*. 2006, *American Society of Microbiology*. p. 133-155.
5. DiSalvo, L., J. Blecka, and R. Zebal, *Vibrio anguillarum* and larval mortality in a California coastal shellfish hatchery. *Applied and Environmental Microbiology*, 1978. 35(1): p. 219-221.
6. Crab, R., A. Lambert, T. Defoirdt, P. Bossier, and W. Verstraete, The application of bioflocs technology to protect brine shrimp (*Artemia franciscana*) from pathogenic *Vibrio harveyi*. *Journal of applied microbiology*, 2010. 109(5): p. 1643-1649.

7. Frans, I., C.W. Michiels, P. Bossier, K. Willems, B. Lievens, and H. Rediers, *Vibrio anguillarum* as a fish pathogen: virulence factors, diagnosis and prevention. *Journal of fish diseases*, 2011. 34(9): p. 643-661.
8. Travers, M.-A., K.B. Miller, A. Roque, and C.S. Friedman, Bacterial diseases in marine bivalves. *Journal of invertebrate pathology*, 2015. 131: p. 11-31.
9. Velji, M., L. Albright, and T. Evelyn, Immunogenicity of various *Vibrio ordalii* lipopolysaccharide fractions in coho salmon *Oncorhynchus kisutch*. *Diseases of aquatic organisms*, 1992. 12(2): p. 97-101.
10. Paillard, C., F. Le Roux, and J.J. Borrego, Bacterial disease in marine bivalves, a review of recent studies: trends and evolution. *Aquatic Living Resources*, 2004. 17(4): p. 477-498.
11. Pruzzo, C., G. Gallo, and L. Canesi, Persistence of *vibriosis* in marine bivalves: the role of interactions with haemolymph components. *Environmental microbiology*, 2005. 7(6): p. 761-772.
12. Beaz-Hidalgo, R., S. Balboa, J.L. Romalde, and M.J. Figueras, Diversity and pathogenicity of *Vibrio* species in cultured bivalve molluscs. *Environmental microbiology reports*, 2010. 2(1): p. 34-43.
13. De Decker, S. and D. Saulnier, *Vibriosis* induced by experimental cohabitation in *Crassostrea gigas*: Evidence of early infection and down-expression of immune-related genes. *Fish & shellfish immunology*, 2011. 30(2): p. 691-699.
14. Liu, X., C. Ji, J. Zhao, and H. Wu, Differential metabolic responses of clam *Ruditapes philippinarum* to *Vibrio anguillarum* and *Vibrio splendidus* challenges. *Fish & shellfish immunology*, 2013. 35(6): p. 2001-2007.
15. Gay, M., T. Renault, A.-M. Pons, and F. Le Roux, Two *Vibrio splendidus* related strains collaborate to kill *Crassostrea gigas*: taxonomy and host alterations. *Diseases of aquatic organisms*, 2004. 62(1-2): p. 65-74.
16. Liu, R., L. Qiu, Z. Yu, J. Zi, F. Yue, L. Wang, H. Zhang, W. Teng, X. Liu, and L. Song, Identification and characterisation of pathogenic *Vibrio splendidus* from Yesso scallop

- (*Patinopecten yessoensis*) cultured in a low temperature environment. *Journal of invertebrate pathology*, 2013. 114(2): p. 144-150.
17. Kogut, M. and N.J. Russell, The growth and phospholipid composition of a moderately halophilic bacterium during adaptation to changes in salinity. *Current Microbiology*, 1984. 10(2): p. 95-98.
  18. Eguchi, M., E. Fujiwara, and N. Miyamoto, Survival of *Vibrio anguillarum* in freshwater environments: adaptation or debilitation? *Journal of Infection and Chemotherapy*, 2000. 6(2): p. 126-129.
  19. Sarita, G.B., Multiple antibiotic resistances of *Vibrio* isolates from coastal and brackish water areas. *American Journal of Biochemistry and Biotechnology* 2005.
  20. Masini, L., G. De Grandis, F. Principi, C. Mengarelli, and D. Ottaviani, Research and characterization of pathogenic *vibrios* from bathing water along the Conero Riviera (Central Italy). *Water research*, 2007. 41(18): p. 4031-4040.
  21. Soto, W., J. Gutierrez, M. Remmenga, and M. Nishiguchi, Salinity and temperature effects on physiological responses of *Vibrio fischeri* from diverse ecological niches. *Microbial ecology*, 2009. 57(1): p. 140-150.
  22. Phillips, D.J., The use of biological indicator organisms to monitor trace metal pollution in marine and estuarine environments—a review. *Environmental Pollution (1970)*, 1977. 13(4): p. 281-317.
  23. Olsen, C.f., N. Cutshall, and I. Larsen, Pollutant—particle associations and dynamics in coastal marine environments: a review. *Marine Chemistry*, 1982. 11(6): p. 501-533.
  24. Nixon, S.W., Coastal marine eutrophication: a definition, social causes, and future concerns. *Ophelia*, 1995. 41(1): p. 199-219.
  25. Baquero, F., J.-L. Martínez, and R. Cantón, Antibiotics and antibiotic resistance in water environments. *Current opinion in biotechnology*, 2008. 19(3): p. 260-265.
  26. Kümmerer, K., Antibiotics in the aquatic environment—a review—part I. *Chemosphere*, 2009. 75(4): p. 417-434.

27. Riedel, T., M. Zark, A.V. Vähätalo, J. Niggemann, R.G. Spencer, P.J. Hernes, and T. Dittmar, Molecular signatures of biogeochemical transformations in dissolved organic matter from ten world rivers. *Frontiers in Earth Science*, 2016. 4: p. 85.
28. Hancock, R.E., The bacterial outer membrane as a drug barrier. *Trends in microbiology*, 1997. 5(1): p. 37-42.
29. Shai, Y., Mechanism of the binding, insertion and destabilization of phospholipid bilayer membranes by  $\alpha$ -helical antimicrobial and cell non-selective membrane-lytic peptides. *Biochimica et Biophysica Acta (BBA)-Biomembranes*, 1999. 1462(1): p. 55-70.
30. Mateo, D.R., A. Siah, M.T. Araya, F.C. Berthe, G.R. Johnson, and S.J. Greenwood, Differential in vivo response of soft-shell clam hemocytes against two strains of *Vibrio splendidus*: changes in cell structure, numbers and adherence. *Journal of invertebrate pathology*, 2009. 102(1): p. 50-56.
31. Turcotte, F., J.-L. Mouget, B. Genard, K. Lemarchand, J.-S. Deschênes, and R. Tremblay, Prophylactic effect of *Haslea ostrearia* culture supernatant containing the pigment marennine to stabilize bivalve hatchery production. *Aquatic Living Resources*, 2016. 29(4): p. 401.
32. Oliver, J.D. and R.R. Colwell, Extractable lipids of gram-negative marine bacteria: phospholipid composition. *Journal of bacteriology*, 1973. 114(3): p. 897-908.
33. Oliver, J.D. and W.F. Stringer, Lipid composition of a psychrophilic marine *Vibrio sp.* during starvation-induced morphogenesis. *Applied and Environmental Microbiology*, 1984. 47(3): p. 461-466.
34. Byers, D.M., Elongation of exogenous fatty acids by the bioluminescent bacterium *Vibrio harveyi*. *Journal of bacteriology*, 1989. 171(1): p. 59-64.
35. Brown, R.N. and P.A. Gulig, Regulation of fatty acid metabolism by FadR is essential for *Vibrio vulnificus* to cause infection of mice. *Journal of bacteriology*, 2008. 190(23): p. 7633-7644.
36. Zhang, Y.-M. and C.O. Rock, Transcriptional regulation in bacterial membrane lipid synthesis. *Journal of lipid research*, 2009. 50(Supplement): p. S115-S119.

37. Freese, E., H. Rütters, J. Köster, J. Rullkötter, and H. Sass, *Gammaproteobacteria* as a possible source of eicosapentaenoic acid in anoxic intertidal sediments. *Microbial ecology*, 2009. 57(3): p. 444-454.
38. Davis, J.H., The description of membrane lipid conformation, order and dynamics by 2H-NMR. *Biochimica et Biophysica Acta (BBA)-Reviews on Biomembranes*, 1983. 737(1): p. 117-171.
39. Li, J., T. Vosegaard, and Z. Guo, Applications of nuclear magnetic resonance in lipid analyses: An emerging powerful tool for lipidomics studies. *Progress in lipid research*, 2017. 68: p. 37-56.
40. Seelig, J., Deuterium magnetic resonance: theory and application to lipid membranes. *Quarterly reviews of biophysics*, 1977. 10(3): p. 353-418.
41. Chauton, M.S., O.I. Optun, T.F. Bathen, Z. Volent, I.S. Gribbestad, and G. Johnsen, HR MAS <sup>1</sup>H NMR spectroscopy analysis of marine microalgal whole cells. *Marine Ecology Progress Series*, 2003. 256: p. 57-62.
42. Arnold, A.A., B. Genard, F. Zito, R. Tremblay, D.E. Warschawski, and I. Marcotte, Identification of lipid and saccharide constituents of whole microalgal cells by <sup>13</sup>C solid-state NMR. *Biochimica et Biophysica Acta (BBA)-Biomembranes*, 2015. 1848(1): p. 369-377.
43. Simpson, A.J., Y. Liaghati, B. Fortier-McGill, R. Soong, and M. Akhter, Perspective: *in vivo* NMR—a potentially powerful tool for environmental research. *Magn. Reson. Chem*, 2015. 53: p. 686-690.
44. Warnet, X.L., A.A. Arnold, I. Marcotte, and D.E. Warschawski, In-cell solid-state NMR: an emerging technique for the study of biological membranes. *Biophysical journal*, 2015. 109(12): p. 2461-2466.
45. Laadhari, M., A.A. Arnold, A.E. Gravel, F. Separovic, and I. Marcotte, Interaction of the antimicrobial peptides caerin 1.1 and aurein 1.2 with intact bacteria by <sup>2</sup>H solid-state NMR. *Biochimica et Biophysica Acta (BBA)-Biomembranes*, 2016. 1858(12): p. 2959-2964.

46. Warnet, X.L., M. Laadhari, A.A. Arnold, I. Marcotte, and D.E. Warschawski, A  $^2\text{H}$  magic-angle spinning solid-state NMR characterisation of lipid membranes in intact bacteria. *Biochimica et Biophysica Acta (BBA)-Biomembranes*, 2016. 1858(1): p. 146-152.
47. Pius, J., M.R. Morrow, and V. Booth,  $^2\text{H}$  solid-state nuclear magnetic resonance investigation of whole *Escherichia coli* interacting with antimicrobial peptide MSI-78. *Biochemistry*, 2011. 51(1): p. 118-125.
48. Tardy-Laporte, C., A.A. Arnold, B. Genard, R. Gastineau, M. Morançais, J.-L. Mouget, R. Tremblay, and I. Marcotte, A  $^2\text{H}$  solid-state NMR study of the effect of antimicrobial agents on intact *Escherichia coli* without mutating. *Biochimica et Biophysica Acta (BBA)-Biomembranes*, 2013. 1828(2): p. 614-622.
49. Nedwell, D. and M. Rutter, Influence of temperature on growth rate and competition between two psychrotolerant Antarctic bacteria: low temperature diminishes affinity for substrate uptake. *Applied and Environmental Microbiology*, 1994. 60(6): p. 1984-1992.
50. Wang, H., H. Cheng, F. Wang, D. Wei, and X.J.J.o.m.m. Wang, An improved 3-(4, 5-dimethylthiazol-2-yl)-2, 5-diphenyl tetrazolium bromide (MTT) reduction assay for evaluating the viability of *Escherichia coli* cells. *Journal of microbiological methods* 2010. 82(3): p. 330-333.
51. Burnett, L. and B. Muller, Deuteron quadrupole coupling constants in three solid deuterated paraffin hydrocarbons: C<sub>2</sub>D<sub>6</sub>, C<sub>4</sub>D<sub>10</sub>, C<sub>6</sub>D<sub>14</sub>. *The Journal of Chemical Physics*, 1971. 55(12): p. 5829-5831.
52. Marcotte, I. and V. Booth,  $^2\text{H}$  Solid-State NMR Study of Peptide–Membrane Interactions in Intact Bacteria, in *Advances in Biological Solid-State NMR*. 2014. p. 459-475.
53. Davis, J.-H., Deuterium magnetic resonance study of the gel and liquid crystalline phases of dipalmitoyl phosphatidylcholine. *Biophysical journal*, 1979. 27(3): p. 339-358.
54. Farmer, J., The family *Vibrionaceae*, in *The prokaryotes*. 2006, *Springer*. p. 495-507.
55. Gauthier-Clerc, S., I. Boily, M. Fournier, and K. Lemarchand, *In vivo* exposure of *Mytilus edulis* to living enteric bacteria: a threat for immune competency? *Environmental Science and Pollution Research*, 2013. 20(2): p. 612-620.

56. Dal Molin, M., G. Gasparini, P. Scrimin, F. Rastrelli, and L.J. Prins, <sup>13</sup>C-isotope labelling for the facilitated NMR analysis of a complex dynamic chemical system. *Chemical Communications*, 2011. 47(46): p. 12476-12478.
57. Schuck, S., M. Honsho, K. Ekroos, A. Shevchenko, and K. Simons, Resistance of cell membranes to different detergents. *Proceedings of the National Academy of Sciences*, 2003. 100(10): p. 5795-5800.
58. Johnson, M., Detergents: Triton X-100, tween-20, and more. *Mater Methods*, 2013. 3(1): p. 163.
59. le Maire, M., P. Champeil, and J.V. Møller, Interaction of membrane proteins and lipids with solubilizing detergents. *Biochimica et Biophysica Acta (BBA)-Biomembranes*, 2000. 1508(1): p. 86-111.
60. Shibuya, I., Metabolic regulation and biological functions of phospholipids in *Escherichia coli*. *Progress in lipid research*, 1992. 31(3): p. 245-299.
61. Barton, L.L., Cellular Growth and Reproduction, in *Structural and Functional Relationships in Prokaryotes* Springer, Editor. 2005: New York,. p. 292-346.
62. Silbert, D.F., F. Ruch, and P.R. Vagelos, Fatty acid replacements in a fatty acid auxotroph of *Escherichia coli*. *Journal of bacteriology*, 1968. 95(5): p. 1658-1665.
63. Beney, L. and P. Gervais, Influence of the fluidity of the membrane on the response of microorganisms to environmental stresses. *Applied microbiology and biotechnology*, 2001. 57(1): p. 34-42.
64. Mykytczuk, N., J. Trevors, L. Leduc, and G. Ferroni, Fluorescence polarization in studies of bacterial cytoplasmic membrane fluidity under environmental stress. *Progress in biophysics and molecular biology*, 2007. 95(1): p. 60-82.
65. Yoon, Y., H. Lee, S. Lee, S. Kim, and K.-H. Choi, Membrane fluidity-related adaptive response mechanisms of foodborne bacterial pathogens under environmental stresses. *Food Research International*, 2015. 72: p. 25-36.
66. Rock, C. and S. Jackowski, Pathways for the incorporation of exogenous fatty acids into phosphatidylethanolamine in *Escherichia coli*. *Journal of Biological Chemistry*, 1985. 260(23): p. 12720-12724.

67. Denich, T., L. Beaudette, H. Lee, and J. Trevors, Effect of selected environmental and physico-chemical factors on bacterial cytoplasmic membranes. *Journal of microbiological methods*, 2003. 52(2): p. 149-182.
68. Carty, C. and L. Ingram, Lipid synthesis during the *Escherichia coli* cell cycle. *Journal of bacteriology*, 1981. 145(1): p. 472-478.
69. Morein, S., A.-S. Andersson, L. Rilfors, and G.J.J.o.B.C. Lindblom, Wild-type *Escherichia coli* cells regulate the membrane lipid composition in a window between gel and non-lamellar structures. 1996. 271(12): p. 6801-6809.
70. O'Leary, W.M., The fatty acids of bacteria. *Bacteriological reviews*, 1962. 26(4): p. 421.