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Cellular Effects of Bacterial N-3-Oxo-Dodecanoyl-L-Homoserine Lactone on the Sponge Suberites domuncula (Olivi, 1792): Insights into an Intimate Inter-Kingdom Dialogue

Johan Gardères1, Joël Henry2, Benoit Bernay3, Andrés Ritter4, Céline Zatylny-Gaudin2, Matthias Wiens5, Werner E. G. Müller5, Gaël Le Pennec1*

1 Université de Bretagne-Sud, Laboratoire de Biotecnologie et de Chimie Marines, EA 3884, Institut Universitaire Européen de la Mer, Lorient, France, 2 Laboratoire des Mollusques Marins et des Ecosystèmes associés, CNRS INEE FRE 3484, Université de Caen Basse-Normandie, Caen, France, 3 Post Genomic Platform PROTEOGEN, SF ICORE 4206, Université de Caen Basse-Normandie, Caen, France, 4 Pontificia Universidad Católica de Chile - Departamento de Ecologia Facultad de Ciencias Biológicas - Santiago - Chile, 5 European Research Council Advanced Investigator Grant Research Group at Institute for Physiological Chemistry, University Medical Center of the Johannes Gutenberg University, Mainz, Germany

Abstract
Sponges and bacteria have lived together in complex consortia for 700 million years. As filter feeders, sponges prey on bacteria. Nevertheless, some bacteria are associated with sponges in symbiotic relationships. To enable this association, sponges and bacteria are likely to have developed molecular communication systems. These may include molecules such as N-acyl-L-homoserine lactones, produced by Gram-negative bacteria also within sponges. In this study, we examined the role of N-3-oxododecanoyl-L-homoserine lactone (3-oxo-C12-HSL) on the expression of immune and apoptotic genes of the host sponge Suberites domuncula. This molecule seemed to inhibit the sponge innate immune system through a decrease of the expression of genes coding for proteins sensing the bacterial membrane: a Toll-Like Receptor and a Toll-like Receptor Associated Factor 6 and for an anti-bacterial perforin-like molecule. The expression of the pro-apoptotic caspase-like 3/7 gene decreased as well, whereas the level of mRNA of anti-apoptotic genes Bcl-2 Homolog Proteins did not change. Then, we demonstrated the differential expression of proteins in presence of this 3-oxo-C12-HSL using 3D sponge cell cultures. Proteins involved in the first steps of the endocytosis process were highlighted using the 2D electrophoresis protein separation and the MALDI-TOF/TOF protein characterization: α and β subunits of the lysosomal ATPase, a cognin, cofilin-like proteins and cytoskeleton proteins actin, α tubulin and α actin. The genetic expression of some of these proteins was subsequently followed. We propose that the 3-oxo-C12-HSL may participate in the tolerance of the sponge apoptotic and immune systems towards the presence of bacteria. Besides, the sponge may sense the 3-oxo-C12-HSL as a molecular evidence of the bacterial presence and/or density in order to regulate the populations of symbiotic bacteria in the sponge. This study is the first report of a bacterial secreted molecule acting on sponge cells and regulating the symbiotic relationship.

Introduction
Sponges and bacteria have lived in an intimate association for the last 700 million years [1,2]. This association may be defined as a symbiosis sensu De Bary [3]. About 25 bacterial phyla have been identified as being associated with sponges within the Porifera phylum [2]. Among them, the Poribacteria contains bacteria specifically associated with sponges [2]. Living together, sponges and bacteria have likely developed means to communicate and to regulate the association. For a number of years, research efforts have focused on understanding the relationships between sponge and bacteria. Recent studies demonstrate that some sponge-associated bacterial species possess specific genes coding for proteins with domains found in eukaryotic proteins such as ankyrin, adhesin, fibronectin type III, tetracopeptide repeats, which may be involved in protein-protein interactions in eukaryote organisms [4,5]. These specific proteins may represent a means for some bacteria to be recognized by sponge cells.

The sponges possess innate immune and apoptotic systems very similar to those of higher vertebrates [6,7,8,9,10]. The sponge immune system is able to detect bacterial membrane molecules from pathogenic strains and to trigger a differential response [7,8]. Some proteins involved in the immune pathway have been identified in Suberites domuncula and Amphimedon queenslandica such as LPS-binding protein [7], TLR (Toll-Like receptor) [9], MyD88 [7], IRAK (Interleukin Receptor Associated Kinase) [9], TRAF 6...
3-oxo-C12-HSL, regardless of the tested concentration, did not
in presence of 3-oxo-C12-HSL. The characterization of these
differently expressed in a 3D cell culture model, the primmorph,
proteomic approach demonstrated that some proteins are
expression of sponge immune and apoptotic genes. Moreover, a
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S. domuncula

in vitro

AHL Effects on the Sponge S. domuncula

2.2 Immune and Apoptotic Responses to 3-oxo-C12-HSL

The variations in gene expression were studied using quanti-
tative RT-PCR in the presence of 3-oxo-C12-HSL for the immune
markers: Toll-like receptor, TRAF 6-like and MPEG-like protein,
and for the apoptotic markers: caspase 3/7-like, BHP 1 and BHP 2
and statistically examined according to the U-Mann Whitney
test (p<0.05). The mRNA levels of the anti-apoptotic genes BHP-
1 and BHP-2 did not statistically change in the presence of
10^{-6} M 3-oxo-C12-HSL compared to the control samples, since
the average ratios of gene expression are 1 between the treated and
the control samples. In contrast, the expression of TLR, TRAF 6-
like, MPEG and caspase 3/7-like genes changed statistically in the
presence of this AHL. The mRNA levels of these genes decreased
on average by a factor of 2 in the presence of 10^{-6} M 3-oxo-C12-
HSL (Figure 2).

2.3 General Protein Response of Sponge Primmorphs to

10^{-6} M 3-oxo-C12-HSL

2.3.1 Total protein fraction. The analysis of 24 h-treated
primmorph proteins showed that 12 proteins were over-expressed
in the presence of 10^{-6} M 3-oxo-C12-HSL (Figures 3 A, B and C).
After characterization and data bank analyses, 7 proteins matched
with EST sequences: 5 with S. domuncula EST sequences and
2 with A. queenslandica EST sequences (Table 1). The alignment of
these sequences with the GenBank data base led to the
identification of 5 proteins according to their function. Three
proteins corresponded to the α and β subunits of a lysosomal
ATPase (spots 104, 154 and 157), α actinin (spot 99) and the α
subunit of tubulin (spot 169) were also over-expressed in the
presence of 10^{-6} M 3-oxo-C12-HSL. Two EST sequences, not
identified, were translated and submitted to the Prosite software
(spots 17 and 121). No positive match was obtained. However, the
protein sequence of spot 121 presented a conserved glutaredoxin
domain in N-terminal position (Prosite score = 10.439).

2.3.2 Membrane protein fraction. After statistical analysis
of 24 h-treated primmorph proteins, 9 spots were over-represent-
ed in the membrane protein fractions either in the presence or in
the absence of the 3-oxo-C12-HSL (Figures 3 C and D): 6 spots

Results

2.1. Cytotoxicity of 3-oxo-C12-HSL on Sponge Cells

The cytotoxicity of 3-oxo-C12-HSL was evaluated on sponge
cells according to the MTT assay in the presence of 10^{-4} M,
10^{-3} M and 10^{-6} M of the molecule. The non-treated
cell cultures were used as a reference. The highest quantity of DMSO
(1%) used to dissolve the molecule was also assayed to evaluate the
cytotoxic potential of this solvent on sponge cells. No significant
difference in cell viability was observed between non-treated and
treated cultures (Figure S1). Furthermore, the amount of DMSO
used in this experiment did not lead to any difference throughout
the length of the experiment, i.e., after up to 48 h. The presence of
3-oxo-C12-HSL, regardless of the tested concentration, did not
induce any difference in the rate of formazan production compared
to reference and DMSO-treated cultures.

We also examined the morphology of primmorphs in the
presence of 3-oxo-C12-HSL. Macroscopically, the morphology of
primmorphs was not modified after 24 h and 48 h of incubation in
the presence of 3-oxo-C12-HSL regardless of the concentrations
tested (Figure 1). We therefore chose to test the effect of the 3-oxo-
C12-HSL at the lowest concentration, 10^{-6} M, corresponding to
the lowest amount of homoserine lactone found in sponge extracts
[18].

Figure 1. Primmorph cultures stimulated for 48 h with 10^{-6} M
of N-3-oxododecanoyl- L-homoserine (A) or not stimulated (B).
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were over-represented in the membranes of 3-oxo-C12-HSL-stimulated primmorphs whereas the intensity of 3 spots was higher in the control condition. Five of these characterized proteins matched with *S. domuncula* EST sequences (Table 2). In presence of 10^{-6} M 3-oxo-C12-HSL, an actin, a cognin and 2 cofilins/actin-depolymerizing factors (ADF) were found in higher amounts in primmorph membranes. α tubulin associated to cell membranes was less abundant in the treated samples compared to the control samples. No domain was identified within the four unknown over-represented proteins using the Prosite software.

2.4 Sponge mRNA Levels of Genes Encoding the Differentially Primmorphs Expressed Proteins

The mRNA levels of genes encoding the differentially expressed *S. domuncula* proteins, α actinin, α ATPase, α tubulin and the protein from spot 121, were compared in the sponge organism stimulated or not by 10^{-6} M 3-oxo-C12-HSL for 8 h. The values shown in Figure 4 represent the average ratio between the expressions of each gene in presence of the AHL versus in the control condition. Significant differences were examined according to the U-Mann Whitney test (p<0.05). α actinin mRNA level did not vary statistically in the presence or in the absence of this AHL. The expression of genes encoding the α ATPase, the α tubulin and the spot 121 protein increased 1.63, 1.94 and 1.76 fold, respectively, in the presence of 10^{-6} M 3-oxo-C12-HSL (Figure 4). The statistical analysis showed that their expression differed significantly in the presence of 10^{-6} M 3-oxo-C12-HSL.

![Figure 2. Relative amounts of transcripts for Toll-like receptor (TLR), Toll-like Receptor associated factor 6-like protein (TRAF 6), Macrophage-Expressed Gene protein (MPEG), caspase-like 3/7, BCI-2 homolog protein-1 (BHP-1) and BCI-2 homolog protein-2 (BHP-2) in *N*-3-oxododecanoyl-L-homoserine lactone (3-oxo-C12-HSL)-stimulated *Suberites domuncula* compared to control *S. domuncula*. The mRNA levels in 8 h-stimulated *S. domuncula* were evaluated by quantitative reverse transcription-PCR and compared to those in control sponges. Reactions were performed in triplicate with three different specimens. Relative mRNA level values resulted from calculating values: values above and below 1 show a higher and a lower mRNA level in the presence of 10^{-6} M 3-oxo-C12-HSL, respectively. Significant expression changes (p<0.05) in the presence of *N*-3-oxododecanoyl-L-homoserine are pointed out by an asterisk. doi:10.1371/journal.pone.0097662.g002

### Materials and Methods

#### 3.1 Live Material, Primmorph Culture, and Stimulation

*Suberites domuncula* is the sponge used in this study. No specific authorization is requested to collect sponges in open areas for scientific purposes. This study did not involve endangered or protected species.

Live specimens were collected along the Brittany coasts (Bay of Brest, Brittany, France) by scuba diving (at a water depth of 5 m) and kept alive in an artificial seawater aquarium at 11°C. The physical and chemical parameters were controlled twice a week prior to feeding [22]. For each experiment, sponge cells were dissociated individually from 3 different specimens for cell culture purposes [18,22]. Briefly, a piece (2 cm^3) of each sponge specimen was cut individually into small cubes (1 mm^3) in calcium- and magnesium-free seawater (CMFSW) (460 mM NaCl, 7 mM Na,HSO₄, 10 mM KCl, 10 mM Hepes, 73 μg mL⁻¹ of penicillin G potassium, 34.5 μg mL⁻¹ of streptomycin sulfate, pH 7.4) containing EDTA (250 mM) under sterile conditions. The resulting fragments were transferred into a 50-mL conical tube and incubated at room temperature (RT°C, namely 20°C ± 1) on a rotary shaker for 30 min. The supernatant was filtered through a nylon cloth with pores of 20 μm diameter. Fresh CMFSW-EDTA solution was added on the remaining pieces of sponge, and the suspension was incubated once again on the rotary shaker for 30 min. The resulting filtered cell suspensions were centrifuged at 800 g at RT°C for 5 min. The supernatants were discarded, and the cells were suspended twice in CMFSW to remove the EDTA. Finally, the cells from the two incubations were pooled and...
centrifuged at 800 g at RT \(^{\circ}C\) for 5 min. The cell pellet was then suspended in 0.2 \(\mu\)m-filtered natural seawater collected at seashore at Ploemeur, Brittany, France. The seawater was supplemented with sea sand (Sigma-Aldrich, France), 10 \(\mu\)M ferrous citrate (Sigma-Aldrich, France), 1 mM pyruvate (Sigma-Aldrich, France) and 75 \(\mu\)g mL\(^{-1}\) of Penicillin G potassium and 34.5 \(\mu\)g mL\(^{-1}\) of Streptomycin sulfate to prevent bacterial growth. The cell suspension was separated in two fractions of equal volumes, and both were incubated into Petri dishes, at 15 \(^{\circ}C\) under permanent gentle shaking. During the first two days of incubation, the cells clumped and aggregated, forming axenic primmorphs. At this stage, two identical cultures from the same sponge were available. After 3 days of culture, the culture medium was completely renewed with fresh culture medium without antibiotic. Old culture medium was spread on Marine growth agar (Difco, France) to check for bacterial growth. In order to study early primmorph extract separated with a linear gradient pH 4–7 (A) or pH 5–8 (C). Spots with amounts significantly higher (p < 0.05) changed are highlighted on the gels with white and black boxes for protein, the amount of which is significantly higher or lower in presence of 3-oxo-C\(_{12}\)-HSL, respectively. Enlargements of these spots are shown in D (left part: 3-oxo-C\(_{12}\)-HSL -treated sample; right part: untreated sample).

**Figure 3. 2D electrophoretic profiling of Suberites domuncula primmorph extracts in response to 10\(^{-6}\) M of N-3-oxododecanoyl-L-homoserine lactone (3-oxo-C\(_{12}\)-HSL).** Images correspond to representative gels of a total 3-oxo-C\(_{12}\)-HSL-stimulated protein primmorph extract separated with a linear gradient pH 4–7 (A) or pH 5–8 (B), and of a membrane 3-oxo-C\(_{12}\)-HSL-stimulated protein primmorph extract separated with a linear gradient pH 5–8 (C). Spots with amounts significantly (p<0.05) changed are highlighted on the gels with white and black boxes for protein, the amount of which is significantly higher or lower in presence of 3-oxo-C\(_{12}\)-HSL, respectively. Enlargements of these spots are shown in D (left part: 3-oxo-C\(_{12}\)-HSL -treated sample; right part: untreated sample). doi:10.1371/journal.pone.0097662.g003

3.2 Cytotoxicity Assays

The cytotoxic assays were performed according to Zhang et al. (2004) [23] in triplicate with cells from two different specimens. After tissue dissociation, the sponge cells were cultured in 96 well plates into supplemented seawater. Briefly, 200 microliters of the cell suspension (10\(^{6}\) cells mL\(^{-1}\)) were laid in each well and incubated for 16 h at 15 \(^{\circ}C\). The cells were then incubated for 24 h and 48 h in presence of 3-oxo-C\(_{12}\)-HSL (10\(^{-4}\) M, 10\(^{-5}\) and 10\(^{-6}\) M) or DMSO 0.1% (v: v). Cell cultures without AHL or DMSO supplementation were used as a reference.

Cell viability was determined with a solution of tetrazolium compound (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium) (MTT) (Sigma-Aldrich, France). Twenty microliters of a MTT solution (5 mg mL\(^{-1}\)) were added into each culture well and incubated for 2 h at 15 \(^{\circ}C\). After centrifugation at 800 g for 10 min at 4 \(^{\circ}C\), the supernatant was removed and replaced by 200 \(\mu\)L DMSO. The plate was shaken in the darkness and then sonicated to promote the cell lysis. The production of formazan, which is related to cell viability [24], was determined by measuring its absorbance at 540 nm with a spectrophotometric 96-well plate reader (Tecan, France). A U-Mann Whitney test was performed as a statistical test with the following hypothesis: the results are different between the controls and the samples (p<0.05) using the Statistica software (StatSoft, France).

3.3 Preparation of Total and Membrane Proteins

Protein extractions were performed on primmorphs. Primmorphs were collected by centrifugation at 800 g for 5 min at 4 \(^{\circ}C\) and washed with CMFSW. Primmorphs were then crushed using a Polytron homogenizer in 2 mL of lysis solution (1% Triton 100X, 20 mM Tris-HCl, 3 mM MgCl\(_{2}\), 1 mM EDTA, 0.15 mM NaCl and 1 mM PMSF, pH 7.4) and further incubated on ice for 2 h under gentle agitation. The mixture was then centrifuged at 400 g for 10 min at 4 \(^{\circ}C\). The supernatant was collected and precipitated overnight at −20 \(^{\circ}C\) by 4 volumes of precipitating solution (0.1 M ammonium acetate, acetone 80% (v: v)) in order to pellet the total protein fraction. For membrane preparation, an additional step was added. The centrifuged lysate was laid onto a saccharose gradient (10, 15, 35 and 40% (w: v)) and centrifuged at 200,000 g for 15 h at 4 \(^{\circ}C\). The 15% fraction was collected and precipitated as described above. The precipitate was collected after centrifugation at 10,000 g for 20 min at 4 \(^{\circ}C\). The protein pellet was subsequently washed twice in ice-cold acetone. The pellet was quickly dried at RT \(^{\circ}C\) and suspended in a protein solubilization buffer (7M Urea, 2M Thiourea, CHAPS 4% (w: v), 60 mM DTT, 10 mM Tris-HCl, protease inhibitor mix (GE Healthcare, France), pH 7.4). A final cleaning step was added using the 2-D Clean-Up Kit (Bio-Rad Laboratories, France). The total protein concentration was assayed by using the Quick Start Bradford (Bio-Rad Laboratories, France). The extracts were stored at −80 \(^{\circ}C\).

3.4 2-D protein separation

For the three replicates of each condition, either for the total proteins or for the membrane proteins, 600 \(\mu\)g of proteins were solubilized into 300 \(\mu\)L of the solubilization buffer supplemented by 1X Biolyte, pH 3-10 (Bio-Rad Laboratories, France) and 0.005% (w: v) bromophenol blue. The protein solution was loaded onto a 17 cm ReadyStrip, pH range 4–7 or 5–8 (Bio-Rad Laboratories, France) according to the manufacturer’s instructions. After an overnight active rehydration step at 50 V in the Protean IEF Cell (Bio-Rad Laboratories) thermo-regulated at 20 \(^{\circ}C\), the isoelectrofocalisation, the SDS-
Table 1. MS identification of the proteins from total primmorph extract and from the membrane fractions, which displayed differential abundances in N-3-oxodecanoyl-L-homoserine lactone (3-oxo-C_{12}-HSL)-stimulated *Suberites domuncula* primmorphs compared to control primmorphs (p<0.05).

| Protein spots | Protein analysis | Protein identification |
|---------------|------------------|------------------------|
|               | protein number regulation | sequence bank | GenBank accession number | Mascot score | recognized peptide numbers | sequence coverage (%) | homology (species) | E-Value |
| 24 h-stimulated primmorphs (total soluble protein fraction) | | | | | | |
| 17 | + | S. domuncula | gi|300467112 | 59 | 1 | 11 |
| 39 | + | | | | | |
| 70 | + | | | | | |
| 99 | + | S. domuncula | gi|300479356 | 93 | 2 | 10 | α-actinin 1 (*Homo sapiens*) | 5.0 · 10^{-68} |
| 102 | + | | | | | |
| 104 | + | S. domuncula | gi|300478742 | 167 | 4 | 13 | α subunit lysosomal ATPase (*Homo sapiens*) | 5.0 · 10^{-75} |
| 114 | + | | | | | |
| 121 | + | S. domuncula | gi|300479590 | 172 | 3 | 16 |
| 143 | + | | | | | |
| 154 | + | A. queenslandica | Aqu1.228276 | 83 | 3 | 1 | β subunit lysosomal ATPase (*Homo sapiens*) | 8.0 · 10^{-67} |
| 157 | + | A. queenslandica | Aqu1.228276 | 84 | 4 | 1 | β subunit lysosomal ATPase (*Homo sapiens*) | 8.0 · 10^{-67} |
| 169 | + | S. domuncula | gi|300467815 | 125 | 3 | 17 | tubulin α-1 chain (*Parentrotus lividus*) | 1.0 · 10^{-124} |
| 24 h-stimulated primmorphs (membrane soluble protein fraction) | | | | | | |
| 394 | + | S. domuncula | gi|300469085 | 143 | 4 | 26 | actin (*Aedes aegypti*) | 2.0 · 10^{-132} |
| 503 | + | S. domuncula | gi|300465889 | 74 | 2 | 12 | cognin (*Gallus gallus*) | 5.0 · 10^{-58} |
| 1201 | + | S. domuncula | gi|300465842 | 78 | 3 | 11 | cofilin/Actin depolymerizing factor (*Grosmannia clavigera*) | 1.0 · 10^{-15} |
| 1402 | + | | | | | |
| 3608 | – | | | | | |
| 4204 | + | | | | | |
| 4502 | – | S. domuncula | gi|300467049 | 128 | 4 | 23 | α-tubulin (*Suberites ficus*) | 6.0 · 10^{-137} |
| 4504 | + | S. domuncula | gi|300468062 | 67 | 1 | 4 | cofilin/Actin depolymerizing factor (*Grosmannia clavigera*) | 1.0 · 10^{-15} |
| 5202 | – | | | | | |

*The amount of proteins in fractions is higher (+) or lower (−) in presence of 3-oxo-C_{12}-HSL.

Protein MS spectra were compared to theoretical spectra of proteins generated from *S. domuncula* and *Amphimedon queenslandica* EST data bases.
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3.5 Image Analysis

Gels were scanned using the Molecular Imager G800 Calibrated Densitometer (Bio-Rad Laboratories, France) at 400 dpi by Quantity One software (Bio-Rad Laboratories, France). The gels were then analyzed with the Melanie software (GE Healthcare, France). Manual editing and normalization were applied after automated spot detection and matching. Spot quantification was based on spot density as a percentage of the total spot density of the gel to normalize for possible staining differences between gels. Gel annotations and matching fidelity were checked manually to eliminate matching errors caused by the software. All spots selected for MS analyses presented statistically significant variations (p < 0.05) using the U-Mann Whitney test (Statistica software, StatSoft, France).

**Table 2.** Primers used to quantify gene expression in *Suberites domuncula* using real-time PCR.

| Genes            | forward primers                      | reverse primers                      |
|------------------|---------------------------------------|--------------------------------------|
| Toll-like receptor | 5’-CGCTTTTACTTCAGCTGCC-3’            | 5’-CCTCGGGGACAAAGACAAG-3’            |
| Caspase 3/7-like  | 5’-AATGGCATCCAGAAAATCAGGGG-3’        | 5’-GGTGGCATCTGCGCACTGATG-3’          |
| TRAF6-like       | 5’-GGAATCGCACAATGGCCCT-3’            | 5’-CAGCAAGATCAGGAGTTGG-3’            |
| α ATPase         | 5’-GCGTCTGAGCTGAACAGGAC-3’           | 5’-GCGTCTGAGCTGAACAGGAC-3’           |
| actin α1         | 5’-GACTGGGAATCTCCACAGACG-3’          | 5’-GGTGGATGTCTGGCGACGT-3’            |
| tubulin α        | 5’-GCATGGGAATCTCCACAGACG-3’          | 5’-GGTGGATGTCTGGCGACGT-3’            |
| spot 121         | 5’-AGCACCTGGCCAGTACGAG-3’            | 5’-GGTGGATGTCTGGCGACGT-3’            |
| HPRT             | 5’-TACATGGAGGCGACGTTGACGGAC-3’        | 5’-TACATGGAGGCGACGTTGACGGAC-3’        |
| GAPDH            | 5’-TCCAAACCGCAGCAAGTGATCAG-3’        | 5’-AGTGAAGTGCTCCCTGAAACGTC-3’        |

**Figure 4.** Relative amounts of the α subunit of ATPase (ssu α ATPase), α actinin, α tubulin and protein spot 121 transcripts in N-3-oxododecanoyl-L-homoserine lactone (3-oxo-C12-HSL)-stimulated *Suberites domuncula* compared to the control. The mRNA levels in stimulated *S. domuncula* were evaluated by quantitative reverse transcription-PCR and compared to non-stimulated sponges. Reactions were performed in triplicate with three different specimens. Relative mRNA level values resulted from calculating values: values above and below 1 show a higher and a lower mRNA level in the presence of 10^{-6} M 3-oxo-C12-HSL, respectively. Significant expression changes (p < 0.05) in the presence of N-3-oxododecanoyl-L-homoserine are pointed out by an asterisk.

doi:10.1371/journal.pone.0097662.g004
3.6 In Gel Digestion and Protein Analysis

The spots of interest were manually excised from the gel. The gel pieces were washed individually for 30 min in 200 μL of solution A (ammonium bicarbonate and acetonitrile mix: 2.5 mL of 1 M ammonium bicarbonate added to 47.5 mL water and 50 mL acetonitrile). Washings with ammonium bicarbonate 25 mM and solution A were repeated until the gel was discolored. The subsequent washings were performed with 200 μL of ultrapure HPLC grade water, then with 200 μL of 100% HPLC grade acetonitrile. Each washing lasted approximately 15 min at RT under shaking. The supernatants were discarded and the gels were dried using a vacuum pump for 5 min at RT/C. Twenty-five microliters of a diluted trypsin solution (0.006 μg μL−1 in 25 mM ammonium bicarbonate) were added to each gel piece and rehydration was done on ice for 15 min. Thirty microliters of 25 mM ammonium bicarbonate were added to complete the rehydration, and the samples were incubated overnight at 37°C under continuous shaking. The supernatant was discarded, and the peptides were extracted for 15 min successively with 30 μL of a solution of 50% (v/v) of acetonitrile in water, 30 μL of a 5% formic acid (v/v) solution in water, and finally with 30 μL 100% acetonitrile. The solutions were gathered together prior to drying using a vacuum pump or a dry bath at 55°C until complete evaporation. The sample was stored at −20°C until analysis.

3.7 Mass Spectrometry and Bank Search

MS experiments were carried out on an AB Sciex 5800 proteomics analyzer equipped with TOF TOF ion optics and an OptiBeam on-axis laser irradiation with 1000 Hz repetition rate (AB Sciex, USA). The system was calibrated immediately before analysis with a mixture of des-Arg-Bradykinin, Angiotenin I, Glu1-Fibrinopeptide B, ACTH (18–39), ACTH (7–38) and a mass precision less than 5 ppm. 0.8 μL of the peptide solution was mixed with 1.6 μL of 9-cyano-4-hydroxycinnamic acid (CHCA) matrix dissolved in a solution of 50% acetonitrile supplemented with 0.1% TFA (v/v). The mixture was spotted on a stainless steel Opti-TOF 384 targets (Applied Biosystems, USA); the droplet was evaporated before introducing the target into the mass spectrometer. All acquisitions were taken in automatic mode. A laser intensity of 3,000 A was typically used for ionizing. MS spectra were acquired in the positive reflector mode by summing 1000 single spectra (5×200) in the m/z 700–4,000 range. MS/MS spectra were acquired in the positive MS/MS reflector mode by summing a maximum of 2,500 single spectra (10×250) with a laser intensity of 3,900 A. For the tandem MS experiments, the acceleration voltage applied was 1 kV, and air was used as the collision gas. The fragmentation pattern was used to determine the sequence of the peptide. Database searching was performed using the Mascot 2.3.02 program (Matrix Science, USA). Two Expressed Sequence Tags (EST) databases corresponding to updated compilation downloaded from the NCBI database were used with the demosponges S. domuncula and A. queenslandica as selected species (including 13,684 and 30,060 entries respectively). The variable modifications allowed were as follows: N-terminal acetylation, methionine oxidation, and dioxidation. “Trypsin” was selected as enzyme, and three misclevagions were also allowed. Each matching cDNA sequence was submitted to the NCBI protein database (blastx) to find a potential homology with known proteins of other species. Homologous proteins possessing an E-value lower than 10−10 were considered to possess the same identity as the studied protein. The sequences of unknown proteins were then analyzed by Scanproas (expasy.org/tools/scanproasite) to predict putative functions for the proteins under study.

3.8 Quantitative Reverse Transcription-PCR (qRT-PCR) Analysis

Three sponge specimens were separated in two pieces, incubated in 100 mL of 0.2 μm-filtered seawater and stimulated for 8 h either by 10−6 M 3-oxo-C12-HSL or by 0.1% DMSO (v:v) as control sample, respectively. Eight hours were chosen according to Smith et al. (2001) [25]. Total RNAs were isolated from fresh sponge tissues in the extraction solution RNA now (Epicentre, USA), and DNase (Epicentre, USA) treated according to the manufacturer’s instructions. Five hundred nanograms of total RNAs were used to synthesize first-strand cDNAs using oligo(dT) primers with MultiScribe Reverse Transcriptase (Applied Biosystem, USA) according to the manufacturer’s instructions. A negative control was included using total RNA without the MultiScribe Reverse Transcriptase. The mRNAs of interest were quantified by real-time PCR amplification of their cDNAs. The relative mRNA transcript change of each gene was studied for immune markers: Toll-like receptor, TRAF 6-like and MPEG-like protein, and for apoptotic markers: caspase 3/7-like, BHP 1 and BHP 2. Primers (Table 2) were designed with Primer Express 3 software (Applied Biosystems, USA) in order to have a melting temperature (Tm) between 58 and 60°C. Each primer pair was validated by verifying that the PCR efficiency E was above 0.95, and that a single PCR product with the expected Tm was obtained. PCR reactions were performed in triplicate with the 7300 Real Time PCR System apparatus (Applied Biosystems, USA). The 20 μL reactions contained 10 μL SYBR Green PCR Master Mix (including AmpliTaq Gold DNA Polymerase) (Applied Biosystems, USA), 2 μL of each primer (3 μM) and 8 μL of cDNAs. For each experiment, three serial cDNA dilutions were used: 0.25, 0.025 and 0.0025 ng μL−1. The PCR conditions were 95°C for 10 min for polymerase activation, and 40 cycles at 95 and 60°C for 60 and 30 s, respectively. The relative quantification of the mRNAs of interest was obtained by the comparative Pfaffl method using HPRT or GAPDH as endogenous control (Table 2) [26]:

\[
\text{Ratio}(R) = \frac{E^{Ct\text{control}} - E^{Ct\text{stimulated}}}{E^{Ct\text{sample gene}} - E^{Ct\text{reference gene}}}
\]

E: efficiency of the primer couple, Ct: cycle threshold. Relative mRNA level values resulted from calculated values: values above and below 1 showed a higher and a lower mRNA level in the presence of 10−6 M 3-oxo-C12-HSL or by 0.1% DMSO (v:v), respectively. A U-Mann Whitney test was performed as a statistical test with the following hypothesis: the relative transcript level ratios are different between the controls and the samples (p<0.05), using the Statistica software (StatSoft, France).

Discussion

Sponges and bacteria have been associated within consortia for approximately 700 million years [1,2]. As foreign organisms, on the one hand, the bacteria need to find a means to protect themselves from the host chemical defense or predation and, on the other hand, the host needs to sense the population of bacteria to discriminate between the pathogenic and the non-pathogenic ones and to regulate the density of resident bacteria. Both organisms are able to express molecules to communicate between themselves such as quorum-sensing molecules for the bacteria [11].
and hormone-like factors for sponges [27]. Some of these molecules may be able to act as cross-kingdom dialog factors. Among these potential molecules, AHLs are produced in vivo by bacteria within the sponge *S. domuncula* [18]. These secreted molecules, produced by Gram-negative bacteria, were recognized as acting on eukaryotic cells of higher vertebrates [12,13,14,15]. Nevertheless, these studies have always been performed in pathological contexts, and never in a symbiotic one sensu De Bary [3]. The purpose of this study was to investigate the potential of 3-oxo-C12-HSL, an AHL which was found in crude sponge extracts [18] and in culture supernatants of sponge-associated bacteria [18,19,20,21], as a symbiotic paracrine factor in the sponge bacterium consortium.

As a xenobiotic molecule, 3-oxo-C12-HSL may trigger an answer of the immune system and/or the apoptotic pathway, both present in this Porifera phylum [6,7,8,9,10]. In order to avoid a cross-contamination by bacteria established in the sponge, axenic 3-D cultures (primmorphs) were used. Primmorphs were first incubated in presence of 10^−6 M 3-oxo-C12-HSL, for 48 h. This primary contact did not influence the shape or the color of the primmorphs maintained in vitro, indicating that 3-oxo-C12-HSL was devoid of a deleterious effect at the macroscopic level. The cell cytotoxicity has been also evaluated: 3-oxo-C12-HSL at 10^−4, 10^−5 and 10^−6 M, as well as the solvent DMSO (1%), did not have any significant cytotoxic effect on sponge cells. These results were in agreement with those observed on human polynuclear neutrophile cells at 10^−5 and 10^−4 M [4].

The different experiments performed on eukaryotic cells with 3-oxo-C12-HSL showed that this molecule can have a negative impact on the immune and apoptosis systems of the host cells. For example, the bacterium *Pseudomonas aeruginosa* uses this molecule to promote its installation and proliferation into the lungs or the intestine. Indeed, 3-oxo-C12-HSL modifies the integrity of the barrier formed by human intestinal epithelial cells [12] and is able to inhibit the vasoconstriction of blood vessels in the heart and lungs [4]. It blocks the proliferation of leucocytes [13] and the differentiation of human T lymphocytes [14]. This molecule also induces the apoptosis in human T lymphocytes by activating the mitochondrial apoptotic pathway [15]. 3-oxo-C12-HSL is also able to influence the secretion of cytokine by immune cells [30,31,32,33]. Sponges possess an innate immune system and an apoptotic pathway close to those of higher eukaryotes [6,7,8,9,10]. [34,35,36,37]. It triggers the transcription of a lot of vertebrate genes transcription observed in whole individual varied in a same way.

In the presence of 10^−6 M 3-oxo-C12-HSL, some proteins were differentially expressed in the total sponge protein extracts. The protein spot 121, over-expressed in presence of 3-oxo-C12-HSL, has not been identified but possesses a glutaredoxin domain. Its gene is also over-expressed after 8 h in the presence of this molecule. This kind of protein, often involved in detoxification processes, is also over-expressed in the plant *Medicago truncatula* in the presence of two AHLs [39]. Moreover, glutaredoxin-1 is involved in the activation of the TRAF-6 protein in Hela cells, which is bound to a S-glutathione group in its inactive state. This mechanism promotes the activation of the IL-1 R/TLR 4 pathway [40]. The sponge may use this protein to try to activate its immune system and/or to eliminate 3-oxo-C12-HSL. Some subunits of the lysosomal ATPase, the α and β subunits, were over-expressed, forming the catalytic site of ATPase [41]. Two spots with different isoelectric points corresponded to the same β subunit. This difference may be explained by posttranslational modifications encountered in phosphorylated proteins [42]. 3-oxo-C12-HSL at 10^−6 M stimulates the expression of the lysosomal α ATPase gene after 8 h of incubation with sponges. Nevertheless, over-expressed cytoskeleton associated-proteins have also been identified: an α actinin and an α tubulin. 3-oxo-C12-HSL stimulates the transcription of the α tubulin gene after 8 h, whereas this molecule did not affect the transcription of the α actinin gene. The increase of a posttranslational form of this protein in the presence of 3-oxo-C12-HSL may explain the higher amount of this protein in 3-oxo-C12-HSL-stimulated primmorph extracts. The incubation time may also be inappropriate to observe the effect of the molecule on the gene expression. The genes transcription observed in whole individual varied in a same manner as the expression of proteins observed in primmorph in the presence of 10^−6 M 3-oxo-C12-HSL. A correlation between the level of genes expression and the corresponding protein is
difficult to establish since regulation processes of the transcription and the regulation of proteins are independent in eukaryotes. Furthermore, the gene expression level between the sponge and the prymnophore may also be somehow different. In the presence of 10^-6 M 3-oxo-C12-HSL, some proteins were also differentially recruited to the sponge cell membranes. Actin and 2 cofillins/ADF proteins were recruited to the membranes, whereas the α tubulin seems to be more represented in the cytoplasm of 3-oxo-C12-HSL-stimulated sponge cells.

The proteins identified in this study correspond to proteins involved in the first steps of endocytosis [43,44]. Indeed, the α actinin is a protein involved in the link between the cell membrane and the intracellular actin. In higher vertebrates, this protein is recruited during the activation of integrins [45], participating for example to the bacteria phagocytosis [43,44]. It links the β subunit of the integrin to actin and participates in the engulfment of bacteria by the cell. Moreover, β integrin homolog sequences have been discovered in the genome of the sponge *A. queenslandica* [10].

The lysosomal ATPase is recruited very early in this process directly in the phagosomes of mouse macrophages. It is transported by tubular lysosomes, formed by tubulin and α tubulin, and contributes to the acidification of early phagosomes [45]. Cofilin/ADF proteins are adjoined to the membrane during the phagosome formation. They regulate the polymerization of actin filaments around the Dictostelium phagosome [47]. Nevertheless, these proteins are also involved in the internalization of the parasite *Listeria monocytogenes* [48,49]. A cognin-like protein is also recruited to the membrane in the presence of 3-oxo-C12-HSL. This membrane protein intervenes in cell aggregation thanks to its disulfide isomerase activity, which creates temporary covalent links with membrane proteins of the other cells [50,51]. Some data demonstrate that some sponge-associated bacteria possess proteins with eukaryotic protein-protein interaction domains [5]. The cognin-like protein may intervene in the capture of these bacteria. 3-oxo-C12-HSL seems to stimulate the de novo protein expression as well as the recruitment of proteins involved in the internalization of bacteria and further in the first step of the endocytosis/phagocytosis process. Indeed, the over-expression of lysosomal V-ATPase, early recruited to the phagosomes via tubular lysosomes to establish the hostile acidic environment [46], suggests that 3-oxo-C12-HSL promotes the phagocytosis process in the sponge cells. In the same way, the phagocytosis activity is stimulated in response to 3-oxo-C12-HSL in immune cells of higher vertebrates [28,29,52]. This increase of activity due to this molecule may correspond to an ancestral mechanism conserved in the evolution.

The 3-oxo-C12-HSL effects on the plant *M. truncatula* also lead to a modification of the expression of cytoskeletal protein such as tubulin and a cofilin/ADF protein [39].

To conclude, 3-oxo-C12-HSL may participate in the control of the immune and apoptotic *S. domuncula* systems. This takeover does not presume of the destiny of bacteria in the eukaryotic cells: taking advantage like in pathological contexts or long-lasting installation like in symbiosis. But the sponge may perceive this signal as a molecular evidence of the bacterial presence/density and may then trigger the first steps of bacterial endocytosis and detoxification mechanism in order to control its bacteriophage.

Indeed, this mechanism may lead the sponge to react to the multiplication of the inhabiting bacteria in order to regulate the population. This secreted 3-oxo-C12-HSL is the first molecule demonstrating a paracrine inter-kingdom action in the sponge and in a non-pathological context. These results open up a new perspective in the understanding of the mechanism of regulation of sponge/bacterium relationships.

**Supporting Information**

**Figure S1** Effect of 3-oxododecanoyl-L-homoserine lactone (3-oxo-C12-HSL) on the viability of *Suberites domuncula* cells. Histogram of the optical density of the cell lysate at 540 nm corresponding to the amount of formazan formed by the alive *S. domuncula* cells. Sponge cells were cultured and then stimulated with 10^-6 (soft grey), 10^-5 (medium grey) and 10^-4 M (dark grey) 3-oxo-C12-HSL, with 1% DMSO (v: v) (white) and with only culture medium (black) for 24 h and 48 h. (TIF)

**Table S1** Complementary information regarding the proteomic experiments. (XLS)

**Author Contributions**

Conceived and designed the experiments: JG GLP JH. Performed the experiments: JG GLP BB JH. Analyzed the data: JG GLP JH BB AR MW. WEGM CZG. Contributed reagents/materials/analysis tools: JG GLP BB JH MW. Wrote the paper: JG GLP JH.

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