

UC Berkeley

UC Berkeley Previously Published Works

Title

A bacterial sulfonolipid triggers multicellular development in the closest living relatives of animals

Permalink

<https://escholarship.org/uc/item/2v96d00r>

Journal

eLife, 1(1)

ISSN

2050-084X

Authors

Alegado, Rosanna A

Brown, Laura W

Cao, Shugeng

et al.

Publication Date

2012

DOI

10.7554/elife.00013

Copyright Information

This work is made available under the terms of a Creative Commons Attribution License, available at <https://creativecommons.org/licenses/by/4.0/>

Peer reviewed



A bacterial sulfonolipid triggers multicellular development in the closest living relatives of animals

Rosanna A Alegado^{1†}, Laura W Brown^{2†}, Shugeng Cao², Renee K Dermenjian², Richard Zuzow³, Stephen R Fairclough¹, Jon Clardy^{2*}, Nicole King^{1*}

¹Department of Molecular and Cell Biology, University of California, Berkeley, Berkeley, United States; ²Department of Biological Chemistry and Molecular Pharmacology, Harvard Medical School, Boston, United States; ³Department of Biochemistry, Stanford University School of Medicine, Stanford, United States

Abstract Bacterially-produced small molecules exert profound influences on animal health, morphogenesis, and evolution through poorly understood mechanisms. In one of the closest living relatives of animals, the choanoflagellate *Salpingoeca rosetta*, we find that rosette colony development is induced by the prey bacterium *Algoriphagus machipongonensis* and its close relatives in the Bacteroidetes phylum. Here we show that a rosette inducing factor (RIF-1) produced by *A. machipongonensis* belongs to the small class of sulfonolipids, obscure relatives of the better known sphingolipids that play important roles in signal transmission in plants, animals, and fungi. RIF-1 has extraordinary potency (femtomolar, or 10^{-15} M) and *S. rosetta* can respond to it over a broad dynamic range—nine orders of magnitude. This study provides a prototypical example of bacterial sulfonolipids triggering eukaryotic morphogenesis and suggests molecular mechanisms through which bacteria may have contributed to the evolution of animals.

DOI: [10.7554/eLife.00013.001](https://doi.org/10.7554/eLife.00013.001)

*For correspondence: jon_clardy@hms.harvard.edu (JC); nking@berkeley.edu (NK)

†These authors contributed equally to this work

Competing interests: See page 12


Funding: See page 12

Received: 22 May 2012

Accepted: 18 July 2012

Published: 15 October 2012

Reviewing editor: Peter Greenberg, University of Washington, United States

 Copyright Alegado et al. This article is distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use and redistribution provided that the original author and source are credited.

Introduction

Eukaryotes evolved in a world filled with bacteria and throughout their shared history these two branches of life have developed a complex set of ways to compete and cooperate with each other. While research on these interactions has historically emphasized bacterial pathogens, bacteria also regulate the biology of eukaryotes in many other ways (McFall-Ngai 1999; Koropatnick et al. 2004; Mazmanian et al. 2005; Falkow 2006; Hughes and Sperandio 2008; Desbrosses and Stougaard 2011) and may have exerted critical influences on animal evolution. Choanoflagellates, microscopic bacteria-eating eukaryotes that are the closest living relatives of animals (James-Clark 1868; Saville Kent 1880; Hibberd 1975; Carr et al. 2008; King et al. 2008; Ruiz-Trillo et al. 2008), could provide particularly important insights into the mechanisms underlying bacterial influences on animal biology and evolution. Moreover, some choanoflagellates have both solitary and multicellular stages in their life histories (Leadbeater 1983; Karpov and Coupe 1998; Dayel et al. 2011) and understanding the environmental cues that regulate choanoflagellate colony formation could provide a molecular model for animal multicellularity.

Results

In the choanoflagellate *Salpingoeca rosetta*, rosette-shaped multicellular colonies develop when a single founder cell undergoes multiple rounds of incomplete cytokinesis, leaving neighboring cells physically attached by fine intercellular bridges (Fairclough et al. 2010; Dayel et al. 2011). Although the original stock of *S. rosetta* (ATCC50818) was established from a rosette colony (Dayel et al.

eLife digest All animals, including humans, evolved in a world filled with bacteria. Although bacteria are most familiar as pathogens, some bacteria produce small molecules that are essential for the biology of animals and other eukaryotes, although the details of the ways in which these bacterial molecules are beneficial are not well understood.

The choanoflagellates are water-dwelling organisms that use their whip-like flagella to move around, feeding on bacteria. They can exist as one cell or a colony of multiple cells and, perhaps surprisingly, are the closest known living relatives of animals. This means that experiments on these organisms have the potential to improve our understanding of animal development and the transition from egg to embryo to adult.

Alegado *et al.* have explored how the morphology of *Salpingoeca rosetta*, a colony-forming choanoflagellate, is influenced by its interactions with various species of bacteria. In particular, they find that the development of multicellularity in *S. rosetta* is triggered by the presence of the bacterium *Algoriphagus machipongonensis* as well as its close relatives. They also identify the signaling molecule produced by the bacteria to be C₃₂H₆₄NO₇S; this lipid molecule is an obscure relative of the sphingolipid molecules that have important roles in signal transmission in animals, plants, and fungi. Moreover, Alegado *et al.* show that *S. rosetta* can respond to this molecule – which they call rosette-inducing factor (RIF-1) – over a wide range of concentrations, including concentrations as low as 10⁻¹⁷ M.

The work of Alegado *et al.* suggests that interactions between *S. rosetta* and *Algoriphagus* bacteria could be a productive model system for studying the influences of bacteria on animal cell biology, and for investigating the mechanisms of signal delivery and reception. Moreover, the molecular mechanisms revealed by this work leave open the possibility that bacteria might have contributed to the evolution of multicellularity in animals.

DOI: [10.7554/eLife.00013.002](https://doi.org/10.7554/eLife.00013.002)

2011), laboratory cultures consistently produced single cells, with small numbers of rosette colonies forming only sporadically (**Figure 1A**, **Figure 1—figure supplement 1**). Serendipitously, we discovered that the bacterial community influences rosette colony development. Treatment of the ATCC50818 culture with an antibiotic cocktail resulted in a culture of *S. rosetta* cells that proliferated robustly by feeding on the remaining antibiotic-resistant bacteria but never formed rosette colonies, even upon removal of antibiotics (**Figure 1B**). This culture line is hereafter referred to as RCA (for 'Rosette Colonies Absent'). Supplementation of RCA cultures with bacteria from ATCC50818 restored rosette colony development, revealing that *S. rosetta* cells in the RCA culture remained competent to form colonies and would do so when stimulated by the original community of environmental bacteria.

To determine which co-isolated bacterial species stimulate rosette colony development in *S. rosetta*, the RCA cell line was supplemented with 64 independent bacterial isolates from ATCC50818 and monitored for the appearance of rosette colonies. Only one bacterial species from ATCC50818, the previously undescribed *Algoriphagus machipongonensis* (phylum Bacteroidetes; Alegado *et al.* 2012), induced rosette colony development in the RCA cell line (**Figure 1C**). *S. rosetta* cultures fed solely with *A. machipongonensis* yielded high percentages of rosette colonies (**Figure 1—figure supplement 1**), demonstrating that no other co-isolated bacterial species is required to stimulate rosette colony development.

What was not clear was whether other bacteria might also be competent to induce rosette colony development. Therefore, representative Bacteroidetes and non-Bacteroidetes bacteria were grown and fed to RCA cultures (**Figure 2**, **Table 1**). None of the non-Bacteroidetes species tested, including members of the γ -proteobacteria, α -proteobacteria, and Gram-positive bacteria, were competent to induce rosette colony development. In contrast, all 15 *Algoriphagus* species tested induced rosette colony development, as did six of 16 other closely related species tested in the Bacteroidetes phylum (**Table 1**). Therefore, the ability to induce rosette colony development is enriched in *Algoriphagus* bacteria and their relatives.

Although Bacteroidetes bacteria regulate morphogenetic processes in such diverse lineages as animals, red algae, and green algae (Provasoli and Pintner 1980; Matsuo *et al.* 2005; Mazmanian

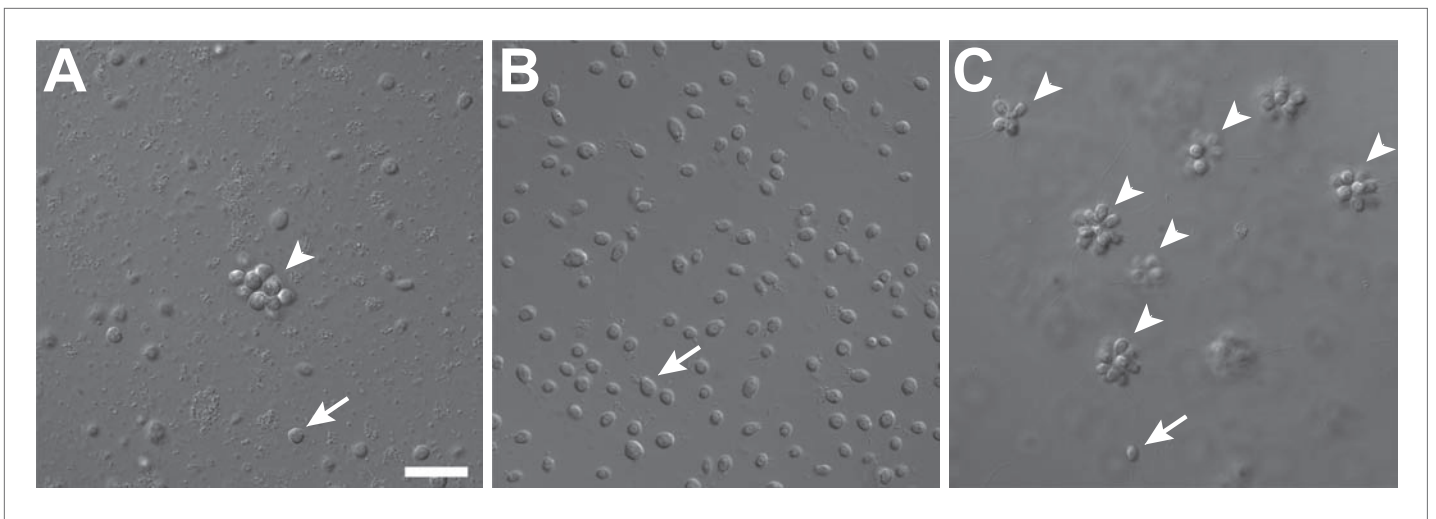


Figure 1. Rosette colony development in *S. rosetta* is regulated by *A. machipongonensis*. (A) The original culture of *S. rosetta*, ATCC 50818, contains diverse co-isolated environmental bacteria and forms rosette colonies (arrowheads) rarely. (B) Treatment of ATCC50818 with a cocktail of antibiotics reduced the bacterial diversity and yielded an *S. rosetta* culture line, RCA, in which rosette colonies never formed. (Representative single cells indicated by arrows.) (C) Addition of *A. machipongonensis* to RCA cultures was sufficient to induce rosette development. Scale bar, 2 μm .

DOI: [10.7554/eLife.00013.003](https://doi.org/10.7554/eLife.00013.003)

The following figure supplements are available for figure 1:

Figure supplement 1. Frequency of rosette colonies in *S. rosetta* environmental isolate ATCC 50818, RCA with and without *A. machipongonensis* and a monoxenic line with *A. machipongonensis* feeder bacteria (Px1).

DOI: [10.7554/eLife.00013.004](https://doi.org/10.7554/eLife.00013.004)

et al. 2005), the bacterially produced chemical cues that regulate most of these partnerships remain obscure. The limited phylogenetic distribution of bacteria capable of inducing rosette colony development suggested that *A. machipongonensis* and its close relatives may produce a characteristic molecule that could be identified biochemically. The complete absence of rosette colonies in RCA cultures provided the basis for a robust bioassay that we developed to identify the rosette-inducing molecule(s), which we named RIFs (Rosette-Inducing Factors), from *A. machipongonensis* cultures. Preliminary studies demonstrated that RIF activity was present in conditioned medium from *A. machipongonensis*, even when grown in the absence of choanoflagellates. Furthermore, the activity was also found in the *A. machipongonensis* cell envelope and was heat, protease, and nuclease resistant, revealing that the compound is not a protein, RNA, or DNA (**Table 2**).

The bacterial cell envelope components lipopolysaccharide (LPS) and peptidoglycan (PGN) from Gram-negative bacteria have long been known to affect host biology (**Cohn and Morse 1960; Hoffmann et al. 1999; Kopp and Medzhitov 1999; Takeuchi et al. 1999; Medzhitov and Janeway 2000; Kimbrell and Beutler 2001; Koropatnick et al. 2004**), but neither LPS nor PGN from *A. machipongonensis* triggered rosette development, alone or in combination (**Figure 3A**). Instead, we found that *A. machipongonensis* crude lipid extracts enriched in sphingolipids robustly induced rosette development (**Figure 3A**). In animals, sphingolipid signaling pathways regulate developmental processes such as cell death, survival, differentiation, and migration (**Prieschl and Baumruker 2000; Pyne and Pyne 2000; Spiegel and Milstien 2000; Hannun et al. 2001; Merrill et al. 2001; Herr et al. 2003**). Moreover, sphingolipids serve essential functions both as structural components of cell membranes and as signaling molecules in diverse eukaryotes (**Hannich et al. 2011**). In contrast, the phylogenetic distribution of sphingolipids in bacteria is largely limited to Bacteroidetes and *Sphingomonas*, where their endogenous functions are poorly understood (**Olsen and Jantzen 2001; An et al. 2011**).

To isolate and characterize the molecule(s) underlying RIF activity, we focused on the fraction enriched in sphingolipids. Lipids isolated from 160 L of *A. machipongonensis* culture were separated using preparative liquid chromatography–mass spectrometry (LC-MS) and the activity of each fraction was measured using the rosette colony induction bioassay. RIF activity tracked with a single fraction, which was further purified by several rounds of preparative thin-layer chromatography (**Figure 3—figure supplement 1**) to yield approximately 700 μg of active compound (RIF-1) with sufficient purity

Table 1. Species tested for colony induction

Species	16S rDNA accession number	Reference	Rosette colonies
<i>Algoriphagus machipongonensis</i> PR1	NZ_AAAXU000000000	Alegado et al. (2012)	+
<i>Algoriphagus alkaliphilus</i> AC-74	AJ717393	Tiago et al. (2006)	+
<i>Algoriphagus boritolerans</i> T-22	AB197852	Ahmed et al. (2007)	+
<i>Algoriphagus mannitolivorans</i> JC2050	AY264838	Yi and Chun (2004)	+
<i>Algoriphagus marincola</i> SW-2	AY533663	Yoon et al. (2004)	+
<i>Algoriphagus ornithinivorans</i> JC2052	AY264840	Yi and Chun (2004)	+
<i>Algoriphagus vanfongensis</i> KMM 6241	EF392675	Van Trappen et al. (2004)	+
<i>Algoriphagus antarcticus</i> LMG 21980	AJ577141	Nedashkovskaya et al. (2004)	+
<i>Algoriphagus aquimarinus</i> LMG 21971	AJ575264	Nedashkovskaya et al. (2004)	+
<i>Algoriphagus chordae</i> LMG 21970	AJ575265	Nedashkovskaya et al. (2004)	+
<i>Algoriphagus halophilus</i> JC2051	AY264839	Yi and Chun (2004)	+
<i>Algoriphagus localis</i> MSS-170	AY835922	Yoon et al. (2005a)	+
<i>Algoriphagus ratkowskyi</i> LMG 21435	AJ608641	Bowman et al. (2003)	+
<i>Algoriphagus terrigena</i> DS-44	DQ178979	Yoon et al. (2006)	+
<i>Algoriphagus winogradskyi</i> LMG 21969	AJ575263	Nedashkovskaya et al. (2004)	+
<i>Algoriphagus yeomjeoni</i> MSS-160	AY699794	Yoon et al. (2005b)	+
<i>Agrobacterium tumefaciens</i> C58	AE007870	Wood et al. (2001)	+
<i>Aquiflexum balticum</i> BA160	AJ744861	Brettar et al. (2004a)	-
<i>Bacillus subtilis</i> 168	AL009126	Kunst et al. (1997); Burkholder and Giles (1947); Spizizen (1958)	-
<i>Bacteroides fragilis</i> NCTC9343	CR626927	Cerdeno-Tarraga et al. (2005)	-
<i>Belliella baltica</i> BA134	AJ564643	Brettar et al. (2004b)	-
<i>Caulobacter crescentus</i> CB15	AE005673	Nierman et al. (2001)	-
<i>Croceibacter atlanticus</i> HTCC2559	NR_029064	Cho and Giovannoni (2003)	-
<i>Cyclobacterium marinum</i> LMG 13164	AJ575266	Raj and Maloy 1990)	+
<i>Cytophaga hutchinsonii</i> ATCC 33406	M58768	Lewin (1969)	+
<i>Dyadobacter fermentans</i> DSM 18053	NR_027533	Chelius and Triplett (2000)	+
<i>Echinicola pacifica</i> KMM 6172	NR_043619	Nedashkovskaya et al. (2006)	-
<i>Escherichia coli</i> MG1655	U00096	Blattner et al. (1997)	-
<i>Flavobacteria johnsoniae</i> UW101	CP000685	Bernardet et al. (1996)	-
<i>Flectobacillus major</i> DSM 103	M62787	Raj and Maloy (1990)	+
<i>Listeria monocytogenes</i> 10403S	CP002002	Edman et al. (1968)	-
<i>Magnetospirillum magneticum</i> AMB-1	AP007255	Matsunaga et al. (2005)	-
<i>Microscilla marina</i> ATCC 23134	M123134	Garrity (2010)	-
<i>Oceanostipes pacificus</i> HTCC2170	CP002157	Oh et al. (2011)	-
<i>Robiginitalea biformata</i> HTCC2501	CP001712	Cho and Giovannoni (2004)	-
<i>Salinibacter ruber</i> DSM13855	CP000159	Anton et al. (2002)	-
<i>Sphingomonas wittichii</i> RW1	CP000699	Miller et al. (2010)	-
<i>Vibrio fischeri</i> ES114	CP000021	Ruby et al. (2005)	-
<i>Zobellia galactonovorans</i> Dsij	NR_025053	Barbeyron et al. (2001)	+
<i>Zobellia uliginosa</i> ATCC 14397	M62799	Matsuo et al. (2003)	+

-: no rosette colonies observed; +: rosette colonies observed

DOI: [10.7554/eLife.00013.005](https://doi.org/10.7554/eLife.00013.005)

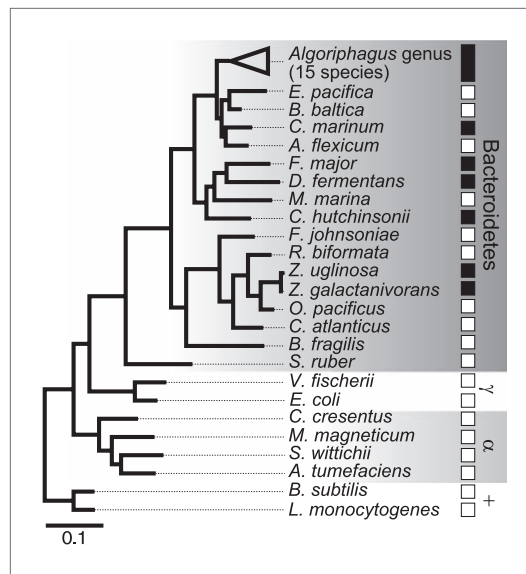


Figure 2. Diverse members of the Bacteroidetes phylum induce rosette colony development. A maximum likelihood phylogeny inferred from 16S rDNA gene sequences reveals the evolutionary relationships among *A. machipongonensis*, other members of the Bacteroidetes phylum, and representative γ -proteobacteria (γ), α -proteobacteria (α), and Gram-positive (+) bacteria. All 15 members of the *Algoriphagus* genus (Table 1), as well as six other species in the Bacteroidetes phylum, were competent to induce colony development (filled squares). In contrast, no species outside of Bacteroidetes and most of the non-*Algoriphagus* bacteria tested failed to induce rosette colony development (open squares). Scale bar, 0.1 substitutions per nucleotide position. DOI: 10.7554/eLife.00013.006

any activity in our assay system. To our knowledge, RIF-1 is the first sulfonolipid demonstrated to influence developmental processes in eukaryotes.

Finally, we investigated the potency of RIF-1 and its ability to induce colony development under plausible environmental conditions. Purified RIF-1 induces rosette formation with a bell-shaped dose-response curve over a broad range of concentrations, from 10^{-2} to 10^7 fM or some nine orders of magnitude (Figure 4). No observable effects were seen below 10^{-5} fM, and RIF-1 appears to be inactive above 10^8 fM. *A. machipongonensis* conditioned medium contains 10^4 fM RIF-1 (Figure 4—figure supplements 1–3), and even if this conditioned medium measurement exaggerates natural concentrations by a factor of 10^6 , *S. rosetta* could still respond to its presence. The shape of the dose-response curve and the potency of RIF-1 suggest that *S. rosetta* perceives RIF-1 in a manner consistent with a receptor-ligand interaction, albeit a receptor of exquisite sensitivity and remarkable dynamic range. While RIF-1 is the only molecule detected with rosette-inducing activity, its maximal activity ($5.6 \pm 0.5\%$ colonial cells/total cells) differs from that of the sphingolipid-enriched lipid fraction ($19.2 \pm 4.6\%$ colonial cells/total cells; Figure 4). This difference may be due to delivery issues of the purified and highly hydrophobic molecule, which in nature resides in membranes and potentially in membrane vesicles. Alternatively, the full potency of RIF-1 as an inducer of colony development may require additional *A. machipongonensis* molecules not identified in this study.

Discussion

These data reveal that RIF-1, a sulfonolipid produced by the prey bacterium *A. machipongonensis*, regulates morphogenesis in its predator, *S. rosetta*. The ecological relevance of this signaling

for structural analysis. RIF-1 represents only 0.015% of the *A. machipongonensis* sphingolipid pool. Based on high-resolution mass spectrometry, RIF-1 has a molecular formula of $C_{32}H_{64}NO_7S$ (M-H: exptl. 606.44027, calcd. 606.44035, Figure 3—figure supplement 2). Detailed analysis of one- and two-dimensional (COSY, HMBC, TOCSY, Figure 3—figure supplements 3–15) nuclear magnetic resonance (NMR, 600 MHz, Table 3) spectra revealed the planar structure of RIF-1, an unusual sulfonolipid shown in Figure 3B.

Sulfonolipids like RIF-1 resemble sphingolipids, but there are important differences between the two. In sphingolipids, a sphingoid base (1,3-dihydroxy-2-aminoalkane) is linked through an amide bond to a fatty acid. The long alkyl chains of both the sphingoid base and fatty acid vary in length, branching, number of double bonds, and placement of hydroxyl substituents. In RIF-1, a capnoid base (2-amino-3-hydroxy-15-methyl-1-sulfonic acid) replaces the sphingoid base, and the sphingolipid hydroxyl, which is the attachment point for the major diversifying elements of the sphingolipid family, is replaced by a sulfonic acid. While members of the sphingolipid family, such as the ceramides, glycosphingolipids, sphingomyelins, and gangliosides, differ by the groups attached to the hydroxyl, the sulfonic acid function in sulfonolipids like RIF-1 has no reported diversifying modifications. In this sense sulfonolipid diversity appears more limited than sphingolipid diversity. Significantly, commercial sphingolipids (sphingomyelin, monosialoganglioside, galactocerebroside, and N-palmitoyl-DL-dihydrolacto cerebroside; Table 2) failed to show

Table 2. Responses of RCA culture to various supplements

Treatment	Rosette colonies	Interpretation
Sea water	–	
CM from ATCC50818	+	RIF-1 present in environmental isolate ATCC 50818
CM from RCA	–	RIF-1 is absent in RCA lines
Live <i>A. machipongonensis</i> (cell pellet)	++	RIF-1 is produced by <i>A. machipongonensis</i>
Heat killed <i>A. machipongonensis</i> (cell pellet)	++	RIF-1 is resistant to heat
<i>A. machipongonensis</i> CM	+	RIF-1 is released by live <i>Algoriphagus</i>
<i>A. machipongonensis</i> CM, boiled 10 min	+	RIF-1 is not labile
<i>A. machipongonensis</i> CM + Proteinase K	+	RIF-1 is not a protein
<i>A. machipongonensis</i> CM + DNase	+	RIF-1 is not DNA
<i>A. machipongonensis</i> CM + RNase	+	RIF-1 is not RNA
<i>A. machipongonensis</i> CM, MeOH extract	+	RIF-1 is an organic compound
<i>A. machipongonensis</i> cell pellet, MeOH extract	++	RIF-1 is present in the <i>Algoriphagus</i> cell envelope
<i>A. machipongonensis</i> cell pellet, Bligh-Dyer extract	++	RIF-1 is a lipid
Sphingomyelin (20 mg mL ⁻¹)	–	Sphingomyelin does not induce rosette colony development
Monosialoganglioside (20 mg mL ⁻¹)	–	Monosialoganglioside does not induce rosette colony development
Galactocerebroside (20 mg mL ⁻¹)	–	Galactocerebroside does not induce rosette colony development
N-palmitoyl-DL-dihydrolacto cerebroside (20 mg mL ⁻¹)	–	N-palmitoyl-DL-dihydrolacto cerebroside does not induce rosette colony development

–: no induction; +: low induction; ++: high induction

CM: conditioned medium; RCA: rosette colonies absent; RIF-1: rosette inducing factor 1

DOI: [10.7554/eLife.00013.007](https://doi.org/10.7554/eLife.00013.007)

interaction is indicated both by the coexistence of *S. rosetta* and *A. machipongonensis* in nature and by the fact that the activity of RIF-1 at femtomolar concentrations makes it markedly more potent than other marine signaling molecules [e.g., *Vibrio* autoinducer (Schaefer et al. 1996) and the tripeptide pheromones of the Caribbean spiny lobster (Ziegler and Forward 2007)]. The potency of RIF-1 signaling compares favorably with that of silkworm moth sex pheromone signaling, in which vapors from an ~4 fM solution of bombykol, the sex pheromone of the silkworm moth, induce a pronounced wing fluttering response in males (Butenandt et al. 1961; Agosta 1992; Roelofs 1995). While it is formally possible that RIF-1-dependent rosette colony development is a promiscuous response to sphingolipid-type molecules, only a handful of sulfonolipids like RIF-1 have been reported (Godchaux and Leadbetter 1980, 1983, 1984, 1988; Drijber and McGill 1994; Kamiyama et al. 1995a, 1995b; Kobayashi et al. 1995) and no other *A. machipongonensis* lipid tested in this study induced rosette colony development. Therefore we favor a model in which *A. machipongonensis* cell density, as revealed by RIF-1 concentration, provides *S. rosetta* with an indication of conditions under which rosette colony development would be advantageous, for instance by promoting more efficient capture of planktonic bacteria (Kreft 2010). In analogy to the chemotaxis system of bacteria (Falke et al. 1997), the ability of *S. rosetta* to respond to increasing bacterial cell density likely requires the hypothesized RIF-1 receptor to become less sensitive at higher concentrations. The high concentration cutoff in the dose-response curve reflects a complete loss of sensitivity at high, but non-physiological, RIF-1 concentrations. Although the presence of RIF-1 in the *A. machipongonensis* cell envelope suggests that it may be encountered by *S. rosetta* during phagocytosis, it can also function at a distance. We hypothesize that RIF-1 may be released into the environment in membrane vesicles, which have been described in Gram-negative bacteria such as Bacteroidetes (Zhou et al. 1998; Møller et al. 2005), and that additional membrane constituents might be required for the full potency of RIF-1. In the future,

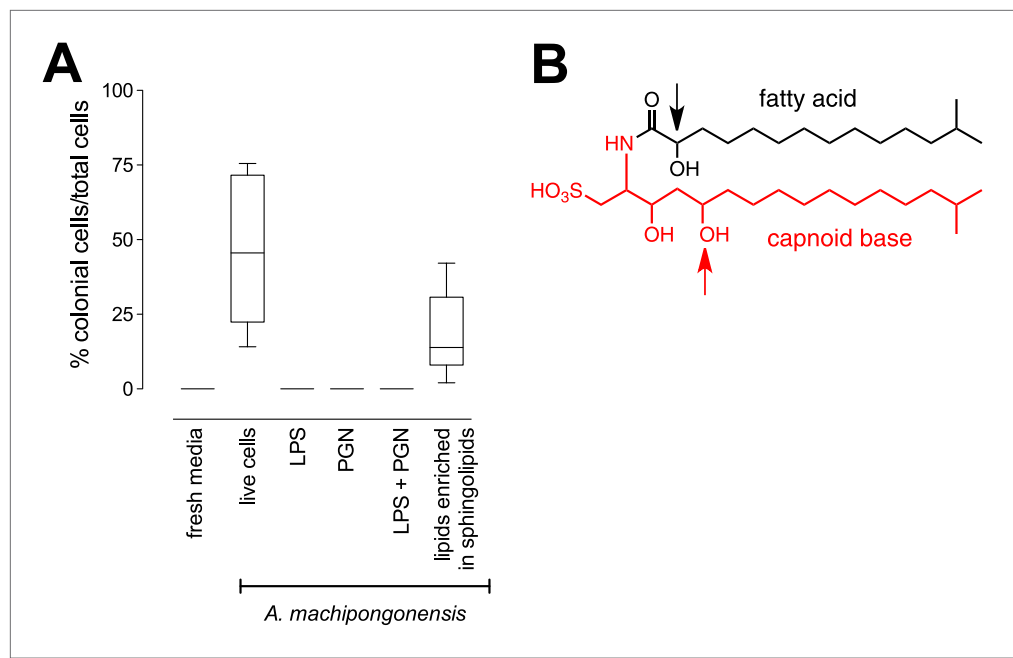


Figure 3. RIF-1, a sulfonolipid that induces rosette colony development. **(A)** Rosette colony development is induced by live *A. machipongonensis* and the sphingolipid-enriched lipid fraction (20 mg mL⁻¹), but not by fresh medium, *A. machipongonensis* LPS (10 mg mL⁻¹), PGN (50 mg mL⁻¹), or LPS+PGN. Shown are the whisker-box plots of the % colonial cells/total cells under each condition in three independent experiments. **(B)** The molecular structure of RIF-1 deduced from MS and 1D- and 2D-NMR data. The RIF-1 structure, 3,5-dihydroxy-2-(2-hydroxy-13-methyltetradecanamido)-15-methylhexadecane-1-sulfonic acid, has two parts: a base (shown in red) that defines the capnoid, and a fatty acid (shown in black). Features that distinguish RIF-1 from other known capnoids are shown with colored arrows: the 2-hydroxy on the fatty acid (black) and the 5-hydroxy on the capnoid base (red).

DOI: [10.7554/eLife.00013.008](https://doi.org/10.7554/eLife.00013.008)

The following figure supplements are available for figure 3:

Figure supplement 1. Separation of *A. machipongonensis* sphingolipids by thin layer chromatography (TLC).

DOI: [10.7554/eLife.00013.009](https://doi.org/10.7554/eLife.00013.009)

Figure supplement 2. MS/MS analysis of RIF-1.

DOI: [10.7554/eLife.00013.010](https://doi.org/10.7554/eLife.00013.010)

Figure supplement 3. Key two-dimensional (2D) correlations of RIF-1: Observed COSY correlations.

DOI: [10.7554/eLife.00013.011](https://doi.org/10.7554/eLife.00013.011)

Figure supplement 4. Key two-dimensional (2D) correlations of RIF-1: Observed HMBC spin system.

DOI: [10.7554/eLife.00013.012](https://doi.org/10.7554/eLife.00013.012)

Figure supplement 5. Key two-dimensional (2D) correlations of RIF-1: Observed TOCSY spin system.

DOI: [10.7554/eLife.00013.013](https://doi.org/10.7554/eLife.00013.013)

Figure supplement 6. ¹H NMR spectrum of RIF-1.

DOI: [10.7554/eLife.00013.014](https://doi.org/10.7554/eLife.00013.014)

Figure supplement 7. gHMBC spectrum of RIF-1.

DOI: [10.7554/eLife.00013.015](https://doi.org/10.7554/eLife.00013.015)

Figure supplement 8. gCOSY spectrum of RIF-1.

DOI: [10.7554/eLife.00013.016](https://doi.org/10.7554/eLife.00013.016)

Figure supplement 9. Expanded dqfCOSY spectrum of RIF-1.

DOI: [10.7554/eLife.00013.017](https://doi.org/10.7554/eLife.00013.017)

Figure supplement 10. Expanded dqfCOSY spectra of RIF-1.

DOI: [10.7554/eLife.00013.018](https://doi.org/10.7554/eLife.00013.018)

Figure supplement 11. gHMBC spectrum of RIF-1.

DOI: [10.7554/eLife.00013.019](https://doi.org/10.7554/eLife.00013.019)

Figure supplement 12. Expanded gHMBC spectrum of RIF-1 (δ_H 0–4.00 ppm/ δ_C 15.0–85.0 ppm).

DOI: [10.7554/eLife.00013.020](https://doi.org/10.7554/eLife.00013.020)

Figure 3. Continued on next page

Figure 3. Continued

Figure supplement 13. Expanded gHMBC spectrum of RIF-1 (δ_H 0.80–1.80 ppm/ δ_C 20.0–40.0 ppm).

DOI: [10.7554/eLife.00013.021](https://doi.org/10.7554/eLife.00013.021)

Figure supplement 14. TOCSY spectrum of RIF-1.

DOI: [10.7554/eLife.00013.022](https://doi.org/10.7554/eLife.00013.022)

Figure supplement 15. Expanded TOCSY spectrum of RIF-1 (δ_H 0.50–4.25 ppm/ δ_C 0.50–4.25 ppm).

DOI: [10.7554/eLife.00013.023](https://doi.org/10.7554/eLife.00013.023)

elucidating RIF-1 delivery, along with determining the three-dimensional structure of RIF-1 and characterizing sulfonolipids from other Bacteroidetes will begin to provide the needed foundation for a molecular understanding of how *S. rosetta* perceives RIFs.

The morphogenetic interaction described here between *S. rosetta* and *A. machipongonensis* raises the possibility that bacterially-produced sphingolipids in general, and sulfonolipids in particular, may be essential for the chemical signaling that allows Bacteroidetes to influence cell differentiation and morphogenesis in diverse animals (Falkow 2006; Mazmanian et al. 2008; Lee and Mazmanian 2010; An et al. 2011). Sulfonolipids like RIF-1 have been reported to have therapeutic activities, but their endogenous functions are not known. Sulfobacins A and B, which were isolated from the culture broth of a *Chryseobacterium* sp. were reported as von Willebrand factor receptor antagonists, and flavocristamide A, from a related bacterial species, was reported as a DNA polymerase α inhibitor (Kamiyama et al. 1995a; Kobayashi et al. 1995). The pervasiveness of interactions between Bacteroidetes and animals (Webster et al. 2004; Wexler 2007), coupled with the close evolutionary relationship between choanoflagellates and animals (King and Carroll 2001; King 2004; King et al. 2008; Ruiz-Trillo et al. 2008), raise the possibility that the connection between Bacteroidetes and animal development has deep evolutionary roots (McFall-Ngai 1999). The discovery of RIF-1 and its biological activity toward *S. rosetta* provides both the molecular basis and model organism for further understanding a new and potentially important class of small molecule information transfer.

Materials and methods

Choanoflagellate husbandry and microscopy

The environmental isolate of *Salpingoeca rosetta* is deposited at the American Tissue Culture Collection (ATCC) under the designation ATCC50818 (King et al. 2003). The Rosette Colonies Absent (RCA) culture line was produced from ATCC50818 by serial treatment with chloramphenicol (68 $\mu\text{g mL}^{-1}$), ampicillin (50 $\mu\text{g mL}^{-1}$), streptomycin (50 $\mu\text{g mL}^{-1}$), and erythromycin (50 $\mu\text{g mL}^{-1}$) (Fairclough et al. 2010). A monoxenic line of *S. rosetta* (Px1) was generated by treating ATCC 50818 with a combination of ofloxacin (10 $\mu\text{g mL}^{-1}$), kanamycin (50 $\mu\text{g mL}^{-1}$), and streptomycin (50 $\mu\text{g mL}^{-1}$) antibiotics to kill the undefined environmental bacteria. Following several rounds of serial dilution, a single cell was isolated by FACS and supplemented with *A. machipongonensis* (Dayel et al. 2011). All three *S. rosetta* cell lines (ATCC 50818, RCA, and Px1) were grown in cereal grass infused seawater at 25°C and maintained by splitting cultures 1:10 into fresh medium every 3 days (King et al. 2009). Live cells were imaged with a Leica DMI6000B microscope equipped with a DFC350 FX camera.

Bioassay for rosette colony development

Under laboratory conditions, *S. rosetta* differentiates into a variety of cell types including attached thecate cells, solitary swimmers, rosette colonies, chain colonies and loose, disorganized associations of cells attached to one another at the collar or to bacterial biofilms (Dayel et al. 2011). *S. rosetta* rosette colonies can be distinguished from other cell types in that they contain clusters of at least four closely associated cells with organized polarity; each cell oriented with its flagellum pointing outward from a central focus. In the qualitative bioassay, RCA cultures were diluted in fresh medium to a density of approximately 10^4 – 10^5 cells mL^{-1} , aliquoted into 24-well flat bottom culture dishes (Costar, Corning, NY, USA), supplemented with various treatments, and scored for the presence or absence of rosette colonies after 48 hr. For quantitative measurements, RCA cultures were diluted as before into six-well flat bottom culture dishes. To measure the percentage of cells within rosette colonies, each well was scraped to detach thecate cells and the total number of cells and the total number of cells in each rosette colony were counted with a Bright-Line hemacytometer (Hausser Scientific, Horsham, PA, USA).

Table 3. Table of NMR chemical shifts

Position	δ ^1H (multiplicity, J, #H)	^{13}C (δ , ppm)
NH	8.21 (d, J=9.1 Hz, 1H)	
1	3.01 (dd, J=14.2, 5.1 Hz, 1H) 2.56 (dd, J=14.3, 3.6 Hz, 1H)	51.87
2	3.88 (ddd, J=13.0, 8.6, 4.5 Hz, 1H)	50.89
3	3.78 – 3.71 (m, 1H)	71.51
OH3	5.20 (d, J=4.2 Hz, 1H)	
4	1.51 – 1.47 (m, 1H) 1.33 – 1.29 (m, 1H)	41.36
5	3.61 – 3.53 (m, 1H)	70.20
OH5	4.31 (d, J=3.5 Hz, 1H)	
6	1.34 – 1.29 (m, 1H) 1.24 – 1.20 (m, 1H)	37.27
7–13	1.21 – 1.27 (br s, 14H)	22.5– 29.6
14	1.16 – 1.11 (m, 2H)	38.91
15	1.52 – 1.47 (m, 1H)	27.79
16, 17	0.84 (d, J=6.6 Hz, 6H)	22.09
1'		173.23
2'	3.80 (dd, J=6.6, 4.2 Hz, 1H)	71.29
OH2'	5.52 (d, J=5.0 Hz, 1H)	
3'	1.59 – 1.54 (m, 1H) 1.50 – 1.45 (m, 1H)	34.85
4'?	1.35 – 1.30 (m, 2H)	24.99
5'–11'	1.21 – 1.27 (brs, 14H)	22.5– 29.6
12'	1.16 – 1.11 (m, 2H)	38.91
13'	1.52 – 1.47 (m, 1H)	27.79
14', 15'	0.84 (d, J=6.6 Hz, 6H)	22.09

DOI: [10.7554/eLife.00013.024](https://doi.org/10.7554/eLife.00013.024)

members of the Bacteroidetes phylum, and eight species representing three additional major clades within Bacteria. Each species was screened for morphogenic activity using the bioassay for rosette colony development. Live cells from individual colonies grown from solid agar plates were added directly to RCA cultures and scored for the presence or absence of rosette colonies 48 hr after inoculation. Each bacterial species was tested three times.

To determine the phylogenetic distribution of morphogenic activity in the bacterial species tested (**Table 1**), a sequence alignment of 16S rDNA genes from each species was generated by iterative pairwise comparisons using FSA (**Bradley et al. 2009**). Poorly aligned regions were removed by Gblocks version 0.91b (**Castresana 2000; Talavera and Castresana 2007**) using default block parameters. A distance matrix (distance options according to the Kimura two-parameter model), including clustering with the maximum likelihood algorithm, was calculated using Phylip version 3.67 (**Falstenstein 1989**). Support for the resulting tree topology was estimated using bootstrap analysis (1000 replicates).

Biochemical analysis of Rosette Inducing Factor (RIF-1)

To determine the biochemical nature of RIF-1, *A. machipongonensis* cell fractions and conditioned medium were subjected to a battery of treatments. The results of these tests are summarized in **Table 2**. Conditioned medium (CM) was generated by pelleting either choanoflagellates grown

Isolation and identification of *A. machipongonensis*

A partial representation of the bacterial flora from ATCC50818 was isolated by standard dilution-plating technique on modified Zobell medium agar (**Carlucci and Pramer 1957**) at 25°C. Individual isolates were tested for their morphogenic activity by supplementing RCA cultures with a single colony of each isolate. Of 64 isolates tested, the only one that restored rosette colony development to the RCA cell line was a species that formed pink-pigmented colonies (designated strain PR1). Strain PR1 was used to inoculate liquid modified Zobell medium at 25°C and grown with aeration overnight. PR1 cells were harvested by centrifugation, and genomic DNA was isolated using a Bacterial Genomic DNA Mini-prep Kit (Bay Gene, Burlingame, CA, USA) according to the manufacturer's specifications. The 16S rRNA gene was amplified using universal primers 8F (5'-AGAGTTTGATCCTGGCTCAG-3') and 1492R (5'-ACCTGTTACGRCTT-3') (**Weisburg et al. 1991**); comparison of the PR1 16S rRNA sequence to the Greengenes 16S rRNA database (**DeSantis et al. 2006**) revealed strain PR1 to be most closely related to members of the *Algoriphagus* genus within the Bacteroidetes phylum. PR1 was subsequently named *Algoriphagus machipongonensis* (**Bradley et al. 2009**).

Generating a phylogenetic framework for testing the diversity of bacteria that induce rosette colony development

To investigate whether the ability to trigger rosette colony development was specific to *A. machipongonensis*, we tested three classes of bacterial species for their morphogenic capacity: 15 species in the *Algoriphagus* genus, 16 non-*Algoriphagus*

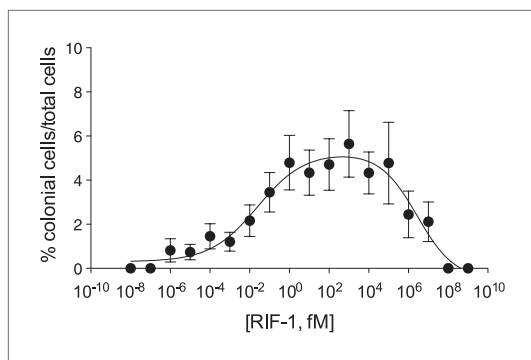


Figure 4. Purified RIF-1 is active at plausible environmental concentrations. RIF-1 concentrations ranging from 10^{-2} to 10^7 fM induce rosette colony development in RCA cultures. Frequency of rosette colony development was quantified in RCA cultures 2 days after treatment with a dilution series of purified RIF-1. Data are mean \pm s.e. from three independent experiments. Line indicates non-linear regression of the RIF-1 activity profile.

DOI: [10.7554/eLife.00013.025](https://doi.org/10.7554/eLife.00013.025)

The following figure supplements are available for figure 4:

Figure supplement 1. Detection of purified RIF-1.

DOI: [10.7554/eLife.00013.026](https://doi.org/10.7554/eLife.00013.026)

Figure supplement 2. Detection of RIF-1 in the conditioned medium of *A. machipongonensis*.

DOI: [10.7554/eLife.00013.027](https://doi.org/10.7554/eLife.00013.027)

Figure supplement 3. Co-injection of concentrated conditioned medium with purified RIF-1.

DOI: [10.7554/eLife.00013.028](https://doi.org/10.7554/eLife.00013.028)

A. machipongonensis cell pellet was extracted according to the Bligh–Dyer method (Bligh and Dyer 1959). Briefly, the cell pellet was resuspended in 3 vol of 1:2 (vol/vol) CHCl_3 :MeOH and vortexed. One volume of CHCl_3 was added, and the mixture vortexed. One volume of distilled water was then added, and the mixture vortexed. The same was then centrifuged at 1000 rpm for 5 min and the bottom layer recovered and dried.

To test whether RIF-1 was a component of lipopolysaccharide (LPS), *A. machipongonensis* LPS was isolated using a method from Apicella (2008). Lyophilized *A. machipongonensis* cells were ground with a mortar and pestle and suspended in 10 mM Tris–Cl buffer (pH 8.0), containing 2% sodium dodecyl sulfate (SDS), 4% 2-mercaptoethanol, and 2 mM MgCl_2 . The mixture was vortexed and incubated at 65°C until solubilized. Proteinase K (20 mg mL^{-1}) was added to the mixture, and incubated at 65°C for an additional hour, followed by 37°C incubation overnight. 3 M sodium acetate was then added and the sample mixed. Following addition of cold absolute ethanol to the cell suspension, the sample was incubated overnight at -20°C to allow precipitate to form. The mixture was centrifuged at 4000 \times g for 15 min, and the supernatant discarded. The precipitate was suspended in distilled water. 3 M sodium acetate was added, and the mixture vortexed. Following addition of cold absolute ethanol, the mixture was vortexed again, and the suspension again allowed to precipitate overnight at -20°C . After the centrifugation, the precipitate was suspended in 10 mM Tris–Cl (pH 7.4), and DNase I (100 $\mu\text{g mL}^{-1}$; NEB) and RNase (25 $\mu\text{g mL}^{-1}$; NEB) added. The mixture was incubated at 37°C for 4 hr, then placed in a 65°C water bath for 30 min. Ninety percent phenol preheated to 65°C was added, and allow to set at 65°C for 15 min. The mixture was placed in an ice bath to cool, and then centrifuged at 6000 \times g for 15 min. The top aqueous layer was removed, and the phenolic layer re-extracted with an equal volume of distilled water. This sample was again incubated at 65°C for 15 min and then placed in ice water. After centrifugation at 6000 \times g for 15 min, the two aqueous layers were combined and dialyzed against multiple changes of distilled water over 2 days.

in cereal grass infused with seawater or *A. machipongonensis* cultures grown in seawater complete medium (Atlas 2004) and filtering the culture supernatant through a 0.22 μm pore filter (Millipore) to remove live bacteria. To test whether RIF-1 activity required live bacteria, *A. machipongonensis* was grown overnight at 25°C, centrifuged at 16,000 \times g for 1 min to pellet cells, and heated for 30 min at 80°C to kill viable bacteria. To test whether RIF-1 activity might be heat labile (e.g., a polypeptide), *A. machipongonensis* CM was boiled for 10 min. To test whether RIF-1 was a protein, *A. machipongonensis* CM was incubated with 200 $\mu\text{g mL}^{-1}$ proteinase K (New England Biolabs, Ipswich, MA, USA) for 2 hr at 37°C. To test whether RIF-1 was a nucleic acid, 25 mL of *A. machipongonensis* CM was lyophilized, resuspended in 2.5 mL of water, and extracted with 100% ethanol to a final concentration of 80% (vol/vol) for 2 hr at -20°C and the precipitate was collected by centrifugation for 30 min at 4000 \times g at 4°C. The precipitate was dissolved in 0.01 M PBS (containing 10 mM MgCl_2 and 1 mM CaCl_2) and incubated with either RNase A (100 $\mu\text{g mL}^{-1}$; Sigma) or DNase I (100 $\mu\text{g mL}^{-1}$; Sigma) for 2.5 hr at 37°C. To test whether RIF-1 activity was in the methanolic extract, *A. machipongonensis* cell pellet and CM were lyophilized and vortexed with methanol. Each suspension was centrifuged at 8000 rpm for 5 min and the methanol layer recovered and dried.

To test whether RIF-1 was a lipid, *A. machipon-*

To test whether RIF-1 was a peptidoglycan, *A. machipongonensis* peptidoglycan was isolated using a method adapted from *de Jong et al. (1992)*, *A. machipongonensis* cell pellet was washed with 0.8% NaCl. The cells were resuspended in hot 4% SDS, boiled for 30 min, and then incubated at room temperature overnight. The sample was boiled for an additional 10 min and then centrifuged at 15,000×g for 15 min at room temperature. The pellet was washed four times with water and resuspended in water. The sample was digested for mutanolysin (10 µg mL⁻¹; Sigma) overnight at 37°C. The enzyme was inactivated by incubation at 80°C for 20 min.

Isolation and purification of RIF-1 from *A. machipongonensis*

A. machipongonensis was cultured in seawater complete medium (16×1 L) at 30°C for 2 days. The cells were harvested by centrifugation and extracted with CHCl₃:MeOH (2:1, 4 L). The organic extract was filtered, dried over sodium sulfate (Na₂SO₄), and concentrated to give approximately 4 g crude lipid extract. The crude extract was dissolved in a minimum amount of CHCl₃:MeOH (2:1), and purified by preparative high performance liquid chromatography (HPLC). All solvents were purchased from Fisher Scientific unless otherwise noted. Preparative reversed phase HPLC (RP-HPLC) was performed on an Agilent Technologies 1200 Series HPLC using a Phenomenex Luna 5 µm C8(2) 100 Å 250×21.2 mm column. Isolation of RIF-1 continued with a crude fractionation in which compounds were eluted at 10 mL min⁻¹ in a gradient of solvents A (0.1% NH₄OH in water) and B (0.1% NH₄OH in methanol): 65% B increasing to 100% B over 30 min, isocratic at 100% B for 1 min. before returning to 65% B and re-equilibrating over 10 min. Fractions were analyzed by low-resolution mass spectrometry (LC-MS) on an Agilent 6130 LC/MS using a Phenomenex Gemini-NX 5 µm C18 110 Å 100×2 mm column. The next stage involved a higher resolution separation in which compounds were eluted at 0.5 mL min⁻¹ in a gradient of solvents A (0.1% NH₄OH in water) and B (0.1% NH₄OH in methanol): 65% B increasing to 100% B over 30 min, isocratic at 100% B for 1 min before returning to 65% B and re-equilibrating over 3 min and those which contained a mass peak corresponding to RIF-1 ([M-H]=606.4) were combined and concentrated. This material was then purified by preparative TLC (1 mm, silica gel 60), eluted with CHCl₃:MeOH:AcOH:H₂O (100:20:12:5, Rf=0.5). RIF-1 was visualized by staining with ammonium molybdate in 10% H₂SO₄. The portion of the plate (Fraction F; **Figure 3—figure supplement 1**) that induced colony formation and contained RIF-1 (LC/MS: [M-H] 606) was scraped off after RIF-1 was visualized by staining with ammonium molybdate in 10% H₂SO₄, and the silica was extracted with CHCl₃:MeOH (5:1). This material was further purified by preparative TLC on a 250 µm TLC plate (silica gel 60), eluted with CHCl₃:MeOH:AcOH:H₂O (100:20:12:5). From 16 L of *A. machipongonensis* culture, approximately 50 µg RIF-1 was obtained in sufficient purity. The entire process, from growth of the cells to isolation of pure RIF-1, was repeated nine times in order to obtain approximately 0.7 mg RIF-1 from a total of 160 L of *A. machipongonensis* culture.

High Resolution Mass Spectrometry (HRMS) was carried out by Ted Voss at the WM Keck Foundation Biotechnology Resource Laboratory at Yale University on a Bruker 9.4T FT-ICR MS. RIF-1 was dissolved in 200 µL DMSO-*d*₆ and transferred into a 3 mm NMR tube. ¹H, TOCSY, gCOSY and dqfCOSY were recorded on a Varian Inova 600 spectrometer. HMQC and gHMBC experiments were performed on a Bruker Advance (sgu) 900 MHz and Varian Unity Inova 600 MHz equipped with a cryoprobe, respectively. Chemical shifts are reported in ppm from tetramethylsilane with the solvent resonance resulting from incomplete deuteration as the internal standard (DMSO: δ 2.50). Data are reported in **Table 3** as follows: chemical shift, multiplicity (s = singlet, d = doublet, t = triplet, q = quartet, br = broad, m = multiplet), coupling constants, and integration. Optical rotation was measured on a Jasco P-2000 digital polarimeter with a sodium lamp at 21.4°C. Unless otherwise noted, all solvents and reagents were purchased from VWR or Fisher and used without further purification.

¹H NMR (600 MHz, DMSO) and ¹³C NMR (600 MHz, DMSO): see **Table 3**. Optical rotation: [α]_D^{21.4} +6.4 (c=0.07, MeOH). HRMS *m/z* calcd for C₃₂H₆₄NO₇S (M-H): 606.44035. Found: 606.44027 (M-H)⁻. MS/MS analysis: A major fragment derived from *m/z*=606 (M-H) in the MS/MS spectrum of RIF-1 corresponds to amino-sulfonic acid, **Figure 3—figure supplement 2**. HRMS/MS *m/z* calculated for C₁₇H₃₆NO₅S (M-H): 366.23142. Found: 366.2310 (M-H)⁻.

Quantification of RIF-1 levels in conditioned medium

Conditioned medium was prepared from *A. machipongonensis* grown in seawater complete medium (750 mL) at 30°C for 2 days. The conditioned medium was lyophilized and extracted with CHCl₃:MeOH

(2:1; 78 mL). The organic extract was filtered, further extracted with CHCl_3 (60 mL \times 2), and filtrates were combined and concentrated to dryness under vacuum. The crude extract was suspended in 5 mL 50% MeOH:H₂O and was passed through a C-18 SPE (1 g) column. The open column was then washed with 10 mL 90% MeOH:CHCl₃. The organic eluate was concentrated and dissolved in 3 mL CHCl₃:MeOH (2:1) for LC/MS analysis. The chromatography was carried out using an Agilent 6130 Quadrupole LC/MS system with a C18 reverse-phase column (4.6 \times 100 mm; Phenomenex Luna; 5 μ) for 30 min in a linear gradient from solvent A (60% methanol/water with 0.1% ammonium hydroxide) to solvent B (100% methanol with 0.1% ammonium hydroxide). The RIF-1 was detected in the conditioned medium at a concentration of 80 ng L⁻¹. The purified RIF-1 was used as the standard (**Figure 4—figure supplements 1–3**).

Activity profile of RIF-1

The potency of pure RIF-1 was determined using the quantitative bioassay for rosette colony development. Briefly, 100 μ g of pure RIF-1 was solubilized in 100 μ L DMSO and this 1 g L⁻¹ stock was stored at -80°C. For each experiment, serial dilutions ranging from 10⁻¹ g L⁻¹ down to 10⁻¹⁷ g L⁻¹ were made in DMSO. 2 μ L of each dilution was premixed with 1 mL of fresh cereal grass infused seawater (**King et al. 2003**) to avoid precipitation of RIF-1 and the premixed RIF-1 dilution was then added to 1 mL RCA cultures to yield final concentrations ranging from 10⁻³ to 10⁻²⁰ g L⁻¹, equivalent to 1.6 \times 10⁹ fM down to 1.6 \times 10⁻⁸ fM. The percentage of rosette colonial cells was determined as described above in three independent cell lines in triplicate. From the percent rosette colony development, a bell-shaped dose-response model was determined to be the nonlinear regression curve of best fit determined using GraphPad Prism 5 statistical software.

Acknowledgements

We thank Michael Fischbach, Richard Losick, and Russell Vance for critical reading of the manuscript. NK is a Fellow in the Integrated Microbial Biodiversity Program of the Canadian Institute for Advanced Research.

Additional information

Competing interests

JC: Reviewing Editor, *eLife*. The remaining authors have no competing interests to declare.

Funding

Funder	Grant reference number	Author
Gordon and Betty Moore Foundation Marine Microbiology Initiative		Nicole King
National Institutes of Health	F32 GM086054	Rosanna A. Alegado
National Institutes of Health	F32 GM089018	Laura W. Brown
National Institutes of Health	R01 GM086258	Jon Clardy
National Institutes of Health	R01 GM099533	Jon Clardy, Nicole King
National Institutes of Health	T32 HG00047	Stephen R. Fairclough

The funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.

Author contributions

RA: Conception and design, Acquisition of data, Analysis and interpretation of data, Drafting or revising the article; LB: Conception and design, Acquisition of data, Analysis and interpretation of data, Drafting or revising the article; SC: Acquisition of data, Analysis and interpretation of data, Drafting or revising the article; RD: Acquisition of data, Analysis and interpretation of data; RZ: Acquisition of data, Analysis and interpretation of data; SF: Acquisition of data, Analysis and interpretation of data; JC: Conception and design, Analysis and interpretation of data, Drafting or revising the article; NK: Conception and design, Analysis and interpretation of data, Drafting or revising the article

References

- Agosta WC.** 1992. *Chemical communication*. Scientific American Press, New York.
- Ahmed I, Yokota A, Fujiwara T.** 2007. Chimaericella boritolersans sp nov., a boron-tolerant and alkaliphilic bacterium of the family Flavobacteriaceae isolated from soil. *Int J Syst Evol Microbiol* **57**: 986–992.
- Alegado RA, Grabenstatter JD, Zuzow R, Morris A, Huang SY, Summons RE, King N.** 2012. Algoriphagus machipongonensis sp. nov. co-isolated with a colonial choanoflagellate. *Int J Syst Evol Microbiol* [epub ahead of print].
- An D, Na C, Bielawski J, Hannun YA, Kasper DL.** 2011. Membrane sphingolipids as essential molecular signals for Bacteroides survival in the intestine. *Proc Natl Acad Sci U S A* **108** Suppl. 1: 4666–4671.
- Anton J, Oren A, Benlloch S, Rodriguez-Valera F, Amann R, Rossello-Mora R.** 2002. Salinibacter ruber gen. nov., sp nov., a novel, extremely halophilic member of the bacteria from saltern crystallizer ponds. *Int J Syst Evol Microbiol* **52**: 485–491.
- Apicella MA.** 2008. Isolation and characterization of lipopolysaccharides. *Methods Mol Biol* **431**: 3–13.
- Atlas RM.** 2004. *Handbook of microbiological media*, p. 2051. Boca Raton: CRC.
- Barbeyron T, L'Haridon S, Corre E, Kloareg B, Potin P.** 2001. Zobellia galactanovorans gen. nov., sp. nov., a marine species of Flavobacteriaceae isolated from a red alga, and classification of [Cytophaga] uliginosa (ZoBell and Upham 1944) Reichenbach 1989 as Zobellia uliginosa gen. nov., comb. nov. *Int J Syst Evol Microbiol* **51**(Pt 3): 985–997.
- Bernardet J, Segers P, Vancanneyt M, Berthe F, Kersters K, Vandamme P.** 1996. Cutting a Gordian knot: Emended classification and description of the genus Flavobacterium, emended description of the family Flavobacteriaceae, and proposal of Flavobacterium hydatis nom nov (basonym, Cytophaga aquatilis Strohl and Tait 1978). *Int J Syst Bacteriol* **46**: 128–148.
- Blattner FR, Plankett G III, Bloch CA, Perna N, Burland V, Riley M, Collado-Vides J, Glasner JD, Rode CK, Mayhew GF, et al.** 1997. The complete genome sequence of Escherichia coli K-12. *Science* **277**: 1453–1462.
- Bligh EG, Dyer WJ.** 1959. A rapid method of total lipid extraction and purification. *Can J Biochem Physiol* **37**: 911–917.
- Bowman JP, Nichols CM, Gibson JAE.** 2003. Algoriphagus ratkowskyi gen. nov., sp. nov., Brumimicrobium glaciale gen. nov., sp. nov., Cryomorpha ignava gen. nov., sp. nov. and Crocinitomix catalasitica gen. nov., sp. nov., novel flavobacteria isolated from various polar habitats. *Int J Syst Evol Microbiol* **53**(Pt 5): 1343–1355.
- Bradley RK, Roberts A, Smoot M, Juvekar S, Do J, Dewey C, Holmes I, Pachter L.** 2009. Fast statistical alignment. *PLoS Comput Biol* **5**: e1000392.
- Brettar I, Christen R, Hofle M.** 2004a. Aquiflexum balticum gen. nov., sp nov., a novel marine bacterium of the Cytophaga-Flavobacterium-Bacteroides group isolated from surface water of the central Baltic Sea. *Int J Syst Evol Microbiol* **54**: 2335–2341.
- Brettar I, Christen R, Hofle MG.** 2004b. Belliella baltica gen. nov., sp. nov., a novel marine bacterium of the Cytophaga-Flavobacterium-Bacteroides group isolated from surface water of the central Baltic Sea. *Int J Syst Evol Microbiol* **54**(Pt 1): 65–70.
- Burkholder PR, Giles NH.** 1947. Induced biochemical mutations in Bacillus subtilis. *Am J Bot* **34**: 345–348.
- Butenandt A, Beckmann R, Hecker E.** 1961. On the sex attractant of silk-moths. I. The biological test and the isolation of the pure sex-attractant bombykol. *Hoppe-Seylers Z Physiol Chem* **324**: 71–83.
- Carlucci AF, Pramer D.** 1957. Factors influencing the plate method for determining abundance of bacteria in sea water. *Proc Soc Exp Biol Med* **96**: 392–394.
- Carr M, Leadbeater BSC, Hassan R, Nelson M, Baldauf SL.** 2008. Molecular phylogeny of choanoflagellates, the sister group to Metazoa. *Proc Natl Acad Sci U S A* **105**: 16641–16646.
- Castresana J.** 2000. Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. *Mol Biol Evol* **17**: 540–552.
- Cerdeno-Tarraga AM, Patrick S, Crossman L, Blakely GW, Abratt V, Lennard N, Poxton I, Duerden B, Harris B, Quail MA, et al.** 2005. Extensive DNA inversions in the B. fragilis genome control variable gene expression. Blakely GW, editor. *Science* **307**: 1463–1465.
- Chelius M, Triplett E.** 2000. Dyadobacter fermentans gen. nov., sp nov., a novel gram-negative bacterium isolated from surface-sterilized Zea mays stems. *Int J Syst Evol Microbiol* **50**: 751–758.
- Cho J-C, Giovannoni SJ.** 2003. Croceibacter atlanticus gen. nov., sp. nov., a novel marine bacterium in the family Flavobacteriaceae. *Syst Appl Microbiol* **26**: 76–83.
- Cho J-C, Giovannoni SJ.** 2004. Robiginitalea bifurcata gen. nov., sp. nov., a novel marine bacterium in the family Flavobacteriaceae with a higher G+C content. *Int J Syst Evol Microbiol* **54**(Pt 4): 1101–1106.
- Cohn ZA, Morse SI.** 1960. Functional and metabolic properties of polymorphonuclear leucocytes. II. The influence of a lipopolysaccharide endotoxin. *J Exp Med* **111**: 689–704.
- Dayel MJ, Alegado RA, Fairclough SR, Levin TC, Nichols SA, McDonald K, King N.** 2011. Cell differentiation and morphogenesis in the colony-forming choanoflagellate Salpingoeca rosetta. *Dev Biol* **357**: 73–82.
- DeSantis TZ, Hugenholtz P, Larsen N, Rojas M, Brodie EL, Keller K, Huber T, Dalevi D, Hu P, Andersen GL.** 2006. Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. *Appl Environ Microbiol* **72**: 5069–5072.
- Desbrosses GJ, Stougaard J.** 2011. Root nodulation: A paradigm for how plant-microbe symbiosis influences host developmental pathways. *Cell Host Microbe* **10**: 348–358.
- Drijber R, McGill W.** 1994. Sulfonolipid content of Cytophaga and Flexibacter species isolated from soil and cultured under different nutrient and temperature regimes. *Can J Microbiol* **40**: 132–139.
- Edman DC, Pollock MB, Hall ER.** 1968. Listeria monocytogenes L forms. I. Induction maintenance, and biological characteristics. *J Bacteriol* **96**: 352–357.

- Fairclough SR**, Dayel MJ, King N. 2010. Multicellular development in a choanoflagellate. *Curr Biol* **20**: R875–R876.
- Falenstein J**. 1989. PHYLIP—Phylogeny inference packages (version 3.2). *Cladistics*. **5**: 164–166.
- Falke JJ**, Bass RB, Butler SL, Chervitz SA, Danielson MA. 1997. The two-component signaling pathway of bacterial chemotaxis: A molecular view of signal transduction by receptors, kinases, and adaptation enzymes. *Annu Rev Cell Dev Biol* **13**: 457–512.
- Falkow S**. 2006. Is persistent bacterial infection good for your health? *Cell* **124**: 699–702.
- Garrity GM**. 2010. *Bergey's manual of systematic bacteriology: Bacteroidetes, spirochetes, tenericutes (mollicutes), acidobacteria, fibrobacteres, fusobacteria, dictyoglomi, gemmatimonadetes, lentisphaerae, verrucomicrobia, chlamydiae, and planctomycetes*, p. 949. New York: Springer Verlag.
- Godchaux W**, Leadbetter ER. 1980. Capnocytophaga spp. contain sulfonolipids that are novel in procaryotes. *J Bacteriol* **144**: 592–602.
- Godchaux W**, Leadbetter ER. 1983. Unusual sulfonolipids are characteristic of the Cytophaga-Flexibacter group. *J Bacteriol* **153**: 1238–1246.
- Godchaux W**, Leadbetter ER. 1984. Sulfonolipids of gliding bacteria. Structure of the N-acylamino-sulfonates. *J Biol Chem* **259**: 2982–2990.
- Godchaux W**, Leadbetter E. 1988. Sulfonolipids are localized in the outer membrane of the gliding bacterium *Cytophaga johnsonae*. *Arch Microbiol* **150**: 42–47.
- Hannich JT**, Umehayashi K, Riezman H. 2011. Distribution and functions of sterols and sphingolipids. *Cold Spring Harb Perspect Biol* **3**: pii: a004762. doi: [10.1101/cshperspect.a004762](https://doi.org/10.1101/cshperspect.a004762).
- Hannun YA**, Luberto C, Argraves KM. 2001. Enzymes of sphingolipid metabolism: From modular to integrative signaling. *Biochemistry* **40**: 4893–4903.
- Herr DR**, Fyrst H, Phan V, Heinecke K, Georges R, Harris GL, Saba JD. 2003. Sply regulation of sphingolipid signaling molecules is essential for Drosophila development. *Development* **130**: 2443–2453.
- Hibberd DJ**. 1975. Observations on the ultrastructure of the choanoflagellate *Codosiga botrytis* (Ehr.) Saville-Kent with special reference to the flagellar apparatus. *J Cell Sci* **17**: 191–219.
- Hoffmann JA**, Kafatos FC, Janeway CA, Ezekowitz RA. 1999. Phylogenetic perspectives in innate immunity. *Science* **284**: 1313–1318.
- Hughes DT**, Sperandio V. 2008. Inter-kingdom signalling: Communication between bacteria and their hosts. *Nat Rev Microbiol* **6**: 111–120.
- James-Clark H**. 1867. On the spongiae ciliatae as infusoria flagellata; or observations on the structure, animality, and relationship of *Leucosolenia botryoides*, Bowerbank. *Memoirs Boston Soc. Of Nat. Hist.* I, two plates.
- de Jonge BL**, Chang YS, Gage D, Tomasz A. 1992. Peptidoglycan composition in heterogeneous Tn551 mutants of a methicillin-resistant *Staphylococcus aureus* strain. *J Biol Chem* **267**: 11255–11259.
- Kamiyama T**, Umino T, Iteazono Y, Nakamura Y, Satoh T, Yokose K. 1995a. Sulfobacins A and B, novel von Willebrand factor receptor antagonists. II. Structural elucidation. *J Antibiot* **48**: 929–936.
- Kamiyama T**, Umino T, Satoh T, Sawairi S, Shirane M, Ohshima S, Yokose K. 1995b. Sulfobacins A and B, novel von Willebrand factor receptor antagonists. I. Production, isolation, characterization and biological activities. *J. Antibiot* **48**: 924–928.
- Karpov SA**, Coupe SJ. 1998. A revision of choanoflagellate genera *Kentrosiga*, Schiller, 1953 and *Desmarella*, Kent, 1880. *Acta Protozoologica* **37**: 23–27.
- Kimbrell DA**, Beutler B. 2001. The evolution and genetics of innate immunity. *Nat Rev Genet* **2**: 256–267.
- King N**. 2004. The unicellular ancestry of animal development. *Dev Cell* **7**: 313–325.
- King N**, Carroll SB. 2001. A receptor tyrosine kinase from choanoflagellates: Molecular insights into early animal evolution. *Proc Natl Acad Sci U S A* **98**: 15032–15037.
- King N**, Hittinger CT, Carroll SB. 2003. Evolution of key cell signaling and adhesion protein families predates animal origins. *Science* **301**: 361–363.
- King N**, Westbrook MJ, Young SL, Kuo A, Abedin M, Chapman J, Fairclough S, Hellsten U, Isogai Y, et al. 2008. The genome of the choanoflagellate *Monosiga brevicollis* and the origin of metazoans. *Nature* **451**: 783–788.
- King N**, Young SL, Abedin M, Carr M, Leadbeater BSC. 2009. Starting and maintaining *Monosiga brevicollis* cultures. *Cold Spring Harb Protoc.* **2009**: pdb.prot5148.
- Kobayashi J**, Mikami S, Shigemori H, Takao TYS, Izuta S, Yoshida S. 1995. Flavocristamides A and B, new DNA polymerase α inhibitors from a marine bacterium sp. *Tetrahedron* **51**: 10487–10490.
- Kopp EB**, Medzhitov R. 1999. The Toll-receptor family and control of innate immunity. *Curr Opin Immunol* **11**: 13–18.
- Koropatnick TA**, Engle JT, Apicella MA, Stabb EV, Goldman WE, Mcfall-Ngai MJ. 2004. Microbial factor-mediated development in a host-bacterial mutualism. *Science* **306**: 1186–1188.
- Kreft JM**. 2010. Effects of forming multicellular colonies or attaching to surfaces on feeding rates of the choanoflagellate *Salpingoeca rosetta*. Koehl M, editor. *Thesis (M.A. in Integrative Biology)*. University of California, Berkeley.
- Kunst F**, Ogasawara N, Moszer I, Albertini AM, Alloni G, Azevedo V, Bertero MG, Bessières P, Bolotin A, Borchert S, et al. 1997. The complete genome sequence of the gram-positive bacterium *Bacillus subtilis*. *Nature* **390**: 249–256.
- Leadbeater BSC**. 1983. Life-history and ultrastructure of a new marine species of Proterospongia (Choanoflagellida). *J Mar Biol Assoc UK* **63**: 135–160.
- Lee YK**, Mazmanian SK. 2010. Has the microbiota played a critical role in the evolution of the adaptive immune system? *Science* **330**: 1768–1773.

- Lewin R.** 1969. A classification of flexibacteria. *J Gen Microbiol* **58**: 189–206.
- Matsunaga T, Okamura Y, Fukuda Y, Wahyudi AT, Murase Y, Takeyama H.** 2005. Complete genome sequence of the facultative anaerobic magnetotactic bacterium *Magnetospirillum* sp. strain AMB-1. *DNA Res* **12**: 157–166.
- Matsuo Y, Suzuki M, Kasai H, Shizuri Y, Harayama S.** 2003. Isolation and phylogenetic characterization of bacteria capable of inducing differentiation in the green alga *Monostroma oxyspermum*. *Environ Microbiol* **5**: 25–35.
- Matsuo Y, Imagawa H, Nishizawa M, Shizuri Y.** 2005. Isolation of an algal morphogenesis inducer from a marine bacterium. *Science* **307**: 1598.
- Mazmanian SK, Liu CH, Tzianabos AO, Kasper DL.** 2005. An immunomodulatory molecule of symbiotic bacteria directs maturation of the host immune system. *Cell* **122**: 107–118.
- Mazmanian SK, Round JL, Kasper DL.** 2008. A microbial symbiosis factor prevents intestinal inflammatory disease. *Nature* **453**: 620–625.
- McFall-Ngai M.** 1999. Consequences of evolving with bacterial symbionts: Insights from the squid-vibrio associations. *Ann Rev Ecol Syst* **30**: 235–256.
- Medzhitov R, Janeway C.** 2000. Innate immune recognition: Mechanisms and pathways. *Immunol Rev* **173**: 89–97.
- Merrill AH, Sullards MC, Wang E, Voss KA, Riley RT.** 2001. Sphingolipid metabolism: Roles in signal transduction and disruption by fumonisins. *Environ Health Perspect* **109** Suppl. 2: 283–289.
- Miller TR, Delcher AL, Salzberg SL, Saunders E, Detter JC, Halden RU.** 2010. Genome sequence of the dioxin-mineralizing bacterium *Sphingomonas wittichii* RW1. *J Bacteriol* **192**: 6101–6102.
- Møller JD, Barnes AC, Dalsgaard I, Ellis AE.** 2005. Characterisation of surface blebbing and membrane vesicles produced by *Flavobacterium psychrophilum*. *Dis Aquat Organ* **64**: 201–209.
- Nedashkovskaya OI, Vancanneyt M, Van Trappen S, Vandemeulebroecke K, Lysenko AM, Rohde M, Falsen E, Frolova GM, Mikhailov VV, Swings J.** 2004. Description of *Algoriphagus aquimarinus* sp. nov., *Algoriphagus chordae* sp. nov. and *Algoriphagus winogradskyi* sp. nov., from sea water and algae, transfer of *Hongiella halophila* Yi and Chun 2004 to the genus *Algoriphagus* as *Algoriphagus halophilus* comb. nov. and emended descriptions of the genera *Algoriphagus* Bowman, et al. 2003 and *Hongiella* Yi and Chun 2004. *Int J Syst Evol Microbiol* **54**(Pt 5): 1757–1764.
- Nedashkovskaya O, Kim S, Vancanneyt M, Lysenko A, Shin D, Park M, Lee KH, Jung WJ, Kalinovskaya NI, Mikhailov VV, et al.** 2006. *Echinicola pacifica* gen. nov., sp. nov., a novel flexibacterium isolated from the sea urchin *Strongylocentrotus intermedius*. *Int J Syst Evol Microbiol* **56**: 953–958.
- Nierman WC, Feldblyum TV, Laub MT, Paulsen IT, Nelson KE, Eisen JA, Heidelberg JF, Alley MR, Ohta N, Maddock JR, et al.** 2001. Complete genome sequence of *Caulobacter crescentus*. *Proc Natl Acad Sci U S A* **98**: 4136–4141.
- Oh H-M, Kang I, Yang S-J, Jang Y, Vergin KL, Giovannoni SJ, Cho JC.** 2011. Complete genome sequence of strain HTCC2170, a novel member of the genus *Maribacter* in the family *Flavobacteriaceae*. *J Bacteriol* **193**: 303–304.
- Olsen I, Jantzen E.** 2001. Sphingolipids in bacteria and fungi. *Anaerobe* **7**: 103–112.
- Prieschl EE, Baumruker T.** 2000. Sphingolipids: Second messengers, mediators and raft constituents in signaling. *Immunol Today* **21**: 555–560.
- Provasoli L, Pintner I.** 1980. Bacteria induced polymorphism in an axenic laboratory strain of *Ulva lactuca* (Chlorophyceae). *J Phycol* **16**: 196–201.
- Pyne S, Pyne NJ.** 2000. Sphingosine 1-phosphate signalling in mammalian cells. *Biochem J* **349**(Pt 2): 385–402.
- Raj H, Maloy S.** 1990. Proposal of *Cyclobacterium-Marinus* gen-nov, comb-nov for a marine bacterium previously assigned to the genus *Flectobacillus*. *Int J Syst Bacteriol* **40**: 337–347.
- Roelofs WL.** 1995. Chemistry of sex attraction. *Proc Natl Acad Sci U S A* **92**: 44–49.
- Ruby EG, Urbanowski M, Campbell J, Dunn A, Faini M, Gunsalus R, Lostroh P, Lupp C, McCann J, Millikan D, et al.** 2005. Complete genome sequence of *Vibrio fischeri*: A symbiotic bacterium with pathogenic congeners. *Proc Natl Acad Sci U S A* **102**: 3004–3009.
- Ruiz-Trillo I, Roger AJ, Burger G, Gray MW, Lang BF.** 2008. A phylogenomic investigation into the origin of metazoa. *Mol Biol Evol* **25**: 664–672.
- Saville Kent W.** 1880. *A manual of the infusoria*. David Bogue, London.
- Schaefer AL, Hanzelka BL, Eberhard A, Greenberg EP.** 1996. Quorum sensing in *Vibrio fischeri*: Probing autoinducer-LuxR interactions with autoinducer analogs. *J Bacteriol* **178**: 2897–2901.
- Spiegel S, Milstien S.** 2000. Sphingosine-1-phosphate: Signaling inside and out. *FEBS Lett* **476**: 55–57.
- Spizizen J.** 1958. Transformation of biochemically deficient strains of *Bacillus subtilis* by deoxyribonucleate. *Proc Natl Acad Sci USA* **44**: 1072–1078.
- Takeuchi O, Hoshino K, Kawai T, Sanjo H, Takada H, Ogawa T, Takeda K, Akira S.** 1999. Differential roles of TLR2 and TLR4 in recognition of gram-negative and gram-positive bacterial cell wall components. *Immunity* **11**: 443–451.
- Talavera G, Castresana J.** 2007. Improvement of phylogenies after removing divergent and ambiguously aligned blocks from protein sequence alignments. *Syst Biol* **56**: 564–577.
- Tiago I, Mendes V, Pires C, Morais PV, Veríssimo A.** 2006. *Chimaereicella alkaliphila* gen. nov., sp. nov., a Gram-negative alkaliphilic bacterium isolated from a nonsaline alkaline groundwater. *Syst Appl Microbiol* **29**: 100–108.
- Van Trappen S, Vandecandelaere I, Mergaert J, Swings J.** 2004. *Algoriphagus antarcticus* sp. nov., a novel psychrophile from microbial mats in Antarctic lakes. *Int J Syst Evol Microbiol* **54**(Pt 6): 1969–1973.
- Webster NS, Smith LD, Heyward AJ, Watts JEM, Webb RI, Blackall LL, Negri AP.** 2004. Metamorphosis of a scleractinian coral in response to microbial biofilms. *Appl Environ Microbiol* **70**: 1213–1221.

- Weisburg WG**, Barns SM, Pelletier DA, Lane DJ. 1991. 16S ribosomal DNA amplification for phylogenetic study. *J Bacteriol* **173**: 697–703.
- Wexler HM**. 2007. Bacteroides: The good, the bad, and the nitty-gritty. *Clin Microbiol Rev* **20**: 593–621.
- Wood DW**, Setubal JC, Kaul R, Monks DE, Kitajima JP, Okura VK, Zhou Y, Chen L, Wood GE, Almeida NF Jr, et al. 2001. The genome of the natural genetic engineer *Agrobacterium tumefaciens* C58. *Science* **294**: 2317–2323.
- Yi H**, Chun J. 2004. *Hongiella mannitolivorans* gen. nov., sp. nov., *Hongiella halophila* sp. nov. and *Hongiella ornithinivorans* sp. nov., isolated from tidal flat sediment. *Int J Syst Evol Microbiol* **54**(Pt 1): 157–162.
- Yoon J-H**, Yeo S-H, Oh TK. 2004. *Hongiella marincola* sp. nov., isolated from sea water of the East Sea in Korea. *Int J Syst Evol Microbiol* **54**(Pt 5): 1845–1848.
- Yoon J-H**, Kang S-J, Oh TK. 2005a. *Algoriphagus locisalis* sp. nov., isolated from a marine solar saltern. *Int J Syst Evol Microbiol* **55**(Pt 4): 1635–1639.
- Yoon J-H**, Kang S-J, Jung S-Y, Lee C-H, Oh TK. 2005b. *Algoriphagus yeomjeoni* sp. nov., isolated from a marine solar saltern in the Yellow Sea, Korea. *Int J Syst Evol Microbiol* **55**(Pt 2): 865–870.
- Yoon J-H**, Lee M-H, Kang S-J, Oh TK. 2006. *Algoriphagus terrigena* sp. nov., isolated from soil. *Int J Syst Evol Microbiol* **56**(Pt 4): 777–780.
- Zhou L**, Srisatjaluk R, Justus DE, Doyle RJ. 1998. On the origin of membrane vesicles in gram-negative bacteria. *FEMS Microbiol Lett* **163**: 223–228.
- Ziegler TA**, Forward RB. 2007. Larval release behaviors in the Caribbean spiny lobster, *Panulirus argus*: Role of peptide pheromones. *J Chem Ecol* **33**: 1795–1805.