

## ORIGINAL ARTICLE

# A small predatory core genome in the divergent marine *Bacteriovorax marinus* SJ and the terrestrial *Bdellovibrio bacteriovorus*

Lisa C Crossman<sup>1,2</sup>, Huan Chen<sup>3</sup>, Ana-M Cerdeño-Tárraga<sup>4</sup>, Karen Brooks<sup>5</sup>, Michael A Quail<sup>5</sup>, Silvia A Pineiro<sup>6</sup>, Laura Hobley<sup>7</sup>, R Elizabeth Sockett<sup>7</sup>, Stephen D Bentley<sup>5</sup>, Julian Parkhill<sup>5</sup>, Henry N Williams<sup>3</sup> and O Colin Stine<sup>8</sup>

<sup>1</sup>Department of Bioinformatics, The Genome Analysis Centre, Norwich Research Park, Norwich, UK; <sup>2</sup>School of Biological Sciences, University of East Anglia, Norwich, UK; <sup>3</sup>School of the Environment, Florida A&M University, Tallahassee, FL, USA; <sup>4</sup>ENA, European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, UK; <sup>5</sup>Pathogen Genomics, Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, UK; <sup>6</sup>US Food and Drug Administration, Rockville, MD, USA; <sup>7</sup>School of Biology, University of Nottingham, Nottingham, UK and <sup>8</sup>Department of Epidemiology, University of Maryland, Baltimore, MD, USA

***Bacteriovorax marinus* SJ is a predatory delta-proteobacterium isolated from a marine environment. The genome sequence of this strain provides an interesting contrast to that of the terrestrial predatory bacterium *Bdellovibrio bacteriovorus* HD100. Based on their predatory lifestyle, *Bacteriovorax* were originally designated as members of the genus *Bdellovibrio* but subsequently were re-assigned to a new genus and family based on genetic and phenotypic differences. *B. marinus* attaches to Gram-negative bacteria, penetrates through the cell wall to form a bdelloplast, in which it replicates, as shown using microscopy. *Bacteriovorax* is distinct, as it shares only 30% of its gene products with its closest sequenced relatives. Remarkably, 34% of predicted genes over 500 nt in length were completely unique with no significant matches in the databases. As expected, *Bacteriovorax* shares several characteristic loci with the other delta-proteobacteria. A geneset shared between *Bacteriovorax* and *Bdellovibrio* that is not conserved among other delta-proteobacteria such as *Myxobacteria* (which destroy prey bacteria externally *via* lysis), or the non-predatory *Desulfo-bacteria* and *Geobacter* species was identified. These 291 gene orthologues common to both *Bacteriovorax* and *Bdellovibrio* may be the key indicators of host-interaction predatory-specific processes required for prey entry. The locus from *Bdellovibrio bacteriovorus* is implicated in the switch from predatory to prey/host-independent growth. Although the locus is conserved in *B. marinus*, the sequence has only limited similarity. The results of this study advance understanding of both the similarities and differences between *Bdellovibrio* and *Bacteriovorax* and confirm the distant relationship between the two and their separation into different families.**

*The ISME Journal* (2013) 7, 148–160; doi:10.1038/ismej.2012.90; published online 6 September 2012

**Subject Category:** integrated genomics and post-genomics approaches in microbial ecology

**Keywords:** *Bacteriovorax*; *Bdellovibrio*; genome sequence; BALO; subtractive hybridization; host-interaction locus

## Introduction

*Bacteriovorax* is a genus of bacteria within the unique group of predatory prokaryotes known as the *Bdellovibrio* and like organisms (BALOs) that prey upon Gram-negative bacteria. These predatory bacteria share a unique lifecycle consisting of two distinct phases, the predatory attack phase that is

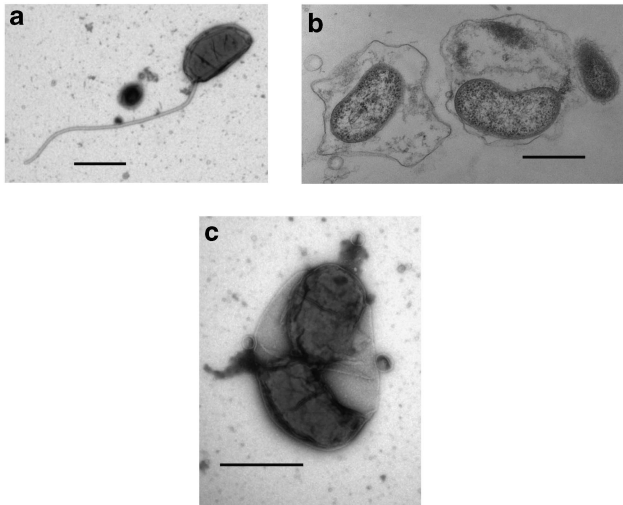
highly motile, which facilitates predation and an intraperiplasmic growth phase. On colliding with their prey, the BALOs penetrate the cell wall and lodge in the periplasm where they alter the cell wall to form a bdelloplast, grow, multiply and finally free themselves by lysing the prey cell wall.

Although *Bacteriovorax* share some attributes with *Bd. bacteriovorus*, they are distinct in several important features including the requirement of the former for sodium chloride (>0.5%), for growth and multiplication and a lower % G + C ratio, in the mid 30%*s* (Marbach *et al.*, 1976), compared with about 50% for the freshwater group (Seidler *et al.*, 1972). Salt tolerant or marine *Bacteriovorax* organisms also differ from their terrestrial cousins by

Correspondence: LC Crossman, Bioinformatics, The Genome Analysis Centre, Norwich Research Park, Norwich, Norfolk NR4 7UH, UK.

E-mail: lisa.crossman@bbsrc.ac.uk

Received 29 March 2012; revised 18 June 2012; accepted 20 June 2012; published online 6 September 2012



**Figure 1** Electron micrographs of *B. marinus* SJ (a) single attack phase flagellate *B. marinus* cell (b) inhabiting the intraperiplasmic space of *Vibrio parahaemolyticus* prey cells, and (c) septating into progeny.

being generally smaller, *Bdellovibrio* are typically 0.2–0.5  $\mu\text{m}$  in width and 0.5–2.5  $\mu\text{m}$  in length (Burnham *et al.*, 1968; Burnham and Conti, 1984), whereas *Bacteriovorax* ranges from 0.6 to 1.0  $\mu\text{m}$  in length in our collection of electron micrographs (Figures 1a–c), thereby passing through a 0.2  $\mu\text{m}$  filter. *Bacteriovorax* also thrive at lower temperatures than freshwater BALOs (Uematsu and Wakimoto, 1971; Williams, 1979) and have a preference for prey native to estuarine or other saltwater environments (Marbach *et al.*, 1976; Sutton and Besant, 1994). Formerly, *Bacteriovorax* was in the genus *Bdellovibrio* (Conti and Burnham, 1984) but was not given a species name. The designation of marine *Bdellovibrio* sp., persisted for more than a decade.

Recent advances in the taxonomy and systematics of BALOs have proceeded with knowledge of 16S ribosomal DNA sequences. This approach was most useful as wild type obligate predators have not been grown in pure culture, a necessary step for many metabolic and biochemical methods traditionally used to characterize and classify bacteria. These predators can be grown in co-culture solely with prey bacteria. The 16S ribosomal DNA sequence data from isolates of the saltwater and freshwater species revealed major differences and have resulted in establishment of new genera, *Bacteriovorax*, and family, Bacteriovoraxaceae, for the marine groups (Baer *et al.*, 2000; Snyder *et al.*, 2002; Baer *et al.*, 2004; Davidov and Jurkevitch, 2004) and a second family, Peredibacteraceae that includes some of the freshwater strains (Pineiro *et al.*, 2007). Subsequently, further differentiation based on sequence comparisons of the *rpoB* gene revealed that there were at least eight operational taxonomic units within the marine group (Pineiro *et al.*, 2007). Prey or host-independent (HI) mutants of marine

(*Bacteriovorax marinus* and *Bacteriovorax litoralis*) and freshwater (*Bd. bacteriovorus* 109J) species have been isolated in the laboratory, and tested for metabolic characteristics (Shoeffield, 1990; Seidler and Starr, 1969).

Both *Bd. bacteriovorus* and *B. marinus* are members of the delta-proteobacteria. This phylum includes organisms highly diverse in terms of niche, metabolic strategies and adaptations (Karlin *et al.*, 2006). Members of the delta-proteobacteria share a few particular genomic features but use distinct ecological strategies such as using iron as electron acceptor (*Geobacter metallireducens*), swarming with self-organizing behavior, (*Myxococcus xanthus*), and as with *B. marinus*, exhibiting a predatory lifestyle (Coppi *et al.*, 2004; Goldman *et al.*, 2006).

*B. marinus* strains are unusual and potentially useful (Socket and Lambert, 2004), but have not been studied extensively. To date, only a terrestrial strain *Bd. bacteriovorus* HD100, has been sequenced (Rendulic *et al.*, 2004). Here, we report the complete sequencing and analyses of the first halophilic *Bacteriovorax* genome. *B. marinus* SJ<sup>T</sup> (= ATCC BAA-682<sup>T</sup> = DSM 15412<sup>T</sup>) was isolated from coastal waters near St John's Island, US Virgin Islands (Baer *et al.*, 2004). *Bacteriovorax* have a ubiquitous distribution in saltwater environments. However, not all operational taxonomic units are similarly distributed. Some have a widespread distribution and others are restricted to certain ecosystems. *B. marinus* is placed in operational taxonomic units phylogenetic Cluster III based upon similarity of the 16S ribosomal RNA gene sequences. In a global survey this group was found to be the most widely distributed in oceans and seas among the eight phylotype clusters identified (Pineiro *et al.*, 2007). It is typically found in higher salinity marine environments than in lower salinity brackish waters and estuarine systems. Differences between ocean and estuarine isolates were revealed by 16S rDNA sequence analysis.

Comparisons between the genomes of *Bdellovibrio* and *Bacteriovorax* will advance knowledge of these unique predators, their predatory behavior and other common and distinct features. The results of this study will also expand interest in sequencing *Bacteriovorax* and other BALO phylotypes that vary in their ecology and genomic profile.

## Materials and methods

For DNA isolation, *B. marinus* SJ was grown in prey seawater broth using *Vibrio parahaemolyticus* as the prey bacterium as previously described (Williams and Baer, 2005). Briefly, prey ( $10^8$  to  $10^9$ ) was inoculated into sterile seawater to which a 24–48 h culture (filtered through 0.2  $\mu\text{m}$  filter to remove prey cells) of SJ was added and the turbid suspension was incubated on a shaker at 25°C until the turbidity cleared. The culture was filtered to remove

prey cells and the filtrate centrifuged to pellet the SJ cells from which DNA was extracted.

DNA sequencing was carried out using Sanger sequencing technology. DNA was sonicated, size selected and libraries were constructed in pUC19, pMAQ1b and pBACe3.6. The genome assembly was based on paired end-reads from pUC19 and pMAQ1b libraries to give 10-fold sequence coverage of the genome. Directed finishing reads were used to produce scaffolds from large-insert libraries in pBACe3.6. Repeats were bridged using read-pairs or end-sequenced PCR products. Gene prediction was carried out on the complete finished genome sequence using the programs Glimmer3 and Orpheus, and manually curated (Frishman *et al.*, 1998; Delcher *et al.*, 1999). Annotation was carried out using the Artemis (Rutherford *et al.*, 2000) platform, with marked InterPro (Hunter *et al.*, 2009), TMHMM (Sonnhammer *et al.*, 1998) and SigP (Bendtsen *et al.*, 2004) domains. The transfer RNAs (tRNAs) were determined using tRNAscan-SE (Lowe and Eddy, 1997) and ribosomal RNAs were determined using BLASTN and manual markup.

Phylogenetic Tree analysis was carried out with 1000 replicates using the RAXML-VI-HPC (Stamatakis, 2006), Phylip (Felsenstein, 2005) and NJ Plot (Perriere and Gouy, 1996) programs. This was independently verified using neighbor joining and whole-genome composition vector Tree (Xu and Hao, 2009a) approaches.

Gene orthologues were calculated by reciprocal best match (bidirectional best hit analysis using Fasta global alignments with sequence identity cut-offs as described in the text. Orthologues were removed from the *B. marinus* annotation using Artemis Select Function to leave genes shared only with *Bdellovibrio* that are not found in other members of the delta-proteobacteria. This geneset was additionally verified using a unidirectional (BLASTP) best hit analysis and visualized manually. Accession numbers of the strains used in the study are as follows: *Bd. bacteriovorus* HD100 (NC\_005363.1), *Lawsonia intracellularis* PHE/MN1-00 (NC\_008011.1), *Myxococcus xanthus* DK1622 (NC\_008095.1), *Anaeromyxobacter dehalogenans* 2CP-1 (NC\_011891.1), *Pelobacter carbinolicus* DSM238 0 (NC\_007498.2), *Geobacter metallireducens* GS-15 (NC\_007517.1), *Haliangium ochraceum* DSM14365 (NC\_013440.1), *Desulfatibacillum alkenivorans* AK-01 (CP001322.1), *Desulfovibrio desulfuricans* subsp. *desulfuricans* strain ATCC27774 (NC\_011883.1), *Desulfovibrio vulgaris* str. Hildenborough (NC\_002937), *Desulfococcus oleovorans* Hxd3 (NC\_009943.1), *Desulfohalobium retbaense* DSM 5692 (NC\_13223.1), *Sorangium cellulosum* 'Soce56' (NC\_010162.1), *Syntrophus aciditrophicus* SB (NC\_007759.1), *Syntrophobacter fumaroxidans* MPO (NC\_008554.1).

Electron microscopy was carried out at University of Florida, USA (UF) and University of Nottingham, UK. A 50 ml sample of 4 and 24 h culture of the predators and prey was fixed for electron

microscopy examination according to Koval and Bayer (1997) with modification. Briefly, samples were centrifuged for 30 min at 27 485 g, resuspended in 1 ml of 0.1 M sodium phosphate buffer (pH 7) and centrifuged for 20 min at 20 142 × g. The pellets were resuspended in 2 ml of 0.1 M cacodylate buffer containing 2% glutaraldehyde and 1% formaldehyde, both diluted from 25% (v/v) and 16% (v/v) stock solutions, respectively. After 1 h at 4 °C and centrifugation at 20 142 g for 20 min, the pellets were overlaid with cacodylate buffer. Samples were embedded in epoxy for further study of thin sections. Cells were post-fixed in OsO<sub>4</sub>, washed, dehydrated and embedded in resin. Ultrathin sections were counterstained with uranyl acetate and lead citrate and examined with a Hitachi H-7600 transmission electron microscope Hitachi high technologies America Inc., Pleasanton, CA, USA.

## Results

### *Electron microscopy studies show B. marinus SJ as a predatory species*

To determine whether *B. marinus* carries out the same predatory strategy as the terrestrial *Bd. bacteriovorus*, or other halophilic *Bacteriovorax*, we examined cells co-cultured with *Vibrio parahaemolyticus*. The results from the laboratories of two independent groups show conclusively the invasion and replication tactic employed by *B. marinus* is the same as *Bd. bacteriovorus*. Typically, the first observable interaction of BALOs with its prey is attachment (Figure 1a). Following attachment is penetration (not shown) and invasion into the periplasmic space of the prey (Figure 1b) where a predator cell alters the prey cell wall, consumes the cytoplasmic contents of the prey and grows to fully occupy the area within the prey cell. The final steps in the intracellular cycle are multiplication (Figure 1c shows predator cells septating to form new cells) and lysis of the prey cell releasing predator progeny. The predatory growth of *Bx. marinus* had not previously been demonstrated unequivocally.

### *Comparison of B. marinus to the features of delta-proteobacteria*

The genome of *B. marinus* strain SJ comprises a single circular chromosome and a small plasmid. The chromosome is moderately short at 3 435 933 bp with 3230 predicted coding sequences. Eighteen pseudogenes and two ribosomal RNA operons were identified in the sequence. The general features of the chromosome are shown in Table 1. Remarkably, 1116 (34.5%) of the predicted genes of over 500 nt in length were found to have no significant hit in the databases (including the GenBank marine metagenomics samples), nor did they possess any Pfam domains. Overall, 4496 hits to *Bacteriovorax* were found in the MG-RAST databases.



The delta-proteobacteria are a highly diverse class of the phylum Proteobacteria. A phylogenetic tree shows the positioning of *B. marinus* SJ within the delta-proteobacteria (Figure 2). While the closest sequenced relative to *B. marinus* SJ is *Bd. bacteriovorus*, no genomic synteny is observed by dotplot or by Artemis Comparison Tool (Carver *et al.*, 2005) BLASTN analysis. Using Artemis Comparison Tool with a more sensitive TBLASTX indicates only very short match regions. MUMmer (Kurtz *et al.*, 2004) alignments indicated only one short region showing direct synteny that corresponds to the ribosomal proteins (Supplementary Figure 1).

**Table 1** General characteristics of the *B. marinus* SJ genome

	Chromosome overview	Plasmid overview
Number of bases	3 435 933 bp	1973 bp
Number of coding sequences	3249	1
Gene Density genes kb <sup>-1</sup>	0.94	0.506
Average length	988 bp	723 bp
Coding percentage	92.9%	36.6%
G + C content	36.75%	36.2%
Pseudogenes	18	0
Ribosomal RNA operons	2	0

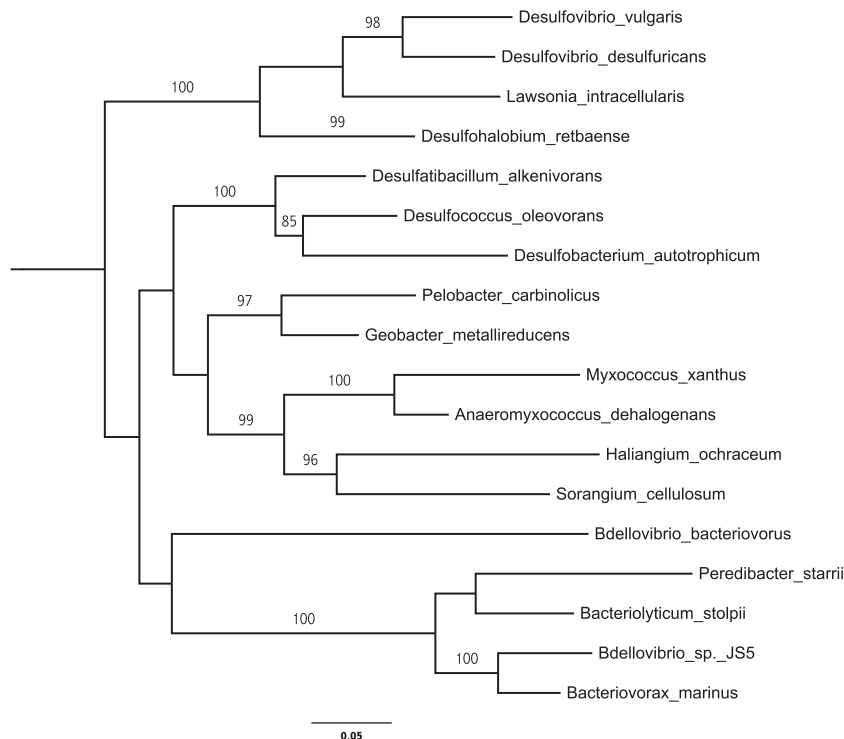
Major features of the *B. marinus* SJ genome sequence in terms of both the chromosome and plasmid DNA.

From investigations by Karlin *et al.* (2006), the major characteristics of delta-proteobacteria are as follows:

1. Delta-proteobacteria have two giant S1 ribosomal proteins genes compared with one or none in other bacteria.
2. In most delta-proteobacteria, the major ribosomal protein gene cluster near the origin.
3. Delta-proteobacteria have a rare combination of discriminating asparagine and glutamine tRNA synthetases to modify Asp-tRNA into Asn-tRNA and Glu-tRNA into Gln-tRNA.
4. Delta-proteobacteria have numerous TonB receptors and ferric siderophore receptors.
5. Anaerobic deltas have multiple copies of reuberythrin.
6. Sigma 54 has a more important role in delta-proteobacteria than other bacteria.
7. There are multiple beta lactamases.

The genome of *B. marinus* appears to conform to some, but not all of these findings.

Surprisingly, there is only one giant S1 protein in *B. marinus*, only five TonB Pfam domains and only three large putative TonB receptor proteins encoded in the genome. However, in keeping with other delta-proteobacteria, the major ribosomal protein gene cluster is located near the *ori*.



**Figure 2** Phylogenetic tree based on small subunit ribosomal RNA to show the placing of *B. marinus* SJ among the delta-proteobacteria. Numbers on branches correspond to bootstrap values based on 1000 replicates. This phylogenetic tree was produced with maximum likelihood with bootstrapping by RAxML (Stamatakis, 2006) and Phylip (Felsenstein, 2005). Species included in this analysis are as listed on the tree and in the methods. The topology of the tree was conserved (excluding *B. marinus* SJ) using the neighbor-joining method in the Integrated Microbial browser and with the composition vector Tree (Xu and Hao, 2009b) approach (excluding *Desulfatibacillum alkenivorans* and *Myxococcus xanthus*). *Escherichia coli* was used to root the tree.

**Table 2** shows the top BLASTP hits of some highly conserved predicted proteins found in *B. marinus* SJ

Gene name	Top BLASTP hit (% id) (excluding SJ)
<i>dnaA</i>	38%
<i>gyrA</i>	57%
<i>nuoA</i>	46%
<i>lon</i>	48%
<i>topA</i>	48%
<i>rpoN</i>	46%
<i>clpA</i>	53%
<i>mutS</i>	38%
<i>rpmA</i>	67%
<i>pfkA</i>	63%
<i>hemN</i>	34%
<i>rpoA</i>	57%
<i>gidA</i>	40%
<i>dnaX</i>	32%
<i>ftsZ</i>	65%
<i>recA</i>	73%

BLASTP was carried out using default parameters on the non-redundant sequence databases. Results show that despite this organism carrying common gene orthologues they are highly divergent with respect to other genes in the databases.

Discriminating asparagine and glutamine tRNA synthetases are found in the genome, and there are 11 Pfam domains classified as beta lactamases or beta-lactamase-like.

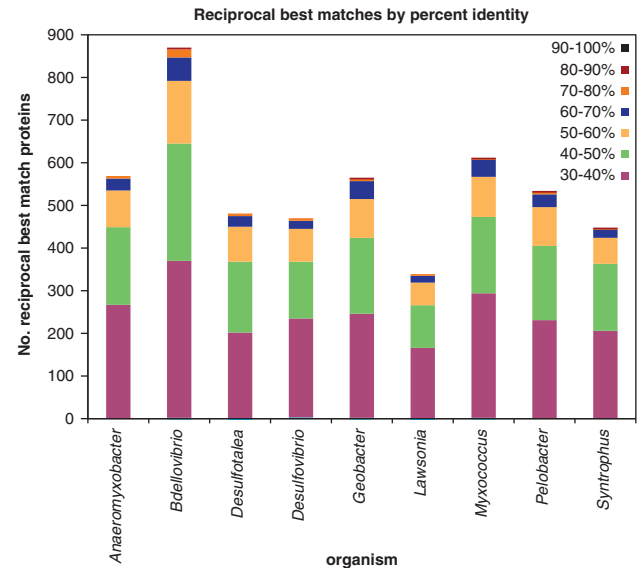
#### Plasmid, general structure and function

*B. marinus* possesses a unique plasmid of 1973 bp and of 36.2% GC content, designated pBMS1. The % GC content is in accordance with that of the chromosome. There is only one strongly predicted coding sequence on the plasmid, *repA*. Throughout the remainder of this short plasmid, there are also a number of short direct and palindromic DNA repeats and a potential stem-loop structure. This plasmid may represent a truly selfish piece of DNA, in that it may only carry one gene specifying its replication. A selfish plasmid, pKL1, has been described from *E. coli* that carries only a *repA* gene (Burian *et al.*, 1997). In addition, the German outbreak *E. coli* O104:H4 also carries a selfish plasmid (BGI, 2011).

Although the *repA* gene remains the only strongly predicted coding sequence, BLAST analysis indicates a predicted 38-amino-acid polypeptide with N-terminal matches to conserved hypothetical genes. Recently, two plasmids have been characterized from *Bd. bacteriovorus* (Roschanski and Strauch, 2011), however, these plasmids do not resemble pBMS1.

#### Orthologous genes shared with delta-proteobacteria

To date, *B. marinus* SJ remains divergent from all other sequenced prokaryotes. Table 2 shows a list of important genes with their June 2012 top BLASTP hit against the non-redundant databases shown by sequence identity, while Figure 3 indicates the number of orthologous genes shared with other delta-proteobacteria. Only four coding sequences have



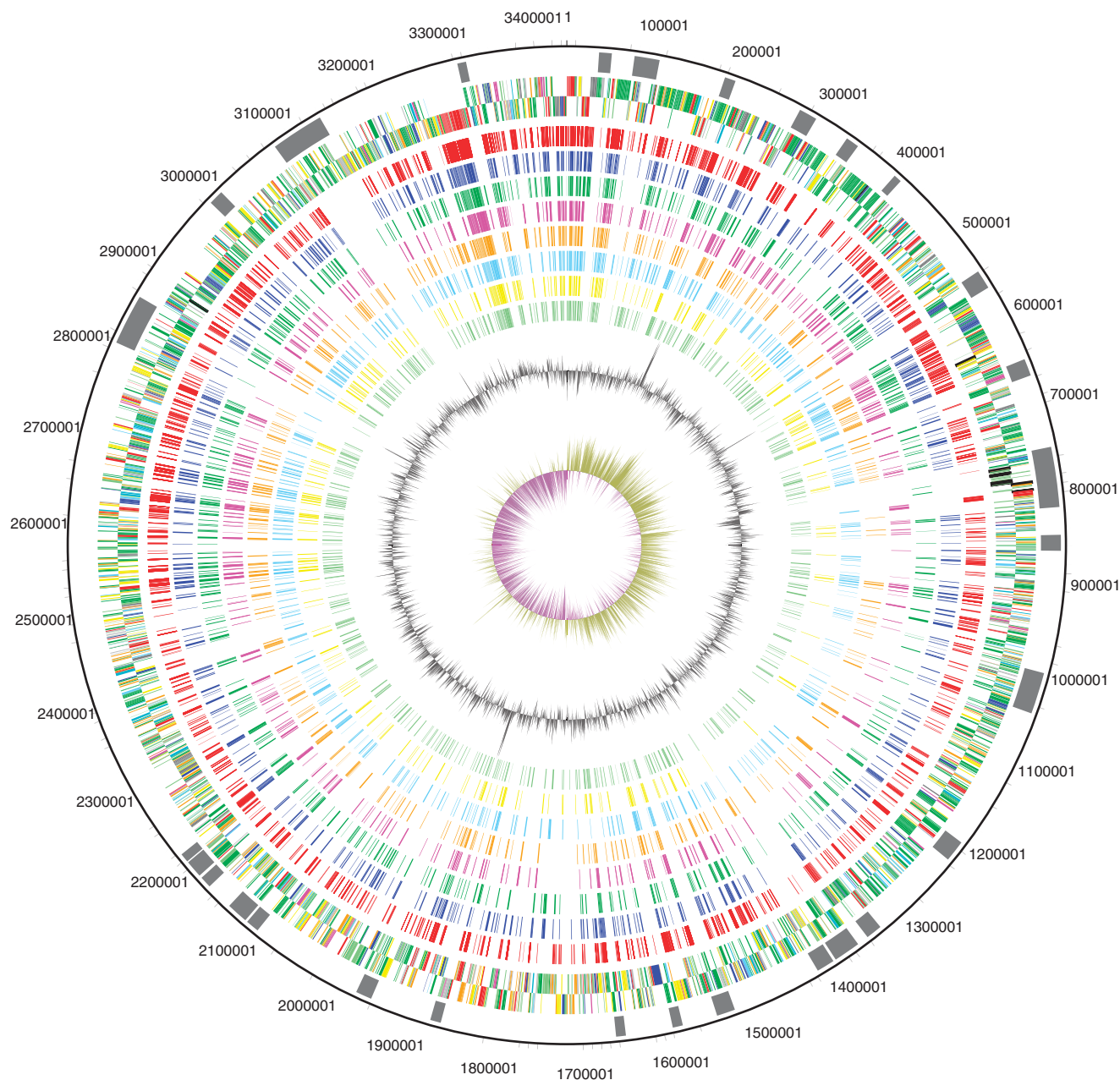
**Figure 3** Orthologous genes shared between delta-proteobacteria (by percentage identity) as determined by bidirectional best hit analysis. Bar graph to show the percentage identities of *B. marinus* SJ gene orthologues with other delta-proteobacteria. Orthologues were calculated by bidirectional best hit analysis, altering the percentage identity cutoff between 30–90%. The species of delta-proteobacteria used in the investigation were: *Anaeromyxobacter dehalogenans*, *Desulfotalea psychrophila*, *Bdellovibrio bacteriovorus*, *Desulfovibrio vulgaris*, *Geobacter metallireducens*, *Lawsonia intracellularis*, *Myxococcus xanthus*, *Pelobacter carbinolicus* and *Syntrophus aciditrophicus*.

an 80% or higher identity shared with its closest sequenced relative, *Bd. bacteriovorus*. Investigations indicate a common delta core solely consisting of 891 genes in bidirectional best hit analyses with the genome sequences of the species described in the Materials and methods section that represent different clades of the delta-proteobacteria.

#### Genomic islands of *B. marinus*

Regions of difference were determined. Some of these genomic islands of *B. marinus* were (i) unique to *B. marinus* among delta-proteobacteria or (ii) shared only with *Bd. bacteriovorus* (Figure 4). Each of these genetic regions has been systematically numbered, and the key coding sequences (CDS) carried on these islands are listed in Supplementary Table 1.

Following alien hunter analysis (Vernikos and Parkhill, 2006), approximately half of the genomic islands detected above were potentially acquired by horizontal gene transfer. These regions have been numbered systematically and are listed in and summarized in Table 3. The phylogenetic origin of the potentially horizontally transferred regions was accessed by dividing the regions into 150 bp sequences and compared with Uniprot using BLAST. The output was entered into MEGAN (Huson *et al.*, 2007). Approximately 1/3 of the sequences had no hit, 1/3 matched unassigned sequences and 1/4 matched proteo-bacterial sequences (Supplementary Figure 2). In the main,



**Figure 4** Orthologous genes shared with delta-proteobacteria as determined by bidirectional best hit analysis. The circles on the diagram are as follows (outermost to innermost): *B. marinus* SJ DNA coordinates. Regions of major differences, known as BMRD for *B. marinus* regions of difference (marked in black). Orthologous genes from the following genera, with all predicted orthologues shown on the forward strand only, for clarity: *Bdellovibrio*, *Myxococcus*, *Anaeromyxobacter*, *Desulfovibrio*, *Desulfococcus*, *Pelobacter*, *Lawsonia*, *Sorangium*, GC content, GC skew.

the regions of difference carry large amounts of conserved and hypothetical proteins, many of which are predicted by the SigP program to be exported (Emanuelsson *et al.*, 2007). For example, BMRD8 and 14 carry secondary efflux transporters of the RND family. BMRD27 carries a predicted ABC transporter and a putative sigma factor, while BMRD28 and 29 carry pili and glycosyl transferases and a methyl-accepting chemotaxis protein, respectively. BMRD1 carries some amino acid biosynthetic enzymes and BMRD9 carries CDS of bacteriophage

origin in addition to a putative type I restriction-modification system.

In addition to the larger islands described above, there are potentially laterally transferred regions that comprise few or single genes. One such gene, *BMS1619*, shares high sequence similarity with a hemagglutinin/hemolysin of *Staphylococcus epidermidis*, a surface protein from the planctomycete *Rhodopirellula baltica*, and two separate CDS from *Bd. bacteriovorus*. This potential island has a very high alien hunter score (>54) consistent with horizontal gene transfer. A second gene, *BMS\_3202*,



**Table 3** shows a summary of the *B. marinus* major regions of difference (BMRD) islands

Region of difference	Range	U/S	Alien	Characteristics
BMRD1	BMS0031-0045	U	Y	Many transmembrane proteins
BMRD2	BMS0069-0101	S	Y	Beta-lactamase/flagellar
BMRD3	BMS0170-0184	S	Y	<i>hit</i> locus
BMRD4	BMS0257-0272	U	N	Many exported/transmembrane
BMRD5	BMS0313-0327	U	N	Antiporter/exported/chaperone
BMRD6	BMS0382-0389	U	Y	Transferases/transmembrane
BMRD7	BMS0518-0536	S	N	Iron-regulated/siderophore uptake system
BMRD8	BMS0631-0644	U	N	Efflux transporter/exported
BMRD9	BMS0733-0814	S	Y	Type I restriction system/phage
BMRD10	BMS0855-0879	S	N	Oxygenase/glutathione peroxidase
BMRD11	BMS1029-1078	S	Y	Hypotheticals/histone deacetylase
BMRD12	BMS1245-1266	S	N	DNAGyrase/transmembrane
BMRD13	BMS1373-1392	S	Y	Motility/transmembrane
BMRD14	BMS1408-1430	U	Y	Efflux system/exported
BMRD15	BMS1436-1456	U	N	Exported
BMRD16	BMS1551-1567	U	Y	Exported
BMRD17	BMS1612-1617	U	Y	Exported
BMRD18	BMS1668-1674	U	Y	Lysyl tRNA synthetase/exported
BMRD19	BMS1866-1878	U	N	CoA transferases/aminotransferases
BMRD20	BMS1941-1958	U	Y	Protease/exported/cation transporter
BMRD21	BMS2076-2091	U	N	Poly (A)polymerase/LysR regulator
BMRD22	BMS2093-2115	U	Y	ABC transporter/ACR effluxer
BMRD23	BMS2149-2154	U	Y	Hypothetical/cell surface
BMRD24	BMS2158-2169	S	Y	Serine protease/flagellin/exported
BMRD25	BMS2173-2181	S	Y	Conserved hypothetical/exported
BMRD26	BMS2818-2862	S	Y	Efflux/resistance/xanthine dehydrogenase
BMRD27	BMS2995-3009	U	N	ABC transporter/sigma factor
BMRD28	BMS3094-3150	U	N	O antigen/polysaccharide
BMRD29	BMS3325-3335	U	N	Exported/chemotaxis

Alien, Alien hunter suggests possibility of horizontal gene transfer; N, No; S, mainly shared between *B. marinus* and *Bd. bacteriovorus*; U, mainly unique to *B. marinus*; Y, yes.

The islands are marked up according to locus tag numbering and whether they carry genes that are mainly unique to *B. marinus* or genes that are shared between *B. marinus* and *Bd. bacteriovorus*. If the BMRD was also predicted as horizontally transferred using the Alien Hunter (Vernikos and Parkhill, 2006) program this is noted along with the major findings on each island.

has another high alien hunter score (>32) and shares sequence similarity with a cell surface/hemagglutinin protein of the plant pathogenic bacterium *Xanthomonas campestris*.

Larger genomic islands present in *Bd. bacteriovorus* and *B. marinus* and not in free-living delta-

proteobacteria are of interest in that they may represent islands involved or required for predation and/or host-interaction. Most of these islands carry high quantities of transmembrane and exported proteins. BMRD11 carries glycosyl transferases in addition to other transmembrane/exported proteins. BMRD26 carries a gene with similarity to microcin immunity (BMS2821), together with xanthine dehydrogenase, chemotaxis and efflux transporter proteins.

#### *Genes important in predation*

A small common core of 891 genes is shared between *Bacteriovorax* and *Bd. bacteriovorus* genomes. Using an *in silico* subtractive hybridization using both bidirectional and unidirectional best hit analysis revealed 291 genes were shared between *Bacteriovorax* and *Bdellovibrio* but not shared with the common core gene data set of delta-proteobacteria. The orthologous genes from the *in silico* subtractive hybridization may represent the core set required for bacterial invasion, macromolecular consumption and escape from the (eventually) degraded prey cell or bdelloplast. Identifying them by comparative genomics is a potential insight into the machinery of intracellular bacterial predation.

Gene expression in *Bdellovibrio* at the beginning of the predatory cycle has been studied by a transcriptomic analysis at only 30 min of predator-prey interaction (Lambert *et al.*, 2010). At this time-point the *Bdellovibrio* are attaching to the outer-membrane of the prey, entering the prey periplasm, resealing the prey outer-membrane and inducing the genes whose products will commence the systematic digestion of the prey cell. Remarkably, only 15 of the 291 genes were observed as upregulated in *Bdellovibrio* at this time-point. Ten of these genes (*BMS\_1308*, *BMS\_0406*, *CMS\_2372*, *BMS\_2940*, *BMS\_2521*, *BMS\_1074*, *BMS\_0590*, *BMS\_1798*, *BMS\_0407*) and *BMS\_2266* are homologous to *Bdellovibrio* genes (*Bd0301*, *Bd0370*, *Bd0965*, *Bd1176*, *Bd2033*, *Bd2288*, *Bd2480*, *Bd3094*, *Bd3134*, *Bd3748* and *Bd3823*) in the conserved hypothetical category and as such may represent unexplored novel pathways contributing to predator-prey interactions. The genes are scattered throughout the genomes *Bacteriovorax* and *Bdellovibrio*, reflecting the variable synteny that is evident between the genomes; however, they are enriched particularly in BMRD26, which also shares genes in common with the predator-lysis bacterium *Myxococcus xanthus* and are not found in non-predatory delta-proteobacteria. Present in this region are transmembrane proteins and regulators (Supplementary Table 1).

The remaining five orthologues with a predicted encoded function include *BMS\_2143*, the homolog of *Bd0087*. This resembles a guanosine triphosphate cyclohydrolase that encodes the *de novo* synthesis pathway for tetrahydrofolate, a coenzyme involved in transfer of one-carbon groups. A second

orthologue, *BMS\_0990* (a *Bd1990* homolog), is annotated as a gene encoding a putative auxin regulated protein as it has a Pfam domain denoted as plant auxin responding. Third, *BMS3383* (*Bd3359*) has a RAS-like guanosine-5'-triphosphatase motif and may be involved in signal transduction as is the case in *Myxobacteria* (Leonardy *et al.*, 2010). Fourth, *BMS\_1097* (*Bd3533*) has serine esterase similarity and finally, *BMS\_2214* (*Bd1370*) is annotated as an RNA helicase.

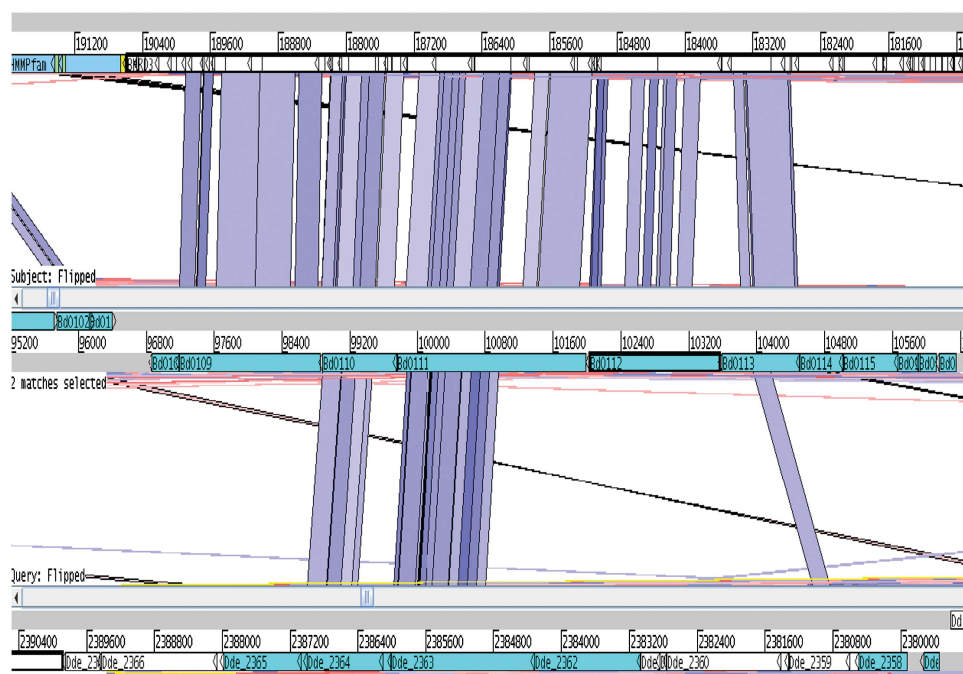
#### Motility/chemotaxis

Motility and chemotaxis is important for predation in *Bd. bacteriovorus* (Lambert *et al.*, 2003, 2006). In *B. marinus*, there are eight predicted methyl-accepting chemotaxis proteins (MCPs), with one extra MCP found as a pseudogene with a central stop codon. The MCPs are important in predation in *Bd. bacteriovorus* where chemotaxis aids detection of high concentrations of prey bacteria (Lambert *et al.*, 2003, 2006) *B. marinus* has an apparent full complement of motility and chemotaxis genes, although the number of *fliC*s encoding the flagellar filament is five rather than the six found in *Bdellovibrio* genes (Lambert *et al.*, 2006). A key *fliC3* gene, required for motility in *Bd. bacteriovorus* and important in predation has a close homolog in *B. marinus*. In contrast to the three pairs of *motAB* genes found in *Bd. bacteriovorus* (Morehouse *et al.*, 2011), a sole pair of flagellar motor protein genes is present in *B. marinus*.

Type IV pili are encoded by both of the above predatory species. Type IV pili are generally implicated in gliding/twitching motility, biofilm formation and pathogenicity/host interaction (Evans *et al.*, 2007). Type IV pili are essential for predation in *Bdellovibrio* (Evans *et al.*, 2007; Mahmoud and Koval, 2010). This homology may reflect the common prey invasion mechanisms of these bacteria.

#### Host interaction (*hit*) locus

Spontaneous mutants of *Bd. bacteriovorus* that did not require host cells for growth on rich media (Cotter and Thomashow, 1992) were referred to as HI mutants and shown to have lesions in the *hit* locus. A short open reading frame within a gene cluster encoding structural elements of a type IV pilus (*tadAB*) and a cellulose binding protein (*wapA*) was mutated in these mutants and termed *hit* locus (Cotter and Thomashow, 1992; Rendulic *et al.*, 2004). Predatory growth can be restored on introduction of a wild-type *hit* gene to saprophytic mutants (Roschanski *et al.*, 2011). A subsequent study has shown that Flp pilus-like proteins encoded at this locus show increased transcription in synchronized cultures with prey bacteria by reverse transcription-PCR, whereas transcriptional activity was reduced in intracellular replication phase (Schwudke *et al.*, 2005). More recently, mariner transposon mutants were isolated in this locus and implicated in predation of *E. coli* biofilms



**Figure 5** tBLASTx analysis of the *hit* locus region comparing conservation and genome synteny. Artemis comparison tool (ACT (Carver *et al.*, 2005)) tBLASTx investigation of the *hit* locus. The top of the figure shows the *hit* locus in *B. marinus* SJ. The middle line constitutes the *hit* locus of *Bd. bacteriovorus* HD100. The extent of the described *hit* locus in *Bd. bacteriovorus* (Schwudke *et al.*, 2005) is shown. The base of the figure shows a partial match equivalent to the *hit* locus region in *Desulfovibrio desulfuricans* G20. This organism, as all other sequenced delta-proteobacteria, does not have a *hit* orthologue present.



(Medina *et al.*, 2008). Thus, the *hit* locus is thought to be involved in host invasion and penetration.

Synteny in the core region of the *hit* locus (Figure 5) is conserved between *Bd. bacteriovorus* and *B. marinus* where genes upstream of *cpaBC* in *B. marinus* also show limited similarity with pilus assembly genes, including *tadV* and *pilA*. The position of the *tad* genes for Flp pilus assembly being conserved in the *hit* locus of *B. marinus* and *Bd. bacteriovorus* suggests these genes are important. This region is syntenic except that in *Bacteriovorax* the region is inverted with respect to the *Bdellovibrio* sequence. It has been suggested that the *hit* locus bears some resemblance to the widespread colonization island (Tomich *et al.*, 2007). Although there is one putative Flp pilus coding sequences in *Myxococcus xanthus*, and *Desulfovibrio desulfuricans* G20 has two potential coding sequences involved in *flp* pili production, the *hit* locus is not intact in other delta-proteobacteria. This is as expected should the *hit* locus have an important involvement in predation, as the other sequenced delta-proteobacteria are free-living and non-parasitic.

Recent findings highlighted the importance of a single gene, *hit*, in *Bd. bacteriovorus* within the *hit* locus in the conversion from HI growth to predatory growth (Wurtzel *et al.*, 2010; Roschanski *et al.*, 2011). Deletion of *hit* abolished plaque formation on prey lawns, which was restored by complementation with just this gene. Additionally, mutations that genuinely affected HI growth resided solely within *hit*, implying that *hit* is required, in a direct or regulatory role, for predatory entry to other bacteria. Given this importance it is striking that at the same locus in *Bacteriovorax*, a gene duplication event has given rise to two gene products, BMS0183 and BMS0184, each with limited similarity to *Bd. bacteriovorus hit*. The 18-N-terminal amino-acids of all three genes are highly conserved. Both *B. marinus* genes are 34-amino-acids shorter than 101 amino acids of *hit* and have limited similarity in the 60-C-terminal amino-acids of *hit*. This low similarity was unexpected because C-terminal deletions and point mutations causing truncations or frameshifts after codon 30 in *hit* were common in *Bdellovibrio* HI strains (Barel and Jurkevitch, 2001).

#### Other aspects

Analysis of the *B. marinus* genome was undertaken using the program Pathway Tools (Karp *et al.*, 2002), including the pathway hole filler (Green and Karp, 2004), and KEGG analysis (Ogata *et al.*, 1999). The results indicate that *B. marinus* is able to synthesize many but not all amino acids, for example, complete pathways are lacking for the biosynthesis of arginine, histidine, isoleucine, phenylalanine, threonine, tryptophan, tyrosine and valine (or selenocysteine). *Bd. bacteriovorus* is similarly predicatively unable to synthesize the

following amino acids: arginine, histidine, isoleucine, methionine, phenylalanine, tryptophan and valine (Rendulic *et al.*, 2004). These findings are suggestive that the organism can gain essential amino acids from its prey.

It remains possible that these metabolic pathways are unusual in these organisms, and that the method of synthesizing these amino acids cannot be recognized. Interestingly, asparagine synthetase along with a divergently transcribed AsnC family transcriptional regulator is found in a region unique to *B. marinus* among deltas. A tRNA-Arg is also located here (BMRD1; see Supplementary Table 1). A full complement of tRNA synthetases is present in the genome. In terms of nucleotide synthesis, the ready-made DNA supplied by the prey is sufficient for one extra progeny predator cell to form, yet to form several progeny the predator must convert other prey cellular materials *de novo* to DNA and RNA.

## Discussion

The delta-proteobacteria are a highly diverse phylogenetic group and as expected, the sequenced *B. marinus* SJ strain conforms to most, but not all of the expected characteristics of phylum. *B. marinus* SJ is most closely related to *Bd. bacteriovorus*, however, they are very distinct genomically. *B. marinus* SJ has a unique gene content that comprises 66% of the genome when bidirectional best hit analyses are performed against other sequenced delta-proteobacteria at a 30% level of identity across most of the sequence. In addition, hypothetical genes of larger than 500 nucleotides predicted by *ab-initio* and manual curation methods with no significant BLASTP matches in the non-redundant sequence databases as of July 2011 constitute 35% of the genome. These regions did not appear to be repetitive when searched using the Reputer (Kurtz and Schleiermacher, 1999) and MUMmer (Kurtz *et al.*, 2004) packages. Several of these predicted hypothetical coding sequences are found in pairs in the genome. Of these pairs, five were related by sequence albeit slightly to other pairs in the genome, and a further, separate two pairs were related. The size and organization of these gene pairs is reminiscent of insertion sequence mobile elements, but there is no indication that these could represent such elements by domain or sequence similarity.

The high level of sequence diversity is rarely seen in current sequencing projects (Young *et al.*, 2006; Crossman *et al.* 2008a, b; Holden *et al.*, 2009; Crossman *et al.*, 2010; Carter *et al.*, 2011; Crossman, 2011; Heavens *et al.*, 2011; Seipke *et al.*, 2011). It raises the question of the origin of such unique DNA. *Bacteriovorax marinus* SJ appears to be related to *Bd. bacteriovorus* by phylogenetic analysis with long branch length and may represent an

ancient delta-proteobacterium. The unusual lifestyle of this predatory bacterium lends weight to a suggestion that some of the unique DNA could represent sequences that have been gained from prey consistent with our analysis that 25% of the sequences are most closely related to bacterial sequences (Supplementary Figure 2). We have observed in our laboratory that SJ is capable of preying on several other bacteria including *V. vulnificus*, *V. cholera*, a *Vibrio sp.* and *E. coli* and may prey on the wealth of bacteria in oceans that have never before been cultured or sequenced. Effectively this organism may have been carrying out its own DNA sampling of prey bacteria.

Unique hypothetical genes are sprinkled throughout the genome rather than being confined to predicted islands, although BMRD9 carries the highest concentration of these genes. In addition to the BMRD, there are also short islands that carry a few or single genes such as one with similarity to haemagglutinins implicated in adhesion in *Xanthomonas campestris* that may be involved in attachment/recognition. Hemagglutinins have been implicated in adhesion and may be involved in plant–parasite relationships in plant pathogenic bacteria (Alavi *et al.*, 2008).

Orthologous genes shared between *Bacteriovorax* and *Bdellovibrio* from an *in silico* subtractive hybridization may represent the core set required for the invasive predatory processes. Little is known about the mechanisms employed by the invasive *Bdellovibrio*-like predatory bacteria (also known as BALOs) during invasion and intraperiplasmic growth phase when they utilize prey macromolecules for biosynthesis and energy metabolism. However, it is known that motility/chemotaxis and pili are important factors in predation in *Bd. bacteriovorus*.

Few studies have addressed the metabolic and energy pathways for the BALOs and much remains to be done in this area. Of the studies that have been carried out, nearly all have been on strains of *Bd. bacteriovorus* or other freshwater/soil BALOs. None have focussed on the saltwater species, *Bacteriovorax*, other than to study the utilization patterns of some nutrient substrates. It is obvious that the prey cell can provide all the nutrients necessary for the intraperiplasmic growth of the predators in the case of both the freshwater and saltwater species. Beyond that, results of studies on *Bd. bacteriovorus* have shown that the organisms are capable of utilizing prey cell-derived amino acids as a major energy source for growth within the prey's intraperiplasmic space (Hespell *et al.*, 1973). Hespell later reported that *Bd. bacteriovorus* has many of the enzymes of the tricarboxylic acid cycle and that during intraperiplasmic growth these enzymes increase (Hespell, 1976). A number of proteolytic enzymes associated with BALO predation cycle have been reported from studies on the freshwater BALOs. A recent report describes the twin-arginine translocation system in *Bdellovibrio*, which transports

folded proteins across the cytoplasmic membrane as it does in other bacteria (Chang *et al.*, 2011). Recent observations in our laboratory have revealed that the *Bacteriovorax* and *Bdellovibrio* and other freshwater BALOs, with few exceptions, are not capable of predation on the same genera of bacteria perhaps because a different set of enzymes are required. Additional study on the metabolic machinery and growth requirements of the saltwater *Bacteriovorax* is needed to clarify the similarities or differences between this group and the freshwater BALOs.

Specific flagellar gene differences between *Bacteriovorax* and *Bdellovibrio* genomes can reflect the marine versus terrestrial lifestyles of the two bacteria but reinforce the importance of motility in encountering prey in both environments. Previous investigators (Lambert *et al.*, 2006; Iida *et al.*, 2009) showed that in *Bd. bacteriovorus* of six *fliC* genes only, *fliC3*, is essential for flagellar motility and hence efficient location of/collision with prey. The highest similarity among the *fli* orthologues is with the *fliC3* gene product at 70%. Thus, the importance of flagellar motility for prey encounters is strong in *Bacteriovorax* to hunt prey-rich regions in the oceans. Related to that marine lifestyle, a sole pair of flagellar ion-channel flagellar motor protein genes are present in the *Bacteriovorax* genome rather than the three pairs, which were all shown to contribute to the single flagellar motor of *Bd. bacteriovorus* (Morehouse *et al.*, 2011).

A host-interaction (*hit*) locus identified in *Bd. bacteriovorus* is only partially conserved in *B. marinus*. A *hit* gene is tandemly duplicated giving rise to the BMS0183 and BMS0184 genes of divergent proteins. We found this surprising given that this protein has been implicated in *Bdellovibrio*, by two separate research groups, as being uniquely important to strains switching between predatory and prey-independent HI growth (Wurtzel *et al.*, 2010; Roschanski *et al.*, 2011) and suggesting that the conserved genes may be the only ones necessary for a successful predator–prey interaction.

There is a theory that these predatory bacteria or certain of their enzymes could be used as therapeutic agents in a biological control type scenario. Furthermore, predators could be designed to invade specific cell types should the molecular machinery of predation be fully understood. The halophilic nature of *B. marinus* could be beneficial in its use for treating infections in humans and certain animals whose body environment is at 0.85 percent salts, tolerable for many of the halophilic predators. This theory will be interesting to explore and the genome sequence of *Bacteriovorax*, together with the comparison with *Bd. bacteriovorus*, provides us with a major stepping-stone to achieve the application of the predators as antibacterial agents. Understanding the machinery of predation may advance consideration of the possible use of these predatory bacteria or their enzymes as therapeutic agents or alternative applications in biological control.

## Acknowledgements

Sequencing and annotation of *Bacteriovorax marinus* SJ was funded by the Wellcome Trust. Microscopy was supported by National Science Foundation award HRD 0932137 to HW and by BBSRC UK G003092/1 to RES. LC is funded by BBSRC in partnership with East of England Development Agency, Norfolk County, Norwich City and South Norfolk Councils and the Greater Norwich Development Partnership, UK. The complete manually annotated chromosome of *Bacteriovorax marinus* SJ is available at FQ312005; plasmid pBMS1 has been assigned accession number HE610506.

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