

Bdellovibrio exovorus sp. nov., a novel predator of Caulobacter crescentus

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The life cycle, prey range and taxonomic status of a Bdellovibrio-like organism, strain JSST, were studied. Strain JSST was isolated from sewage in London, Ontario, Canada, in enrichment culture with Caulobacter crescentus prey cells. During predation, this strain remained attached to the outside of a stalked C. crescentus cell. No periplasmic growth stage was observed and no bdelloplast was formed. The stalked cells of C. crescentus retained their shape and, after predation, were devoid of cytoplasmic content, as shown by transmission electron microscopy. A periplasmic growth stage has been a definitive character in the description of members of the genera Bdellovibrio, Bacteriovorax, Bacteriolyticum and Peredibacter. This is the first description of an epibiotic predator in this group of prokaryotic predators. The G+C content of the genomic DNA of strain JSST was 46.1 mol%. 16S rRNA gene sequence analysis showed that this strain was related to Bdellovibrio bacteriovorus strains HD100T, 109J, 114 and 127 (90–93% similarity). Phylogenetic analysis based on 16S rRNA gene sequences grouped strain JSST with the Bdellovibrio cluster, but at a distance from other Bdellovibrio isolates. On the basis of features of the life cycle and phylogenetic data, it was concluded that strain JSST merits classification as the type strain of a novel species, for which the name Bdellovibrio exovorus sp. nov. is proposed (type strain JSST = ATCC BAA-2330T = DSM 25223T).

Bdellovibrio bacteriovorus is a small, rapidly motile, Gram-negative bacterium that is an obligate predator of other Gram-negative bacteria. It has a life cycle characterized by a free-living, non-replicating attack phase and a reproductive phase within the periplasm of the prey cell. The first report of Bdellovibrio bacteriovorus described the isolates as predatory, ectoparasitic and bacteriolytic micro-organisms (Stolp & Starr, 1963). Subsequent studies by Starr & Baigent (1966) and Burnham et al. (1968) described prey cell penetration and the intraperiplasmic growth of the parasite. For many years, new isolates of predatory bacteria were assigned to the genus Bdellovibrio, as strains of Bdellovibrio bacteriovorus, based on their morphological characteristics (comma-shaped rods; motile by means of a single, polar, sheathed flagellum) and predatory life cycle. Seidler & Starr (1969) reported the DNA G+C contents of 11 isolates of prey-dependent bdellovibrios and noted that two isolates of uncertain nomenclature status had G+C contents of ~43 mol%, less than that of all other isolates, which had G+C contents of ~50 mol%. Two novel species were described by Seidler et al. (1972): Bdellovibrio starrii (the A3.12T isolate from the original work of Stolp and Starr) and Bdellovibrio stolpii (the UKi2 isolate from the Conti lab). These two species were subsequently transferred to a new genus, Bacteriovorax (Baer et al., 2000), and then each to other new genera, as Peredibacter starrii (Davidov & Jurkevitch, 2004) and Bacteriolyticum stolpii (Pineiro et al., 2008). Collectively, Bdellovibrio, Bacteriovorax, Bacteriolyticum and Peredibacter species and strains and taxonomically uncharacterized isolates of intraperiplasmic, predatory prokaryotes are referred to as ‘Bdellovibrio-and-like organisms’ (BALOs) (Snyder et al., 2002). As predators, BALOs have been defined as having a cell cycle featuring an obligate, intraperiplasmic developmental stage inside the substrate bacterium (Jurkevitch, 2006).
In a study on the protective function of paracrystalline protein surface layers (S-layers) against predation by *Bdellovibrio bacteriovorus* (Koval & Hynes, 1991), we isolated on *Caulobacter crescentus* CB2A, a predatory bacterium, strain JSST, which resembled *Bdellovibrio bacteriovorus* in many respects. This BALO is a small, motile, comma-shaped rod that possesses a single, polar, sheathed flagellum (29 nm wide) (Koval & Hynes, 1991). It is a prey-dependent predator that forms plaques on lawns of *C. crescentus*. In the present study, we report further characterization of strain JSST and provide evidence for the description of a novel species of *Bdellovibrio*.

Initial studies on the growth of strain JSST were done in co-cultures in 1/10-strength yeast extract-peptone medium supplemented with calcium (YP/10 plus Ca\(^{2+}\)) (Koval & Hynes, 1991). This was necessary because the *C. crescentus* strain with an S-layer (strain CB2NY66R) was unstable in the HEPES plus Ca\(^{2+}\) buffer used in other co-cultures in this study. However, the S-layer-negative strain of *C. crescentus* (strain CB2A) (=ATCC BAA-2331 =DSM 25117) is stable in HEPES buffer. HM buffer [3 mM HEPES (pH 7.6) with 1 mM CaCl\(_2\) and 0.1 mM MgSO\(_4\)] was used for further studies, to correlate with other studies on *Bdellovibrio bacteriovorus* 109J (Thomashow & Rittenberg, 1978; Flannagan et al., 2004). Dilute nutrient broth medium (Cotter & Thomashow, 1992) may also be used for co-cultures. For maintenance, co-cultures containing 1 ml strain JSST and 4 ml of a 24 h peptone-yeast extract (PYE) broth culture (Johnson & Ely, 1977; Koval & Hynes, 1991) of *C. crescentus* CB2A were incubated in 125 ml flasks with 20 ml HM buffer. The co-culture was incubated at 30 °C with shaking at 150 r.p.m. for 24–48 h. Cultures were transferred to sterile screw-capped tubes and kept at 4 °C for up to 1 month. Cell suspensions were plated for plaques using yeast extract-peptone-aceate medium (YPSC) (Koval & Hynes, 1991) or dilute nutrient broth medium. Plaques were small. For long-term storage, a 24–48 h culture of strain JSST cells was frozen in the presence of 25% (w/v) glycerol at −80 °C. *Bdellovibrio bacteriovorus* strain 109J was grown on *Escherichia coli* ML35 (Flannagan et al., 2004) and strain 6-5-S on *Aquatiridae* sp serum phosphorus VHL (Koval & Hynes, 1991). *Bacterio-lyticum stolpii* UKi2T was obtained from J. Tudor (St. Joseph’s University, Philadelphia, PA, USA); it was maintained on peptone-yeast extract medium (1% peptone, 0.3% yeast extract, 1% agar, pH 6.8) (Seidler & Starr, 1969).

The *C. crescentus* strains used in this study are listed in Table 1 and were obtained from J. Smit (University of British Columbia, Vancouver, BC, Canada) and J. Poindexter (Barnard College, Columbia University, New York, NY, USA). All *C. crescentus* strains were maintained on PYE medium. Other Gram-negative bacteria used to test the prey range of strain JSST were from the culture collection of the Department of Microbiology and Immunology, University of Western Ontario.

### Table 1. Predation of *Caulobacter crescentus* strains by strain JSST

<table>
<thead>
<tr>
<th>Strain</th>
<th>S-layer</th>
<th>Predation</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>CB2A</td>
<td>−</td>
<td>+</td>
<td>J. Smit</td>
</tr>
<tr>
<td>CB2NY66R</td>
<td>+</td>
<td>−</td>
<td>J. Smit</td>
</tr>
<tr>
<td>CB13bla</td>
<td>−</td>
<td>+</td>
<td>J. Smit</td>
</tr>
<tr>
<td>CB15A KSAC</td>
<td>−</td>
<td>+</td>
<td>J. Smit</td>
</tr>
<tr>
<td>Rmg1</td>
<td>−</td>
<td>+</td>
<td>J. Poindexter</td>
</tr>
<tr>
<td>A-19</td>
<td>+</td>
<td>−</td>
<td>J. Poindexter</td>
</tr>
<tr>
<td>CB15-BE</td>
<td>−</td>
<td>+</td>
<td>J. Poindexter</td>
</tr>
</tbody>
</table>

The age of prey cells affected the growth of strain JSST. When *C. crescentus* CB2A was grown in PYE medium, cells entered late exponential phase/early stationary phase in about 10–12 h. In co-cultures, strain JSST grew well on prey cells grown for 8, 14 and 24 h but, with prey cells grown for 48 h, predation was incomplete. There were always some residual, unattacked prey cells in the co-culture. Therefore, *C. crescentus* CB2A cells were routinely grown for 24 h before use.

Initial observations on the growth of strain JSST were made by phase-contrast light microscopy, at which time the lack of intraperiplasmic growth was noted (Koval & Hynes, 1991). Co-cultures were then examined by transmission electron microscopy. For thin sections, samples were fixed with acrolein (5% v/v) and glutaraldehyde (0.25%, v/v) in 50 mM cacodylate buffer, enrobed in Noble agar and post-fixed with 1% osmium tetroxide and 1% uranyl acetate. After dehydration in an ethanol series, samples were embedded in Spurr resin. Thin sections were post-stained with uranyl acetate and lead citrate. All preparations were examined in a Philips EM300 operating at 60 kV. Predators remained attached to the outside of the prey cell (Fig. 1) and did not enter the periplasmic space. At the attachment site (Fig. S1, available in IJSEM Online), a ‘bulge’ of prey outer membrane formed around the attached end of strain JSST. There was a localized degradation of peptidoglycan, but the electron-dense bilayer of the prey plasma membrane remained intact (Fig. S1b). No bdelloplast-like structures were ever seen in thin sections and the prey cells did not round up after attack by strain JSST. The stalked cells retained their original shape and, at the end of predation, were devoid of cytoplasmic content (Fig. 1b). Strain JSST is thus an example of an epibiotic predator (Davidov et al., 2006).

How do strain JSST cells replicate? No long, aseptate filaments (analogous to those seen inside bdelloplasts) were ever seen on the outside of prey cells by light or electron microscopy. In thin sections (Fig. 1), cells of strain JSST appeared to be dividing by binary fission. For analysis by scanning electron microscopy (SEM), a 20 ml culture of strain JSST was centrifuged, resuspended in 5 ml YP/10 plus Ca\(^{2+}\) medium and added to 2 ml of a 24 h culture of *C. crescentus* CB2A in 18 ml YP/10 plus Ca\(^{2+}\) in a 125 ml side-arm flask. The co-culture was incubated at 30 °C with
The prey range of strain JSST was tested on a panel of prey. JSST divides by binary fission. SEM preparations confirmed the evacuation and collapse of stalked prey cells during predation (Fig. S2b).

To determine the DNA base composition, late-stage co-cultures were filtered (0.45 μm) to remove residual prey cells. DNA isolation was performed using standard methods (Sambrook et al., 1989). The genomic DNA G+C content was determined by thermal denaturation in 1× SSC. The G+C content was calculated using the equation of Mandel et al. (1970) \[ G+Cl=1.99(Tm−66.0) \]. DNA from *Escherichia coli* K-12 and prey-independent *Bdellovibrio bacteriovorus* HI100 was used as reference DNA. The base composition of DNA from strain JSST was 46.1 mol% G+C. The base composition of DNA prepared from *Bdellovibrio bacteriovorus* HI100 was 49.7 mol% G+C. This value compares favourably with the published value of 50.4 mol% G+C (Burnham & Conti, 1984; Williams et al., 2005). The thermal denaturation curve of the DNA preparation from strain JSST gave no indication of contaminating *C. crescentus* DNA (62–67 mol% G+C; data not shown).

Schwudke et al. (2001) proposed that the genetic locus hit (for host interaction) was restricted to *Bdellovibrio bacteriovorus* strains and could be used as a specific probe for this species. Therefore, we screened the genomic DNA of strain JSST for the presence of the hit locus by PCR amplification (according to Schwudke et al., 2001) and Southern blotting (as described by Flannagan et al., 2004) with a DIG-labelled hit locus probe. The hit locus was not identified in strain JSST by either method (data not shown). As positive controls, genomic DNA of *Bdellovibrio bacteriovorus* strains 109J and 6-5-S was screened. As a negative control, genomic DNA of *Bacteriolyticum stolpii* UKi2T was screened. These results support the identification of strain JSST as a member of a novel species of *Bdellovibrio*.

For identification purposes, the 16S rRNA gene of strain JSST was amplified and sequenced in almost its entire length (1432 bp) as described by Jurkevitch et al. (2000). The 16S rRNA gene sequence (Genbank accession no. EF687743) had 93% similarity to that of *Bdellovibrio bacteriovorus* HD100T. Other *Bdellovibrio bacteriovorus* isolates (strains 109J, 114, 127) had similarity values of 90–93% to strain JSST. Therefore, the closest relatives to strain JSST are members of the genus *Bdellovibrio*.
A phylogenetic tree was reconstructed based on 16S rRNA gene sequences. Eleven good-quality, long (>1200 bp), representative cultured 16S rRNA gene sequences from Bdellovibrio strains were downloaded from GenBank on October 2011 and aligned by MUSCLE (Edgar, 2004). The alignment was trimmed at both ends in order for all the sequences to overlap each other fully, and a maximum-likelihood tree was reconstructed using MEGA5 (Tamura et al., 2011), with Bacteriovorax as an outgroup. Our phylogenetic analysis confirmed that strain JSS\textsuperscript{T} is a member of the class Deltaproteobacteria and that it belongs to the \textit{Bdellovibrio} cluster (Fig. 2). It is distantly related to \textit{Bdellovibrio bacteriovorus} strains, though not as distant as isolate TRA2. A more extensive phylogenetic analysis (not shown) was undertaken using all 16S good-quality, long \textit{Bdellovibrio} 16S rRNA gene sequences available at the RDP-II database, from both cultured and environmental samples. This phylogenetic tree confirmed the position of strain JSS\textsuperscript{T} in the \textit{Bdellovibrio} lineage, and also revealed an interesting observation: the \textit{Bdellovibrio} sequences split into two major clusters, one encompassing all the cultured strains alongside some sequences from uncultured organisms and another composed solely of sequences from uncultured bacteria. This suggests that many groups in this latter cluster may be very different from the ‘classic’ \textit{Bdellovibrio}, thus providing ample opportunity for further study of the diversity of this genus.

Since the report of strain JSS\textsuperscript{T} by Koval & Hynes (1991), more BALOs have been isolated on lawns of \textit{C. crescentus} CB2A, this time from another sewage treatment plant in London, Ontario, Canada, and from compost samples. These strains (KL1 to 8) had similar properties to strain JSS\textsuperscript{T}: extracellular attachment, no bdelloplast formation and no lysis of \textit{Escherichia coli} ML35 (Shemesh et al., 2003). The partial sequence of the 16S rRNA gene of strain KL8 (GenBank accession no. JQ080535) showed 99% similarity to the 16S rRNA gene sequence of strain JSS\textsuperscript{T}.

A summary of the phenotypic characteristics of strain JSS\textsuperscript{T} and \textit{Bdellovibrio bacteriovorus} HD100\textsuperscript{T} is provided in Table 2. Strain JSS\textsuperscript{T} lacks an intracellular, periplasmic growth phase, and no bdelloplast is formed during the life cycle. The prey range, as studied so far, is limited to \textit{C. crescentus}. Additional chemotaxonomic data would be useful to support this proposal for a novel species of \textit{Bdellovibrio}. However, these analyses need to be done with prey-independent mutants of predators, a rationale stated by Schwudke et al. (2001). The presence of remaining prey cells in a co-culture necessitates their separation from predators by filtration or differential centrifugation. This is not an easy task, especially on a large scale. Caution would have to be exercised in interpretation of chemotaxonomic data from prey-independent mutants, as the chemical composition of mutants may not be the same as that of the wild-type strain. Furthermore, analyses of properties such as fatty acid composition need to be conducted under standardized conditions, as the results vary with experimental conditions (temperature, growth stage, growth medium). For BALOs, the chemical composition of cells may also vary between the attack and growth phases.

Strain JSS\textsuperscript{T} differs from \textit{Bdellovibrio bacteriovorus} as it does not demonstrate a periplasmic growth stage or form bdelloplasts. Strain JSS\textsuperscript{T} therefore represents a novel species, for which the name \textit{Bdellovibrio exovorus} sp. nov. is proposed.

**Description of \textit{Bdellovibrio exovorus} sp. nov.**

\textit{Bdellovibrio exovorus} (ex.o.vo’rus. Gr. pref. exo- outside; L. v. vorare to devour, to consume; L. suff. -vorus eating; N.L. masc. adj. exovorus eating outside, referring to the epibiotic life cycle).

Gram-negative, comma-shaped rods (0.5 \(\mu\)m wide, 0.5–1.4 \(\mu\)m long) with a single, polar, sheathed flagellum (29 \(\mu\)m wide). Obligate predator; the type strain was isolated from sewage in enrichment cultures with \textit{Caulobacter crescentus} CB2A. Does not prey on \textit{Escherichia coli}. Cells exhibit a biphasic life cycle: a free swimming attack phase and a growth phase whereby the predator attaches to and remains on the outside of the prey cell. There is no periplasmic stage within the prey cell. No bdelloplast is formed. Empty stalked \textit{C. crescentus} cells remain after predation is complete. Small plaques are formed on lawns.

**Table 2. Phenotypic characteristics of strain JSS\textsuperscript{T} and \textit{Bdellovibrio bacteriovorus} HD100\textsuperscript{T}**

Both strains form vibroid cells with a single, polar, sheathed flagellum and both strains form plaques.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Strain JSS\textsuperscript{T}</th>
<th>\textit{B. bacteriovorus} HD100\textsuperscript{T}</th>
</tr>
</thead>
<tbody>
<tr>
<td>Width of flagellum</td>
<td>29</td>
<td>28</td>
</tr>
<tr>
<td>Intracellular growth</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>Bdelloplast formation</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>Prey range</td>
<td>\textit{Caulobacter}</td>
<td>Wide</td>
</tr>
</tbody>
</table>
of prey cells. Growth is by binary fission while attached to the prey cell. On the basis of 16S rRNA gene sequence similarity, belongs to the class Deltaproteobacteria, related to *Bdellovibrio bacteriovorus* (93% similarity). Differs from *Bdellovibrio bacteriovorus* as it does not demonstrate a periplasmic growth stage or form bdelloplasts.

The type strain, JSST (=ATCC BAA-2330 =DSM 25223T), was isolated from sewage in enrichment cultures with *Caulobacter crescentus* CB2A. Similar isolates were obtained from compost and soil. The DNA G+C content of the type strain is 46.1 mol%.

### Acknowledgements

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