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(Article begins on next page)
Sigma E Regulators Control Hemolytic Activity and Virulence in a Shrimp Pathogenic Vibrio harveyi

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Abstract

Members of the genus Vibrio are important marine and aquaculture pathogens. Hemolytic activity has been identified as a virulence factor in many pathogenic vibrios including V. cholerae, V. parahaemolyticus, V. alginolyticus, V. harveyi and V. vulnificus. We have used transposon mutagenesis to identify genes involved in the hemolytic activity of shrimp-pathogenic V. harveyi strain PSU3316. Out of 1,764 mutants screened, five mutants showed reduced hemolytic activity on sheep blood agar and exhibited virulence attenuation in shrimp (Litopenaeus vannamei). Mutants were identified by comparing transposon junction sequences to a draft of assembly of the PSU3316 genome. Surprisingly none of the disrupted open reading frames or gene neighborhoods contained genes annotated as hemolysins. The gene encoding RsEB, a negative regulator of the sigma factor (σE), was interrupted in 2 out of 5 transposon mutants, in addition, the transcription factor CytR, a threonine synthetase, and an efflux-associated cytoplasmic protein were also identified. Knockout mutations introduced into the rpoE operon at the rsEB gene exhibited low hemolytic activity in sheep blood agar, and were 3-to 7-fold attenuated for colonization in shrimp. Comparison of whole cell extracted proteins in the rsEB mutant (PSU4030) to the wild-type by 2-D gel electrophoresis revealed 6 differentially expressed proteins, including two down-regulated porins (OmpC-like and OmpN) and an upregulated protease (DegQ) which have been associated with σE in other organisms. Our study is the first report linking hemolytic activity to the σE regulators in pathogenic Vibrio species and suggests expression of this virulence-linked phenotype is governed by multiple regulatory pathways within the V. harveyi.

Introduction

Vibrio harveyi is one of several closely-related species of Vibrio that cause disease in marine organisms [1–3]. Outbreaks of highly virulent Vibrio strains have caused major losses to shrimp farmers in Thailand and elsewhere [4–8]. The mechanisms of pathogenesis in these vibrios are not clearly understood and are likely mediated in part by strain-specific virulence factors. Hemolytic activity has been linked to virulence in many species of Vibrio where several different classes of hemolysins have been described. The V. harveyi hemolysin (VHH) is a member of the broadly distributed thermostable hemolysin (TLH) family [9–12] and appears to be sufficient for hemolytic activity in some, but not all, strains of V. harveyi [12,13]. We have previously determined that the vhh gene is present in all V. harveyi isolates from both healthy and diseased marine animals collected in Southern Thailand [14]. However, hemolytic activity on blood agar was variable in the vhh bearing isolates, suggesting that hemolytic activity is influenced by additional factors.

In order to better understand mediators of hemolytic activity and virulence in V. harveyi we have investigated genes that control hemolytic activity in the shrimp-virulent V. harveyi strain PSU3316. Results of an initial transposon screen led us to hypothesize that regulators of the cell envelope stress sigma factor RpoE control the elaboration of V. harveyi hemolytic activity and that this phenotype correlates with virulence in shrimp. Recent work in Vibrio vulnificus has revealed that the regulatory network of RpoE controls virulence in a mouse model [15]. To investigate whether the RpoE-operon regulatory proteins mediate the virulence of V. harveyi we have carried out targeted mutagenesis, in vitro and in vivo activity assays, and proteomic analysis to identify genes differentially expressed in wild-type and non-hemolytic mutants. Surprisingly, none of the differentially regulated proteins or gene products of loci inactivated in hemolysis-attenuated transposon mutants were similar to known hemolysins. These results suggest that hemolysis activity per se may be a phenotype that is influenced by a variety of different factors including the RpoE-operon mediated cell envelope stress response of V. harveyi.

Materials and Methods

Bacterial strains and plasmids

All bacterial strains and plasmids used in this study are listed in Table 1. V. harveyi PSU3316 was isolated in 2004 from the...
hemolymph of a diseased shrimp (*Penaeus monodon*) in Southern Thailand, and an early passage of this strain was archived in glycerol at −80°C. PSU3316 was identified as being most similar to type strains of *V. harveyi* by biochemical testing, genome sequencing, and phylogenetic analysis of the gyrB gene [16]. Although the systematics of the *V. harveyi-*group is subject to debate based on emerging genomic data we have chosen to retain the original designation pending official taxonomic revision of type strains. PSU3354 is a spontaneous streptomycin-resistant (SmR) derivative of PSU3316. Confirmation of virulence of *V. harveyi* PSU3316 and PSU3354 was performed by determining the LD$_{50}$ of each strain in shrimp (*P. monodon*) and through a competition assay involving co-infection of these strains and measurement of hepatopancreas colonization levels. All strains were maintained in 20% glycerol at −80°C.

Media and growth conditions

*Vibrio* strains were grown at 30°C on Luria-Bertani medium (LB) or Tryptic Soy Broth (TSB) containing 1% or 1.5% NaCl. When required, chloramphenicol (Cm) (2 μg mL$^{-1}$) or streptomycin (Sm) (200 μg mL$^{-1}$) was added into broth or agar. *Echerichia coli* DH5α::kpm and BW20767::kpm were grown at 30°C for 6 h followed by selection of SmR harboring rseB from PSU3345 cloned into the XbaI site. PSU3316 was identified as being most similar to type strains of *V. harveyi* by biochemical testing, genome sequencing, and phylogenetic analysis of the gyrB gene [16]. Although the systematics of the *V. harveyi-*group is subject to debate based on emerging genomic data we have chosen to retain the original designation pending official taxonomic revision of type strains. PSU3354 is a spontaneous streptomycin-resistant (SmR) derivative of PSU3316. Confirmation of virulence of *V. harveyi* PSU3316 and PSU3354 was performed by determining the LD$_{50}$ of each strain in shrimp (*P. monodon*) and through a competition assay involving co-infection of these strains and measurement of hepatopancreas colonization levels. All strains were maintained in 20% glycerol at −80°C.

Sequencing and draft assembly of the PSU3316 genome

Libraries suitable for sequencing using the Illumina Genome Analyzer (Illumina, Inc.) were generated using a modified version of the standard Illumina GA protocol. 5 μg of genomic DNA from strain PSU3316 was sheared using Adaptive Focused Acoustic technology (Covaris, Inc.) to generate fragments 100–300 bp in length. Fragments were blunt-ended, A-tailed and ligated with T nucleotide overhang Illumina forked paired end-sequencing adapters (Illumina, Inc.) containing custom bar-codes for multiplex sequencing. Libraries were then PCR amplified for 16 cycles after identifying the optimum number of cycles using qPCR, sequenced to a depth of ~6× and assembled into contigs using CLC Genomics Workbench 4 (Aarhus, Denmark). Genome fragments were uploaded to the Rapid Annotations using Subsystems Technology (RAST) server for annotation [17]. Genome regions containing open reading frames for genes and proteins identified in this study have been deposited at NCBI with accessions XXX-YYY (to be provided with final submission).

Transposon mutagenesis of *V. harveyi*

The mariner-based transposon pSC189 (KmR) [18] containing a kanamycin resistance gene was modified by insertion of a chloramphenicol marker into the Psl restriction site to obtain pJT064. This plasmid carries a transposon fragment which was designated as TnJT064. pJT064 was transformed into competent *E. coli* BW20767 [19]. Conjugation of *E. coli* donor strain and *V. harveyi* PSU3316 was performed by mixing each strain at ratio of 1:1 on LB plates supplemented with 1% NaCl and incubation at 30°C for 6 h followed by selection of *V. harveyi* mutants carrying TnJT064 insertions on *Vibrio*-selective Thiosulfate citrate bile salt-sucrose agar (TCBS) containing chloramphenicol (2 μg mL$^{-1}$).

Screening transposon insertion mutants for hemolytic activity and shrimp virulence

TnJT064 transposon insertion mutants were screened for hemolytic activity by spotting cultures on sheep blood agar (PMI Microbiologicals, USA) and then scoring for the appearance of a lytic zone after incubation at 30°C for 48 h. Wild type *V. harveyi* PSU3316 and its streptomycin resistant derivative PSU3345 are β-hemolytic in this assay and any mutant that caused incomplete hemolysis (defined here as α-hemolysis) were subjected to a second screen for virulence in shrimp. Cells grown overnight in TSB were harvested by centrifugation, washed, and suspended in a sterile saline solution. Shrimp were challenged by intramuscular injection of a 100 μl of saline suspensions of approximately 2.4 × 10$^{6}$ CFU (corresponding to four times LD$_{50}$ for wild-type PSU3316), of either selected transposon mutants, PSU3316, PSU3345, or sterile saline (mock infection control). The challenge experiment was repeated twice, first with three shrimp per challenge followed by a second experiment with seven shrimp per challenge. Differences in mortality after 18 h in wild-type strains (PSU3316 and PSU3345) and mutant strains with attenuated hemolysis were evaluated using the Fisher’s exact test. Relative risk (RR) of mortality compared with the wild type-strain was also determined for each mutant.
Characterization of genes involved in hemolytic activity

The identity of genes disrupted in hemolysis- and virulence-attenuated mutants was determined by PCR amplification and sequencing of the transposon insertion junctions using primers targeting outward facing priming sites in the Tn7T064 transposon (Mar2018 and MarEC6) and arbitrary primers ARB6/7 and ARB2 which bind throughout the genome [20]. Nucleotide sequences from transposon insertion junctions were compared to the PSU3316 genome by BLAST and identified based on annotation of the corresponding open reading frames disrupted by the transposon insertion.

rseBC disruption

A spontaneous streptomycin resistant V. harveyi PSU3316 (designated as PSU3545) was used as the parental strain in the construction of two independent insertions in the rseB gene by homologous recombination-based gene disruption [21] which is expected to also inactivate the downstream gene rseC. PCR amplification of inserts for gene disruption was performed using specific primers designed in this study (Table 2). The PCR products were cloned into pJF084 (a derivative of suicide plasmid pDTR901 which carries the R6K origin of replication , the RP4 mob region, the smB gene for sucrose-based counter selection from pCVD422 [22] modified by removal of the bla gene encoding ampicillin resistance by partial PsiI digestion (NEB) and addition of a chloramphenicol acetyltransferase (cat gene for chloramphenicol resistance), transformed into E. coli BW20767/kpiR and conjugated with PSU3545. V. harveyi mutants containing gene disruptions were selected on TCBS containing chloramphenicol (2 μg mL−1) and streptomycin (200 μg mL−1).

Quantification of hemolytic activity

Hemolytic activity expressed by rseBC mutant and wild-type strains on solid media was visualized using a standard sheep blood agar assay [23,24]. Cell-associated hemolytic activity was quantified as the percentage of red blood cells lysed in liquid suspension assay. In brief, bacterial strains were grown 18 h at 30 °C in LB agar containing 1.5% NaCl.

Immobiline Drystrip (IPG gel strip) and was transferred to Quant Kit (GE Healthcare). The test sample was then applied to concentration of protein was determined using PlusOne 2-D manufacturer's protocol (GE Healthcare). Briefly, tested samples were cleaned by 2D clean-Up Kits (GE Healthcare) and the were kept at C until required.

Table 2. Nucleotide sequences of PCR primers for gene disruption mutagenesis.

<table>
<thead>
<tr>
<th>Primers</th>
<th>Primer sequence 5′ → 3′</th>
<th>Product size (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>rseA-F1676 rseB-R2903</td>
<td>CATGGTCTCTAGATAGAGCAAGACCAGGACGCTGCTGCTGTAGACACCACTACATCCGAGTTACTG</td>
<td>1228</td>
</tr>
<tr>
<td>rseB-F2410 rseB-R2925</td>
<td>CATGGTCTCTAGATAGAGCAAGACCAGGACGCTGCTGCTGTAGACACCACTACATCCGAGTTACTG</td>
<td>516</td>
</tr>
</tbody>
</table>

doi:10.1371/journal.pone.0032523.t002

Growth and competition assays during shrimp infections

Growth rates of V. harveyi rseBC mutants (PSU4030 and PSU4031) were compared to the wild-type strain PSU3545. Strains were grown in LB broth containing 1.5% NaCl for 16 h at 30 °C and growth was quantified by optical density at 600 nm every 60 min. Colony morphologies were observed on sheep blood agar. The competitive index (CI) of mutant strains was determined in vivo using juvenile L. vannamei shrimp (10 to 13 g with a length of 4 to 5 inches). Shrimp were obtained from a farm in Pattani province, Thailand, and were maintained in a 70 L glass tank containing artificial seawater (salinity 17 ppt) at a temperature of 29±1 °C for at least 7 days before testing. For competition assays, cell suspensions of wild-type PSU3545 (CmS SmR) and a mutant strain (CmR SmR) were mixed at a ratio of 1:1 in sterile saline and then approximately 1×10⁶ CFU were injected intramuscularly into each shrimp. Each competition was performed in duplicate using 7 shrimp per group. Approximately 18 h post infection, the hepatopancreas of each infected shrimp was removed, homogenized, and the proportion of V. harveyi parental and mutant strains determined by plating on TCBS supplemented with streptomycin. After colonies were recovered several hundred were picked on to TCBS supplemented with chloramphenicol and streptomycin to determine the ratio of PSU3545 (CmS SmR) to either PSU4030 and PSU4031 (CmR SmR).

The CI was calculated as follows: CI = (number of mutant CFU/number of wild type CFU isolated from hepatopancreas)/(number of mutant CFU/number of wild type CFU in injected cell suspension). A CI of less than 1 indicates the ability of the mutant strain to infect shrimp is lower than the wild type. Statistical analysis of results obtained from competition assays were evaluated by the Mann-Whitney U test [25,26].

Characterization of whole cell proteins from rseBC mutant

Protein extracts of rseBC mutant (PSU4030) and wild-type V. harveyi (PSU3545) were investigated to identify differentially expressed proteins that may mediate hemolytic activity. Strains were grown on sheep blood agar at 30 °C for 24 h. Whole-cell protein extracts were prepared by suspending bacterial cells in 1 mL phosphate-buffered saline (PBS). Cells were washed three times with PBS. The cell pellets were then resuspended in lysis buffer (7 M Urea, 2 M Thiourea, 4% CHAPS, 2% Pharmalyte 4–7, 40 mM DTT) and incubated at 4 °C for 6 h. The supernatant was collected by centrifugation at 14,000×g for 5 min at 4 °C and was kept at −70 °C until required.

2-D gel electrophoresis was performed according to the manufacturer’s protocol (GE Healthcare). Briefly, tested samples were cleaned by 2D clean-Up Kits (GE Healthcare) and the concentration of protein was determined using PlusOne 2-D Quant Kit (GE Healthcare). The test sample was then applied to Immobiline Drystrip (IPG gel strip) and was transferred to
IPGhor system (GE Healthcare). Isoelectric focusing (IEF) was conducted in the first dimension at 300 V for 0.30 h, 1000 V for 0.30 h, 5000 V for 1.20 h, and then 5000 V for 0.25 h. (total 6.5 kVh). After IEF, the IPG gel strips were equilibrated in sodium dodecyl sulfate (SDS) equilibration buffer (6 M Urea, 75 mM Tris-HCl (pH 8.8), 29.3% glycerol, 2% SDS, 0.002% bromophenol blue) containing 1% DTT for 15 min followed by a further 15-min incubation in the same buffer containing 2.5% iodoacetamide. The strips were transferred onto 12.5% Tris-glycine SDS polyacrylamide gel and subjected to SDS-polyacrylamide gel electrophoresis as the second dimension. Electrophoresis was performed with miniVE electrophoresis system (Amersham Bioscience AB, Sweden) with an initial constant current of 10 mA/gel for 15 min followed by 20 mA/gel. Proteins were visualized by staining with Coomassie Brilliant Blue R250, which is compatible with subsequent mass spectrometry-based protein identification. Gels were scanned by ImageScanner and the protein spots were analyzed using an ImageMaster 2D Platinum (Amersham Bioscience AB, Sweden). The experiment was performed in duplicate. Differentially expressed proteins from mutant and wild type were analyzed by nano liquid chromatography–electrospray ionisation tandem mass spectrometry (nano LC–ESI-MS/MS). Proteins were identified using MS/MS ion search of the Mascot search engine (Matrix Science, London, UK) and nonredundant protein databases (NCBInr; National Center for Biotechnology Information, Bethesda, MD, USA) with the

### Table 3. Transposon mutants with reduced hemolytic activity on sheep blood agar.

<table>
<thead>
<tr>
<th>Mutants</th>
<th>ORF Annotation in PSU3316 genome*</th>
<th>Homologous ORF in reference genome BAA-1116</th>
<th>E valueb</th>
<th>Mortality in shrimpc,d (#dead/total)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. EG6</td>
<td>DNA-binding transcriptional regulator CytR</td>
<td>VIBHAR00726</td>
<td>0</td>
<td>1/3 and 2/7</td>
</tr>
<tr>
<td>2. EH12</td>
<td>Putative cytoplasmic protein, probably associated with Gluthathione-regulated potassium-efflux</td>
<td>VIBHAR00067</td>
<td>1E-91</td>
<td>1/3 and 2/7</td>
</tr>
<tr>
<td>3. FH3</td>
<td>σ factor regulatory protein RseB</td>
<td>VIBHAR03540</td>
<td>0</td>
<td>1/3 and 1/7</td>
</tr>
<tr>
<td>4. GG7</td>
<td>σ factor regulatory protein RseB</td>
<td>VIBHAR03540</td>
<td>0</td>
<td>1/3 and 2/7</td>
</tr>
<tr>
<td>5. FD6</td>
<td>Threonine synthetase</td>
<td>VIBHAR00941</td>
<td>0</td>
<td>2/3 and 2/7</td>
</tr>
</tbody>
</table>

*aBased on Rapid Annotation using Subsystem Technology (RAST) of de novo assembled genome fragments from PSU3316.

bE values determined using NCBI BLASTN using the full open reading frame of PSU3316.

cControl challenges with wild-type PSU3316 or transposant mutants with wild-type hemolysis activity exhibited mortality of 100% at the challenge dose.

dHemolysis attenuated mutants exhibited variable mortality that was statistically different from wild-type as evaluated by Fisher’s exact test (p<0.05).

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Figure 1. V. harveyi PSU3316 genome regions containing sites interrupted and the flanking open reading frames. Each region (A–D) was interrupted by transposon or targeted mutagenesis (orange stars). The corresponding full contigs from the draft genome assembly have been deposited at NCBI.

doi:10.1371/journal.pone.0032523.g001
following parameters; taxonomy: other proteobacteria; fixed modifications: cysteine carbamidomethylation; variable modifications; methionine oxidation, three missed cleavages allowed, peptide tolerance of 1.2 Da, and MS/MS tolerance of 0.6 Da. The identification of proteins was based on the Probability-Based MOWSE (molecular weight search) scores, whereby individual ion scores of greater than 53 indicates significant identities (p<0.05).

Results

Transposon mutagenesis of *V. harveyi* and screen for hemolysis and virulence

Using the mariner-based transposon mutagenesis, 1,764 *V. harveyi* PSU3316 mutants were generated and screened for a loss of hemolytic activity on sheep blood agar. Five mutants displayed low hemolytic activity (Table 3) and were subsequently screened for virulence in shrimp at a dose of four times the LD₅₀ of the wild-type strain (2.4×10⁶ CFU shrimp⁻¹). This dose of wild-type *V. harveyi* PSU3316 (or PSU3545, see below) consistently resulted in 100% shrimp mortality. Hemolysis attenuated mutants exhibited lower rates of mortality (Fisher’s exact test p<0.05) where the relative risk of mortality of mutant strains was 2.5 to 5-fold less than wild-type. Other randomly chosen transposon mutants without disruption of the hemolysis phenotype were not attenuated for virulence (data not shown), indicating that the acquisition of the transposon per se is not associated with reduced shrimp virulence. Shrimp infected with *V. harveyi* exhibited characteristic disease symptoms including lethargy, and upon dissection, their hepatopancreas appeared discolored.

The DNA sequences corresponding to the junction of transposon insertions were determined for the attenuated *V. harveyi* mutants. Annotation of sequences adjacent to the transposon insertions were not associated with reduced shrimp virulence (data not shown), indicating that the acquisition of the transposon per se is not associated with reduced shrimp virulence. Shrimp infected with *V. harveyi* exhibited characteristic disease symptoms including lethargy, and upon dissection, their hepatopancreas appeared discolored.

The DNA sequences corresponding to the junction of transposon insertions were determined for the attenuated *V. harveyi* mutants. Annotation of sequences adjacent to the transposon insertion sites revealed that 2 hemolysis-attenuated mutants (designated as FH3 and GG7) carried insertions that disrupted the gene encoding the G₄ factor negative regulatory protein (RseB) (Table 3 & Figure 1A). The other mutants carried insertions that interrupted genes encoding putative proteins annotated as a transcriptional repressor cytR, a threonine synthase, and a hypothetical protein in the kspC operon associated with glutathione-regulated potassium-efflux (Table 3 & Figure 1B, C, D). These genes were also present in the genomes of closely-related strains (i.e. *V. harveyi* BAA-1116, *V. harveyi* HY01, and *V. parahaemolyticus* RIMD 2210633). Analysis of neighboring genes on contigs assembled from the *V. harveyi* PSU3316 genome and in

![Figure 2. Growth of *V. harveyi* in LB broth with 1.5% NaCl, pH 7.5 at 30°C.](https://www.plosone.org/figure/2)

![Figure 3. Hemolytic activity of wild type and mutants strains of *V. harveyi* on sheep blood agar.](https://www.plosone.org/figure/3)

![Figure 4. Percent hemolytic activity of *V. harveyi* wild type PSU3545 and *rseBC* mutants relative to controls.](https://www.plosone.org/figure/4)
In vivo competition assays

The virulence of *V. harveyi* rseBC mutants (PSU4030 and PSU4031) was evaluated by quantification of shrimp colonization relative to wild-type *V. harveyi* (PSU3545). The competitive indexes (CI) for rseBC mutants PSU4030 and PSU4031 against the wild type were determined to be 0.15 and 0.31, respectively (Figure 5) indicating three to seven-fold reduction in the ability of either rseBC mutant to colonize shrimp relative to the wild-type strain.

Comparative analysis and identification of proteins using 2D gel electrophoresis

Two-dimensional protein gel electrophoresis revealed 6 proteins that were differentially expressed in the rseBC mutant (PSU4030) compared to the wild-type *V. harveyi* (PSU3545). These proteins were analyzed by nano LC-ESI-MS/MS and five proteins could be identified with significant identity (*p* < 0.05) to proteins in the NCBInr database. In the non-hemolytic *V. harveyi* rseBC mutant, three proteins were significantly under-expressed (Figure 6-A, spots 1, 2, 3) corresponding to two outer membrane porins (OmpC-like and OmpN) and an unidentified protein (Figure 7-A, B; Table 4). Expression of three proteins was elevated in the rseBC mutant relative to the wild type (Figure 6-B, spots 4, 5, 6) corresponding to a phosphosugar mutase, S-(hydroxymethyl) glutathione dehydrogenase, and the protease (DegQ) (Figure 7 C, D, E & Table 4).

Discussion

In the present study transposon and targeted insertion mutagenesis of *V. harveyi* PSU3316 revealed that disruption of regulatory elements in the rpoE operon modulate hemolytic activity and the ability of this pathogenic organism to colonize shrimp. The ability to lyse blood cells is an important virulence factor for *V. harveyi* [12] and other microbial pathogens [28] however modulation of hemolysis by the activity of RpoE operon regulatory proteins was previously unknown. In *E. coli* the σE operon contains the gene for the sigma(E) factor (rpoE) as well as the regulator elements rseA, rseB and rseC which are co-transcribed by a promoter upstream of the rpoE gene [29]. RseA and RseB are transmembrane and periplasmic negative regulatory proteins while RseC is a positive regulatory protein [30,31]. Genome sequencing and draft assembly revealed an identical rpoE-rseABC operon structure in *V. harveyi* PSU3316 (Figure 1A). RpoE has been implicated in virulence as well as adaptive responses for survival in natural habitats [30,32–35] and in Gram negative bacteria, stressors trigger accumulation of unfolded- or misfolded-proteins in the periplasm, and this in turn activates σE through RseA and RseB signal transduction [36,37]. In *E. coli* the transcription factor encoded by *rpoE* (σE) becomes more active when rseB is disrupted leading to increased transcription of σE.
dependent genes [27]. In *V. vulnificus* *rseB* mutants are attenuated for virulence in a mouse model through putative modulation of *rpoE* activity [15]. If regulation of the *rpoE* operon in *V. harveyi* is the same as in *E. coli* and as proposed for *V. vulnificus*, then the attenuated virulence phenotypes associated with the *V. harveyi* *rseBC* mutants may be due to changes in activity of RpoE due to relief of regulatory control by RseB or RseC. Studies in *E. coli* suggest deletion of the negative regulator *rseB* induces RpoE activity while deletion of the positive regulator *rseC* has a negligible effect [27,30]. In *E. coli* the double mutant (*rseBC*) either has a net inducing effect on RpoE activity similar to a *rseB* deletion mutant (in the case of a transposon insertion in *rseB* with expected polar effects on *rseC*) [27] or revealed less induction of RpoE activity than the single *rseB* deletion mutant (in the case of a double deletion mutant in both *rseB* and *rseC*) suggesting competing effects of negative and positive regulation by RseB and RseC respectively on RpoE activity [30]. In *V. harveyi*, if the activity of RseB is dominant to that of RseC then elevated RpoE activity in the *rseB* gene-disruption mutants would be responsible for alterations in protein expression that are negatively correlated with hemolysis and virulence. Alternatively, our transposon and plasmid insertions in *rseB* may have had a polar effect on expression of the downstream RpoE positive regulatory gene *rseC*. In the latter case, inactivation of either *rpoE* or *rseC* would be predicted to produce the same phenotype as such postulated polar *rseB* insertion mutations. Unfortunately we were not successful in making mutations in the *rpoE* region other than in *rseB* and it is possible that *rpoE* is an essential gene in *V. harveyi*. In addition, we were unable to select for in-frame deletions of *rseB* using sucrose- or streptomycin-based counter selection via the sacB or rpsL genes, respectively, due to the limited genetic tractability of this shrimp pathogenic *V. harveyi* strain. Additional genetic analysis (including the construction of double mutants in *rseB* together with *rseC* or *rpoE* and complementation with each gene) will be needed to resolve these two possible models for the phenotype associated with *rseB* insertion mutations.

Figure 7. Contigs from the PSU3316 genome draft assembly bearing genes for differentially expressed proteins (A–E) in the *rseBC* mutant PSU4030 (spots 2 to 6, respectively). Peptide sequences from differentially expressed proteins were identified by mass spectrometry. doi:10.1371/journal.pone.0032523.g007

Regulatory Control of *V. harveyi* Virulence
To shed light on how disruption of the RpoE operon at the rseB gene controls virulence, we used proteome analysis to determine whether any protein level changes could be distinguished between non-hemolytic (rseBC mutant) and wild-type V. harveyi grown on sheep blood agar. We found that two outer membrane porins (OmpN- and OmpC-like) and an additional unidentified protein were decreased in the rseBC mutant relative to the wild-type (Table 4). This observation is consistent with down-regulation of OmpN during enhanced expression of σE in E. coli [38]. Several porins are established components of the RpoE regulon, controlling transport of solutes through the outer membrane and modulating the periplasmic environment [39]. Our data show that reduced porin expression and reduced hemolytic activity are both linked to disruption of the RpoE operon at the rseB gene in V. harveyi and characterization of these proteins and their potential involvement in RpoE-regulated virulence of V. harveyi will be a priority for future work in this system.

We also observed that three proteins were over-expressed in the rseBC mutant relative to the wild type. These proteins are a phosphosugar mutase, a S-(hydroxymethyl)glutathione dehydrogenase, and the DegQ protease which is homologous, and shares overlapping function with DegP [40,41], a positively regulated member of the tpoE regulon in E. coli [42]. RpoE-directed regulation of DegQ in fish pathogenic V. harveyi has been suggested recently [41] and our data supports this model. It should be noted that differentially expressed RpoE, RseA, RseB, and RseC were not detected during proteomic analysis because the theoretical molecular weight of RpoE, RseA and RseC proteins were less than 30 kDa (21.7, 23.5 kDa, and 16.6 kDa respectively) and the theoretical pI of RseB was more than 7 (pI = 8.6) which were out of molecular weight and pI ranges respectively) and the theoretical pI of RseB was more than 7 (pI = 8.6) which were out of molecular weight and pI ranges respectively. The obtained peptides had ion scores of greater than 53 indicating significant identities (p < 0.05).

### Table 4. Summary of MS/MS data for protein spots showing altered expression levels on 2-D gels for wild-type and rseBC mutant cell extracts.

<table>
<thead>
<tr>
<th>Spot no.</th>
<th>Predicted product in PSU3316b</th>
<th>Homolog in reference genome BAA-1116 (E valuec)</th>
<th>Identified peptides</th>
<th>Ion scored</th>
<th>Theoretical p/ MW (kDa)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Unidentified</td>
<td>NA*</td>
<td>NA*</td>
<td>NA*</td>
<td>MW (kDa)</td>
</tr>
<tr>
<td>2</td>
<td>Outer membrane protein N, non-specific porin (ompN)</td>
<td>VIBHAR06284 (0.0)</td>
<td>IGYYNQGDIQANFVGK</td>
<td>109</td>
<td>4.53/37.80</td>
</tr>
<tr>
<td>3</td>
<td>Outer membrane protein C precursor (ompC)</td>
<td>VIBHAR06741 (3e-47)</td>
<td>LGYGATHDQYGR</td>
<td>83</td>
<td>4.40/36.29</td>
</tr>
<tr>
<td>4</td>
<td>Phosphosugar mutase of unknown sugar</td>
<td>VIBHAR06273 (0.0)</td>
<td>GVVGYDGRPDKS VKAPWAFGVR</td>
<td>134</td>
<td>5.03/62.03</td>
</tr>
<tr>
<td>5</td>
<td>S-(hydroxymethyl) glutathione dehydrogenase</td>
<td>VIBHAR06925 (0.0)</td>
<td>SELPEIVNR</td>
<td>55</td>
<td>5.17/41.38</td>
</tr>
<tr>
<td>6</td>
<td>Outer membrane stress sensor protease DegQ, serine protease</td>
<td>VIBHAR00878 (0.0)</td>
<td>VTPAVSIAVEGK GLGSGVIDAK GAFYSQWPSADA DK ADTFSER ITLIR VI TSVTVLR</td>
<td>538</td>
<td>5.88/48.03</td>
</tr>
</tbody>
</table>

*Spot no. corresponds to region of stained gel in Figure 6. Spots 1–3 were under-expressed and spots 4–6 were over-expressed in the rseBC mutant relative to WT.

bBased on Rapid Annotation using Subsystem Technology (RAST) of de novo assembled genome fragments, or by homology to reference genome BAA-1116.

cE values determined using NCBI BLASTN using full open reading frame in PSU3316.

dIndividual ion scores of greater than 53 indicates significant identities (p < 0.05).
References


