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A pandemic *Vibrio parahaemolyticus* O3:K6 clone causing most associated diarrhea cases in the Pacific Northwest coast of Mexico

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Between September and October of 2004, more than 1230 cases of gastroenteritis due to pandemic O3:K6 strains of *Vibrio parahaemolyticus* (*V. parahaemolyticus*) were reported in the relatively small geographical area of Southern Sinaloa, a state located in Northwest Mexico. Since then, *V. parahaemolyticus*-associated gastroenteritis cases have gradually increased in prevalence spreading from south to north. The present study conducted an epidemiological surveillance of *V. parahaemolyticus* strains in both environmental and clinical samples along the Pacific coast of Sinaloa from 2011 to 2013. The genetic relatedness, serotype dominance and antibiotic resistance of isolates were investigated. A total of 46 strains were isolated from environmental samples (e.g., sediment, seawater and shrimp), whereas 249 strains were obtained from stools of patients with gastroenteritis. Nine different O serogroups and 16 serovars were identified. Serovars O3:K6 and O6:K46 were identified in both environmental and clinical strains. Whereas most environmental isolates carried the *tdh* gene (71.74%, 33/46), only three (6.52%) belonged to pandemic clones (O3:K6, O3:KUT and OUT:KUT). In contrast, 81.1% (202/249) of clinical isolates belonged to pandemic serotypes, with O3:K6 (*tdh*, toxRS/new, and/or *orf8*) representing the predominant serovar (97%, 196/202). This prevalence of pathogenic (*tdh* and/or *trh* positive) and O3:K6 pandemic *V. parahaemolyticus* isolates in this study were similar to those found from 2004 to 2010. As investigated by REP-PCR, genetic lineages of selected O3:K6 strains isolated in this study and some isolated earlier were nearly identical. Antimicrobial susceptibility testing showed that most strains (93.8%) were resistant to ampicillin but sensitive to chloramphenicol (98.8%). Multidrug resistance significantly increased from 8.6% (2004–2010) to 22.93% (2011–2013; *p* < 0.05). Our data indicate that pandemic O3:K6 clone has endemically established in the Pacific Coast of Mexico.

**Keywords:** serologic, isolation, *Vibrio parahaemolyticus*, biosurveillance, public health
Introduction

*Vibrio parahaemolyticus* is a Gram stain-negative bacterium autochthonous of marine and estuarine environments worldwide (Kaneo and Colwell, 1973, 1978; Joseph et al., 1982). While the majority of environmental strains are innocuous members of the marine microbiota, small subpopulations are opportunistic pathogens of humans (Johnson et al., 2008). Potentially virulent strains are commonly differentiated from likely avirulent strains by the presence of the thermostable direct (*tdh*) and/or *tdh*-related (*trh*) hemolysin genes (Shirai et al., 1990; Bej et al., 1999). Acute gastroenteritis is the most common manifestation of illness and often associated with the consumption of raw or undercooked oysters, which can bioaccumulate the bacterium through filter-feeding (Daniels et al., 2000; Su and Liu, 2007; Iwamoto et al., 2010).

Previously, *V. parahaemolyticus* infections have been typically sporadic cases attributed to multiple serotypes, with at least 13 O serogroups and 71 K serotypes detected (Ishibashi et al., 2000). There was not a clear association between *V. parahaemolyticus*-mediated infection and serovars until 1996. Serogroup O3:K6 was first isolated in 1996 from diarrhea patients in Kolkata, India (Okuda et al., 1997) and subsequently worldwide. Since then an increasing incidence of gastroenteritis caused by the serogroup O3:K6 has been reported in many countries, including Africa (Ansaruzzaman et al., 2005), Europe (Martinez-Urtaza et al., 2004, 2005), and Latin America (Gonzalez-Escalona et al., 2005). Serotype O3:K6 strain was then identified as a dominant pandemic clone from clinical cases of *V. parahaemolyticus*-induced diarrhea reported globally (Okuda et al., 1997; Chowdhury et al., 2000).

Up to now, a wide variety of O3:K6 clone derivatives, including O4:K68, O1:K25, O1:K26, and O1:KUT, have been recognized as the predominant group responsible for most outbreaks since 1996 (Okuda et al., 1997; Matsumoto et al., 2000; Okura et al., 2004; Ansaruzzaman et al., 2005; Hayat Mahmud et al., 2006). Pandemic strains typically belong to serotype O3:K6 and encode a unique *orfβ* gene (Nasu et al., 2000). It has been hypothesized that *orfβ* encodes for an adherent protein that increases the ability of *V. parahaemolyticus* to adhere to host intestinal cells or the surfaces of marine plankton (Okuda et al., 2000; Yeung et al., 2002). Several studies reported that the *toxRS* operon of pandemic strains contains a unique sequence, thereby referred as *toxRS*/*new*, encoding transmembrane proteins involved in the regulation of virulence associated genes (Chowdhury et al., 2000; Okura et al., 2003, 2005). In general, an isolate possessing both *tdh* and *toxRS/new* can be considered as a pandemic strain (Okura et al., 2003). Another known virulence gene, *trh*, is not specific to pandemic strains and it is rarely present in environmental strains compared to clinical ones (DePaola et al., 2000; Parvathi et al., 2006).

In Mexico, the first outbreak of gastroenteritis caused by the pandemic strain of *V. parahaemolyticus* O3:K6 was reported in 2004 (Cabanillas-Beltran et al., 2006). More than 1230 cases of infection with *V. parahaemolyticus* were associated to consumption of contaminated seafood in a relatively small geographic area in southern Sinaloa (Cabanillas-Beltran et al., 2006). The incidence of *V. parahaemolyticus* infections in Mexico was unknown until 2004 when the O3:K6 pandemic strain with the *tdh* virulence gene was detected in this region. In subsequent years, recurrent sporadic cases has been detected in both South and North areas with the pandemic strain O3:K6 causing >79% of reported cases between 2004 and 2010 (Velazquez-Roman et al., 2012).

In an effort to understand the prevalence and dissemination of *V. parahaemolyticus* strains (toxigenic and pandemic O3:K6) we have characterized since 2004 strains of *V. parahaemolyticus* isolated from both clinical cases and environmental samples obtained from South and North areas of the Sinaloa state (Velazquez-Roman et al., 2012). The present report describes a more extensive investigation that evaluated the prevalence of *V. parahaemolyticus* strains in clinical and environmental samples collected from 2011 through 2013 from along all Sinaloa state. Our studies characterized the isolates by serotyping, investigated their antimicrobial susceptibility or non-susceptibility and assessed the presence of toxigenic and pandemic genetic markers. We also investigated the genetic relationships of strains isolated between 2004 and 2010 to those investigated in this study and isolated in 2011–2013. Our results indicate the persistence in the environment and clinical cases of the O3:K6 pandemic strain in Northwest Mexico from 2004 to 2013 To our knowledge, this is the first report describing that the pandemic O3:K6 clone has endemically established in the Pacific Coast of Mexico and causes most *V. parahaemolyticus* attributable diarrhea cases.

Materials and Methods

Area of Study, Collection of Environmental Samples, and Stool Samples

This study was performed in the state of Sinaloa, which is located in Northwest Mexico. Sinaloa has over 650 km of coastline, with most of it (~75%) facing the Sea of Cortez and the rest (~25%) bordering the Pacific Ocean. Sample collection was performed in eleven sites from the southern to the northern region in Sinaloa, during the years of 2011, 2012, and 2013. Regions sampled include were leading shrimp producers in Sinaloa are located; clinical cases were also detected near these regions. A total of 1,895 environmental samples (shrimp *N* = 204, sediment *N* = 9, and seawater *N* = 1,682) were collected (Figure 1). Stool specimens or rectal swabs (*N* = 10,521) were collected in Cary-Blair transport medium from persons with clinical gastroenteritis who had eaten seafood and requested attention in public-sector health care agencies during the period 2011–2013 (Figure 1). Written informed consent was obtained from patients or their families. Procedures for collection of stool samples were approved by the ethics committee of the Faculty of Medicine-UAS and the Sinaloa State Public Health Laboratory.

Bacteriological Analyses

Samples were processed following procedures found in the Bacteriological Analytical Manual of the Food and Drug Administration (Kaysner and De Paola, 2004) and as described by Canizalez-Roman et al. (2011). Briefly, 50 g of shrimp, or
sediment samples, or 50 mL of seawater, were homogenized with 450 mL of sterile alkaline peptone water (APW; pH 8.6) in a Stomacher 400 circulator. The APW homogenate was incubated at 37°C for 6–8 h. Stool samples, or rectal swabs, were placed in Cary-Blair transport medium and transported at room temperature (RT) to the laboratory within 2 h and immediately processed. These specimens were also enriched in APW (pH 8.6) for 6–8 h at 37°C. After incubation, the enrichment broths were streaked onto thiosulfate-citrate-bile salts-sucrose (TCBS) agar plates and/or CHROMagar Vibrio (CV) medium (CHROMagar, Paris, France) and incubated at 37°C for 18–24 h. At least three typical colonies of *V. parahaemolyticus* were isolated from each plate and subjected to identification by biochemical test and polymerase chain reaction (PCR) as mentioned below. After identification of *V. parahaemolyticus* a single colony from each sample was used to continue the analysis (serotyping and virulence genes).

**Extraction and Purification of Chromosomal DNA**

Chromosomal DNA was extracted using the Wizard genomic DNA purification kit (Promega Corp.) according to the manufacturer’s instructions. Briefly, strains were inoculated in LB broth containing 3% NaCl an incubated overnight at 37°C. This culture (3 mL) was pelleted by centrifugation at 16,000 × g for 5 min. Cells were lysed at 80°C in nucleic lysis solution. RNase solution was added to the cell lysate, followed by incubation at 37°C for 1 h and cooling at RT. Protein precipitation solution was added to the RNase-treated cell lysate and vortexed vigorously. DNA was precipitated by adding 0.6 volumes of isopropanol at RT and then washed with 70% ethanol; air dried, and solubilized using DNA rehydration solution. Our DNA preparations were stored at −20 or −80°C until use.

**PCR Assays**

Polymerase chain reaction amplification was performed in 25 µL reactions consisting of 1X GoTaq green master mix (Promega), primers targeting either the *tl* gene (Bej et al., 1999), pR72H plasmid (Lee et al., 1995; Robert-Pillot et al., 2002), *tdh* or *trh* genes (Bej et al., 1999), and 0.5 µL of purified genomic DNA template, with the remaining volume consisting of molecular biology grade water. PCR was routinely carried out in a Thermal Cycler C1000 (Bio-Rad Laboratories, Hercules, CA, USA) under the following cycling conditions: an initial period of DNA denaturation at 94°C for 3 min, followed by 35 cycles of 1 min at 94°C, 1 min at 58°C, and 1 min at 72°C, and a final extension of 5 min at 72°C. PCR assays to amplify the *toxRS/new* and *orf8* genes (pandemic markers) were performed using specific primers previously reported.
Serotyping

Serotyping of *V. parahaemolyticus* isolates was done by using a commercially available *V. parahaemolyticus* antiserum test kit (Denka Seiken, Tokyo, Japan) with O1–O11 antisera and 71 K antisera according to the manufacturer’s instructions. Briefly, strains were grown overnight at 37°C on LB agar containing 3% NaCl. A pool of colonies was suspended in 1 mL of saline and then split in two 500 µL aliquots. For serotyping, an aliquot was heated up to 121°C for 1 h for O serotyping; if the serotype could not be obtained, the bacterial lysate was heated for an additional hour and then used for O serotyping. The second aliquot was used for serotyping based on the K antigen.

**REP-PCR**

More than 50% (*n* = 150) of strains isolated between 2004–2010 and 2011–2013 were selected for repetitive extragenic palindromic PCR (REP-PCR) analysis. Of these only nine strains are shown in the results section. Strains from the 2004 to 2010 period were obtained from the previous study (Velazquez-Roman et al., 2012), and 77 clinical and 32 environmental isolates from 2011 to 2013, were tested by a standard disk diffusion method on Mueller-Hinton II agar (CLSI, 2011). The antibiotic sensi-disk (BD BBL, Sensi-Disc, Becton, Dickinson and Company, USA) used were the following: ampicillin (10 µg), tetracycline (30 µg), trimethoprim–sulfamethoxazole (1.25 µg/23.75 µg), chloramphenicol (30 µg), nalidixic acid (30 µg), ciprofloxacin (5 µg), cefazidime (30 µg), gentamicin (10 µg), and cefotaxime (30 µg).

**Antibiotic Susceptibility Testing**

To evaluate antimicrobial-susceptibility of *V. parahaemolyticus* strains, 65 clinical and 87 environmental isolates from 2004 to 2010 (from MEMC, a previous study (Velazquez-Roman et al., 2012), and 77 clinical and 32 environmental isolates from 2011 to 2013, were tested by a standard disk diffusion method on Mueller-Hinton II agar (CLSI, 2011). The antibiotic sensi-disk (BD BBL, Sensi-Disc, Becton, Dickinson and Company, USA) used were the following: ampicillin (10 µg), tetracycline (30 µg), trimethoprim–sulfamethoxazole (1.25 µg/23.75 µg), chloramphenicol (30 µg), nalidixic acid (30 µg), ciprofloxacin (5 µg), cefazidime (30 µg), gentamicin (10 µg), and cefotaxime (30 µg).

In the absence of Clinical and Laboratory Standards Institute (CLSI) definitive standards for interpreting *V. parahaemolyticus* susceptibility to antibiotics, zone diameters were determined and recorded as sensitive, intermediate, or resistant according to established standards for *V. cholerae* and *Enterobacteriaceae*. The following *V. parahaemolyticus* strains were used as a control organism: ATCC 17802, (tdh–) and multidrug resistant strain 727 (Leon-Sicaire et al., 2009).

**Statistical Analysis**

All statistical analysis was performed using SPSS v.20.0 (IBM Corp., Armonk, NY, USA). We carried out Chi-square to evaluate significance.

**Results**

**Isolation of *V. parahaemolyticus* from Environmental and Stool Samples**

From 2011 to 2013, a total of 1,895 environmental samples were analyzed for the presence of *V. parahaemolyticus* strains; these samples included 204 shrimp, 1682 seawater and nine sediment
samples (Figure 1). Overall, V. parahaemolyticus strains were isolated from 2.4% (N = 46) of samples. Of these 46 strains, 38 (82.6%) were obtained from shrimp samples, 5 (10.9%) from sediment, and 3 (6.5%) from seawater. In clinical samples taken during the same period, V. parahaemolyticus strains were isolated in 249 (2.4%) out of 10,521 stool specimens or rectal swabs collected from persons with gastroenteritis who had eaten seafood. The presence of V. parahaemolyticus in both, environmental samples and in cases of diarrhea by this bacterium were detected from southern to northern Sinaloa state (Figure 1).

Virulence Genes, Serotypes and Pandemic Characteristics of V. parahaemolyticus Isolates

Based on the presence or absence of virulence genes, we classified the isolates into three groups: pandemic (tdh+, toxRS/new+, and/or orf8+), pathogenic (tdh− and/or trh+), and non-pathogenic strains (tdh− and trh−). Among environmental V. parahaemolyticus strains, three strains (6.5%) were identified as pandemic isolates. One of these strains belonged to serotype O3:K6 and carried the tdh, toxRS/new, and orf8 genes (isolated from shrimp), whereas two pandemic O3:KUT strains carried the tdh, toxRS/new and/or orf8 genes (isolated from sediment and shrimp). A total of 65.2% (30/46) of environmental isolates carried the virulence tdh gene and therefore are considered as pathogenic strains. We did not detect isolates encoding the trh gene (Table 1). Approximately 28% (13/46) of environmental isolates were non-pathogenic. The most prevalent serovars were O3:K6 and carried the tdh, toxRS/new, and orf8 genes (isolated from shrimp), whereas two pandemic O3:KUT strains carried the tdh, toxRS/new and/or orf8 genes (isolated from sediment and shrimp). A total of 80.3% (200/249) of these isolates were identified as pandemic serotypes (Table 1). Of these, 97% (196/202) belonged to serovar O3:K6, carrying the tdh, toxRS/new and/or orf8 genes. One isolate belonged to serovar O3:K29 (tdh+ and toxRS/new+), and one isolate belonged to serotype OUT:KUT (tdh+, toxRS/new+, and orf8+). A total of 16.1% (40/249) of these clinical isolates were pathogenic strains (tdh+ and/or trh+) including several serotypes (e.g., O1:KUT, O4:K12, O4:K29, O4:K55, O6:K18, O10:KUT, OUT:KUT, OUT:K53, O1:K56, O3:KUT, O4:KUT, O8:K21). Only few clinical isolates, 2.8% (7/249), were classified within the non-pathogenic group. Unlike serovars detected in environmental isolates, pandemic serotype O3:K6 (80.3%, 200/249) was the most prevalent among those isolated from clinical samples (Table 1). Serotypes O1:KUT, O2:KUT, O3:KUT, O3:K6, O6:K46, and OUT:KUT were isolated from both environmental samples and stool samples.


The pandemic clone O3:K6 serotype was the most prevalent strain isolated from gastroenteritis cases in both periods 2004–2010 (81.8%) and 2011–2013 (80.3%). Among environmental strains the prevalence of serotype O3:K6 was also similar, 2.7 or 2.1%, for those isolated in 2004–2010, or 2011–2013, respectively (Figure 2). The percentage of clinical pathogenic strains isolated during the period 2011–2013 (16.1%) was slightly higher than that obtained during the period 2004–2010 (11%) but statistical analysis revealed no significant difference (p > 0.05).

In the case of environmental pathogenic strains the prevalence increased from 52% in 2004–2010 to 65.3% in our period of analysis 2011–2013 (Figure 2). Similarly, no statistically significant difference was detected (p > 0.05). This indicates that the incidence of V. parahaemolyticus infection by the pandemic strains (O3:K6) in this region of Mexico had remained constant since 2004. It is noteworthy that between 2004 and 2013, O3:K6 strains were isolated from clinical samples in high proportions (80.3–81.8%) whereas pathogenic strains were detected in low proportions (11–16.1%). Conversely, in environmental samples the pandemic clone O3:K6 was detected in low proportions (2.1–2.7%) and pathogenic strains were detected in high proportions (52–65.3%).

REP-PCR Typing of Clinical and Environmental V. parahaemolyticus Strains

To investigate whether infections due to pandemic isolates were caused by genetic related clones throughout the years, DNA fingerprints of 150 strains obtained during 2004–2013 were examined using REP-PCR, but only seven randomly selected O3:K6, one O3:KUT and one O1:K20 isolates are shown in the Figure 3. Our REP-PCR studies revealed 11 discernible products (i.e., PCR bands) ranging in size from 400 to 3000 bp. Several REP-PCR products with molecular size of 600, 750, and 1500 bp were common to most strains, while products of 400, 800, 1000, and 3000 bp were present in all V. parahaemolyticus strains (Figure 3). One REP-PCR banding pattern was obtained for O3:K6 (tdh+, toxRS/new+, orf8+, and trh+) strains; these seven isolates (Figure 3, lanes 1–5, 7, 9), yielded an identical banding pattern to that observed for the control strains (Figure 3, lane 10). A second banding pattern comprised one isolate, O3:KUT (tdh+, toxRS/new+, orf8+, and trh+), (Figure 3, lane 6) and a third REP-PCR banding pattern was obtained with one isolate, O1:K20 (tdh+, toxRS/new+, orf8+, and trh+) (Figure 3, lane 8). Similar REP-PCR banding patterns were observed when REP-PCR was repeatedly performed, at least three times, demonstrating the reproducibility of our data. Except for the O3:KUT, lane 6 and O1:K20, lane 8 which displayed non-identical REP-PCR profiles, isolates from any year with the same serotype mostly produced identical REP-PCR profiles.

Antibiotic Resistance Profiles of V. parahaemolyticus Strains

Of the environmental and clinical strains tested, a significant increase in cefotaxime resistance was observed from 2004–2010 to 2011–2013 (p < 0.05) and most isolates were resistant to ampicillin (Table 2). However, among clinical strains a significantly ampicillin-resistance decreased was observed from 2004–2010 to 2011–2013 (p < 0.05). Low resistance was determined for gentamicin, nalidixic acid, sulfamethoxazole-trimethoprim, cefadroxil, chloramphenicol, and tetracycline from 2004–2010 to 2011–2013 (Table 2). Clinical and environmental isolates were all susceptible to ciprofloxacin or chloramphenicol, respectively.
TABLE 1 | Serovar and virulence attributes of 295 Vibrio parahaemolyticus strains isolated between 2011 and 2013.

<table>
<thead>
<tr>
<th>O serogroup and serovar</th>
<th>Total no. of isolates</th>
<th>Presence of each virulence gene</th>
<th>No. of clinical isolates (from feces)</th>
<th>No. of environmental isolates from:</th>
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<td>tdh    trh  toxRS/new Orf8</td>
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<td>1</td>
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<td>1</td>
</tr>
<tr>
<td>OUT:K53</td>
<td>+ + − −</td>
<td>1</td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>TOTAL</td>
<td>295</td>
<td>38</td>
<td></td>
<td>38 3 5</td>
</tr>
</tbody>
</table>

Sh, Shrimp; Sw, Seawater; S, Sediment.

FIGURE 3 | Agarose gel (1.5%) electrophoresis showing the results of polymerase chain reaction (PCR) amplification of representative fingerprint patterns for the REP-PCR of *Vibrio parahaemolyticus* strains of serotype O3:K6 (tdh\(^+\), toxRS/new\(^+\), orf8\(^+\), and trh\(^-\)), isolated from 2004 to 2013. Lane M, 1 kb molecular size markers; lane 1, clinical isolate (2004, O3:K6); lane 2, clinical isolate (2006, O3:K6); lane 3, clinical isolate (2008, O3:K6); lane 4, clinical isolate (2010, O3:K6); lane 5, clinical isolate (2011, O3:K6); lane 6, shrimp isolate (2011, O3:KUT, tdh\(^+\), toxRS/new\(^+\), orf8\(^+\), and trh\(^-\)); lane 7, clinical isolate (2012, O3:K6); lane 8, clinical isolate (2012, O1:K20, tdh\(^-\), toxRS/new\(^-\), orf8\(^-\), and trh\(^-\)); lane 9, clinical isolate (2013, O3:K6); lane 10, control strain *V. parahaemolyticus* RIMD 2210633 (tdh\(^+\), toxRS/new\(^+\), orf8\(^+\), and trh\(^-\)); lane 11, negative control (no DNA template added to the rep-PCR reaction); lane 12, molecular size markers.

Regarding overall antibiotic resistance, most environmental (>78%) and clinical strains (>70%) were non-susceptible to at least one antibiotic (Table 3). This high prevalence of resistance decreased in strains isolated in 2011–2013 in comparison to previous period, 2004–2010, with an expected increase on the prevalence of strains resistant to two or more antibiotics (multidrug-resistant; Table 3). The increased prevalence, however, of strains with resistance to two antibiotics was only statistically significant among clinical isolates (p < 0.05). Importantly, strains with resistance to 5 or 7 antibiotics were detected among clinical strains isolated in the period 2011–2013 (Table 3).

**Discussion**

In Mexico, the first outbreak of gastroenteritis caused by pandemic *V. parahaemolyticus* strain O3:K6 was reported in a relatively small geographical area of the Southern part of the Sinaloa State (Velazquez-Roman et al., 2012). Since its arrival back in 2004, Sinaloa has experienced recurrent sporadic cases of gastroenteritis caused by *V. parahaemolyticus* strains which have gradually spread from south to north from 2004 to 2010 (Velazquez-Roman et al., 2012). The present study conducted an epidemiological surveillance of *V. parahaemolyticus* strains in both environmental and clinical samples along the Pacific coast...
of Sinaloa from 2011 to 2013. We demonstrate that the pandemic clone O3:K6 (encoding the tdh and toxRS/new genes and with or without orf8) still remains the most prevalent serotype isolated from cases of *V. parahaemolyticus*-induced diarrhea cases. The pandemic clone has endemically established in the Pacific Coast of Mexico. Furthermore, most strains were resistant to ampicillin and resistance to multiple first-line antibiotics significantly increased from 2004–2010 to 2011–2013. These observations represent, to the best of our knowledge, the first report demonstrating 10 years of persistence of the pandemic clone O3:K6 in the Mexico’s pacific coast.

As in our previous study where most strains isolated from 2004 to 2010 belonged to the O3:K6 serotypes, most strains isolated from 2011 to 2013 were serotype O3:K6 (Velazquez-Roman et al., 2012). The prevalence of O3:K6 pandemic and pathogenic strains isolated from environmental and clinical samples was not significantly different from that detected in 2004–2010. This indicates that (1) the incidence of *V. parahaemolyticus* infection by the pandemic strains remains similar and (2) that the pandemic clone is a permanent resident of the environment in this region of Mexico. We hypothesize that the presence of pandemic strains in the environment is at least partially due to shedding in the feces of patients with gastroenteritis.

Regional persistence of O3:K6 pandemic strains have been reported in different geographic areas. For example, O3:K6 was the predominant serovar in studies conducted in Peru in 2007.
More recently, however, isolates obtained in Mexico and the US. (Paranjpye et al., 2012; Li et al., 2014) demonstrated high serodiversity in the environment of V. parahaemolyticus, with serovars O4:K29, O4:K55, O6:K18, and OUT:K53, and three from environmental samples (O4:K4, O5:K30, and OUT:K6). Data from the present study are in accordance with other reports in which V. parahaemolyticus environmental strains show a high serological variability (Nair et al., 2007; Chao et al., 2009; Garcia et al., 2009).

Previous studies have demonstrated that up to 90% of clinical strains encode the tdh and/or trh gene (Okuda et al., 1997; Chao et al., 2009; Garcia et al., 2009; Velazquez-Roman et al., 2012; Li et al., 2014; Pazhani et al., 2014), whereas their presence in environmental isolates is rare (Shirai et al., 1990; DePaola et al., 2000; Yeung and Boor, 2004; Nair et al., 2007; Chao et al., 2009; Velazquez-Roman et al., 2012). More recently, however, an increased proportions (48–52%) of strains encoding virulence genes (i.e., tdh and/or trh) have been detected in environmental isolates obtained in Mexico and the US. (Paranjpye et al., 2012; Velazquez-Roman et al., 2012; Gutierrez West et al., 2013). Accordingly, our studies detected high prevalence of the tdh gene (encoding for the TDH hemolysin) as it was carried by 58.6% of all environmental strains isolated from 2004 to 2013. Besides this demonstrated high serovariability in the environment of V. parahaemolyticus strains with pathogenic potential (i.e., non-O3:K6 strains encoding the tdh gene), the pandemic strain O3:K6 caused >81% of reported cases of gastroenteritis, attributable to V. parahaemolyticus between 2004 and 2013 in the Pacific Northwest coast of Mexico. The detection of tdh gene in environmental isolates suggests that tdh alone is not an adequate marker for potentially virulent V. parahaemolyticus strains (Paranjpye et al., 2012).

As expected, our studies found a high serodiversity of V. parahaemolyticus in the environment, including isolates obtained from shrimp, sediment, and seawater. It is worth to mention that in 2013 we observed a high mortality of cultured Penaeus vannamei in shrimp farms located in northern Mexico including the states of Nayarit, Sinaloa and Sonora. Mortality was due to acute hepatopancreatic necrosis disease (AHPN), which has also been referred to as early mortality syndrome (EMS), and the pathogen associated with EMS was V. parahaemolyticus (Gomez-Gil et al., 2014; Gomez-Jimenez et al., 2014; Nunan et al., 2014). Additional studies should provide a link between pathogenic traits of V. parahaemolyticus strains and/or serotype or serovars, if any, associated to this syndrome in shrimps

Rep-PCR genomic fingerprinting is known to have a greater resolving power than serotyping (Maluping et al., 2005). Our rep-PCR studies intended to demonstrate genetic similarities, or differences, between pandemic strains isolated from the environment with those isolated from human cases of gastroenteritis. Whereas molecular divergence was noticed on the banding profile obtained from O1:K20 and O3:KUT strains, we obtained a similar rep-PCR profile in all O3:K6 pandemic isolates utilized which indicates that O3:K6 strains circulating in the environment have the same clonal origin than those infected patients and therefore a source of infection and transmission.

Another important contribution in our work was the investigation of susceptibility, or not, of the isolated V. parahaemolyticus strains to first-line antibiotics utilized in the region. In agreement with our genetic evidences (i.e., rep-PCR) indicating genetic relationships of the isolated strains, our results revealed similar resistance patterns in both clinical and environmental isolates. Most V. parahaemolyticus isolates were resistant to ampicillin which was not a surprise as non-susceptibility to ampicillin is very common in V. parahaemolyticus strains isolated from environmental and clinical samples (Okuda et al., 1997; Wong et al., 2000; Roque et al., 2001; Sun et al., 2013), suggesting that these drugs have a negligible role in the treatment of V. parahaemolyticus. In contrast, most isolates were sensitive to tetracycline, trimethoprim–sulfamethoxazole, chloramphenicol, nalidixic acid, ciprofloxacin, ceftazidime and gentamicin, which can be used as an alternative antibiotic therapy. Resistance to cefotaxime increased from 4.6% in 2004–2010 to 19.3% in 2011–2013. A similar prevalence of resistance to cefotaxime (20%) has also been reported in resistant strains isolated in Italy from shellfish and clinical samples (Ottaviani et al., 2013). While the percentage of isolates expressing resistance to the newer generation of cephalosporins was relatively low, these antibiotics are considered to be some of the best defenses against the severe infections that these organisms can elicit, so even a small percentage of resistant isolates could be cause for concern. Therefore, all isolates must be tested for antimicrobial susceptibility to monitor resistance patterns of each antibiotic. In Mexico and others countries, patients suffering V. parahaemolyticus disease are treated with empiric antibiotic therapy which generates more resistance to first line antibiotics. Unlike other bacterial infections, little to nothing is reported about antibiotic resistance of V. parahaemolyticus in Mexico, and perhaps other Latin American countries, as clinical laboratories do not routinely test susceptibility to different classes of antimicrobial agents. Furthermore, until 2004 where we reported the first outbreak of gastroenteritis caused by V. parahaemolyticus in Mexico, there had not been other outbreaks published in the scientific literature (Velazquez-Roman et al., 2012, 2014). Prior to our studies, only
few environmental strains had been isolated from water and fish in Mexico (Cabrera-Garcia et al., 2004).

To the best of our knowledge, our findings represent the first investigation in Mexico about the prevalence, pathogenic potential, and antimicrobial susceptibility over a 10-years period of continuous surveillance of *V. parahaemolyticus* (pathogenic and pandemic O3:K6 clone) in both clinical specimens and environmental samples. Most gastroenteritis cases attributable to *V. parahaemolyticus* strains are caused by the same pandemic clone which warrants extended surveillance in the region and across the country. Continued monitoring of *V. parahaemolyticus* strains and their susceptibility to antibiotics seem to be necessary to ensure the best treatment, and prognosis, to patients with *V. parahaemolyticus* diseases in the area. This information should also be relevant to health authorities in the case of a local or multistate foodborne outbreak of *V. parahaemolyticus* gastroenteritis.

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References


Cabrera-Garcia, et al. (2004). Several environmental strains had been isolated from water and fish in Mexico (Cabrera-Garcia et al., 2004).


Pandemic V. parahaemolyticus at Northwest Mexico


Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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