International Dissemination of Epidemic Vibrio cholerae by Cargo Ship Ballast and Other Nonpotable Waters

SUSAN A. McCARTHY^{1*} AND FARUKH M. KHAMBATY²
Gulf Coast Seafood Laboratory, Food and Drug Administration, Dauphin Island, Alabama 36528,¹ and Gulf Coast Seafood Laboratory, Food and Drug Administration, Dauphin Island, Alabama 36528,1 and Division of Microbiological Studies, Food and Drug Administration, Washington, D.C. 202042

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In 1991 and 1992, toxigenic *Vibrio cholerae* O1, serotype Inaba, biotype El Tor, was recovered from nonpotable (ballast, bilge, and sewage) water from five cargo ships docked in ports of the U.S. Gulf of Mexico. Four of these ships had taken on ballast water in cholera-infected countries; the fifth took on ballast in a noninfected country. Isolates examined by pulsed-field gel electrophoresis were indistinguishable from the Latin American epidemic strain, C6707; however, they differed significantly from the endemic Gulf Coast strain (VRL 1984), the sixth-pandemic strain $(569-B)$, and a V. cholerae non-O1 strain isolated from a ship arriving $\mathbf{X}(\mathbf{X})$ and a vertex strain $\mathbf{X}(\mathbf{X})$, and a $\mathbf{Y}(\mathbf{X})$, the sixth-pandemic strain isolated from a ship arriving $\mathbf{X}(\mathbf{X})$ from a foreign port. On the basis of our findings, the Food and Drug Administration recommended that the basis
So Coost Cuard issues on advisory to chinning coants and contains requesting that hellest waters he U.S. Coast Guard issue an advisory to shipping agents and captains requesting that ballast waters be exchanged on the high seas before entry of ships into U.S. ports.

In January 1991, epidemic cholera was reported in Peru (4, In July and September 1991 and June 1992, toxigenic Vibrio. cholerae O1 was isolated from five oysters and one fish collected from Mobile Bay, Ala. $(6, 7, 24)$. Biochemical and serological characterization of the isolates showed their resemservation characterization of the isolates showed their resemblance to the Latin American epidemic strain, V. cholerae 01, biotype El Tor, serotype Inaba.
Since 1973, 91 sporadic cholera cases unrelated to the Latin

American epidemic have occurred in the United States. Most of these cases, which were related to the consumption of raw or undercooked shellfish from the Gulf of Mexico (2, 25), were undercooked shellfish from the Gulf of Mexico $(z, 25)$, were
the distribution of C_0 . cholerae 01 strain VRL 1984, which is endemic to the Gulf Coast (6, 17). Unlike strain VRL 1984, the Latin American strain lacks hemolysin and the VcA-3 vibrio- $\frac{1}{2}$ and the strain density in their shelpes to $\frac{1}{2}$ vibrioage, and the strains differ in their cholera toxin gene

we investigated gas exploration and marine transportation
We investigated gas exploration and marine transportation to determine if these activities might serve to introduce the Latin American strain locally. The toxigenic strains isolated during this investigation were characterized by biochemical and serological tests, PCR, and pulsed-field gel electrophoresis (PFGE). Our results showed that cargo ships are vehicles for the transmission of epidemic cholera. In order to manage the problem, it was recommended that ships exchange their ballast polem, it was recommended that sinps exenange their banast $\frac{1}{2}$ while on the high seas. (Premimary accounts of this work were presented elsewhere [19, 20].)

MATERIALS AND METHODS

Sample collection and analysis. Along with U.S. Coast Guard authorities, Food and Drug Administration (FDA) investigators boarded vessels to collect samples from 19 cargo ships at the ports of Mobile, Ala., and Gulfport and Pascagoula, Miss. (Table 1). Samples (50 to 100 ml) from ballast tanks, fire mains, bilge tanks, oily-water separators, holding $t_{\rm max}$, first mains, bilge tanks, only $\frac{1}{2}$ and $\frac{1}{2}$ an tanks, or marine sanitation devices were collected into sterile polyethylene Falcon containers and maintained on ice until were determined. Salinity was measured with a Reichert refractometer (Cambridge Instruments, Inc., Buffalo, N.Y.); refractometer (Cambridge Instruments, Inc., Buffalo, N.Y.); 1 was measured with Colorphast Store paper (EN Science,
paper Hill NH Cherry Hill, N.J.).
To detect the presence of *V. cholerae*, 10-fold serial dilutions

of each test sample were inoculated into alkaline peptone water (APW); duplicate sets of APW enrichments were incubated at 35 and 42° C for 18 to 24 h. From evident pellicles, 3to 5-mm loopfuls of inoculum were transferred to thiosulfatecitrate-bile salts-sucrose (TCBS) agar and incubated at 35° C for 18 to 24 h; suspect colonies on TCBS were streaked to tryptone salt (T_1N_1) [1% tryptone, 1% NaCl]) (9) agar. If no pellicles were evident in APW enrichments at 24 h, incubation was extended an additional 48 to 72 h at room temperature. we calculate an additional 48 to 72 h at room temperature. anibers of fecal collibrius per 100 ml were determined by the membrane filter method (8).
Biochemical and serological characterization of suspect V.

cholerae isolates. V. cholerae isolates were characterized by the oxidase reaction, the string test in 0.5% sodium desoxycholate (29), growth in 1% tryptone broth, and biochemical reactions in API 20E strips (Analytab Products, Plainview, N.Y.).

Biotype determinations were based on Voges-Proskauer reaction and resistance to polymyxin B on Mueller-Hinton agar (9) . *V. cholerae* antigen was typed by serological agglutination with V . cholerae polyvalent antiserum (Difco Laboratories, Detroit, Mich.) and by slide latex agglutination with the V . ries, Detroit, Mich.) and by slide latex agglutination with the V. cholerae AD Seiken kit (Denka Seiken Co., Ltd., Tokyo,

Japan).
Determination of toxigenicity. *V. cholerae* enterotoxin was identified by reversed passive latex agglutination (RPLA) (VET-RPLA; Oxoid, Basingstoke, Hampshire, United Kingdom); cultures were grown in AKI medium before testing (9). $\lim_{n \to \infty}$ used to detect the A subunit of the cholera toxin
the PCR was used to detect the A subunit of the cholera toxin
no from 1 ml ABW enrichments (10) CTY2 and CTY3 gene from 1-ml APW enrichments (10). CTX2 and CTX3 primers were obtained from the Enteric Diseases Branch, Division of Bacterial and Mycotic Diseases, Centers for Disease Control, Taq polymerase, deoxynucleoside triphosphates, $\frac{d}{d}$ 10X PCR buffer were obtained from Perkin-Elmer Cetus,
and lOX PCR buffer were obtained from Perkin-Elmer Cetus, Norwalk, Conn. The PCR was performed with ^a Hybaid thermal reactor (National Labnet Co., Woodbridge, N.J.).

^{*} Corresponding author. Mailing address: FDA Gulf Coast Seafood Laboratory, P.O. Box 158, Dauphin Island, AL 36528. Phone: (205) 694-4480. Fax: (205) 694-4477. Electronic mail address: SAM@ FDACF.SSW.DHHS.GOV.

TABLE 1. Description of ships sampled

Ship	Date ^a	Location	LPC^b
1	10/30/91	Mobile, Ala.	Japan
2	10/30/91	Mobile, Ala.	South Africa
3	10/31/91	Mobile, Ala.	Mexico
4	11/01/91	Mobile, Ala.	Nova Scotia
5	11/01/91	Mobile, Ala.	Venezuela
6	11/05/91	Mobile, Ala.	Louisiana
7	11/05/91	Mobile, Ala.	Puerto Rico
8	11/06/91	Mobile, Ala.	Brazil
9	11/07/91	Mobile, Ala.	Colombia
10	11/19/91	Pascagoula, Miss.	Chile
11	11/25/91	Gulfport, Miss.	Venezuela
12	11/25/91	Gulfport, Miss.	Venezuela
13	11/26/91	Mobile, Ala.	Venezuela
14	11/26/91	Mobile, Ala.	Venezuela
15	12/02/91	Mobile, Ala.	Venezuela
16	12/03/91	Mobile, Ala.	Venezuela
17	12/03/91	Mobile, Ala.	Venezuela
18	06/11/92	Mobile, Ala.	Puerto Rico
19	06/12/92	Mobile, Ala.	Brazil

 μ LPC, last port of call.

Amplified DNA was analyzed by electrophoresis through a 0.8% agarose gel in Tris-borate-EDTA buffer at 90 V for 1.5 to 2 h. The gel was stained for 10 min in a solution of ethidium bromide (2.0 μ g/ml) and photographed under UV light. Control organisms used were V . cholerae O1 El Tor strains C6706 and C6707 from the Latin American epidemic, V. cholerae O1 El Tor strain VRL 1984 (the Gulf Coast strain), V. cholerae O1 classical strain 569-B, and V. cholerae non-O1 strain 566-454 μ classical strain 569-B, and V. cholerae non-O1 strain 566-454. isolated from sewage from a ship that had a last port of call in

PFGE. Agarose plugs containing DNA were prepared by a modification of the method of Smith and Cantor (28) . Calla modification of the method of Smith and Cantor (28). Cells
were grown aerobically at 35° C in Luria-Bertani broth to an $A₆₁₀$ of about 0.6. From each culture, 5 ml was centrifuged $(12,000 \times g$ for 10 min); the cells were washed once and (12,000 \times g for 10 min); the cens were washed once and
resuspended in 5 ml of an ice-cold solution of 10 mM Tris-Cl,
1.0 M NoCl and 50 mM EDTA (pH 8.0), A 1 ml aliquot of the 1.0 M NaCl, and 50 mM EDTA (pH 8.0). A 1-ml aliquot of the cell suspension was briefly warmed to 52°C, mixed with an equal volume of molten 1% PFGE-grade agarose (tempered to 52° C), and dispensed into molds. After the plugs solidified, they were transferred to sterile tubes containing 2.0 ml of a they were transferred to sterile tubes containing 2.0 ml of a
lysozyme solution (1 mg/ml in 1 M NaCl-0.5% sarcosyl-0.2%) sodium deoxycholate–6 mM Tris-Cl-100 mM EDTA, pH 8.0) and incubated at 37°C for 1 h. The lysozyme solution was and included at 37°C for 1 h. The lysozyme solution was
removed, and 2.0 ml of a proteinase K solution (2 mg/ml in 0.1% sarcosyl-0.5 M EDTA, pH 9.0) was added. The plugs were incubated at 55° C for 8 to 12 h. The proteinase K solution were incubated at 55°C for 8 to 12 h. The proteinase K solution
was then replaced with 2.0 ml of a phonylmathylaulfonyl was then replaced with 2.0 ml of a phenymichlylsulfonyl fluoride solution (1.5 mM in 10 mM Tris-Cl-1 mM EDTA, pH 8.0). The tubes were agitated gently at room temperature for 1 h; the solution was discarded and the phenylmethylsulfonyl fluoride rinse was repeated. Finally, the plugs were rinsed three times was repeated. Finally, the plugs were rinsed
three times (1 h each) with 10 mM Tris-Cl-50 mM EDTA (pH 8.0) with gentle agitation. Plugs were stored at 4°C in the final

wash solution.
Slices (1 to 2 mm thick) from the plugs were aseptically cut
of the plug strain in the plug strain of the slices and transferred to 1.5-ml microcentrifuge tubes. The slices were first rinsed with 0.5 ml of sterile distilled water for 5 min and then for 10 min with the digestion buffer recommended for the restriction enzyme. Finally, the slices were incubated at the the restriction enzyme. Finally, the slices were incubated at the recommended temperature for ⁸ to ¹² h in ¹⁵⁰ RI of digestion buffer containing 20 U of either $ApaI$ or Notl. After incubation, the digestion buffer was aspirated and the slices were tion, the digestion buffer was aspirated and the slices were
rinsed for 10 min with 0.5 ml of gel running buffer (45 mM Tris-borate–1 mM EDTA, pH 8.0). Slices were then transferred to a 1% agarose gel and analyzed by electrophoresis, by ferred to a 1% agarose gel and analyzed by electrophoresis, by the correction of the correction using the CHEF DR II system (Bio-Rad, Hercules, Calif.). The
DNA in the cals was visualized and photographed after DNA in the gels was visualized and photographed after staining with ethidium bromide $(1 \mu g/ml)$ for 30 min.

TABLE 2. Recovery of fecal coliforms and V . cholerae O1 from nonpotable water

Ship	Water source	pH ^a	Salinity $(ppt)^a$	Concn of fecal coliforms (CFU/100 ml)	Presence of V. cholerae
1	Bilge Sewage			1.2×10^{2} 2.7×10^4	$\overline{}$
2	Bilge Sewage			ND^b 0	
3	Bilge Sewage			ND 2.8×10^{4}	
4	Ballast Sewage	7	32	0 0	
5	Ballast Sewage	7	17	$\bf{0}$ 0	$\overline{}$
6	Ballast Bilge Sewage	7	30	1.2×10^{1} ND 3.0×10^6	- Ļ
7	Ballast Bilge	6	32	3.0 ND	
8	Ballast Fire main	7 7	13 14	2.0×10^{1} 5.8×10^2	$^+$ $\mathrm{+}$
9	Ballast Bilge Sewage	6	14	$\bf{0}$ 0 1.5×10^{5}	$+$ $\mathrm{+}$ $\! + \!$
10	Ballast Bilge	7	32	$\bf{0}$ 0	$^{+}$ $^{+}$
11	Ballast Sewage	7	31	0 $\bf{0}$	\overline{a}
12	Ballast Sewage	7	28	0 0	— —
13	Ballast Sewage	7	26	0 $\bf{0}$	$\overline{}$
14	Ballast	7	26	$\bf{0}$	
15	Ballast	7	32	$\bf{0}$	
16	Ballast	7	18	9.0×10^{1}	
17	Ballast	7	21	5.1×10^{2}	
18	Ballast	6	20	$\bf{0}$	$^{+}$
19	Ballast	6	12	0	$^{+}$

MD, not done.

TABLE 3. Toxigenicity of V. cholerae isolates

Ship or organism	Water source	RPLA titer	ctxA detection by PCR
8	Ballast	1:64	$^{+}$
	Fire main	1:64	$\ddot{}$
9	Ballast	1:32	$^{+}$
	Bilge	1:4	$^{+}$
	Sewage	1:32	$+$
10	Ballast	1:64	$\, +$
	Bilge	1:64	$\ddot{}$
18	Ballast	1:64	$+$
19	Ballast	1:64	$^{+}$
V. cholerae O1			
C6706		1:16	$^{+}$
C6707		1:32	$^{+}$
569B		1:64	$\ddot{}$
VRL1984		1:64	$+$
V. cholerae non-O1		0	

RESULTS AND DISCUSSION

The salinity of the ballast waters from the ships examined ranged from 12 to 32 ppt, whereas the pH values were either 6 or 7 (Table 2). Culturable *V. cholerae* O1 cells were isolated from ballast water (ballast tanks and fire main), bilge water (bilge and oily-water separator), and sewage from 5 of the 19 ships. On the basis of growth in APW, viable counts of V . cholerae were 10^6 /ml or greater. The five contaminated ships had last ports of call in Brazil, Colombia, Chile, and Puerto Rico (Table 1). Fecal coliforms were found in two of the eight

Rico (Table 1). Fecal coliforms were found in two of the eight

samples from which *V. cholerae* was isolated (Table 2). This result suggests that in these types of samples, fecal coliforms are not a reliable indicator of V . cholerae. V . cholerae was recovered from ballast water with salinities of 12, 13, 14, 20. and 32 ppt, indicating its ability to survive in a variety of estuarine and marine environments.

The isolates were identified as El Tor biotype, Inaba serotype. All isolates were positive by PCR for the $ctxA$ gene and by RPLA for V. cholerae enterotoxin production, with titers of 1:4 to 1:64 (Table 3). Of the control V. cholerae O1 strains, C6706, C6707, 569-B, and VRL 1984 also tested positive by RPLA and PCR; the *V. cholerae* non-O1 strain was negative in both tests.

It is possible that viable nonculturable V . cholerae cells were also present in ballast water. Since we detected an alarming number of culturable cells and identified the source of the strain by conventional methods, we did not attempt to determine the presence of viable nonculturable cells. However, if viable nonculturable cells constituted a significant portion of the V . *cholerae* population, they could pose a potential threat under appropriate conditions.

PFGE analysis showed that the toxigenic isolates from ships shared an essentially identical $ApaI$ restriction pattern (Fig. 1, lanes 1 through 7). This pattern was indistinguishable from that of the Latin American strain C6707 (Fig. 1, lane 8), a strain reported to have two copies of the $c\alpha A$ gene region (16). The other Latin American strain tested (C6706) had a single copy of the toxin gene region (16) and an $ApaI$ pattern that differed from that of $C6707$ by a single band (Fig. 1, lane 9). These bands in C6706 and C6707, approximately 100 and 108 kb, respectively, differed in size by about 8 kb. This value matches that of a reported tandem duplication observed in the genome of other EI Tor strains (21). Thus, it is likely that the toxin gene operon is located on these $Apal$ fragments. The results also suggest that the Latin American strains may be able to switch between having either one or multiple copies of the toxin operon.

FIG. 1. PFGE of ApaI restriction digests of total DNA. Isolates from ships were as follows: lane 1, ballast water, ship 8; lane 2, fire main, ship 8; lane 3, ballast water, ship 9; lane 4, bilge, ship 9; lane 5, ballast wa Other isolates were as follows: lane 8, V. cholerae C6707 (Latin American epidemic strain carrying two copies of the toxin gene region); lane 9, V. cholerae C6706 (Latin American epidemic strain carrying one copy of the toxin gene region); and lane 10, V. cholerae 134-9 (toxigenic strain from a Mobile Bay oyster). Arrows point to bands by which patterns in lanes 8 and 9 differ. from a Mobile Bay oyster). Arrows point to bands by which patterns in lanes 8 and 9 differ.

FIG. 2. PFGE of ApaI restriction digests of total DNA. Lane 1, toxigenic V. cholerae O1 isolate from ship 8; lane 2, V. cholerae C6707 (Latin American epidemic strain); lane 3, V. cholerae 409-1C2i (non-O1, cholera toxin-negative isolate from shrimp); lane 4, V. cholerae 566-454 (non-O1, cholera toxin-negative isolate from ship); lane 5, V . cholerae VRL 1984 (toxigenic Gulf Coast strain); lane 6, V. cholerae 569-B (sixth-pandemic strain, classical biotype); lane 7, 48.5-kb lambda ladder (size standards).

PFGE analyses showed that the patterns of eight isolates from oysters and fish harvested near ship traffic lanes in Mobile Bay $(7, 24)$ were indistinguishable from that of C6706. The pattern of an isolate from an oyster is seen in Fig. 1, lane 10. Although all of the isolates from seafoods examined in this study had the single-copy pattern, all of those from ships had the double-copy pattern. However, in another study (23), additional isolates from oysters revealed both the single- and double-copy patterns. Strains with higher numbers of toxin gene copies were found to have growth advantages in vivo (1, 13, 14, $\overline{2}2$). Our findings suggest that the double-copy version may have survival advantages in seawater as well.

The highly conserved $ApaI$ patterns of the strains described. above (Fig. 2) differed significantly from those of (i) a non-O1 V. cholerae strain recovered from shrimp from Ecuador (lane 3); (ii) a non-O1 V. cholerae ship isolate (lane 4); (iii) the toxigenic Gulf Coast strain VRL 1984 (lane 5); and (iv) the sixth-pandemic strain, 569-B (lane 6). Thus, the data rule out the possibility that the toxigenic isolates from seafood examined in this study were derived from either the endemic Gulf Coast strain or from the sixth-pandemic strain. It points to the Latin American area as the most likely source of the isolates and strongly implicates cargo ships as the vectors for transmission of these strains to U.S. coastal areas.

To ascertain the origin of the Latin American epidemic strain, we compared the $ApaI$ restriction pattern of C6707 with those of clinical El Tor isolates from Bangladesh, India, Indonesia, Saudi Arabia, Thailand, and Vietnam and of El Tor isolates from food from Korea. All of the El Tor isolates examined had highly conserved patterns, although no two were identical (data not shown). This conservation confirmed the findings of others (32) that the Latin American outbreak is an extension of the seventh pandemic. The strain is, however, evolving over time, as indicated by the distinct differences seen among the various patterns. The pattern of C6707 most closely matched that of an Indonesian strain. The fact that Indonesia is a maritime country and the Latin American epidemic started in a coastal region of Peru (4) suggests that transmission of the epidemic to this hemisphere also may have involved ships.

Comparison by PFGE of the *Not*I restriction patterns of the strains showed that patterns of all the toxigenic isolates from ships, both Latin American strains, and the toxigenic isolates from seafoods were indistinguishable from one another (data not shown). Those of the other control strains differed significantly from one another and from the isolates from ships and seafood. This finding reiterates the $ApaI$ digest findings that the Latin American strains and the isolates from ships and seafood are clonal. However, the inability of *Not*I to distinguish C6706 from C6707 underscores the importance of using more than one enzyme for comparative studies and marks ApaI as the enzyme of choice for studying V . cholerae even though the patterns obtained are more crowded than those of tot the patterns obtained than the patterns obtained than those of tot

The diversity in restriction patterns among V. cholerae strains increases the value of PFGE as an epidemiological tool. Previously, Kaper et al. (15) used Southern blots and restriction digest patterns to study the molecular epidemiology of V . cholerae non-O1 and Vibrio mimicus in the U.S. Gulf Coast region. Our study illustrates the advantage of using the remarkable resolving ability of the PFGE method to conduct comparative restriction fragment analysis. The need for blotting and probing is eliminated, and, unlike ribotyping (26) , this approach allows essentially the entire genome to be examined, thereby providing a greater degree of strain-specific discrimi- $\sum_{i=1}^n$

Ballast discharge is a major factor in the transmission of aquatic organisms worldwide; it has been implicated in the introduction of several exotic aquatic organisms into new areas, e.g., the European cladoceran into the Great Lakes (3), the Asian clam into San Francisco Bay (3), and toxic dinoflagellates into Australian waters $(12, 27)$. Our findings show that ballast and other nonpotable waters from cargo ships are likely vehicles for the transmission of epidemic cholera as well. In July 1991, the Marine Environmental Protection Committee of the International Maritime Organization adopted a resolution: the International Guidelines for Preventing the Introduction of Unwanted Pathogens from Ships' Ballast Water and Sediment Discharges. Because of our findings, these guidelines were published in the Federal Register on December 12, 1991 (30), and the U.S. Coast Guard requested that shipping agents and ships' captains comply with the recommendation that ballast water be exchanged twice on the high seas to reduce the possibility of introducing pathogens into U.S. coastal waters.

In a nationwide effort conducted in 1991 to 1992, the FDA. with the U.S. Coast Guard and quarantine officers from the Centers for Disease Control, sampled nonpotable water from an additional 90 ships arriving in U. S. ports from Latin America (18). Six of the 109 ships sampled were contaminated with the Latin American strain of V . cholerae O1. The FDA, in with the Latin American strain of V. cholerae of V collaboration with the Alabama Department of Public Health and the Mobile County Health Department, monitored the occurrence of V . cholerae O1 in oysters and the environment until October 1992. No additional contaminated seafood was recovered after June 1992 (24). At that point, the problem appeared to have been resolved and surveillance was terminated. No cases of cholera have been reported in the immediate area. The detection of V . cholerae O1 by our research surveys and the measures implemented as a result of our finding the pathogen in the nonpotable waters of cargo ships may have averted further contamination of coastal seafood resources and thus prevented human illnesses.

The recent advent and pandemic spread of a non-O1 strain of V . cholerae has caused much concern. This strain, which was serogrouped as O139, genetically and physiologically resembles the seventh-pandemic $O1$ El Tor strains (11) . We suggest that control measures effective against the seventh-pandemic strain, including ballast water surveillance and exchange advi s_{max} may be notain the spread of *V* cholerae Ω 130 as s_{max} may help to contain the spread of λ cholerae 0139 as

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