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Identification of Atypical El Tor V. cholerae O1 Ogawa Hosting SXT Element in Senegal, Africa

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Vibrio cholerae O1 is the causative agent of cholera with classical and El Tor, two well-established biotypes. In last 20 years, hybrid strains of classical and El Tor and variant El Tor which carry classical ctxB have emerged worldwide. In 2004–2005, Senegal experienced major cholera epidemic with a number of cases totalling more than 31719 with approximately 458 fatal outcomes (CFR, 1.44%). In this retrospective study, fifty isolates out of a total of 403 V. cholerae biotype El Tor serovar Ogawa isolates from all areas in Senegal during the 2004–2005 cholera outbreak were randomly selected. Isolates were characterized using phenotypic and genotypic methods. The analysis of antibiotic resistance patterns revealed the predominance of the S-Su-TCY-Tsu phenotype (90% of isolates). The molecular characterization of antibiotic resistance revealed the presence of the SXT element, a self-transmissible chromosomally integrating element in all isolates. Most of V. cholerae isolates had an intact virulence cassette (86%) (ctx, zot, ace genes). All isolates tested gave amplification with primers for classical CT, and 10/50 (20%) of isolates carried classical and El Tor ctxB. The study reveals the presence of atypical V. cholerae O1 El Tor during cholera outbreak in Senegal in 2004–2005.

Keywords: Vibrio cholerae, O1 virulence, antibioresistance, SXT element, Senegal

INTRODUCTION

Cholera is an epidemic diarrheal disease caused by toxigenic Vibrio cholerae, serogroup O1 or O139. There are two biotypes in the serogroup O1, classical and El Tor. The seventh pandemic of cholera were due to V. cholerae O1, biotype El Tor, began in Celebes (Islands) in 1961 and spread in West African countries in the early 1970s while the fifth and the sixth pandemics of cholera were caused by the classical biotype (Kaper et al., 1995). For over a decade, Africa has been the continent most affected by cholera in terms of the number of individuals infected and the frequency of outbreaks recorded1. In 2004–2005, cholera outbreaks occurred in eight countries in Africa with 125,082 cases and 2,230 deaths, CFR 1.78 (WHO, 2006). However, in some areas, the CFR exceeded 10%. In Senegal, the cholera outbreak has caused 31,719 cases with approximately

1 http://www.who.int/wer
458 deaths (CFR, 1.44%) and the most affected regions were Diourbel and Dakar; the index case was a young Guinean living in a populous district in Dakar (Manga et al., 2008). Smaller scale epidemics have been reported from 2006 to 2008. However, no cases have been reported since July 2010, this is probably due to the monitoring implemented by the Senegalese Ministry for Health (Global Task Force on Cholera Control, 2006).

The pathogenicity of *V. cholerae* O1 and O139 isolates depends on a combination of factors including the coordinated expression of virulence factors, and the secretion of cholera toxin (CT). Molecular analysis of *V. cholerae* revealed the presence of two genetic elements in the genome of pathogenic strains: the lysogenic bacteriophage (CTXo), which hosts at least six genes including toxin genes: ctxAB, ace, and zot encoding, respectively A and B subunits CT, accessory enterotoxin, and zonula occludens toxin), and the *Vibrio cholerae* pathogenicity island (VPI), which carries genes for the pilus colonization factor, toxin coregulated pilus (TCP) (Pearson et al., 1993; Waldor et al., 1997). Strains named “atypical El Tor” have traits of both classical and El Tor (Nair et al., 2002). Recently, several atypical El Tor strains have been reported, including Matlab variants (Safa et al., 2006), Mozambique variants (Ansaruzzaman et al., 2004), altered El Tor (Nair et al., 2006), and hybrid El Tor strains, harboring the classical CT allele ctxB1 (Goel et al., 2008; Safa et al., 2008). Safa et al. (2010) proposed the term “atypical El Tor” for all *V. cholerae* O1 El Tor that harbor classical traits.

*Vibrio cholerae* O1 strains isolated in Africa are known to be resistant to many antibiotics (Ceccarelli et al., 2006; Quilici et al., 2010). Drug-resistance of bacteria is linked to the mobilization and the dissemination of resistance genes through genetic determinants such as plasmids, integrons, and transposons. The SXT element is a self-transmissible mobile genetic element belonging to the family of integrating and conjugative elements (ICEs) that originally was discovered in a *V. cholerae* O139 isolate from India (MO10) which is resistant to streptomycin (Sm), trimethoprim (Tm), sulfamethoxazole (Su), and chloramphenicol (Wozniak et al., 2009; Ceccarelli et al., 2010). The SXT element is always integrated into the 5′ end of the chromosomal gene prfC and able to replicate with the host chromosome (Waldor et al., 1997). Capture and spread of antibiotic resistance determinants by integrons is an effective route of antimicrobial resistance dissemination among Gram-negative bacteria (Mazel, 2006). Several of integrons have been described based on integrase gene. The class 1 integron is widely spread among *V. cholerae* isolates with various types of resistance gene cassettes (Dalsgaard et al., 2001; Ceccarelli et al., 2006). Class 4 integron named superintegrons is a component SXT element found in several bacteria in particular in *V. cholerae*. Superintegrons are the ancestors of multiresistant integrons (Mazel, 2006). Integrons and ICEs have been found in *V. cholerae* isolated in Mozambique, Iran, and India and they have largely contributed to the spread of antibiotic resistance (Amita et al., 2003; Adabi et al., 2009; Pugliese et al., 2009).

In Senegal, there is little data available on the genetic determinants of virulence and antibiotic-resistance among epidemic *V. cholerae* isolates. Despite the description of multiresistant isolates during the lastest cholera outbreaks in Senegal in 1994 (Aidara et al., 1998) and in 2004–2006 (Manga et al., 2008), the molecular mechanisms of antibiotic resistance have never been studied. The objective of this work was to characterize the genetic determinants of virulence and antibiotic-resistance in *V. cholerae* O1 isolated during the latest cholera outbreak in Senegal.

**MATERIALS AND METHODS**

**Bacterial Isolates**

A total of 403 *V. cholerae* serogroup O1 strains were isolated in different areas in Senegal between November 2004 to May 2005 from patients with acute diarrhea. A sampling of fifty isolates were randomly selected to represent the most affected population: Dakar (39); Diourbel (09); Kaolack (01); Louga (01) (Figure 1).

All isolates were identified with the API 20E (Biomerieux, Marcy l’Etoile, France) and serotyped using anti-Ogawa, anti-Inaba antisera.

**Susceptibility to Antibiotics**

Antimicrobial susceptibility testing was performed using the Kirby Bauer disk diffusion method on Muller Hinton agar. The following antibiotics were tested: ampicillin (AM, 10 µg), amoxicillin-clavulanic acid (AMC, 20 µg/10 µg), cefotaxime (CTX, 30 µg), streptomycin (S, 10 µg), tetracycline (TCY, 30 µg), chloramphenicol (CHL, 30 µg), nalidixic acid (NA, 30 µg), pefloxacin (5 µg), trimethoprim (T, 5 µg), sulfamethoxazole (Su, 200 µg), trimethoprim-sulfamethoxazole (TSu, 1.25 µg/23.25 µg). The diameter of inhibition zones was interpreted following the CLSI recommendations for enterobacteria.

**DNA Extraction**

Total DNA was obtained by using QIAamp DNA Mini Kit (Qiagen SA, Courtaboeuf, France).

**PCR Amplifications**

**Detection of Antibiotic Resistance and Virulence Molecular Markers**

PCR analysis was performed for detection of genetic determinants of antibiotic resistance and virulence. Amplification was carried out and virulence with primers described elsewhere (Ploy et al., 2000; Hochhut et al., 2001; Shi et al., 2006), and GenBank accession number AF099172. For the detection of virulence genes, primers used as those described by Ogawa et al. (1990), Keasler (1993), and Shi et al. (1998) (Table 1) and GenBank accession numbers (AF262318, GQ485654). Chromosomal integration was detected by amplification of the right SXT element chromosome junction (attP-prfC gene sequence) (Table 1).

All amplified DNA fragments were resolved by conventional electrophoresis in 1% agarose gel, stained with ethidium bromide and visualized under UV light.

2http://www.clsi.org/
**ctxB Typing by MAMA PCR**

Mismatch Amplification Mutation Assay (MAMA) based PCR was performed to detect the presence of *ctxB* classical and or El Tor biotype *V. cholerae* O1 isolates, using specific primers described elsewhere (Morita et al., 2008).

**Cloning and Sequencing**

The integrase SXT fragment (*intSXT*) was purified with the QIAquick kit (Qiagen SA, Courtaboeuf, France), and cloned with the pGEMT vector (Promega, Madison, WI, USA), transformed into XL1-Blue competent cells (Stratagene, Garden Grove, CA, USA).

The insert of the recombinant plasmid was sequenced with dye terminator on ABI Prism automatic sequencer as described by the manufacturers. The sequences were analyzed by nucleotide BLAST search at the National Center for Biotechnology Information (NCBI) website. Primers were used for cloning and sequencing are listed on Table 1.

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**Conjugation Experiments**

Conjugation experiments were used to transfer resistance determinants from *V. cholerae* O1 isolates into nalidixic acid-resistant *E. coli* C1 strain. Mating experiments were carried out by mixing volumes of Luria Bertani (LB) broth in a ratio 2:1 overnight culture of donor and recipient strains. The cultures were transferred to LB agar plates containing trimethoprim (32 µg/ml), sulfamethoxazole (160 µg/ml), and nalidixic acid (50 µg/ml). To confirm the transfer of antibiotic resistance genes, transconjugants were tested for sensitivity to antibiotic and by PCR.

This study was carried out in accordance with the recommendations of Senegalese Ethical Committee, with informed consent from all subjects. The isolates used in this study were taken for the purposes of research, and the protocol was approved by the Senegalese Ethical Committee (N°0046/MSAS/DRPS/CNERS).
### TABLE 1 | Primers used in this study.

| Primer sequence (5′-3′) | Primers | Target gene | Reference |
|------------------------|---------|-------------|-----------|
| ACA TGT GAT GGC GAC GCA CGA | int1L | intI1 | Ploy et al., 2000 |
| ATT TCT GTC CTG GCT GGC GA | int1R | intI1 | Ploy et al., 2000 |
| CAC GGA TAT GGC ACA AAA AGG T | int2L | intI2 | Ploy et al., 2000 |
| GTA GCA AAC GAG TGA CGA AAT G | int2R | intI2 | Ploy et al., 2000 |
| GCC TCC GGC AGC GAC TTC TGG | int3L | intI3 | Ploy et al., 2000 |
| ACG GATCTGCAAACCTGACT | int3R | intI3 | Ploy et al., 2000 |
| GTG TTC GCG AAT TTA TGC | int4-1 | intI4 | Shi et al., 2006 |
| ACG GGA TAG TGG TGG CTT TAA | int4-2 | intI4 | Shi et al., 2006 |
| GCT GGA TAG GTT AAG GGC GG | SXT1 | intSXT | Hochhut and Waldor, 1999 |
| CTC TAT GGG CAC TGT CCA CAT TG | SXT2 | intSXT | Hochhut and Waldor, 1999 |
| CAA GCG GAA AAA AAT CCA TA | SXT-R1F | SXT | Pugliese et al., 2009 |
| AGAATCGAATGCGTACAGG | SXT-R1R | prfC | Keasler, 1993 |
| CTCAGCCGCTTGGTATTGCGCAGC | ctxA-1 | ctxA | Shi et al., 1998 |
| TCTATCTGATGACCTATTAGC | ctxA-2 | ctxA | Shi et al., 1998 |
| GGG CTA AAC GAG TGA CGA AAT G | Zot-1 | zot | Shi et al., 1998 |
| CCT TGT AGG GGT AGC CGT G | Zot-2 | zot | Shi et al., 1998 |
| TAA GGA TGT CTC TAT GAT GGA CAC CC | Ace-1 | ace | Shi et al., 1998 |
| CGT GAT GAA TAA AGA TAC TCA TAG G | Ace-2 | ace | Shi et al., 1998 |
| CAC GAT AAG AAA AAC GGT CAAGAG | TcpA-F | tcp (Classical) | Ogawa et al., 1990 |
| ACC AAA TGC AAC GGC GAA TGG AGC | TcpA-R | tcp (El Tor) | Ogawa et al., 1990 |
| GAA GAA GTT TGT AAA AAG AAG ACC C | TcpA-F | tcp (El Tor) | Ogawa et al., 1990 |
| GAA AGG ACC TTC TTT CCC GAT G | TcpA-R | tcp (El Tor) | Ogawa et al., 1990 |
| ATC AG TGC TTC CAT ATC | RestC-F | RST | AF 262318 |
| ATT AAAGAG TTG AGA GAG AT | RestC-R | RST | AF 262318 |
| AGA ATG TCT TAT CAG CAT AC | RestE-F | RST | AF 262318 |
| TAG CCA CCC AAA GAA AGG CA | RestE-R | RST | AF 262318 |
| GAGTGGCACGTCGCGCCCAACGTCC | SXT-X | intSXT | This study |
| GGAATTCCGAGCATGCGAGGAGCACC | SXT-X-M | intSXT | This study |
| CATCGAGAATTAGAAGAATTGGACTTG | SXT-X-2 | intSXT | This study |
| TGTACGATGACCCATTAGAAATAAAGACC | SXT-X-3 | intSXT | This study |
| GGAATTCCCGCTGGTCGACCGCAGCTTC | SXT-1-M | intSXT | This study |
| CCGGATCGGTCTGAGAGCAATTTTACGTTA | SXT-1-M | intSXT | This study |
| CCTGATATGCTGACGATCC | SXT-1 | intSXT | This study |

### RESULTS

#### Antimicrobial Susceptibility

In this retrospective study, we show that isolates were resistant to at least four antibiotics including streptomycin (S), trimethoprim (T), sulfamethoxazole (Su), trimethoprim-sulfamethoxazole (Tsu). The analysis of antibiotic resistance patterns reveals three phenotypes: S-Su-T-TSu (90%), S-Su-T-TSu-C (8%), S-Su-T-TSu-AM (2%). All isolates were resistant to trimethoprim-sulfamethoxazole but susceptible to tetracyclines.

#### Detection of Genetic Determinants of Antimicrobial Resistance: Detection of Integrons, Resistance Genes, and SXT Element

All isolates were negative for class 1, 2, and 3 integrons. A 900 bp PCR product of the intI4 gene was obtained for all isolates.

The amplification of SXT integrase revealed an amplicon size of 3 kb in all isolates, different from the expected size, i.e., 592 bp. The SXT integrase from senegalese isolates was identical to a fragment of V. cholerae KN14, isolated in Kenya GenBank accession number (AB535680). The integration of the SXT element in the chromosome was highlighted by the amplification of the right SXT element-chromosome junction (attP-prfC) which produced a 785 bp PCR product.

To identify genes hosted by the ICE circulating in Senegal, PCR analysis revealed the presence of the following antibiotic resistances genes (sulI, floR, strA, and dfrA1), except dfr18 gene.

#### Detection of Virulence Markers

The ctxR, zot, ace genes in the CTX element were present, respectively, in 98, 92, and 88% of isolates. All isolates gave positive results for tcpA (classical and El Tor) (Figure 2) and for bacteriophage rstR repressor gene of the El Tor and classical types. The detection of virulence genes revealed the presence of the genome of filamentous bacteriophage CTXø.
of the expressed by each of the transconjugants. The PCRs for detection transconjugants showed that resistance profiles were *V. cholerae* SXT-related elements. Antimicrobial susceptibility testing of ICE-mediated resistance, transconjugants were tested for xazole, and trimethoprim by conjugation. To identify a possible determinants to chloramphenicol, streptomycin, sulfamethoxazole and chloramphenicol, they lack multiple resistant integrons.

Further studies are needed to characterize and completely sequenced the SXT-related ICE in senegalese isolates.

*Vibrio cholerae* O1 strains isolated during the lastest outbreak (2004–2005) in Senegal were “atypical” as appointed by Safa et al. The presence of these atypical isolates may explain the disease severity After 2001, atypical *V. cholerae* O1 strains have emerged in India and spread worldwide, particularly in Africa. Indeed, atypical *V. cholerae* O1 strains were described in Mozambique (B33) (Ansaruzzaman et al., 2004), and Angola (Cecarelli et al., 2011a). The apperance of atypical strains in Senegal is enigmatic, and suggest that probably these new strains followed the same West African path used by cholera to enter Africa in the early 1970s. The presence of int*AT* identical to a fragment of *V. cholerae* KN14 could confirm this hypothesis. The global replacement of El Tor prototype by atypical strains indicates the evolution of *V. cholerae* O1. Our study revealed that atypical strains are also in the process of replacing El Tor strains; this phenonenon has been described in Eastern Africa (Cecarelli et al., 2011a). This global replacement is believed to be due to unknown environmental factors and phages contribution (Faruque and Mekalanos, 2012).

**CONCLUSION**

Based to our results, atypical *V. cholerae* O1 El Tor strains were responsible for cholera outbreak in Senegal in 2004–2005.

According to our study integrons were not involved in the spread of resistance among senegalese isolates of *V. cholerae* O1 even though they have been detected in other Gram-negative enteric bacteria in Senegal. However, the detection of the SXT element in all isolates, irrespective of their resistance phenotypes, could have a clinical significance and should be monitored to avoid dissemination in other bacteria. The understanding of the basis of antimicrobial resistance patterns could inform guidelines for empirical treatment to reduce injudicious antimicrobial use. Further studies should be conducted to characterize the SXT element identified in Senegalese *V. cholerae* isolates. The genetic changes occurred in *V. cholerae* O1 El Tor strains need to be monitored to prevent severe cholera outbreaks in Africa.

**AUTHOR CONTRIBUTIONS**

BS-B participated in the molecular genetic studies and drafted the manuscript. MD carried out the molecular genetic studies.
AW participated in the molecular genetic studies. AS participated on the identification of isolates. GC helped in drafting the manuscript. AGS helped on the collection and the identification of isolates in all sites. CB participated in the design and coordination of the study. AG-S designed the study, and wrote the manuscript. All authors read and approved the final manuscript.

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**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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