

Risk of Vibrio Transmission Linked to Consumption and Contact with Water in Benin.

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Introduction: Vibrio infections have increased in Benin, and this phenomenon is expected to increase due to climate change, increased consumption of contaminated water and the number of people who are immunocompromised. The objective of this study was to evaluate the risk of Vibrio transmission linked to the use of contaminated water in Benin. .

Méthodologie

Water samples [n = 220] were analyzed to isolate Vibrio strains using their biochemical and cultural characteristics. The species were identified by the Polymerase Chain Reaction technique by monitoring the search for genes encoding the cholera toxin of Vibrio cholerae [*ctxA* and *ctxB*] and the direct thermostable and thermostable hemolysins linked to *Vibrio parahaemolyticus* [*tdh* and *trh*].

Table 1. List of used primers for the molecular characterization of Vibrio strains

Gènes cibles	Amorces	Séquence (5-3)	Taille des fragments amplifiés
16S/23S	VC-F	5'-TTA AGC SIT TTC RCT GAG AAT G- 3'	295-310 pb
ISR	VCM-R	5'-AGT CAC TTA ACC ATA CAA CCC G- 3'	
<i>Pr72H</i>	VP32	5'-CGA ATC CTT GAA CAT ACG CAG C- 3'	320-387 pb
<i>ToxR</i>	VP33	5'-TGC GAA TTC GAT AGG GTG TTA ACC-3'	368
	ToxR 4	5'-GTC TTC TGA CGC AAT CGT TG- 3'	
	ToxR 7	5'-ATA CGA GTG GTT GCT GTC ATG- 3'	
<i>ctxA</i>	CTX2	5'-CGG GCA GAT TCT AGA CCT CCT G- 3'	564 pb
	CTX3	5'-CGA TGA TCT TGG AGC ATT CCC AC- 3'	
<i>ctxB</i>	CTX7	5'-GGT TGC TTC TCA TCA TCG AAC CAC- 3'	460 pb
	CTX9B	5'-GAT ACA CAT AAT AGA ATT AAG GAT G- 3'	
<i>tdh</i>	L.tdh	5'-GTA AAG GTC TCT GAC TTT TGG AC- 3'	269 pb
	R.tdh	5'-TGG AAT AGA ACC TTC ATC TTC ACC- 3'	
<i>trh</i>	L.trh	5'-TTG GCT TCG ATA TTT TCA GTA TCT- 3'	500 pb
	R.trh	5'-CAT AAC AAA CAT ATG CCC ATT TCC G- 3'	

Résultats

The results of the incidence of vibrio's and other strains in the different communes are summarized in figure 2 and 3. Thus, it appear that the collected water samples were contaminated by *Citrobacter freundii* (17.73%), *Vibrio spp* (32.73%), *Proteus spp* (20.45%), *Salmonella spp* (28.18%) and *Escherichia coli* (23.18%). The lowest rate of *Vibrio spp* (15%) was obtained in the communes of Athiémé and Sèmè-Podji while a high rate of *Vibrio spp* (65%) was obtained in the commune of Savalou. In addition, *Salmonella sp.* was highly identified (60%) in the samples collected in the municipality of Aguégué. Concerning the *Escherichia coli* strains, they were highly isolated from the samples collected in the northern (85% for Parakou and 55% for Djougou) part of the country.

Molecular Identification of Vibrio species

Of the 86 strains of Vibrio isolated from sampled waters, 13.95% belong to the species *V. alginolyticus*, 18.60% to the species *V. parahaemolyticus*, 35% to the species *V. cholerae* and 32.56% to the species *Vibrio spp*

Acknowledgements : The authors express their gratitude to the LBTMM staff for their contribution to this study. .

Distribution of virulence factors in Vibrio species.

The genes encoding major virulence factors, cholera toxin of *V. cholerae* [*ctxA* and *ctxB*] and the direct and thermostable heat-stable hemolysins of *V. parahaemolyticus* [*tdh* and *trh*] were detected in strains of *V. cholerae* and *V. parahaemolyticus* which we characterized by PCR. Thus, the characterized *Vibrio cholerae* strains harbor the gene encoding for *ctxA* [6.67%], *ctxB* [10%] and the couple *ctxA-ctxB* [3.33%] toxins [Figure 1]. Likewise, the 12.5% *V. parahaemolyticus* strains contain the encoding for *tdh* toxins and 31.25% of them harbor both *tdh* and *trh* [Figure 2]. The search for genes [*tdh* and *trh*] in *V. alginolyticus* was also negative.

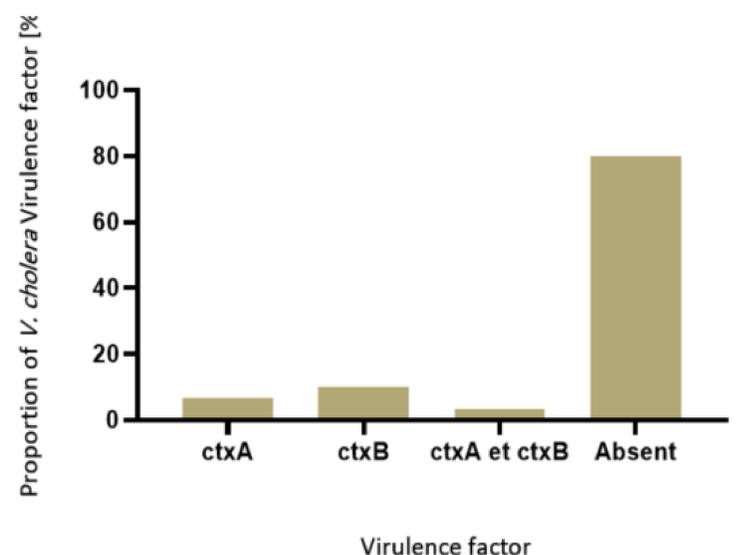


Figure [1]: Percentage of *Vibrio cholerae* species carrying genes encoding cholera toxin.

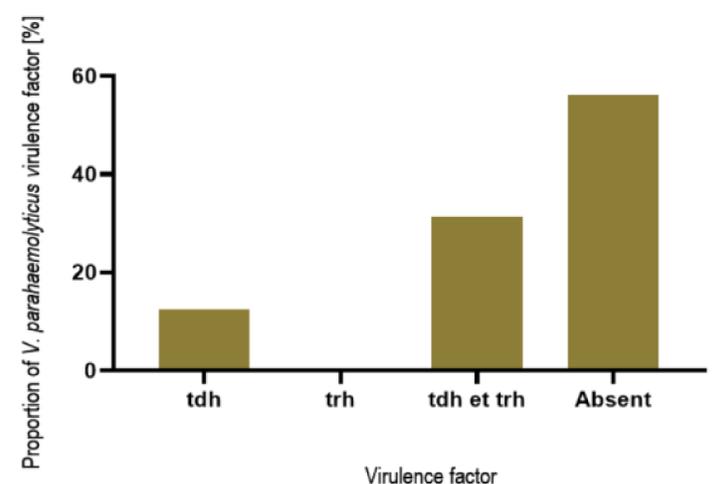


Figure [2]: Percentage of *Vibrio parahaemolyticus* species harboring genes encoding the hemolysins *tdh* and *trh*.

Conclusion

Epidemics can be triggered by natural or fabricated events that contaminate drinking water or compromise access to safe drinking water and sanitation. The incidence of vibriosis is increasing, perhaps in part because of the spread of *Vibrio* species promoted by climate change and increasing water temperature.

Mots-Clés Water; *Vibrio* species; Polymerase Chain Reaction; Virulence Genes; Bacterial Resistance.