

Table 1. *Distribution and comparison of ctxB genotypes in V. cholerae strains**

Subtype	ctxB genotype	Nucleotide position (amino-acid position)								Ref.
		58 (20)	72 (24)	83 (28)	101 (34)	115 (39)	138 (46)	165 (55)	203 (68)	
O1	1 (Classical, 569B)	C (His)	A (Gln)	A (Asp)	A (His)	C (His)	T (Phe)	A (Lys)	C (Thr)	[3, 6]
	2 (El Tor, Australia)	C (His)	A (Gln)	A (Asp)	A (His)	C (His)	G (Leu)	A (Lys)	C (Thr)	
	3 (El Tor, N16961)	C (His)	A (Gln)	A (Asp)	A (His)	T (Tyr)	T (Phe)	A (Lys)	T (Ile)	
	7 (Altered El Tor)	A (Asn)	A (Gln)	A (Asp)	A (His)	C (His)	T (Phe)	A (Lys)	C (Thr)	
	10	C (His)	A (Gln)	A (Asp)	C (Pro)	T (Tyr)	T (Phe)	A (Lys)	T (Ile)	[1]
	11	C (His)	A (Gln)	A (Asp)	C (Pro)	C (His)	T (Phe)	A (Lys)	C (Thr)	(this study)
O139	3	C (His)	A (Gln)	A (Asp)	A (His)	T (Tyr)	T (Phe)	A (Lys)	T (Ile)	[3, 7]
	4	C (His)	A (Gln)	A (Asp)	A (His)	T (Tyr)	T (Phe)	A (Lys)	C (Thr)	
	5	C (His)	A (Gln)	C (Ala)	A (His)	C (His)	T (Phe)	A (Lys)	C (Thr)	
	6	C (His)	A (Gln)	A (Asp)	C (Pro)	T (Tyr)	T (Phe)	A (Lys)	C (Thr)	
O27	8	C (His)	C (His)	C (Ala)	A (His)	C (His)	T (Phe)	A (Lys)	C (Thr)	[8]
O37	9	C (His)	A (Gln)	A (Asp)	A (His)	C (Leu)	G (Leu)	C (Asn)	C (Thr)	[9]

* Adapted from Safa *et al.* [4].

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M. A. MARIN, A. C. P. VICENTE

Laboratory of Molecular Genetics of Microorganisms,
Oswaldo Cruz Institute (IOC) – Oswaldo Cruz Foundation
(FIOCRUZ), Rio de Janeiro, Brazil

Author for correspondence:

Dr A. C. P. Vicente, Instituto Oswaldo Cruz (IOC)/
FIOCRUZ,
Av. Brasil, 4365, PO Box 926 CEP 21045-900,
Rio de Janeiro, Brazil
(Email: anapaulo@ioc.fiocruz.br)

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Variants of *Vibrio cholerae* O1 El Tor from Zambia showed new genotypes of ctxB: a reply to Marin & Vicente

We appreciate and thank Marin & Vicente for a quick analysis of *ctxB* sequences that we deposited in GenBank under the accession numbers EU932878–EU932884 [1].

In fact the sequences of the *ctxB* gene of Zambian strains were deposited as additional information to confirm the result of MAMA-PCR as well as to type the strains following Olsvik *et al.* overlooking the actual result of the genotype [2]. After the report by Safa and co-workers [3] we are now sequencing a large number of variant strains of *V. cholerae* O1 for the *ctxB* gene that were isolated from cholera-endemic areas globally in order to understand the actual number and location of new genotypes of *ctxB*. In our published paper, we concentrated our analysis on targeting the pattern of nine virulence regions of *V. cholerae* O1 especially the regions for VSP-I and VSP-II [1]. However, Marin & Vicente, in their letter, have clearly identified the new genotypes 10 and 11 in Zambian strains. They have correctly identified three distinct *ctxB* alleles among Zambian strains, not the two types that we stated in our published paper [1]. We did not analyse the clonal lineages in terms of genotype of the strain. However, as

new genotype 10 (EU932878) belongs to cluster A, genotype 11 belongs to cluster B as the other strain 224/12 (EU932882) isolated in 2004 was included for pulsed-field gel electrophoresis in this study from Zambia [1].

References

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M. ANSARUZZAMAN, N. A. BHUIYAN

Enteric and Food Microbiology Unit, Laboratory Sciences Division, ICDDR,B, Bangladesh
(Email: ansar@icddr.org)
(Email: bhuiyan@icddr.org)