

TITLE: Phenotypic and genotypic characteristics of *Vibrio cholerae* O1 isolated from 1991 to 2001 in Brazil

AUTHORS: RODRIGUES, E.C.P.¹; PRIBUL, B.R.^{1,3}; SANTOS, A.F.M.^{1,3}; ROGES, E.M.¹; IASBICK, L.L.F.¹; COSTA, R.G.¹; GONÇALVES, V.D.¹; BERTO, L.H.²; RODRIGUES, D.P.¹

INSTITUTION:

1- FUNDAÇÃO OSWALDO CRUZ, AV. BRASIL, 4365 - MANGUINHOS, RIO DE JANEIRO - CEP: 21040-360

2 - SVS /MS - SECRETARIA DE VIGILÂNCIA EM SAÚDE/ MINISTÉRIO DA SAÚDE (SRTVN Q701 BLD - ED PO700, BRASÍLIA/DF, BRASIL)

3-UNIVERSIDADE FEDERAL FLUMINENSE, PÓS-GRADUAÇÃO EM HIGIENE VETERINÁRIA E PROCESSAMENTO TECNOLÓGICO DE P.O.A. - RUA VITAL BRAZIL FILHO, Nº 64 – NITERÓI – RJ – CEP 24.230. 340

It has been suggested that the original ecosystem for the growth of the species of *Vibrio cholerae* O1 is the sea, however *V.cholerae* O1 persists environmentally in river, estuarine, and coastal waters around the world. In Brazil *Vibrio cholerae* O1 reappeared in 1991 after its reintroduction in Peru, having spread to almost all the countries of Latin America, facilitated by the lack of sanitation. Particularly in Brazil, the introduction of this microorganism occurred through the Amazon region, and in a short time arrived in the Northeast where, due to the geographic characteristics established in the environment in different aquatic systems, however like what occurs in the Indian subcontinent strains isolated from the environment loses the virulence. *V. cholerae* presents about 250 serovars, with serogroups O1 and O139 being the only ones recognized for causing epidemics. Considering the knowledge acquired during the 7th pandemic, in the present evaluation we aim to verify the capacity that strains isolated from 1991 to 2001 maintains characteristics as antimicrobial resistance, virulence genes and identity in its clonal profile. Seventy-four strains isolated in different states of the north and northeast regions were randomly selected among the strains, maintained at room temperature in buffered nutrient agar. These were isolated in TCBS Agar, performed the identification of the genus and in sequence characterized antigenically using poly and monovalent somatic antisera. Antimicrobial susceptibility profile was reconfirmed by the agar diffusion method according to the recommendations of the Clinical and Laboratory Standards Institute (CLSI, 2017), using disks impregnated with the following drugs and their concentrations (OXOID): Ampicillin (10 µg), FOX (30µg), CAZ (30µg), NAL (30µg), Ciprofloxacin (5µg), SXT (23.75 / 1.25µg); the virulence genes will be characterized by PCR and subtyping by PFGE according to the PULSENET / CDC protocol. The strains were resistant to: FOX 63.5%, AMP 21.6%, NAL 5.4% and no resistance had been observed to SXT and CIP. The results obtained with the strains isolated between 1991 and 1992 showed that 33.3% isolated in the states of the Amazon region presented resistance to 3rd generation cephalosporins, while the dispersion of *V.cholerae* among the different states to the Northeast and Southeast of Brazil, the percentage of strains with this characteristic decreases to 22.2%.

Key words: *Vibrio cholera* O1, Antimicrobial Resistance, PFGE