

MOLECULAR CHARACTERIZATION OF *VIBRIO CHOLERAE* O26 STRAINS  
ISOLATED FROM HUMAN ENTERIC PROCESSES IN BRAZIL

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The identification of the *Vibrio cholerae* serogroup O139 as causative agent for epidemic cholera, a second etiologic agent distinct from the O1 serogroup known to cause this disease, raised the possibility of other serogroups being associated with new outbreaks. In Brazil, six strains of the O26 serogroup were isolated from humans during the 1990s' cholera epidemic. We proposed to characterize at the molecular level the genes associated with their pathogenicity. First, we amplified fragments of 12 genes known to be associated with the pathogenicity of the O1 serogroup, confirming the presence of the CTXphi prophage and the *Vibrio* Pathogenicity Island. One of the amplified fragments, part of the *ctxA*, was sequenced and found to be 100% identical to equivalent regions from *V. cholerae* O1. In contrast, no amplification products were obtained from PCR reactions aimed at the chromosomal *rfbN* locus (specific for the O1 serogroup), nor any of these strains were capable of expressing cholera toxin (CT) as assayed through Western-Blots. The seroconversion of strains of *V. cholerae* O1 in other serogroups justifies the presence of virulence genes in these strains. Thus, we aim to sequence the 16S and 23S spacer region to compare their phylogenetic relationship with those of the O1 serogroup.

Keywords: *Vibrio cholerae*, CTXphi prophage, *Vibrio* Pathogenicity Island, phylogenetic relationship