

Genetic diversity of toxigenic *Vibrio cholerae* O1 from Sabah, Malaysia 2015

ABSTRACT

Background

Cholera is an important health problem in Sabah, a Malaysian state in northern Borneo; however, *Vibrio cholerae* in Sabah have never been characterized. Since 2002, serogroup O1 strains having the traits of both classical and El Tor biotype, designated as atypical El Tor biotype, have been increasingly reported as the cause of cholera worldwide. These variants are believed to produce clinically more severe disease like classical strains.

Purpose

The purpose of this study is to investigate the genetic diversity of *V. cholerae* in Sabah and whether *V. cholerae* in Sabah belong to atypical El Tor biotype.

Methods

ERIC-PCR, a DNA fingerprinting method for bacterial pathogens based on the enterobacterial repetitive intergenic consensus sequence, was used to study the genetic diversity of 65 clinical *V. cholerae* O1 isolates from 3 districts (Kudat, Beluran, Sandakan) in Sabah and one environmental isolate from coastal sea water in Kudat district. In addition, we studied the biotype-specific genetic traits in these isolates to establish their biotype.

Results

Different fingerprint patterns were seen in isolates from these three districts but one of the patterns was seen in more than one district. Clinical isolates and environmental isolate have different patterns. In addition, Sabah isolates harbor genetic traits specific to both classical biotype (*ctxB-1*, *rstRCl α*) and El Tor biotype (*rstRET*, *rstC*, *tcpAET*, *rtxC*, VC2346).

Conclusion

This study revealed that *V. cholerae* in Sabah were genetically diverse and were atypical El Tor strains. Fingerprint patterns of these isolates will be useful in tracing the origin of this pathogen in the future.