

ABSTRACT

Infections by strains belonging to the O3:K6 pandemic clone of *Vibrio parahaemolyticus* are prevalent in southern Thailand, and serovariants of these strains have also been detected. *V. parahaemolyticus* strains lacking important virulence genes (*tdh* and *trh*) were isolated from 6.5 to 10.9% of clinical specimens during 2000-2003. In order to understand if changes to the characteristics of *V. parahaemolyticus* occur during infection, 10 isolates collected from each of 63 patients who presented with diarrhea at Hat Yai hospital from 2003 to 2004 were examined for the presence of the *tdh* and *trh* genes, the O:K serotype, and genetic markers for the pandemic clone. Forty-two patients (66.7%) yielded identical isolates (homogeneous populations), and 21 of the patients (33.3%) yielded isolates that differed in at least one character from the other isolates (heterogeneous populations). The DNA fingerprints (examined by arbitrarily primed PCR and pulsed-field gel electrophoresis) of some, but not all, of the heterogeneous populations from single patients were indistinguishable. The results indicated that some patients were infected with a unique strain, and that *in vivo* changes (*tdh* deletion or serotype conversion) might have occurred in certain individuals. It is therefore important to bear in mind that epidemiological studies based on the analysis of a single colony from a single patient might lead to misleading conclusions. Finally, this study did not rule out the possibility that *tdh*⁻, *trh*⁻ isolates have unknown virulence mechanism other than the *tdh* and *trh* genes.