

Multilocus sequence typing reveals genetic diversity of *Vibrio parahaemolyticus* from southeastern China with clonal complexes 3 seen from 2006

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*Vibrio parahaemolyticus* has been the leading cause of foodborne infections in coastal China. Multilocus sequence typing system (MLST, <http://pubmlst.org/vparahaemolyticus/>) was used to examine the genetic diversity of seventy one *V. parahaemolyticus* strains (clinical, seafood and environmental strains) isolated from 2003-2009 in our laboratory. Seventy-one strains were classified into 62 sequence types (STs). With all the 201 STs (included those from our laboratory) in the web database, 4 clonal complexes (CCs), 18 groups and 141 singletons were observed. Out of 141 singletons, 59 were from our isolates. Other 8 STs scattered in 2CCs and 6 Groups. Phylogenetic tree showed great diversity of Chinese *V. parahaemolyticus* isolates. Strains in CC3 were considered as the founder strains responsible for worldwide outbreak of Vibriosis due to pandemic *V. parahaemolyticus* isolates. There were also CC3 strains in China from 2006-2009. The minimum evolution tree divided strains in 111 STs into four major branches. Vast majority of our isolates and those from other countries were into the two major branches, while 5 STs (representing 5 strains) were categorized in the other two minor branches due to divergence of *recA* gene.