

**GENETIC DIVERSITY IN POPULATIONS OF *SEPIELLA JAPONICA* BASED ON THE
MITOCHONDRIAL DNA SEQUENCE ANALYSIS**

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ABSTRACT: Part of the 16S rRNA gene was amplified with PCR and sequenced for 57 individuals from 5 populations of common Chinese cuttlefish *Sepiella japonica*: three from the South China Sea, one from East China Sea and one from Nagasaki water (Japan). The result showed that a total of 5 nucleotide positions were found to have insertions/deletions among these individuals, and 13 positions were examined to be variable in all the sequences, which ranged from 494 to 509 base pairs. All of the individuals were grouped into 7 haplotypes (h1–h7). The individuals from Nagasaki belonged to h1 and the h3 haplotype was found only in the coastal waters of China. A↔G transition in Nucleotide 255 was suggested to be taken as a kind of genetic marker to identify the populations distributed in East-South China Sea and the Nagasaki water of Japan.
