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Bioinformatics analysis of *Helicobacter pylori metalloprotease* gene

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To determine the sequence of the *metalloprotease* gene (*mtp*) of *Helicobacter pylori* MEL-Hp27 strain and investigate the structural characters and biological function of the *mtp*-encoded protein using bioinformatic methods. The H. *pylori mtp* gene was applified by PCR from H. *pylori* MEL-Hp27 strain, and the mtp nucleotide sequence was obtained by gene sequencing. The amino acid sequence, physicochemical properties, transmembrane region, signal peptide, glycosylation and phosphorylation sites, secondary and tertiary structure of the *mtp*-encoded protein (Mtp) were analyzed using bioinformatics software. The coding region of MEL-HP27 *mtp* gene is 615 bp in length, encoding a protein comprising 204 amino acids. Bioinformatics analysis resulted in that the homology of *mtp* among various *H. pylori* strains is 91%-98%, the metalloprotease is an unstable and alkaline hydrophilic protein, without transmembrane region and signal peptide, but contains glycosylation and phosphorylation sites. The secondary structure of metalloprotease includes alpha helix, extended strand, beta turn, and random coil, which account for 52.45%, 16.67%, 4.41% and 26.47% of the whole molecular length, respectively. The conserved structures found in Mtp suggested that this protein might belong to the M48 protein family. Mtp contains B cell-associated antigenic epitopes and CTL cell antigenic epitopes. The results indicate that Mtp is alkaline hydrophilic protein with low molecular mass, located in cytoplasm or the nucleus might play crucial role in cellular signaling, regulation of cellular function, the mechanism of host immune response to *H. pylori* infection and the pathogenesis. The findings lay novel basis for approaching pathogenic mechanism and immune prevention of *H. pylori* infection.

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