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Research progress of *Helicobacter pylori* genomics in China

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Abstract

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In the last three years there has been a dramatic increasement of genomic sequences for *Helicobacter pylori* (*H.pylori*) in the GenBank genomics database (46 completed and 189 draft , till 16th May,2013). More and more studies focus on investigation of potential molecular genetics mechanism based on the large amount of genome sequences.

We have previously used a high density tiling microarray to explore genomic features of strains isolated from patients with different gastro duodenal diseases in China, and found series differential regions that would be probably contributed to various clinical outcomes. To confirm these initial results, also to extend our knowledge of *H.pylori* genomics, we have finished whole genome sequencing of dozens of strains isolated from different geographic areas of China by using Illumina HiSeq 2000. Paired-end libraries (500 bp and 2 kb) were generated and more than 100 Mb of high-quality data were obtained for all strains. Finally, the paired-end reads from the two libraries were de novo assembled into scaffolds. Gene prediction and annotation, as well as a preliminary comparative genomics and population structure analysis were performed to understand potential microevolution correlated with geography and ethics. Since these isolates were recovered from gastric cancer, ulcer and gastritis patients respectively. The comprehensive comparisons of genomes from different diseases were also done. These strains were shown have a high genomic diversity compared to isolates involved in chronic superficial gastritis and gastric cancer in the previous studies.

Biography

Prof. Jianzhong Zhang, Ph.D & MD, advisor for Ph.D candidates. President of Chinese Society of Public Health, Chinese Medical Association (CMA). Deputy director of National Institute for Communicable Disease Control and Prevention (ICDC), Chinese Center for Disease Control and Prevention (China CDC). Director of Department of Diagnosis, ICDC, China CDC (involving in the study of Helicobacter pylori(H.pylori), Campylobacter jejuni （C. jejuni）, Streptococcosis , Staphylococcus aureus, Mycoplasma , Acinetobacter baumannii and MALDI-TOF Mass Spectrometry -based Identification of bacterial pathogens). He is the member of the editorial committee for Helicobacter. As the Member of Chinese Society and American Society for Microbiology, Prof. Zhang has great interests in the molecular biological studies on bacteria, including the biological characters and pathogenicity of H.pylori, H.pylori vaccine, Guillain-Barre Syndrome related C. jejuni, the relationship of H.pylori infection and gastric cancer, epidemic diseases diagnosis, DNA chip development, the proteomic research and the antibiotic resistance study of bacteria. He has published more than 170 papers and books. He is currently in charge of two ongoing projects on the diagnostic method development for communicable diseases control and prevention.