

Human migration

Type: Book Chapter

Abstract:

Helicobacter pylori strains from different geographic areas exhibit clear phylogeographical differentiation. The genotype of the virulence genes is useful as a tool to track human migration utilizing the high genetic diversity and frequent recombination between different *H. pylori* strains. Using combinations of the virulence genes, five major groups have been defined according to geographical associations. Multilocus sequence typing (MLST) analysis using seven housekeeping genes also are widely used markers for genomic diversity. It was revealed that seven modern population types of *H. pylori* which derived from six ancestral populations provide more detailed information on human migration than does the analysis of human genetics. Although approaches by MLST and virulence factors are effective, these methods focus on a small number of genes and may miss information conveyed by the rest of the genome. Genome-wide analyses using DNA microarray or whole-genome sequencing technology give a broad view on the genome of *H. pylori*. In particular, next-generation sequencers, which can read DNA sequences in less time and at lower costs than Sanger sequencing, enabled us to efficiently investigate not only the evolution of *H. pylori*, but also novel virulence factors and genomic changes related to drug resistance.

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