

ZMIENNOŚĆ GENETYCZNA *CAMPYLOBACTER JEJUNI*

Elżbieta Katarzyna Jagusztyn-Krynicka,
Elżbieta Brzuszkiewicz

1. Wstęp. 2. Podstawowe cechy genomu *C. jejuni* NCTC 11168. 3. Typowanie bakterii rodzaju *Campylobacter*. 3.1. Fenotypowanie. 3.1.1. Serotypowanie. 3.1.2. Biotypowanie. 3.2. Genotypowanie. 4. Zmienność genetyczna szczepów rodzaju *Campylobacter*. 4.1. Fakty dokumentujące różnorodność genetyczną szczepów *C. jejuni*. 4.2. Mechanizmy warunkujące genetyczną różnorodność szczepów *C. jejuni*. 5. Podsumowanie

Genetic diversity of *Campylobacter jejuni*

Abstract: *Campylobacter jejuni* is one of the most common causes of bacterial diarrhea worldwide. It is also the primary bacterial cause of food-borne illness. Variability in the clinical symptoms of *Campylobacter* infection has been observed for many years. The clinical picture ranges from asymptomatic infection to secretory diarrhea and, less frequently, inflammatory diarrhea. Other clinical presentations of *Campylobacter* infection are meningitis, bacteremia, localized extraintestinal infections, and immunoreactive complication such as Guillain-Barré syndrome and reactive arthritis. variability of the infection symptoms and the phenotypic traits of isolates may be related to genetic diversity of *Campylobacter* strains. The diversity within *C. jejuni* isolates has been well established and is detectable at both, the phenotypic and genotypic level. The lack of the genetic, physiological and pathogenic information of this pathogen was the driving force behind the *C. jejuni* NCTC 11168 genome project. Completion of genome sequence offers unrivalled opportunities to understand the molecular basis of virulence of this pathogen and revealed a few mechanisms by which the organism can generate genetic diversity. Among a lot of novel features revealed by the genome sequence are at least 25 hypervariable sequences mostly found in genes encoding surface structures. Variation of the length of poly G/C tracts in genes containing these hypervariable sequences is likely to play a key role in enabling *C. jejuni* to evade the host immune response. The ability of the *C. jejuni* genome sequence data has coincided with important technological advances in bioinformatics, gene mutagenesis, proteome analysis and DNA microarrays. Given the range of disease associated with *C. jejuni* infection, combined with the diverse genotyping and phenotypic properties of clinical and environmental isolates, a *Campylobacter* DNA microarray will be particularly useful in determining correlates of pathogenicity and in deciphering the epidemiology of the microorganism.

1. Introduction. 2. Basic features of the genome sequence of *C. jejuni* NCTC 11168. 3. Typing of *Campylobacter* spp. 3.1. Fenotyping. 3.1.1. Serotyping. 3.1.2. Biotyping. 3.2. Genotyping. 4. Genetic diversity of *Campylobacter* spp. 4.1. Facts improving genetic diversity of *C. jejuni*. 4.2. Mechanisms of genetic diversity of *C. jejuni*. 5. Summary

Zakład Genetyki Bakterii
Instytut Mikrobiologii
Uniwersytet Warszawski
Warszawa 02-096
ul. Miecznikowa 1
tel. 554-12-16

Wpłynęło we wrześniu 2002 r.