

## **Abstract**

**The purpose of PulseNet Taiwan project is to build a national molecular subtyping network for real time surveillance of bacterial diseases. The network is comprised of the laboratories in the Northern Branch, Central Branch, Southern Branch, and Eastern Branch of Center for Disease Control, Department of Health. In this year, isolates of *Neisseria meningitidis*, *Shigella* spp., and *Salmonella enterica* subsp. *enterica* serovar Typhi (*S. Typhi*) and *S. Paratyphi* were analyzed by standardized pulsed-field gel electrophoresis (PFGE) protocols and the PFGE patterns were compared with those in the DNA fingerprint databases for the bacterial species to early detect cluster of infection and monitor long-term evolution of bacterial strains. In 2004, 23 *N. meningitidis*, 42 *S. flexneri*, 20 *S. sonnei*, 24 *S. Typhi*, and 6 *S. Paratyphi* were analyzed. No cluster of meningococcal infections was detected in this year. Twenty *N. meningitidis* isolates were confirmed belonging to the previously identified clonal groups in Taiwan, the other three isolates could be originated from new genetic clones. Several clusters of *S. flexneri* infections were identified. Forty *S. flexneri* infections were caused by indigenous strains, most of them have been circulating in Central and Eastern Taiwan for years. Eleven of 20 *S. sonnei* infections occurred in traveling in Southeastern Asian countries, strengthening the observation that most of *S. sonnei* strains in Taiwan in the past years could be originated from Southeastern Asian countries or China. Typhoid fever cases were caused by indigenous and exogenous strains. A major indigenous *S. Typhi* clonal group could have been circulating in the island for years. However, exogenous strains could be the major *S. Typhi* source. Further study is needed to trace *S. Typhi* source and the route of transmission. All *S. Paratyphi* isolates were genetic homogenous, they could have evolved from a common ancestor. This surveillance network is powerful in confirming cluster of infection and disease outbreak, the databases of bacterial DNA fingerprint and of host-related epidemiological information can serve as a basis for observing long-term dynamic change of the bacterial strains.**

**Keywords : Taiwan PulseNet ; Laboratory-based surveillance ; Molecular typing ; Pulsed-field gel electrophoresis**