

Application of Bacterial Genotyping Techniques in Molecular Epidemiology of Foodborne Diseases

Chien-Shun Chiou, Yen-Yi Liu, Ying-Shu Liao*

Abstract

Genotyping of bacterial isolates has been performed as a routine measure in most public health laboratories for disease surveillance and disease outbreak investigation. Among bacterial genotyping methods, pulsed-field gel electrophoresis (PFGE) and multilocus variable number tandem repeat analysis (MLVA) are the most frequently used methods for their high discriminatory power in most bacterial pathogens. When using genotyping data to elucidate a disease outbreak investigation, three hypothetical modes should be considered: H1, a disease outbreak is caused by one genotype of a pathogen (by one strain); H2, a disease outbreak is caused by multiple genotypes of a pathogen (multiple strains) or by multiple pathogens; H3, various disease outbreaks are caused by one genotype of a pathogen. With the advance of next generation sequencing (NGS) techniques, whole genome sequencing (WGS) of bacterial isolates has become practical in public health laboratories. WGS can provide genetic data for retrieving useful information including serotypes, virulence gene profiles, antimicrobial resistance genes, and genetic fingerprints to represent short-term and long-term evolutionary relationships among bacterial strains. WGS will replace PFGE and MLVA within a few years to be the determining subtyping tool for bacteria in public health laboratories. Taiwan Centers for Disease Control has to establish the laboratory capability and capacity in WGS and data analysis as soon as possible.

Keywords: Genotyping, Molecular epidemiology, Pulsed-field gel electrophoresis (PFGE), Next generation sequencing (NGS), Whole genome sequencing (WGS)

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Epidemiological Analysis of Diarrhea Outbreaks in Taipei Region, April 2015–April 2016

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Abstract

We analyzed the outbreaks of diarrhea occurred in the Taipei region from April 2015 to April 2016, and found that the major causative pathogen was norovirus, followed by rotavirus and *Vibrio parahaemolyticus*. Most outbreaks were considered as "direct person-to person transmission" (40%), or "difficult to determine the transmission mode" (32%). To clarify the source of infection and the mode of transmission, the health authority should investigate the contact history and food consumed within three days before onset date immediately after been notified. Since most cases were occurred mainly in school, the Taiwan Centers for Disease Control, the Taiwan Food and Drug Administration, and local health authorities should cooperate with each other to formulate and implement preventive measures, and regard schools as important target group. Implementing hand hygiene and food safety are the best methods to prevent outbreaks of diarrhea. By utilizing surveillance and reporting system, the health authority should conduct investigation early and take appropriate preventive measures to block the spread of disease.

Keywords: Diarrhea outbreak, Norovirus, Transmission mode, Hand hygiene

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Weekly Data of Notifiable Infectious Diseases (by week of diagnosis)

Case diagnosis week		Week 1		Week 1–1		
Classification	Disease Diagnosed ¹	2017	2016	2016	2015	
Category I	Plague	0	0	0	0	
	Rabies	0	0	0	0	
	SARS	0	0	0	0	
	Smallpox	0	0	0	0	
Category II	Acute Flaccid Paralysis	0	0	0	0	
	Acute Viral Hepatitis type A	13	2	13	2	
	Amoebiasis	7	6	7	6	
	Anthrax	0	0	0	0	
	Chikungunya Fever	0	1	0	1	
	Cholera	0	0	0	0	
	Dengue Fever	6	203	6	203	
	Diphtheria	0	0	0	0	
	Enterohemorrhagic E. coli Infection	0	0	0	0	
	Epidemic Typhus Fever	0	0	0	0	
	Hantavirus Pulmonary Syndrome	0	0	0	0	
	Hemorrhagic Fever with Renal Syndrome	0	0	0	0	
	Malaria	0	0	0	0	
	Measles	0	0	0	0	
	Meningococcal Meningitis	0	0	0	0	
	Paratyphoid Fever	1	0	1	0	
	Poliomyelitis	0	0	0	0	
	Rubella	0	0	0	0	
	Shigellosis	6	2	6	2	
	Typhoid fever	0	0	0	0	
West Nile Fever	0	0	0	0		
Category III	Acute Viral Hepatitis type B	5	2	5	2	
	Acute Viral Hepatitis type C ⁵	5	4	5	4	
	Acute Viral Hepatitis type D	0	0	0	0	
	Acute Viral Hepatitis type E	1	2	1	2	
	Acute Viral Hepatitis untype	0	0	0	0	
	Congenital Rubella Syndrome	0	0	0	0	
	Enteroviruses Infection with Severe Complications	0	1	0	1	
	Haemophilus Influenza type b Infection	0	0	0	0	
	Japanese Encephalitis	0	0	0	0	
	Legionellosis	1	0	1	0	
	Mumps ²	9	18	9	18	
	Neonatal Tetanus	0	0	0	0	
	Pertussis	0	1	0	1	
	Tetanus ²	0	0	0	0	
	Category IV	Botulism	0	0	0	0
		Brucellosis	0	0	0	0
Complicated Influenza		14	16	14	16	
Complicated Varicella ⁴		0	0	0	0	
Endemic Typhus Fever		0	1	0	1	
Herpesvirus B Infection		0	0	0	0	
Invasive Pneumococcal Disease		10	19	10	19	
Leptospirosis		3	1	3	1	
Lyme Disease		0	0	0	0	
Melioidosis		0	0	0	0	
Q Fever		0	0	0	0	
Scrub Typhus		6	12	6	12	
Toxoplasmosis		0	0	0	0	
Tularremia	0	0	0	0		
Category V	Ebola Virus Disease	0	0	0	0	
	Ebola-Marburg Hemorrhagic Fever	0	0	0	0	
	Novel Influenza A Virus Infections ⁶	0	0	0	0	
	Lassa Fever	0	0	0	0	
	Rift Valley Fever	0	0	0	0	
	Middle East Respiratory Syndrome Coronavirus	0	0	0	0	
	Yellow Fever	0	0	0	0	

1. The following 8 chronic diseases are excluded from the table: MDR-TB, Tuberculosis, Syphilis, Gonorrhoea, HIV Infection, AIDS, Hansen Disease and Creutzfeldt-Jakob Disease.
2. Reported cases.
3. Since 2014/1/1, "Varicella" was modified to "Complicated Varicella".
4. Since 2014/3/6, the case definition for confirmed Acute hepatitis C was changed from "meet the clinical and laboratory conditions" to "meet the clinical or laboratory conditions".
5. Since 2014/7/1, various subtypes of human cases of avian influenza are reported as "novel influenza A virus infections", a Category V Notifiable Infectious Disease. The original "H5N1 flu" and "H7N9 flu", which were respectively listed as a Category I Notifiable Infectious Disease and a Category V Notifiable Infectious Disease were removed from the list on the same day.
6. Since 2016/1/22, "Zika Virus Infection" was listed as a Notifiable Infectious Disease.

Suspected Clusters

- Twenty-one clusters were reported, including 12 diarrhea clusters, 3 influenza-like illness clusters, 3 tuberculosis clusters, 2 upper respiratory tract infection clusters, and 1 varicella cluster.

Imported Infectious Diseases

- 24 confirmed cases were imported from 9 countries during Week 1 of 2017.

Country Disease	Indonesia	Vietnam	Philippines	India	Australia	Cambodia	China	Thailand	Malaysia	Total
Amoebiasis	7			1	1					9
Dengue Fever	1	2	1					1	1	6
Typhoid fever	2									2
Shigellosis	2									2
Hepatitis B		2								2
Hepatitis A							1			1
Paratyphoid Fever						1				1
Chikungunya Fever	1									1
Total	13	4	1	1	1	1	1	1	1	24

Note: The statistics listed in this table include imported cases that were either confirmed or updated* in the previous week.

- A total of 13 confirmed cases were imported from 7 countries in 2017.
- Top 3 imported diseases : Dengue fever (3), Amoebiasis (3), Shigellosis (1).
- Top 3 countries responsible for most imported cases : Indonesia (5), Vietnam (3), Philippines (1).

Summary of Epidemic

- **Influenza** : Since the northeast monsoon has become prevalent, the recent temperature has dropped and fluctuated drastically from day to night. As a result, influenza activity is expected to gradually increase. H3N2 is currently the dominant strain circulating in the community.
- **Diarrhea** : As the viral gastroenteritis season is upon us, the epidemic is expected to gradually increase.
- **Enterovirus** : The epidemic has slowed down in the community. The number of visits to outpatient services and ER for enterovirus infection is expected to lower than the epidemic threshold this week. Coxsackie A virus is currently the dominant strain circulating in the community. Sporadic cases of enterovirus 71 infection have been recently confirmed.
- **Zika Virus Infection** : As the epidemic in affected areas has continued to increase, the risk of importing Zika virus into Taiwan from those countries remains elevated.

Weekly Data of Notifiable Infectious Diseases (by week of diagnosis)

Classification	Case diagnosis week Disease Diagnosed ¹	Week 2		Week 1–2	
		2017	2016	2017	2016
Category I	Plague	0	0	0	0
	Rabies	0	0	0	0
	SARS	0	0	0	0
	Smallpox	0	0	0	0
Category II	Acute Flaccid Paralysis	0	1	0	1
	Acute Viral Hepatitis type A	14	7	27	9
	Amoebiasis	10	4	17	10
	Anthrax	0	0	0	0
	Chikungunya Fever	0	0	0	1
	Cholera	0	0	0	0
	Dengue Fever	7	118	13	321
	Diphtheria	0	0	0	0
	Enterohemorrhagic E. coli Infection	0	0	0	0
	Epidemic Typhus Fever	0	0	0	0
	Hantavirus Pulmonary Syndrome	0	0	0	0
	Hemorrhagic Fever with Renal Syndrome	1	0	1	0
	Malaria	0	2	0	2
	Measles	0	0	0	0
	Meningococcal Meningitis	0	0	0	0
	Paratyphoid Fever	0	0	1	0
	Poliomyelitis	0	0	0	0
	Rubella	0	0	0	0
	Shigellosis	6	4	12	6
Typhoid fever	1	0	1	0	
West Nile Fever	0	0	0	0	
Category III	Acute Viral Hepatitis type B	7	1	12	3
	Acute Viral Hepatitis type C ⁵	3	3	8	7
	Acute Viral Hepatitis type D	1	0	1	0
	Acute Viral Hepatitis type E	0	1	1	3
	Acute Viral Hepatitis untype	0	0	0	0
	Congenital Rubella Syndrome	0	0	0	0
	Enteroviruses Infection with Severe Complications	0	0	0	1
	Haemophilus Influenza type b Infection	0	0	0	0
	Japanese Encephalitis	0	0	0	0
	Legionellosis	2	2	3	2
	Mumps ²	16	12	25	30
	Neonatal Tetanus	0	0	0	0
	Pertussis	0	0	0	1
	Tetanus ²	1	0	1	0
Category IV	Botulism	0	0	0	0
	Brucellosis	0	0	0	0
	Complicated Influenza	13	23	27	39
	Complicated Varicella ⁴	0	0	0	0
	Endemic Typhus Fever	0	1	0	2
	Herpesvirus B Infection	0	0	0	0
	Invasive Pneumococcal Disease	13	6	23	25
	Leptospirosis	4	0	7	1
	Lyme Disease	0	0	0	0
	Melioidosis	0	0	0	0
	Q Fever	1	0	1	0
	Scrub Typhus	8	12	14	24
	Toxoplasmosis	0	0	0	0
Tularremia	0	0	0	0	
Category V	Ebola Virus Disease	0	0	0	0
	Ebola-Marburg Hemorrhagic Fever	0	0	0	0
	Novel Influenza A Virus Infections ⁶	0	0	0	0
	Lassa Fever	0	0	0	0
	Rift Valley Fever	0	0	0	0
	Middle East Respiratory Syndrome Coronavirus	0	0	0	0
Yellow Fever	0	0	0	0	

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6. Since 2016/1/22, "Zika Virus Infection" was listed as a Notifiable Infectious Disease.

Suspected Clusters

- Twenty-seven clusters were reported, including 13 diarrhea clusters, 6 upper respiratory tract infection clusters, 4 tuberculosis clusters, 3 varicella clusters, and 1 influenza-like illness cluster.

Imported Infectious Diseases

- 22 confirmed cases were imported from 5 countries during Week 2 of 2017.

Country Disease	Indonesia	Philippines	Thailand	Vietnam	Malaysia	Total
Shigellosis	11					11
Dengue Fever		2	3	1	1	7
Amoebiasis	3	1				4
Total	14	3	3	1	1	22

Note: The statistics listed in this table include imported cases that were either confirmed or updated* in the previous week.

- A total of 28 confirmed cases were imported from 7 countries in 2017.
- Top 3 imported diseases : Dengue fever (9), Amoebiasis (7), Shigellosis (5).
- Top 3 countries responsible for most imported cases : Indonesia (12), Vietnam (4), Philippines (4).

Summary of Epidemic

- **Diarrhea** : As the viral gastroenteritis season is upon us, the epidemic is expected to gradually increase.
- **Influenza** : Since the northeast monsoon has become prevalent, the recent temperature has dropped. As a result, influenza activity is expected to gradually increase. H3N2 is currently the dominant strain circulating in the community.
- **Enterovirus** : The epidemic has slowed down in the community. The number of visits to outpatient services and ER for enterovirus infection is expected to dip lower than the epidemic threshold this week. Coxsackie A virus is currently the dominant strain circulating in the community. Sporadic cases of enterovirus 71 infection have been recently confirmed.
- **Zika Virus Infection** : As the epidemic in affected areas has continued to increase, the risk of importing Zika virus into Taiwan from those countries remains elevated.

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