

# Foodborne Outbreak Investigation and Whole Genome Sequences Analysis in Korea MFDS

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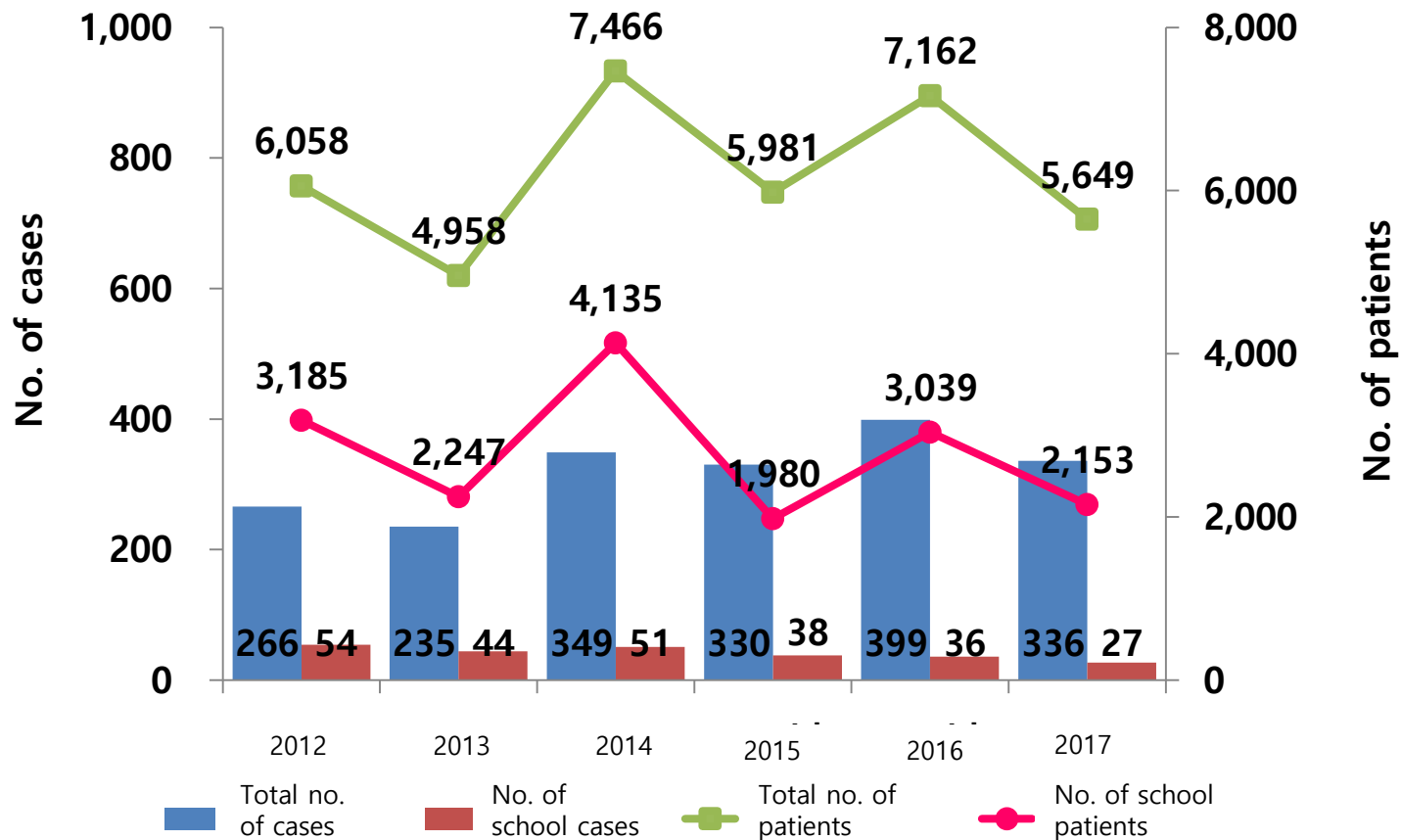
1. Foodborne Outbreaks Trend in Korea
2. Foodborne Outbreaks Investigation and Establishment of DB for Characteristics Analysis
3. Foodborne Outbreaks Investigation through WGS Analysis



# 1. Foodborne Outbreak Trend in Korea

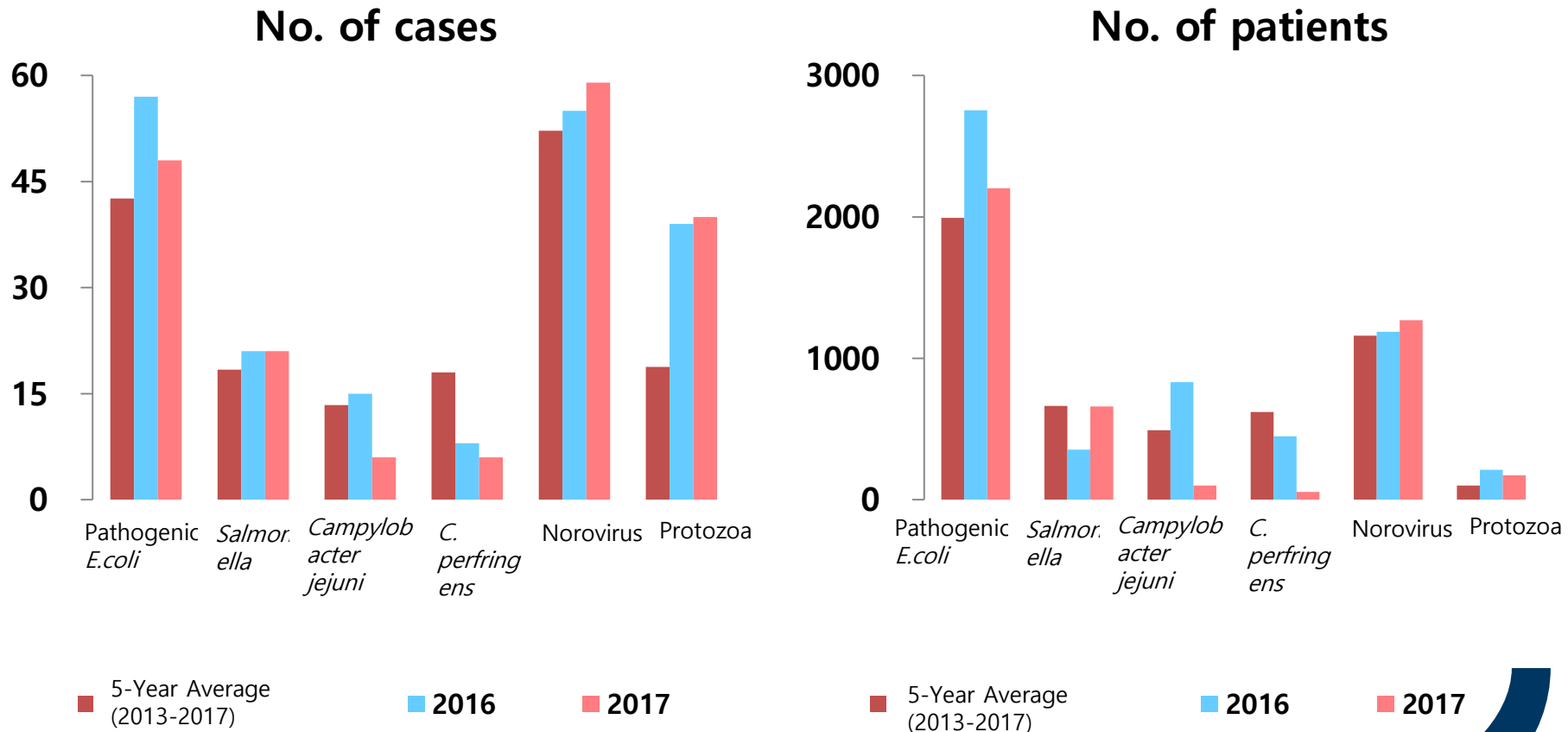
# Foodborne Outbreak Trend

Foodborne outbreak **increases** and **decreases** repeatedly every year. In particular, **foodborne outbreak in schools** significantly changes the total number of foodborne outbreak cases.



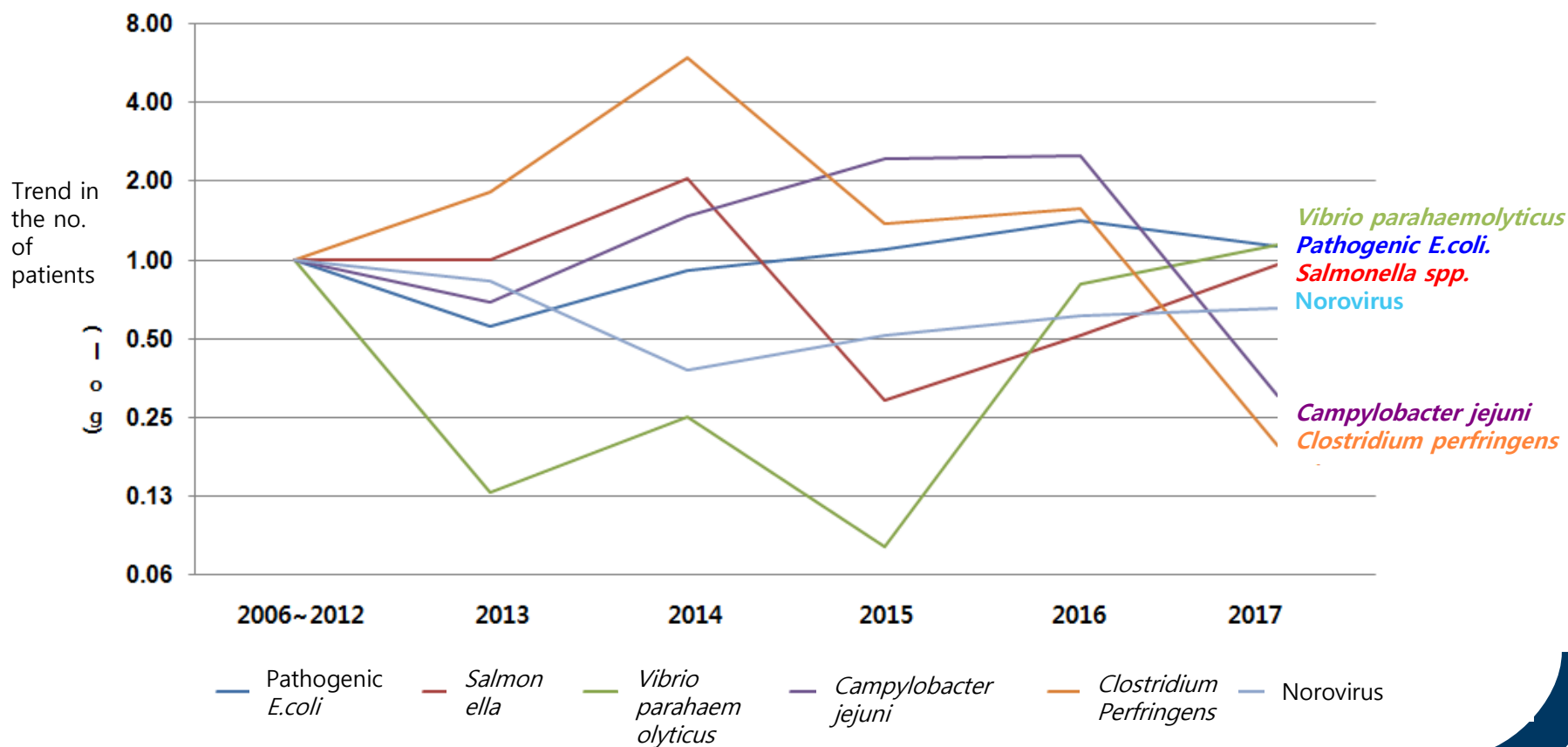
# Trend by Causative pathogens

- No. of cases : The number of **Norovirus** cases is the highest.
- No. of patients : The number of **pathogenic *E.coli*** patients is the highest.



# The relative trend of Causative pathogens

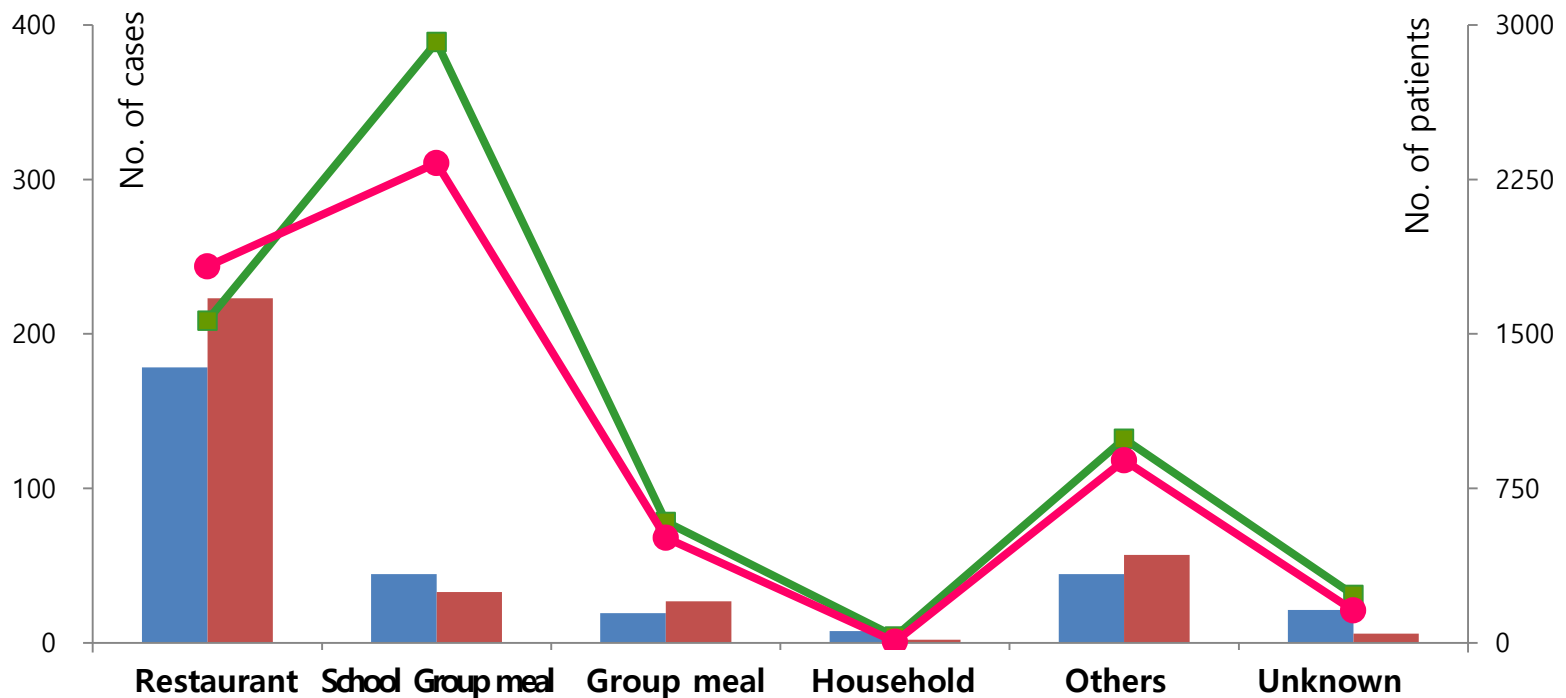
- The relative trend of occurrence shows that *Vibrio parahaemolyticus*, pathogenic *E.coli* and *Salmonella spp.* have an increasing trend
- norovirus continues to occur.





# Foodborne Outbreak Occurrence Pattern (by place)

- (No. of cases) **Restaurants (62%)** and (No. of patients) **schools (43%)** with many number of people who take school meal at a time.



5-Year average  
No. of cases (2012-2016)

No. of cases  
(2017)

5-Year average  
No. of patients (2012-2016)

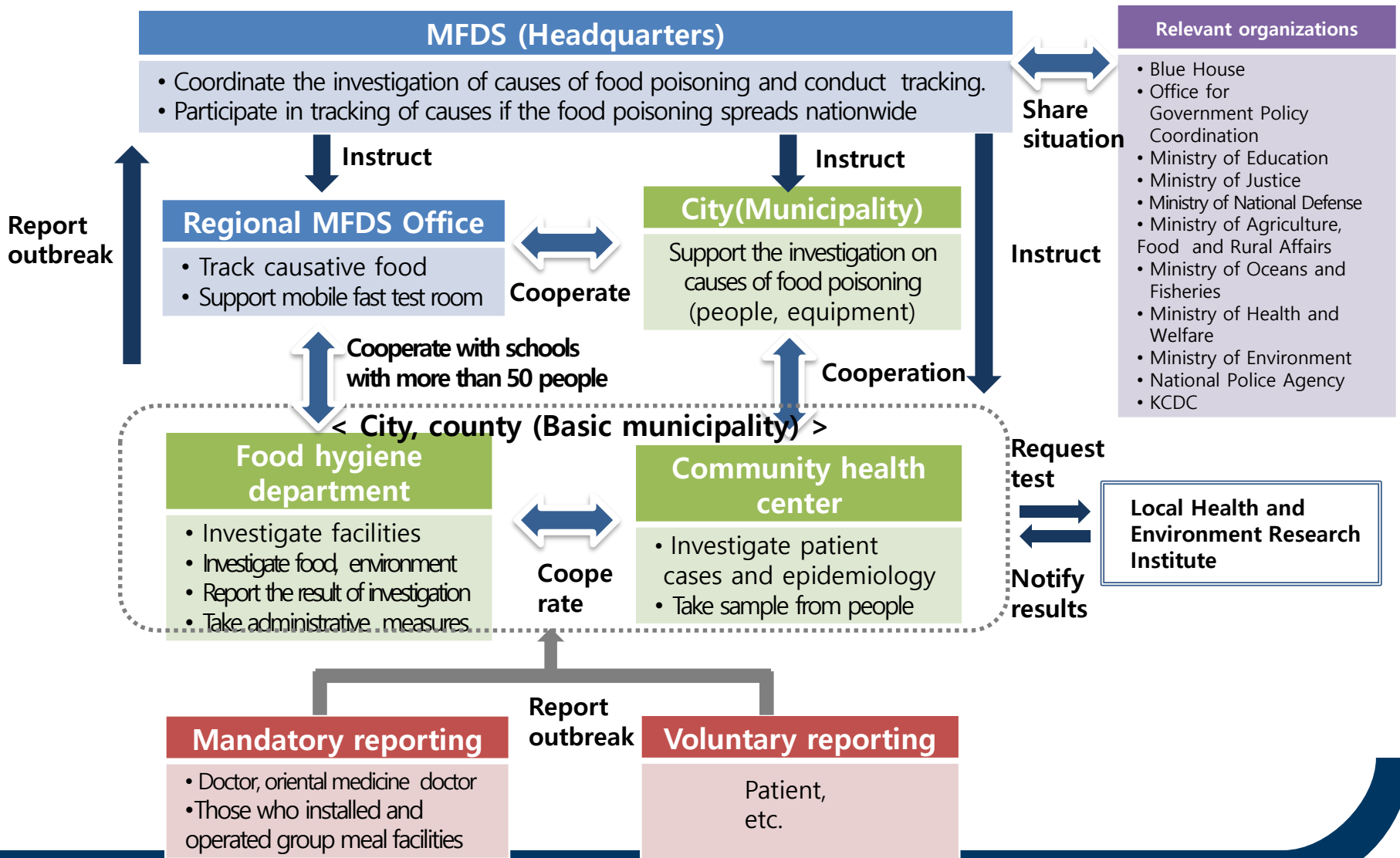
No. of patients  
(2017)



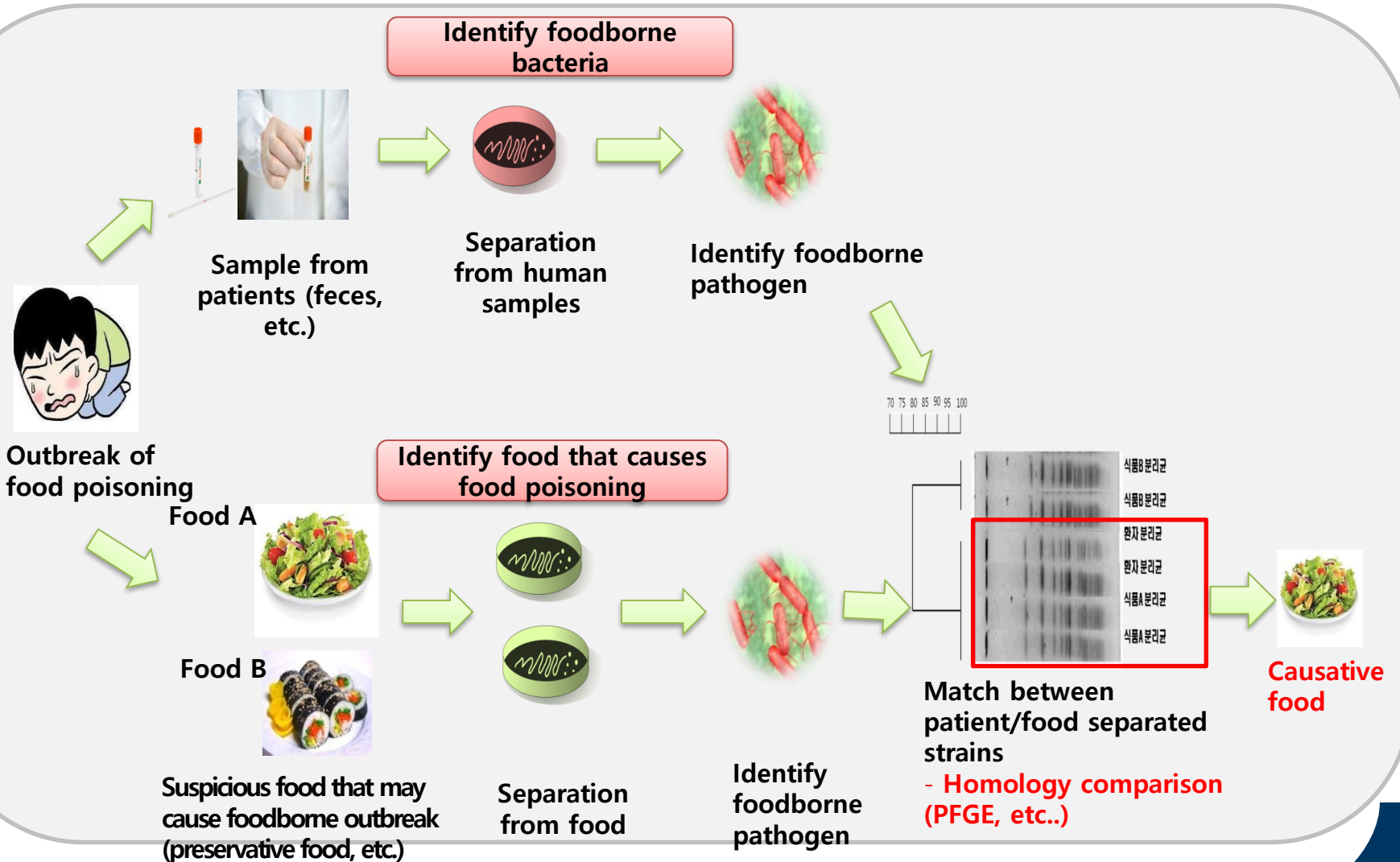


## **2. Foodborne outbreak Investigation and Establishment of DB for Characteristics Analysis**

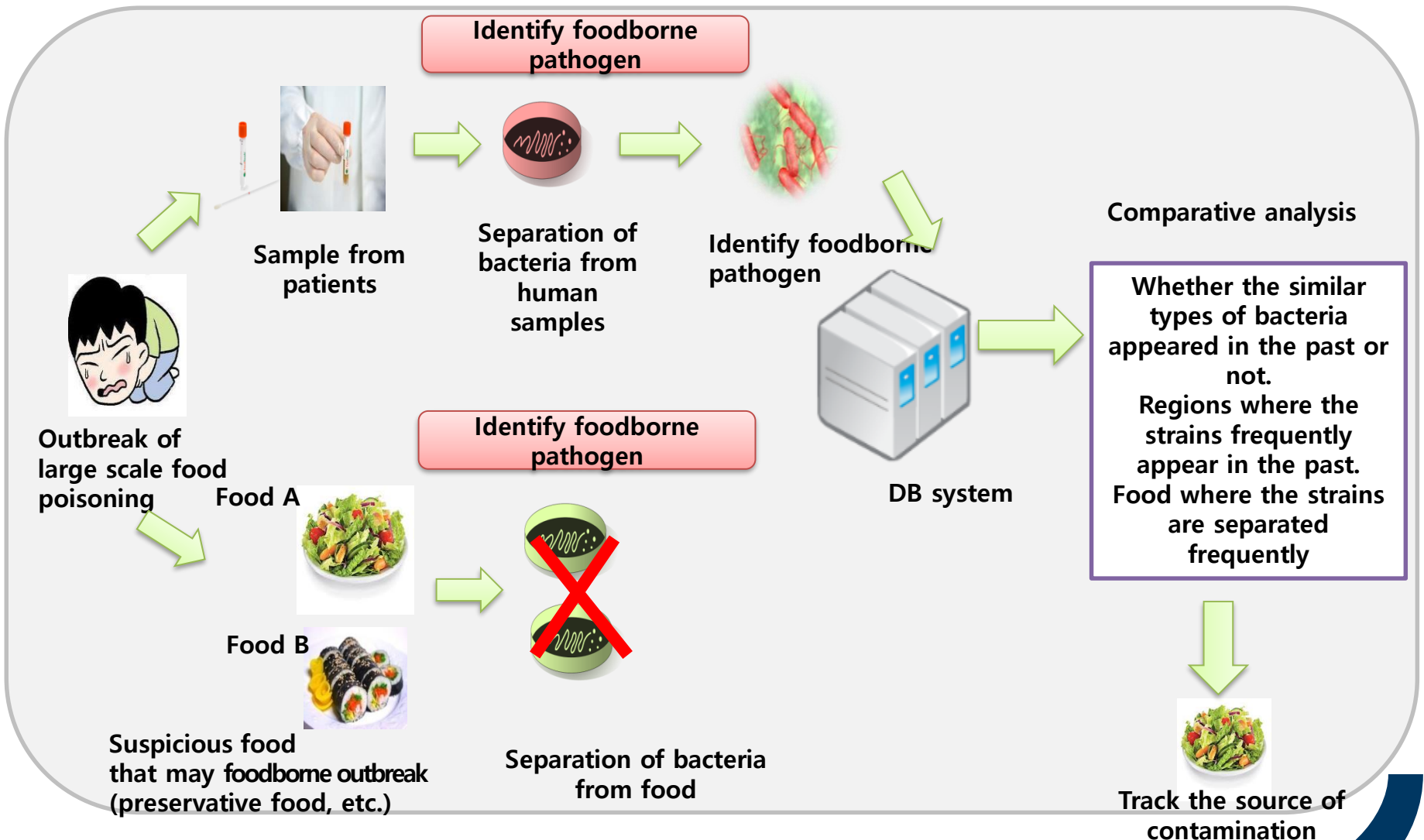
# Structure of Foodborne Outbreak Investigation in KOREA



# Process of Foodborne Outbreak Investigation

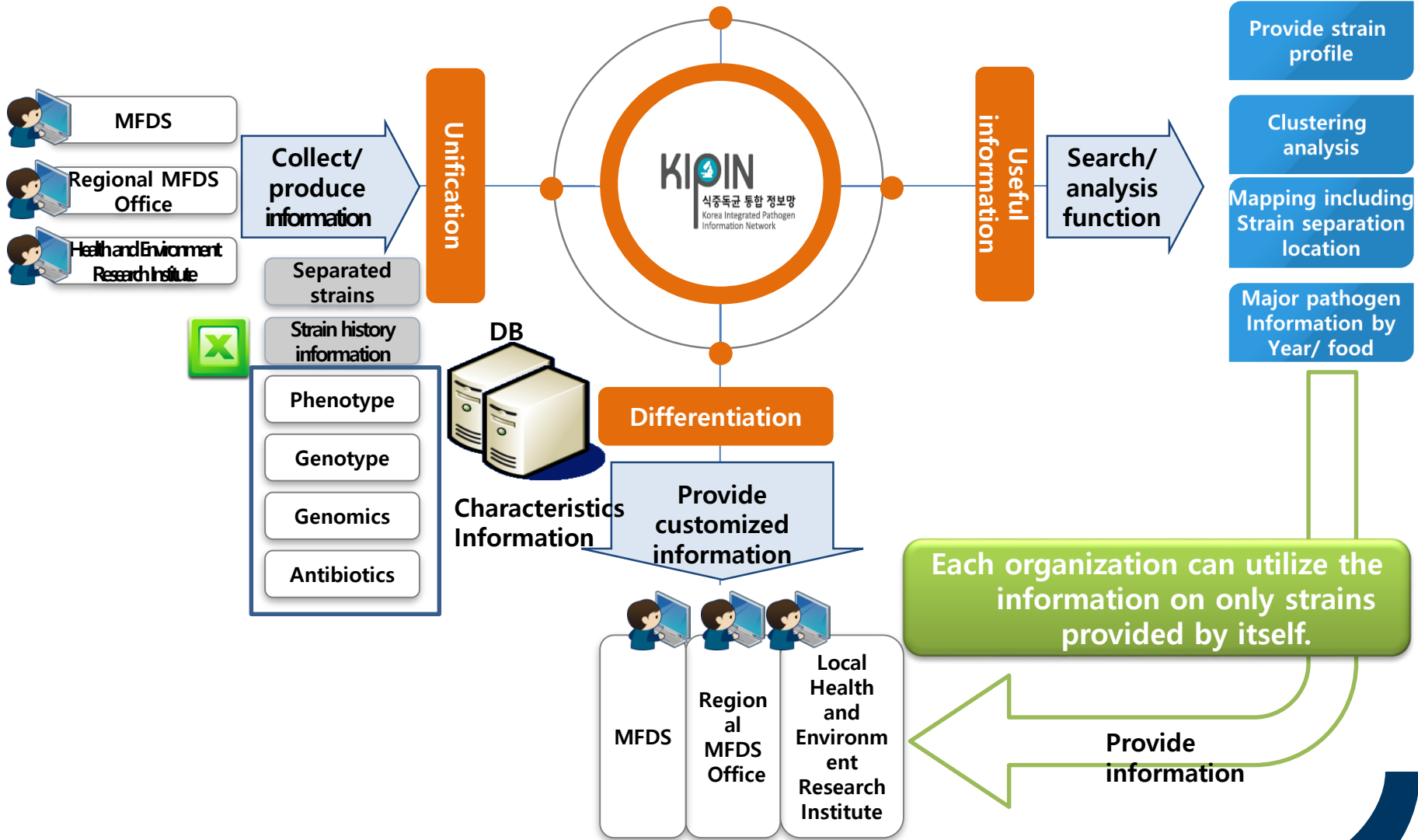


# Need for Characteristics Analysis and DB for Foodborne Pathogen



Need for DB on foodborne pathogen which can be used for tracking sources of contamination with foodborne pathogen

# Korea Integrated Pathogen Information Network (KIPIN)



# Foodborne pathogen Resources Center



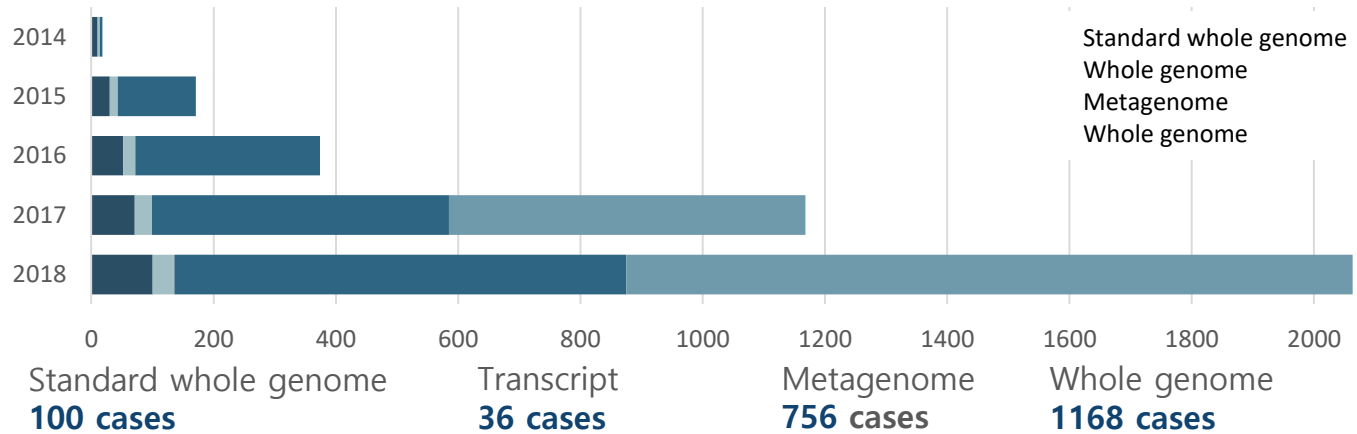
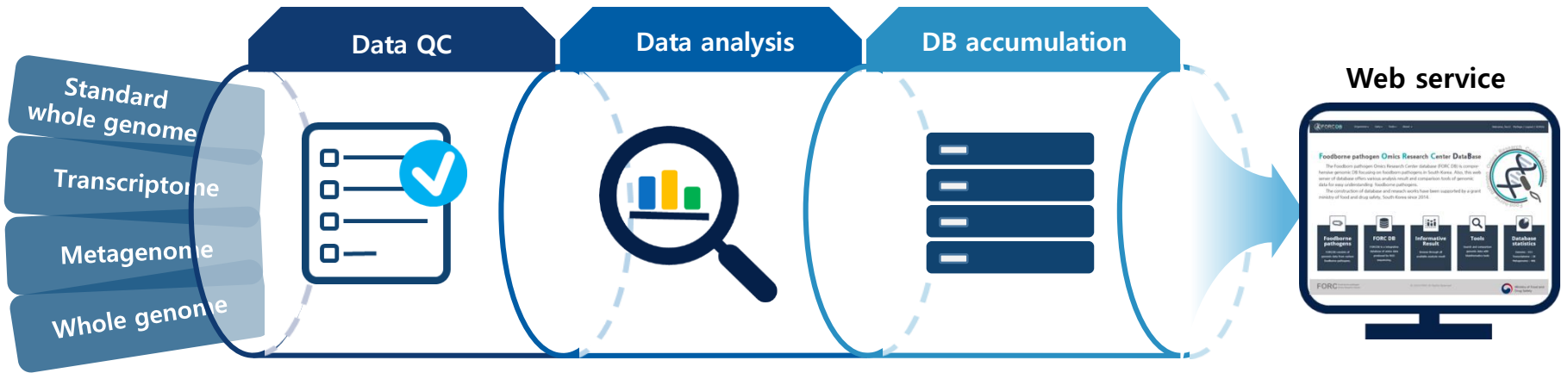


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Drug Safety Evaluation

### **3. Foodborne Outbreak Investigation through WGS Analysis**

# Establishment of Genome DB

- ✓ Establishment of genome DB: identify and analyze genome-level information on foodborne pathogens that are found in domestic food.





# Genome Homology Analysis- *Salmonella*

SNP-based genome homology analysis results for 54 strains separated from 5 foodborne outbreak cases caused by *Salmonella* between 2014 and 2018.

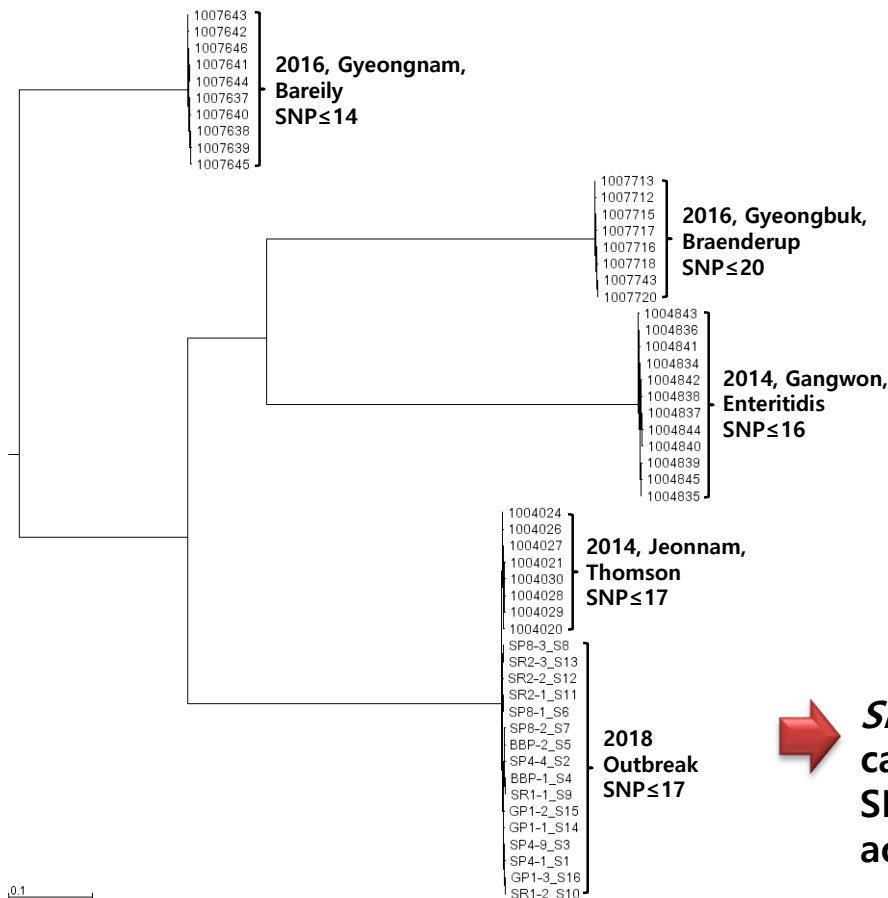


Table. No. of SNPs per case

SNP	2016 Gyeongnam	2016 Gyeongbuk	2014 Gangwon	2014 Jeonnam	2018
2016 경남	≤14	> 30982	> 31892	> 29989	> 29991
2016 경북	> 30982	≤20	> 31591	> 30021	> 30021
2014 강원	> 31892	> 31591	≤16	> 31571	> 31573
2014 전남	> 29989	> 30021	> 31571	≤17	43~56
2018	> 29991	> 30021	> 31573	43~56	≤17



**SNP analysis on 5 *Salmonella* foodborne outbreak cases confirmed that there are differences of SNP ≤ 20 within an accident and SNP ≥ 43 between accidents.**

# Genome Homology Analysis- Pathogenic *E.coli*

SNP-based genome homology analysis results for 52 strains separated from 5 foodborne outbreak cases caused by Pathogenic *E. coli* between 2013 and 2017.

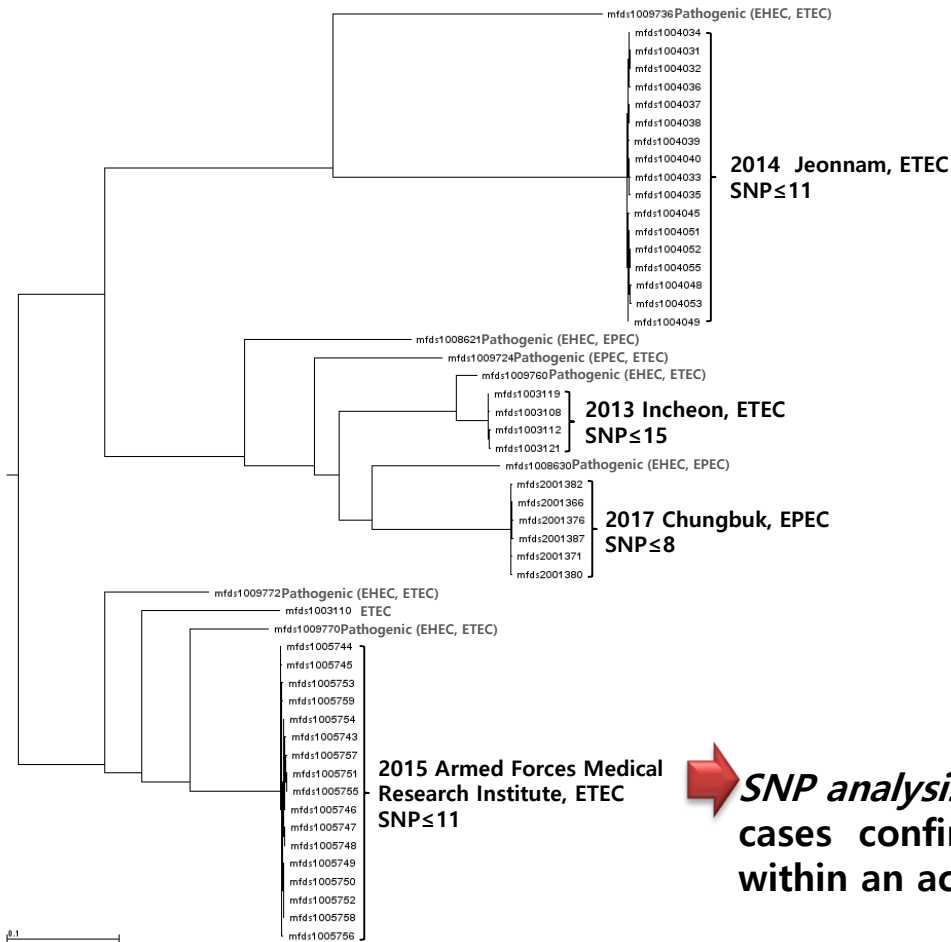


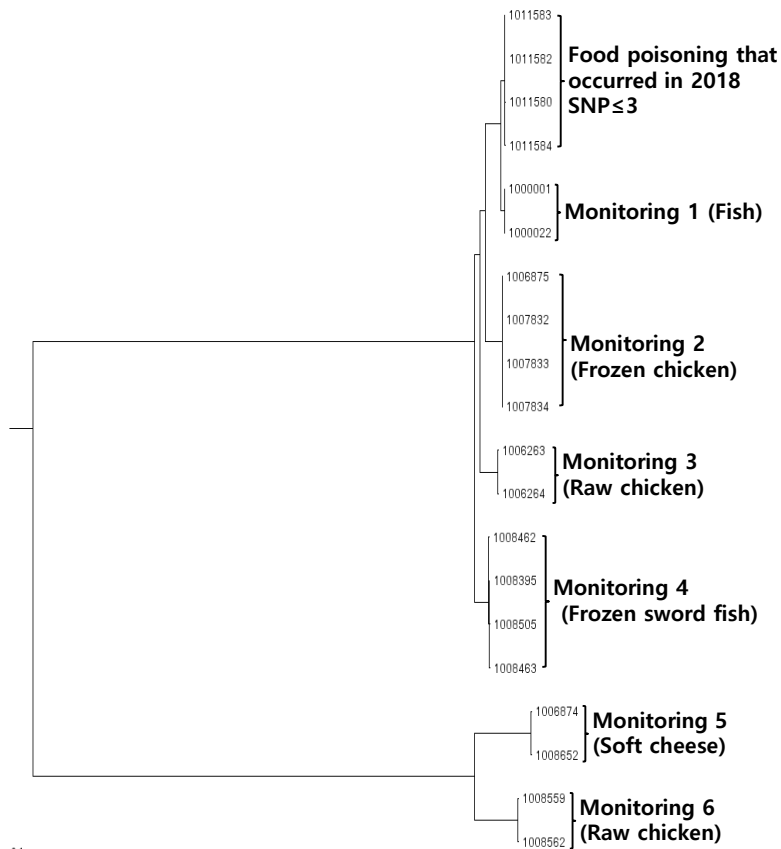
Table. No. of SNPs per case

SNP		ETEC			EPEC
		2014 Jeonnam	2013 Incheon	2015 Armed Forces Medical Research Institute	2017 Chungbuk
ETEC	2014 Jeonnam	≤11	>20302	>20404	>20272
	2013 Incheon	>20302	≤15	>16086	>8687
	2015 Armed Forces Medical Research Institute	>20404	>16086	≤11	>16101
EPEC	2017 Chungbuk	>20272	>8687	>16101	≤8

→ SNP analysis on 4 pathogenic *E. coli* foodborne outbreak cases confirmed that there are differences of SNP ≤ 15 within an accident and SNP ≥ 8687 between accidents.

# Genome Homology Analysis- *Listeria*

**SNP-based genome homology analysis results** related to 4 strains separated from *Listeria monocytogenes* foodborne outbreak cases and 16 strains separated from monitoring and standard specification test in 2018



**Table. No. of SNPs per case**


	Food poisoning that occurred in 2018	Monitoring 1	Monitoring 2	Monitoring 3	Monitoring 4	Monitoring 5	Monitoring 6
Food poisoning that occurred in 2018	≤3	> 865	> 3973	> 4315	> 4323	> 52624	> 51826
Monitoring 1	> 865	≤2	> 3986	> 4305	> 4343	> 52650	> 51840
Monitoring 2	> 3973	> 3986	≤10	> 4087	> 4266	> 52558	> 51740
Monitoring 3	> 4315	> 4305	> 4087	≤17	> 4311	> 52635	> 51808
Monitoring 4	> 4323	> 4343	> 4272	> 4311	≤13	> 52514	> 51711
Monitoring 5	> 52624	> 52650	> 52558	> 52635	> 52514	≤15	> 10673
Monitoring 6	> 51826	> 51840	> 51740	> 51808	> 51711	> 10673	≤3



**SNP analysis results confirmed that there are differences of  $SNP \leq 3$  within an accident and  $SNP \geq 865$  between foodborne outbreak cases and other strains.**

# Summary of Genome Homology Analysis Results

Type	Food Poisoning		No. of SNPs in an accident	No. of SNPs in between accidents
Salmonella	A	2016 Gyeongnam	≤14	29989~31892
Salmonella	B	2016 Gyeongbuk	≤20	30021~31591
Salmonella	C	2014 Gangwon	≤16	31571~31892
Salmonella	D	2014 Jeonnam	≤17	43~31571
Salmonella	E	2018	≤17	43~31573
Pathogenic E.coli	F	2014 Jeonnam	≤11	20272~20404
Pathogenic E.coli	G	2013 Incheon	≤15	8687~20302
Pathogenic E.coli	H	2015 Armed Forces Medical Research Institute	≤11	16086~20404
Pathogenic E.coli	I	2017 Chungbuk	≤8	8687~20272
Listeria	J	2018	≤3	865~52624


**MFDS SNPing was applied to utilize homology analysis method. It is necessary to expand and validate more foodborne pathogens for SNP-based genome homology analysis.**

# Foodborne Pathogen Genome Network

## Foodborne Pathogen Genome Network

Genome DB

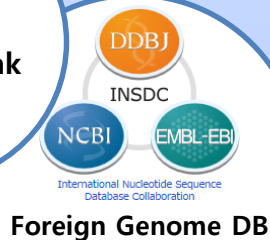
Analysis system

### WGS data Standardize & Transfer

[Total genome information: 1,000 ('18) → 3,000 ('19) → 5,500 ('20) → 8,500 ('21) → 12,000 ('22)]

Isolates  
from outbreak

Isolates from  
contaminated  
food/environment



### GUI-based Analysis Reports

- Identification of causes of foodborne disease
- SNPing and Clustering

### Genome characterization

- Comparative genomic analysis
- Virulence marker search
- Domestic vs Foreign isolates comparison



MFDS and regional offices

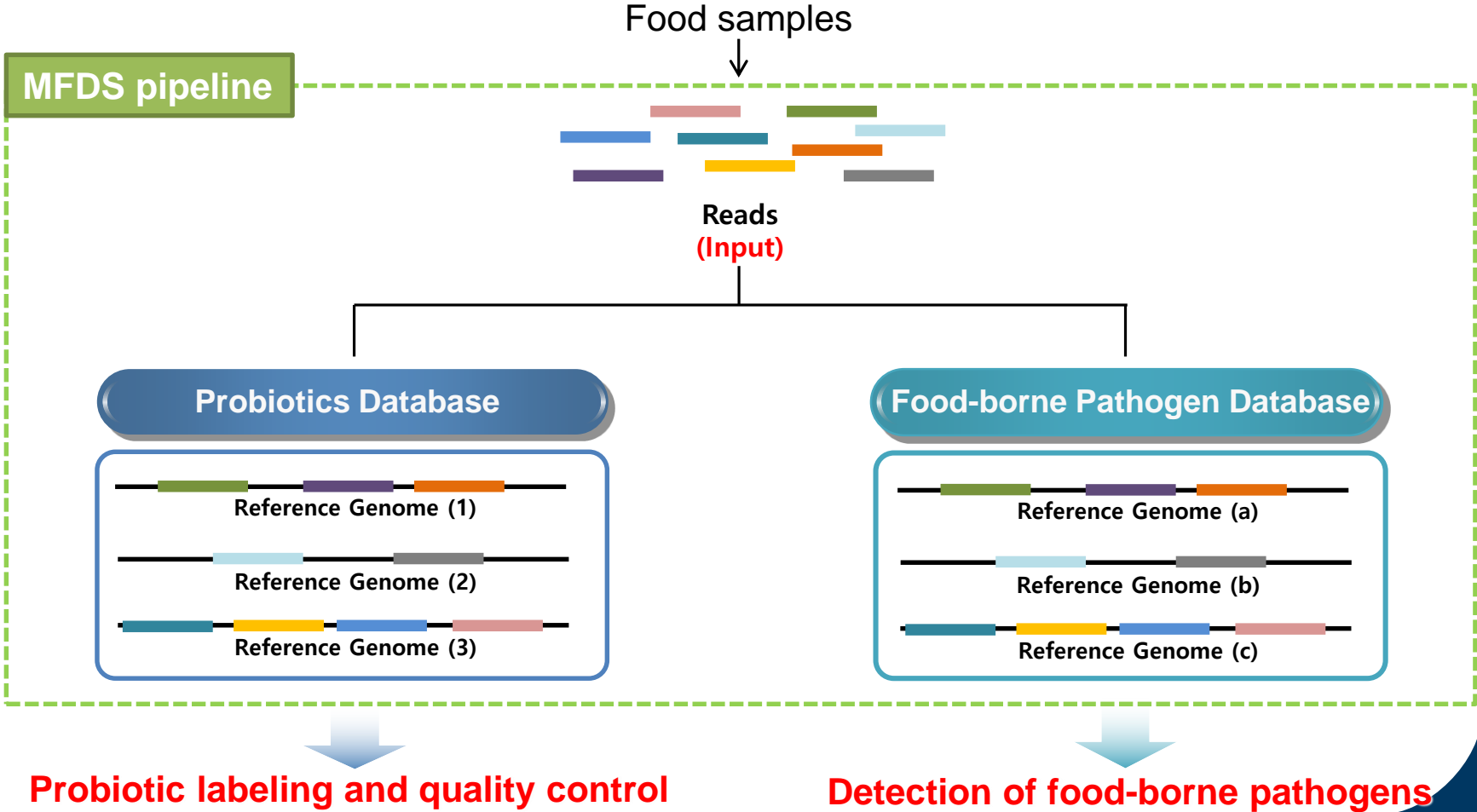
Relevant organizations  
(National Institute of Fisheries Science,  
National Institute of Animal Science)

Health and Environment  
Research Institute

Domestic researchers

# Database expansion for foodborne pathogen using metagenomic analysis pipeline

✓ Application of metagenomic sequencing to Food Safety





# Thank you for attention

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National Institute of Food and Drug Safety Evaluation

