

# ENB Quarterly

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- Local and Global Swine Influenza Monitoring Programme



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## *Editor's note*

Our theme for the April issue of ENB Quarterly is urban health security, a subject which is oft taken for granted but highly relevant to globally connected cities like Singapore. We have an interesting line-up of five articles covering diverse public health issues facing city dwellers.

The first article deals with dengue as an important vector-borne disease endemic in many tropical urban locales. Authors from NEA review our dengue situation in 2018 and highlight the prospects for more cases in 2019. Key to the control of this disease is control of *Aedes aegypti*, a complex and challenging task in densely populated housing estates. The authors call for further cooperation and involvement by the community in responding to this major disease threat.

Our next two articles provide examples of how our health protection framework involving *One Health* responds to the issues of food safety at the human-animal health interface. Salmonellosis is a major food-borne illness locally and the second article presents findings of a joint study by MOH, AVA and NEA which examines the distribution of *Salmonella* along the chain from food supply points and retail to human cases. The third article documents how we look at local and global swine influenza surveillance programmes to strengthen pandemic preparedness.

We take a more global view in our fourth article reporting on measures to maintain urban health security in Singapore, including five core areas that have evolved in tandem with our city state. Last but not least, in *Notes from the Field*, we discover how these health security efforts have been subject to a Joint External Evaluation with WHO on its core capacities to safeguard public health implemented under the International Health Regulations.

Enjoy!

*Steven*

# Review of the 2018 Dengue Situation and Outlook for 2019

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## INTRODUCTION

A total of 3,285 dengue cases were reported in 2018. This was similar to the estimate produced by predictive modelling at beginning of the year. The dengue virus 2 (DENV-2) has been dominant in Singapore since 2016 and remained so through 2018. The low number of dengue cases observed in 2018 is consistent with the 8-year cyclical pattern dominated by DENV-1 and DENV-2, observed since 2004. It is also consistent with the relatively calm dengue situation in our neighbouring countries. Although there is no signal for a major outbreak, the increased *Aedes aegypti* mosquito population in the community may lead to a surge in the number of cases in 2019. Increased efforts in arresting the escalation of the *Aedes aegypti* mosquito population may be necessary to avoid a surge in cases in 2019.

## DENGUE SITUATIONAL REVIEW

### Low number of dengue cases in 2018 - Consistent with the cyclical epidemic patterns

Dengue in 2018 had panned out as forecasted in the beginning of the year.<sup>1</sup> A total of 3,285 dengue were reported to the Ministry of Health, 20% more than 2017. However, the 2018 incidence remained relatively low when compared to all years since 2001 (Figure 1). The relatively low number of cases in 2017 and 2018 mirrored the pattern in 2008 and 2009 when DENV-2 was also predominant. Since 2013, Singapore has been experiencing a similar epidemic pattern as the decade before. Comparison of the epidemiological trend of 2004 to 2012 (1<sup>st</sup> cycle) and 2013 to 2017 (2<sup>nd</sup> cycle) showed a cyclical epidemic pattern that was associated with alternating dominance of DENV-1 and DENV-2 serotypes.<sup>2</sup> (Figure 2)

Many countries in South East Asia had also experienced a relatively calm dengue situation in 2018, when compared to two previous years, 2016 and 2017 (Figure 3). The often synchronised peaks and troughs of dengue in the region suggest the influence of environmental factors, among many others, in shaping the epidemiology of dengue.<sup>3</sup>

### Dengue viruses in circulation

The year 2018 saw lower diversity of dengue viruses in circulation, corresponding to the calm local and regional situation. A previous study had shown that the diversity of dengue viruses was driven by in-situ evolution and importations.<sup>4</sup> There was a 31.1% reduction in the total number of virus strains (new + pre-circulating) detected in Singapore in 2018, compared to 2017 (Figure 4).

DENV-2 has remained as the predominant dengue serotype in Singapore since 2016, and the primary genotype, Cosmopolitan Clade Ib of the DENV-2, caused 42.1% of the cases analysed in 2018 (n=492). Clade Ib is not a new strain as it has been circulating in Singapore since February 2013 and has dominated the local dengue scene since August 2015 (Figure 5). It was associated with 40.7% of large dengue clusters (>10 cases) in 2018. The same clade was reported to have associated with large dengue outbreaks in Johor and Melaka in 2013-2014.<sup>5</sup>

### Increasing trend of adult *Aedes aegypti* population

Although the weekly number of dengue cases remained below its 5-year mean +1 standard deviation (SD) for the whole of 2018, a persistently high vector population was observed in 2018. (Mean +1 standard deviation of dengue cases five years prior to 2018, after removal of outliers)

Figure 1. Annual number of dengue cases and dengue incidence, 2001-2018

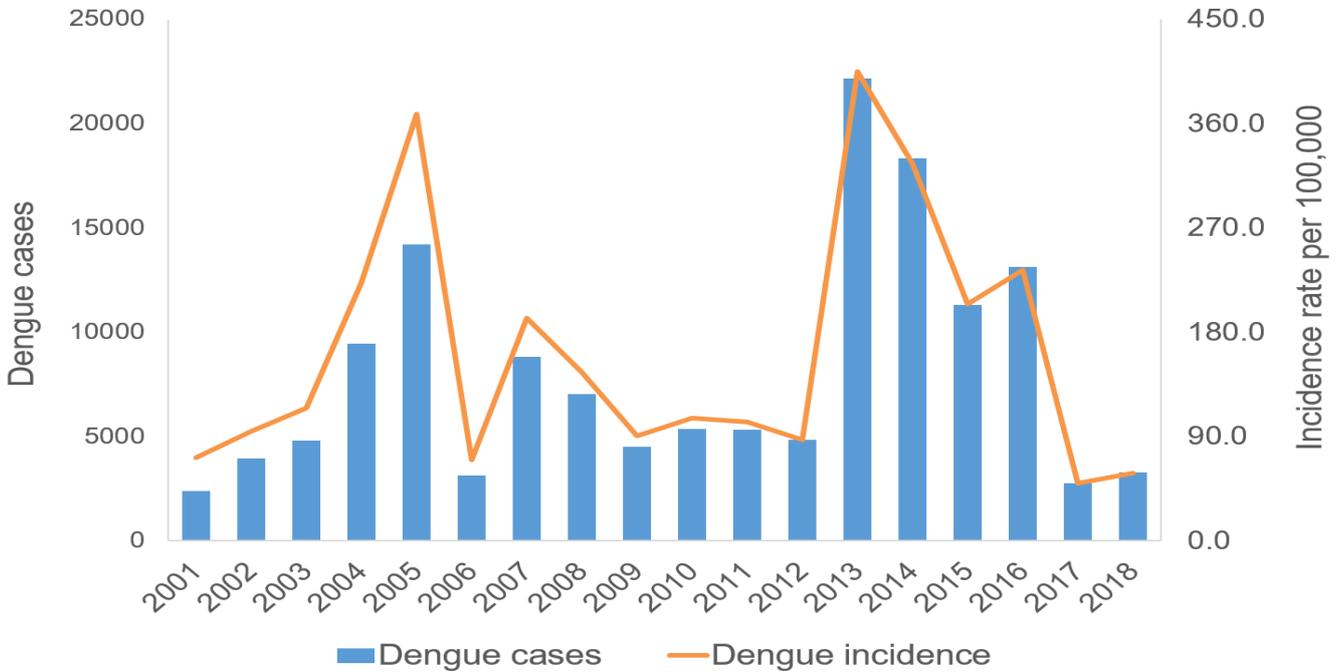


Figure 2. Weekly serotype distribution and number of dengue cases, 2004-2018

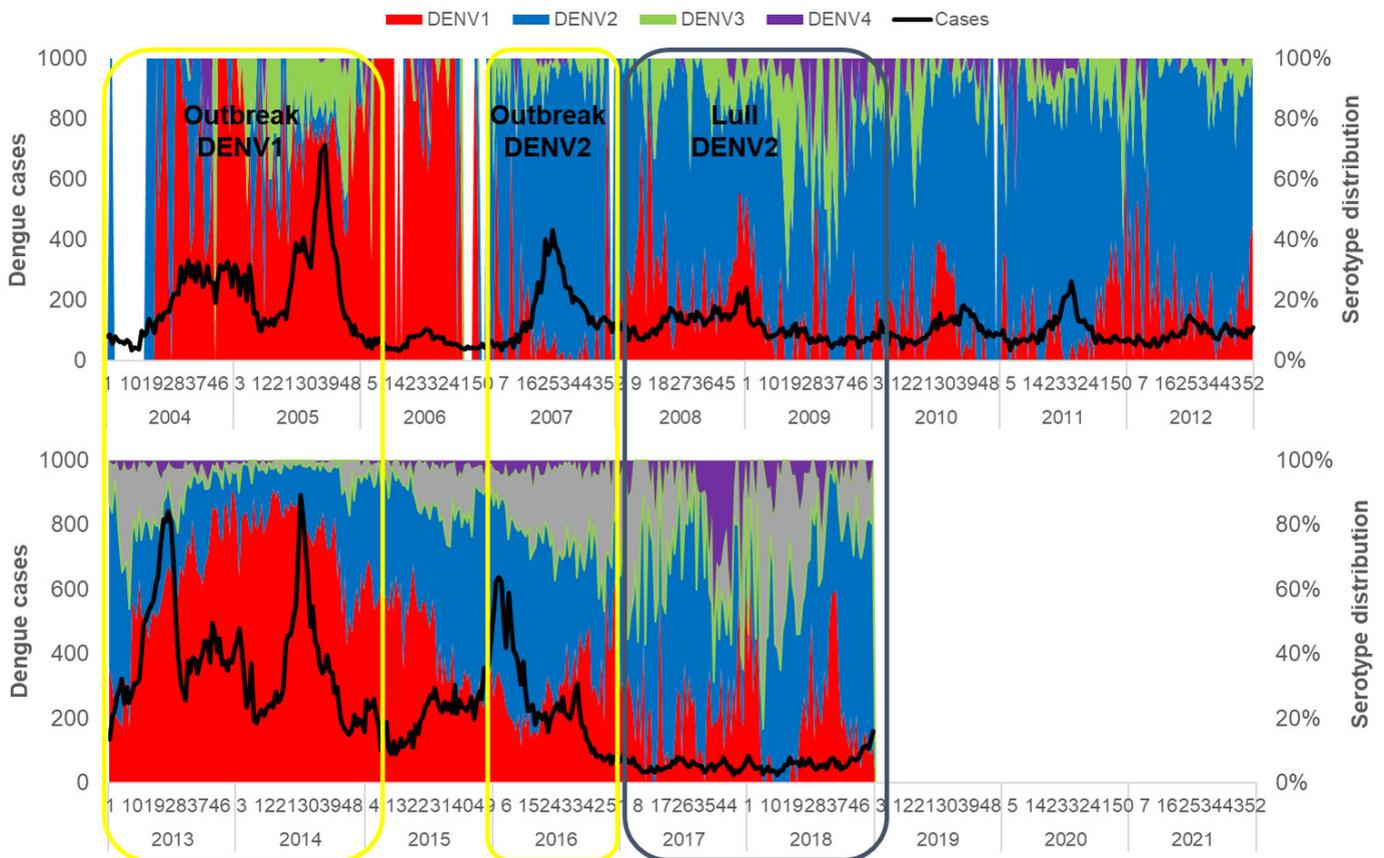
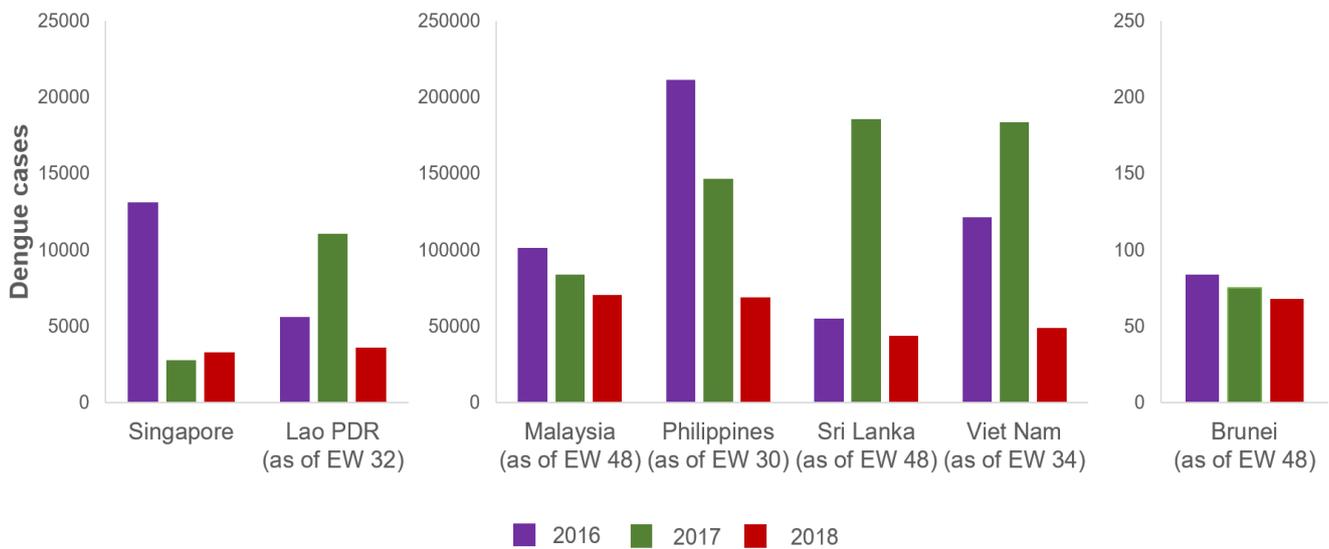
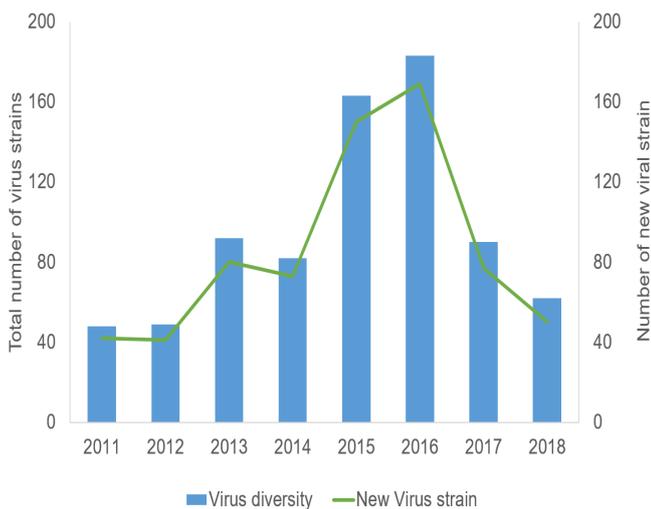


Figure 3. Annual number of dengue cases in Singapore and regional countries, 2016-2018



Source: Data from UniteDengue (<https://www.unitedengue.org/index.html>) & WHO Western Pacific Region (WPRO (<https://www.who.int/westernpacific/emergencies/surveillance/dengue>))

Figure 4. Annual numbers of circulating viruses and new viral strains in Singapore, 2011-2018



The Gravitrap sentinel surveillance, which has been put in place since 2013, has detected an upward trend in the *Aedes aegypti* population since 2016 (Figure 6). The *Aedes aegypti* population in 2018 (20.1%) was almost double that of 2016 (11.5%). Correspondingly, the islandwide Gravitrap surveillance, which was implemented later in 2016, also showed similar trend, consistent with the sentinel surveillance data.

The mean national Gravitrap *aegypti* index (percentage of Gravitrap traps that caught at least one *Aedes aegypti* mosquito) in 2018 was 94% higher than that of 2017. The increase in Gravitrap *aegypti* index indicated a higher abundance of vector population within the community.

**DENGUE OUTLOOK FOR 2019**

Figure 7 shows the dengue forecast for 2019 based on Environmental Health Institute (EHI)/ National University of Singapore (NUS)'s dengue model.<sup>6</sup> The dengue model was developed using historical dengue cases, vector surveillance data, meteorological data, population-based national statistics, and used the seasonality and trend of DENV-2 years (2008-2012) to generate the forecast. In the absence of a serotype switch in 2019 (i.e. following the epidemiological pattern of post outbreak years of 2008-2012), the total number of dengue cases in 2019 is expected to be about 50% more than that in 2018.

Singapore registered a high number of dengue cases at the start of 2019, with an average of 207 weekly cases between E-week 1 and 3. This was significantly higher than in the same period in 2017 and the whole of 2018 when the average number of weekly cases was 78 and 68 respectively. The higher number of dengue cases at the beginning of the year suggested a surge

Figure 5. Monthly distribution of DENV genotypes, January 2013-December 2018

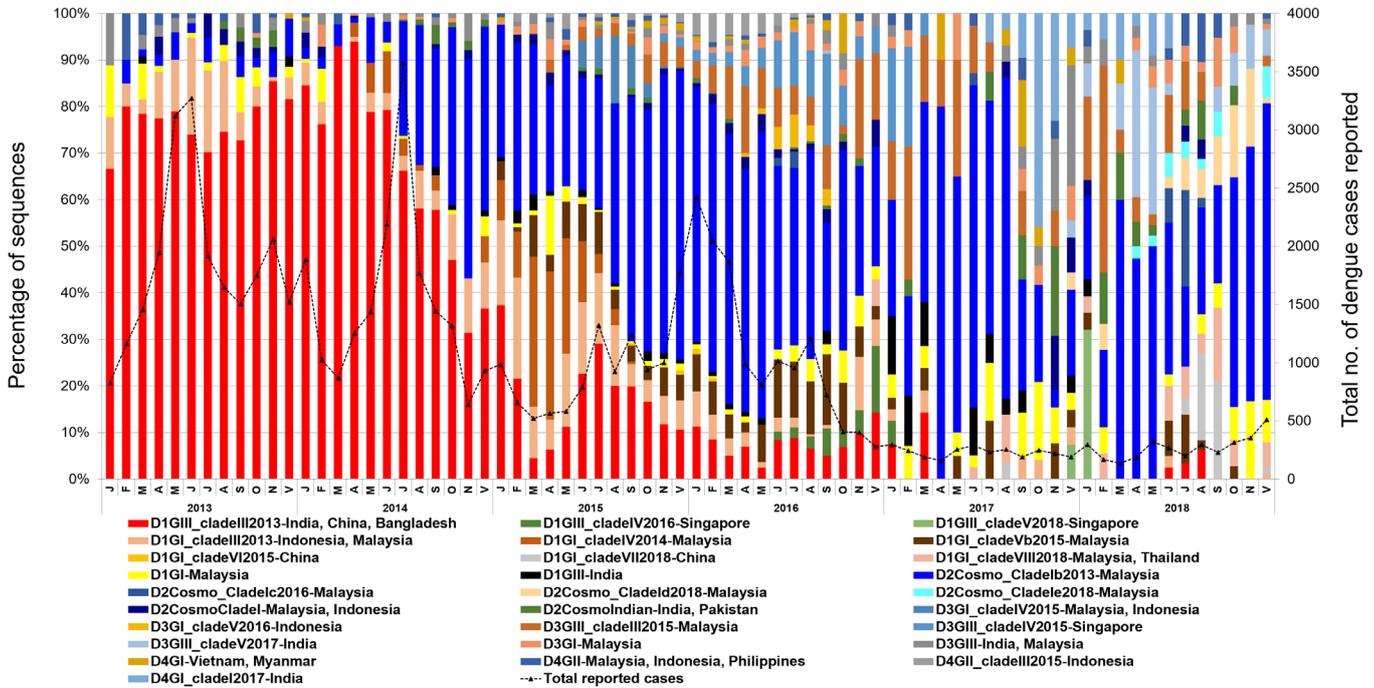


Figure 6. Weekly Gravitrap *aegypti* index, Sentinel and Islandwide Gravitrap Surveillance, 2016-2018

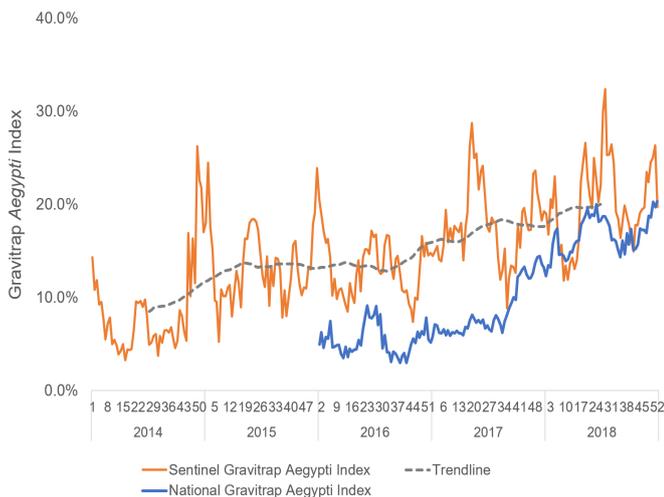
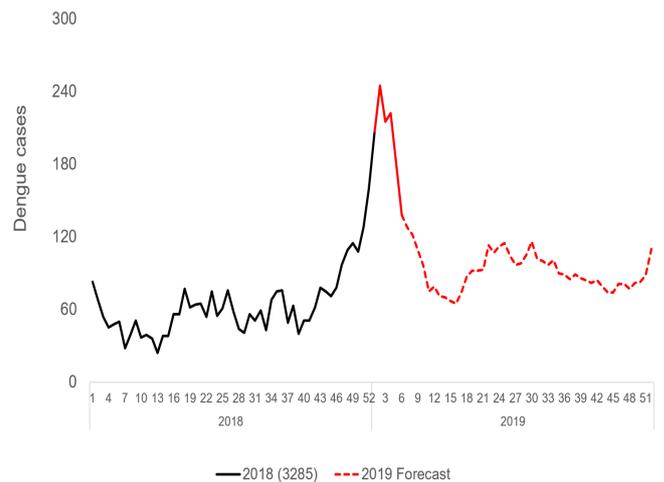


Figure 7. Projection of dengue trend for 2019

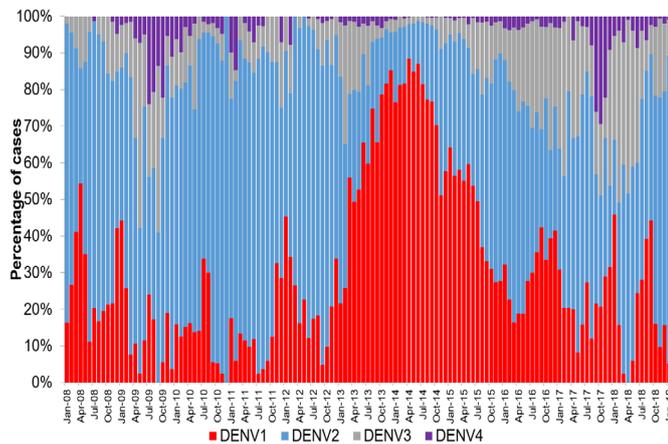


in the number of dengue cases in 2019, despite having no signal of a serotype switch (Figure 8).

Our previous study had shown an increased risk of dengue among older adults >55 years old during DENV-2 outbreak years<sup>2</sup>. This could be contributed by the characteristic of DENV-2, which has been observed to be most often associated with a higher risk of severe cases among secondary

infections.<sup>7,8</sup> Considering that the older adult residents in Singapore have a seroprevalence of 85%, while youth of 16-20 years old has 16% seroprevalence<sup>9</sup>, it is likely that a substantial number of older adults remain susceptible to a secondary dengue infection. A surge in the transmission of DENV-2 Cosmopolitan Clade Ib could thus potentially have a more negative impact on the elderly.

**Figure 8. Monthly distribution of dengue serotypes, January 2007-December 2018**



The persistently high vector population seen in the last few months remains a key concern. The islandwide Gravitrap surveillance has detected about 40% more *Aedes aegypti* mosquitoes in December 2018 as compared to the same period in 2017. Since E-week 1 of 2019, the Gravitrap *aegypti* index has been hovering around 17.2%, indicating a high abundance of vector population within the community.

The increased *Aedes aegypti* mosquito population coupled with the high dengue baseline may lead to a surge in dengue cases in 2019, therefore, concerted efforts are needed to reduce or prevent the further rise of *Aedes* population.

## CONCLUSION

2018 was a dengue lull year as expected. While our risk analysis suggests that there is no signal of an epidemic in 2019, there has been an increase in the *Aedes aegypti* population as well as dengue cases as we enter 2019. Even in the absence of a serotype switch, 2019 may see about 50% more dengue cases than 2018. The high *Aedes* population poses a risk of increased dengue transmission, and potentially increased transmission of other arboviruses like Zika and chikungunya as well. Early robust efforts in reducing the *Aedes aegypti* population ahead of the next dengue season are essential to avoid a surge in dengue cases in 2019.

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# Distribution of *Salmonella* spp. along the Food Chain in Singapore, 2008-2016

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## INTRODUCTION

Salmonellosis is one of the leading causes of food poisoning in Singapore<sup>1</sup> and globally. Its symptoms include diarrhoea, fever, abdominal cramps, and vomiting. The illness is caused by nontyphoidal *Salmonella* enterica serovars (other than *S. enterica* serovar Typhi and *S. Paratyphi* A). There are over 2,500 serovars that have been identified based on the Kauffmann-White classification system.<sup>2</sup> *Salmonella* are also categorised into serogroups (A-Z) based on the O (somatic) antigens. Most serovars of *Salmonella* can cause gastroenteritis in humans, which is often mild and usually resolves without specific treatment. However, in the young, elderly and immunocompromised individuals, salmonellosis can be severe and even fatal.

*Salmonella* are ubiquitous in nature and naturally present in the digestive tracts in animals as well as in household pets, including cats, dogs, birds, and reptiles such as turtles. *Salmonella* is usually transmitted through the consumption of contaminated food from animal origin, such as eggs, meat, poultry, or fruits and vegetables contaminated by manure or water<sup>3</sup>. Person-to-person transmission can also occur through the faecal-oral route due to poor or improper personal hygiene.

Nontyphoidal salmonellosis became a notifiable disease in Singapore from 2008. Strict licensing and

accreditation requirements are in place on food sources, establishments and retailers to ensure the safety of foods imported, produced and sold in Singapore. Cases of nontyphoidal salmonellosis have been on an increasing trend (Figure 1) and the *One Health* agencies, comprising the Ministry of Health (MOH), the Agri-food & Veterinary Authority (AVA) and the National Environment Agency (NEA), undertook a joint study to examine the distribution of *Salmonella* spp. isolated from food supply points, retail and clinical cases. This report presents One Health agencies' combined retrospective data on *Salmonella* from 2008 to 2016, as a step towards identifying factors contributing towards the rising trend of salmonellosis.

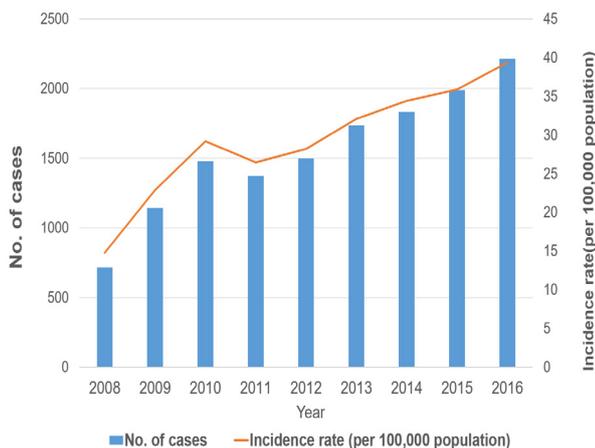
## METHODS

Surveillance data on incidence rates of human cases of Salmonellosis was provided by MOH. Laboratory data on isolation rates, serovar and serogroup was provided by the national reference laboratories for public health, food safety, animal health and environmental health: The National Public Health Laboratory (NPHL), Veterinary Public Health Laboratories (VPHL) and Animal Health Laboratories (AHL) of AVA, and the Environmental Health Institute (EHI) of NEA.

### *Salmonella* from food supply points

A total of 3,727 *Salmonella* isolates were obtained from AVA's routine surveillance and monitoring

**Figure 1. Incidence rate of salmonellosis cases in Singapore, 2008-2016**



programmes for food products in Singapore from 2008 to 2016. This comprised 3,716 isolates from 73,428 samples submitted for *Salmonella* spp. testing and 11 *S. Enteritidis* isolates from 8,412 consignments of imported shell eggs. Samples were obtained from points of import, wholesalers, slaughterhouses, local produce and food processing establishments. Singapore imports from over 160 countries<sup>4</sup> and imported food accounts for over 95% of food consumed, thus forming the bulk of surveillance samples. All raw poultry and meat are imported only from approved sources and countries accredited by AVA. They are imported as fresh (chilled), frozen or as live animals for slaughter. Sampling is conducted on a risk-based schedule, taking into consideration factors such as risk category, compliance history, origin of source and importers' track records. Upon initial detection, additional sampling of the 'problem source' would be triggered. These criteria and actions result in an intrinsically biased sampling for imports.

*Salmonella* spp. was isolated from 25g of food samples following enrichment in buffered peptone water. Shell eggs were screened serologically for *Salmonella* spp. antibodies; positive consignments were then tested for the presence of *S. Enteritidis* only. Pathogen identification was performed using the Vitek 2 (bioMérieux) biochemical system. Isolates obtained were serotyped by the slide agglutination method according to the Kauffman-White scheme.

Isolates were also obtained from non-food samples obtained from local slaughterhouses. These samples include poultry viscera from carcasses sampled prior to the evisceration process (uneviscerated poultry), water and ice used for spin chilling (water used to cool down

eviscerated carcasses) at poultry slaughterhouses, and condemned pig organs from the abattoir, such as liver, lung, kidneys and spleen. Although these samples did not enter the food chain, they were included as potential sources of contamination and to reflect the full range of serovars associated with these food animals.

### ***Salmonella* from retail raw foods and cooked/ready-to-eat (RTE) foods**

A total of 690 raw food samples including raw poultry (chicken), meat (pork, beef and mutton) and seafood (squid, salmon, prawns, cockles, clams and mussels) were collected in 2016 and 26,257 cooked/ready-to-eat food samples were collected between 2008 and 2016 as part of the microbiological surveillance of retail food by the National Environment Agency. Food samples were collected from various food premises at retail such as hawker centres, restaurants, food courts, markets and supermarkets across Singapore. Food samples were sent to an accredited commercial laboratory for the isolation of *Salmonella* species. Qualitative tests (FDA BAM Chapter 5)<sup>5</sup> were performed by the commercial laboratory on 25g of the samples with a further confirmation step using ROMER RapidCheck. Serogrouping was done in EHI laboratory using Wellcolex colour *Salmonella* latex test kit (Oxoid) to identify the serogroups A, B, C, D, E or G. Multi-locus sequence typing (MLST) was carried out in EHI laboratory to identify sequence types and to predict the serotypes based on Enterobase *Salmonella* MLST database.

### ***Salmonella* from clinical cases**

*Salmonella* isolates were submitted to NPHL under the Infectious Disease Act (Singapore) by the diagnostic laboratories at the public hospitals. At NPHL, these isolates were confirmed to be *Salmonella* spp. by matrix-assisted laser desorption ionisation-time of flight mass spectrometry (MALDI-TOF-MS) (Bruker) prior to serotyping using the Kauffmann-White classification scheme. PCR and sequencing of the flagellin genes *fljB* and *fliC* were performed for *Salmonella* isolates that did not undergo phase conversion. Finally, biochemical test and PCR were also done to differentiate d-Tartrate-fermenting (dT+) and d-Tartrate-non-fermenting (dT-) *Salmonella*.

## **RESULTS**

### ***Salmonella* from food sampled at supply points**

Between 2008 to 2016, *Salmonella* was isolated from 4.6% (3,727/81,840) of samples submitted for *Salmonella* testing, ranging from 2.3 to 6.7% per year (Figure 2). Raw chicken meat was the most common

source of *Salmonella* spp., (41.3%, 1538/3,727), followed by pork meat (11.3%, 421/3,727), duck meat (6%, 223/3,727) and other types of poultry such as quail and turkey (2.7%, 100/3,727). *Salmonella* was also frequently isolated from gut samples of uneviscerated poultry and water used for chilling eviscerated poultry at slaughterhouses (Figure 3). Chicken for consumption is largely imported either frozen or as live chickens from Malaysia for slaughter. *Salmonella* spp. was isolated from 9.4% of fresh chickens sampled at slaughterhouses, and 3.2% of frozen chicken meat sampled at import.

**Salmonella from raw food samples at retail**

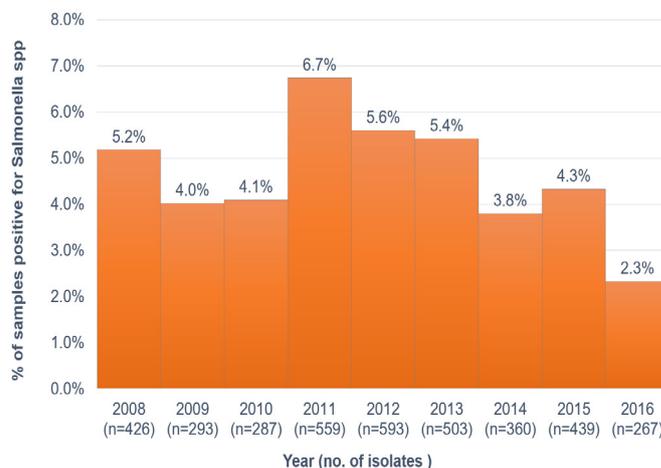
Raw poultry products were one of the most common source of *Salmonella* among raw foods from retail end (Figure 4). Microbiological survey on raw foods was conducted by NEA in 2016 on 690 samples. These samples included raw poultry (chicken), meat (pork, beef and mutton) and seafood (squid, salmon, prawns, cockles, clams and mussels) samples. Results from this survey showed that *Salmonella* was detected mostly in raw poultry (21.3%, 286/690) followed by raw meat (4.5%, 154/690) and raw seafood (2.8%, 250/690). Results from NEA’s routine surveillance programme on cooked and RTE foods showed that only 0.06% (16/26,257) of the samples were detected with *Salmonella* spp. (Table 1). Of these, 56.3 % (9/16) was associated with food containing poultry or eggs, such as chicken rice (n=5), duck rice (n=2) and cakes or pastries (n=2) (Table 1).

**Comparison of Salmonella isolates from clinical and food samples**

*Salmonella* serogroup D was the predominant serogroup identified from clinical samples from foodborne Salmonellosis between 2012 and 2016 (Figure 5). In comparison, *Salmonella* serogroup B was the predominant serogroup isolated from food supply samples (Figure 6). The reported food poisoning clusters involving salmonellosis in Singapore have been largely attributed to serogroup D, with majority of the cases caused by *S. Enteritidis*. The number of cases attributed to serogroup D has remained relatively high but stable, while an increasing trend for serogroup B was observed. In contrast, a downward trend of serogroup D *Salmonella* in food and slaughterhouse samples was observed.

We compared the ten most common serovars found in clinical and food supply samples in the last five years of data collection period (Table 2). *S. Enteritidis* was the predominant serovar implicated in human cases in all five years, followed by *S. Stanley*, *S. Weltevreden*, *S. Typhimurium* and serovar 4,5,12:b:- (dT+).

**Figure 2. Frequency of isolation of Salmonella spp. from the samples tested**

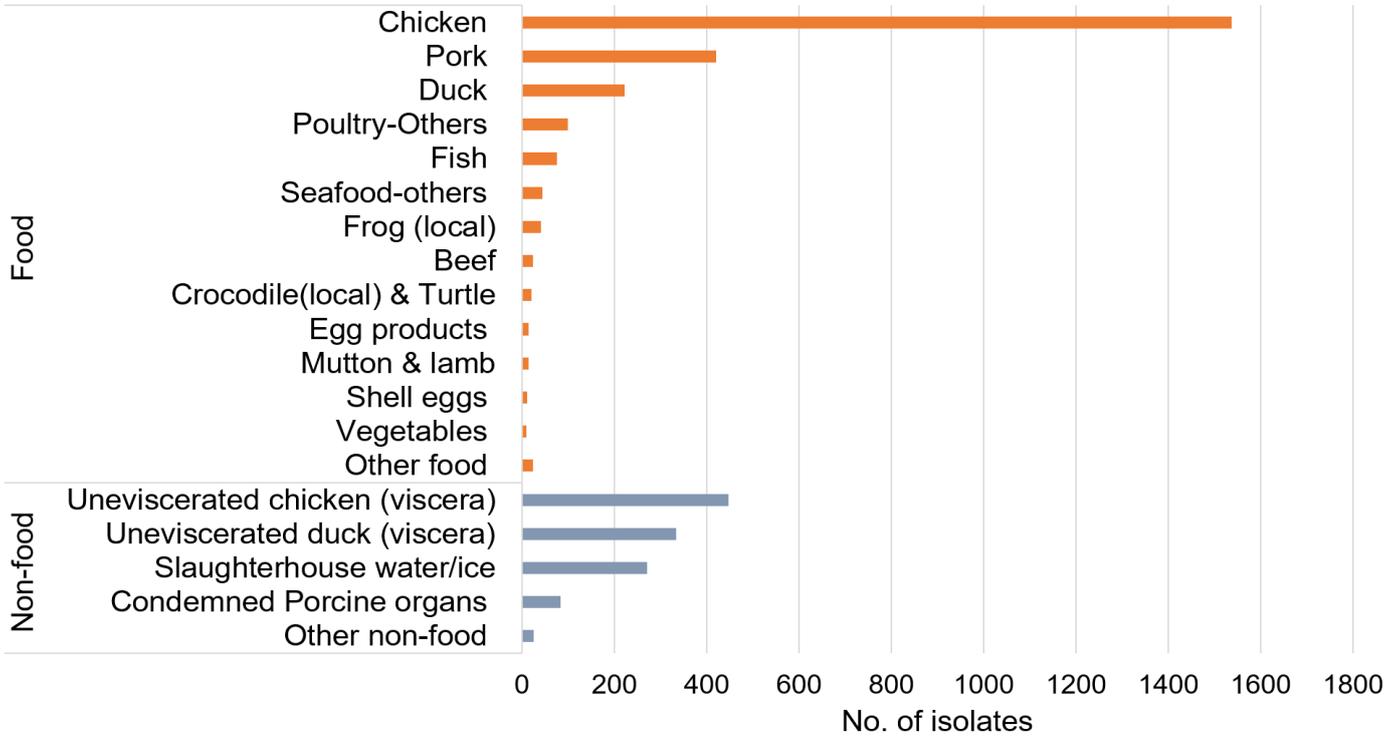


*S. Saintpaul* and *S. Brancaster* were identified for the first time among the top 10 common serovars in 2015 and 2016, respectively (Table 2A). In food supply samples, *S. Typhimurium* was the most common serovar identified from 2012 to 2014, followed by *S. Enteritidis*, *S. Heidelberg* or *S. Albany* in 2015 and 2016 (Table 2B).

In RTE retail food (n=16) the serovars identified from 2008 to 2016 included *S. Enteritidis*, *S. Weltevreden*, *S. Braenderup*, *S. Newport*, *S. Corvallis*, *S. Stanley/Sarajane*, *S. Agona*, *S. London*, *S. Mbandaka* and *S. Typhimurium*. Due to the very low rate of isolation from retail RTE food (0.06%, 16/26257), it was not possible to determine any predominant serovar in RTE food.

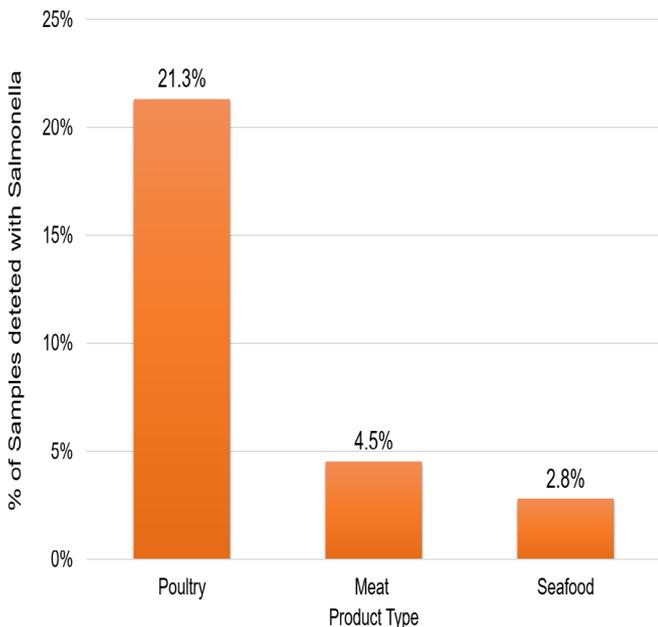
To identify the common food sources of various serovars found at the supply end, isolates were categorised according to food sample type (Table 3). Over 180 different *Salmonella* spp. serovars were isolated from 2008 to 2016, of which 20 serovars constituted over 80% of all serovars isolated. *S. Enteritidis* was most commonly found in raw poultry meat and egg products. *S. Stanley* was also predominantly in poultry meat, but occasionally found in pork. Although *S. Weltevreden* was among the three most common human isolates, it was less frequently isolated from food and usually associated with fish and seafood samples. *S. Typhimurium* had a wider distribution that included raw duck meat, pork, seafood, beef, crocodile and frog meat. Two serovars were predominantly associated with pork or porcine samples: *S. Derby* in pork samples and *S. Anatum* was associated with condemned pig organs from the abattoir, which, at the time of this study, slaughtered pigs from a single export farm in Indonesia.

**Figure 3. Distribution of *Salmonella* spp across various food and non-food types from supply end**



**Chicken:** Includes fresh, frozen and prepared meats, such as breaded or smoked. **Pork:** Includes fresh, frozen and processed pork such as ham and sausages. **Poultry-Others:** Quail, turkey. **Fish:** Includes local and imported fish, includes processed fish such as fillet and fish balls. **Seafood-Others:** Crab, prawn, shellfish, raw and frozen cooked seafood. **Egg Products:** Liquid egg, salted egg. **Shell eggs:** Imported shell eggs. **Vegetables:** Bean sprouts and RTE vegetables such as salad, chives, chilli. **Other food:** Cooked food, drinks, mixed products. **Condemned porcine organs:** Rejected organs found with lesions such as kidney, spleen, lung. **Other non-food:** Animal feed, environmental swabs.

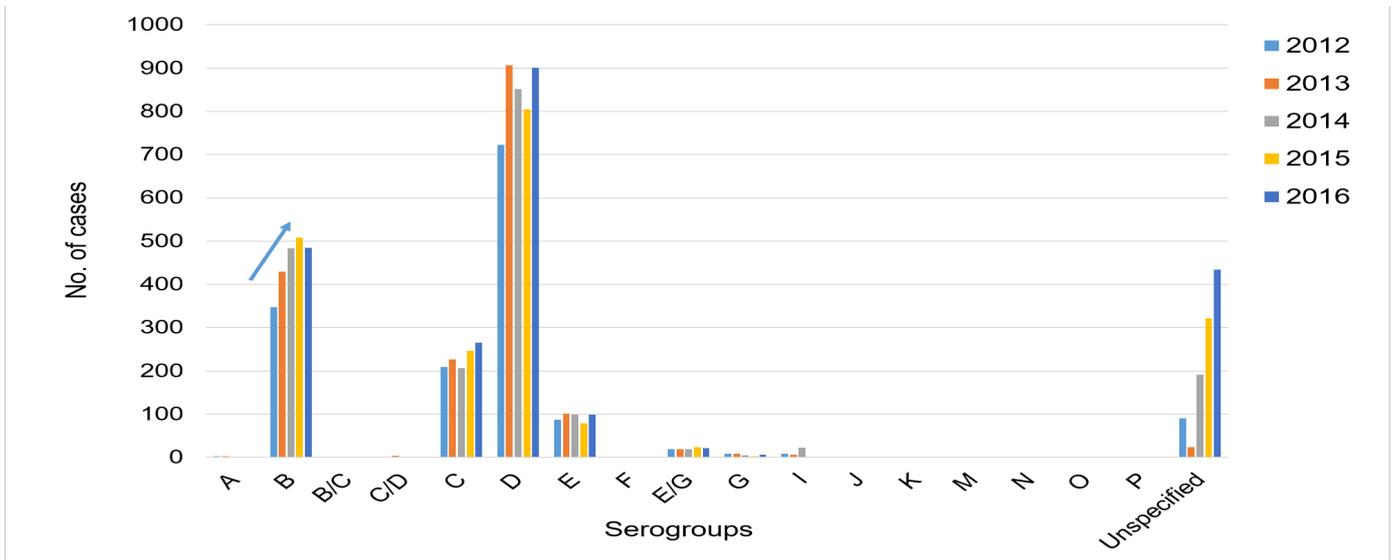
**Figure 4. Percentage detection of in raw poultry, meat and seafood samples from retail, 2016**



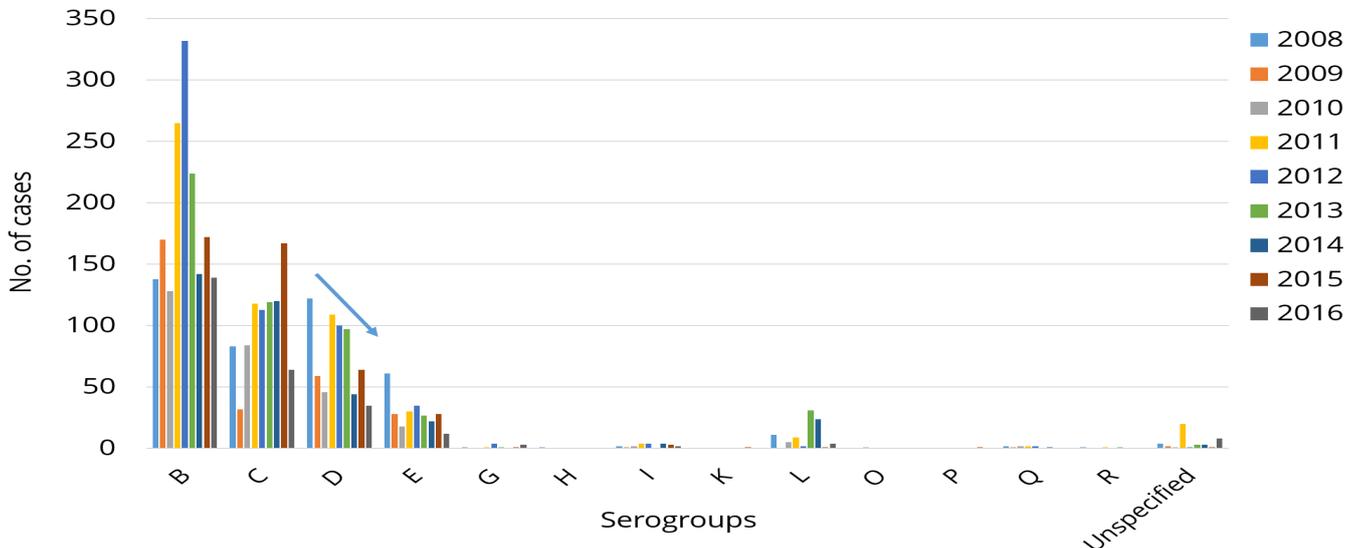
**Table 1. Detection of *Salmonella* from different types of ready-to-eat foods, 2008-2016**

RTE Food	No. of isolates	% of total isolates
Rice		
Chicken	5	31.30%
Duck	2	12.50%
Breads/Confectionery-Cakes/Pastries	2	12.50%
Beverages - Juice	1	6.30%
Noodles		
Laksa	1	6.30%
Pasta	1	6.30%
Wonton/Shrimp	1	6.30%
Others		
Plain appom	1	6.30%
Vegetables	1	6.30%
Salads	1	6.30%
<b>Total</b>	<b>16</b>	<b>100.00%</b>

**Figure 5. Reported salmonellosis cases categorised by serogroups from 2012-2016 (arrow indicates an increasing trend of serogroup B cases)**



**Figure 6. Serogroup of *Salmonella* isolates from food supply samples 2008-2016 (arrow indicates a decreasing trend of serogroup D, mostly *S. Enteritidis*)**



Further examination of poultry-associated serovars showed that *S. Brancaster* and *S. Saintpaul* were primarily found in fresh chicken. *S. Typhimurium* was found more frequently in fresh than frozen chickens, while *S. Enteritidis*, *S. Stanley* and *S. Albany* were found in both frozen and fresh chickens. *S. Heidelberg*, *S. Minnesota* and *S. Schwarzengrund* were predominantly associated with frozen poultry. (Table 4)

In general, the predominant serovars found in chicken viscera and spin-chill water (non-food) mirrored those found in chilled chicken meat.

## DISCUSSION

To our knowledge, this is the first report comparing *Salmonella* spp. isolated from food supply points, retail and clinical cases in Singapore.

Raw chicken was the most common source of *Salmonella* spp. at food supply points, which is consistent with current knowledge of its close relationship with poultry populations.<sup>6</sup> Furthermore, chicken is the most commonly consumed meat in Singapore, with a per capita consumption of 35 kg or 206,000 tonnes imported in 2016, compared

**Table 2. Top ten most common *Salmonella* serovars isolated from food samples at supply points (A) and from clinical cases (B) by year, 2012–2016.**

Salmonella serovars and number of isolates per year										
Rank	2012		2013		2014		2015		2016	
	Serovar	n	Serovar	n	Serovar	n	Serovar	n	Serovar	n
<b>A. Clinical isolates</b>										
1	Enteritidis	161	Enteritidis	271	Enteritidis	269	Enteritidis	200	Enteritidis	251
2	Stanley	91	Stanley	107	Stanley	151	Weltevreden	100	Weltevreden	104
3	Weltevreden	81	Weltevreden	73	Weltevreden	97	<b>Saintpaul</b>	96	Stanley	100
4	4,5,12:b:(dT+)	47	Typhi	56	Typhimurium	72	Stanley	80	<b>Saintpaul</b>	80
5	Typhimurium	42	4,5,12:b:(dT+)	52	4,5,12:b:(dT+)	62	4,5,12:b:(dT+)	49	4,5,12:b:(dT+)	60
6	Typhi	36	Typhimurium	44	Albany	34	Typhi	38	Typhi	47
7	Bareilly	32	Bareilly	26	Typhi	33	Typhimurium	36	Bareilly	35
8	Albany	23	Javiana	22	Bareilly	23	Paratyphi B Var Java	28	Hvittingfoss	31
9	Paratyphi A	20	Paratyphi B var Java	18	Javiana	22	Albany	24	Typhimurium	29
10	Javiana	19	Braenderup	17	Hvittingfoss	22	Bareilly	23	<b>Brancaster</b>	25
-	Others	185	Others	161	Others	190	Others	227	Others	240
	<b>Total</b>	<b>737</b>	<b>Total</b>	<b>847</b>	<b>Total</b>	<b>975</b>	<b>Total</b>	<b>901</b>	<b>Total</b>	<b>1002</b>
<b>B. Food supply isolates (all food types)</b>										
1	Typhimurium	135	Typhimurium	95	Typhimurium	54	<b>Brancaster</b>	65	<b>Brancaster</b>	32
2	Heidelberg	132	Enteritidis	91	Albany	39	Albany	65	Typhimurium	30
3	Enteritidis	95	Heidelberg	68	Enteritidis	34	Enteritidis	60	Heidelberg	22
4	Albany	34	Minnesota	31	Heidelberg	29	Typhimurium	27	Enteritidis	20
5	Stanley	24	Albany	30	Minnesota	23	Mbandaka	24	Stanley	19
6	Kentucky	23	Stanley	26	Braenderup	16	Heidelberg	15	<b>Saintpaul</b>	14
7	Anatum/ var 15	12	Infantis	24	Corvallis	13	Corvallis	14	Mbandaka	10
8	Weltevreden	11	Mbandaka	21	Istanbul	12	<b>Saintpaul</b>	12	Potsdam	9
9	Schwarzengr- und	10	Weltevreden/ var15	10	Kentucky	12	Stanley	11	Weltevreden/ var15	9
10	Derby	10	Braenderup	9	Derby	11	Derby	9	Derby	6
-	Others	107	Others	98	Others	113	Others	136	Others	90
	<b>Total</b>	<b>593</b>	<b>Total</b>	<b>503</b>	<b>Total</b>	<b>356</b>	<b>Total</b>	<b>438</b>	<b>Total</b>	<b>261</b>

Serovars in bold indicates emerging serovars not identified among the top 10 in prior to 2015.

**Table 3. Distribution of *Salmonella* serovars from food supply points, categorised by sample type, 2012-2016.**

Food supply & slaughterhouse sample type (no. of isolates)											
Rank	Sero-group	Serovar	Total		Chicken / chicken products	Uneviscerated chicken (viscera)	Duck	Uneviscerated duck (viscera)	Spin-chill water/ice	Other Poultry	Pork / pork products
			3727	%	1538	448	223	335	272	100	421
1	B	Typhimurium	711	19.1	145	41	98	155	66	21	148
2	D	Enteritidis	633	17	438	63	17	13	78	1	2
3	B	Heidelberg	342	9.2	333	2	0	0	0	2	1
4	C2	Albany	224	6	103	92	4	5	16	0	0
5	B	Stanley	154	4.1	40	59	3	0	11	2	18
6	B	Brancaster	101	2.7	16	61	0	10	7	0	0
7	B	Derby	101	2.7	2	1	1	15	3	0	79
8	C2	Corvallis	85	2.3	42	17	4	2	13	2	0
9	B	Agona	84	2.3	23	24	2	14	10	4	5
10	L	Minnesota	83	2.2	80	0	0	0	0	0	3
11	E1	Anatum & variants	81	2.2	7	0	9	6	4	0	7
12	C1	Mbandaka	80	2.1	24	10	1	21	9	1	0
13	C2	Kentucky	76	2	60	1	5	6	3	0	1
14	E1	Weltevreden/var15+	72	1.9	4	13	4	12	6	3	1
15	C1	Infantis	61	1.6	13	0	5	2	1	13	22
16	C1	Braenderup	54	1.4	28	8	1	1	2	0	3
17	B	Schwarzengrund	53	1.4	37	5	1	2	4	0	3
18	B	Saintpaul	42	1.1	21	9	1	4	1	0	6
19	C2	Hadar	37	1	1	0	20	5	9	1	0
20	C2	Bovismorbificans	31	0.8	5	9	0	1	0	1	5
		<b>Total</b>	<b>3105</b>	<b>83.3</b>	<b>1422</b>	<b>415</b>	<b>176</b>	<b>274</b>	<b>243</b>	<b>51</b>	<b>304</b>
		Others	622	16.7	116	33	47	61	29	49	117

**Table 3 (continued). Distribution of *Salmonella* serovars from food supply points, categorised by sample type, 2012–2016.**

Food supply & slaughterhouse sample type (no. of isolates)											
Rank	Sero-group	Serovar	Total		Con-demned pig organs	Beef/mutton	Fish	Other seafood	Frog / crocodile /turtle	Egg/egg products	Other
			3727	%	84	38	76	44	63	26	59
1	B	Typhimurium	711	19.1	7	6	6	7	3	4	4
2	D	Enteritidis	633	17	0	0	0	1	0	16	4
3	B	Heidelberg	342	9.2	4	0	0	0	0	0	0
4	C2	Albany	224	6	0	0	2	0	1	0	1
5	B	Stanley	154	4.1	8	2	3	1	5	0	2
6	B	Brancaster	101	2.7	0	0	1	5	0	0	1
7	B	Derby	101	2.7	0	0	0	0	0	0	0
8	C2	Corvallis	85	2.3	0	0	2	0	2	0	1
9	B	Agona	84	2.3	2	0	0	0	0	0	0
10	L	Minnesota	83	2.2	0	0	0	0	0	0	0
11	E1	Anatum & variants	81	2.2	44	0	0	1	2	0	1
12	C1	Mbandaka	80	2.1	0	2	4	0	0	1	7
13	C2	Kentucky	76	2	0	0	0	0	0	0	0
14	E1	Weltevreden/var15+	72	1.9	0	0	10	13	0	0	6
15	C1	Infantis	61	1.6	0	4	1	0	0	0	0
16	C1	Braenderup	54	1.4	0	0	2	0	4	2	3
17	B	Schwarzengrund	53	1.4	1	0	0	0	0	0	0
18	B	Saintpaul	42	1.1	0	0	0	0	0	0	0
19	C2	Hadar	37	1	1	0	0	0	0	0	0
20	C2	Bovismorbificans	31	0.8	0	5	1	1	0	0	3
<b>Total</b>			<b>3105</b>	<b>83.3</b>	<b>67</b>	<b>19</b>	<b>32</b>	<b>29</b>	<b>17</b>	<b>23</b>	<b>33</b>
Others			622	16.7	17	19	44	15	46	3	26

SCIENTIFIC CONTRIBUTIONS

**Table 4. Top five most common *Salmonella* serovars found in chicken and slaughterhouse samples, 2012-2016**

Sample Type	Rank	Serovars and number of isolates per year (chicken & slaughterhouse samples)									
		2012	n	2013	n	2014	n	2015	n	2016	n
<b>Frozen chicken</b>	1	Heidelberg	128	Heidelberg	68	Heidelberg	29	Enteritidis	46	Heidelberg	22
	2	Typhimurium	42	Minnesota	31	Minnesota	20	Albany	29	Enteritidis	3
	3	Enteritidis	39	Enteritidis	11	Enteritidis	15	Heidelberg	15	Schwarzengrund	3
	4	Kentucky	20	Infantis	5	Albany	9	Virchow	9	Stanley	3
	5	Schwarzengrund	7	Schwarzengrund	4	Braenderup	7	Liverpool	5	Kentucky	2
			Others	26	Others	18	Others	32	Others	28	Others
<b>Slaughterhouse samples:</b>											
<b>Fresh chicken</b>	1	Enteritidis	16	Enteritidis	42	Albany	7	Albany	8	Brancaster	9
	2	Albany	15	Albany	17	Corvallis	7	Brancaster	6	Saintpaul	9
	3	Typhimurium	8	Braenderup	5	Typhimurium	4	Enteritidis	5	Typhimurium	4
	4	Stanley	7	Typhimurium	4	Enteritidis	3	Corvallis	5	Enteritidis	4
	5	Corvallis	2	Stanley	4	Braenderup	3	Saintpaul	3	Mbandaka	2
			Others	7	Others	4	Others	8	Others	10	Others
<b>Uneviscerated chicken (viscera)</b>	1	Enteritidis	22	Stanley	16	Albany	18	Brancaster	45	Brancaster	13
	2	Albany	15	Typhimurium	14	Typhimurium	5	Albany	24	Enteritidis	7
	3	Stanley	11	Enteritidis	11	Stanley	4	Saintpaul	7	Albany	4
	4	Corvallis	4	Albany	6	Corvallis	3	Enteritidis	4	Saintpaul	2
	5	Typhimurium	4	Agona	3	Braenderup	3	Stanley	4	Mbandaka	2
			Others	12	Others	10	Others	10	Others	19	Others
<b>Spin chill Water</b>	1	Enteritidis	11	Enteritidis	17	Typhimurium	12	Typhimurium	6	Typhimurium	3
	2	Typhimurium	9	Typhimurium	10	Enteritidis	6	Brancaster	4	Enteritidis	3
	3	Stanley	2	Albany	5	Albany	3	Enteritidis	3	Brancaster	2
	4	Albany	1	Stanley	2	Mbandaka	2	Corvallis	2	Corvallis	2
	5	Corvallis	1	Mbandaka	2	Indiana	2	Mbandaka	2	Albany	1
			Others	5	Others	8	Others	7	Others	6	Others

with 117,000 tonnes of pork and 94,000 tonnes of fish.<sup>4</sup> This in turn translates to a relatively higher proportion of chicken samples tested for *Salmonella*. While *Salmonella* spp. was rarely isolated from RTE retail food, 56% of positive detections were similarly associated with food containing poultry products and undercooked poultry, such as pastries containing egg and chicken rice.

The average detection rate from freshly slaughtered chickens was found to be 9.4%. This was lower than the estimated prevalence in fresh chicken meat sold at retail by Zwe et al<sup>7</sup>, together with NEA, which had estimated the prevalence of *Salmonella* spp. to be 25% (30/120) from markets and 12.7% (19/150) from supermarkets. The difference in detection rates suggests that contamination along the supply chain from slaughterhouse to retail points may have occurred. Zwe et al had suggested that relatively inferior hygiene practices could contribute to increased cross-contamination events at wet markets. In addition, it could also suggest better cold-chain management at supermarkets than at wet markets, where stalls are managed by individual sellers. A breakdown of cold chain may result in an overgrowth of bacteria above detection limits. More data would determine if a consistent difference exists between slaughterhouse, wet market and supermarket fresh chicken.

Problems related to temperature abuse may be exacerbated by climate factors in tropical cities. Aik et al had demonstrated a statistically significant association between climatic conditions and *Salmonella* infections in Singapore, and proposed that higher ambient temperatures could pose a challenge for food production. Local regulations require freshly-slaughtered chickens be chilled immediately after evisceration, transported in chiller vans and stored at retail premises at temperature of 4°C and below. A better understanding of practices from the time chickens are picked up from the slaughterhouse, to the time they are delivered, stored and sold will help shed light on possible breakdown points. While frozen-thawed chicken is not allowed to be sold as fresh chicken, the extent of such practices at wet markets could also be investigated.

Analysis of the data collected over time enabled us to observe a changing diversity of *Salmonella* serogroups and serovars found in food and clinical samples. From 2012, we observed an overall decline in serogroup D (characterised by *S. Enteritidis*) detections in food supply samples. Concurrently, there was an increase in serogroup B detections in clinical samples

against a high but stable serogroup D detections. *S. Enteritidis*, followed by *S. Stanley* and *S. Weltevreden*, were the three most common serovars in clinical samples. In contrast, *S. Typhimurium*, *S. Enteritidis* and *S. Heidelberg* were the three most common serovars isolated from imported food samples, of which poultry samples were the most common sources.

*S. Typhimurium* was the most common serovar detected in food supply samples. It has a wide distribution that included poultry, pork, beef, seafood and frog meat. In poultry, it was more frequently isolated from fresh than frozen poultry samples. While an important cause of nontyphoidal salmonellosis in Singapore, it was less frequently isolated in clinical samples after 2014.

*S. Enteritidis* was the second most common serovar detected and associated mainly with poultry samples. From 2011, there was an overall decline in *S. Enteritidis* (Group D) detection from food supply samples. This could be attributed to improving standards of export sources as a result of Singapore's regulatory action on *Salmonella* spp., particularly on *S. Enteritidis* detection. These actions include a ban of affected consignments from sale, more rigorous testing of affected products and potential loss of farm accreditation status. A survey of fresh retail chickens by Zwe et al did not find *S. Enteritidis* in fresh chicken samples from local wet markets and supermarkets. The authors proposed that fresh chicken meat may not play a major role in the epidemiology of salmonellosis due to *S. Enteritidis* here. Nevertheless, despite strict regulatory action at supply and retail, *S. Enteritidis* remains the predominant serovar associated with human illness in Singapore. The possibility of other sources of contamination warrants further investigation.

Another notable trend was an increasing detection of *S. Brancaster* and *S. Saintpaul* in 2015 from both food and clinical cases, alongside an increase in serogroup B *Salmonella* among clinical cases. *S. Saintpaul* emerged among the 10 most common serovars causing human illness in 2015, followed by *S. Brancaster* in 2016. At the supply end, *S. Brancaster* and *S. Saintpaul* were also increasingly detected in fresh chicken and associated slaughterhouse samples from 2015. Similarly, Zwe et al had identified *S. Saintpaul* (32.7%, 17/52), *S. Brancaster* (21.2%, 11/52), *S. Albany* (11.5%, 6/52), and *S. Stanley* (9.6%, 5/52) as the most common serovars found in fresh retail chicken meat over a similar period. We propose that the emergence of *S. Brancaster* and *S. Saintpaul* may be contributing to the increase in Group B clinical cases.

S. Heidelberg was the third most common serotype detected in food supply samples and predominantly associated with frozen chicken. In the US, S. Heidelberg was identified as one of the top human and poultry serotypes implicated in large multistate outbreaks.<sup>9</sup> However, it is not among the serovars commonly associated with human illness in Singapore. More information on consumer preferences and practices here will help us understand if frozen poultry present lower risks for consumers. Conversely, serovar 4,5,12:b:- (dT+) was commonly found in clinical samples, but not frequently detected in food samples.

Some of the limitations of this study include inherent bias in risk-based sampling of imported food. *Salmonella* data from supply points should therefore be interpreted with caution. The data presented here do not represent the prevalence of *Salmonella* in a specific source or food type, but does provide information on the distribution of various serovars found in various food types imported into Singapore. Nonetheless, the observed association of the increasing trend in serogroup B *Salmonella* detections in raw food and clinical samples merits further investigation in the future.

Under current regulations, layer farms are mandated to be free from *S. Enteritidis*, eggs being the most important vehicle for *S. Enteritidis*.<sup>10,11</sup> Local layer farms are monitored closely at farm level and if *S. Enteritidis* is detected in the farm, eggs are not allowed to be sold, unless there has been further treatment to eliminate potential SE contamination, such as by heat-treatment or pasteurisation. Imported shell eggs are also primarily monitored for *S. Enteritidis*. Hence, information on *Salmonella* serovar diversity in shell eggs is incomplete. This gap is recognised and surveillance programmes for *Salmonella* spp. in local farms are being reviewed.

The cause of the rising salmonellosis cases is likely multifactorial. On-going molecular characterisation using whole-genome sequencing will shed some light on the relationships between *Salmonella* spp. isolated along the food chain and those detected from clinical cases. Together with a better understanding of local practices along the food supply chain, these investigations will contribute towards identifying areas for risk mitigation to reverse the rising trend of salmonellosis in Singapore.

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# Local and Global Swine Influenza Monitoring Programme

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## INTRODUCTION

Genetic reassortment is a strategy for influenza viruses to persist in the animal and human population. The ability for a virus to change its genetic make-up and incorporate genetic segments from different host species further enables inter-species transmission, and pigs are an intermediary host to facilitate the spread of novel avian influenza viruses to humans.<sup>1</sup> In 2009, the combination of previous triple reassortment of pigs, humans and birds with Eurasian swine influenza viruses resulted in the emergence of a novel influenza A virus - A(H1N1)pdm09.<sup>2</sup> Sustained human-to-human transmission of A(H1N1)pdm09 marked the start of the 2009 H1N1 pandemic and underscored the importance to monitor and strengthen influenza pandemic preparedness at the human-animal interface.

The veterinary authorities of countries such as New Zealand, United Kingdom (UK) and United States of America (USA) do not consider A(H1N1)pdm09 in pigs a notifiable disease while the veterinary authority of Australia considers all Influenza A viruses in pigs a notifiable disease<sup>3</sup>, on the premise that it is a production disease. As swine influenza surveillance in agricultural production can enhance our understanding of the disease circulation patterns and its epidemiological characteristics,<sup>4,5</sup> we undertook a *One Health*\* project to review the swine influenza monitoring programme in Singapore and other parts of the world, and explore how our findings can be used by respective agencies during peacetime.

## SWINE INFLUENZA MONITORING IN SINGAPORE

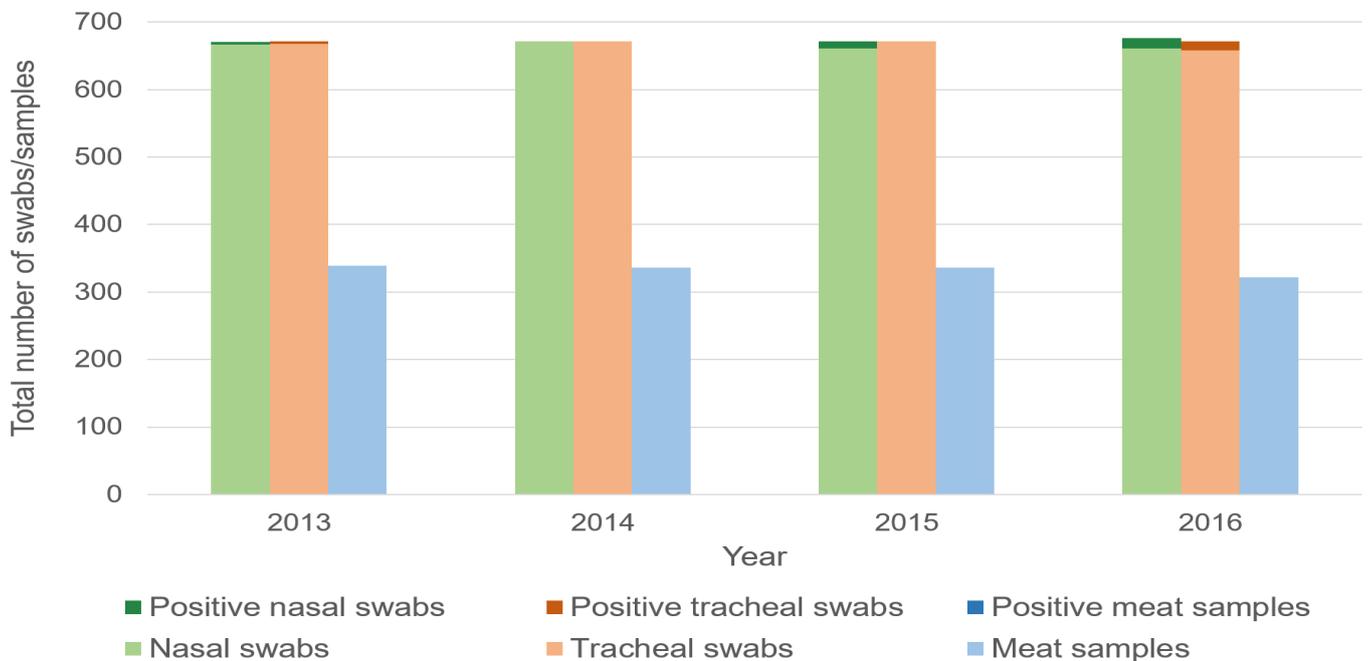
In April 2009, monitoring of A(H1N1)pdm09 in imported pigs from Indonesia was initiated due to public health concerns, in light of the unknown zoonotic potential of the pathogen. Under the monitoring programme, nasal swabs from imported pigs, as well as tracheal and meat swabs from slaughtered imported pigs were collected once every two weeks and sent to the Animal Health Laboratory in Singapore for testing by real-time reverse transcription polymerase chain reaction (RT-PCR) assay. The results of samples collected from imported pigs intended for slaughter between 2013 and 2016 are shown in Figure 1.

Between 2013 and 2016, 2.1% (range, 1.7-2.5%) of nasal and tracheal samples from imported pigs were detected positive for A(H1N1)pdm09. Detection rates were higher between November to April, indicating that there was more viral shedding during these months. Detection rates were also higher in nasal swab samples compared to tracheal swabs, and as a result, collection of tracheal swabs was discontinued in 2017.

All meat swabs were tested negative for A(H1N1)pdm09. This result demonstrated a high level of confidence that A(H1N1)pdm09 was not found in pork, consistent with the statements from the World Organisation for Animal Health (OIE) and the World Health Organisation (WHO)<sup>6,7</sup>. Considering the aforementioned and that there was no evidence of foodborne transmission of the virus, collection of meat swab samples was discontinued in 2017.

\**One Health* for Singapore involves applying coordinated, collaborative, multidisciplinary and cross sectoral approaches at the animal-human environment interface to address public health concerns, and to prevent, prepare against, respond to and recover from public health threats.

**Figure 1. Real-time RT-PCR results for A(H1N1)pdm09 from swabs collected from imported pigs for slaughter between 2013 and 2016**



Apart from A(H1N1)pdm09, other influenza A viruses such as A(H1N2), A(H3N2) and other strains of A(H1N1) are also known to circulate in pigs which can mutate to become a public health threat. Hence, the monitoring programme was expanded in 2017 to cover all relevant influenza A subtypes.

**SWINE INFLUENZA IN OTHER PARTS OF THE WORLD**

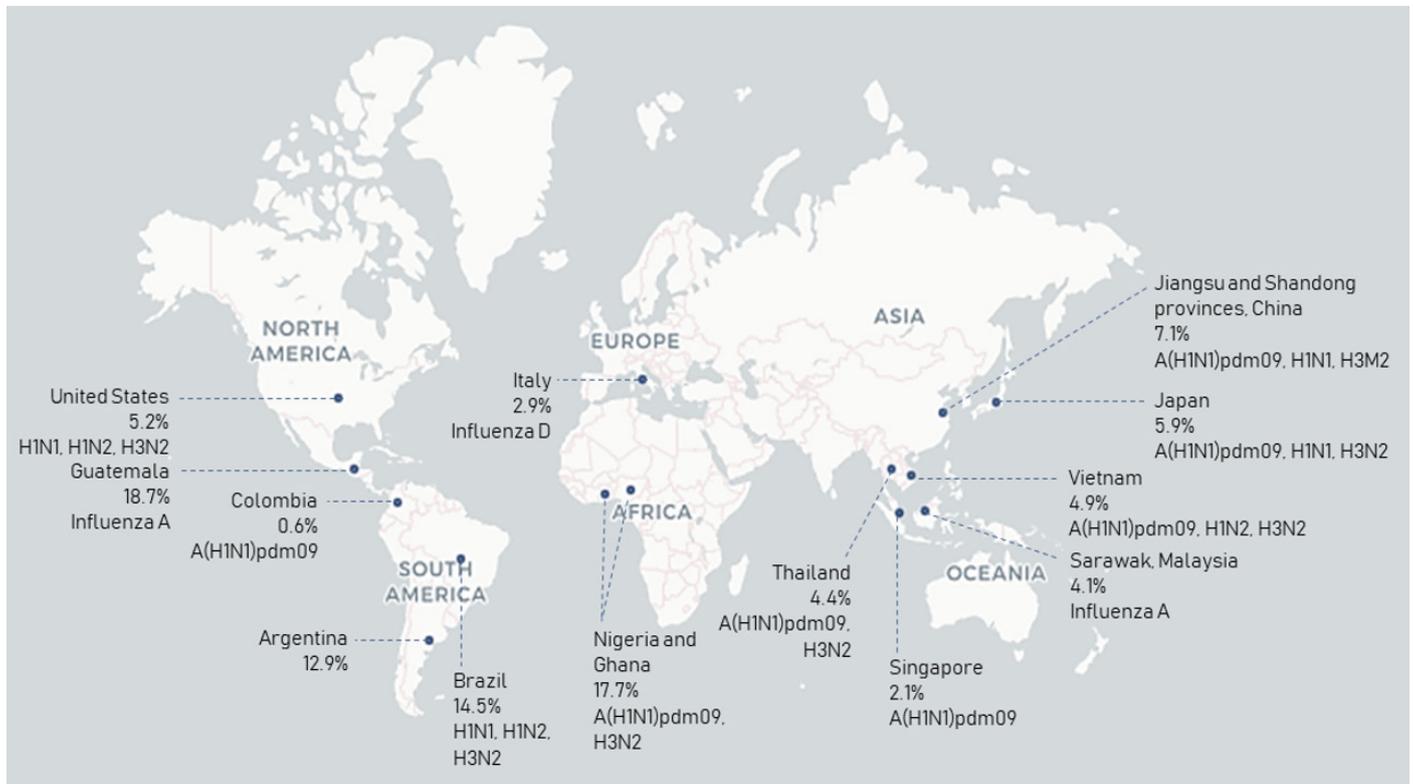
Existing literature on swine influenza surveillance programmes with a study period that overlaps any time between 2015 and 2018 was reviewed and the average detection rate of influenza in a country’s or region’s swine population was plotted in Figure 2. Singapore is one of few countries with a monitoring programme for swine influenza, and the detection rates were relatively low compared to other countries. This could be due to the monitoring programme focusing only on A(H1N1) pdm09 prior to 2017.

Other countries reported detection rates of less than 1% to over 15%. The wide contrast in detection rates can be attributed to the differing porcine health status when sampling was conducted and infection control measures undertaken at farms to minimise influenza transmission, among other factors. In most parts of the world, the outcomes of swine influenza surveillance were not routinely reported or have yet to be established.

**COMMENTS**

In 2009, the initial transmission of A(H1N1)pdm09 from pigs to humans could have occurred through inhalation of respiratory droplets, direct contact with the nasal or throat secretions of an infected animal, or indirect contact with surfaces contaminated with these secretions. The virus is generally restricted to the respiratory tract and is not detected in the muscle of pigs. In other words, A(H1N1)pdm09 is not considered a foodborne pathogen and there have been no documented cases of human infections associated with eating foods contaminated with the virus since 2009. A(H1N1)pmd09 infection in animals is not an OIE notifiable disease. After establishing sustained human-to-human transmission, the A(H1N1)pdm09 is currently considered a seasonal influenza virus circulating in human populations and can circulate in pig herds with few or no clinical signs.

Singapore is a global hub with high trade and travel volume and thus the threat of zoonotic diseases importation is ever present despite the limited interactions between humans and wild animals/ livestock. The 2009 pandemic has highlighted the importance of animal-health surveillance and reinforced the need for information sharing between animal and human health agencies.

**Figure 2. Country/Area-specific average influenza detection rate**

Our swine influenza monitoring programme in Singapore was initiated soon after the pandemic and this programme has been refined over the years to focus on collection of nasal samples during periods of the year with increased influenza activity, thereby enhancing viral detection and cost effectiveness. The coverage has also been expanded to include more swine influenza subtypes.

Beyond swine influenza surveillance, our frequent collaborative work in urban health security between One Health agencies has allowed us to pool our skills and knowledge in identifying areas for improvement in our human-animal health surveillance systems. We will continue to strengthen our pandemic preparedness plans and monitor the local and global situation to calibrate our response measures towards outbreaks of zoonotic diseases.

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# Upholding Urban Health Security in Singapore

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## INTRODUCTION

With global transformations in politics, economics and culture, increasing connectivity and cosmopolitanism, our world is becoming very vulnerable to the threat of outbreaks. Urban health security involves the implementation of quick and targeted public health interventions with the aid of epidemic intelligence methods. Health authorities in cities today face multiple challenges, from emerging and re-emerging infections to the spread of antimicrobial drug-resistance, which all demand improvements to surveillance, epidemiology and response. Singapore has also observed this convergence of circumstances that condition our set of disease control measures, and notable local features that make our situation unique. In this report, we provide a field epidemiologic perspective on five key areas that are core to our city state's public health safeguards against communicable diseases.

## SURVEILLANCE AND OUTBREAK MANAGEMENT

The communicable diseases situation in Singapore is closely monitored through a comprehensive system of public health surveillance. While Singapore's international connectivity always placed it at an increased risk of imported infections, the SARS outbreak has been a defining moment in our nation-building experience.<sup>1-3</sup> In February 2003, infection was introduced into the country with the return of three unsuspecting young travellers from Hong Kong, and further imported infections from symptomatic patients to other passengers and crew were documented in at least three flights flying outbound from Hong Kong.<sup>4</sup> In order to stem its spread, we set up a contact tracing centre which catered for 200 officers who sought to identify all contacts of SARS cases and observation cases in whom SARS could not be ruled out. In total, 238 cases with 33 deaths were reported and the large-scale quarantine operations cost the government approximately US\$5.2 million.<sup>5,6</sup>

The SARS outbreak had shown that disease control required a whole of government approach and could not be the sole purview of the health authority. Fear and uncertainty over an unknown disease rapidly ignites panic, with adverse repercussions on the economy and social fabric. Hence, in the aftermath of SARS, Singapore invested heavily into contingency planning, pandemic preparedness, and epidemic intelligence.<sup>7-9</sup> With these resources, external surveillance, risk assessments and horizon scanning are routinely undertaken to monitor and analyse changes in overseas disease landscapes. Intelligence acquired from this process is used to track potential threats, trigger public health response, and inform the relevant stakeholders when necessary.

We maintain vigilance over Middle East respiratory syndrome (MERS), Ebola virus disease (EVD), yellow fever and other global developments. Our national strategy is premised on a well-established surveillance and response system that forewarns, detects, and contains the importation of a novel agent, and on mitigation measures when community spread is sustained, i.e., showing no epidemiological link to imported source cases. As part of our outbreak response, we have introduced a colour-coded national DORSCON [Disease Outbreak Response System CONDITION] risk communications plan with flexible and step-wise advisories to be provided by the public health authority to members of the public according to the nature and transmissibility of the agent, and the evolving situation.

## HEALTH PROTECTION FRAMEWORK

Singapore's rapid urbanization has resulted in an increasingly built environment with new dynamic interactions between the natural biosphere and the man-made technosphere (Figure 1).<sup>10-12</sup> Further, our dependency on food imports, growth of high-tech farming, hawker culture, and taste for exotic produce all pose food safety challenges that are compounded by high tropical ambient temperatures and ample opportunities for cross-contamination.<sup>13,14</sup>

**Figure 1. Singapore's urban health security involves risk assessments and management of our highly built environment in a natural tropical biosphere**



To safeguard public health, the city state has established a *One Health* framework as the mechanism for expanding cross-sectoral coordination between the human, animal, food and environmental health sectors. This framework is supported by international organisations such as the World Health Organization (WHO), World Organization for Animal Health (OIE), Food and Agriculture Organization (FAO) and Asia-Pacific Economic Cooperation (APEC).

In 2007, actions at the human-animal-environment interface were tested by our first locally acquired human *Plasmodium knowlesi* malaria infection, requiring ecological studies into simian malaria transmission from local macaque populations. Following the first case, four additional human cases occurred within the same year, and one in 2008. All cases involved military personnel who had undergone training in restricted-access forested areas in Singapore.<sup>15</sup> The risks of exposure persist and, although Singapore has been certified malaria-free by the WHO since 1982 and the *Anopheles spp.* vector population has been reduced to low levels, urban malaria outbreaks can still be triggered by returning travellers, or foreign workers with relapsing *P. vivax* infection.<sup>16,17</sup>

Our health protection is made more effective through a larger platform of international cooperation.<sup>18,19</sup> This is because the country's status as a trade and travel hub together with the presence of vectors renders us both vulnerable and receptive to the introduction of emerging infections from the region. Hence,

we maintain professional exchanges with regional neighbours and are strong supporters of WHO's global outbreak alert and response network (GOARN). The benefits are mutual because our officers who deployed overseas have gained useful experience as well as technical, operational, and logistics skills.

#### **CAPACITY BUILDING FOR INTEGRATED RESPONSE**

Core capacities to mount an integrated public health response across agencies were put to the test during the 2009 influenza pandemic. The multiple introductions of novel influenza A (H1N1) virus was thought to be related to a high number of flights coming in from major urban centres, and investigations into a cluster of six cases revealed transmission on board a commercial aircraft which confirmed the capability for rapid spread across borders by convenient air travel.<sup>20-22</sup>

In a public health emergency such as SARS, border closure may not be feasible because we are highly dependent on international trade and food supplies. Nonetheless, while maintaining continuity of services and supplies, morbidity and mortality could be reduced through early isolation and treatment of cases, nationwide contact tracing, and enhancement of prevention and control measures.<sup>23</sup>

Vector-borne epidemics are also occasions for integrated response. The quintessential dengue continued to see cyclical outbreaks and in 2005 and

2013-14, a serotype switch from DEN-2 to DEN-1 unleashed epidemics with record high numbers.<sup>24,25</sup> The Ministry of Health (MOH) oversaw clinical management while the National Environment Agency (NEA) stepped up vector surveillance and control operations through an inter-agency dengue taskforce. Chikungunya infection also became a serious concern when it surfaced in 2008.<sup>26</sup> Genetic analysis showed that the first three local episodes were most likely the result of independent importations of the virus from neighbouring Asian countries while locally acquired cases around July in the same year were largely due to a single strain which was closely related to the strain detected in cases imported from Malaysia.<sup>27</sup> In addition, the first local outbreak of Zika occurred in 2016.<sup>28</sup> Integrated response ensured clear and timely provision of information, advocacy for social responsibility, and promotion of good housekeeping practices that helped to strengthen social trust and morale.

Capacity building in peacetime leads to better public health coordination in an emergency.<sup>29</sup> In 2018, our ongoing collaborative efforts in preparedness and response across four ministries and seven government agencies culminated in a highly favorable joint review of our core capacities by a multi-sectoral team of international experts coordinated by the WHO Western Pacific Region (Figure 2).

### UNCERTAINTIES AND PUBLIC HEALTH RESEARCH

We live in an ambiguous and volatile world full of uncertainties - unusual outbreaks, stress-related disorders and other curious aetiologies have occurred from time to time.<sup>30-34</sup> The role of lifestyle became more evident in an outbreak of *Fusarium* keratitis associated with contact lens wear (ReNu with Moisture Lock, manufactured by Bausch and Lomb) which we investigated in 2006.<sup>35,36</sup> Of the 66 patients diagnosed, close to 82% reported poor contact lens hygiene practices, highlighting the potential harm posed by novel products if not used properly. In 2016, the Group B *Streptococcus* outbreak associated with consumption of ready-to-eat raw fish in porridge sounded another cautionary note against the increasing sophistication of city life and behavioural determinants finding a greater role in disease aetiology.<sup>37</sup>

A long-term variable that may amplify disease transmission is climate change, as evident by extreme weather events, particularly the unprecedented flash flooding in the 2010s. Our national environment agency has acknowledged difficulties in rainfall prediction, which may augur unfavourably for infrastructural planning. Extreme weather events demonstrate

larger forces at work that remain poorly understood and addressed even as the country grapples with new realities. New disease control requires study into the epidemiologic triad as host, environment, and agent rebalances dynamically.<sup>38</sup>

Singapore, to attain its vision of a distinctive global city with a relatively affluent, well-educated, and upwardly mobile population enjoying good access to environments, goods, and services, requires a first world public health service to match.<sup>39</sup> Practicing field epidemiologists understand the importance of establishing professional credibility with stakeholders through scholarship in research and publication. This work involves making applied research contributions to the scientific community, designing field studies to test novel hypotheses, and adding to the growth of knowledge via medical journals, news bulletins and surveillance reports.

### POLICY LEADERSHIP AND COMMUNITY OUTREACH

In the global village where many potential threats loom ominously over the horizon, we need forward-looking strategies and administrative processes to future-proof public health. Leadership and support for Singaporeans to lead healthier lives is provided by the Ministry of Health in a key shift of focus beyond hospitals to the community. We are currently re-engineering public health systems to improve work-streams and policy decisions using modalities to process large amounts of incoming data, new ways of visualisation, functionalities to splice data by important variables, spatiotemporal analyses, and thresholds to trigger alarms.

Since 2010, our Singapore field epidemiology training programme has been building a cadre of field specialists who are highly competent to lead and support the public health mission.<sup>40-42</sup> Modelled after the US Centers for Disease Control and Prevention's epidemic intelligence service, our graduate fellows have moved on to gain peer recognition through involvement in WHO, GOARN and TEPHINET (Training-programs in Epidemiology and Public Health Interventions NETwork) activities worldwide. We are also an active founding member of the regional ASEAN+3 field epidemiology training network.<sup>43-44</sup>

Working within our local communities, we are promoting shared values through outreach programmes such the *One Health* diploma course at Temasek Polytechnic and a mini medical school at Khoo Teck Puat hospital. The School of Public Health was established at the National University of Singapore in 2011 to produce future leaders and innovate new

## SCIENTIFIC CONTRIBUTIONS

**Figure 2. Public health experts hosted by our Director of Medical Services in a joint external evaluation of national core capacities, 16-20 April 2018**



technologies to address complex challenges. And this year, our new National Centre for Infectious Diseases will operate as a purpose-built state-of-the-art facility for the public health and clinical management of communicable diseases.

### CONCLUSION

We have briefly described our experience of upholding urban health security that perhaps offers a case study in communicable diseases control. Singapore's territorial compactness, population heterogeneity, and affluent lifestyles mirror the characteristics of many cities today. To beat the odds of tropical disease outbreaks, policy and control measures must evolve with the dynamics of modern life. The presence of a flexible and responsive field epidemiologic service contributes strongly to our capability for managing outbreaks and guiding positive human behaviour.

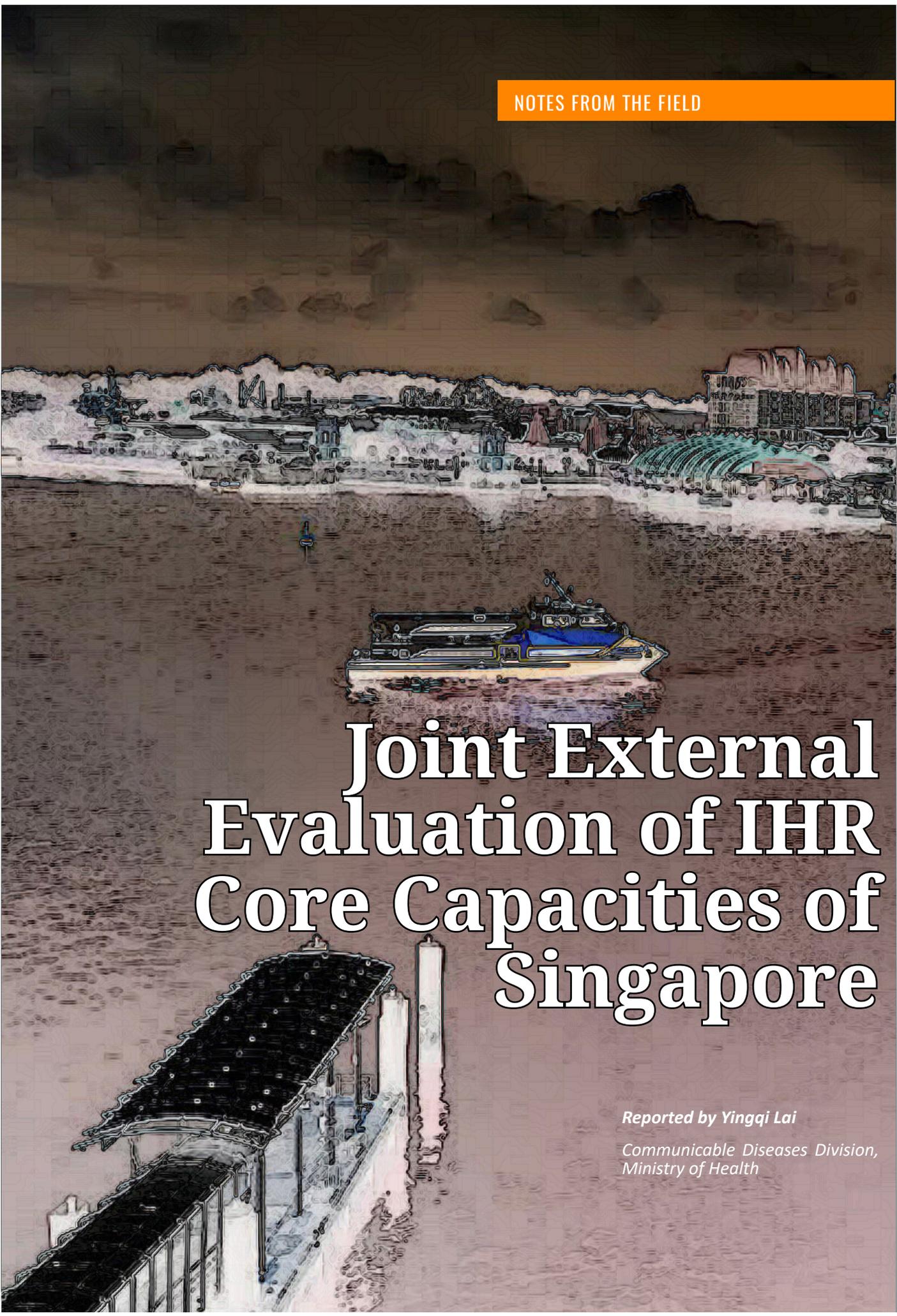
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## SCIENTIFIC CONTRIBUTIONS

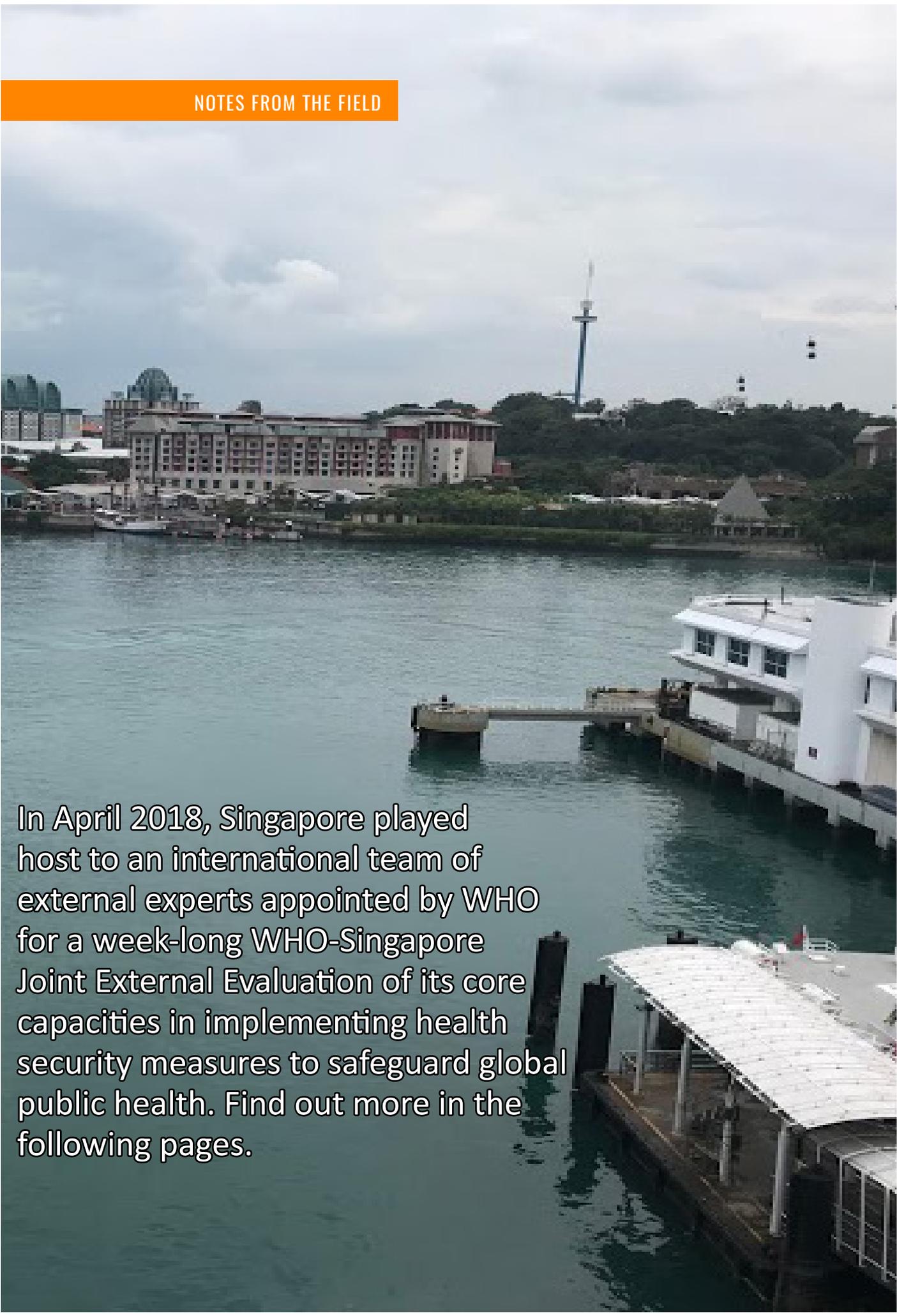
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An aerial photograph of a harbor in Singapore. In the center, a blue and white motorboat is moving across the water. The background shows a cityscape with various buildings and structures. In the foreground, a large, dark, rectangular structure, possibly a pier or a covered walkway, is visible. The overall scene is captured from a high angle, showing the layout of the harbor and the surrounding urban environment.

# Joint External Evaluation of IHR Core Capacities of Singapore

*Reported by Yingqi Lai*

*Communicable Diseases Division,  
Ministry of Health*



In April 2018, Singapore played host to an international team of external experts appointed by WHO for a week-long WHO-Singapore Joint External Evaluation of its core capacities in implementing health security measures to safeguard global public health. Find out more in the following pages.

### What is Joint External Evaluation (JEE)?

The JEE was developed to ensure countries' implementation of the International Health Regulations (2005) [IHR (2005)]. The IHR (2005) is an international framework that is legally binding on all 196 WHO member states. It articulates specific measures that member states can take to limit the spread of diseases and uphold global public health security, including the report of certain disease outbreaks and health events.

Prior to the JEE, the progress of IHR Core Capacities development was self-evaluated exclusively. The JEE is a voluntary process in which a team of external experts appointed by WHO, together with internal country experts, jointly assess a country's capacity to prevent, detect, and rapidly respond to major public health threats. The move to external evaluation comes from the recognition that transparency and mutual accountability in the international community are essential in implementing IHR collectively.

### Why did we participate in the JEE?

Singapore went through a major national crisis during the outbreak of Severe Acute Respiratory Syndrome (SARS) in 2003. The SARS outbreak revealed gaps in Singapore's preparedness and response capabilities to manage a major public health emergency. In its aftermath, we invested heavily in strengthening our systems and capabilities to manage public health emergencies and threats, taking reference from the IHR (2005). We are looking continuously to improve our policies and practices based on evaluation and after action reviews. Therefore, despite participation in the WHO JEE not being compulsory, we were committed to improve our readiness through receiving external validation and invaluable feedback on areas for improvement. Singapore's participation in the JEE provided an objective evaluation of our national capacity, and feedback from international experts enabled us to identify the most urgent needs within our system and prioritize efforts to further



Experts from Singapore and World Health Organization discussing urban health security issues

**Assessing clinical and laboratory core capacities for dealing with a public health emergency**



strengthen our preparedness and response. We believe that this whole-of-government effort better prepares Singapore to face future public health emergencies.

**What happens during the JEE?**

The development of national capacity for public health preparedness and response cuts across the work of four ministries and seven agencies, namely the Ministry of Health (MOH), Ministry of Defence, Ministry of Home Affairs, Ministry of Manpower, National Environment Agency, Agri-Food & Veterinary Authority of Singapore, Civil Aviation Authority of Singapore, Changi Airport Group, Maritime and Port Authority of Singapore, Singapore Cruise Centre and Singapore Civil Defence Force.

Over the course of a year, starting from 2017, the MOH JEE team worked closely with partner MOH divisions and all other agencies to prepare answers to over 600 Self-Evaluation Technical Questions, draft a 100-page Self-Assessment Report and finalise presentations to be made to the JEE external evaluators. This culminated in a joint review of our core capacities by a multi-sectoral team of international experts, coordinated by the WHO Western Pacific Region, from 16 to 20 April 2018. As the WHO JEE Evaluation Framework comprises 48 indicators across nineteen technical areas, we made presentations, provided relevant documentation and organized site visits covering the various technical areas for the WHO JEE team. These included visits to our emergency operations centre, border checkpoints, laboratories, and the National Centre for Infectious Diseases.

## Vigilant officers screening inbound passengers for travellers' health at Singapore ferry checkpoint



### How did we perform in the JEE?

The JEE team assessed that Singapore had a highly developed capacity to detect and respond to potential public health emergencies, and commended Singapore's system as one of the best in the world. Strengths identified included the whole-of-government mechanism for emergency preparedness and response, scalable depending on the event; use of innovation and new technologies to strengthen detection and response systems; strong leadership and forward planning in workforce development; and demonstration of continuous improvement of policies and practice based on evaluation and after action reviews. Priority areas identified to require further strengthening included surveillance information systems, the MOH emergency operations centre and the national capacity for infectious disease management. More details can be viewed in the published *Mission report on the Joint External Evaluation of IHR Core Capacities of Singapore on 24 Oct 2018* here: <http://www.who.int/ihr/publications/WHO-WHE-CPI-REP-2018.25/en/>.

This was the first time Singapore underwent an international evaluation of such scale. The findings are a validation of the whole-of-government's achievement

in strengthening our health security capabilities and safeguarding public health for all Singaporeans.

### What's next?

We will continue to work with our partner agencies to address the identified priority areas. During the JEE preparation process, regular staff meetings between agencies have fostered working relationships between staff across agencies. Since the JEE, agencies have also become more cognizant of public health priorities in their areas of responsibilities and of the areas needing collaboration.

Participation in the JEE will also continue, so as to identify priority areas for strengthening and to reach a sustainable level of capacity. We will conduct the self-evaluation every year and participate in the JEE every five years to ensure our preparedness for the next public health threat.

# Formation of New Agency and New Cluster



The Singapore Food Agency (SFA) was formed on 1 April 2019 to oversee Singapore's food safety and security. The SFA serves as the single point of contact for public feedback on food-related issues and strengthen management of foodborne disease outbreaks to protect public health. The SFA will also facilitate more business-friendly regulations with oversight of all food safety policies and consolidation of food laboratory capabilities to deepen competencies in food diagnostics, and research and development in food safety.



With the transfer of functions, National Parks Board (NParks) is now the lead agency and provides one-stop service for animal and wildlife management, as well as animal and plant health. Animal and Veterinary Service (AVS), a cluster under NParks, is the main touch-point on animal-related issues for pet owners and businesses, and animal welfare groups. It will also be the first responder for animal-related feedback, and continue to uphold high standards in animal welfare and health.

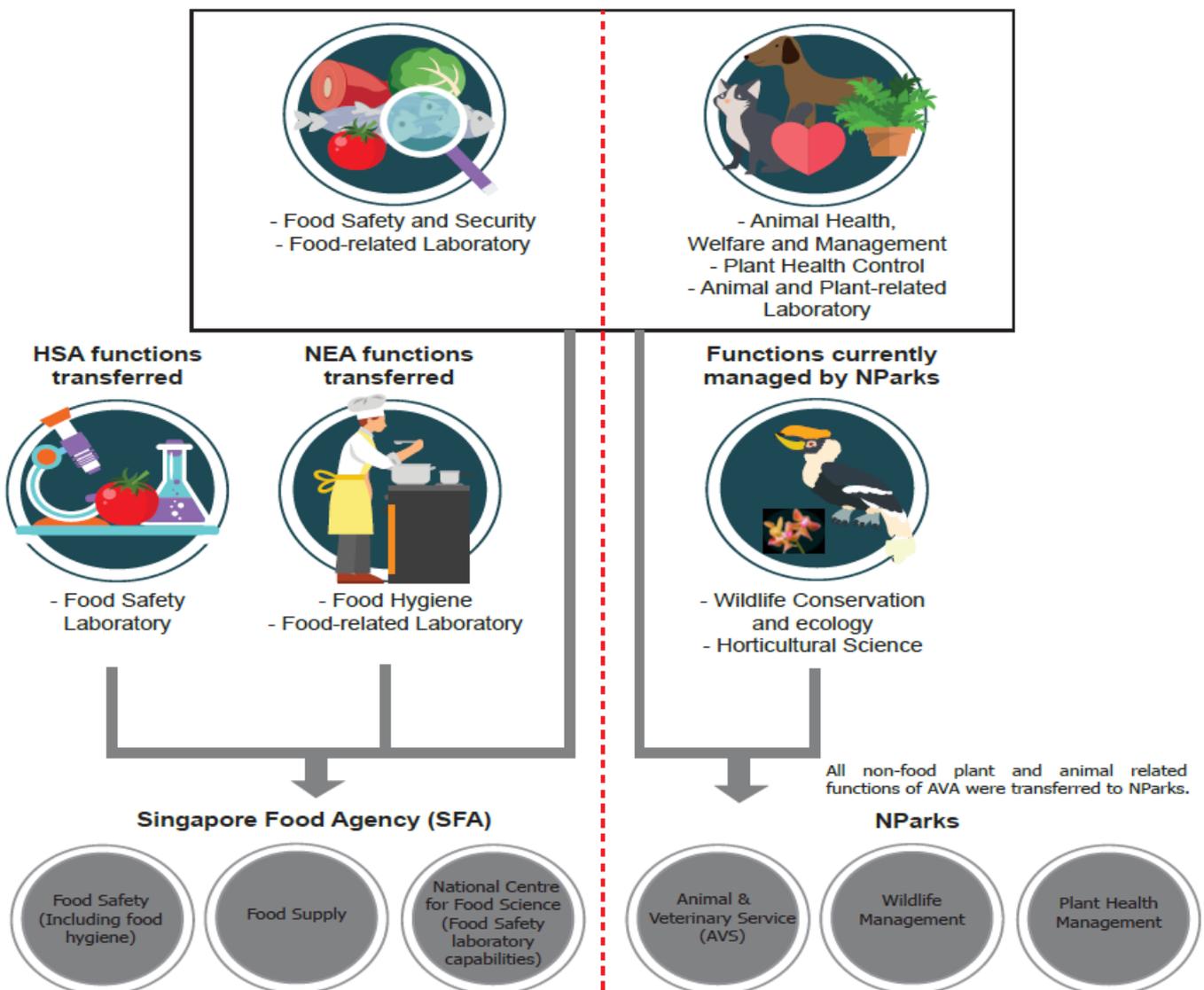
## New Singapore Food Agency to Oversee Food Safety and Security... Animal & Veterinary Service in NParks to Protect Animal Health and Safeguard Animal Welfare...

As of 1 April 2019, all food-related functions previously under the Agri-Food & Veterinary Authority (AVA) of Singapore, Health Sciences Authority (HSA), and National Environment Agency (NEA) have been consolidated into a new statutory board called the Singapore Food Agency (SFA).

In parallel, all plant and animal matters that are unrelated to food have been transferred from AVA to National Parks Board (NParks), which is now the lead agency for animal and wildlife management, as well as animal and plant health.

A new Animal & Veterinary Service (AVS) has been formed under NParks as the main touch-point on animal-related issues for pet owners, pet businesses, and animal welfare groups. It also takes on AVA's previous role as the first responder for animal-related feedback, and continues to uphold high standards in animal health and welfare.

### AVA functions distributed



# Infectious Diseases Update

As of E Week 13 (24-30 Mar 2019)

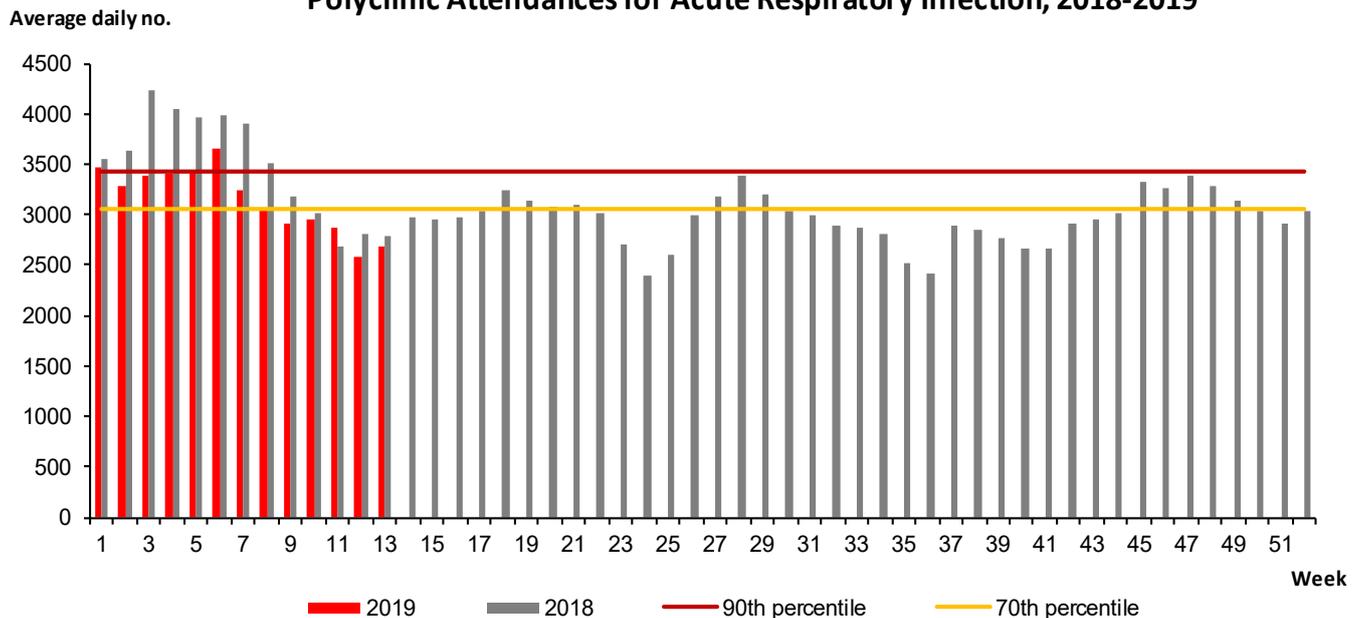
	E Week 13			Cumulative first 13 Weeks		
	2019*	2018	Median	2019	2018	Median
			2014 -2018			2014 -2018
<b>FOOD/WATER-BORNE DISEASES</b>						
Acute Hepatitis A	1	1	1	18	15	15
Acute Hepatitis E	0	1	1	8	15	14
Campylobacteriosis	8	11	10	114	87	104
Cholera	0	0	0	1	1	0
Paratyphoid	0	0	0	4	5	6
Poliomyelitis	0	0	0	0	0	0
Salmonellosis	70	22	39	536	334	400
Typhoid	2	0	0	21	9	16
<b>VECTOR-BORNE DISEASES</b>						
Chikungunya Fever	1	0	0	8	1	
Dengue Fever	100	24	90	2199	599	2245
Dengue Haemorrhagic Fever	1	0	1	25	3	6
Japanese Encephalitis <sup>^</sup>	0	0	NA	0	0	NA
Leptospirosis <sup>^</sup>	0	1	NA	0	6	NA
Malaria	1	0	0	9	7	4
Murine Typhus <sup>^</sup>	0	0	NA	2	2	NA
Nipah virus infection	0	0	0	0	0	0
Plague	0	0	0	0	0	0
Yellow Fever	0	0	0	0	0	0
Zika Virus Infection	0	0	NA	4	1	NA
<b>AIR/DROPLET-BORNE DISEASES</b>						
Avian Influenza	0	0	NA	0	0	NA
Diphtheria	0	0	0	0	0	0
Ebola Virus Disease	0	0	NA	0	0	NA
<i>Haemophilus influenzae</i> type b	0	0	0	1	0	0
Legionellosis	0	0	1	2	2	5
Measles	2	1	2	42	12	15
Melioidosis	2	0	1	12	8	12
Meningococcal Disease	0	0	0	2	3	3
Mumps	12	10	12	103	127	127
Pertussis	2	1	0	26	27	17
Pneumococcal Disease (invasive)	4	2	2	36	34	34
Rubella	0	0	0	0	0	3
Severe acute respiratory syndrome	0	0	0	0	0	0
Tetanus <sup>^</sup>	0	0	0	0	1	0
<b>OTHER DISEASES</b>						
Acute hepatitis B	1	2	1	13	13	NA
Acute hepatitis C	0	1	0	6	5	NA
Botulism <sup>^</sup>	0	0	NA	0	1	NA
<b>MERS-CoV</b>						
Suspect cases tested	11	8	NA	66	71	NA
Other patients tested	8	6	NA	42	32	NA
<b>POLYCLINIC ATTENDANCES - AVERAGE DAILY NUMBER</b>						
Acute upper respiratory infections	2687	2797	2530			NA
Acute conjunctivitis	84	109	83			NA
Acute Diarrhoea	584	532	452			NA
Chickenpox	13	21	NA			NA
Hand, Foot And Mouth Disease	85	121	NA			NA
<b>HIV/STI/TB NOTIFICATIONS</b>						
	<b>2019</b>	<b>Feb</b>		<b>Cumulative 2019</b>		
HIV/AIDS	13			36		
Legally Notifiable STIs	477			1062		
Tuberculosis	131			290		

\* Preliminary figures, subject to revision when more information is available.

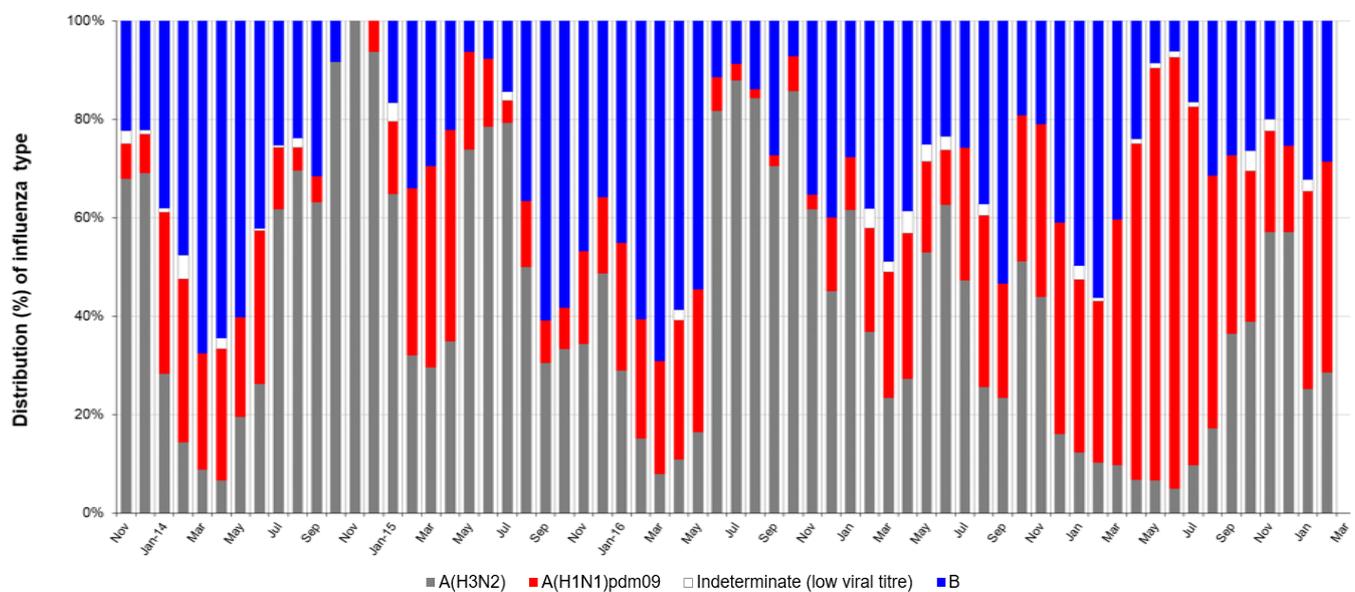
### INFLUENZA SURVEILLANCE

The average daily number of patients seeking treatment in the polyclinics for Acute Respiratory Infection (ARI) fluctuated above 70th percentile in January and February 2019. It declined and remained below 70th percentile in March. The proportion of patients with influenza-like illness (ILI) among the polyclinic attendances for ARI is 1.7%. The overall positivity rate for influenza among ILI samples (n=213) in the community was 22.5% in the past 4 weeks. Of the specimens typed for influenza in February 2019, these were positive for influenza A (H3N2) (28.6%), influenza A (H1N1) pdm09 (42.9%), and influenza B (28.6%).

**Polyclinic Attendances for Acute Respiratory Infection, 2018-2019**



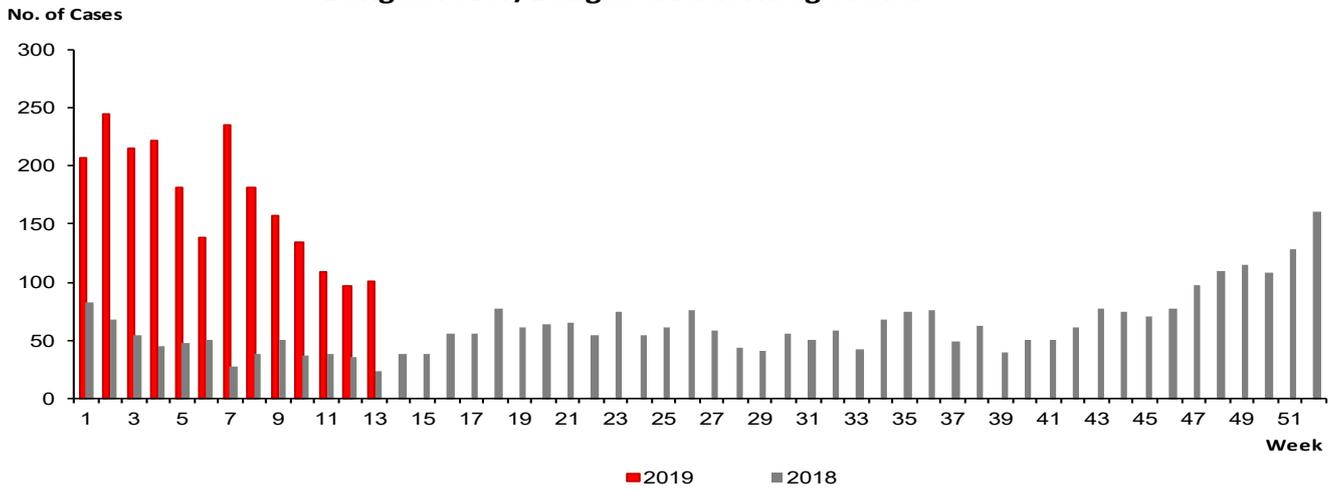
**Monthly Influenza Surveillance**



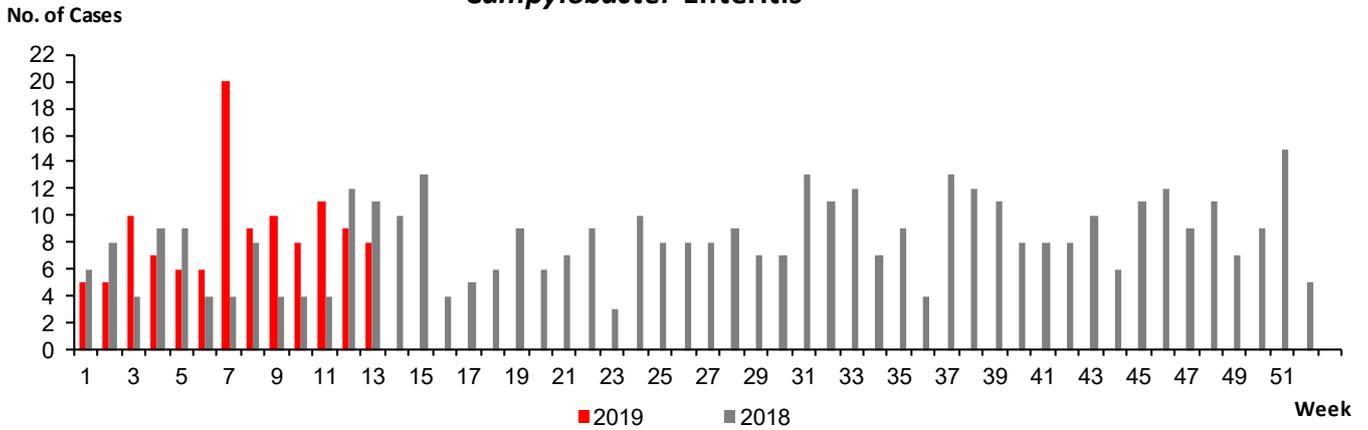
## SURVEILLANCE SUMMARY

### SURVEILLANCE OF OTHER SELECTED DISEASES

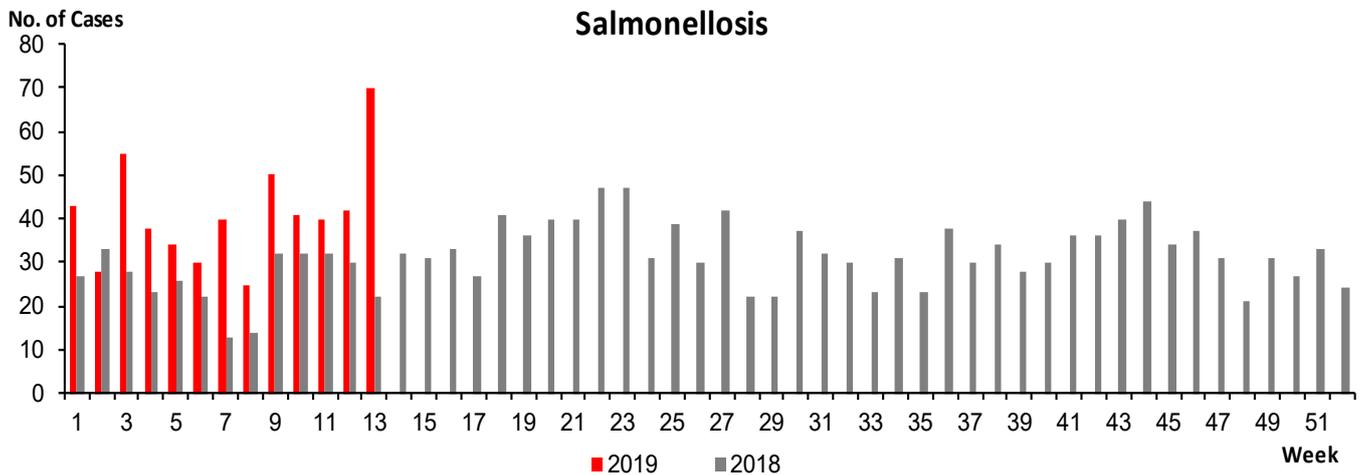
#### Dengue Fever/Dengue Haemorrhagic Fever

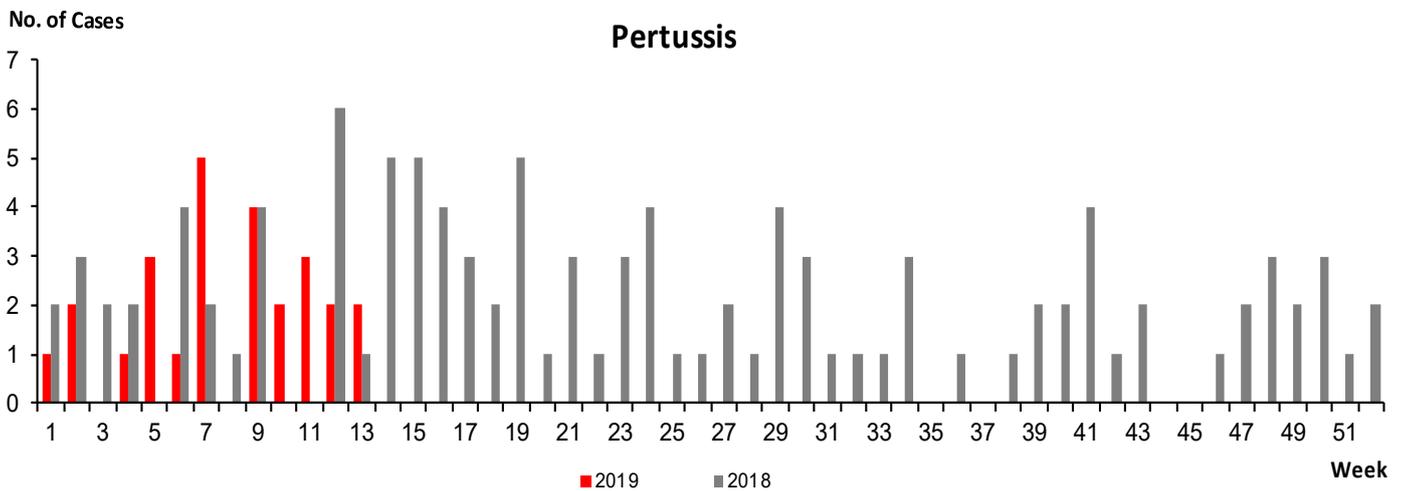
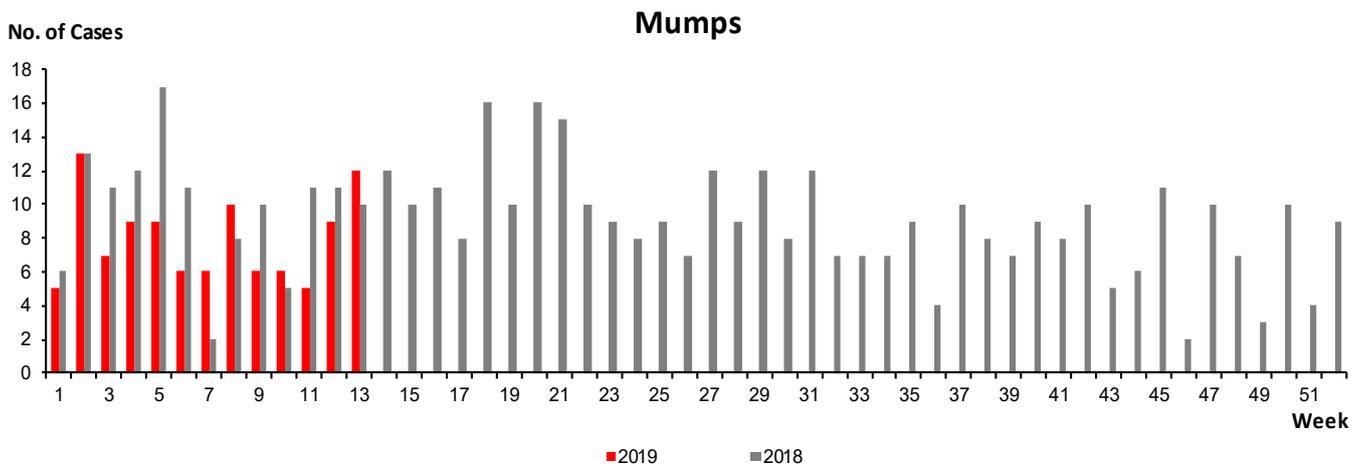
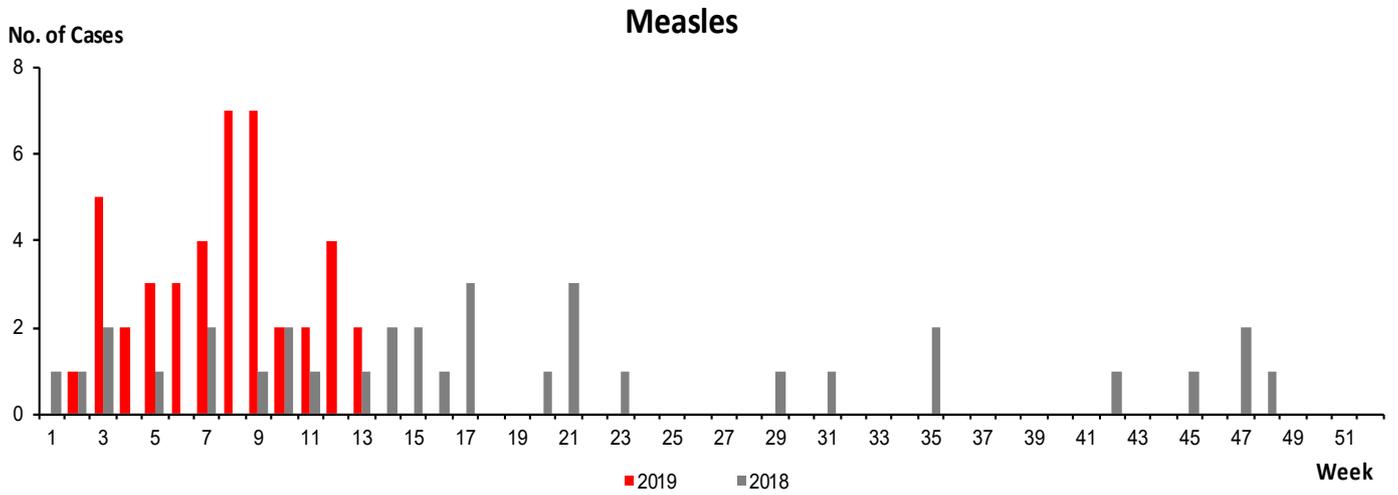


#### Campylobacter Enteritis



#### Salmonellosis





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