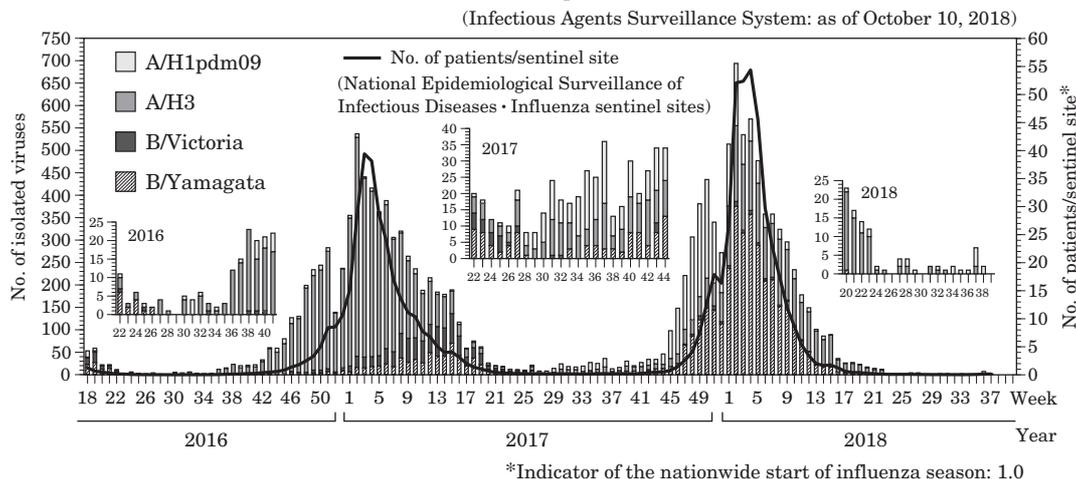


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<THE TOPIC OF THIS MONTH> Influenza 2017/18 season, Japan

Figure 1. Weekly number of isolated influenza viruses and reported influenza patients/sentinel sites from week 18, 2016 to week 38, 2018, Japan



The 2017/18 influenza season (from week 36 in September 2017 to week 35 in August 2018) was characterized by the predominance of the influenza B/Yamagata lineage, followed by A/H3 and A/H1pdm09 subtypes.

Epidemiology of the 2017/18 influenza season: Under the National Epidemiological Surveillance of Infectious Diseases (NESID) system, approximately 5,000 influenza sentinel sites (approximately 3,000 pediatric and 2,000 internal medicine health facilities) report patients diagnosed as influenza on a weekly basis. The number of patients reported per sentinel exceeded 1.0 (indicator of the nationwide start of influenza season) in week 47 of 2017 (Fig. 1) (<http://www.niid.go.jp/niid/en/10/2096-weeklygraph/2572-trend-week-e.html>) and exceeded 10.0 (indicator for the alert level, used at the prefectural level) in all 47 prefectures by week 2 of 2018. The peak was in week 5 of 2018 with 54.3 patients/sentinel, which was the highest since April 1999 when the Infectious Diseases Control Law was implemented.

Based on the reported sentinel surveillance data, the estimated number of influenza patients who visited medical facilities from week 36 of 2017 to week 17 of 2018 was 22,490,000. According to hospitalized influenza patient surveillance (data from approximately 500 designated sentinel hospitals with ≥ 300 beds), the number of hospitalized influenza patients during the same period was 20,584. Among 479 patients diagnosed as “acute encephalitis” (a category V notifiable infectious disease), 166 were reported as cases whose causative pathogen was influenza virus (as of October 2, 2018) (see p. 191 of this issue).

The 2017/18 influenza season was characterized by a greater number of influenza-associated hospitalizations than the 2016/17 season (when influenza A/H3 subtype predominated) and fewer cases of influenza-associated encephalitis/encephalopathy than the 2015/16 season (when influenza A/H1pdm09 predominated). Other information, such as excess mortality data, are reported in the 2017/18 annual influenza season report (<https://www.niid.go.jp/niid/images/idsc/disease/influ/fludoco1718.pdf>, in Japanese).

Isolation/detection of influenza virus in the 2017/18 season: Prefectural and municipal public health institutes (PHIs) reported the isolation/detection of 10,244 influenza viruses (7,681 isolations and 2,563 detections without isolation) (Table 1 in p. 183). Among them, 9,209 were reported from the influenza sentinel sites and 1,035 from non-sentinel sites (Table 2 in p. 183). Influenza type B comprised 45% (Yamagata lineage 96%, Victoria lineage 3%, and unknown lineage 1%), A/H3 comprised 32%, and A/H1pdm09 comprised 23% (Table 2). Although isolations of A/H1pdm09 began increasing from week 45 of 2017, it was surpassed by those of A/H3 from week 3 of 2018. Isolation of influenza type B began increasing from week 47 of 2017, earlier than usual, and

(THE TOPIC OF THIS MONTH-Continued)

surpassed that of type A from week 3 of 2018 (Fig. 1 and Fig. 2 in p. 183). In some regions, circulation of A/H3 was reported in the early spring of 2018 (Fig. 2 and p. 189 of this issue). During the 2017/18 season in the northern hemisphere, including Japan, influenza B/Yamagata lineage was predominant and detected for a long period of time (see p. 202 of this issue).

Genetic and antigenic characteristics of 2017/18 isolates: The National Institute of Infectious Diseases (NIID) conducts genetic and antigenic analyses of isolates from Japan and other Asian countries. For the antigenic analysis, the sera obtained from infected ferrets were used (see p. 184 of this issue). All A/H1pdm09 isolates analyzed belonged to genetic clade 6B.1. The majority of isolates tested were antigenically similar to A/Singapore/GP1908/2015 (the vaccine strain used in Japan for the 2017/18 season) and A/Michigan/45/2015 (WHO recommended vaccine strain for the 2017/18 season). All A/H3 isolates analyzed belonged to genetic clade 3C.2a or 3C.3a, and all but one isolate were 3C.2a. Antigenic analysis indicated that 50-60% of isolates tested were antigenically similar to the cell-grown reference virus A/Hong Kong/4801/2014 (original vaccine strain for the 2017/18 season). All B/Yamagata lineage isolates analyzed belonged to genetic clade 3, and more than 90% of the isolates tested were antigenically similar to B/Phuket/3073/2013 (the vaccine strain for the 2017/18 season). All B/Victoria lineage strains tested belonged to genetic clade 1A. Among the isolates analyzed, although 90% were antigenically similar to B/Texas/2/2013 (the vaccine strain for the 2017/18 season) until January 2018, the antigenic similarity dropped to 60% from February 2018.

Resistance to antivirals among 2017/18 isolates: Among 1,538 A/H1pdm09 isolates from Japan, 24 (1.6%) isolates were resistant to both oseltamivir and peramivir. All A/H3 isolates from Japan (209 isolates) and all influenza type B isolates from Japan (289 isolates) were sensitive to oseltamivir, peramivir, zanamivir, and laninamivir (see p. 184 of this issue).

Seroprevalence among the Japanese population prior to the 2017/18 season: Based on seroprevalence surveys conducted under the National Epidemiological Surveillance of Vaccine-Preventable Diseases program, the seroprevalence levels were measured from 4,356 serum samples collected from July to September 2017 (see p. 193 of this issue). The age groups with the highest seroprevalence (measured as HI antibody-positive, titer $\geq 1:40$) were 10-24 year olds (63-69%) for A/Singapore/GP1908/2015 [A(H1N1)pdm09], 5-19 year olds (78-86%) for A/Hong Kong/4801/2014 [A(H3N2)], and 15-34 year olds (61-69%) for B/Phuket/3073/2013 (B/Yamagata lineage). The sero-positivity for B/Texas/2/2013 (B/Victoria lineage) was less than 40% for all age groups except for 40-44 year olds (42%).

Influenza vaccine: The tetravalent vaccine for the 2017/18 season contained antigens of two type A and two type B strains. Approximately 26,430,000 vial-equivalent doses (estimated on the assumption that 1 vial contained 1 mL) were produced in the 2017/18 season, of which an estimated 24,910,000 vials were used.

For the 2018/19 season, the A/H1 strain selected was A/Singapore/GP1908/2015 (IVR-180), as in the 2017/18 season. The newly selected A/H3 strain was A/Singapore/INFIMH-16-0019/2016 (IVR-186). The B/Yamagata strain selected was B/Phuket/3073/2013, as in the 2017/18 season, and the newly selected B/Victoria strain was B/Maryland/15/2016 (NYMC BX-69A) (see p. 195 of this issue).

The multicenter case-control study conducted in the 2013/14 to 2016/17 seasons demonstrated that, for each respective season, two doses of vaccination to children under 6 years of age was significantly associated with protection against symptomatic influenza (see p. 197 of this issue).

Human infection with avian and swine influenza virus (see p. 200 of this issue): Since 2003, 860 confirmed human cases (454 fatal cases) of highly pathogenic avian influenza A(H5N1) virus infection have been reported from 16 countries, and since 2014, 21 confirmed human cases of avian influenza A(H5N6) virus infection have been reported from China (both as of October 4, 2018). Additionally, since 2013, China has reported many human cases of low pathogenic avian influenza A(H7N9) virus infection, with a total of 1,567 human cases (615 fatal cases) as of October 4, 2018. During the fifth epidemic (from October 2016 to September 2017) of this virus, highly pathogenic A(H7N9) viruses emerged and were also detected in 32 human cases. During the sixth epidemic (from October 2017 to September 2018) of this virus, only three human cases, all of which were due to a highly pathogenic virus, were reported. In February 2018, a human case of A(H7N4) virus infection was reported from China for the first time. Human cases of avian influenza A(H9N2) virus infection have been sporadically reported from China and Egypt.

Regarding swine influenza viruses, human cases of A(H3N2) variant (v), A(H1N1)v, and A(H1N2)v virus infections, associated with exposure at agricultural fairs in the United States, have been reported.

Conclusion: The response to influenza will continue to require sustained, comprehensive monitoring. Important activities include monitoring of trends in the occurrence of influenza patients, isolation of influenza viruses, analysis of the antigenic and genetic properties of circulating strains, vigilance against the emergence of drug-resistant strains, and monitoring of seroprevalence levels. Based on the revised Infectious Diseases Control Law implemented in April 2016, virological surveillance for influenza has been strengthened, including considerations for the number of tests conducted for seasonal influenza and positivity (see p. 192 of this issue). Furthermore, as a preventive measure against pandemic influenza in Japan, discussions regarding the future strategy for stockpiling pre-pandemic vaccines are ongoing at the national government level (see p. 199 of this issue).

Note: For IASR reporting, influenza nomenclature is based on the virus information available. Influenza viruses are classified by type, subtype, and strain based on hemagglutination (HA), neuraminidase (NA), and other information:

- When both HA and NA typing have been performed, names are listed fully [e.g. A(H1N1)pdm09, A(H3N2), A(H5N1)].
- When NA typing has not been performed, only HA information is listed (e.g. A/H1pdm09, A/H3).
- The strain name is represented by the location of isolation; in the case of isolation in Japan, the location is written in Japanese kanji, and in the case of isolation in foreign countries, in English.
- To distinguish swine influenza viruses recovered from humans from seasonal influenza viruses, the term "variant virus" is used with a letter "v" added after the subtype name [e.g. A(H3N2)v].

The statistics in this report are based on 1) the data concerning patients and laboratory findings obtained by the National Epidemiological Surveillance of Infectious Diseases undertaken in compliance with the Act on the Prevention of Infectious Diseases and Medical Care for Patients with Infectious Diseases, and 2) other data covering various aspects of infectious diseases. The prefectural and municipal health centers and public health institutes (PHIs), the Department of Environmental Health and Food Safety, the Ministry of Health, Labour and Welfare, and quarantine stations, have provided the above data.

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(特集つづき) (THE TOPIC OF THIS MONTH-Continued)

表1. インフルエンザウイルス分離・検出報告数, 2014/15~2017/18シーズン
Table 1. Isolation/detection of influenza viruses during the 2014/15-2017/18 influenza seasons

型 Type	シーズン* Season*			
	2014/15	2015/16	2016/17	2017/18
A/H1pdm09	41 (22)	3,032 (608)	281 (101)	1,859 (459)
A/H3	3,701 (1,530)	415 (217)	5,322 (2,326)	2,260 (996)
A NT	-(12)	1 (6)	1 (26)	-(15)
B/Victoria	57 (8)	1,174 (198)	817 (112)	113 (31)
B/Yamagata	653 (104)	1,526 (234)	656 (114)	3,403 (996)
B NT	11 (39)	2 (146)	2 (109)	6 (50)
C	2 (1)	22 (43)	-(1)	40 (16)
合計 Total	4,465 (1,716)	6,172 (1,452)	7,079 (2,789)	7,681 (2,563)

A NT: A亜型未同定, B NT: B系統未同定
A NT: A not subtyped, B NT: B lineage not determined

*各シーズン(当年9月~翌年8月)に採取された検体から各地方衛生研究所で分離されたウイルス報告数, -報告なし, ()内はウイルスは分離されていないが, 遺伝子検出または抗原検出による報告数を別掲

(病原微生物検出情報: 2018年10月10日現在報告数)

*Sampling season from September through August in the following year.

(): Nos. in parentheses denote gene or antigen detection without isolation, not included in the total.

[Infectious Agents Surveillance System: as of October 10, 2018 from prefectural and municipal public health institutes (PHIs)]

表2. インフルエンザウイルス分離・検出報告数, 2017/18シーズン
Table 2. Isolation/detection of influenza viruses during the 2017/18 influenza season

型 Type	Total (A+B)		(A)	(B)
	(A+B)	(A)		
A/H1pdm09	2,318	1,991	327	
A/H3	3,256	2,957	299	
A NT	15	15	-	
B/Victoria	144	131	13	
B/Yamagata	4,399	4,012	387	
B NT	56	49	7	
C	56	54	2	
合計 Total	10,244	9,209	1,035	

(A)インフルエンザ定点(小児科+内科)

Reports from influenza sentinels (pediatric & internal medicine sites)

(B)インフルエンザ定点以外(基幹定点+その他)

Reports from sites other than influenza sentinels

A NT: A亜型未同定, B NT: B系統未同定

A NT: A not subtyped, B NT: B lineage not determined

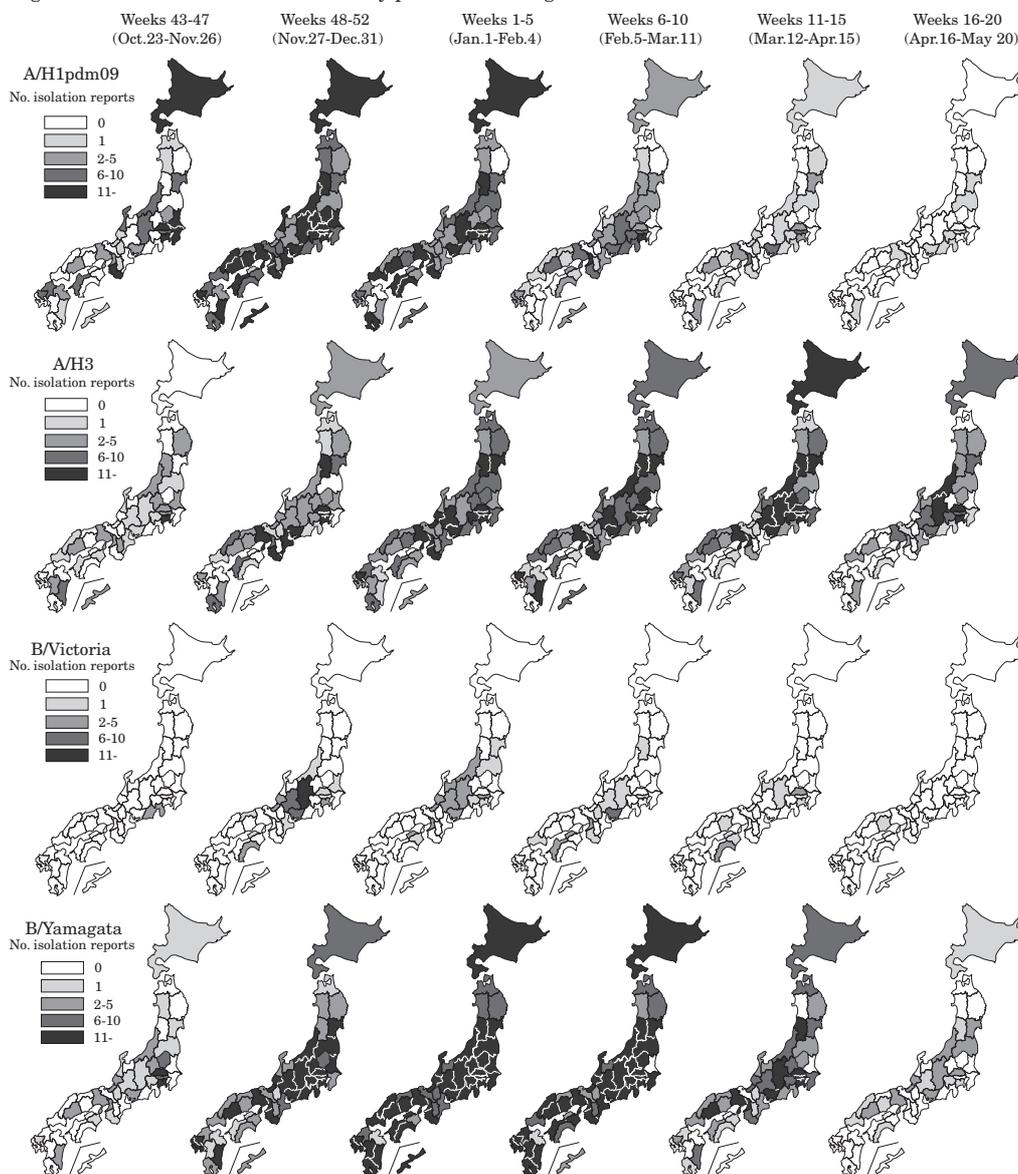
2017年9月~2018年8月に採取された検体から各地方衛生研究所で分離・検出されたウイルス報告数, -報告なし

(病原微生物検出情報: 2018年10月10日現在報告数)

Based on samples collected from September 2017-August 2018 (Infectious Agents Surveillance System: as of October 10, 2018 from PHIs)

図2. 都道府県別インフルエンザウイルス分離報告状況, 2017/18シーズン

Figure 2. Isolation of influenza viruses by prefecture during the 2017/18 influenza season



(病原微生物検出情報: 2018年10月18日現在報告数)

[Infectious Agents Surveillance System: As of October 18, 2018 from PHIs]