Margaret McCarron et al.

Global influenza surveillance

United States Centers for Disease Control and Prevention support for influenza surveillance, 2013–2021

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Abstract

Objective To assess the stability of improvements in global respiratory virus surveillance in countries supported by the United States Centers for Disease Control and Prevention (CDC) after reductions in CDC funding and with the stress of the coronavirus disease 2019 (COVID-19) pandemic.

Methods We assessed whether national influenza surveillance systems of CDC-funded countries: (i) continued to analyse as many specimens between 2013 and 2021; (ii) participated in activities of the World Health Organization’s (WHO) Global Influenza Surveillance and Response System; (iii) tested enough specimens to detect rare events or signals of unusual activity; and (iv) demonstrated stability before and during the coronavirus disease 2019 (COVID-19) pandemic. We used CDC budget records and data from the WHO Global Influenza Surveillance and Response System.

Findings While CDC reduced per-country influenza funding by about 75% over 10 years, the number of specimens tested annually remained stable (mean 2261). Reporting varied substantially by country and transmission zone. Countries funded by CDC accounted for 71% (range 61–75%) of specimens included in WHO consultations on the composition of influenza virus vaccines. In 2019, only eight of the 17 transmission zones sent enough specimens to WHO collaborating centres before the vaccine composition meeting to reliably identify antigenic variants.

Conclusion Great progress has been made in the global understanding of influenza trends and seasonality. To optimize surveillance to identify atypical influenza viruses, and to integrate molecular testing, sequencing and reporting of severe acute respiratory syndrome coronavirus 2 into existing systems, funding must continue to support these efforts.
Introduction
Global surveillance of influenza guides prevention and control decisions and monitors pandemic threats. Investment in global capacity-building for influenza surveillance was prompted by concerns about the pandemic potential of human infections with the highly pathogenic H5N1 avian influenza virus. As a result, dramatic improvements were made in testing capacity. While the coronavirus disease 2019 (COVID-19) pandemic highlighted the usefulness of strong disease surveillance systems, it strained insufficiently funded public health infrastructure and threatened the sustainability of surveillance systems.

In 2004, the Influenza Division of the United States Centers for Disease Control and Prevention (CDC) began support to health ministries to conduct influenza surveillance and improve pandemic preparedness using a funding model designed to gradually shift costs from donors to countries. These surveillance systems were critical during the 2009 H1N1 influenza pandemic response, and testing of respiratory specimens for influenza surged in the post-pandemic period. The Influenza Division’s early funding was intended to build sustainable capacity, with programmed reductions in its support after 10 years. Since 2013, 35 partner countries have transitioned to alternative funding sources, and by 2021, more than 70 countries had received some support from CDC for influenza surveillance.

We aimed to assess the sustainability of the surveillance improvements made by countries supported by the Influenza Division as funding decreased. Of 64 partner countries continuing to receive funds from the Influenza Division in 2021, we assessed if their national influenza surveillance systems: (i) continued to analyse as many specimens as before funding decreases; (ii) participated in activities of the World Health Organization’s (WHO) Global Influenza Surveillance and Response System, e.g. national influenza centres reported to WHO FluNet (a global influenza surveillance reporting platform) and contributed specimens to WHO consultations on the composition of influenza virus vaccines; (iii) tested and shipped enough specimens to detect rare events or signals of unusual activity; and (iv) demonstrated stability both before the COVID-19 pandemic and when facing the stress associated with the pandemic, that is, if they maintained levels of testing and reporting consistent with pre-pandemic levels.

Methods
Funding to countries
We used budget records of the Influenza Division from 2013 to 2021 to explore relationships between CDC funding and surveillance activity. We consulted progress reports of WHO’s Pandemic Influenza...
Preparedness Framework, a global framework for pandemic influenza preparedness, for 2013–2021 to identify our partner countries that received additional external funding via that mechanism. To estimate changes in gross cost per specimen among partner countries funded for 10 years or more, we conducted a linear regression analysis between median annual award and annual median number of specimens reported to FluNet.

**FluNet participation and molecular testing**

To evaluate the contribution of countries funded by the division to global influenza situational awareness, i.e. observation of circulating viruses, intensity of activity and identification of atypical activity, we calculated the proportion of Influenza Division partners among all countries reporting to FluNet. We reported the number of specimens tested and influenza-positive specimens per week reported to FluNet by partner countries aggregated by geographically contiguous areas with similar influenza transmission patterns (transmission zones).

We explored increases in the volume of molecular testing reported to the Global Influenza Surveillance and Response System by partner countries throughout the CDC investment period using linear regression analysis. Finally, to assess the capacity of our partner countries to maintain surveillance during the COVID-19 pandemic, we compared the number of specimens tested annually, weekly and by epidemic period in 2019 and 2021.

**Advanced characterization of specimens**

We explored the impact of the Influenza Division programme on the representativeness of data informing the biannual consultation to determine influenza vaccine composition and on global capacity to monitor the frequency and geographic diversity of genetic and antigenic change. We collected genetic and antigenic characterization and sequencing data from the WHO collaborating centre at CDC and combined these data with data uploaded to EpiFlu™ database (a global database of influenza genetic sequences) by all other collaborating centres for our partner countries. These data were used as proxies for the quantity and representativeness of specimens assessed in the biannual vaccine composition meeting.

We summed the number of specimens shared with WHO collaborating centres and the sequences uploaded to the EpiFlu™ database to detect temporal changes potentially associated with Influenza Division funding. We analysed submissions by transmission zone for the 3-month period before the vaccine composition meeting to explore geographic representativeness of decisions on vaccine selection.
To identify transmission zones that produce the greatest number of atypical (i.e. non-endemic) viruses, we analysed the frequency of sequences from viruses characterized as antigenic drift variants (i.e. low reactors) submitted to the WHO collaborating centre at CDC or uploaded to the EpiFlu™ database by other collaborating centres. We compared these numbers across transmission zones to identify regions that shared the most atypical viruses. We analysed the relationship between the mean number of influenza-positive viruses reported to FluNet and the mean number of viruses sequenced for each transmission zone to identify the proportion of positive viruses sequenced.

Using 2019 World Bank population estimates for partner countries of the Influenza Division, we calculated the population proportion in each transmission zone and determined the expected number of specimen submissions for each zone if distributed proportionally to population. We calculated the difference between the actual and expected submissions to evaluate population-based representativeness.

**Results**

**Funding to countries**

During 2013–2021, the Influenza Division directly or indirectly funded 70 countries, which had about 70% of the 2021 world population. We analysed data for 64 countries receiving funding before the COVID-19 pandemic, i.e. as of 2019. In 2021, there were 40 funded agreements. Six (15%) agreements had been in place for 1–5 years, five (12%) for 6–10 years and 29 (73%) for more than 10 years. Of the 34 countries that had received 10 years of funding by 2021, the median award was 300,000 United States dollars (US$; interquartile range, IQR: 282,500–400,000) in 2013 and US$ 50,000 (IQR: 24,981–100,000) in 2021 (Fig. 1). Nearly half (48%; 31/64) of the Influenza Division partner countries received at least 1 year of funding from the WHO Pandemic Influenza Preparedness Framework between 2013 and 2021.

**FluNet participation**

The 64 countries in our analysis represented 63% of the 102 WHO Member States reporting data to FluNet in 2021. While the weekly number of specimens tested was similar during 2021 (33; IQR: 11–86) compared with 2019 (35; IQR: 14–90), influenza detections were lower in 2021 (2; IQR: 0–10) than in 2019 (median 4; IQR: 0–17). We observed similar differences in pre- and peri-pandemic testing during epidemic periods (periods of sustained activity above baseline): a median of 4592 (IQR: 1669–18,574) tests and 58 (IQR: 8–512) influenza-positive results were reported to FluNet per epidemic period from each WHO transmission zone included in our analysis in 2021 compared with a median of 5529 (IQR: 1142–13,369) tests and 1355 (IQR: 366–2761) influenza-positive results in 2019.
annual average number of specimens tested and reported to FluNet increased linearly between 2013 and 2021 at a rate of almost 200 000 specimens a year, a statistically significant increase \((P\text{-value } 0.002; \text{Fig. 2})\). In 2020 and 2021, the volume of influenza testing varied monthly, but followed a similar pattern to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) testing (Fig. 3). For most months in 2020 and 2021, influenza testing was higher than the historical monthly average of influenza testing for 2016–2019.

Of the 35 countries that had received 10 years of funding by 2021, the median number of specimens tested was 3247 (IQR: 1312–5042) in 2013 and 3051 (IQR: 892–10 344) in 2021. When comparing the median award with the median number of specimens tested, we saw a linear decrease in cost per specimen from US$ 92 in 2013 to US$ 16 in 2021 \((P\text{-value } 0.002; \text{Fig. 1})\).

**Advanced characterization of specimens**

The number of partner countries that shipped specimens to a WHO collaborating centre significantly increased from 44 (69% of 64) in 2013 to 56 (88%) in 2019 \((P\text{-value } 0.02)\). Shipments from partner countries of the Influenza Division accounted for an average of 71% (range: 61–94%) of specimens included in the genetic sequencing data package submitted to the vaccine composition meeting; partner countries made up 81% (1797/2222) and 94% (4765/5078) of submissions during the February and September 2021 vaccine composition meetings, respectively. This change represented an increase of more than 100% in the annual number of specimens shipped by partner countries, from 14 956 in 2013 to 36 868 in 2019; this number fell during the low circulation of influenza during the peri-pandemic period.6 Partner countries accounted for an average of 44% (range 39–47) of all sequences of human seasonal influenza viruses uploaded to EpiFlu™ by any WHO collaborating centre between 2013 and 2019.

During 2013–2019, 48% (460/5518) of influenza A(H1N1), 21% (1057/5070) of influenza A(H3N2), 16% (370/2373) of influenza B Victoria and 15% (401/2673) of influenza B Yamagata haemagglutinin sequences were classified into clades with a prevalence of less than 10%. Similarly, of 14 059 influenza viruses that were antigenically characterized, 521 (4%) were antigenic drift variants which did not react strongly in laboratory assays (data repository).6 In 2013–2019, 2279 specimens were identified rare genetic clades (i.e. clades comprising less than 10% of clades identified in genetic sequencing). These 2279 clades were most often identified in Eastern Asia (479; 21%), South East Asia (340; 15%) and Eastern Europe (340; 15%; \(P\text{-value } 0.0001; \text{data repository})\).6 Similarly, 521 antigenic variants were identified in 2013–2021. These variants were most often identified among specimens...
shipped from South East Asia (145; 28%) followed by Southern Asia (101; 19%), and Eastern Europe (47; 9%; *P*-value 0.0001; data repository).6

**Geographical representativeness of funded countries**

Reporting varied substantially by country and transmission zone. In 2019, the total population of partner countries was 5 453 110 000. Eastern Asia contained 26% (1 400 520 000) of that population but accounted for 69% (680 186) of the average number of specimens tested per year for 2016–2019 by all partners (991 219), as reported to FluNet, and 87% of specimens shipped to collaborating centres. Tropical South America accounted for 2% (17 338/991 219) of the specimens reported to FluNet, but 5% (243 560 000) of the population of partner countries. In contrast, Southern Asia had 34% (1 835 731 000) of the population of partner countries but accounted for only 4% (40 718) of specimens tested, as reported to FluNet (data repository).6 The greatest proportions of the 1067 specimens included in the February 2019 vaccine composition meeting package were from Eastern Asia (250; 23%), South East Asia (248; 23%) and Eastern Europe (155; 15%). Only 27% (292/1067) of the remaining specimens came from zones with 61% of the northern hemisphere population. Similarly, Eastern Asia (399; 23%), Eastern Europe (230; 13%) and Central America and the Caribbean (198; 12%) accounted for the greatest proportion of the 1717 specimens in the package for the September 2019 vaccine composition meeting. Only 21% (366/1717) of the specimens in the package originated from other southern hemisphere transmission zones, which typically have peak influenza activity in May–September. Overall, 3% (IQR: 1–8) of the positive viruses reported to FluNet were reported to EpiFlu™ as having been sequenced annually. However, this figure varied greatly by transmission zone, with little change from 2013 to 2019. Oceania Melanesia and Polynesia, and Northern Africa, respectively, sequenced a mean of two and six influenza viruses annually, while Central America, Southern Asia and South East Asia, respectively, sequenced an average of 289, 255 and 252 viruses, respectively, each year.

**Ability to identify rare variants**

Before the COVID-19 pandemic, 41 of 48 (85%) countries with > 5 years of data tested enough samples in 2021 to define their epidemic period (required sample size ≥ 100 specimens).7 Two (12%) of the 17 transmission zones tested enough specimens by molecular testing each week to reliably identify atypical viruses circulating at a hypothetical prevalence of 0.1% (required sample size ≥ 3838 specimens; Table 1). Eleven of the 17 transmission zones tested enough specimens over the epidemic period to reliably identify atypical viruses. In 2019, only eight of the 17 transmission zones shipped enough specimens to WHO collaborating centres in the 3 months before the vaccine composition meeting to
reliably identify antigenic variants and rare haemagglutinin genetic clades at a hypothetical prevalence of 3.7% per epidemic period (required sample size ≥ 100 specimens; Table 1). The most underpowered transmission zones for detecting antigenic variants and rare haemagglutinin genetic clades were Middle Africa, Oceania Melanesia and Polynesia, and Central Asia. Of note, all transmission zones except Middle Africa, and Oceania Melanesia and Polynesia tested enough samples to identify hypothetical antigenic drift variants if all influenza-positive samples identified through reverse transcription polymerase chain reaction testing were further characterized.

Discussion

Our findings suggest that Influenza Division investments established sustainable programmes, with a linear decrease in costs to the division per influenza specimen tested. The transition from external to domestic funding was implicit in the funding model and was intended to foster country ownership and investment by local stakeholders, similar to models used by other global health organizations.8,9 Partner countries tested and reported a similar number of specimens before and after transitioning from Influenza Division funding to other funding sources,10 with a surge during the COVID-19 pandemic. These partners continued to participate meaningfully and improve their contributions to the Global Influenza Surveillance and Response System during 2013–2021 despite an average programmed funding decreased. While in some countries additional donors supported influenza surveillance, to our knowledge their contributions have been modest and often focused on research or have been awarded to nongovernment partners.11,12 It is possible that a surge in donor funds during the COVID-19 pandemic facilitated expansion in testing capacity after 2020.

The Global Influenza Surveillance and Response System provides critical information for selection of influenza vaccine strains and surveillance for new viruses. We observed that influenza testing volumes reported to FluNet by partner countries were 3.5 higher in 2021 than in 2013, and the number of specimens submitted to WHO collaborating centres from 2013 to 2019 nearly doubled, which contributed to an overall strengthening of the Global Influenza Surveillance and Response System.13 The volume of molecular influenza testing during the COVID-19 peri-pandemic period was 1.5 times higher in 2021 than in 2019. The increase in the number and geographic breadth of specimens expanded genetic sequencing and identification of antigenic variants, which likely improved the representativeness of influenza vaccine strains. This larger pool of specimens available for sequencing potentially increases global capacity to identify rare viruses.
Information generated by influenza surveillance systems facilitates evidence-based influenza prevention and control policies and programmes. Before the expansion of global testing and reporting, little was known about the circulation of influenza viruses and the burden of influenza disease in tropical and subtropical areas.14 During our analytic time period (2013–2021), 36 partner countries of the Influenza Division published national estimates of the burden of influenza disease or were included in regional estimates and these estimates were used to justify investments in expanding or introducing new vaccination programmes.15–18 These estimates have also been used to plan the timing of national influenza vaccination campaigns.7

Sustained gains among Influenza Division partner countries through the COVID-19 pandemic suggest commitments to conduct national surveillance despite the challenge of a stressed system and other challenges, such as political will to replace donor funding or inaccurate estimates of financial needs.19 Continuity of influenza testing during the pandemic may have been influenced by WHO guidance20,21 and webinars about the integration of SARS-CoV-2 testing using the Global Influenza Surveillance and Response System. Reminders to continue influenza testing in advance of the typical influenza seasons might have contributed to consistent testing for influenza in addition to SARS-CoV-2 during the peri-pandemic period.

The candidates for magnitude of surveillance gains have not been geographically homogeneous. These differences may represent missed opportunities to rapidly identify rare events that could be the first signal of a public health emergency of international concern and identify emerging viruses that could become seasonal or pandemic influenza vaccines.22 The Eastern Asia transmission zone consistently tested enough specimens to detect a rare event weekly, while in the remaining zones, testing was sufficient only when specimens were aggregated during a 3-month influenza epidemic period. The Southern Asia transmission zone, home to 27% of the global population, provided only a small portion of the total specimens reported to FluNet. While 11 of 17 of transmission zones were able to identify non-endemic viruses circulating at a low prevalence (e.g. <0.1%) during a three-peak epidemic months, an insufficient number of specimens were collected during epidemic periods in other zones. Given country-level testing disparities, it may be sensible to aggregate data from epidemic zones to identify rare events. We have identified transmission zones that would benefit most from technical assistance and guidance on identifying atypical events, the target sample sizes needed to do so and the appropriate timeframes. The mismatch in population size to specimen volume may indicate regions with resource-constrained health systems that require greater financial and technical investment and an increase in political interest in surveillance of respiratory viruses and mitigation of their disease burden.
The COVID-19 pandemic tested the pandemic preparedness capacity that the Influenza Division programme intended to build. Partner countries met this challenge by quickly operationalizing their influenza surveillance systems to detect and monitor SARS-CoV-2 activity.23 With similar case definitions10,24,25 and molecular testing and reporting platforms, the surveillance systems supported by the Influenza Division proved agile enough to monitor other respiratory viruses. The COVID-19 pandemic led to substantial increases in testing by national influenza centres, the SARS-CoV-2 testing volume in 2021 was 23 times greater than the 2019 influenza testing volume. COVID-19 response investments are being used so that national influenza centres can routinely test respiratory specimens for multiple viral pathogens, employ new assays, and sequence and improve informatics platforms, thereby enhancing broader respiratory disease surveillance activities globally.

Our evaluation was subject to several limitations. We relied on publicly available data, which might not represent the entirety of each country’s influenza surveillance data, nor differentiate between routine surveillance and outbreak-related testing data. Reporting to the Global Influenza Surveillance and Response System and EpiFlu™ and shipment of specimens to collaborating centres are voluntary, and not all countries share complete information about their activities. As a result, our estimates for power to detect unusual events, proportional representation and overall gains might be biased. We present our analyses using theoretical thresholds to consider potential sample size requirements to detect rare events; we are unaware of a consensus about standard influenza testing sample sizes, thresholds or triggers for public health action. Our analyses included data from Influenza Division partner countries only and do not represent comprehensive global estimates. While our partner countries are worldwide, they do not include high-income countries that typically have well developed influenza surveillance systems. We believe, however, that gains in global surveillance have primarily been in low- and middle-income countries that have expanded their surveillance since donors began funding surveillance in 2004. Likewise, advances in surveillance in tropical and subtropical regions may afford new opportunities to identify emerging viruses and to identify viruses that might start epidemics in temperate regions.26,27 While we believe gains are partially attributable to Influenza Division investments, we cannot quantify the contributions of other donors. We recognize that China has an extensive surveillance network and some of our analyses may be biased by the amount of data from there. Similarly, Brazil expanded surveillance during the COVID-19 pandemic, which may also bias our estimates.

In conclusion, investment in infrastructure led to sustained growth in surveillance capacity among partner countries. The initial 10-year investment in capacity-building yielded gains that, as of 2021, proved sustainable despite decreases in Influenza Division funding and the stress of a respiratory
disease pandemic. Partner surveillance systems demonstrated agility in integrating a non-influenza pathogen into routine surveillance within the Global Influenza Surveillance and Response System.28 While global gains in surveillance have been substantial, groups of neighbouring countries within transmission zones, rather than individual countries, are testing enough specimens to reliably detect unusual events. Strategic improvements, such as increasing capacity to perform next-generation sequencing within transmission zones, may provide opportunities to improve global situational awareness of influenza activity trends and the emergence of atypical viruses.

**Competing interests:**
None declared.

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Table 1. **Samples tested, identified and submitted within the influenza surveillance, by transmission zone, 2013–2021**

| Influenza transmission zone | Characterized months | Mean no. of samples tested,\(^a\) 2013–2021 | Mean no. of influenza-positive samples\(^a\) per epidemic, 2013–2021 | Antigenic drift variants identified 2013–2021, total no. (%) | Samples sent to collaborating centres in 3 months before Sep 2019 vaccine composition meeting, mean no. (%) | Samples sent to collaborating centres in 3 months before Feb 2019 vaccine composition meeting, mean no. (%) | Population-based deficit or surplus in sample submissions in 2019, % |
|----------------------------|----------------------|---------------------------------------------|----------------------------------------------------------------|-------------------------------------------------|-------------------------------------------------|-------------------------------------------------|-------------------------------------------------|
| Eastern Africa | Dec–Jan | 225 | 1553 | 217 | 57 (11) | 86 (3) | 121 (2) | −6 |
| Northern Africa | Dec–Feb | 223 | 4809 | 1149 | 1 (0) | 10 (0) | 55 (1) | −2 |
| Middle Africa | Dec–May | 27 | 761 | 87 | 4 (1) | 17 (1) | 29 (0) | −1 |
| Western Africa | Sep–Mar | 186 | 5891 | 833 | 28 (5) | 68 (2) | 106 (1) | −4 |
| Southern Africa | May–Sep | 144 | 4221 | 788 | 2 (0) | 65 (2) | 28 (0) | −1 |
| Central America and Caribbean | Jun–Oct | 337 | 8257 | 888 | 22 (4) | 105 (3) | 89 (1) | 0 |
| Temperate South America | May–Aug | 166 | 3181 | 570 | 7 (1) | 28 (1) | 20 (0) | 0 |
| Tropical South America | May–Sep | 5137 | 135635 | 1409 | 47 (9) | 179 (6) | 66 (1) | −4 |
| North America | Dec–Mar | 601 | 16032 | 3587 | 26 (5) | 30 (1) | 31 (0) | −2 |
| Eastern Asia | Jan–Mar | 10952 | 176237 | 36441 | 115 (22) | 1910 (60) | 6324 (84) | 63\(^b\) |
| Central Asia | Dec–Feb | 14 | 502 | 151 | 0 (0) | 31 (1) | 27 (0) | 0 |
| Western Asia | Dec–Mar | 36 | 1074 | 352 | 1 (0) | 24 (1) | 33 (0) | 0 |
| Southern Asia | Dec–Apr | 895 | 22260 | 3530 | 37 (7) | 133 (4) | 111 (1) | −32\(^c\) |
| Eastern Europe | Jan–Apr | 2582 | 76268 | 17262 | 38 (7) | 201 (6) | 97 (1) | −3 |
| South West Europe | Dec–Mar | 191 | 6525 | 2512 | 3 (1) | 69 (2) | 57 (1) | 0 |
| Oceania | Jul–Sep | 31 | 475 | 92 | 0 (0) | 78 (2) | 69 (1) | 0 |
| Melanesia and Polynesia | | | | | | | | |
| South East Asia | Jul–Oct | 315 | 5976 | 1106 | 131 (25) | 176 (5) | 259 (3) | −8 |
| **Total** | NA | NA | NA | NA | 519 | 33210 | 7522 | NA |

\(^a\) Identified by polymerase chain reaction test.

\(^b\) Over-represented (more specimens than proportional to the population).

\(^c\) Under-represented (fewer specimens than proportional to the population).

Notes: Tropical South America and Eastern Asia tested enough specimens each week to reliably identify atypical viruses. Central America and Caribbean, Tropical South America, Eastern Asia, Eastern Europe, South West Europe, Southern Asia, Northern Africa, Western Africa, Southern Africa, North America and South East Asia tested enough specimens over the epidemic period to reliably identify atypical viruses. Central America and Caribbean, Tropical South America, Eastern Asia, Eastern Europe, Southern Asia, Eastern Africa, Western Africa and South East Asia sent enough specimens to WHO collaborating centres to reliably detect viruses or rare variants or clades that could not be subtyped.
Fig. 1. **Number of specimens tested in countries supported by the CDC, total funding and cost to CDC per specimen, 2012–2021**

CDC: Centers for Disease Control and Prevention; GISRS: Global Influenza Surveillance and Response System; US$: United States dollars.

Note: $P = 0.002$ for decrease in cost per specimen, 2013–2021.
Fig. 2. Molecular testing volume in countries supported by the Centers for Disease Control and Prevention, 2013–2021

SARS-CoV-2: severe acute respiratory syndrome coronavirus 2.

Note: $P = 0.002$ for increase in average number of specimens tested, 2013–2021.
Fig. 3. **Number of specimens tested for influenza and SARS-CoV-2 molecular testing in countries supported by the Centers for Disease Control and Prevention, by month, 2020–2021**

COVID-19: coronavirus disease 2019; GISRS: Global Influenza Surveillance and Response System; PHEIC: public health emergency of international concern; SARS-CoV-2: severe acute respiratory syndrome coronavirus 2; WHO: World Health Organization.