

Original Article

# Respiratory pathogen trends in Queensland, Australia between 2018 and 2021: A statewide cohort study before and after the initial COVID-19 outbreak

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**Background.** The SARS-CoV-2 pandemic and accompanying public health measures disrupted the normal transmission of respiratory viral pathogens. Less is known about the effects on bacterial pathogens.

**Aims.** To assess the impact of public health restrictions on common respiratory pathogens (influenza viruses, respiratory syncytial virus (RSV) and the following bacterial pathogens: *Streptococcus pneumoniae* (*S. pneumoniae*), *Klebsiella pneumoniae* (*K. pneumoniae*), *Pseudomonas aeruginosa* (*P. aeruginosa*) and *Staphylococcus aureus* (*S. aureus*).

**Methods.** This statewide cohort study used respiratory specimen result data from 237 health facilities in Queensland, Australia, collected between January 2018 and June 2021. Trends and weekly positive rates per 100 tests/cultures for weeks 11–27 (with 95% confidence intervals) were compared between pre-pandemic (2018/2019), early pandemic restrictions (2020), and easing of restrictions (2021) periods.

**Results.** Over 260,000 viral PCRs and 180,000 cultures were analyzed. Decreases in influenza and RSV were observed in 2020 from 10.8 to 1.1 and 9.5 to 2.5 per 100 tests, respectively; *S. pneumoniae* decreased from 1.7 to 1.1 per 100 cultures. Influenza levels remained low until the end of the study period. There was no change in the detection of *S. aureus* or *P. aeruginosa* per 100 cultures, but cultures positive for *K. pneumoniae* increased from 1.2 in 2018/2019 to 1.8 in 2020 and 1.6 in 2021. After restrictions eased, RSV rates increased to levels higher than before the pandemic.

**Conclusions.** Transmission of droplet-spread pathogens decreased after the introduction of public health restrictions due to the COVID-19 pandemic. The increase in *K. pneumoniae*, often associated with nosocomial infections, warrants further investigation. Crown Copyright © 2024 Published by Elsevier Inc. on behalf of Instituto Mexicano del Seguro Social (IMSS). This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>)

**Keywords:** COVID-19, Respiratory, Virus, Microbial, Epidemiology.

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## Introduction

Lower respiratory tract infections (LRTIs) are frequent, affecting 46 out of every 1,000 people annually (1). The most common pathogens associated with severe LRTIs worldwide include *Streptococcus pneumoniae* (*S. pneumoniae*), influenza viruses, and respiratory syncytial virus (RSV) (1). Several other pathogens that cause respiratory disease are classified as emerging threats due to increasing antibiotic resistance and virulence: *Klebsiella pneumoniae* (*K. pneumoniae*), *Pseudomonas aeruginosa* (*P. aeruginosa*), and *Staphylococcus aureus* (*S. aureus*) (2). The clinical significance of these respiratory pathogens and their modes of transmission are described in Table 1 (1–7).

In late 2019, a new respiratory pathogen, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), led to the coronavirus disease of 2019 (COVID-19) pandemic, which caused widespread disruption of social interaction patterns worldwide, including in Queensland, Australia. Queensland imposed a statewide lockdown for approximately 16 weeks from the time the World Health Organization declared the pandemic on March 11, 2020, until the end of June 2020. During this time, residents were required to stay at home for all but essential reasons; schools and non-essential businesses were closed, and borders with other jurisdictions were closed and monitored. Hand hygiene and social distancing messages were widely disseminated (8). These public health measures were somewhat effective in slowing the spread of SARS-CoV-2; Queensland averaged 63 positive SARS-CoV-2 findings per week from March to June 30, 2020, dropping to seven per week from July 1 through the end of December 2020 (9).

Besides SARS-CoV-2, other respiratory pathogens were affected by the public health measures introduced. Changes

in the circulating prevalence of other viral pathogens before and after the first months of the COVID-19 pandemic have been summarized in systematic reviews (10,11). Most studies describe influenza trends, followed by RSV, and a few examined parainfluenza, rhinovirus, and adenovirus. These reviews conclude that there have been substantial and clinically significant reductions worldwide for all viruses investigated and the diseases they cause. However, most report short-term effects, comparing early pandemic incidence (March–June 2020) with historical statistics on the incidence of these viruses. Longer population-based studies (through June 2021) have been conducted using the Systemized Nomenclature of Medicine (SNOMED) and/or the International Classification of Diseases version 10 (ICD-10) that include respiratory diseases (12,13). These studies, which examined both communicable and non-communicable causes of illness, found that presentations and/or admissions for respiratory conditions remained lower than expected through June 2021.

However, few studies have examined potential changes in the prevalence of bacterial pathogens as a result of public health measures. We aim to provide additional evidence on trends in respiratory pathogen detection over 3.5 years for common viral pathogens as well as less studied bacterial pathogens (*K. pneumoniae*, *S. pneumoniae*, *P. aeruginosa*, and *S. aureus*).

## Methods

### Design, setting, and sample

This cohort study conducted in Queensland is reported according to the STROBE statement (14). Queensland is the second largest state in Australia, covering 1.7 million km<sup>2</sup>

**Table 1.** Pathogen studied, most common transmission route, and clinical significance in respiratory diseases.

Pathogen and transmission route	Clinical significance
Influenza viruses (aerosol droplets, fomites)	Seasonal (autumn to winter) <sup>a</sup> , a leading cause of hospitalization for pneumonia and bronchiolitis in children and older adults. Estimated to infect 20% of the population annually, highly variable strains (3).
Respiratory syncytial virus (respiratory droplets and direct contact, common secondary infections in homes).	Seasonal virus (autumn to winter) <sup>a</sup> , a leading cause of croup, bronchiolitis, bronchitis and pneumonia in children, particularly those under two years of age. Most children have been infected by RSV by age two. Estimated to cause 85% of infant LRTI hospitalizations during seasonal outbreaks (4).
<i>Streptococcus pneumoniae</i> (Droplets and direct contact)	Leading cause of serious bacterial infections of the lower respiratory tract worldwide. Estimated to be responsible for more than half of all deaths in children under five from LRTIs (1). Causes pneumococcal disease.
<i>Klebsiella pneumoniae</i> (Direct contact or faecal-oral)	Can be community-acquired, although most occur in healthcare settings. Risk factors include alcohol abuse and diabetes. Common cause of nosocomial pneumonia, especially in immunocompromised and ventilated patients. Emerging global threat from carbapenem-resistant and hypervirulent strains (2,5).
<i>Pseudomonas aeruginosa</i> (Direct contact with contaminated surfaces, devices or water)	Common cause of coinfections and hospital-acquired pneumonia. Estimated to cause one in four ICU-acquired respiratory infections. Common complicating pathogen in patients with cystic fibrosis. Multidrug resistant strains emerging (2,6).
<i>Staphylococcus aureus</i> (transmitted by micro-aspiration from normal flora in nares or skin)	Most commonly occurs after influenza infection and is more severe in the very young and very old. Cause of nosocomial pneumonia (7).

<sup>a</sup>Seasonality is hemisphere specific. Winter is defined as the three months with the lowest average temperatures, i.e. December, January, and February in the northern hemisphere and June, July, and August in the southern hemisphere. LRTI, lower respiratory tract infection; ICU, intensive care unit.

and a population of over four million people. We used data from all respiratory specimens (nasopharyngeal aspirates, bronchoalveolar lavage, sputum) reported through Pathology Queensland's AUSLAB™ data system (PJA Solutions Pty Ltd). Pathology Queensland provides diagnostic pathology services for public hospitals in Queensland as well as for state-run services (e.g., corrective services), some private sector facilities, and point-of-care collections in remote areas. In this study, specimen tests and results recorded in AUSLAB™ came from 237 different facilities; about 70% of the tests were collected at public hospitals. This sample is representative of people requiring in-hospital testing in Queensland. Criteria for undertaking testing were clinician and institution-specific.

#### Data collection

Results from all respiratory specimens, both microbiological cultures and polymerase chain reaction (PCR) results, were available for analysis. Data were extracted, cleaned, and quality checked at the organism count level by Pathology Queensland for all results reported in the AUSLAB™ system for the period January 1, 2018–June 30, 2021. All results for specimens taken from a respiratory sample were retained, not just those in which a pathogen was detected. Eligible samples from any respiratory site (nose, throat, lungs) included nasopharyngeal swabs, bronchial washings, sputum samples, pleural as-

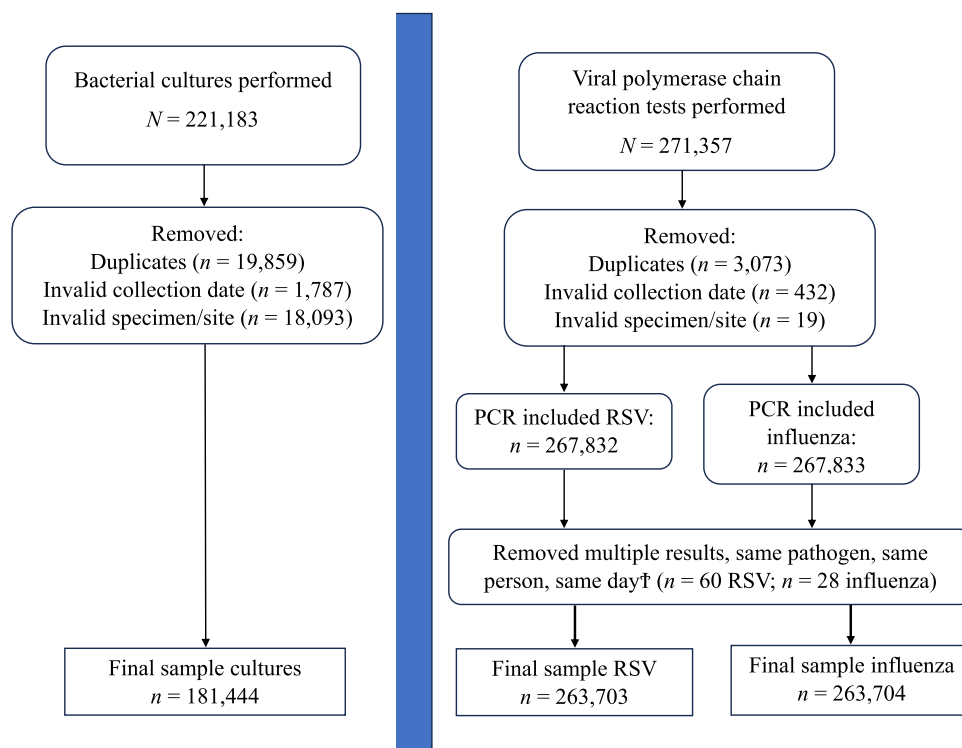
pirates, tracheostomy/endotracheal samples, and biopsies. Urinary antigen testing was not included.

A multiplex PCR test for influenza A, influenza B, and RSV was used during the study period. Variables extracted by Pathology Queensland were an anonymous individual identifier, laboratory number, collection location, ward, collection date and time, age, sex, ethnicity, specimen type, and anatomical site of the specimen. For bacterial cultures, all cultured organisms (if any) were provided.

#### Data cleaning and categorization

Two distinct datasets were provided: one for PCR assays and results and one for cultures. Data were analyzed in RStudio 2022.07.2. For both datasets, exact duplicates were identified by the person's unique identifier, the anatomical site, the collection date and time, and the result. Exact duplicates, invalid dates, illogical respiratory specimens (e.g., blood), and illogical specimen sites (e.g., kidney) were removed from the dataset. Datasets were adjusted according to Fig. 1. More detail on data cleaning and categorization can be found in Supplementary Material 1.

Collection dates were categorized into three seasonally similar periods over the three and a half years. Period one (pre-pandemic) included weeks 11–27 of 2018 and 2019 (mid-March–the end of June each year); period two (early pandemic/restrictions) included weeks 11–27 of 2020, and



**Fig. 1.** Polymerase chain reaction respiratory samples and results from the AUSLAB™ clinical diagnostic reporting system included in the study.

period three (easing of restrictions) included weeks 11–27 of 2021.

### Data analysis

Simple descriptive statistics (frequencies, proportions, means, and standard deviations) were produced to summarize the dataset. The following pathogens were examined: influenza (A and B combined), RSV, *S. aureus*, *S. pneumoniae*, *K. pneumoniae*, and *P. aeruginosa*. Pathogens detected and tests performed were aggregated weekly and graphed as a result per 1000 tests performed to show trends over time. The number of cultures performed each week was the same regardless of the bacterial pathogen detected (if any).

Rate ratios (RR) of pathogen detection per 100 tests along with 95% confidence intervals (95% CI) were calculated and compared by period (pre-pandemic, early pandemic/restrictions, and easing of restrictions). Age-specific trends and changes by year were also assessed for influenza and RSV; methods are reported in Supplementary Material 2.

### Ethical considerations

Approval was obtained from the Gold Coast Hospital and Health Service (LNR/2020/QGC/65436) and Griffith University Human Research (2020/567) ethics committees. Public Health Act 2005 (Qld) approval was received.

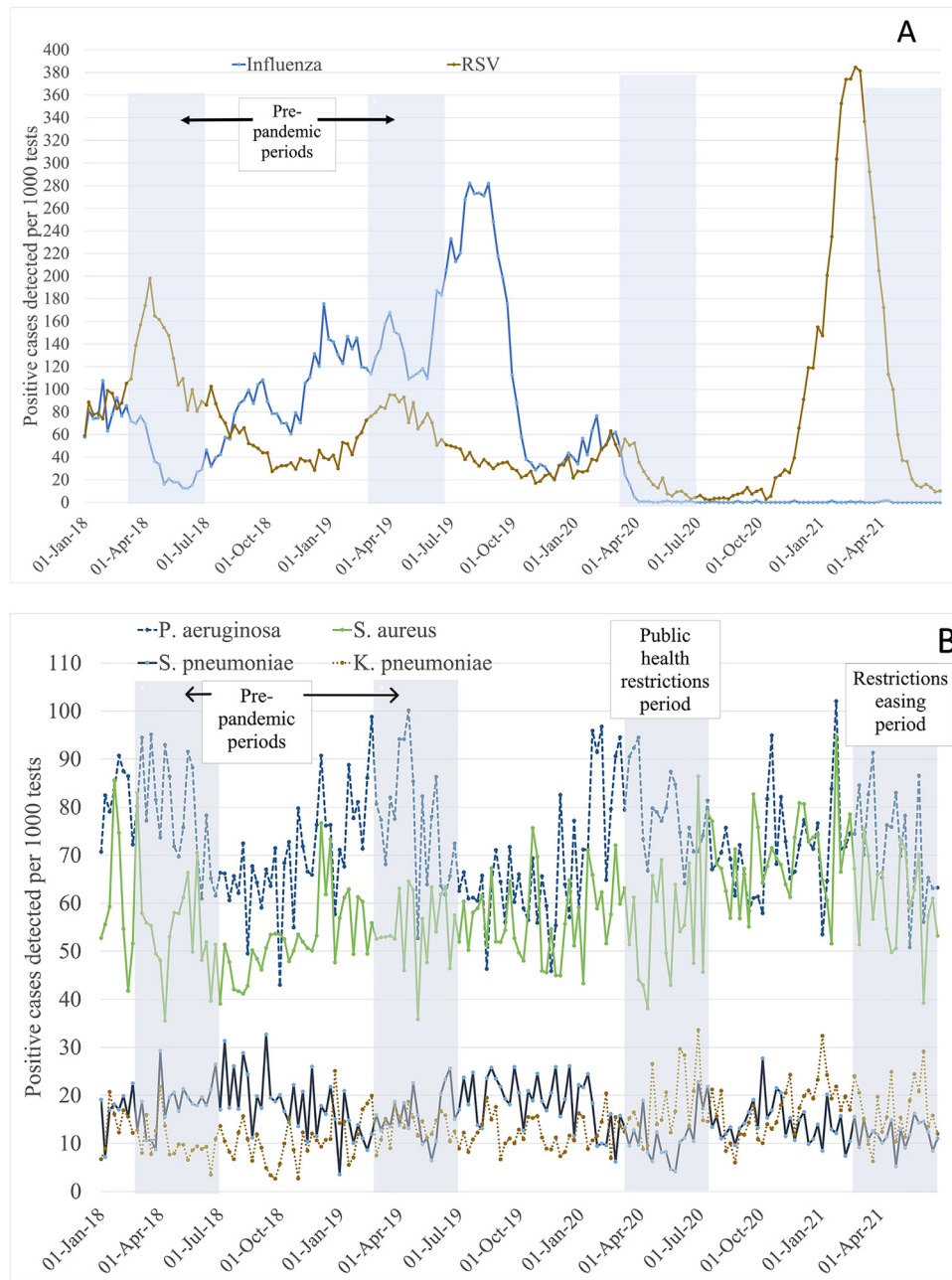
## Results

### Sample characteristics

Table 2 describes the population studied. Samples were collected from a total of 237 unique facilities, including 109 different public hospitals, 52 primary health care centers, 12 correctional centers, eight private hospitals, and 20 other types of private sector facilities. More than 260,000 ( $n = 263,704$ ) PCR tests and 181,444 cultures were included in the analysis. Females were tested in 51.2% ( $n = 135,162$ ) and 42.0% ( $n = 76,279$ ) of PCRs and cultures, respectively. Most PCRs ( $n = 193,452$ ; 73.4%) and cultures ( $n = 126,423$ ; 69.7%) came from public hospitals.

**Table 2.** Characteristics of included respiratory specimens taken from 237 collection centers in Queensland, 2018–2021.

Characteristic	Tested for influenza and/or RSV ( $n = 263,704$ )		Cultures ( $n = 181,444$ )	
	<i>n</i>	%	<i>n</i>	%
Age in years (mean +/- SD)	43.2 (29.8)		56.8 (23.0)	
Age group				
<1 years	20,095	7.6	1,996	1.1
1–4 years	31,441	11.9	4,871	2.7
5–64 years	131,087	49.7	89,523	49.3
65+ years	81,053	30.7	79,494	43.8
Invalid or missing age	28	0.0	5,560	3.1
Sex				
Male	128,365	48.7	100,079	55.2
Female	135,162	51.2	76,279	42.0
Missing	177	0.1	5,086	2.8
Aboriginal and/or Torres Strait Islander people				
Stated as such	26,107	9.9	14,961	8.2
Other	229,686	87.1	148,435	81.8
Not stated/ Missing	7,911	3.0	18,048	9.9
Facility type where specimen collected				
Public hospitals	193,452	73.4	126,423	69.7
Other	21,379	8.1	19,557	10.8
Private day care centers/hospitals	18,178	6.9	10,707	5.9
Aged care facilities	11,939	4.5	11,913	6.6
Home care services	15,341	5.8	9,037	5.0
Community health centre/clinic	1,324	0.5	1,623	0.9
Dental clinics	992	0.4	19	0.0
Correctional centers	1,098	0.4	395	0.2
Not assigned	0	0.0	1,770	1.0
Geographic location where test collected				
Northern Queensland	51,898	19.7	32,681	18.0
Southeast Queensland	176,697	67.0	120,546	66.4
Central Queensland	14,267	5.4	7,065	3.9
Not assigned	20,836	7.9	21,152	11.7



**Fig. 2.** Respiratory pathogens detected per 1,000 tests/cultures: Queensland, Australia January 2018–June 2021. A. Influenza and Respiratory Syncytial Virus. B. Bacterial pathogens.

### Respiratory pathogen trends

Fig. 2 describes the trends in weekly cases detected per 1,000 tests over the three and a half years. Weeks 11-27 of each year are shaded in gray. Supporting data for the figures can be found in Supplementary Material 3.

### Influenza and RSV

Influenza-positive rates increased cyclically from 2018 to early 2020, with the highest rates observed in the southern

hemisphere winter months of 2019 (June–August), exceeding 280 cases per 1,000 tests. RSV-positive rates also followed a seasonal pattern, with maximum detection rates occurring in March–April of each year for 2018–2020, albeit with a decreasing maximum each year until 2021 (Fig. 2A). Shortly after the initial pandemic/restriction period began, influenza cases dropped nearly to zero for the remainder of the study period (Fig. 2A). While RSV rates also decreased during the early pandemic/restriction period, RSV reemerged in February 2021 and peaked at

**Table 3.** Rates of pathogen detection from respiratory sample cases with 95% confidence intervals, weeks 11–27, pre-pandemic (2018/2019), early pandemic/restrictions (2020), and restrictions easing (2021) periods in Queensland, Australia.

	Pre-pandemic wk 11–27 (2018 and 2019)		Early pandemic/restrictions (2020 wk 11–27)		Restrictions easing (2021 wk 11–27)	
	<i>n</i>	Rate per 100 PCRs or cultures (95% CI)	<i>n</i>	Rate per 100 PCRs or cultures (95% CI)	<i>n</i>	Rate per 100 PCRs or cultures (95% CI)
PCRs performed <sup>a</sup>	48,523	NA	28,182	NA	22,293	NA
Influenza detected	5,243	10.81 (10.53–11.08)	304	1.08 (0.96–1.20)	5	0.02 (0.003–0.042)
RSV detected	4,596	9.47 (9.21–9.73)	693	2.46 (2.28–2.64)	2,440	10.95 (10.54–11.35)
Cultures performed	18,569	NA	13,854	NA	15,414	NA
<i>S. aureus</i> detected	997	5.37 (5.14–5.60)	787	5.68 (5.30–6.07)	943	6.12 (5.74–6.50)
<i>P. aeruginosa</i> detected	1,415	7.62 (7.35–7.89)	1,100	7.94 (7.49–8.39)	1,097	7.12 (6.71–7.52)
<i>S. pneumoniae</i> detected	320	1.72 (1.59–1.85)	154	1.11 (0.94–1.29)	184	1.19 (1.02–1.37)
<i>K. pneumoniae</i> detected	225	1.21 (1.10–1.32)	249	1.80 (1.58–2.02)	248	1.61 (1.41–1.81)

PCR, polymerase chain reaction; RSV, respiratory syncytial virus; *S. aureus*, staphylococcus aureus; *P. aeruginosa*, pseudomonas aeruginosa; *S. pneumoniae*, streptococcus pneumoniae; *K. pneumoniae*, klebsiella pneumoniae.

<sup>a</sup>PCRs were combination panels of both influenza and RSV. However, more influenza tests had invalid results recorded (neither detected nor not detected).

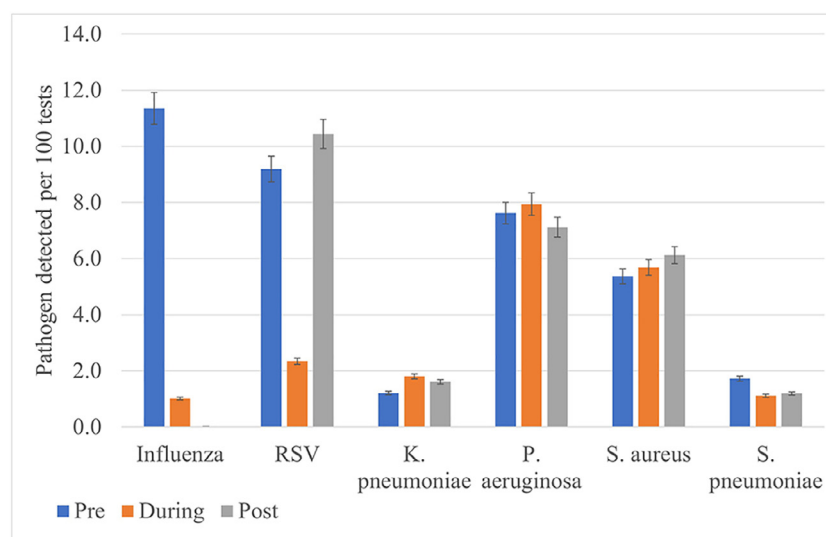
384 per 1,000 tests, a rate six times higher than the peak rate in 2020 (63 per 1,000 tests; RR [95% CI]: 6.1 [4.8–7.7]), and two times higher than the peak rate in 2018 (198 per 1,000 tests; RR [95% CI]: 1.9 [1.7–2.2]), (Fig. 2A).

Age-specific trends and changes by period are shown in Supplementary Figure 1, Supplementary Figure 2, and Supplementary Table 1. The trends observed for influenza were similar across age groups (Supplementary Figure 2). Similarly, the trends observed for RSV were similar by age group (Supplementary Figure 1). The increase in peak weekly rates observed for RSV was highest for people aged 5–64 years, with a 2021:2020 RR (95% CI) of 6.95 (4.85–9.95), and for those aged 65+ years (4.15: 2.72–

6.31). These increases were greater than those observed in infants (2021:2020 RR [95% CI] = 2.26 [1.43–3.59]) or children aged 1–4 years (2.22: 1.56–3.15) (Supplementary Table 1).

#### Bacterial pathogen trends

Weekly trends for the bacterial pathogens studied are shown in Fig. 2B. No remarkable changes in the weekly pattern were observed for *P. aeruginosa* or *S. aureus*. Rates for *S. pneumoniae* appeared to decrease during the early pandemic/restrictions period, whereas weekly rates for *K. pneumoniae* appeared to increase during this period and in 2021.

**Fig. 3.** Rates of respiratory pathogen detection per 100 polymerase chain reaction/culture tests, wk 11–27: pre-pandemic (2018/2019), during early pandemic/restrictions (2020), and post easing of restrictions (2021), Queensland, Australia.

### Changes by pandemic period

Table 3 and Fig. 3 compare pathogen detection rates per 100 PCRs/cultures for similar seasonal periods (weeks 11–27) pre-pandemic, early pandemic/restrictions (2020), and easing of restrictions (2021).

By period, the influenza and RSV rates were consistent with the trends reported in Fig. 2. Comparing the pre-pandemic and easing of restrictions periods to the early pandemic/restrictions period, no change was observed in the detection of *S. aureus* or *P. aeruginosa* per 100 cultures. The *S. pneumoniae* positive rate decreased by 36% from 1.72 to 1.11 in wk 11–27, 2020: RR (95% CI) = 0.64 (0.53–0.78) and remained low in 2021. Cultures positive for *K. pneumoniae* increased by 48% from 1.21 to 1.80 per 100 cultures: RR (95% CI) = 1.48 (1.24–1.77), and remained statistically significantly higher in 2021 compared to the pre-pandemic period.

### Discussion

This study found a decrease in rates of droplet-spread pathogens after the initiation of public health measures due to the pandemic: decreases in influenza and *S. pneumoniae* cases were observed that lasted at least 15 months until the end of the study period, along with a short-lived decrease in RSV (nine months of sustained decrease). After the easing of public health restrictions, cases of RSV and *K. pneumoniae* increased. There were no notable changes in the rates of other bacterial pathogens (*S. aureus*, *P. aeruginosa*).

Influenza rates decreased dramatically during the study period; an entire influenza season was averted in 2020. This phenomenon has been described elsewhere, including in New Zealand, where similar pandemic mitigation strategies were implemented, as in Australia (15) and in private laboratories in Queensland (16). Singapore and other countries in the northern hemisphere also reported a significant decline in influenza cases (17,18). It has been hypothesized that some influenza strains may have been eliminated (19). Seasonal influenza virus, with an estimated reproduction number ( $R_0$ ) of 1.28 (20), is less transmissible than estimates for the SARS-CoV-2 variants ( $R_0$  1.38 [Delta] and 1.90 [Omicron]) (21). Thus, it is likely that public health measures were even more effective in suppressing influenza. Restrictions on interstate and international travel are likely to have played a role in reducing the importation of new strains of influenza to Queensland (22). While influenza vaccination coverage rates increased between 2018/2019 and 2020 for children aged 6–5 months years in QLD (from 25.5 to 40.5%), and for all Australians aged six months and older (26.2–34.2%), they decreased in 2021 (to 22.4% for QLD children and 32.1% for Australians) (23). Improvements in vaccination cover-

age rates are unlikely to explain the ultimate suppression of influenza.

As this study only included data up to June 2021, it may have been too early to see a resurgence of influenza following the return of international travel and social interactions. Recently, South Korea reported a 120-1500-fold increase in specimens positive for influenza A in children under 18 in June/July 2022 (24). Similarly, recent influenza trends in Queensland, based on notifiable disease registries, show an above-average increase in cases in 2022 and an early surge in cases in 2023 (25). The SARS-CoV-2 (Omicron variant) is also now circulating widely in Queensland.

Given the efficacy of public health measures in reducing influenza cases demonstrated in this study, the benefit of implementing additional public health measures to protect the very young, the elderly (and those with chronic respiratory conditions such as chronic obstructive pulmonary disease [COPD], cystic fibrosis, and asthma), during each influenza season is an important consideration (10). Further research into why a resurgence occurs for some viruses but not others and the timing of virus-specific resurgence may inform future prevention efforts.

Unlike influenza, an initial decline in RSV in our sample was reversed following the reopening of interstate borders with Queensland (mid-December 2020). Similar resurgences have been reported following the lifting of public health restrictions throughout Europe, Asia, South America, and South Africa (26–28). In children under five years of age, following notable RSV reductions in the United Kingdom, an unseasonal increase in RSV cases was detected in 2021, including a 1,258% increase over historical trends in laboratory-confirmed cases and a 125% increase in hospital admissions (29). This increase has been suggested to be the result of a decline in natural immunity caused by a lack of exposure to RSV in 2020 (29). However, our analysis of all age groups shows even larger increases in other age groups (e.g., 5–64 years and 65+ years) that would have had prior exposure to RSV. This suggests that some factor other than natural immunity was involved in the RSV resurgence in Australia.

Nonetheless, RSV was able to re-establish itself in the population and cause widespread infection, while influenza remained suppressed, as seen in this study- for at least another season. The science of respiratory virus transmissibility is complicated and influenced by host, viral, and environmental factors (30). Possible reasons for the continued suppression of influenza could be the continued prohibition on international travel (22) and/or the lower transmissibility of seasonal influenza compared to RSV ( $R_0$  1.28 vs. 2.8) (20,31).

After the vaccination of most of the population in Australia, Queensland opened its borders to all states and territories, and Australia opened its borders to international

travel. At that time, Queensland experienced a second wave of COVID-19 due to cases of the Omicron variant of SARS-CoV-2. As this variant is even more transmissible than RSV, this suggests that a pandemic caused by a virus as transmissible as Omicron that emerged before vaccination would have resulted in less effective containment. This has implications for future pandemic planning, considering the possibility that the next pandemic virus may be more like the Omicron variant rather than Delta.

*S. pneumoniae* decreased in this study and remained below the 2018–2019 levels for the next 18 months. Other centers in Taiwan and the United Kingdom reported changes in invasive pneumococcal disease, also suggesting a decrease in *S. pneumoniae* circulation (10). The Invasive Respiratory Infection Surveillance group, representing 27 laboratories in 26 countries, also reported a 68% decrease in *S. pneumoniae* detected 4 weeks after the introduction of public health restrictions and an 82% reduction at 8 weeks (32). That same study suggests that restrictions could be attributed to a 38% short-term (<10 wk) reduction in the incidence of invasive disease caused by *S. pneumoniae* (32), similar to the 35% reduction observed in our study.

The corollary of the above is that the effect of a reduced period of influenza, RSV, and *S. pneumoniae* may have contributed to the reduction in overall respiratory emergency presentations observed in Queensland over the same period (12). Exacerbations in common chronic diseases such as asthma and COPD were substantially reduced in many centers (10,33).

Although the number of positive cases of *S. aureus* and *P. aeruginosa* detected decreased during the statewide lockdown period, the positive rate per 100 cultures did not change significantly. This is consistent with another study of *S. aureus* trends in children, which found no significant reduction in 2020 compared to 2018 and 2019 (34). As these pathogens are associated with nosocomial infections, this may mean that community restrictions did not affect the transmission of these healthcare-associated pathogens (35).

However, the isolation rate for *K. pneumoniae* increased relative to historical times and remained elevated through 2021. *K. pneumoniae* is commonly associated with hospital-acquired pneumonia (36), and multidrug resistance is a concern. Possible reasons for this could be an increase in multidrug-resistant strains associated with increased use of antibiotics to treat patients with influenza-like illnesses in the early pandemic period. A recent study of pathogens involved in acute exacerbations of COPD found an increase in disease caused by *K. pneumoniae*, methicillin-resistant *S. aureus*, and *P. aeruginosa* after the COVID-19 outbreak (33). These authors suggest that pathogens able to colonize susceptible individuals may have become more threatening due to the decline in other competing pathogens, such as influenza and *S. pneumoniae* (33). Our study sup-

ports this finding about *K. pneumoniae*, and analysis of these data using cultures performed rather than the population at risk may have allowed the detection of a small increase in actual disease. However, the absolute number of cases detected increased minimally (by less than one per 100 cultures), and the number of cultures performed increased from year to year. Thus, the observed increase may be due to data artifacts or increases in clinician testing of certain highly susceptible individuals. These findings would benefit from further validation in other settings.

#### Data limitations

This dataset represents patients who present with respiratory symptoms and/or those whose treating clinician believed testing was necessary. Some patients with respiratory illness may have refused to have a sample collected, which would bias the results toward lower detection rates per 100 cultures.

Secondly, it is not known whether or not the pathogens detected in this study caused invasive disease. The pathogens are laboratory-confirmed cases, but the clinical significance is unknown. Some positive results, particularly with the bacterial cultures, may be due to contamination. However, the population from which the samples were collected is hospitalized or seeking medical care, and these cases likely had symptoms that prompted appropriate testing, suggesting clinically important disease.

Finally, while the trends describe pathogen rates per 100 or 1,000 tests, there may have been a shift in patients test seeking behavior or clinician test ordering. We cannot comment on the size or direction of any resulting bias.

#### Conclusions

This study demonstrated a significant decrease in respiratory pathogens, including influenza, RSV, and *S. pneumoniae*, following the declaration of the SARS-CoV-2 pandemic and the implementation of associated public health measures in Queensland, Australia. *K. pneumoniae*-positive rates increased from pre-pandemic levels. As restrictions were relaxed, RSV, which is more transmissible than influenza, could circulate at a higher level than historical RSV seasons.

#### Conflicts of Interest

All authors declare no conflicts of interest in the preparation of this work.

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### Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.arcmed.2024.103144.

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