About the Author

Dr. Bbosa is an assistant professor at the London School of Hygiene and Tropical Medicine; a senior scientist at the Medical Research Council/Uganda Virus Research Institute and the London School of Hygiene and Tropical Medicine Uganda Research Unit, Entebbe, Uganda; and a project investigator at the Uganda Virus Research Institute in Entebbe. His primary research interests are viral genomics, molecular epidemiology, pathogen phylodynamics, and infectious disease pandemic preparedness and response.

References

1. Bbosa N, Nabirye SE, Namagembe HS, Kiiza R, Ssekagiri A, Munyagwa M, et al. Case reports of human monkeypox virus infections, Uganda, 2024. Emerg Infect Dis. 2025;31:144–8. https://doi.org/10.3201/eid3101.241269
2. Uganda Ministry of Health, Mpox Incident Management Team. National mpox situation report [cited 2025 Jun 15]. https://www.afro.who.int/sites/default/files/2025-05/Ug_Mpox_Sitrep_28May25.pdf
3. Jezek Z, Szczeniowski M, Paluku KM, Mutombo M, Grab B. Human monkeypox: confusion with chickenpox. Acta Trop. 1988;45:297–307.
4. Hughes CM, Liu L, Davidson WB, Radford KW, Wilkins K, Monroe B, et al. A tale of two viruses: coinfections of monkeypox and varicella zoster virus in the Democratic Republic of Congo. Am J Trop Med Hyg. 2020;104:604–11. https://doi.org/10.4269/ajtmh.20-0589
5. Nzoyikorera N, Nduwimana C, Schuele L, Nieuwenhuijse DF, Koopmans M, Otani S, et al. Monkeypox clade Ib virus introduction into Burundi: first findings, July to mid-August 2024. Euro Surveill. 2024;29:2400666. https://doi.org/10.2807/1560-7917.ES.2024.29.42.2400666
6. Mmerem JI, Johnson SM, Iroezindu MO. Monkeypox and chickenpox co-infection in a person living with human immunodeficiency virus. J Infect Dev Ctries. 2024;18:1152–6. https://doi.org/10.3855/jidc.18318
7. Bbosa N, Ssemwanga D, Weiss SL, Kalungi S, Mawanda A, Ssentudde R, et al. Identification of anthrax as the cause of a cluster of unexplained deaths, Uganda, 2023: the role of metagenomic next-generation sequencing and postmortem specimens. Am J Trop Med Hyg. 2025;112:835–9. https://doi.org/10.4269/ajtmh.24-0489
8. Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 2015;32:268–74. https://doi.org/10.1093/molbev/msu300
9. Onyango C, Hines JZ, Ochieng M, Amon D, Lidechi S, Anguko E, et al. High prevalence of varicella zoster virus infection among persons with suspect mpox cases during an mpox outbreak in Kenya, 2024. Am J Trop Med Hyg. 2025;113:1411–4. https://doi.org/10.4269/ajtmh.25-0308
10. Tayachew A, Kebede N, Alayu M, Onywera H, Kanyerezi S, Agune A, et al. Genomic evidence of varicella-zoster virus among mpox-suspected cases in Ethiopia during the 2022 mpox multi-country outbreak. Sci Rep. 2025;16:148. https://doi.org/10.1038/s41598-025-29116-w
11. Hoff NA, Morier DS, Kisalu NK, Johnston SC, Doshi RH, Hensley LE, et al. Varicella coinfection in patients with active monkeypox in the Democratic Republic of the Congo. EcoHealth. 2017;14:564–74. https://doi.org/10.1007/s10393-017-1266-5

Address for correspondence: Nicholas Bbosa, Medical Research Council/Uganda Virus Research Institute and London School of Hygiene and Tropical Medicine Uganda Research Unit, Plot 51–59 Nakiwogo Rd, Entebbe, Uganda; email: nicholas.bbosa@mrcuganda.org

Age Differences in Pertussis Epidemics, New South Wales, Australia, 2015 and 2024

Ella F. Madden, Sally L. Ellis, Andrea Parisi, Christine E. Selvey, Janaki Amin

Author affiliations: New South Wales Ministry of Health, St. Leonards, New South Wales, Australia (E.F. Madden, S.L. Ellis, A. Parisi, C.E. Selvey, J. Amin); University of Sydney, Sydney, New South Wales, Australia (A. Parisi); Australian National University, Canberra, Australian Capital Territory, Australia (A. Parisi); Macquarie University, Sydney (J. Amin); University of New South Wales, Kensington, New South Wales, Australia (J. Amin).

DOI: https://doi.org/10.3201/eid3210.260332

We compared data from the 2015 and 2024 pertussis epidemics in New South Wales, Australia. In 2024, we found twice as many notifications and a shift in distribution to older children. COVID-19 interventions and lack of circulation of pertussis likely contributed to an age cohort immunity gap and increased infections.

Pertussis (whooping cough) is a highly contagious respiratory disease caused by *Bordetella pertussis* bacteria. Although infants <6 months of age are at greatest risk for severe disease and death (*1*), infections occur across all age groups. Immunity from both immunization and infection wanes over time. Consequently, pertussis remains endemic in New South Wales (NSW), Australia, and causes epidemics every 3–4 years (*2*,*3*).

Pertussis vaccines are funded in Australia under the national immunization program. Since

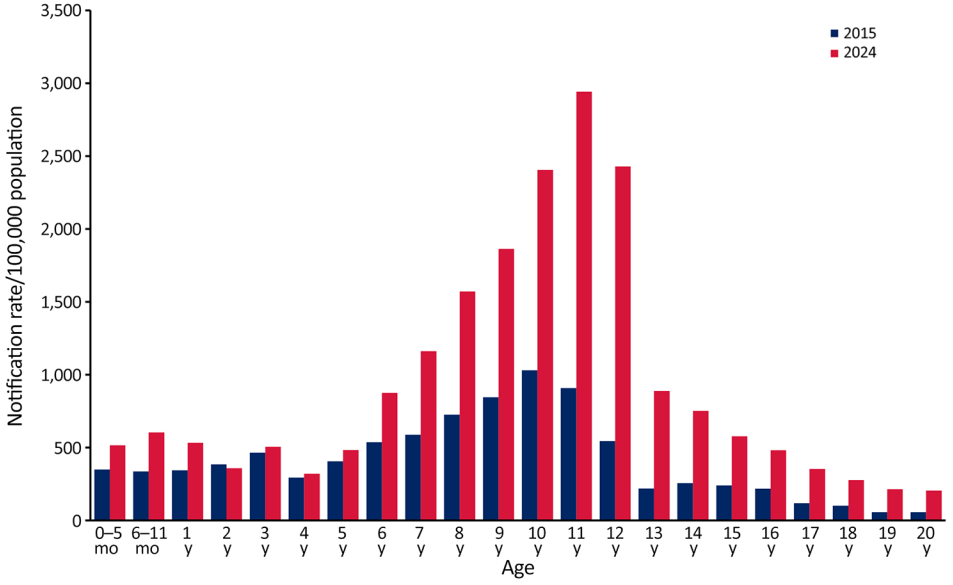

Figure. Age-specific pertussis notification rates per 100,000 population for persons 0–20 years of age, by year notified, New South Wales, Australia, 2015 and 2024. Because no population data were available for children 0–5 months and 6–11 months, the total population estimates for children <1 year of age in 2015 and 2024 was halved. These populations were used for the rate calculations.

2009, pertussis vaccines are administered at 6 weeks, 4 months, 6 months, 18 months, and 4 years of age in NSW; vaccination during pregnancy has been funded since 2015. A booster dose is given at age 12–13 through the NSW school vaccination program (*4*). The COVID-19 pandemic disrupted infection cycles, likely because of widespread nonpharmaceutical interventions that have reduced transmission of multiple respiratory pathogens (*5*). From 2020–2023, NSW reported historically low pertussis activity, with <600 notifications annually (*3*). We describe age- and sex-specific patterns across 2 epidemics in NSW, in 2015 and 2024, and discuss the potential results of pandemic-related interventions and waning immunity as likely contributors to observed pattern changes.

We calculated age-specific rates by using annual NSW population estimates (*6*). Confirmed pertussis cases (*7*) are reported to the NSW notifiable conditions information management system, a statutory public health register of infectious diseases legally notifiable to NSW Health (*8*). Our review of those data reveals NSW experienced a resurgence in 2024, recording the highest annual total since pertussis became notifiable in 1991. After 1991, the most recent NSW epidemic occurred in 2015. During 2015–2024, a total of 68,842 confirmed pertussis cases were reported in NSW, including 12,007 in 2015 and 25,695 in

Table. Demographic characteristics of pertussis cases notified in New South Wales, Australia, 2015 and 2024*

Characteristic	Notifications		Rate, cases/100,000 population†		IRR, 2024 vs. 2015 (95% CI)
	2015	2024	2015	2024	
Age group					
<1 y	336 (2.80)	503 (1.96)	342.47	505.03	1.47 (1.28–1.69)
0–5 mo	171 (1.42)	232 (0.90)	348.58	516.33	1.48 (1.22–1.8)
6–11 mo	165 (1.37)	271 (1.05)	336.35	603.13	1.79 (1.48–2.18)
1–4 y	1,477 (12.30)	1,641 (6.39)	372.04	431.54	1.16 (1.08–1.24)
5–9 y	3,020 (25.15)	5,964 (23.21)	617.39	1,187.25	1.92 (1.84–2.01)
10–14 y	2,666 (22.20)	9,762 (37.99)	594.18	1,904.40	3.21 (3.07–3.35)
15–24 y	981 (8.17)	2,738 (10.66)	99.50	275.72	2.77 (2.58–2.98)
25–34 y	645 (5.37)	859 (3.34)	57.77	73.85	1.28 (1.15–1.42)
35–44 y	905 (7.54)	1,185 (4.61)	87.96	105.64	1.2 (1.1–1.31)
45–54 y	853 (7.10)	1,332 (5.18)	86.51	131.25	1.52 (1.39–1.65)
≥55 y	1,124 (9.36)	1,711 (6.66)	54.41	71.95	1.32 (1.23–1.43)
Sex					
M	5,607 (46.70)	12,883 (50.14)	148.47	317.32	2.14 (2.07–2.21)
F	6,386 (53.19)	12,801 (49.82)	166.32	311.78	1.87 (1.82–1.93)
Unknown/other	13 (0.11)	10 (0.04)	NA	NA	NA
Median age, y (IQR)	11 (7–33)	11 (9–17)	NA	NA	NA
Total cases	12,007 (100.0)	25,695 (100.0)	157.65	314.68	2 (1.95–2.04)

*Values are no. (%) cases except as indicated. IRR, incidence rate ratio. NA, not applicable.
†As no population was available for the groups 0–5 mo and 6–11 mo, the total population estimates for people <1 years of age in 2015 and 2024 respectively was halved. Those populations were then used for rate calculations.

2024. Compared with 2015, notifications in 2024 more than doubled, and the age distribution shifted toward older children, with the greatest proportion of notifications in 10–14-year-olds. The notification rate in 2024 (314.7/100,000 population) was almost double the rate of 2015 (157.7/100,000 population) (Table). The ratio of male to female notifications in 2015 was 0.88; in 2024, the ratio of male to female notifications was 1.08.

In 2015, the highest proportion of cases occurred in children 5–9 years of age (25.2%), followed by those 10–14 years of age (22.2%). By contrast, children 10–14 years of age dominated the 2024 epidemic caseload (38.0%), followed by those 5–9 years of age (23.2%). The percentage of cases in children <5 years of age declined from 15.1% in 2015 to 8.3% in 2024 and in children <6 months of age from 1.4% in 2015 to 0.9% in 2024. Conversely, the notification rate for children 10–14 years of age more than tripled, from 594.2 cases/100,000 population in 2015 to 1,904.4 cases/100,000 population in 2024 (incidence rate ratio [IRR] 3.21 [95% CI 3.07–3.35]) (Table). That increase was not observed to the same extent in other age groups, particularly those ≥25 years of age. The median age at notification remained consistent at 11 years in both epidemics. However, the interquartile range for age narrowed substantially, from 7–33 in 2015 to 9–17 in 2024 (Table), reflecting a more concentrated distribution of cases among school-age children in 2024.

The COVID-19 pandemic likely changed health-seeking and testing behaviors, resulting in a higher proportion of persons with laboratory-confirmed pertussis. That behavior change might have contributed to higher notifications in 2024, but it is unlikely to explain the pronounced shift in age distribution. Several factors possibly contributed. The near absence of circulating pertussis during the pandemic could have disrupted natural immune boosting from exposure to *Bordetella pertussis*. That disruption probably had the greatest effect on children approaching adolescence, as reflected in the age-specific rates (Figure). In 2024, the risk of infection increased with each year of age among school-age children, particularly in those 8–12 years of age, who were several years past their last scheduled vaccine dose and therefore more susceptible to illness because of waning immunity. That immunity gap likely enabled rapid transmission through school populations. In contrast, the relative reduction in the age-specific rates from age 13 years onward, seen in both epidemics but more noticeably in 2024, signals the effect of the adolescent booster and its importance in maintaining immunity (Figure). The NSW pertussis resurgence in 2024 aligns with international observations after the easing of COVID-19 restrictions, with increased incidence among older children reported by several countries (*9*). Those parallels point to global immunity gaps attributable to reduced pathogen circulation during the pandemic.

In conclusion, the 2024 NSW pertussis epidemic differed substantially from the 2015 epidemic in both magnitude and age profile. Waning immunity, exacerbated by reduced natural boosting during the COVID-19 pandemic, likely contributed to the increased effects, particularly in children 8–12 years of age. Future research should explore vaccine effectiveness during extended inter-epidemic periods and the role of adolescent boosters to mitigate transmission. Adjustments should be made to surveillance and outbreak response strategies to prevent and reduce the effects of future outbreaks.

About the Author

Ms. Madden is a senior public health advisor at Health Protection NSW, within the NSW Ministry of Health. Her work focuses on surveillance, reporting, and policy for vaccine-preventable and respiratory diseases.

References

1. Parisi A, Nuñez O, López-Perea N, Masa-Calles J. Reduced pertussis disease severity in infants following the introduction of pertussis vaccination of pregnant women in Spain, 2015–2019. Vaccine. 2024;42:2810–6. https://doi.org/10.1016/j.vaccine.2024.03.028
2. Leong RNF, Wood JG, Turner RM, Newall AT. Estimating seasonal variation in Australian pertussis notifications from 1991 to 2016: evidence of spring to summer peaks. Epidemiol Infect. 2019;147:e155. https://doi.org/10.1017/S0950268818003680
3. NSW Health Communicable Diseases Branch and Centre for Epidemiology and Evidence. Pertussis notifications in NSW residents by year of disease onset and age group. January 2015 to December 2024 [cited 2025 Jul 25]. https://www.health.nsw.gov.au/IDD/#/PERT/periodandagegroup
4. Health NSW. NSW immunisation schedule. 2025 [cited 2025 Sep 22]. https://www.health.nsw.gov.au/immunisation/publications/nsw-immunisation-schedule.pdf
5. van der Kooi S, Beard F, Dey A, McIntyre P, Imai C, Amin J. Pertussis notifications decline in Australia during COVID-19 non-pharmaceutical interventions, 2020–2021. Commun Dis Intell. 2024;48:24. https://doi.org/10.33321/cdi.2024.48.24
6. Australian Bureau of Statistics. Population at 30 June, by sex and single year of age, NSW, from 1971 onwards. June 2025 ed. Canberra (Australia): Australian Government; 2025 [cited 2025 Dec 22]. https://www.abs.gov.au/statistics/people/population/national-state-and-territory-population/jun-2025
7. Australian Centre for Disease Control. Pertussis (whooping cough) surveillance case definition. Canberra (Australia): Australian Government Department of Health; 2025 [cited

2025 Dec 17]. https://www.cdc.gov.au/resources/publications/surveillance-case-definition-pertussis
8. New South Wales Government. Public health act 2010 no. 127 [cited 2025 Feb 25]. https://legislation.nsw.gov.au/view/html/inforce/current/act-2010-127
9. Gorringe A, Cavell B, Beard F, Tsukada K, Otsuka N, Fu P, et al. Global incidence of pertussis after the COVID-19 pandemic. JAMA Netw Open. 2025;8:e2545963. https://doi.org/10.1001/jamanetworkopen.2025.45963

Address for correspondence: Ella Madden, Health Protection NSW, NSW Ministry of Health, Locked Mail Bag 2030, St. Leonards, NSW 1590, Australia; email: ella.madden@health.nsw.gov.au

Estimated Transmissibility and Case Fatality Rate of Bundibugyo Virus, Uganda, 2007

Bianca de Padua and Andrei R. Akhmetzhanov

Authors affiliation: National Taiwan University College of Public Health, Taipei, Taiwan

DOI: https://doi.org/10.3201/eid3210.261175

Because the epidemiology of Bundibugyo virus remains unclear, we reanalyzed the first recognized outbreak (Uganda, 2007). Adjusting for case underascertainment and the effect of control measures, we estimated the effective reproduction number (1.55, falling to <1 after intervention) and case-fatality rate (31%, declining to 25%). The underascertainment rate was 15%.

Bundibugyo virus (BDBV) is 1 of 6 orthoebolaviruses (genus *Orthoebolavirus*), constituting the species *Orthoebolavirus bundibugyoense* (*1*) and causes rare but severe disease in humans (*2*). Two other orthoebolaviruses, Ebola virus (EBOV) and Sudan virus, have caused the largest outbreaks and are highly lethal; case-fatality rates (CFRs) average ≈50% (*2*). BDBV is considered less lethal; CFRs are reported to be 30%–40%, and it has historically caused only small outbreaks (*3*). The ongoing 2026 outbreak in the Democratic Republic of the Congo and Uganda shows a different pattern: first reports in late May 2026 recorded >600 suspected cases, and >2,000 cases were projected within 3 months (*4*). Despite this potential for large outbreaks, the transmissibility and severity of BDBV remain poorly characterized.

Control measures, such as case isolation, active case finding, infection control in hospitals and isolation wards, and safe burial practices, are key to curbing Ebola outbreaks, in part by limiting superspreading and lowering mortality rates (*5*). However, those measures also alter the epidemiologic parameters used to characterize an outbreak: the desirable reduction in the reproduction number can be accompanied by improved case ascertainment and reduced mortality rates. Failing to account for the effect of control measures can bias estimates of transmissibility and severity, whereas adjusting for them yields values closer to the natural history of the virus. In this study, we reanalyzed the first reported BDBV outbreak (Bundibugyo, Uganda, 2007) (*6*) to obtain robust estimates of transmission potential and CFR adjusted for both case underascertainment and the effect of control measures.

We digitized weekly counts of confirmed and probable cases from a 2010 study (*6*), retaining 110 cases (37 deaths) with a known week of symptom onset. We excluded 6 additional cases (2 deaths) lacking onset dates. Those data are consistent with 116 confirmed and probable cases and 39 deaths (crude CFR 34%) reported for the outbreak (*6*). Control measures were initiated in week 48, which we used to define preintervention and postintervention periods. We estimated transmission with a renewal process incorporating intrinsic back-projection to the time of infection (*7*), informed by the incubation period and time from onset to transmission, the latter adapted from EBOV (*8*). That linked the effective reproduction number (R_t) to the time of infection rather than to symptom onset. We modeled the intervention as a step reduction at week 48 in R_t and in case underascertainment, together with a multiplicative reduction in the CFR. We assumed that deaths were fully recorded throughout the outbreak, whereas nonfatal cases that occurred before the intervention could have been missed (*9*). We fitted the model in a Bayesian framework and report posterior means with 95% credible intervals (CrIs) (Appendix, https://wwwnc.cdc.gov/EID/article/32/10/26-1175-App1.pdf).

Before the intervention, BDBV was capable of sustained transmission of R_t of 1.55 (95% CrI 1.02–2.36). The R_t markedly declined to 0.50 (95% CrI 0.17–1.15) after the intervention (Figure; Appendix Figure 1). We estimated that ≈15% (95% CrI 2.7%–31.7%) of cases were under ascertained, corresponding to 20 (95% CrI 3–51) cases predicted to be missed. After adjusting for underascertainment, the preintervention CFR was 31.4% (95% CrI 21.8%–42.8%), which then