In conclusion, we describe 7 indigenous cases of dengue fever in Niger. Dengue fever cases are underreported in Africa, where it is often misdiagnosed as malaria (*1*). Misdiagnosis and underreporting highlights the need to train healthcare staff on the recognition and diagnosis of dengue fever. Strong vector control measures are also beneficial for containing the spread of dengue fever (*4*).

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Large-Scale Outbreak of *Mycoplasma pneumoniae* Infection, Marseille, France, 2023–2024

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We report a large-scale outbreak of *Mycoplasma pneumoniae* respiratory infections encompassing 218 cases (0.8% of 26,449 patients tested) during 2023–2024 in Marseille, France. The bacterium is currently circulating and primarily affects children ≤15 years of age. High prevalence of co-infections warrants the use of a syndromic diagnostic strategy.

Mycoplasma pneumoniae is known to cause upper respiratory tract infections and pneumonia, especially in children 5–15 years of age (*1*). Although mostly sporadic, *M. pneumoniae* infections may occur as successive epidemics every few years (*1*). The precedent outbreak was observed during

the 2019–2020 cold season, simultaneously in several countries, just before onset the COVID-19 pandemic (*2*). Then, the number of cases observed worldwide decreased markedly during this pandemic. However, although the resurgence of most respiratory pathogens was gradually observed from 2021, incidence of *M. pneumoniae* remained particularly low until June 2023, when a major resurgence of cases was reported worldwide (*2*–*3*).

We describe *M. pneumoniae* respiratory infections diagnosed in Marseille, France, university hospitals during January 1, 2014–February 15, 2024. We analyzed retrospectively all respiratory samples tested with 1 of the following specific quantitative PCRs (qPCRs) for *M. pneumoniae*: qPCR carried out by point-of-care laboratories using the Biofire FilmArray Respiratory Panel 2 Plus Assay (bioMérieux, https://www.biomerieux.com); qPCR performed routinely at the core laboratory using the FTD Respiratory Pathogens 21 Assay (Siemens Healthineers, https://www.siemens-healthineers.com); or an in-house specific qPCR (*4*). We used OpenEpi version 3.01 (https://www.openepi.com) for statistical analyses and considered differences significant at $p \leq 0.05$.

Overall, 98,401 samples from 74,355 patients were tested for *M. pneumoniae* as part of the diagnosis of respiratory infections during 2014–2024. Median patient age was 30 years (range 0–108 years); 52% were male and 48% female. *M. pneumoniae* was detected in 449 patients (0.6%). Median age of positive patients was 10 years (range 0–101 years); 57% were male and 43% female.

We observed a few *M. pneumoniae* outbreaks in Marseille during 2014–2020, with a peak in early 2020 (Figure). Incidence then declined until a resurgence was observed beginning in 2023. Initially, 9 cases were observed in January 2023, followed by 6 cases during February–May. Then, a major increase in diagnoses was observed during June 1, 2023–February 15, 2024 (203 total with a peak of 48 cases in December 2023). From January 2023 through mid-February 2024, we diagnosed 218 *M. pneumoniae* infections (0.8% of 26,449 patients tested), compared with 231 cases (0.3% of 71,952 patients tested) during January 2014–December 2022 ($p<0.0001$). Median age was significantly lower for patients diagnosed since 2023 than for previous years (8 vs. 15 years; $p<0.0001$) (Table). Concurrent presence of ≥1 respiratory viruses was found for 114/316 (36%) *M. pneumoniae*–positive patients. The prevalence of co-infections was significantly higher in children <5 years of age than in other age groups ($p<0.0001$). The most common co-infections were with rhinovirus (n = 49), influenza A virus (n = 13), respiratory syncytial virus (n = 12), human coronavirus OC43 (n = 10), influenza B virus (n = 9) and metapneumovirus (n = 9) (Appendix Figure 1, https://wwwnc.cdc.gov/EID/article/30/7/24-0315-App1.pdf). Co-infections were significantly less frequent in patients diagnosed during 2014–2022 (45/164 [27%]) compared with those diagnosed since 2023 (69/152 [45.4%]; p = 0.0008).

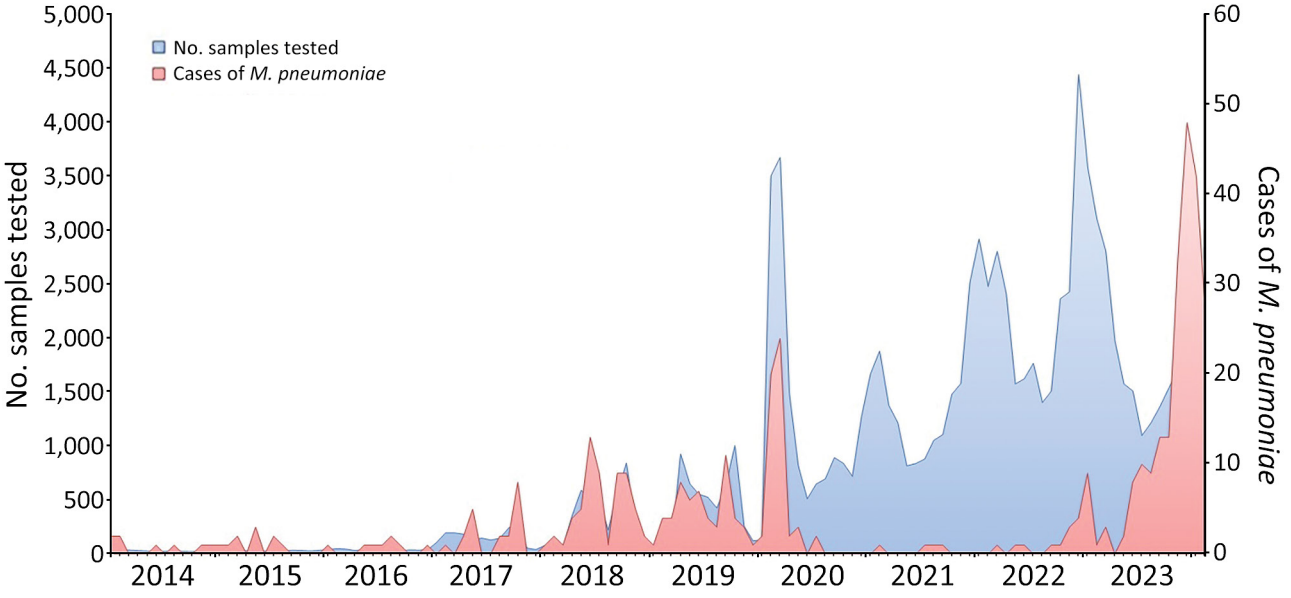

Figure. Monthly number of *Mycoplasma pneumoniae*–specific quantitative PCR tests performed and positive cases at a university hospital, Marseilles, France, January 1, 2014–February 15, 2024. Scales for the y-axes differ substantially to underscore patterns but do not permit direct comparisons.

Table. Demographic characteristics of 449 patients who had *Mycoplasma pneumoniae* infection diagnosed using quantitative PCR, Marseille, France, 2014–2022 versus 2023–2024*

Characteristic	Total	2014–2022	2023–2024	p value
No. patients	449	231	218	
Sex				
M	258 (57)	137 (59)	121 (56)	0.41
F	191 (43)	94 (41)	97 (44)	
Median age, y (range)	10 (0–101)	15 (0–93)	8 (0–101)	<0.001
Age group, y				
0–4	117 (26)	50 (22)	67 (31)	0.028
5–14	146 (32)	63 (27)	83 (38)	0.015
15–44	106 (24)	67 (29)	39 (18)	0.006
45–64	40 (9)	29 (13)	11 (5)	0.005
≥65	40 (9)	22 (9)	18 (8)	0.638
Co-infections				
No. patients tested	316	164	152	
No. patients with co-infection	114 (36)	45 (27)	69 (45)	0.0008
With 1 pathogen	94 (82)	41 (91)	53 (77)	0.049
With ≥2 pathogens	20 (17)	4 (9)	16 (23)	
Median age, y (range)	4 (0–101)	7 (0–86)	3 (0–101)	0.012
Age group, y				
0–4	58 (51)	18 (40)	40 (58)	<0.001
5–14	27 (24)	7 (16)	20 (29)	0.005
15–44	13 (11)	10 (22)	3 (4)	0.089
45–64	8 (7)	6 (13)	2 (3)	0.286
≥65	8 (7)	4 (9)	4 (6)	1

*Values are no. (%) except as indicated.

The increase of *M. pneumoniae* infection cases observed in our center are in line with observations from surveillance networks in France and throughout Europe (i.e., detection of the first epidemic sign in June 2023 until a peak reaching in December 2023) (*2*). High percentages of positivity (up to 50%) have been reported in China (*5*). In Marseille, we observed a lower percentage (1.8%), similar to the 0.89% observed in the United States since September 2023 (*9*). Most previous studies reported an increased incidence of *M. pneumoniae* infection particularly in school-age children and young adults (*3*,*7*). In Marseille, children ≤15 years were more affected during 2023–2024 than in previous seasons. However, we observed a switch regarding the population affected by the epidemic; adults became more affected beginning in January 2024 (Appendix Figure 2), possibly because of a massive transmission of the bacterium from infected children. We also observed a high rate of co-infections (≈50%), compared with 18% in the Netherlands (*3*). A high rate of co-infection with *M. pneumoniae* and other pathogens has also been previously reported in 65% of children and 34% of adults with acute respiratory infections in the United States (*8*). *M. pneumoniae* carriage ranging from 21% to 56% has also been reported in asymptomatic children (*9*). Interactions during co-detected microorganisms are complex, making it difficult to clearly define the contribution of each to respiratory infection. A high rate of asymptomatic carriers suggests a critical role for the nasopharyngeal microbiota in the clinical expression of respiratory infection.

There are several hypotheses for this re-emergence of *M. pneumoniae*, including the emergence of a new strain or a decline in individual and collective immunity. The current outbreak could be the usual periodic recurrence marked by an exacerbation resulting from a period of low exposure linked to restrictive measures during the COVID-19 pandemic. We did not investigate macrolide resistance, but reported resistance is low in Europe (*10*), and most studies described favorable outcomes after macrolide treatment (*7*). The number of *M. pneumoniae* infection cases is probably underestimated, particularly because patients with mild symptoms are not systematically tested. The high prevalence of co-infections with respiratory viruses justifies the use of a syndromic diagnostic strategy.

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Data are available from the corresponding author upon reasonable request.

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Fatal Infection in Ferrets after Ocular Inoculation with Highly Pathogenic Avian Influenza A(H5N1) Virus

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Ocular inoculation of a clade 2.3.4.4b highly pathogenic avian influenza A(H5N1) virus caused severe and fatal infection in ferrets. Virus was transmitted to ferrets in direct contact. The results highlight the potential capacity of these viruses to cause human disease after either respiratory or ocular exposure.

In recent years, clade 2.3.4.4b highly pathogenic avian influenza A(H5N1) viruses have exhibited substantial host expansion, geographic spread, and reassortment with other circulating influenza A viruses (IAVs) in birds, resulting in epornitics on all continents and virus detection in an expanding group of mammals (*1*). Human cases of H5N1 clade 2.3.4.4b virus infection have been reported, typically following direct exposure to infected animals, contaminated environments, or both (*2*). A 2.3.4.4b highly pathogenic avian influenza A(H5N1) virus was isolated from a human patient in Chile during 2023 (A/Chile/25945/2023 [Chile/25945]) (*3*) and caused severe and fatal disease in ferrets intranasally inoculated with 10^6 PFU of virus. Transmission of virus to animals housed in close contact was also reported (*3*), highlighting the pandemic potential of clade 2.3.4.4b viruses.

Although the eyes represent a secondary mucosal surface that is susceptible to respiratory virus exposure (*4*), as evidenced by recent reports of conjunctivitis in 2 dairy workers exposed to clade 2.3.4.4b H5N1 virus (*5*), risk assessment approaches for clade 2.3.4.4b H5N1 viruses to date have been limited to standard intranasal inoculation (*3*,*6*) and have not evaluated the capacity of those viruses to cause disease after alternative portals of entry. To investigate relative similarities between ocular and respiratory exposure to H5N1 virus, we assessed the severity and kinetics of disease after ocular exposure of ferrets to Chile/25945 virus and compared our findings with a previously published assessment of animals intranasally inoculated with