

Resurgence of *Mycoplasma pneumoniae* by macrolide-resistant epidemic clones in China

In *The Lancet Microbe*, Patrick M Meyer Sauteur and colleagues¹ reported about a delayed re-emergence of *Mycoplasma pneumoniae* after the COVID-19 pandemic restrictions. According to initial study findings, China is currently facing a concurrent outbreak of paediatric respiratory diseases, particularly the macrolide-resistant *M pneumoniae* (MRMP) outbreak.² On the basis of more than 30 000 PCR tests and bronchoscopy findings (appendix p 3) in a paediatric hospital in east China from 2017 to 2023, we found a pronounced re-emergence of *M pneumoniae*, with up to 50% positive cases noted since July, 2023 (appendix p 2), compared with a lower incidence of positive cases ranging from 10% to 20% during the COVID-19 period (2020–22).

We obtained 448 metagenomic datasets (appendix pp 4–11) that were derived from findings of bronchoalveolar lavage fluid samples or swabs of infected children and identified *M pneumoniae* in 179 samples when mapping to a reference genome (GCA_900660465.1). A phylogenetic tree was subsequently constructed and showed the presence of two primary epidemic clones in China: EC1 in P1-1 and EC2 in P1-2 (appendix pp 2, 12–20). EC1 has been isolated throughout east Asia since 2010, and is probably responsible for the elevated MRMP frequencies observed there (appendix p 2). In contrast, EC2 has recently emerged from non-resistant strains, with the first isolates identified in 2019 in Taiwan³ and in 2020 in Beijing.

We found that EC2 showed 100% macrolide resistance because of the acquisition of the A2063G mutation in 23S rRNA (appendix pp 2, 21). All three P1-2 strains isolated in Beijing in 2020 were derived from EC2, suggesting that EC2 could be responsible for the

previously reported increase in MRMP frequencies in P1-2 strains detected in the country after 2018.⁴ Moreover, our analyses showed frequent, cryptic cross-regional *M pneumoniae* transmissions in both EC1 and EC2, and the Taiwan strains in 2019 showed that the EC2 MRMP strain had been spreading throughout China before 2020. PCR-based surveillance data also suggested an unusual increase in infections due to the P1-2 MRMP strain in north China from 2021 to 2022.⁵ Our findings suggest that without the restrictions enacted during the COVID-19 pandemic, the MRMP clones could have caused outbreaks across the country as early as 2020; thus, our findings provide evidence to guide future epidemic prevention and treatment in east Asia.

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1 Sauteur PMM, Beeton ML, Pereyre S, et al. *Mycoplasma pneumoniae*: delayed re-emergence after COVID-19 pandemic restrictions. *Lancet Microbe* 2023; published online Nov 23. [https://doi.org/10.1016/S2666-5247\(23\)00344-0](https://doi.org/10.1016/S2666-5247(23)00344-0).

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- 3 Hsieh YC, Li SW, Chen YY, et al. Global genome diversity and recombination in *Mycoplasma pneumoniae*. *Emerg Infect Dis* 2022; **28**: 111–17.
- 4 Wang X, Li M, Luo M, et al. *Mycoplasma pneumoniae* triggers pneumonia epidemic in autumn and winter in Beijing: a multicentre, population-based epidemiological study between 2015 and 2020. *Emerg Microbes Infect* 2022; **11**: 1508–17.
- 5 Jiang TT, Sun L, Wang TY, et al. The clinical significance of macrolide resistance in pediatric *Mycoplasma pneumoniae* infection during COVID-19 pandemic. *Front Cell Infect Microbiol* 2023; **13**: 1181402.



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See Online for appendix