Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Co-infection with SARS-CoV-2 omicron BA.1 and BA.2 subvariants in a non-vaccinated woman

Circulation of contagious SARS-CoV-2 variants and suboptimal vaccine protection create the conditions for simultaneous infections with multiple strains, which could generate inter-lineage SARS-CoV-2 recombinants with novel unpredictable features.[1,2] Mixed infections have been reported since the first epidemic waves.[3,4] Co-infection with omicron and delta have been found in immunocompetent and immunocompromised patients living in different geographical areas.[5,6] Because these variants are characterised by different genomic sequences, their co-presence can be identified promptly. However, recombination between closely related variants is difficult to identify but can also occur. A total of 637 cases of the omicron BA.1 and BA.2 recombinant, known as XE, have been confirmed in the UK up to now, and the number is increasing.[7] These data also suggest that intralineage recombination generates highly transmissible chimeric strains. It is necessary to detect all co-infections to minimise the risk of recombination.

Here, we report a non-vaccinated woman, aged 63 years and with mild respiratory symptoms, who had a nasopharyngeal swab on Jan 31, 2022. The sample scored positive for the *E*, *N*, and *RdRp* or genes using the Allplex SARS-CoV-2 assay (Arrow and Seegene, Seoul, South Korea; appendix p 3). This case was found fortuitously, as it was randomly picked along with 68 other acute infections to do a molecular survey requested by *Istituto Superiore di Sanità*. All isolates were preliminarily examined with a multiplex PCR to detect the mutation signatures of major circulating variants and were found to belong to the omicron variant (appendix p 2). 54 samples were then chosen at random, 24 of which were whole-genome sequenced and 30 of which were Sanger sequenced in the region of the Spike gene. The case sample fell into the Sanger group and the resulting electropherogram showed various polymorphisms and unreadable sequences close to the 142–144 amino acid deletion of omicron variant BA.1. The sample was then examined by whole-genome sequencing and showed 67 mutations defining the omicron variants. Of these, 15 were of BA.1 sublineage and 20 were of BA.2 sublineage (appendix p 2). Nextclade (version 1.14.0) analysis confirmed the presence of two distinct isolates (appendix p 2).

The woman promptly isolated herself, had no other contacts since then, and resolved the infection within 9 days. These results suggest that omicron co-infection induces mild symptoms, even in non-vaccinated individuals, and can go unnoticed. This work underlines the need for effective genomic surveillance to reduce the risk of generating SARS-CoV-2 recombinants with novel pathogenic and immunological properties.

We declare no competing interests.

*Maria Linda Vatteroni, Anna-Lisa Capria, Pietro Giorgio Spezia, Susi Frateschi, *Mauro Pistello*
mauro.pistello@unipi.it

Virology Unit (MLV, A-LC, PGS, SF, MP) and Retrovirus Centre and Virology Section (PGS, MP), University of Pisa, I-56127 Pisa, Italy

1 Jackson B, Boni MF, Bull MJ, et al. Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. *Cell* 2021; **184:** 5179–88.
2 VanInsberghe D, Neish AS, Lowen AC, Koelle K. Recombinant SARS-CoV-2 genomes are currently circulating at low levels. *bioRxiv* 2021; published online March 15. https://doi.org/10.1101/2020.08.05.238386 (preprint).
3 Samoilov AE, Kaptelova VV, Bukharina AY, et al. Case report: change of dominant strain during dual SARS-CoV-2 infection. *BMC Infect Dis* 2021; **21:** 959.
4 Pedro N, Silva CN, Magalhães AC, et al. Dynamics of a dual SARS-CoV-2 lineage co-infection on a prolonged viral shedding COVID-19 case: insights into clinical severity and disease duration. *Microorganisms* 2021; **9:** 300.
5 Combes P, Bisseux M, Bal A, et al. Evidence of co-infection during delta and omicron variants of concern co-circulation, weeks 49-2021 to 02-2022, France. *medRxiv* 2022; published online March 3. https://doi.org/10.1101/2022.03.02.22271694 (preprint).
6 Rockett RJ, Draper J, Gall M, et al. Co-infection with SARS-COV-2 omicron and delta variants revealed by genomic surveillance. *medRxiv* 2022; published online Feb 15. https://doi.org/10.1101/2022.02.13.22270755 (preprint).
7 UK Health Security Agency. SARS-CoV-2 variants of concern and variants under investigation in England. Technical briefing 39. March 25, 2022. https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1063424/Tech-Briefing-39-25March2022_FINAL.pdf (accessed March 31, 2022).

Published **Online** May 24, 2022 https://doi.org/10.1016/S2666-5247(22)00119-7

See **Online** for appendix