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## Letter to the editor

## SARS-CoV-2 recombinant XN, Italy



Dear Editor,

SARS-CoV-2 recombinants can emerge at the time different strains co-circulate and a patient gets super-infected. Recombinants are named with an “X” prefix in the PANGOLIN phylogeny. To date, recombinant lineages have been reported between VOC Alpha and Delta, Delta and BA.1, Delta and BA.2, and BA.1 and BA.2 [1]. Recombinants between BA.1 and BA.2, generally having BA.1 as the donor and BA.2 as acceptor, have already been reported either in individual patients [2–4] or as circulating sublineages, which have been assigned names XE, XG, XH, XJ, XK, XL, XM, XN, XP, XQ, XR, and XT by PANGOLIN [5].

We report here the case of an 88-years old female attending the hospital nephrology ward for maintenance hemodialysis: she was affected by type 1 diabetes mellitus, stage 4 chronic renal failure, and autoimmune hypothyroidism. On April 11 she tested positive for SARS-CoV-2 at a rapid antigen assay on a nasopharyngeal swab (NPS), which was confirmed at RT-PCR (cycle threshold (Ct) = 13; Alinity, Abbott). Despite being at high risk for disease progression, she was not treated with anti-Spike antibodies because at that time the dominant circulating lineage (BA.2) was resistant to clinically approved therapeutic anti-Spike monoclonal antibodies, and she could not tolerate the nephrotoxicity of small-chemical antivirals. She was hence left under monitoring at home: a follow-up NPS on April 22 was still positive (Ct = 28), and on April 26 she was negative.

Whole-genome sequencing (WGS), performed according to Italian flash surveys, showed the genome to correspond to PANGOLIN XN lineage (GISAID entry EPI\_ISL\_12,279,156), originally reported in the UK on February 1, 2022 (PANGO issue #480). XN has the likely breakpoint between nucleotides 2834 and 4183 at NSP3 and can be identified by the occurrence of the unlabeled private mutation G10986A. As of April 25, CoV-Spectrum.org shows that XN has been reported in 876 GISAID sequences across 25 countries (666 in the UK, 46 in Germany, 36 in the USA, 34 in Denmark), including 7 instances in northern Italy (2 in Lombardy, 4 in Trentino Alto Adige and 1 in Emilia-Romagna).

In the Omicron recombinants known to date, the Spike protein remains the same as in BA.2, leaving unaltered the efficacy of Spike-based therapeutics and vaccines. Among such recombinants, only XE has been currently shown to be fit enough to compete with BA.2 [6], but no lineage to date has the potential to become dominant. Nevertheless, genomic surveillance by WGS is needed to monitor the emergence and spread of novel recombinant lineages.

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## Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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