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Clade IIb A.3 monkeypox virus: an imported lineage during a large global outbreak

As of Dec 5, 2022, there were 3730 mpox (formerly known as monkeypox) cases in the UK,[1] with clade IIb B.1 being the predominant lineage. Cases of mpox associated with travel or proven not to be B.1 lineage on whole genome sequencing were managed in airborne high consequence infectious disease (A-HCID) units, following the derogation of mpox associated with men who have sex with men (MSM) by the Advisory Committee on Dangerous Pathogens.[2] To date, successfully sequenced non-B.1 lineage imported mpox cases to the UK have been within clade IIb A.2.[3]

A man aged 33 years who returned to the UK from Nigeria was admitted in status epilepticus. He had developed epilepsy following a traumatic brain injury in 2004. He was HIV-negative and did not have immunosuppression. Presumed secondary bacterial infection of chickenpox lesions was treated with ciprofloxacin in Nigeria before his return to the UK. Skin swabs taken in critical care for monkeypox virus were positive. The patient was transferred to the nearest A-HCID unit to receive specialist infection treatment and critical care support to treat recalcitrant seizures, severe acute kidney injury secondary to severe rhabdomyolysis (creatinine kinase >750 000 units), and bilateral forearm compartment syndrome necessitating bilateral fasciotomies. Mpox encephalitis was excluded with two negative cerebrospinal monkeypox virus PCR tests. Initially he completed 14 days of oral tecovirimat, which was extended to 6 weeks because of a persistent groin lesion and a deep right corneal ulcer. The right corneal ulcer was treated with 1% triflurodine topical eye drops for 4 weeks, and he was eventually discharged. The patient's monkeypox viraemia, in conjunction with poor anti-epileptic compliance and ciprofloxacin use, was the working diagnosis for the status epilepticus.

Whole genome sequencing was done at the UK Health Security Agency using Illumina next-generation sequencing, which identified an imported lineage within clade IIb that was phylogenetically distinct from other imported cases in 2022 (appendix). This was subsequently designated as lineage A.3.[4] Lineage A.3 contains an additional seven single nucleotide mutations (three non-synonymous), whereas lineage A.2 contains 11 single nucleotide mutations (eight non-synonymous), with no mutations shared between the lineages. Evidence suggests there are mutations in clade IIb that are faster than expected, especially in APOBEC3 enzyme editing.[5] Other countries have reported other lineages associated with travel (A.2.1, A.2.2, and now A.3) that phylogenetically originate in Nigeria, which suggests sustained transmission in non-MSM groups.[5] Further sequencing should be done for circulating lineages and their associated pathogenicity and virulence factors.

We declare no competing interests.

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See **Online** for appendix

ChatGPT and antimicrobial advice: the end of the consulting infection doctor?

Generative artificial intelligence (AI) models have proliferated in the past 2 years. ChatGPT—a large language model (LLM) developed by OpenAI (San Francisco, CA)—mimics natural language and solves cognitive problems by reinforcing learning from online resources using human feedback. Despite access to limited medical data, ChatGPT has medical licensing examination performance as an undergraduate third-year medical student, and has, therefore, stimulated urgent discussions within medicine[1]. Stokel-Walker and van Noorden[2] discuss the implications of generative AI for science and describe how ChatGPT "could answer some open-ended medical queries almost as well as the average human physician could, although it still had shortcomings and unreliabilities."[2]

Clinicians make decisions using complex information.[3] In telemedicine, information is generally restricted to language alone,[4] and is potentially suitable for interventions using LLM. ChatGPT, however, cannot ask questions to seek further clarification of questions or scenarios. Infection consultation requires integration of

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