

Case report

Identifying virulent avian paramyxovirus type-1: A paediatric case of progressive encephalitis diagnosed by clinical metagenomics with case series review

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ABSTRACT

Background: Immunocompromised patients presenting with encephalitis can present a diagnostic conundrum as infection can be caused by a broad range of pathogens, many of which are not detected by standard of care testing pathways. Untargeted metagenomics has proven utility in the diagnosis of such infections, particularly for immunocompromised patients.

Methods: An immunosuppressed adolescent presented with idiopathic progressive muscle weakness resulting in respiratory failure, 16 years after haematopoietic stem cell transplant for familial haemophagocytic lymphohistiocytosis type 5. Clinical and radiological findings suggested a diagnosis of isolated central nervous system haemophagocytic lymphohistiocytosis, however the patient demonstrated no improvement on immunosuppressive therapy. Untargeted metagenomics was performed on brain biopsy tissue.

Results: Clinical metagenomics detected avian paramyxovirus 1 (APMV-1) in the brain tissue 12 days after biopsy, confirmed by targeted PCR and immunohistochemistry. The metagenomics results guided treatment;

Abbreviations: APHA, Animal & Plant Health Agency; APMV-1, avian paramyxovirus 1; CSF, cerebrospinal fluid; DNA, deoxyribonucleic acid; FFPE, formalin fixed paraffin embedded; FHL, familial haemophagocytic lymphohistiocytosis; GOSH, Great Ormond Street Hospital for Children; HLH, haemophagocytic lymphohistiocytosis; HSCT, haematopoietic stem cell transplant; IHC, immunohistochemistry; mNGS, metagenomics; MRI, magnetic resonance imaging; N protein, nucleocapsid protein; NDV, Newcastle Disease; NPA, nasopharyngeal aspirate; PCR, polymerase chain reaction; PPMV-1, pigeon paramyxovirus; RNA, ribonucleic acid; TTV, torque teno virus; UAE, United Arab Emirates.

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immunosuppression was stopped and medication with potential activity against RNA viruses started. The patient died 8 months after symptom onset.

Conclusions: We describe the third published case of fatal encephalitis caused by APMV-1, detectable only in brain parenchyma and only by clinical metagenomics, demonstrating the utility of brain biopsy and metagenomics when investigating encephalitis in immunocompromised patients. Case series review suggests profoundly immunocompromised patients are at risk of severe infection caused by APMV-1.

Background

The cause of encephalitis can be difficult to ascertain due to a broad range of potential aetiologies, particularly in immunocompromised patients, or those with a foreign travel history for whom the range of organisms capable of causing infection is greater. In cases of encephalitis with an undefined cause, metagenomics-based approaches can be employed to detect the presence of causative organisms [1,2] by sequencing total DNA and RNA in a clinical specimen to enable agnostic, pan-pathogen detection [3].

Avian paramyxovirus type 1 (APMV-1) is a negative-sense, single-stranded, non-segmented, enveloped RNA virus with a 15,192-nucleotide genome belonging to the *Paramyxoviridae* family of viruses. There are two classes of APMV-1 (Class I and Class II), with Class II APMV-1 containing 20 distinct genotypes. APMV-1 genotypes VI, XX and XXI have established lineages in pigeons, commonly referred to as pigeon paramyxovirus (PPMV-1). PPMV-1 is endemic in many pigeon and dove species.

APMV-1 circulate globally in avian hosts, often in the absence of clinical disease. Birds infected with APMV-1 display a range of clinical signs, ranging from subclinical or mild disease to high levels of morbidity and mortality. In poultry, the disease is termed Newcastle Disease (NDV) when clinical and genetic criteria are met. Highly virulent genotypes can cause necrotising lesions within the nervous, respiratory, lymphoid or digestive systems and up to 100% mortality. The virus is shed and remains infectious in bird faeces, from where it is commonly spread by fomite transfer.

Infections in humans and non-human mammals with APMV-1 are considered very rare. The first human case was described in 1942 following accidental laboratory exposure. Almost 500 cases have been reported globally, however almost all of these occurred through accidental laboratory or occupational exposure and resulted in mild self-limiting conjunctivitis or 'flu-like' symptoms [4]. There is currently no seroprevalence data for exposure to APMV-1s in the human population; therefore, the relationship between human exposure and disease is

unknown.

We describe a rare case of fatal encephalitis caused by APMV-1, diagnosed by untargeted metagenomics, in a child with familial haemophagocytic lymphohistiocytosis (FHL) type 5 and long standing underlying multifactorial immunodeficiency.

Methods

Clinical history and investigations

A 16-year-old male was admitted to Great Ormond Street Hospital for Children (GOSH), London from the United Arab Emirates (UAE) for investigation of progressive neurological deterioration (Fig. 1). At 11 months-of-age he developed HLH secondary to FHL type 5 (homozygous STXBP2 gene c1430C>T, p.Pro477Leu mutations, resulting in MUNC18-2 deficiency). He received allogenic HSCT at 13 months of age (see Supplementary data).

He demonstrated poor immune reconstitution with pancytopenia, no evidence of *de novo* thymic output (naïve CD4 +ve T cells <1%) and no functional B cell reconstitution, requiring immunoglobulin replacement therapy. Despite this, he remained clinically well until nine years post-HSCT when he developed recurrent sinopulmonary infections. He had evidence of progressive secondary graft loss. Prior to the episode described here, he was cognitively normal, attending school with no neurological concerns. He had a significant multifactorial immunodeficiency post-HSCT with 24% donor chimerism in whole blood (CD3 + cells 16%, CD15 +ve cells 28%), absent thymic output, absent functional B cell immunity and CD4 T cell and B cell lymphopenia (both <300 × 10⁶/L).

He presented with progressive headache, body ache and fatigue with subsequent diarrhoea, petechial rash on upper and lower limbs and generalised arthralgia. He then developed progressive facial, upper and lower limb weakness, diplopia, bilateral ptosis, photophobia, phonophobia, difficulty swallowing and chewing and became disorientated.

Over the subsequent two weeks he developed generalised tonic-

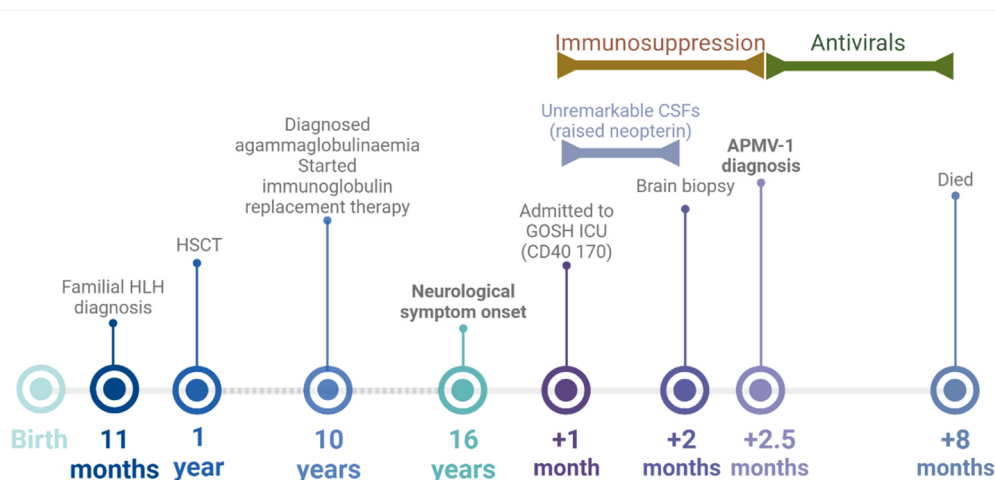


Fig. 1. Timeline of disease progression, diagnosis and treatment. See [supplementary data](#) for details of immunosuppression (HLH, Haemophagocytic lymphohistiocytosis; HSCT, Hematopoietic Stem Cell Transplantation; ICU, Intensive Care Unit; CSF, cerebrospinal fluid; APMV-1, avian paramyxovirus 1). Created in BioRender.

clonic seizures, myoclonic jerks and progressive lower limb and respiratory muscle weakness, resulting in type 2 respiratory failure and the requirement for mechanical ventilation four weeks after the first onset of symptoms. Brain MRI demonstrated widespread cortical, perirolandic and right cerebellar changes with diffusion restriction and associated swelling, in keeping with an immune mediated encephalitic process (Fig. 2). There were no significant spinal lesions.

He was transferred to our centre in the UK 4 weeks into his illness following the requirement for ventilation. On admission his cardiorespiratory status was stable on minimal ventilatory support. He could open his eyes spontaneously but had roving eye movements, with widespread hypotonia and myoclonic jerks of upper and lower limbs.

On admission he was found to be lymphopenic, with a CD4 + count of $170 \times 10^6/L$ and a CD19 count of $160 \times 10^6/L$. A granule release assay was performed to assess cytotoxic degranulation. This was normal with degranulation observed both in NK and CD8 + T cells suggesting some functional immune reconstitution post HSCT in peripheral blood.

Cerebrospinal fluid (CSF) analysis performed at two days, two weeks, and three weeks after admission, were unremarkable (full details in Supplementary). Neopterin was raised at 446nmol/L (normal range 7–65) and a CSF cytokine panel demonstrated detectable IL-6 (14 pg/ml, normal range <1.0 pg/ml) which may indicate CNS inflammation.

A diagnosis was made of immune-mediated inflammatory encephalitis secondary to graft failure with recurrence of MUNC18–2 deficiency and he was treated with incremental immunosuppression (see Supplementary data).

Following no response to immunosuppression, one month after admission, he underwent a brain biopsy of the frontal lobe. Histopathology of the brain biopsy showed no significant active inflammation with mild to moderate, non-specific reactive changes, including leptomeningeal thickening with reactive type of arachnoid proliferation

and macrophage upregulation. The brain parenchyma revealed mild oedema, gliosis and microglial activation with a few dispersed T-cells.

Clinical metagenomics

Metagenomic sequencing of the brain biopsy was performed as previously described [5] and detailed in Supplementary data.

Targeted APMV-1 PCR

Specific real time one-step reverse transcription (RT)-PCR targeting a region of the large polymerase (L)-gene for detection of APMV-1 was undertaken at the Animal & Plant Health Agency (APHA) on residual nasopharyngeal aspirate (NPA), bronchial washings, stool, whole blood, two CSFs and brain biopsy RNA, as described previously [6].

Phylogenetic analysis

Phylogenetic analysis was performed using the consensus sequence generated by metagenomics to denote the genotype and to identify any potential sequence adaptations present. Phylogenetic analysis was undertaken as described previously using the F-gene (1662 bp) region to reconstruct maximum likelihood phylogenetic trees [7] using sequences from NDV consortium or from NCBI (Supplementary Table 1). Phylogenetic trees were visualised using R version 4.5.1 with the libraries ggtree and ggplot2. Sequences from previously described fatal human cases of APMV-1 were included, with the exception of Zou *et al.* as sequence data was unavailable.

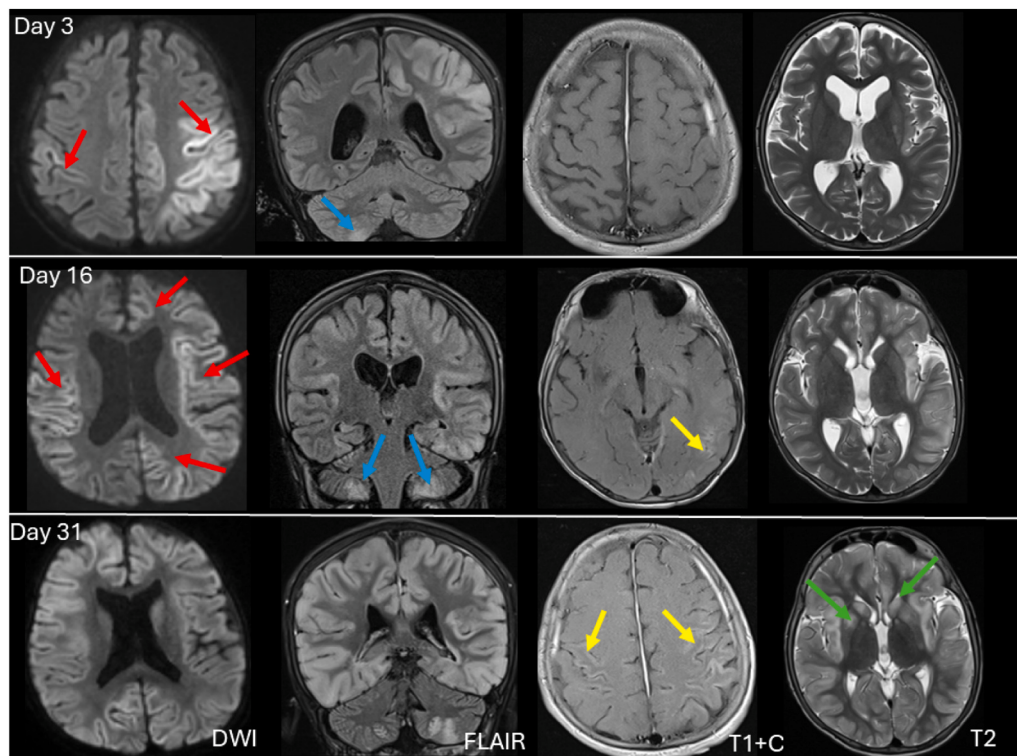


Fig. 2. Serial MRI imaging on days 3, 16 and 31 post-admission showing longitudinal changes. Admission was one month after symptom onset. Imaging shows progressive signal abnormality on all sequences, appearing asymmetrical on initial scans, but progressing to bilateral changes with persisting and worsening restricted diffusion (red arrows) and concomitant signal changes on FLAIR imaging. The cerebellar hemispheres also show progressive abnormality (blue arrows). Note the increasing enhancement within involved cortices over time (yellow arrows). Also, there is progressive involvement of the basal ganglia structures (green arrows) as evidenced on the axial T2 weighted images. The signal changes are accompanied by increasing cerebral swelling. (MRI, magnetic resonance imaging; FLAIR, fluid-attenuated inversion recovery; DWI, diffusion-weighted imaging).

Immunohistochemistry

Sections of formalin fixed paraffin embedded (FFPE) brain tissue were immunohistochemically labelled at APHA with anti-avian paramyxovirus nucleocapsid (N) protein antibody as described previously [8].

Positive and negative controls, comprising APMV-1-infected and non-infected tissues, were included in the immunohistochemistry (IHC) experiment and demonstrated appropriate immunolabelling, confirming the specificity of the staining.

Results

Clinical metagenomics

DNA sequencing generated 79,046,493 reads and identified 165 Torque Teno Virus reads. RNA sequencing generated 67,468,388 reads and identified 1,113,367 reads that had homology to APMV-1. The result was available to treating clinicians 12 days post brain biopsy. Reads were mapped to an APMV-1 reference sequence (Genbank accession KU885949) using CLC workbench [Qiagen] resulting in 100% genome coverage and average 3,849-fold read depth across the genome (Supplementary Figure 1). The consensus sequence generated (Genbank PX463213) was used for downstream analysis.

Targeted APMV-1 PCR

APMV-1 RNA was detected by targeted PCR in RNA purified from brain tissue where it was present at high viral loads with a Ct value of 26 which correlates with an estimated viral load of $10^{4.6}$ Egg infectious dose 50% per millilitre (EID₅₀/ml).

Targeted APMV-1 PCR was negative in all other clinical specimens, including two CSF samples collected two days and two weeks post admission. Blood, plasma, nasopharyngeal aspirate, stool and bronchial washings were also negative by PCR.

Immunohistochemistry

Serial FFPE brain sections demonstrated multifocal, strong intracytoplasmic and intranuclear immunolabelling of APMV viral N protein in neuronal and glial cells (Fig. 3), confirming APMV replication *in situ*.

Treatment and clinical progression

Following diagnosis of APMV-1 infection, immunosuppressive medication was reduced and ribavirin, favipiravir and nitazoxanide were administered daily. Ribavirin (250 milligrams four times daily), favipiravir (600 milligrams twice daily) and nitazoxanide (750 milligrams twice daily) were administered via nasogastric tube for one month. Prior to commencing anti-viral therapy CSF cytokine analyses were repeated and showed very high IL-6 in the CSF (498 pg/ml, normal range <1.0 pg/ml) despite immunosuppression. IL-6 has been described with *in vitro* infection of APMV-1 [9] however raised IL-6 does not discriminate between infectious and neuroinflammatory diseases [10].

Despite combination antiviral treatment targeting RNA viruses the patient continued to experience fevers and poor neurological function. He was transferred back to his country of origin for ongoing palliative care and ultimately died eight months after onset of symptoms.

Three potentially relevant animal exposures were found on history taking after diagnosis of APMV-1 infection. First, the patient had kept pet ducks, one of which died shortly before he became unwell. Secondly, he lived next to a bird sanctuary and thirdly, he regularly participated in falconry sports as a hobby.

Phylogenetic analysis

Phylogenetic analysis determined the sequence to be part of the APMV-1 XXI.1.2 genotype (Fig. 4) therefore this is a PPMV-1-like virus. The publicly available reference sequence with highest homology of the F-gene alone (97.5%, n = 1620/1662) was from a pigeon in Pakistan in 2014 (Genbank accession number KU644586). However, whole genome sequence comparisons showed the closest virus was from a Pakistani

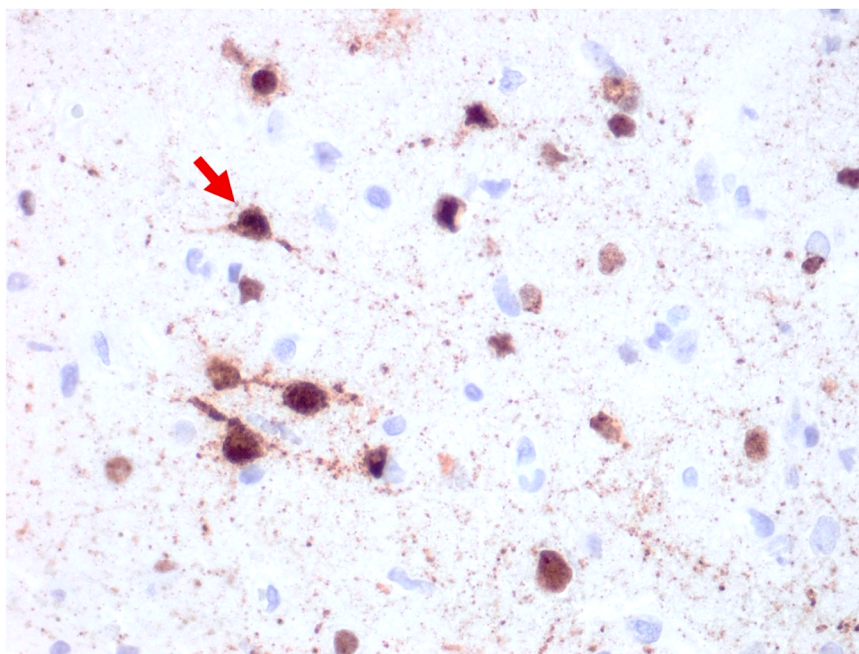


Fig. 3. Immunohistochemical detection of APMV-1 nucleocapsid protein in the neurons (red arrow), glial cells and neuropil of a formalin fixed paraffin embedded (FFPE) brain biopsy collected from the patient two months after symptom onset. Image taken at 400x magnification. Brain FFPE sections were immunohistochemically labelled with anti-avian paramyxovirus nucleocapsid (N) protein antibody, alongside positive and negative controls (not shown). (FFPE, formalin fixed paraffin embedded).



Fig. 4. Maximum likelihood tree of APMV-1 F gene (1664 bp) sequences including case described (GOSH; red). **a)** all APMV-1 genotypes; **b)** genotype XXI, colour coded by country of origin. The human case from France had a travel history to Dubai and the human case from GOSH (UK) originated in UAE. Phylogenetic analysis performed using the consensus sequence derived from clinical metagenomics data. (APMV-1, avian paramyxovirus 1; GOSH, Great Ormond Street Hospital for Children; UAE, United Arab Emirates).

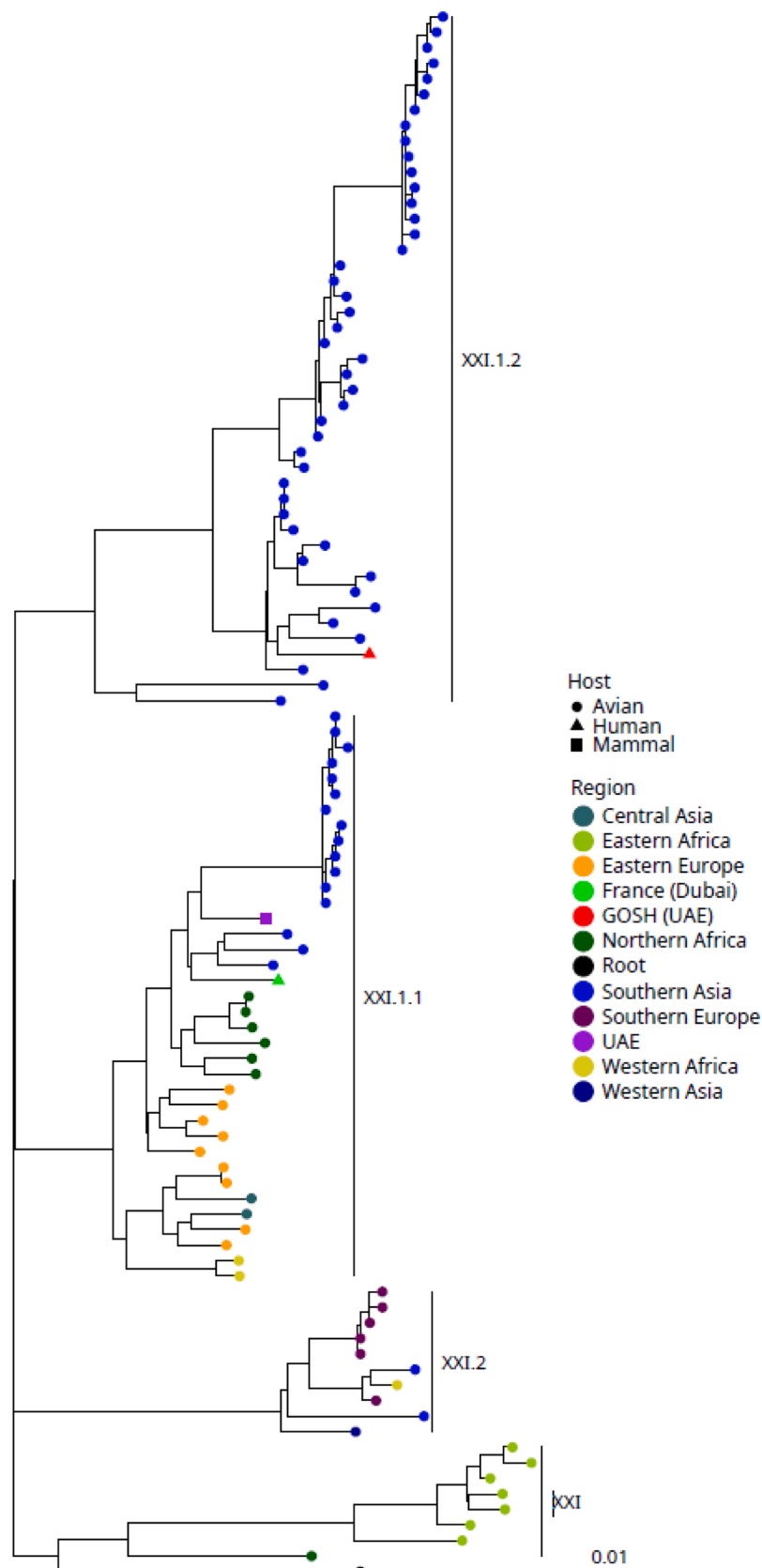


Fig. 4. (continued).

isolate from the same year but from pigeons (KU885949). Pairwise alignment of the whole genome sequence between the consensus sequence of our case and the closest related sequence showed 97.4%

($n = 14798/15192$ nucleotides) homology at the nucleotide level, resulting in 61 amino acid substitutions across the six coding sequences that are unlikely to have altered amino acid characteristics (NP =485/

489, P = 387/395, M = 354/364, F = 547/553, HN = 560/571 and L = 2182/2204).

Discussion

We describe an immunosuppressed patient presenting with progressive and ultimately fatal encephalitis several years post-HSCT with multifactorial immunocompromise in whom, prior to brain biopsy, a diagnosis was made of immune-mediated encephalitis caused by CNS HLH in the context of graft failure and poor immune reconstitution post-HSCT. He was consequently treated with intensive immunosuppression without clinical response. Extensive CSF analysis did not aid in achieving a diagnosis. Brain biopsy two months after symptom onset

facilitated metagenomics and defined the diagnosis as infection with virulent APMV-1 which guided ongoing management.

Once the diagnosis was made, immunosuppressive medication was reduced, and a combination of antiviral medication commenced potentially targeting RNA viruses. The patient continued to have recalcitrant fevers and poor neurological function despite targeted treatment and was transferred back to his country of origin for ongoing care where he died eight months after onset of symptoms.

Combined treatment with favipiravir and ribavirin has been shown to be synergistic *in vitro* [11] and *in vivo* [12]. All RNA polymerase inhibitors are also known to cross the blood brain barrier provided doses are high enough [13]. However at the time of initiation of anti-viral therapy the patient had very extensive and progressive neurological

Table 1

Summary of fatal human cases associated with APMV-1, including the case described here. (BMT, bone marrow transplant; CPE, cytopathic effect; HSCT, Hematopoietic Stem Cell Transplantation; PCR, polymerase chain reaction; APMV-1, avian paramyxovirus 1; HLH, Haemophagocytic lymphohistiocytosis; CSF, cerebrospinal fluid).

Clinical presentation	Country	Year	Age and gender	Underlying diagnosis	APMV-1 Genotype	Method of detection	Notes	Reference
Fatal pneumonia Malaise, fever, diarrhoea, abdominal pain, progressive worsening respiratory signs leading to respiratory failure. Died 8 weeks from symptom onset.	Netherlands	2002	54 years Male	8 weeks post-BMT	VI	Metagenomics on tissue culture cells with CPE	Retrospective diagnosis 15 years after case	[19] Genbank KJ544861
Fatal pneumonia Fever, progressive pulmonary infiltrates, pneumonia leading to respiratory failure. Died 24 days from symptom onset.	USA	2007	42 years Male	18 days post-HSCT for non-Hodgkin's lymphoma	VI	Random PCR based screening method	First published fatal case	[18] Genbank EF555090 to EF555096 (only F-gene sequence available, not full genome)
Fatal pneumonia Fatigue, fever, respiratory failure, acute respiratory distress syndrome (ARDS), severe pneumonia. Died day 21 from symptom onset.	China	2020	64 years Male	None	VI	Metagenomics	Known exposure to infected pigeon (butchered pigeons for restaurant, retrospective PCR testing found PCR positive feather from pigeon hut).	[17] No genbank reference
Fatal encephalitis Sudden onset progressive seizures without fever, myoclonic seizures, unilateral parasthesia. Died day 63 from symptom onset.	France (travel history to Dubai)	2021	12 years Female	3 months post-HSCT for combined immunodeficiency	XXI	Metagenomics	CSF negative for APMV-1	[20] Genbank SAMN13611976
Fatal encephalitis Nausea and vomiting following 3 weeks upper respiratory tract symptoms. Febrile progression with sudden onset super refractory status epilepticus. Died day 48 from symptom onset.	Australia	2023	2 years Female	Acute lymphoblastic leukaemia (ALL)	VI	Metagenomics	CSF not tested	Hurley et al. [21] Genbank OR636618
Fatal encephalitis Headache, body ache, fatigue, petechial rash, diarrhoea, disorientated. Generalized tonic-clonic seizures, myoclonic jerks, progressive limb and muscle weakness leading to respiratory failure. Died month 8 from symptom onset.	UK (symptom onset in UAE)	2022	16 years Male	15 years post-HSCT for familial HLH with agammaglobulinemia and low CD4	XXI	Metagenomics	CSF negative for APMV-1	This manuscript* Genbank PX463213

* Also included in case series [1] and Penner et al. [22]

changes demonstrated on MRI; we suspect his functional neurological defects were irreversible even if the antiviral therapy irradiated the APMV-1 infection. Furthermore, treatment with intensified immunosuppression prior to APMV-1 diagnosis may have accelerated viral replication and clinical decline. Brain biopsy was collected once all diagnostic avenues were exhausted, however the 2.5-month delay in diagnosis and anti-viral treatment likely impacted the chance successful treatment.

Torque teno virus (TTV) was also detected at low levels by metagenomics, however, TTV is a ubiquitous virus with no known disease association and considered part of the human virome [14]. In this case TTV was considered an incidental finding, not causative of encephalitis, and likely present due to the patient's immune deficiency.

APMV-1 is of high virulence when causing infection in poultry [15, 16] and neurotropic, causing encephalitis and death of infected birds. Infections in humans are rare and typically present as mild conjunctivitis or flu-like symptoms. Most reported cases have been associated with accidental occupational exposures, nonetheless there have been five previous reports of fatal human APMV-1 infection. Three cases resulted in fatal pneumonia [17–19] and two cases in fatal encephalitis [20,21] (Table 1). One of the reported cases of fatal encephalitis [21] also had raised neopterin in CSF, suggesting significant central nervous system inflammation in these infections.

As in this report, all but one of the reported fatal cases (4/5) were immunocompromised patients with no defined exposure events. Here we describe a patient with significant CD4 lymphopenia, absent thymic emigrants and no functional B cell immunity at presentation, placing him at significant risk of opportunistic infections and likely contributed to the progressive course of infection. The only reported immunocompetent patient with fatal infection is a restaurant worker in China who had fatal APMV-1 pneumonia after butchering infected pigeons [17], suggesting that without occupational exposure only profoundly immunocompromised individuals are at risk of severe infection.

Genotype XXI.1.2 has been previously described in South and West Asia but has not previously been detected in the United Kingdom (UK). The patient's country of origin, where symptoms began therefore where infection was likely acquired, was the UAE. Several nucleotide and amino acid substitutions were identified compared to other publicly available sequences. However, given the rare detections of APMV-1 in humans it was not possible to ascribe any role of these substitutions to pathogenesis.

The viral sequence included the virulent F-gene cleavage site (¹¹³RQKR/F¹¹⁷) which suggests this virus can infect multiple avian tissues, including the brain. Indeed, the presence of a virulent cleavage site is one of the determinants of Newcastle Disease in poultry. Viral RNA has been detected in the brain of pigeons and chickens following infection [15,16]. It is uncertain what leads to neuroinvasive disease in some human individuals versus conjunctivitis or mild flu-like symptoms in others but given all fatal cases of encephalitis to date have been in immunocompromised patients, immune status is likely to be an important factor.

On review of potential pathogen exposure history in our case, three potential sources of infection were considered, however it has been proposed that APMV-1 can be spread beyond localised environments from pigeon faeces via aerosol and so ascertaining the source of infection in clinical cases is difficult. Since the time of exposure cannot be determined, it was not possible to estimate the incubation period for symptomatic disease.

In this case, APMV-1 was undetectable in CSF with detection of virus restricted to the brain. It is possible the virus was transiently detectable in CSF earlier in the clinical course, with no shedding into CSF once established in the brain parenchyma, however the window for detection outside of the brain is uncertain as we had no access to specimens until one month after symptom onset. There are similar discrepancies in detection between brain parenchyma and CSF in other cases of infective encephalitis including measles SSPE, EBV, Astrovirus VA1, mumps

vaccine virus and *Toxoplasma gondii* [1]. In the other two published fatal APMV-1 encephalitis cases, one was also negative in CSF [20] whilst in the other CSF was not tested [21]. Absence of virus in CSF may be a characteristic feature of APMV-1 encephalitis but more evidence is needed. Nonetheless this case and others demonstrate the diagnostic utility of brain biopsy when a diagnosis cannot be achieved from CSF and imaging.

Brain biopsy and metagenomics facilitated a diagnosis that would otherwise have remained undiagnosed. This case study highlights the need to consider unusual pathogens such as APMV-1 as a cause of fulminant encephalitis in immunocompromised patients and highlights infection causes may not be evident without extensive laboratory investigation. Furthermore, we illustrate the utility of metagenomics to diagnose infection caused by a rare or unexpected organism that is not routinely tested for in clinical laboratories. All but one of the previously reported cases of fatal disease caused by APMV-1 were detected by metagenomics [17,19–21]. Until recently APMV-1 was considered a significant pathogen in avian species but in humans was associated primarily with mild disease linked with occupational exposure [4] therefore this methodology has facilitated recognition of the pathogenic potential of APMV-1 in immunosuppressed patients without occupational exposure risks.

CRedit authorship contribution statement

Ian H. Brown: Writing – review & editing, Formal analysis. **Alejandro Núñez:** Writing – review & editing, Formal analysis. **Joe James:** Writing – review & editing, Formal analysis, Data curation. **Alexander M.P. Byrne:** Writing – review & editing, Formal analysis, Data curation. **Jayne Cooper:** Writing – review & editing, Formal analysis. **Scott M Reid:** Writing – review & editing, Formal analysis, Data curation. **Ashirwad Merve:** Writing – review & editing, Investigation. **Judy Breuer:** Writing – review & editing, Investigation, Formal analysis, Data curation. **Austen Worth:** Writing – review & editing, Investigation. **Ashley C. Banyard:** Writing – review & editing, Investigation, Formal analysis, Data curation. **Craig S Ross:** Writing – review & editing, Investigation, Formal analysis, Data curation. **Fabian ZX Lean:** Writing – review & editing, Formal analysis, Data curation. **Brown Julianne Rose:** Writing – review & editing, Writing – original draft, Validation, Methodology, Investigation, Formal analysis, Conceptualization. **Yael Hacohen:** Writing – review & editing, Investigation. **Nathaniel Storey:** Writing – review & editing, Investigation, Formal analysis, Data curation. **Kshitij Mankad:** Writing – review & editing, Investigation. **Kimberly Gilmour:** Writing – review & editing, Investigation. **Laura Atkinson:** Writing – review & editing, Investigation, Formal analysis. **Hiba M Shendi:** Writing – review & editing, Investigation, Conceptualization. **Marios Kaliakatsos:** Writing – review & editing, Investigation. **Maaie Kusters:** Writing – review & editing, Investigation. **Alasdair Bamford:** Writing – review & editing, Investigation. **Alexander Lennon:** Writing – review & editing, Investigation. **James Hatcher:** Writing – review & editing, Investigation, Data curation. **Reem Elfeky:** Writing – review & editing, Investigation.

Consent

Written informed consent was obtained from the patient's family for publication of this case report and accompanying images. A copy of the written consent is available for review by the Editor-in-Chief of this journal on request

Ethical approval

Not applicable

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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.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at [doi:10.1016/j.idcr.2026.e02555](https://doi.org/10.1016/j.idcr.2026.e02555).

Data availability

Viral genome consensus sequence is available on Genbank (Genbank PX463213).

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