ORIGINAL ARTICLE

Potential viral pathogenic mechanism for new variant inflammatory bowel disease

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Aims: A new form of inflammatory bowel disease (ileocolonic lymphonodular hyperplasia) has been described in a cohort of children with developmental disorder. This study investigates the presence of persistent measles virus in the intestinal tissue of these patients (new variant inflammatory bowel disease) and a series of controls by molecular analysis.

Methods: Formalin fixed, paraffin wax embedded and fresh frozen biopsies from the terminal ileum were examined from affected children and histological normal controls. The measles virus Fusion (F) and Haemagglutinin (H) genes were detected by TaqMan reverse transcription polymerase chain reaction (RT-PCR) and the Nucleocapsid (N) gene by RT in situ PCR. Localisation of the mRNA signal was performed using a specific follicular dendritic cell antibody.

Results: Seventy five of 91 patients with a histologically confirmed diagnosis of ileal lymphonodular hyperplasia and enterocolitis were positive for measles virus in their intestinal tissue compared with five of 70 control patients. Measles virus was identified within the follicular dendritic cells and some lymphocytes in foci of reactive follicular hyperplasia. The copy number of measles virus ranged from one to 300 000 copies/ng total RNA.

Conclusions: The data confirm an association between the presence of measles virus and gut pathology in children with developmental disorder.

An apparently new form of immune mediated inflammatory bowel disease in a cohort of children with developmental disorder has been described.[1] The intestinal pathology includes ileocolonic lymphonodular hyperplasia and non-specific colitis, which manifests as neither Crohn's disease nor ulcerative colitis. The histological and clinical aspects of this new disorder have been reported previously.[2] It has been postulated that reactive follicular hyperplasia in ileal tissue biopsies of affected children may reflect the persistence of viral antigen at this site.[2] Preliminary immunohistochemical data suggested the presence of measles virus (MV) antigen in the extracellular matrix of the midgut mucosal lymphoid tissue in affected children.[2]

MV belongs to the family of single stranded paramyxoviruses. It is the causative agent for several diseases including subacute sclerosing panencephalitis (SSPE) and measles inclusion body encephalitis.[3] Measles ranked as one of the leading causes of childhood mortality in the late 20th century.[4] In developing countries, 1 million deaths each year are related to MV infections.

> "Measles virus is the causative agent for several diseases including subacute sclerosing panencephalitis and measles inclusion body encephalitis"

Our study examines a possible association between MV and the above condition. To achieve this aim, several molecular biological techniques have been used to identify, localise, and measure MV from terminal ileum biopsies in children with ileocolonic lymphonodular hyperplasia and developmental disorder.

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MATERIALS AND METHODS
Patients and RNA extraction
All patient samples were provided by the department of gastroenterology, Royal Free Hospital, London, UK. Ileal lymphoid tissues from 91 affected children were examined (median age, 7 years; range, 3–14; 77 boys). Developmentally normal paediatric controls (n = 70; range, 0–17 years; 47 boys) included: 19 children with normal ileal biopsies, 13 children with mild non-specific chronic inflammatory changes, three children with ileal lymphonodular hyperplasia (LNH) investigated for abdominal pain, eight children with Crohn's disease, one child with ulcerative colitis, and 26 children who had undergone appendicectomy for abdominal pain including appendicitis.

MV positive control material included two cases of SSPE and MV infected Vero cells. Negative control material included uninfected Vero cells, and human tissues, control RNA extracted from Raji cells (Applied Biosystems, Foster City, California, USA) and normal peripheral blood mononuclear cells.

Total RNA was extracted from fresh frozen biopsies, peripheral blood mononuclear cells, and MV infected and uninfected Vero cell lines using the Ultraspec-11 RNA isolation system (Biotecx Laboratories, Houston, Texas, USA). Total RNA was extracted from formalin fixed, paraffin wax embedded tissues using the Purescript® RNA isolation kit (Gentra Systems, Minneapolis, Minnesota, USA).

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Table 1 Measles virus primer and probe sequences

Primer/Probe	Sequence 5′–3′	Amplicon size
N1 forward	5′ TCA GTA GAG CGG TTG GAC CC 3′	
N1 reverse	5′ GGC CCG GTT TCT CTG TAG CT 3′	150 bp
N2 forward	5′ GAG TCG AGG AGA AGC CAG GG 3′	
N2 reverse	5′ GCT GGA CTC CGA TGC AGT GT 3′	120 bp
H1 forward	5′ TTC ATC GGG CAG CCA TCT AC 3′	
H1 reverse	5′ CTC TGA GGT GTC CTC AGG CC 3′	150 bp
H2 forward	5′ TGG GCA CCA TTG AAG GAT AA 3′	
H2 reverse	5′ AAC CGT GTG TGA TCA ATG GC 3′	120 bp
F1 forward	5′ TGA CTC GTT CCA GCC ATC AA 3′	
F1 reverse	5′ TGG GTC ATT GCA TTA AGT GCA 3′	150 bp
F2 forward	5′ CCC ACC GGT CAA ATC CAT T 3′	
F2 reverse	5′ CCC TCG TGC AGT TAT TGA GGA 3′	150 bp
GAPDH 1	5′ GAA GGT GAA GGT CGG AGT 3′	
GAPDH 2	5′ GAA GAT GGT GAT GGG ATT TC 3′	226 bp
N1 probe	5′ CAA ACA GAG TCG AGG AGA AGC CAG GGA 3′	
H1 probe	5′ CCG CAG AGA TCC ATA AAA GCC TCA GCA C 3′	
F1 probe	5′ CTG CAC GAG GGT AGA GAT CGC AGA ATA CAG 3′	
GAPDH probe	5′ CCG ACT CTT GCC CTT CGA AC 3′	

Measles virus N gene primers and probes were designed based on the following Genbank sequence entries (accession numbers): X16565, S58435, NC_002494, NC_002496, X01999, U03661, U03658, and U03656. Measles virus H gene primers and probes were designed based on the following GenBank sequence entries: X16565, U03649, U03654, U03669, U03660, U03671, U03667, Z80793, AF045204, Z66517, and Z80816. Measles virus F-gene primers and probes were designed based on the following Genbank sequence entries: X16565, U03655, U03666, U03648, U03662, U08146, U03657, U03651, U03659, AJ133108, X16567.

Solution phase RT-PCR

Polymerase chain reaction (PCR) primers and probes to conserved regions of the MV Nucleocapsid (N), Haemagglutinin (H), and Fusion (F) genes were designed using Primer Express Software Version 1.5 (ABI Prism; Applied Biosystems). The specificity of selected sequences was checked using the NCBI Blast program (www.ncbi.nml.nih.gov/blast). Table 1 shows the MV primer and probe sequences, amplicon sizes, and GenBank accession numbers used for designing PCR primers and oligonucleotide probes. In some instances primer sets overlap with each other (for example, the sequence of amplicon N1 overlaps partially with the N2 PCR amplicon).

For in situ PCR, oligonucleotide probes were modified at the 5′ end by the addition of a biotin moiety and for Southern blot analysis probes were labelled at the 3′ end with digoxygenin. For TaqMan quantitative reverse transcription PCR (RT-PCR), probes were dual labelled with the fluorescent molecule FAM at the 5′ end and the quencher TAMRA at the 3′ end.

Purified MV RNA (Hu2) was used as a positive control to optimise PCR assays. The following optimal reaction conditions were used for each 25 µl reaction: 0.4mM dNTPs, 0.4µM forward and reverse primers, 2.5mM magnesium acetate, 5 U rTth DNA polymerase, 0.01 U AmpErase, and 1× EZ buffer. The EZ buffer consisted of 50mM bicine, 125mM potassium acetate, 40% (wt/vol) glycerol (pH 8.2) (Applied Biosystems); 50 ng of extracted RNA was used for each reaction. The following RT-PCR thermal cycling conditions were used on a 9700 PCR thermocycler (Applied Biosystems): 50°C for two minutes, 58°C for 30 minutes, 95°C for five minutes, then 40 cycles of 94°C for 20 seconds, 59°C for 20 seconds, and 72°C for 20 seconds, followed by an extension step at 72°C for 10 minutes.

Southern blot analysis

To confirm reaction specificity, solution phase RT-PCR was performed, as described above, on four affected children positive for MV by TaqMan RT-PCR (see below). MV F and H gene amplicons from MV infected Vero cells, SSPE brain, and ileal lymphoid tissues from four affected children, together with a no template control, were examined by Southern blotting[5] using sequence specific probes (table 1). MV specific oligonucleotide probes were labelled at the 3′ end with digoxigenin using a DIG oligonucleotide 3′ end labelling kit (Roche Molecular Biochemicals, Mannheim, Germany), hybridised to the Southern blot at
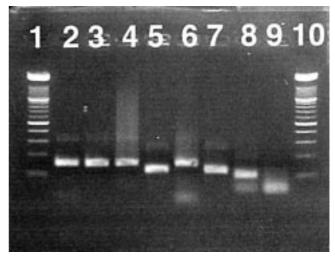

Figure 1 Gel electrophoresis of measles virus cDNA amplicons (HU2 control measles virus RNA) amplified under optimised reaction conditions. Lanes 1 and 10, 100 base pair DNA ladder (Gibco-BRL, Paisley, Scotland, UK). Lanes 2 and 3, Fusion (F) gene cDNA amplicons for two different F gene primer sets. Lanes 4 and 5, Nucleocapsid (N) gene cDNA amplicons for two different N gene primer sets. Lanes 6 and 7, Haemagglutinin (H) gene cDNA amplicons for two different H gene primer sets. Lane 8, positive control human pyruvate dehydrogenase PCR product. Lane 9, no template control for lane 2.

50°C in 5× saline sodium citrate (SSC) with 0.2% sodium dodecyl sulfate for one hour, washed once in 5× SSC at 50°C for 10 minutes, once in 2× SCC at room temperature for 10 minutes, and once in 0.2× SCC at room temperature for 10 minutes. Hybrids were detected using the DIG luminescent detection kit (Roche Molecular Biochemicals).

TaqMan RT-PCR

Real time quantitative RT-PCR based on the 5′ nuclease assay was performed on an ABI 7700 Sequence detector (Applied Biosystems).[6][7] Sequence specific PCR primers and TaqMan probes were designed using Primer Express software as described above. All quantitative PCRs were prepared in a dedicated facility in a class 2 laminar flow benchhood using dedicated pipettors and aerosol resistant pipette tips. Template
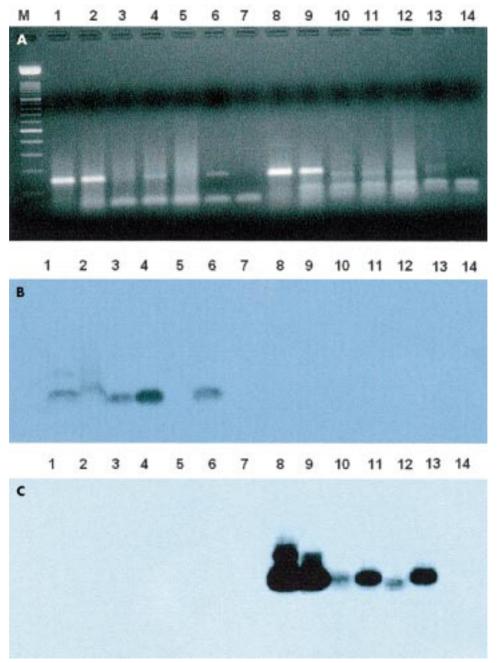
Figure 2 (A) Agarose gel electrophoresis of measles virus Fusion (F) gene and haemagglutinin (H) gene reverse transcription polymerase chain reaction (RT-PCR) amplicons generated using RNA extracted from fresh frozen terminal ileum biopsies from affected children and subacute sclerosing panencephalitis (SSPE) brain tissue and measles infected Vero cells. M denotes 100 base pair molecular weight marker; lanes 1–6 show F gene PCR amplicons from the following RNA samples: measles infected Vero cells, SSPE brain, affected children 1–4, respectively; lane 7, no template control. Lanes 8–14 show H gene PCR amplicons generated from RNA samples in the same order as above. For one sample, RT-PCR for the F gene failed (lane 5). (B) Southern blot of the agarose gel described in (A) probed with a digoxigenin (DIG) labelled F gene specific probe as described in materials and methods. (C) Southern blot of the agarose gel described in (A) stripped and reprobed with a DIG labelled H gene specific probe.

RNA was prepared and added to the PCR mastermix in a separate facility.

TaqMan RT-PCR was performed using EZ TaqMan RT PCR reagents according to the manufacturer's instructions (Applied Biosystems). RT-PCR reactions were performed in duplicate under the following conditions for each 25 µl reaction: 1× EZ buffer, 3mM MnOAc$_2$, 200 nmol of each primer, 100 nmol of TaqMan probe, 0.01 U of AmpErase, 0.1 U of rTth polymerase, and 3 µl (5–50 ng) of total RNA. The thermal cycling conditions on the 7700 were as follows: 50°C for two minutes, 58°C for 30 minutes, 95°C for five minutes, followed by 40 cycles of 94°C for 20 seconds and 60°C for one minute.

Controls for TaqMan RT-PCR included the following: no template control (water added as template), no amplification control (omission of rTth polymerase), irrelevant target primers and specific TaqMan probe (human papillomavirus 16, human herpes virus 8 primers), probe only control (omit PCR primers), human RNA control, spiked RNA control, and asymmetric TaqMan PCR (TaqMan PCR with one or other primer and specific TaqMan probe).

A gene dosage correction was carried out using glyceraldehyde phosphate dehydrogenase as a housekeeping gene. Measles virus quantitative TaqMan RT-PCR was performed by generating standard curves for the F and H genes. Taqman RT-PCR standards were generated by cloning the F and H gene specific PCR products into a vector using the TOPO TA cloning® system (Invitrogen, Gronigen, the Netherlands), according to the manufacturer's instructions. Plasmids containing the PCR

Table 2 Summary of TaqMan RT-PCR and RT in situ PCR results

	TaqMan RT-PCR positive	In situ PCR positive
Affected patients	70 (91)	42 (57)
Controls		
Normal controls	0 (19)	1 (5)
Mild non-specific changes	0 (13)	NT
Lymphonular hyperplasia	0 (3)	NT
Appendicectomies	4 (26)	NT
Ulcerative colitis	0 (1)	NT
Crohn's disease	0 (8)	NT

Total number of patients tested in parentheses.
NT not tested; RT-PCR, reverse transcription polymerase chain reaction.

inserts were then in vitro transcbed into cRNA using the Riboprobe®ription system (Promega, Madison, Wisconsin, USA). Serial dilutions of this cRNA were used to generate standard curves.

RT in situ PCR

RT in situ PCR facilitates low copy gene detection and permits cellular localisation within tissues, with a reported sensitivity of one viral genome copy/cell.[8–10] Sections were dewaxed in xylene and taken through a series of graded alcohols. Endogenous avidin and biotin activity was blocked using the Dako biotin blocking system (Dako, Glostrup, Denmark). Sections were digested with proteinase K (300 µg/ml) for 17 minutes at 37°C.

After pretreatment, MV RNA was amplified using the following protocol: 58°C for 45 minutes and 94°C for five minutes, followed by 25 cycles of 94°C for 45 seconds, 60°C for 45 seconds, and 72°C for 45 seconds. After amplification, sections were fixed in 100% ethanol and air dried.

Hybridisation was carried out with a 5′ biotinylated oligonucleotide probe using previously published protocols.[8] Hybrid detection was achieved using a three step immunocytochemical method[11] or dinitrophenol tyramide signal amplification.[12] Alkaline phosphatase was detected with nitrobluetetrazolium (NBT) and bromochloroindoylphosphate (BCIP) as chromogen. Endogenous alkaline phosphatase was blocked using levamisole, an endogenous AP inhibitor (Dako), during chromogenic detection.

Reaction optimisation experiments were initially carried out using formalin fixed, paraffin wax embedded, measles infected Vero cells, and a variety of probe concentrations (1 µg/ml, 1.5 µg/ml, 2 µg/ml). A concentration of 1 µg/ml yielded optimal signals and was used in subsequent experiments. Biopsies from 73 affected children and five normal controls were examined.

Controls for RT in situ PCR included the following: MV infected and uninfected Vero cells, a mixed population of infected and uninfected Vero cells, MV N gene primers and an irrelevant probe (nonsense pyruvate dehydrogenase probe), and irrelevant primers and N gene specific probe. Hybridisation control experiments were performed using a histone mRNA probe. Other control experiments included RNase digestion of MV infected Vero cells before RT in situ PCR.

Combined RT in situ PCR and immunohistochemistry

To examine MV signal localisation, RT in situ PCR for the MV N gene was performed as described above on tissue sections following immunohistochemistry using the follicular dendritic cell CNA 42 monoclonal antibody[13] (Dako). For in situ hybridisation a 5′ biotin labelled oligonucleotide probe was used as above.

The MV hybridisation signal was developed with horseradish peroxidase and aminoethyl carbazole (AEC; Vector Laboratories, Burlingame, California, USA), and the dendritic cell signal was developed using a three step detection method with AP (Dako) and NBT and BCIP (Roche Molecular Biochemicals) as substrate.

Ethical approval

Approval for these studies was obtained from the ethical practices committee of the Royal Free, Hampstead, NHS Trust. Fully informed, written parental consent was obtained from all trust patients including controls.

RESULTS

Overall, 75 of 91 affected children had MV RNA in their ileal lymphoid tissue compared with five of 70 in the control patient cohort (Fisher exact test, $p < 0.0001$; Analyse-it Software, General 1.62).

A total of six different PCR primer sets were optimised by solution phase RT-PCR to amplify the MV F, H, and N genes from RNA extracted from MV infected Vero cells (fig 1).

The specificity of the primer/probe sets to detect MV F and H genes was established using RNA extracted from: (1) cryopreserved ileal biopsy material from four affected children, (2) SSPE brain, and (3) MV infected Vero cells (fig 2A). All four patient samples were positive for MV F and H genes by TaqMan RT-PCR. Amplicon specificity was confirmed by Southern blot analysis using F and H gene specific probes (fig 2B,C). No template controls run in parallel were negative.

Seventy of 91 affected children were positive for MV compared with four of 70 controls as analysed by TaqMan RT-PCR (table 2). MV copy number in positive biopsies was generally low, but ranged from 1 to 3×10^5 copies of MV/ng of total RNA. Of the paediatric control group, MV was not detected in normal children or children with isolated ileal LNH. However, four of 26 appendicectomy samples harboured the MV genome (table 2).

Figure 3 Reverse transcription (RT) in situ polymerase chain reaction (PCR) experiment using a single stranded biotinylated oligonucleotide probe for the detection of the measles virus Nucleocapsid (N) gene in infected Vero cells. Optimal cytoplasmic staining is achieved in (A) (1 µg/ml), higher probe concentrations in panels (B) (1.5 µg/ml) and (C) (2 µg/ml) showed increasing non-specific nuclear staining.
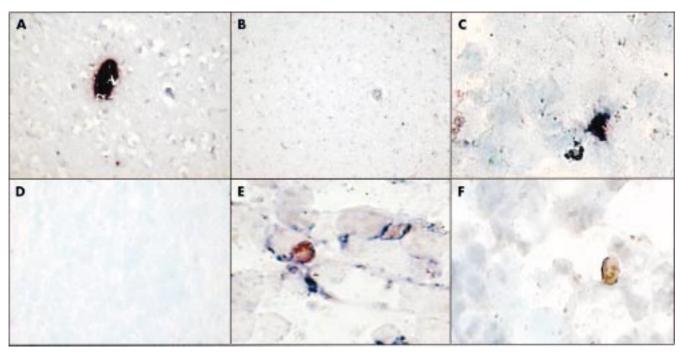
Figure 4 (A) Reverse transcription (RT) in situ polymerase chain reaction (PCR) combined with in situ hybridisation for measles virus (MV) Nucleocapsid (N) gene detection in subacute sclerosing panencephalitis brain tissue showing intense, discrete black signals within the brain parenchyma. (B) Negative control section of (A) treated identically but using irrelevant PCR primers; no MV signal was seen (original magnification, ×400). (C) MV N gene RT in situ PCR combined with in situ hybridisation in a reactive ileal lymphoid follicle centre from an affected child. A positive signal radiates from an intense central core in an apparently beaded, fibrillary pattern (original magnification, ×1000). (D) RT in situ PCR on a serial section of (C) constituting a negative control (irrelevant PCR primers) (original magnification, ×1000). (E) Combined RT in situ PCR for the MV N gene and immunohistochemistry with monoclonal antibody CNA 42, a follicular dendritic cell marker. A single cell is shown, present in a reactive follicle centre from an affected child. Once again, the MV genomic signal (red) appears to exhibit a central pattern that would be consistent with the cell body, whereas CNA 42 (blue/black) delineates dendritic processes radiating from the cell body (enlarged from original magnification of ×1000). (F) RT in situ PCR shows a single mature lymphocyte infected with MV RNA in a hyperplastic area.
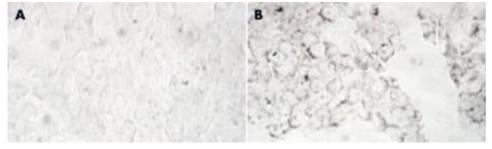

Figure 5 Reverse transcription (RT) in situ polymerase chain reaction (PCR) control experiment for measles virus (MV) Nucleocapsid (N) gene on MV infected Vero cells (A) with and (B) without an RNase digestion step. (A) No signal was seen when RNase digestion was performed before in situ RT-PCR. (B) Shows a cytoplasmic signal in the absence of an RNase digestion step.

RT in situ PCR optimisation experiments were performed as described (fig 3). A probe concentration of 1 µg/ml yielded optimal signals and was used in subsequent experiments.

In MV infected Vero cells, MV amplicons were identified as a cytoplasmic signal (fig 3). In SSPE brain material, discrete, intense foci of MV amplicons were detected in grey matter using RT in situ PCR (fig 4A). Signal was not detected in similarly processed normal brain, or when irrelevant PCR primers were used on sections of SSPE brain (fig 4B).

Of the 57 tissue biopsies from affected children, 42 were positive for the MV N gene by RT in situ PCR and amplicons could be detected in serial sections of ileal biopsies. Four samples were inconclusive for the presence of MV because of high background staining, and 11 biopsies were negative for MV. Of the control group, one of five children with histologically normal small and large bowel mucosa had detectable MV N gene RNA, present in a distribution that was identical to that seen in biopsies from affected children (table 2). MV amplicon localised to reactive follicle centres, and was associated with cells possessing dendritic processes (fig 4C,E) and some lym-

phocytes (fig 4F). No MV signal was seen in serial control sections where irrelevant PCR primers were used (fig 4D). Additional RT in situ PCR control experiments were performed on measles infected Vero cells. No signal was obtained on MV infected Vero cells after RNase digestion (fig 5).

Overall, 91 biopsies have been examined, 56 of which were analysed by a combination of in cell RT-PCR (MV N gene) and TaqMan RT-PCR. Thirty seven of these biopsies were positive for MV and five were negative for MV using both techniques, six were positive by TaqMan RT-PCR but negative by in situ PCR, and five were positive by in situ PCR only (table 2).

DISCUSSION

We describe an association between persistent MV infection and ileocolonic lymphonodular hyperplasia and ileocolitis in children with developmental disorder.[1] The molecular data indicate the presence of MV genomes in 75 of 91 affected children with the disorder compared with five of 70 control children. In addition, there appears to be a strong segregation of

the disease phenotype with male children, in keeping with the reported male predominance of the developmental disorder.

MV localisation was demonstrated in tissue biopsies by RT in situ PCR and combined immunohistochemistry. The signal had a fibrillary character, and appeared to associate with the dendritic cell matrix confirmed by immunohistochemical staining using a specific CNA 42 antibody (fig 4E).

MV was predominantly detected in dendritic cells in reactive follicular hyperplastic centres in ileal biopsies from affected children (fig 4C,E), but was also identified in mature lymphocytes in these hyperplastic areas (fig 4F). This result indicates a possible interaction between MV and the immune response in the pathogenesis of ileocolitis in these children. MV may be a potential "immunological trigger" in the pathogenesis of lymphoid hyperplasia and ileocolitis. Potential initiators for this type of immunological response are dendritic cells. Dendritic cells capture and process viral antigens in the periphery, express costimulatory molecules, and serve as vehicles for viral antigens to the mediators of immunity (B and T cells) in lymphoid tissue. As a result, cytokines are released and initiate an immune response.[14]

MV localisation in follicular dendritic cells mirrors the human immunodeficiency virus type 1 (HIV-1) infection patterns seen in HIV-1 enteropathy. The presence of MV antigen in follicular dendritic cells may reflect a transient stage in the progression from latent to persistent MV infection.[15–17] The hypothetical parallel with HIV infection is interesting: HIV, like measles virus, potentially disrupts cellular immunity, and induces follicular hyperplasia and lymphadenopathy in the early stage of infection. This is associated with expansion of the follicular dendritic cell network and trapping of HIV within germinal centres.[15–17] During the early latent phase of infection, HIV antigens are detectable upon the surface of follicular dendritic cells[15] in a pattern similar to that reported here for MV. Such a location may favour the induction of immunological tolerance and failure of viral clearance. The mechanisms by which MV, immunological abnormalities, and chronic intestinal pathology may be linked are currently not known. Precedents for delayed intestinal and immunological sequelae to MV exposure include chronic immunodeficiency, diarrhoeal disease, and death following early natural measles exposure.[18] Natural measles infection induces an initial T helper cell type 1 (Th1) response and protective cytotoxic immunity (characterised by the classic measles rash and gastrointestinal upset), followed by a prolonged Th2 response with antibody production.[19] In most individuals, this leads to lifelong immunity without delayed pathological sequelae. Nonetheless, immune activation during the measles attack is set against a profound reduction in non-specific cellular immune responsiveness, reflecting the potent immunosuppressive properties of MV. Recent studies suggest that this may be achieved through impaired interleukin 12 (IL-12) production by infected dendritic cells,[20] and blocking of IL-2 receptor α expression by activated T cells.[21] In such circumstances, impaired Th1 immunity, with a shift towards a dominant Th2 response, might occasionally contribute not only to establishing persistent infection, but also to delayed immunopathology.

> "Measles virus may be a potential immunological trigger in the pathogenesis of lymphoid hyperplasia and ileocolitis"

MV was not detected in three children with isolated LNH or in biopsies from normal children. Of the 26 children who underwent apendicectomy, only four harboured MV RNA. The presence of measles virus in the intestine of a small minority of apparently healthy children is not surprising in light of the finding of Warthin-Finkeldy giant cells in inflamed appendices in children with measles infection. However, the prevalence of persistent MV infection in the general population is not known and warrants further investigation.

Take home messages

- Of 91 patients with a histologically confirmed diagnosis of ileal lymphonodular hyperplasia and enterocolitis, 75 were positive for measles virus in their intestinal tissue compared with five of 70 controls
- Measles virus was found within the follicular dendritic cells and some lymphocytes in foci of reactive follicular hyperplasia
- These data confirm an association between the presence of measles virus and gut pathology in children with developmental disorder

These preliminary studies have focused principally on MV. We have not excluded the presence of alternative infections. Viruses may persist elsewhere, or exert a transient effect not requiring subsequent persistence. One such transient risk may be that concurrent exposure to measles and another infection may increase the risk of MV establishing persistent infection: this atypical pattern of exposure has been identified as a risk factor for both SSPE (chicken pox and encephalitogenic enterovirus).[22 23]

Our study raises many questions—most importantly, does MV play an aetiological role in intestinal inflammation in developmental disorder? The study reports for the first time an association between MV infection and ileocolonic lymphonodular hyperplasia and ileocolitis in children with developmental disorder.

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