

**ID:** 1603

**Primary Contact:**

Qandeel Sadiq, Mayo Clinic  
Rochester, United States

**All Authors:**

Qandeel Sadiq, Mayo Clinic (**Primary Presenter**)  
Bohdana Fedyshyn, Mayo Clinic  
David Danko, Biotia  
Niamh O'Hara, Biotia  
Dorottya Nagy-Szakal, Biotia  
Elizabeth Ann L Enninga, Mayo Clinic  
Andrew Norgan, Mayo Clinic

**Is this abstract original material?:**

Yes

**Has this abstract been previously published?:**

No

**Has this abstract been accepted for publication or presentation at another meeting before March 11, 2023?:**

No

**Are you planning to submit a manuscript based off your abstract to any of the following journals prior to March 11, 2023?:**

NA

**Eligibility Attestation:**

Agree

**IRB Approval:**

Affirm

**Applicant Type:**

Fellow

**Category Preference:**

Infectious Disease Pathology

**Presentation Tag:**

Infectious Disease

**Presentation Choice:**

Either Poster or Platform

**Platform Attestation:**

I agree

**Title:**

Investigation into the Potential Role of Cryptic Viral Infection in Villitis of Unknown Etiology Using Pan-Viral Metagenomic Sequencing

**Background:**

Chronic villitis (CV) is characterized by the presence of lymphocytes, histiocytes or rarely plasma cells within villous stroma. Infectious causes of CV account for approximately 5% of cases; for the remainder (approximately 95%), pathogenesis is unclear. Chronic villitis of unknown etiology (VUE) is associated with adverse fetal outcomes, including intrauterine growth restriction and fetal demise. Aberrant maternal immune responses have been implicated as a cause of VUE, but undetected causative or precipitating infections have been difficult to exclude. Herein, we performed pan-viral sequencing of placentas with infectious villitis and VUE to potentially detect the presence of undetected viruses in cases of VUE.

**Design:**

CV and control cases from the period 2013-2021 were selected for evaluation, including infectious villitis due to CMV (n=4), VUE (n=31), non-CV pathology accessioned controls (n=5). All cases were re-reviewed by a single pathologist and gestational data, morphologic findings, and immunohistochemical (IHC) and special stain results were abstracted. Metagenomic sequencing using a panviral capture panel was then performed on all cases.

**Results:**

Of the 31 VUE cases, all were classified as high grade, while 2 of 4 CMV villitis cases showed only low grade villitis. Cytomegalovirus (and additional pathogen) staining was negative for all 31 VUE cases, while CMV was detected in the 4 infectious villitis cases. Panviral sequencing and metagenomic analysis detected CMV reads in all CMV villitis cases, ranging from 166734 to 6339077 reads (0.37% to 18.62% of total reads, respectively). By contrast, clinically significant viral reads of similar fractional abundance were not detected in any of the 31 VUE samples or 5 non-CV control cases.

**Conclusion:**

This work helps to exclude the possibility of cryptic viral infection as a direct cause of morphologic VUE. However, the possibility that VUE results from a transient infectious is not directly addressed and remains to be explored in future studies. In addition, the utility of panviral sequencing for detection of viruses in formalin-fixed paraffin embedded tissue is established, with implications for clinical detection of viral pathogens within the placenta (and other tissues).

**Stowell-Orbison Award:**

No