The Dried Umbilical Cord is a Tenable Sample for CMV Diagnosis by Real-Time PCR

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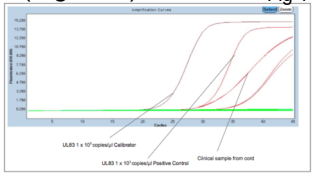
Background: Congenital cytomegalovirus (cCMV) is the most common infectious disease resulting in disabilities in children. Universal cCMV screening of all newborns is increasingly being considered, but for older children retrospective diagnosis of congenital infection requires analysis of archived, stored samples from the neonatal period. Some families save the dried newborn umbilical cord as a "memento". We were interested in determining if such a sample was a useful substrate for cCMV diagnosis.

Methodology: An umbilical cord was available from an infant with cCMV identified in a universal screening study. DNA was extracted from 0.045 grams of tissue using the Qiagen DNeasy Blood and Tissue Kit. Quantitative PCR was compared using primers to the CMV UL83 gene. In addition, glycoprotein B (gB) genotyping was performed on both the urine and umbilical cord samples.

Results:
Umbilical cord was positive for CMV DNA with a viral load of 3.15E+04 copies/µg (Figure 1).

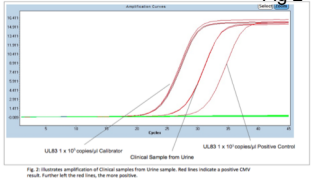
Fig 1



Umbilical Cord Sample

Fig. 1: Illustrates amplification of Clinical samples from Umbilical Cord. Red lines indicate a positive CMV result. Further left the red lines, the more positive.

Fig 2



Urine Sample

Fig. 2: Illustrates amplification of Clinical samples from Urine sample. Red lines indicate a positive CMV result. Further left the red lines, the more positive.

Multiplex gB genotyping identified both the cord and urine samples as encoding gB clade 1 (gB1) (Figure 3).

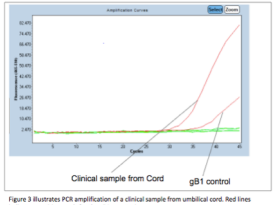
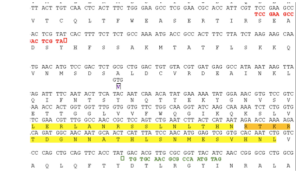


Figure 3 Illustrates PCR amplification of a clinical sample from umbilical cord. Red lines indicate a positive result for the gB1 genotyping assay

Fig 3



Conclusion 1: Umbilical cord tissue can be used to identify cCMV infection by PCR. This may have implications for infants who live in states in the USA where blood spots are destroyed shortly after birth, if the family has saved the cord sample. In addition, we show that real-time PCR can identify the CMV gB genotype.

Conclusion 2:
Since the leading CMV vaccine candidate is based on the gB protein, identifying genotypes can be valuable in future vaccine studies by gauging breakthrough infections based on variant strains that don't "match" the vaccine strain variant.

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