P0408 Prevalence and Genotypic Distribution of Cytomegalovirus in Taiwanese Childbearing Mother and Newborn

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Introduction and Purpose

Cytomegalovirus (CMV) can result in a congenitally transmitted infection, affecting approximately 0.3 to 6.1% of neonates worldwide. Congenital CMV infection is one of the leading infectious causes of sensorineuronal hearing loss and is related to neurodevelopmental disability. There was limited information addressing the genotypic diversity and update prevalence of congenital CMV infection on both mother and newborn sides. This study was set to (1) prospectively screen both maternal blood at delivery and umbilical cord blood for CMV by real time quantitative polymerase chain reaction (PCR), and (2) to determine the genotypic distribution.

Materials and Methods

A cross-section prospective screening study was conducted at Chang Bing Show Chwan Memorial hospital, a community based hospital in central Taiwan, between June 29, 2012 and July 1, 2015. The residual maternal and umbilical cord blood samples at delivery were collected after obtaining the inform consent. The DNA was extracted by using Roche MagNA Pure LC 2.0 System according to the manufacturer's instructions. A fixed amount of 70 to 100ng DNA was tested for CMV using an in-house Taqman based quantitative real time PCR assay developed by Taipei Veterans General Hospital. Genotypes of UL55, UL144 and US 28 were determined by sequencing of the PCR-amplified fragments.

The sample processing flow and the primers used in this study were shown in Figure 1 and 2

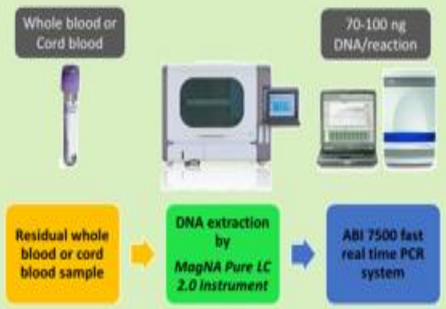


Fig. 1

Fig. 2

Results

1. Demographic characters and positive rate of CMV

A total of 1464 mothers were enrolled during the study period. The mean age of case mother was 30.1± 4.5 year-old. Of them, 95.3% was Taiwanese and 47.1% was the first parity and 39.6% was the second parity. CMV PCR was positive in 5.6% (82/1464) of maternal blood samples. On the other hand, 1324 umbilical cord blood samples were obtained. Of them, 88.6% was derived from full term baby and the mean birth body weight was 3,048± 446.4gm (range: 865 to 4535gm). CMV PCR was positive in 5.3% (70/1324).

Mother (N=1464)			Baby (N=1324)		
Age(Year)	30.1± 4.5	(16-45)	Birth weight(gm)	3045.8 ±446.4	(865-4535)
Cesarean section	553	37.8%	Head circumstance (cm)	33.6± 1.6	(24.0-39.0)
Taiwanese	1395	95.3%			
Parity			Birth age (weeks)		
1	689	47.1%	> 37	1173	88.6%
2	580	39.6%	36- ≦37	72	5.4%
3	166	11.3%	35- ≦36	33	2.5%
4	24	1.6%	34- ≦35	24	1.8%
5	5	0.3%	<34	22	1.7%

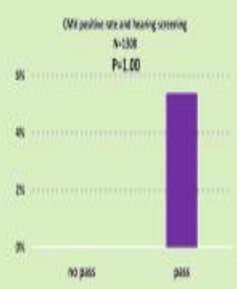
2. Genotype distribution

Most of newborns and mothers had identical virus genotypes (78.9%), which included UL55 gB2-UL144 A1-US28 A2 and UL55 gB1-UL144 C4-US 28 A1. The distribution of UL55 genotype was gB1 (16.7%), gB2 (73.8%) and gB5 (9.5%) in mother group and gB1 (21.9%), gB2 (73.2%) and gB5 (2.4%) in baby group. The distribution of UL144 genotype was A1 (62.5%), B4 (3.1%) and C4 (34.3%) in mother group and A1 (42.8%), B4 (9.5%) and C4 (47.6%) in baby group, respectively. The distribution of US28 genotype was A1 (16.9%) and A2 (83.1%) in mother group and A1 (14.9%) and A2 (85%) in baby group, respectively.

3. Association with newborn hearing screening test and gestational age and birth body weight

Universal newborn hearing screening in Taiwan is using AABR and the failure to pass rate was 3/1000

In present study, we failed to identify the significant association between the presence of CMV in newborn and the failure to pass hearing screening(p=1.00), the gestational age(p=0.28) and birth body weight(p=0.24), respectively.



Conclusions

Screening for CMV DNAemia with PCR can be easily incorporated into routine labor and delivery care using discarded cord blood specimen. The prevalence of CMV DNAemia amongst newborns and mothers was estimated as 5.3 to 5.6%. Two predominant genotypes UL55 gB2-UL144 A1-US28 A2 and UL55 gB1-UL-144 C4-US 28 A1 were identified in this study.

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