

Prevalence and Genotype Distribution of Cytomegalovirus in Taiwanese Childbearing Mother and Newborn

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Background/Objective

Cytomegalovirus (CMV) infection is the most common congenitally transmitted infection, affecting approximately 0.3 to 6.1% of neonates worldwide. There was little information on congenital CMV infection in Taiwan. This study was aimed to (1) prospectively screen both maternal blood at delivery and umbilical cord blood by utilizing real time CMV PCR and (2) determine the CMV UL55 and UL144 genotype distribution

Method

A prospective screening study was conducted at a community based hospital in central Taiwan, between June 29, 2012 and March 31, 2014. The residual maternal blood sample at delivery and umbilical cord blood were collected after obtaining the informed consent. A fixed amount of 100ng of extracted DNA was tested for CMV DNAemia using an in-house Taqman based quantitative real time PCR assay. Genotyping of UL55 and UL144 was performed by a sequencing analysis of PCR-amplified fragments.

Result

During the study period, a total of 1038 mothers were enrolled. The mean age of case mother was 29.3 years-old. CMV PCR was positive in 4.8% (50/1038) of maternal bloods. On the other hand, 980 umbilical cord blood samples were obtained. Of them, 89.2% was derived from full term baby and the mean birth body weight was 3,046.2 > 447.7gm (range: 865 to 4535gm). CMV PCR was positive in 3.5% (35/980). UL55 genotype was obtained successfully from 25 out of 50 CMV positive maternal samples and 22 out of 35 CMV positive baby samples, respectively. All of them was classified as UL55 genotype 2, which was 99% identical to GenBank M60931. The distribution of UL144 genotype was A1(95.5%) and B4(4.5%) in mother group and A1(81.8%) and B4(18.2%) in baby group, respectively.

Conclusion

The prevalence for babies with DNAemia was estimated as 3.5% but without symptoms. UL55 genotype 2 and UL144 A1 were the predominant genotypes in both groups in this study.