



Genetic mechanism associated with congenital cytomegalovirus infection and analysis of effects of the infection on pregnancy outcome

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ABSTRACT. We aimed to compare the diagnostic value of various detection methods for cytomegalovirus (CMV) infection, to investigate the genetic mechanism associated with CMV infection in pregnant women, and to analyze the risk of sequelae development in fetuses with CMV infection. A total of 300 participants who had the same immunosuppressive regimen and received preemptive therapy for CMV infection were prospectively enrolled in this study; they included 289 vaccine trial participants. The gB-absorbed CMV IgG assay was performed for each vaccine trial participant. The healthy women were divided into 2 groups, and amniotic fluids were collected from them at 15-18 weeks of gestation to test for CMV

seropositivity before conception by using IgM specific antibodies, CMV-DNA, and IgG analysis. In 104 cases, cord blood sera and urine specimens were also collected from the infants and examined. The sensitivity and specificity of immediate-early messenger RNA and pp67 (late) messenger RNA detection by the nucleic acid sequence-based amplification technique was comparable to those of virus isolation and PCR. Furthermore, an association between single nucleotide polymorphisms in the TLR-2 gene and congenital CMV infection was observed and confirmed. Moreover, CMV infection during early pregnancy has been shown to have a much more severe effect on the pregnancy outcome compared to infection during later stages of pregnancy.

Key words: Cytomegalovirus; Pregnancy; Gene diagnosis