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DIAGNOSTIC ALGORITHM AND PROGNOSIS OF CONGENITAL CYTOMEGALOVIRUS INFECTION

Daminov F. A.
DSc, Ass. Professor, Head of the Department of Clinical Laboratory Diagnosis with the Course of Clinical Laboratory Diagnostics of PGD

Djabbarova N. R.
Assistant of the Department of Clinical Laboratory Diagnosis with the Course of Clinical Laboratory Diagnostics of PGD

Isokova G. B.
Cadet of the Department of Clinical Laboratory Diagnosis with the Course of Clinical Laboratory Diagnostics of PGD; Samarkand State Medical University Samarkand, Uzbekistan

Abstract
The relevance of the problem of congenital viral infectious diseases is due to their wide prevalence, high frequency of latent and subclinical forms, as well as significant economic damage associated with the costs of diagnosis, treatment and rehabilitation [17,18,19,20].

Keywords: Pregnancy, cytomegalovirus infection, new strain, diagnosis, superinfection, laboratory diagnosis.

Introduction

Cytomegalovirus infection (CMVI) is the most common cause of congenital infectious diseases (CID) in the world. The frequency of congenital CMVI among newborns ranges from 0.6% to 6.1% and is more common than Down syndrome, fetal alcohol syndrome and spina bifida [1,2,3,4,5].

It is known that only 10-15% of children have clinically expressed forms of the disease [6,7]. The most common manifestations are low gestational weight, intrauterine developmental delay syndrome, thrombotic thrombocytopenic purpura, hepatitis, jaundice, meningoencephalitis, seizure syndrome, hydrocephalus and hypertension-liquor syndrome, chorioretinitis. A wide range of clinical manifestations of the disease is explained by the unique ability of the virus to infect virtually all cells of the body [8,9,10].

Despite the prevalence of subclinical forms of the disease, congenital CMVI can cause long-term adverse effects, such as sensorineural hearing loss, epilepsy, cerebral palsy, microcephaly, delayed motor and mental development. Adverse outcomes develop in 15% of cases in asymptomatic course and in 90% - in the manifest form of the disease [11,12,13].

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Unlike other infections included in the TORCH complex (rubella, toxoplasmosis), the presence of specific immunity to CMV in the mother does not prevent vertical transmission of the virus to the foetus. Recurrent CMV infection as a result of reactivation of latent virus or infection with a new strain can also lead to the development of manifest forms of HIV [19,20,21].

CMVI in pregnant women in most cases runs in a subclinical form or with non-specific manifestations of acute respiratory infection, which greatly complicates the diagnosis of HIV in the antenatal period. Only in isolated cases, detected abnormal ultrasound signs of fetal development may be a reason to test the mother for CMVI [22].

The question of the management of pregnant women with CMV infection, the timing and appropriateness of their examination and treatment remains debatable. Since 2019, in the Russian Federation, screening of pregnant women for CMV is not recommended, and if it is carried out at the initiative of the pregnant woman or the attending physician, it is mainly serological methods (ELISA), the predictive value of which is only 15-40%, and if pathological changes in fetal development are detected on ultrasound, the pregnant woman is referred only to a medical genetics centre (if available) to exclude chromosomal diseases [23,24,25].

The lack of data on CMV infection in the pregnant woman and polymorphism of the clinical picture in the newborn do not allow a reliable judgement about the specific etiological form of the disease in the early neonatal period until the results of laboratory examination are obtained. It is relevant to clarify the epidemiological situation of CMV infection among women of reproductive age, which will allow us to assess the feasibility of mandatory laboratory examination of pregnant women. From a practical point of view, it is necessary to develop an algorithm for comprehensive diagnosis of CMV infection in the antenatal period. In addition, when CMV infection is detected in a pregnant woman, it is important to identify factors that can predict the development of congenital CMV infection [2,3,4,5,6].

Despite the large number of domestic and foreign studies on CMV infection, there are still a large number of unresolved issues concerning the optimisation of antenatal and congenital CMV infection diagnosis. At the same time, timely verification of CMV infection in a pregnant woman is an integral part of preventing the development of unfavourable outcomes in the newborn. In the field of scientific research, there is increasing interest in studying the genetic variability of CMV genes in children with congenital CMV infection. The identification of certain genotypes and their association with different variants of the course of the disease will make it possible to revise diagnostic and therapeutic approaches to the management of pregnant women with CMV infection [1,7,8,9,10,11].

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