

# CMV infection of liver transplant recipients: comparison of antigenemia and molecular biology assays

## ABSTRACT

The current findings indicate that the use of antigenemia and pp67 mRNA assays is the most effective method for identifying patients with an increased risk of CMV disease.

## INTRODUCTION

The first report of CMV infection of liver transplant recipients was published in 1990. The discovery of CMV infection of liver transplant recipients has been attributed to the use of a non-specific antibody in the preparation of the transplanted organs. This discovery was of great interest to the medical literature. The cytomegalovirus, which belongs to the human herpesvirus family, causes a persistent infection that is typically well-controlled by the host immune system. However, patients with defective immunity, as recipients of SOT and bone marrow transplants, and those infected with HIV, still face significant clinical problems due to CMV infections. To address this, diagnostic methods must quickly and clearly identify emerging CVM biologic activity, preferably by discriminating between subclinical and symptomatic infection. During active infection, the spread of CMV in the blood is acknowledged as the primary cause of clinical disease, and viremia has been identified as a significant risk factor for the development of disease. Several studies have investigated the association between systemic CVM viral load and immunocompromised patients, with quantification of polymorphonuclear leucocytes expressing the CAV tegument pp65 protein using the antigenemia assay. We analyzed three methods for diagnosing CMV infection and identifying patients with high risk of CVM disease before the disease developed by analyzing quantitative pp65 antigenemia results (CMV Monitor) and qualitative mRNA assay (Nuclisens CMP CIVIL 10), which were obtained in a series of consecutive samples from 10 liver transplant recipients, without any prophylactic treatment.

## CONCLUSION

The ability of antigenemia to predict CMV disease risk in patients was not better than that of molecular biology methods. As a result, the limited number of available patients does not provide sufficient information for drawing definitive conclusions, and it seems unlikely that any other test will do as well.