

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

ABSTRACT

The present data, suggests that the concomitant use of antigenemia and pp67 mRNA assay gives the best identification of patients at risk of developing CMV disease.

INTRODUCTION

Background Cytomegalovirus (CMV), a member of the human herpesvirus family, causes a lifelong persistent infection that is usually well controlled by the host immune system. However, in patients with defective immunity, as recipients of allogeneic solid organ (SOT), bone marrow transplants (BMT) and individuals infected with HIV, CMV remains a major clinical problem. For this reason, diagnostic methods that rapidly and unequivocally identify emerging CMV biologic activity (i.e. replication, viral gene expression), preferably discriminating between subclinical and symptomatic infection are required for optimal surveillance and management of CMV infections. CMV dissemination in the blood occurs during active infection and viremia has been recognized as the major virological risk factor for the progression to clinical disease. In this respect, there have been numerous studies that investigate the correlation of systemic CMV viral load with symptomatic CMV disease in immunocompromised patients. Quantification of the polymorphonuclear leucocytes expressing the CMV tegument pp65 protein by the antigenemia assay, can be used to predict CMV disease and to monitor antiviral treatment. Equally, quantification of CMV DNA load by PCR has been used as a marker for the prediction of CMV disease. The detection of mRNA for the viral matrix tegument pp67 protein in blood leukocytes reflects viral transcriptional activity and has also been showed to be a specific assay for monitoring the onset of symptomatic CMV infection and antiviral therapy. In the present study we evaluated 3 methods for the diagnosis of CMV infection and the identification of patients at risk of developing CMV disease, before the onset of disease. Quantitative pp65 antigenemia prospective results were compared to the retrospectively obtained data by quantitative PCR (CMV Monitor) and a qualitative pp67 mRNA assay (Nuclisens CMV pp67) in a series of consecutive samples from 10 liver transplant recipients, who had not received prophylactic treatment for CMV infection.

CONCLUSION

Molecular biology methods alone did not seem to discriminate patients at risk of developing CMV disease better than antigenemia. Thus, although the small number of patients studied does not allow us to reach definite conclusions, if only one test is to be used, antigenemia seems to be the best choice. It appears however that molecular biology methods have a better performance in discriminating the kinetics of the onset of infection, which seemed to correlate well to the risk of developing CMV disease. Furthermore, despite its qualitative nature, CMV pp67 mRNA assay was, in our hands, without the need to use arbitrarily defined cut-off values, the method with the best negative and positive predictive values for the development of CMV disease. Thus, our results support the need for larger studies testing the possible advantage of concomitantly use antigenemia and pp67 mRNA assays to the prediction of CMV disease in liver transplant recipients.