

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

Human immunodeficiency virus (HIV) infection is a global public health emergency that is not uncommon in modern times. It is prevalent in many parts of the world, including Southeast Asia. In Thailand, compared to other regional countries, HIV infection remains endemic. In Thailand, it is estimated that one million people are infected with HIV, and the risk of undetected HIV infection may increase. Superimposed infection is a major health issue for HIV seropositive patients due to immunity defect. A cross-sectional study was carried out to document the prevalence of colony infection caused by intestinal parasites, which is a common health issue among patients in the tropical region with HIV.

CONCLUSION

Findings The current study showed that HPV DNA could be found in DNA isolated from the plasma of some CC patients, and more importantly, that the HPG genomes from both the tumor and plasma were of the same type and physical status by integrating into the host genome. Hence, the viral DNA probably came from the tumor itself and the plasma HPV DNA represented the circulating free cell CC DNA. Furthermore, although not sensitive to a specific genetic marker, this particular DNA was strongly associated with CMMT.