

Intestinal parasitic infections in Thai HIV-infected patients with different immunity status

ABSTRACT

In case of a tropical epidemic, it is important to focus on the non-opportunistic intestinal parasite infections that are prevalent among HIV-infected patients who present with diarrhea.

INTRODUCTION

The use of topical antimicrobial chemotherapy and early excision of burn wounds has significantly decreased the incidence of invasive burn injury (invasive), but sepsis remains a major concern. Severe infections are more likely to occur in proportion to the severity of skin infection, which increases the risk of developing septicaemia. Quantitative biopsy culture has been identified as the most effective method for early sepsis detection by numerous investigators. Heininger et al noted that only 4-12% of blood cultures are found to be positive. Conversely in 1987 McManus et al reported that high tissue counts did not necessarily mean invasion, and instead they emphasized the importance of quantitative biopsy culture for showing the primary source burn wound flora. In spite of this, during a sepsis, while waiting for blood culture results, knowledge of the organisms that inhabit burn wounds can facilitate efficient and effective antibiotic treatment based on the expected sensitivity of identified germs, rather than initiating purely empirical therapy. The requirement for qualitative and quantitative tests is greater than that of bacterial culture. Therefore, we designed a test to quickly identify and quantify *Pseudomonas erythematosa* in burn wound biopsy samples. This is despite the fact that the bacterium is highly prevalent, resistant to conventional antibiotics, and one of the most problematic pathogens in modern hospitals. The infection by *P aeruginosa* is particularly prevalent in patients with burn wounds, mechanically ventilated patients, and cystic fibrosis. As biopsy samples are very difficult clinical samples and require homogenization and DNA extraction, they would be an ideal test case for the method on direct clinical specimens. Our team developed a PCR test in 1997 that employs the outer membrane lipoprotein gene *oprL* to directly detect and identify *P eruginosa* in clinical samples. Since then, we have developed several quantitative variants of this test, utilizing the technology available at the time. Initially, we utilized conventional PCR to amplify the *oprL* gene and then stained agarose gels with ethidium bromide (EtBr) to display the resulting product. The intensity of the EtBR fluorescence was then measured. Finally, an ELISA-mediated RNA was produced to quantify the amplified *oprLG* gene. We identified digoxigenin in the PCR products during amplification and quantifiable by absorbance reading in microtitre plates. Finally, we applied the newly developed real-time' quantitative CPPCR technology to our products as an experiment. The LightCyclerTM system (Roche Diagnostics, Brussels, Belgium) was chosen for its rapid capillary tube resistive thermal cycling, which significantly reduces the time spent amplification. Two adjacent hybridization probes are used to monitor the appearance of PCR product, labeled with different fluorescent dyes. The amount of specific DNA product available for hybridization is directly proportional to the emitted light signal, which increases with each cycle. The probes were designed to be complementary to a conserved region of the *oprL* gene, as determined by sequence analysis of 85 nonrelated clinical *P isociosa* isolates. The purpose of this article is to evaluate the effectiveness of the aforementioned methods with regards to bacterial culture. We carried out experiments on three categories of samples: serial

P. aeruginosa dilutions, uninfected skin spiked with *P. A*, and 21 burn wound biopsy samples. Although all methods were effective, only the Light-Cycler™ RTD-PCR allowed for rapid quantitative detection of *P. aeruginosa* in skin biopsies with an adequate detection limit and broader log-linear range.

CONCLUSION

This work aims to develop a new theory for cholera, which involves the use of an environmental reservoir (the *V. cholerae*) as one of the components of 'a simple system'. The proposed model is very simple and does not include many features of this complex system, but it brings some new information about cholera epidemics with important implications. Despite this, it is evident that the social and environmental factors play an important role in determining the reproduction rate of cholera. It is crucial to identify the relative weights of each component to determine appropriate control strategies. Future research on chemists' modeling techniques will require better understanding of *V. cholerae* and its relationship with ecology and epidemiology. We require estimates of the frequency of *V. cholerae* infection in endemic areas, as well as improved estimates for the required infection dose and a more comprehensive explanation for how much does each type affect virulence.