TT 病毒感染在台灣族群中的流行率以及基因分型

Prevalence and genotyping of TT virus infection in Taiwanese population

中文摘要

TT 病毒首先由 Nishizawa 等人於 1997 年所發現，因其基因組序列的變異性極高，因此可區分爲許多種基因型。先前的研究報告以 PCR 法偵測 TT 病毒的 DNA，結果顯示 TT 病毒的流行率在不同國家的族群以及各種不同的疾病之間有很大的差異，主要決定於所使用的 primers 以及檢體的來源不同。本實驗利用高靈敏度的 primers 偵測台灣地區 108 個體的 TT 病毒 DNA，包括健康的個體、肝炎患者、血液透析病患以及其他疾病的患者，所有 108 位個體的血清、血漿以及白血球層細胞分別萃取 DNA 並進行巢式 PCR。本實驗分別利用非轉錄區的 UTR primers 以及轉錄區的 N22 region 的 N22 primers 進行 PCR，我們發現 UTR primers 與 N22 primers 的黏合溫度在 52-58℃之間並無明顯差別，利用 UTR primers 偵測血清、血漿以及白血球層細胞中的 TT 病毒 DNA，陽性率分別爲 69%、75%以及 99%，而以 N22 primers 所測得的陽性率則分別爲 31%、37%以及 60%，由此可知 UTR primers 所測得的 TT 病毒陽性率高於 N22 primers，且年齡層較高的族群的 TT 病毒陽性率高於年齡層較低的族群。65 位 N22 PCR 陽性的個體進一步以具有基因型特異性的 primers 進行 PCR 來偵測 TT 病毒第一到第四型的 DNA，我們發現感染第一型的有 40%，第二型的爲 27%，感染第三型的占 12%，感染第四型的有 15%，可見台灣族群感染的基因型以第一型爲主。本實驗的結果再度證明多重感染不同基因型的 TT 病毒的存在性，然而僅感染一種基因型的比例最高，約佔整個研究族群的 50%。另外，在不同臨床特徵的族群所檢測的 TT 病毒陽性率並無明顯的關聯性，除了在感染 C 型肝炎病毒患者似乎有較高的陽性率，而其中的關聯性有待進一步的實驗探討。綜合本實驗的結果，我們認爲 TT 病毒普遍存在於台灣族群，且 TT 病毒的感染應不會造成肝臟疾病。

英文摘要

TT virus (TTV) was first described by Nishizawa et al in 1997 and consists of many genotypes and variants. The prevalence rate of TTV investigated by polymerase chain reaction (PCR) showed tremendous variations among different ethnic populations and patients with different diseases. These various results indicated that TTV DNA detection is highly dependent on the primers used for the PCR assay and on the source DNA samples. Our present study was conducted to examine the TTV prevalence in the apparently healthy subjects and patients with hepatitis B, C virus infection, hemodialysis or others in Taiwan using highly sensitive primers. A total of 108 DNA samples extracted from sera, plasma and buffy coat was individually subjected to 2

rounds of PCR amplification. UTR PCR and N22 PCR performed at temperatures ranging from 52oC to 58oC produced expected products without any obvious difference. Using primers for untranslational region (UTR) amplification, TTV DNA was detected in the sera, plasma and buffy coat fraction with a positive rate of 69%, 75% and 99%, respectively. However, only 31%, 37% and 60% respectively showed positive results when primers (N22) specific for the open reading frame (ORF) region 1 were applied. Subsequently, the existing genotypes among 65 N22 PCR-positive samples were determined using specific primers for genotypes 1 to 4. Our results showed that 40% was infected by genotype 1; 27% by 2; 12% by 3 and 15% by 4. Moreover, our results supported the existence of multiple infection even though one single type TTV infection was found in near 50% of the studied subjects. In addition, the prevalence rate in different groups fluctuates without any apparent correlation except in the HCV infected population. The correlation of TT virus and HCV infection requires further investigation. Viewed as a whole, we concluded that TTV infection is highly prevalent in the general populations in Taiwan and is unlikely involved in the pathogenesis of liver function.