Hepatitis C virus genotypes in Myanmar

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Myanmar is adjacent to India, Bangladesh, Thailand, Laos and China. In Myanmar, the prevalence of hepatitis C virus (HCV) infection is 2%, and HCV infection accounts for 25% of hepatocellular carcinoma. In this study, we reviewed the prevalence of HCV genotypes in Myanmar. HCV genotypes 1, 3 and 6 were observed in volunteer blood donors in and around the Myanmar city of Yangon. Although there are several reports of HCV genotype 6 in Myanmar, the distribution of HCV genotypes has not been well documented in areas other than Yangon. Previous studies showed that treatment with peginterferon and a weight-based dose of ribavirin for 24 or 48 wk could lead to an 80%-100% sustained virological response (SVR) rates in Myanmar. Current interferon-free treatments could lead to higher SVR rates (90%-95%) in patients infected with almost all HCV genotypes other than HCV genotype 3. In an era of heavy reliance on direct-acting antivirals against HCV, there is an increasing need to measure HCV genotypes, and this need will also increase specifically in Myanmar. Current available information of HCV genotypes were mostly from Yangon and other countries than Myanmar. The prevalence of HCV genotypes in Myanmar should be determined.

Key words: Direct-acting antivirals; Genotypes; Hepatitis C virus; Interferon-free; Myanmar

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lead to an 80%-100% sustained virological response in Myanmar.

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INTRODUCTION

The hepatitis C virus (HCV) is a single and positive-stranded RNA virus that is approximately 9600 nucleotides in length[1,2]. HCV infection causes acute and chronic hepatitis, cirrhosis and hepatocellular carcinoma (HCC)[3]. HCV is classified into at least 7 confirmed genotypes and 67 subtypes[4].

Myanmar is located in Southeast Asia and has recently emerged as a nation that is pursuing a peaceful transition to democracy[5]. In Myanmar, the prevalence of HCV infection is 2%, and it accounts for 25% of HCC[5]. HCV genotypes influence the outcome and the duration of interferon-based[6,7] and interferon-free treatments[8]. Direct-acting antivirals (DAAs) against HCV could lead to higher sustained virological response (SVR) rates with fewer adverse events[9,10]. HCV genotypes are very important factors in the selection of DAAs and treatment regimens[11,12].

Myanmar is adjacent to India, Bangladesh, Thailand, Laos and China. In India, HCV genotypes 3a, 3b, 1b and 1a have prevalence rates of 50%, 25%, 14% and 10%, respectively, whereas HCV genotype 4 has only a 4% prevalence rate and has been found only in Southern and Western India[11,12]. The most common HCV genotypes in patients with chronic HCV infection in Bangladesh were types 3 (50%), 3 and 4 (29%), and 1 (14.4%)[12]. In blood donors in Thailand, the most common HCV genotype was 3a (43%), followed by 1b (13%), 6f (13%), 6i (8.7%), 1a (4.4%), 3b (4.4%), 6c (4.4%), 6j (4.4%), and 6n (4.4%)[13]. In Laos, HCV genotypes 1 and 6 have prevalence rates of 5% and 95%, respectively[14]. In Mainland China, 42%, 44% and 14% of patients have HCV genotypes 1, 2 and 3, respectively[15]. In this article, we reviewed the prevalence of HCV genotypes in Myanmar.

HCV GENOTYPES IN MYANMAR

Distribution of HCV genotypes in Myanmar

Nakai et al[16] reported that the most common HCV genotype among 24 patients with liver diseases who were examined at Yangon General Hospital, Yangon, Myanmar, was 3b (67%), followed by genotypes 1a (13%) and 3a (8%); the genotypes were determined using PCR with genotype-specific primers. Mellor et al[17] used the PCR-restriction fragment length polymorphism method to show that variants of HCV genotype 6 exist in Myanmar. Shinji et al[18] reported prevalence rates of 31%, 47% and 21% for variants of HCV genotypes 1, 3 and 6 variants, respectively, in volunteer blood donors in and around the Myanmar city of Yangon; these findings were determined using direct sequencing of PCR products. Previous reports[16-19] showed the inconsistent data of the prevalence of HCV genotypes among the different area in Myanmar (Table 1), suggesting that this difference may attribute to the regional difference (Figure 1).

HCV genotype 6 in Myanmar

Lwin et al[19] reported that HCV genotype 6 was the most prevalent genotype (49%), followed by HCV genotypes 3 (39%), 1 (11%), and 2 (0.7%). In Myanmar, HCV genotype 6 was most often found in patients in the northern cities and HCV genotype 3 in the southern and western cities, suggesting that there are regional differences in HCV genotype distribution[19].

In the Yunnan province in China, where is located in the far southern part of Mainland China bordering Laos, Vietnam, and Myanmar, HCV genotypes 1a, 1b, 3a, 3b, 6a, 6n, and 6u were found in 1.3%, 20%, 24%, 30%, 5%, 11% and 8.8%, respectively, of patients who were co-infected with HCV and HIV[20,21]. A similar HCV genotype distribution of intravenous drug users was reported in this area[22]. Zhang et al[22] reported that HCV genotype 6 was most common (47%), followed by HCV genotypes 3 (41%) and 1 (12%) in intravenous drug users of the Yunnan province. Lwin et al[19] reported that HCV genotypes 1a, 3a, 3b, and 6 were found in 9%, 11%, 20%, and 60%, respectively, of patients in Muse where is located adjacent to the Yunnan. There seems to be the same association of HCV genotype distribution between Muse in Myanmar and Yunnan province in Mainland China.

In a large number of immigrant workers from Cambodia and Myanmar to Thailand, the predominant HCV genotypes were 1a, 1b, 3a, 3b and 6 (5e, 6f, 6m, 6p and 6r)[23]. The seroprevalence of HCV infection in immigrant workers from Cambodia and Myanmar to Thailand was reported to be 2.3% or 1.7%, respectively. HCV genotypes 1a, 1b, 3a, 3b and 6 were 0%, 24%, 16%, 4% and 56%, respectively, in immigrant workers from Cambodia to Thailand, and those were 6.7%, 6.7%, 26.7%, 33.3% and 26.6%, respectively, in immigrant workers from Myanmar to Thailand. Geographic distribution of HCV genotype 6 covered mainly southern China and the mainland of Southeast Asia, including Vietnam, Laos, Thailand, Cambodia and Myanmar[24-27].

RESPONSE TO PEGINTERFERON AND RIBAVIRIN

Treatment of peginterferon and a weight-based dose of
ribavirin for 24 or 48 wk were given to patients infected with HCV genotypes 2 and 3 or HCV genotypes 1 and 6. SVR rates were 81.2% (39/48), 100% (2/2), 85.5% (94/110), 90.3% (28/31) and 100% (4/4) in patients infected with HCV genotypes 1, 2, 3, 6 and with an indeterminate genotype, respectively.

**CONCLUSION**

DAAs are currently available and will be available in the near future to treat patients infected with HCV. In regards to the use of DAAs, the importance of measuring HCV genotypes is increasing and will also increase specifically in Myanmar. DAAs against HCV could lead to higher SVR rates (90%-95%) in patients infected with almost all HCV genotypes other than HCV genotype 3. With current DAAs, HCV genotype 3 is the most difficult-to-cure HCV genotype. HCV NS5B polymerase nucleotide inhibitor sofosbuvir plus ribavirin for 12 and 24 wk could lead 61%-68% and 94% SVR rates, respectively, in non-cirrhotic treatment-naïve patients with HCV genotype 3. Those could lead only 21%-34% and 92% SVR rates, respectively, in cirrhotic treatment-naïve patients with HCV genotype 3.
HCV genotype 3[20]. In treatment-experienced patients, those treatments could lead to less SVR rates[20]. In patients with HCV genotype 6, HCV NSSA inhibitor ledipasvir plus sofosbuvir could lead to approximately 96% SVR rates[20]. Most of the data of HCV genotypes were from Yangon and countries other than Myanmar. It is important to determine the prevalence of HCV genotypes in Myanmar.

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