Hepatitis B Virus and Hepatitis C Virus Infections in United States-Bound Refugees from Asia and Africa

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Abstract. The aim of this study was to determine the prevalence of active hepatitis B and C virus infections among refugees from various countries in Africa and Asia. Pre-admission serum samples collected during 2002–2007 from refugees originating from Bhutan ($N = 755$), Myanmar ($N = 1076$), Iraq ($N = 1137$), Laos ($N = 593$), Thailand ($N = 622$), and Somalia ($N = 707$) were tested for hepatitis B virus (HBV) DNA and hepatitis C virus (HCV) RNA. The HBV DNA (genotypes A, B, C, and G) was detected in 12.1% of samples negative for anti-HBs. Highest HBV prevalence was found among Hmong; lowest among Bhutanese. The HCV RNA (genotypes 1a, 1b, 1c, 3b, 6n, and 6m) was detected in 1.3% of the samples. Highest HCV prevalence was found among Hmong from Thailand; lowest among Iraqis. Screening specific refugee groups at high risk for viral hepatitis infections will identify infected individuals who could benefit from referral to care and treatment and prevent further transmissions.

INTRODUCTION

From 2009 to 2010, ~74,000 refugees resettled in the United States, with the highest number of refugees from Iraq, Myanmar (formerly known as Burma), and Bhutan; the number of refugees decreased to just over 53,000 in 2011.¹ Children < 17 years of age made up the highest proportion of refugees (~34%), followed by those 25–34 years of age (~20%).¹ A medical examination is mandatory for all refugees before entering the United States to identify applicants with inadmissible medical conditions (<http://www.cdc.gov/immigrantrefugeehealth/exams/medical-examination.html>). The Centers for Disease Control and Prevention (CDC) has issued guidelines for medical screening of refugees during this examination. These guidelines state that immunizations, including those for hepatitis B, are not required before entry into the United States for refugees; however, proof of vaccination is required to apply for adjustment of legal status (e.g., permanent resident status) after the refugee has been in the United States for > 1 year (<http://www.cdc.gov/immigrantrefugeehealth/guidelines/domestic/domestic-guidelines.html>).

More than 85% of the world's population live in areas of intermediate (2–7.9%) or high (> 8%) endemicity for hepatitis B.² Prevalence rates of chronic hepatitis B (CHB) vary among refugee populations; overall estimates of CHB in foreign-born individuals living in the United States range from 2.7% to 11%.^{3–6} Estimates of CHB from specific regions vary from 6–14% in immigrants from Africa, 3.7–10% from Asia, 4% in immigrants from the Caribbean, and 2% in immigrants from Europe.^{4,6,7} It is estimated that over 90% of new cases of CHB in the United States are among foreign-born persons.⁸ Because persons who are chronically infected serve as viral reservoirs and may transmit infection to susceptible individuals and to protect the personal health of infected individuals, they should receive additional testing and be considered for treatment, monitored for progression of disease, and receive prevention counseling. Accordingly, the CDC recommends that all adults, including refugees, who

were born in regions of the world with > 2% prevalence of HBV infection be tested for hepatitis B surface antigen (HBsAg), antibodies to hepatitis B core antigen (anti-HBc), or antibodies to hepatitis B surface antigen (anti-HBs) (<http://www.astho.org/Programs/Infectious-Disease/Refugee-Health/ARHC-Medical-Screening-Recommendations/>). The U.S. Preventative Services Task Force has also recently issued a draft recommendation to screen for HBV infection in persons at high risk for infection (<http://www.uspreventiveservicestaskforce.org/draftrec2.htm>), which includes U.S. foreign-born persons from, Laos, Myanmar, Somalia, Sudan, and a number of other countries.

Routine screening for HCV infection is currently recommended by the CDC for persons born during 1945 through 1965 and those who have known risk factors for HCV infection^{9,10}; however, no specific recommendations for immigrant and refugee testing for HCV infection are currently given. There are limited data available regarding the epidemiology of HCV infection among refugee populations. Small-scale studies in specific populations have found rates of infection ranging from 0.1% to 8%.^{7,11–13} Currently, recommended screening practices for refugees arriving in the United States correspond to CDC recommendations for the general U.S. population (<http://refugeehealthhta.org/chronic-hepatitis-infection/>).

Many individuals with chronic hepatitis B or C are unaware of their infection status, because they can remain asymptomatic for years. Individuals who become infected with HBV during early childhood, particularly when acquired perinatally, are at high risk of progression to chronicity.¹² Chronic infections with HBV or HCV, or both, can lead to end-stage liver disease or hepatocellular carcinoma (HCC), which together account for approximately one million annual deaths worldwide.¹⁴ In the United States, HCC is the fastest growing cause of cancer-related death, with incidence tripling over the past 20 years.^{15,16} Deaths associated with HCV infection have now surpassed those associated with human immunodeficiency virus (HIV) in the United States, with deaths occurring primarily among middle-aged adults.¹⁷

Assessing the prevalence of active viral hepatitis infections in refugee populations is critical to formulate public health policies (e.g., generation of screening and treatment guidelines) and to plan strategies for primary and secondary prevention

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in at-risk populations. The aim of this study was to describe the epidemiologic and virologic characteristics of current HBV and HCV infections among refugees whose sera were available for testing and were properly catalogued and stored at CDC's Migrant Serum Bank.

METHODS

Study population. Residual serum samples collected from individuals undergoing prearrival screening examinations between 2002 and 2007 from Bhutan ($N = 755$), Myanmar ($N = 1076$), Iraq ($N = 1137$), Laos ($N = 593$), Thailand ($N = 622$), and Somalia ($N = 707$), shipped on dry ice and stored in CDC's Migrant Serum Bank at -70°C were tested for virological markers of HBV and HCV infections. Although all refugees 15 years of age and older had blood drawn, only refugee populations with sufficient left-over samples for the testing were included in the study. The refugees from Laos and Thailand were all of Hmong ethnicity and inhabited the same refugee camp in Thailand (WatThamKrab), and those from Somalia were Bantus who also resided in one refugee camp (Kakuma). Refugees from Iraq were urban, and sera

were collected while they were in Jordan; Bhutanese refugees inhabited seven camps and those from Myanmar resided in six (Figure 1). These specimens were collected during medical screening examination before refugee arrival in the United States. De-identified data are collected and maintained by the Division of Global Migration and Quarantine, CDC, in the Migrant Serum Bank. Data were collected using standard forms and the protocol for data collection was approved by CDC's Ethics Review Board.

Testing strategy. Because of the availability of only restricted volumes of the sera and the need to conserve volume for polymerase chain reaction (PCR)-testing for HBV DNA and HCV RNA, serological testing for HBsAg, anti-HBc, and anti-HCV could not be performed. For screening for active HBV infections, serum samples were first tested for anti-HBs using VITROS ECi Immunodiagnostic System (Ortho-Clinical Diagnostics, Inc., Rochester, NY). Those negative for anti-HBs were then tested for HBV DNA. For screening for HCV infections, all samples were directly tested for HCV RNA.

The probe and primer sequences for PCR to amplify HBV DNA and HCV RNA are shown in Table 1. The dual-labeled Taqman HBV probe and HBV primers were designed from

FIGURE 1. Map of the refugee camps and urban sites where the refugees in the study resided at the time of the pre-admission medical screening. Countries with pink shading are the home countries of the refugees, whereas those with green shading are those with refugee camps or refugees within urban areas.

TABLE 1

Probe and primer sequences used for quantitative real-time PCR assays for HBV DNA and HCV RNA detection and sequencing*

Primer ID	Sequence
HBV384P	6FAM TGC GGC GTT TAT CAT MTT CCT CTT CAT-BHQ
HBV359F	TGT CCT GGY TAT CGC TGG AT
HBV425R	CCA ACA AGA AGA TGA GGC ATA GC
HCV259F	AGY GTT GGG TYG CGA AAG
HCV312R	CAC TCG CAA GCR CCC T
HCV278P	6FAM- CCT TGT GGT ACT GCC TGA -BHQ
F15	CGT TGA GGA ACT ACT GTC T
R03	GTG CAC GGT CTA CGA GAC CT
F13	GAA AGC GTC TAG CCA TGG CGT
R04	CCC TAT CAG GCA GTA CCA CAA
S1F	CTAGGACCCCTGCTGGTGTT
S1R	TCGAACCACTGAACAAATGGCACT
SNF	GTTGACAAGAATCCTCACAATACC
SNR	GGCTGAGGCCCACTCCCAT

* PCR = polymerase chain reaction; HBV = hepatitis B virus; HCV = hepatitis C virus.

an alignment of *S*-gene sequences representative of all HBV genotypes. Total nucleic acids were extracted from 200 μ L of serum with the MagNApure Total Nucleic Acid Isolation Kit I (Roche Applied Science, Rochester, NY) using the MagNApure LC instrument (Roche Applied Science, Indianapolis, IN) with a final elution volume of 50 μ L. Taqman quantitative PCR (qPCR) for HBV DNA was performed using 5 μ L of nucleic acid in total reaction volumes of 20 μ L using Express Supermix (Life Technologies, Grand Island, NY). Primer and probe concentrations and reaction conditions are given in Table 1. Amplification, detection, and data analysis were performed using the LightCycler 480 system (Roche Applied Science). Standard curves were generated from 10-fold serial dilutions of the Acrometrix HBV DNA Panel (Life Technologies). All HBV-DNA-positive samples were re-amplified for sequencing using nested Sybr qPCR targeting the *S* gene as previously described¹⁸ using primers S1F and S1R in the primary reaction and SNF and SNR in the nested reaction (Table 1).

The qPCR primers and probe used for detection of HCV RNA were designed from a highly conserved region of the 5'UTR.¹⁹ Total nucleic acid extraction was performed as described previously. Quantitative reverse transcriptase real-time PCR for HCV RNA was performed using the Superscript III Platinum 1 Step qRT-PCR kit (Life Technologies) with 10 μ L of RNA in a total volume of 25 μ L using the concentrations and conditions given in Table 1. Standard curves were generated from 10-fold serial dilutions of Acrometrix HCV RNA Panel (Life Technologies). All HCV-

RNA-positive samples were re-amplified for sequencing by nested PCR targeting the 5'UTR with the Qiagen One-Step RT-PCR kit (Qiagen, Valencia, CA) according to the manufacturer's specifications using 24 μ L RNA extract in a 50 μ L reaction volume with primers F15 and R03 (Table 1). Second-round PCR was performed using Quant SybrGreen Master Mix (Quanta BioSciences, Gaithersburg, MD) according to the manufacturer's specifications using 2 μ L primary product in a final volume of 20 μ L with primers F13 and R04 (Table 1).

All sequences generated were assembled and multiple alignments made using Laser Gene software (DNA Star, Madison, WI). Neighbor-joining trees were constructed in MEGA 5.²⁰

Statistical Analyses. Differences in the mean ages of the refugees based on sex or country of origin was investigated with analysis of variance, whereas associations of HBV and HCV infections with gender, age group, and country of birth was evaluated with χ^2 analysis implemented in Minitab16.²¹ Kruskal-Wallis one-way analysis of variance was used to determine if differences in HBV and HCV viral loads in study participants from the various countries were significant. A *P* value of ≤ 0.05 was considered statistically significant.

RESULTS

Of the 4,890 sera tested, 15.4% (*N* = 755) were from refugees from Bhutan, 22.0% (*N* = 1076) from Myanmar, 23.3% (*N* = 1137) from Iraq, 12.1% (*N* = 593) from Hmong born in Laos, 12.7% (*N* = 622) from Hmong born in Thailand, and from Somali, 14.5% (*N* = 707). The number of sera from males was 2,409 (49.3%). The mean age of the refugees was 34.8 years (range 15–95 years) and differences among the study subpopulations were not significant except for the Hmong from Laos (mean 48.7 years [range 29–94]) and the Hmong from Thailand (mean 21.1 years [range 16–28] [*P* < 0.001, Tables 2, and 3]). No significant associations were observed between country of origin and gender.

Prevalence of markers of HBV Infection. Of the total specimens tested, 2,127 (43.5%) were positive for anti-HBs. Greater than 50% of Myanmar refugees, Hmong from Laos, Hmong from Thailand, and refugees from Somali tested positive for anti-HBs. Country of origin was significantly associated with differences in anti-HBs status (*P* < 0.001, Table 3); fewer refugees from Bhutan and Iraq were anti-HBs negative compared with other refugees. Of the anti-HBs negative samples, HBV DNA was detected in 331 (12.1%). The HBV-DNA-detection rates varied depending upon the country of origin: Bhutan, 1.8%; Myanmar, 18.9%; Iraq, 3.2%; the Hmong, 33.3%; and Somali, 14.6%. There was a significant

TABLE 2
Summary characteristics of test population HBV and HCV test data

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Study population	No. (M:F)	Age range (mean [±SD])	HBV markers					HCV RNA	
			Anti-HBs		HBV DNA*				
			Positive (%)	Negative	Positive/total number % (95% CI)	Median viral titer	Positive/total number % (95% CI)	Median viral titer	
Bhutan	755 (384:371)	16–92 (35.9 [±16.7])	139 (18.4)	616	11/755 1.46 (0.06, 2.3)	8.26E + 02	5/755 0.66 (0.08, 1.2)	2.21E + 07	
Myanmar	1076 (522:554)	15–94 (33.3 [±15.0])	558 (51.9)	518	98/1137 9.11 (7.4, 10.8)	1.32E + 04	4/1076 0.37 (0, 0.9)	3.65E + 05	
Iraq	1137 (605:532)	16–95 (37.9 [±15.6])	271 (23.8)	866	28/1137 2.46 (1.6, 3.4)	6.62E + 02	0/1137 0	0	
Hmong (Laos)	593 (304:289)	29–94 (48.7 [±15.2])	389 (65.6)	204	75/593 12.65 (10, 15.3)	5.58E + 03	3/593 0.51 (0, 1.8)	1.10E + 06	
Hmong (Thai)	622 (314:308)	16–28 (21.1 [±3.7])	360 (57.9)	262	80/622 12.86 (10.2, 15.4)	6.48E + 03	45/622 7.23 (5.2, 9.3)	4.80E + 03	
Somalia	707 (352:355)	16–75 (31.0 [±11.7])	410 (58.0)	297	39/707 5.52 (3.8, 7.1)	2.24E + 03	6/707 0.85 (0.17, 1.5)	2.95E + 03	

* = Only anti-HBs negative samples were tested for HBV DNA.

HBV = hepatitis B virus; HCV = hepatitis C virus; HB = hepatitis B,

TABLE 3
Parameters associated with infection with HBV or HCV

Association tested	χ^2	df	P value
Sex and country of origin	5.25	5	0.39
Age and country of origin	1335.5	30	< 0.001
Age and Hmong Thai/Hmong Lao	996.3	6	< 0.001
Age and Hmong Thai/other refugees	789.98	24	< 0.001
Anti-HBs detection rate and country of origin	656.2	5	< 0.001
Detectable HBV DNA and country of origin	290.69	5	< 0.001
Gender and detectable HBV DNA	3.22	1	0.07
Age (≥ 30 years) and detectable HBV DNA	0.282	1	0.595
HCV RNA positivity and country of origin	201.15	5	< 0.001
HCV RNA positivity and country of origin (Hmong Thai excluded)	6.49	4	0.166
Gender and HCV RNA	0.0002	1	0.987
Age (≥ 30 years) and detectable HCV RNA	40.7	1	< 0.001
Country HBV prevalence and country HCV prevalence	65.2	5	< 0.001

HBV = hepatitis B virus; HCV = hepatitis C virus; df = degrees of freedom.

association between HBV-DNA-positivity and country of origin (with the Hmong from Laos and Thailand considered as one group) ($P < 0.001$); a higher proportion of Hmong and Burmese refugees were positive for HBV DNA. There was no association between HBV-DNA-positivity and gender or age. The median HBV viral load was $3.71e3$ (range $18-7e11$) IU/mL, with significant differences in mean viral load among the six countries ($P = 0.015$), and the highest observed among Myanmar refugees ($1.32e4$ IU/mL). The genotype distribution was as follows: A, 2.7%; B, 49.5%, C, 41.4%; and G, 0.3% (Figure 2). Twenty specimens could not be genotyped because of poor sequence data. Genotype A was found in all populations, except refugees from Myanmar. Genotype G was found in a single sample from a Myanmar refugee.

FIGURE 2. Genotype distribution and phylogenetic relatedness among hepatitis B virus (HBV) strains infecting U.S.-bound refugees.

Prevalence of HCV Infection. Of the total specimens tested, 63 (1.1%) were positive for HCV RNA (Table 2). Detection rates varied: the Hmong, 4%; Somali, 0.9%; Bhutan, 0.7%; and Myanmar, 0.4%. There was a statistically significant association between HCV-RNA-positivity and country of origin (with the Hmong considered as one group) ($P < 0.001$); Hmong from Thailand had greater numbers of HCV-positive samples than refugees from other countries. No association is found if the Hmong from Thailand are excluded ($P = 0.166$). Positivity also was associated with age, being significantly higher among persons < 30 years of age ($P < 0.001$), but not with gender (Table 3). The median viral load was $1.07e4$ (range $28-4.7e7$) IU/mL, with significant differences in mean viral load among the six countries ($P = 0.019$), and the highest observed for the Bhutan refugees ($2.21e7$ IU/ml) (Table 3). The genotype distribution was as follows: 1a, 61.9%; 1b, 3.2%; 1c, 3.2%; 3b, 1.6%; 6n, 4.8%; and 6m, 4.8% (Figure 3); 13 (20.5%) specimens could not be genotyped. Genotypes 6n and 6m were identified in sera from refugees from Bhutan and Myanmar, respectively. Four samples were HBV-DNA- and HCV-RNA-positive,

FIGURE 3. Genotype distribution and phylogenetic relationships among hepatitis C virus (HCV) strains infecting U.S.-bound refugees.

one from a Myanmar refugee and three from Hmong born in Thailand.

DISCUSSION

Refugees applying for admission to the United States must undergo a medical examination overseas to identify individuals with inadmissible health-related conditions. These pre-departure examinations do not include routine screening for HBV and HCV virus infections. Following arrival in the United States it is recommended that all refugees receive a post-arrival medical examination for the purpose of further medical screening and to facilitate integration into the United States medical system. The CDC has issued guidelines for this examination. These guidelines include routine testing of refugees for hepatitis B for refugees who are from, or who have lived in, countries with rates of hepatitis B that are equal to or exceed 2%. Because of a lack of data, the CDC currently only recommends routine screening for hepatitis C in accordance with existing United States guidelines (e.g., for those with identified risk factors and in those born between 1945 and 1965).⁹ It is further recommended that any individual who screens positive for hepatitis B or C during the post-arrival medical screen will be counseled and evaluated for treatment (<http://www.cdc.gov/immigrantrefugeehealth/guidelines/domestic/immunizations-guidelines.html>); however, there are no mechanisms in place to ensure that those who screen positive receive adequate medical treatment or follow up.

Testing for anti-HBc and HBsAg could not be performed as a result of paucity of sample volumes, instead all samples were tested for anti-HBs to exclude seropositive samples for HBV DNA testing. Seropositivity for anti-HBs ranged from 18% to 65% in these groups of refugees, which suggests these individuals are already immune to HBV infection, likely from past HBV infections rather than prior hepatitis B vaccination; universal vaccination has recently been implemented only in Somalia and Myanmar.^{22,23} Among those who were seronegative for anti-HBs, 12% were seropositive for HBV DNA. We did not conduct serological tests to differentiate acute from chronic hepatitis B, but on the basis of the available epidemiology, the majority of HBV-DNA-positive refugees could be considered chronically infected with HBV. One recent meta-analysis found that pooled estimates of chronic HBV seroprevalence were higher in refugees than in immigrants, with a 42% higher odds of chronic infection as compared with immigrants after controlling for region of origin and study period.²⁴ Since the adoption of universal vaccination against HBV, the rates of incident HBV infection in the United States have declined by more than 80%, to 1.5 per 100,000 individuals in 2009²⁵; however, the number of persons with chronic HBV infection in the United States is still substantial. The major contributing factor to the continuing endemicity of chronic hepatitis B is importation by already HBV-infected foreign-born individuals⁸; the refugees studied here and found positive for HBV DNA contribute to that endemicity.

Refugees from Myanmar and the Hmong were identified to have disproportionately high rates of HBV infection, reflecting the high endemicity of chronic hepatitis B in East Asia caused by frequent perinatal transmission.²⁶ A high prevalence of HBV infection also can reflect practices adopted before migration that have placed persons at risk of HBV infection, such as tattooing, ear piercing, folk remedies, or scarifica-

tion.²⁷⁻²⁹ Tattooing was a widespread custom in many ethnic groups in Myanmar until the mid-20th century, though the practice is regaining popularity among the youth. Similarly, a study among Hmong living in the San Joaquin Valley found almost 17% prevalence of CHB, and high-risk behavior including multiple sex partners, tattooing, and injecting drugs are common within the community.³⁰ These refugee groups could benefit from early screening for HBV infections, identification, and treatment upon their arrival, which can prevent further progression of disease to end-stage liver disease and HCC, and diminish the risk of transmitting HBV to their contacts.

The HBV genotypes B and C were the most common in our study populations, reflecting their high frequency in Asia.³¹ More than 90% of CHB in Asia is caused by infections with genotypes B and C.³² It has been suggested that genotype C may be the most virulent of the HBV genotypes.³³ Genotype C is associated with a delay in HBeAg seroconversion, ensuring perinatal transmission and progression to chronicity.³³ Individuals with genotype C have a higher risk of liver inflammation, cirrhosis, and liver cancer at a younger age than other genotypes,³⁴⁻³⁶ though in one Taiwanese study, genotype B is associated with HCC in younger individuals.³⁷ The implications of the high prevalence of genotypes B and C in these populations may add to the burden of CHB within the United States. The finding of a sample carrying HBV belonging to genotype G is quite surprising, as it is considered uncommon in Asia; nonetheless, this genotype has recently also been reported from Thailand.³⁸

A relatively lower proportion (1%) of refugees tested in this study were HCV RNA positive. This proportion was particularly high among the Hmong born in Thailand (7%); however, Hmong born in Laos had a significantly lower prevalence of HCV RNA (0.51%, $P < 0.001$). The Hmong refugees born in Thailand were on average 20–30 years younger than those born in Laos, so risk factors for acquiring HCV infection may be different between these two Hmong groups. It has been reported that injection drug use has increased among the Hmong,³⁹ thereby potentially contributing to the higher rate of HCV-RNA-positivity observed for the Thai Hmong. Currently, no specific policy exists for hepatitis C screening of immigrants or refugees, although CDC has recently included in its recommendations one-time screening for hepatitis C of all individuals born between 1945 and 1965.¹⁰ Hepatitis C testing recommendations could be extended to include testing of at-risk refugee groups such as Hmong from Thailand.

The most common HCV genotype was 1a, which reflects its worldwide distribution.⁴⁰ Sera from three refugees, from Bhutan and Myanmar, carried HCV strains belonging to genotype 6 (subgenotypes 6m and 6n). Genotype 6 is relatively common in Southeast Asia, and the 6m and 6n subgenotypes particularly circulate in Thailand and Myanmar.⁴¹

There are several limitations to our study. First, as a result of the limited amount of sera available, our testing algorithm was non-traditional. Rather, we tested only samples that were negative for anti-HBs for HBV DNA and all samples for HCV RNA using the nucleic acids from the same extraction to maximize our ability to determine the number of infected individuals in these groups. This study was aimed at determining the prevalence of active HBV and HCV infections in these refugee populations using de-identified left-over samples in the archives of the CDC Migrant Serum

bank, therefore the results were not shared with the participants and/or used for clinical management of any infected individuals. Second, this study was based on convenience samples available in a repository at the CDC; therefore, our findings may not be generalizable to other refugee groups or immigrants entering the United States. For example, the refugees from Bhutan and Myanmar resided in multiple refugee camps before their pre-admission medical screening; thus, the prevalence estimates are likely representative of the specific refugee group rather than a common source of infection within a particular refugee camp. We could not expand the screening for HBV and HCV infections to other refugee populations due to a lack of availability of their sera samples in CDC repository. Finally, there is the possibility that we may have underestimated the number of refugees with active HBV infections, because individuals could potentially be anti-HBs positive and HBV DNA positive, or could be DNA negative, but still transmit because of positive HBsAg. Nevertheless, our data provide valuable insight into the burden of HBV and HCV infections in these selected refugee populations.

In conclusion, our findings show a higher prevalence of HBV and HCV infections in various refugee populations and the difficulty in developing generic medical screening guidelines for such populations. Refugee populations vary over time and risk of infectious diseases varies as these populations change. Hepatitis B testing has been considered standard of care for refugees for many years, with the assumption that all populations are originating in intermediate or highly endemic areas. Similarly, although the rate of HCV infections in refugees generally falls below the rates found in the United States population, there are specific populations with higher rates that would justify more enhanced screening (e.g., Hmong born in Thailand). Even when ethnically similar, different populations may have distinctly different rates, as shown by the variance found in the Hmong originating in Thailand from those originating in Laos. This study shows that generic screening guidelines issued for this diverse population is a sub-optimal approach. Refugee populations admitted into the United States vary over time. These populations are generally identified in advance of migration to the United States. An ideal system would anticipate health conditions in refugees who are planned to arrive by testing before movement to the United States and would base recommendations on data specific to each population (i.e., population-specific recommendations). In summary, it is essential to determine the risk of serious infection in specific refugee populations rather than treating all refugee populations identically so that appropriate guidelines can be issued. Early identification of infections such as HBV and HCV infection is essential to facilitate treatment of those found infected, which will confer medical benefits to the individual, and curtail the continuing spread of HBV and HCV infections in the United States.

Received January 31, 2014. Accepted for publication March 5, 2014.

Published online April 14, 2014.

Acknowledgments: We thank the panel physicians who provided the sera to CDC's Migrant Sera Bank. We thank C. Virginia Lee for producing the map of refugee camps. We acknowledge Zoya Dimitrova for her assistance in statistical analysis of the data. We are grateful to Mar Than, Natasha Khudhakov, and Tracy Green-Montfort for serologic testing of the specimens.

Disclaimer: The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the U.S. CDC.

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