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<td>Author(s)</td>
<td>Nishida, N; Sawai, H; Kashiwase, K; Minami, M; Sugiyama, M; Seto, WKW; Yuen, RMF; Posuwan, N; Poovorawan, Y; Ahn, SH; Han, KH; Matsuura, K; Tanaka, Y; Kurosaki, M; Asahina, Y; Izumi, N; Kang, JH; Hige, S; Ide, T; Yamamoto, K; Sakaida, I; Murawaki, Y; Itoh, Y; Tamori, A; Orito, E; Hiasa, Y; Honda, M; Kaneko, S; Mita, E; Suzuki, K; Hino, K; Tanaka, E; Mochida, S; Watanabe, M; Eguchi, Y; Masaki, N; Murata, K; Korenaga, M; Mawatari, Y; Ohashi, J; Kawashima, M; Tokunaga, K; Mizokami, M</td>
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<tr>
<td>Citation</td>
<td>PLoS One, 2014, v. 9 n. 2, article no. e86449</td>
</tr>
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<td>Issued Date</td>
<td>2014</td>
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<tr>
<td>URL</td>
<td><a href="http://hdl.handle.net/10722/198043">http://hdl.handle.net/10722/198043</a></td>
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New Susceptibility and Resistance HLA-DP Alleles to HBV-Related Diseases Identified by a Trans-Ethnic Association Study in Asia

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Abstract

Previous studies have revealed the association between SNPs located on human leukocyte antigen (HLA) class II genes, including HLA-DP and HLA-DQ, and chronic hepatitis B virus (HBV) infection, mainly in Asian populations. HLA-DP alleles or haplotypes associated with chronic HBV infection or disease progression have not been fully identified in Asian populations. We performed trans-ethnic association analyses of HLA-DPA1, HLA-DPB1 alleles and haplotypes with hepatitis B virus infection and disease progression among Asian populations comprising Japanese, Korean, Hong Kong, and Thai subjects. To assess the association between HLA-DP and chronic HBV infection and disease progression, we conducted high-resolution (4-digit) HLA-DPA1 and HLA-DPB1 genotyping in a total of 3,167 samples, including HBV patients, HBV-resolved individuals and healthy controls. Trans-ethnic association analyses among Asian populations identified a new risk allele HLA-DPB1*02:01 (P = 1.36 × 10−5; OR = 1.97; 95% CI, 1.50–2.59) and a new protective allele DPB1*02:01 (P = 5.22 × 10−5; OR = 0.68; 95% CI, 0.58–0.81) to chronic HBV infection, in addition to the previously reported alleles. Moreover, DPB1*02:01 was also associated with a decreased risk of disease progression in chronic HBV patients among Asian populations (P = 1.55 × 10−2; OR = 0.50; 95% CI, 0.39–0.65). Trans-ethnic association analyses identified Asian-specific associations of HLA-DP alleles and haplotypes with HBV infection or disease progression. The present findings will serve as a base for future functional studies of HLA-DP molecules in order to understand the pathogenesis of HBV infection and the development of hepatocellular carcinoma.


Editor: Ferruccio Bonino, University of Pisa, Italy

Received November 13, 2013; Accepted December 10, 2013; Published February 10, 2014

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Funding: This work was supported by a Grant-in-Aid from the Ministry of Health, Labour, and Welfare of Japan H24-Bsou-kanen-ippan-011 and H24-kanen-fukko-010 to Masashi Mizokami, H23-kanen-005 to Katsushi Tokunaga, H25-kanen-wakate-013 to Nao Nishida, and H25-kanen-wakate-012 to Hiromi Sawai. This work was also supported by The Grant for National Center for Global Health and Medicine 22-shi-302 to Masashi Mizokami and 24-shi-107 to Nao Nishida. Partial funding for the present study was also acknowledged. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.
Introduction

Hepatitis B virus (HBV) infection is a major global health problem, resulting in 0.5–1.0 million deaths per year [1]. The prevalence of chronic HBV infection varies. About 75% of the chronic carriers in the world live in Southeast Asia and East Pacific [2]. Due to the introduction of vaccination programs, the prevalence of HBV infection in many countries has gradually been decreasing with consequent decreases in HBV-related hepatocellular carcinoma (HCC) [3]. Although some HBV carriers spontaneously eliminate the virus, about 10–15% of carriers develop liver cirrhosis (LC), liver failure and HCC [4]. Moreover, the progression of liver disease was revealed to be associated with the presence of several distinct mutations in HBV infections [5]. Genetic variations in STAT4 and HLA-DQ genes were recently identified as host genetic factors in a large-scale genome-wide association study (GWAS) for HBV-related HCC in China [6].

With regard to the genes associated with susceptibility to chronic HBV infection, HLA-DP and HLA-DQ genes were identified by GWAS in Japanese and Thai populations in 2009 [7] and 2011 [8], respectively. In addition, our previous GWAS confirmed and identified the association of SNP markers located on HLA-DPA1 (rs3077) and HLA-DPB1 (rs9277535) genes with susceptibility to chronic hepatitis B (CHB) and HBV clearance in Japanese and Korean subjects[9]. The significant associations of HLA-DP with CHB and HBV clearance have mainly been detected in Asian populations, such as Japanese [8,9], Thai [7], Chinese [10–12], and Korean [9]. In 2012, the association between HLA-DPA1 gene SNPs and persistent HBV infection was replicated in a Germany non-Asian population for the first time; however, this showed no association with HBV infection [13]. These results seem to be explained by the fact that allele frequencies of both rs3077 (0.155, 0.387 and 0.743 for C allele, on HapMap CEU, JPT, and YRI) and rs9277535 (0.261, 0.558 and 0.103 for G allele, on HapMap CEU, JPT, and YRI) are markedly different between populations. Moreover, the previous study showed that HBsAg seropositivity rates were higher in Thai and China (5–12%) than in North America and Europe (0.2–0.5%) [2]. These results suggest that comparative analyses of HLA-DP alleles and haplotypes in Asian populations would clarify key host factors of the susceptible and protective HLA-DP alleles and haplotypes for CHB and HBV clearance. Here, we performed trans-ethnic analyses of HLA-DP alleles and haplotypes in Asian populations comprising Japanese, Korean, Hong Kong and Thai individuals. The findings from this study will serve as a base for future functional studies of HLA-DP molecules.

We performed genotyping for HLA-DPA1 and HLA-DPB1 in all 3,167 samples, and a total of 2,895 samples were successfully genotyped. The characteristics of successfully genotyped samples are shown in Table S1.

Association of HLA-DPA1 and HLA-DPB1 alleles in Asian populations

As for a general Asian population, including 464 Japanese, 140 Korean, 156 Hong Kong, and 122 Thai subjects, five HLA-DPA1 alleles and twenty-four HLA-DPB1 alleles were observed (Table S2). The frequencies of HLA-DPA1 and HLA-DPB1 alleles were similar between Japanese and Korean subjects. On the other hand, the number of alleles with frequencies of 1–2% was larger in Hong Kong and Thai populations, despite the small sample size. Although the frequencies of HLA-DP alleles varied in Asian populations, HLA-DPB1*05:01 was the most prevalent with over 30% in all populations.

The associations of HLA-DPA1 and HLA-DPB1 alleles with chronic HBV infection (i.e., comparison between HBV patients and healthy controls) are shown in Table S2. To avoid false positives caused by multiple testing, the significance levels were corrected based on the numbers of HLA-DPA1 and HLA-DPB1 alleles.
alleles in the focal population. Briefly, the significance level was set at 0.05/(# of observed alleles at each locus) in each population (see Materials and Methods). With regard to high-risk alleles of HLA-DPA1, the most prevalent allele HLA-DPA1*05:01 was significantly associated with susceptibility to HBV infection in Japanese (P = 3.45 × 10^{-4}; OR = 1.39; 95% CI, 1.16–1.60) and Korean subjects (P = 2.66 × 10^{-5}; OR = 1.39; 95% CI, 1.29–1.50), whereas this association was not observed in Hong Kong or Thai subjects. The association of HLA-DPA1*05:01 with susceptibility to HBV infection was significant only in Japanese (P = 2.61 × 10^{-7}; OR = 1.38; 95% CI, 1.46–2.41). The significant association of HLA-DPA1*01:03 with protection against HBV infection was commonly observed among four Asian populations (Table S2). The pooled OR and 95% CI were 0.51 and 0.41–0.63, respectively in a meta-analysis (P = 3.15 × 10^{-10}) (Fig. S1B).

As shown in Table S2, HLA-DPB1 shows higher degree of polymorphism than HLA-DPA1. The most common allele in Asian populations, HLA-DPB1*05:01, was significantly associated with HBV susceptibility in both Japanese and Korean subjects. Although HLA-DPB1*05:01 showed no significant association in the Hong Kong and Thai populations, the same direction of association (i.e., HBV susceptibility) was observed. Meta-analysis of the four populations revealed a significant association between HLA-DPB1*05:01 and susceptibility to HBV infection (P = 1.51 × 10^{-4}; OR = 1.45; 95% CI, 1.19–1.75) (Fig. S1B). The frequency of HLA-DPB1*09:01 was significantly elevated in Japanese HBV patients (15.7%) as compared with healthy controls (8.7%) (P = 3.70 × 10^{-6}; OR = 1.94; 95% CI, 1.45–2.62), and this association was most significant (i.e., the smallest P value) in the Japanese population. Because of lower allele frequencies of HLA-DPB1*09:01 or lack of statistical power in the other populations, no significant associations were observed. A common allele in Thai subjects, HLA-DPB1*13:01, was significantly associated with susceptibility to HBV infection (P = 2.49 × 10^{-4}; OR = 2.17; 95% CI, 1.40–3.47) with the same direction of associations in Japanese and Hong Kong (OR = 1.52 and 1.40, respectively).

HLA-DPB1*04:02 was identified as the most protective allele for HBV infection in Japanese (P = 1.59 × 10^{-7}; OR = 0.37; 95% CI, 0.24–0.55) and Korean subjects (P = 1.27 × 10^{-7}; OR = 0.19; 95% CI, 0.10–0.38). Both HLA-DPB1*02:01 and HLA-DPB1*04:01 were also significantly associated with protection in the Japanese population, and the former was significantly associated with protection in Hong Kong subjects (P = 9.17 × 10^{-4}; OR = 0.49; 95% CI, 0.32–0.76). This common allele among four Asian populations, HLA-DPB1*02:01, showed a significant association with protection against HBV infection (P = 5.22 × 10^{-4}; OR = 0.68; 95% CI, 0.58–0.81) in a meta-analysis (Fig. S1B).

The frequencies of associated HLA-DP alleles in a comparison of HBV patients with healthy controls (Table S2) or with HBV-resolved individuals (Table S3) were similar in all four Asian populations. In the Japanese population, the associations of susceptible and protective HLA-DPB1 alleles to chronic HBV infection seem weaker in the comparison of HBV patients with HBV-resolved individuals than in the comparison of HBV patients with healthy controls. Moreover, the results of association analyses showed no difference in the comparison of HBV patients with HBV-resolved individuals, including or excluding HCV positive individuals (Table S3). In contrast, the association became stronger in the comparison of HBV patients with HBV-resolved individuals among the Korean subjects. The protective allele HLA-DPB1*04:01 was also identified to have a strong association with HBV clearance in Hong Kong subjects (Table S3). Moreover, in Hong Kong subjects, the HLA-DPB1*05:01 associated with the risk for HBV infection showed lower frequency in HBV-resolved individuals (42.9%) than in the healthy controls (48.1%), which accounts for a strong association in the comparison of HBV patients with HBV-resolved individuals (P = 6.24 × 10^{-3}; OR = 1.64; 95% CI, 1.14–2.36). Although the number of samples was insufficient, HLA-DP-100:01 showed a significant association with protection against HBV infection in the Hong Kong population (P = 3.05 × 10^{-6}; OR = 0.03; 95% CI, 0.0007–0.20).

As for disease progression in CHB patients among Asian populations, a protective effect of HLA-DPB1*02:01 on disease progression was observed in the Japanese (P = 4.26 × 10^{-5}; OR = 0.45; 95% CI, 0.30–0.67) and Korean populations (P = 8.74 × 10^{-4}; OR = 0.47; 95% CI, 0.29–0.75) (Table S4). Multivariate logistic regression analysis adjusted for age and sex revealed that the number of DPB1*02:01 alleles (i.e., 0, 1, or 2) was significantly associated with disease progression in CHB patients in Japanese (P = 1.77 × 10^{-4}; OR = 0.47; 95% CI, 0.32–0.70) (Table 2). Moreover, protective effects of DPB1*02:01 on disease progression in Asian populations (P = 1.55 × 10^{-2}; OR = 0.50; 95% CI, 0.39–0.65) were detected in a multivariate logistic regression analysis adjusted for age, gender, and population (Table 2).

Associations of DPA1-DPB1 haplotypes in Asian populations

The estimated frequencies of HLA DPA1-DPB1 haplotypes are shown in Table S5. The most frequent haplotype among the four Asian populations was DPA1*02:02-DPB1*05:01. The number of haplotypes with low frequencies of 1–2% was 10 in both Japanese and Korean subjects, whereas more haplotypes appeared with frequencies of 1–2% in Hong Kong and Thai subjects. The associations of DPA1-DPB1 haplotypes with HBV infection are shown in Table S5. In the Japanese population, DPA1*02:02-DPB1*09:01 showed the most significant association with susceptibility to HBV infection (P = 3.38 × 10^{-8}; OR = 1.95; 95% CI, 1.46–2.64). The most common haplotype in the four Asian populations, DPA1*02:02-DPB1*05:01, was found to be significantly associated with susceptibility to HBV infection in the Japanese and Korean populations (P = 7.40 × 10^{-4}; OR = 1.37; 95% CI, 1.14–1.66 for Japanese, and P = 4.50 × 10^{-6}; OR = 2.02; 95% CI, 1.48–2.78 for Korean). In the Thai subjects, HLA-DPB1*13:01 was the most significant risk allele for HBV infection (Table S2); however, no significant associations were found for the three different haplotypes bearing HLA-DPB1*13:01, DPA1*02:02-DPB1*13:01, and DPA1*04:01-DPB1*13:01, indicating that the association of HLA-DPB1*13:01 with susceptibility to HBV infection did not result from a specific DPA1-DPB1 haplotype or combination with a specific DPA1 allele.
In the Japanese population, both haplotypes DPA1*01:03-DPB1*04:01 and DPA1*01:03-DPB1*04:02 showed significant associations with protection against HBV infection (P = 1.17 × 10^{-3}; OR = 0.32; 95% CI, 0.18–0.56 for DPA1*01:03-DPB1*04:01 and P = 1.95 × 10^{-2}; OR = 0.37; 95% CI, 0.24–0.55 for DPA1*01:03-DPB1*04:02). In the Korean subjects, a significant association of DPA1*01:03-DPB1*04:02 was also demonstrated; however, no association was observed for DPA1*01:03-DPB1*04:01. Because the observed number of each haplotype was small, none of the other haplotypes showed a significant association with protection against HBV infection.

In order to identify trans-ethnic DPA1-DPB1 haplotypes associated with HBV infection, a meta-analysis was performed. A meta-analysis further revealed that the DPA1*01:03-DPB1*02:01 haplotype was significantly associated with protection against HBV infection (P = 1.45 × 10^{-3}; OR = 0.69; 95% CI, 0.58–0.82) (Fig. S1C).

**Discussion**

Among 2.2 billion individuals worldwide who are infected with HBV, 15% of these are chronic carriers. Of chronic carriers, 10–15% develops LC, liver failure and HCC, and the remaining individuals eventually achieve a state of nonreplcitative infection, resulting in HBsAg negative and anti-HBc positive, i.e. HBV-resolved individuals. To identify host genetic factors associated with HBV-related disease progression may lead HBV patients to discriminate individuals who need treatment.

The HLA-DPA1 and HLA-DPB1 genes were identified as host genetic factors significantly associated with CHB infection, mainly in Asian populations [7–12], and not in European populations [13]. In the previous association analyses of HLA-DPB1 alleles with HBV infection, one risk allele HLA-DPB1*05:01 (OR = 1.52; 95% CI, 1.31–1.76) and two protective alleles, HLA-DPB1*04:01 (OR = 0.53; 95% CI, 0.34–0.80) and HLA-DPB1*04:02 (OR = 0.47; 95% CI, 0.34–0.64), were identified in the Japanese population [7]. In this study, we further identified a new risk allele HLA-DPB1*09:01 (OR = 1.94; 95% CI, 1.45–2.62) for HBV infection and a new protective allele HLA-DPB1*02:01 (OR = 0.71; 95% CI, 0.56–0.89) in the Japanese population, in addition to the previously reported alleles (Table S2) [7]. The discrepancy in the association of HLA-DPB1*09:01 allele with risk for HBV infection in a previous study [7] results from the elevated frequency of HLA-DPB1*09:01 in the controls (12.2%), which is higher than our controls (8.7%). In this study, healthy subjects were recruited as controls. In contrast, individuals that were registered in BioBank Japan as subjects with diseases other than CHB were recruited as controls in the previous study [7], which may have included patients with diseases with which HLA-DPB1*09:01 is associated. Although no significant association of HLA-DPB1*09:01 with risk for HBV infection was observed in the Korean subjects, HLA-DPB1*09:01 appears to have a susceptible effect on HBV infection, as it showed the same direction of association. When the association analyses in Japanese and Korean subjects were combined in meta-analysis, the association was statistically significant (P = 1.36 × 10^{-3}; OR = 1.97; 95% CI, 1.50–2.59). Thus, HLA-DPB1*09:01 may be a Northeast Asian-specific allele associated with risk for HBV infection.

Moreover, a significant association of HLA-DPB1*13:01 with risk of HBV infection (OR = 2.17; 95% CI, 1.40–3.47) was identified in the Thai subjects. However, the frequency of HLA-DPB1*13:01 in Thai healthy controls (11.5% in the present study) reportedly varies, ranging from 15.4% to 29.5%, due to the population diversity [15–17]. Therefore, a replication analysis is required to confirm the association of HLA-DPB1*13:01 with HBV infection in the Thai subjects. There were four other marginally associated HLA-DPB1 alleles with low allele frequencies below 5% in HBV patients and healthy controls, including HLA-DPB1*28:01, -DPB1*31:01, -DPB1*100:01, and -DPB1*165:01, in the Hong Kong and Thai subjects. Because these infrequent alleles may have resulted from false positive associations, the association needs to be validated in a large number of subjects.

HLA-DPB1*02:01 showed a significant association with protection against HBV infection in both Japanese and Hong Kong populations (Table S2); however, the HLA-DPB1*02:01 allele was not associated with HBV infection in the previous study [7]. Although HLA-DPB1*02:01 showed no association in either Korean or Thai populations, a significant association of HLA-DPB1*02:01 with protection against HBV infection among four Asian populations was detected in meta-analysis (P = 5.22 × 10^{-6}; OR = 0.68; 95% CI, 0.58–0.81) (Fig. S1B). We therefore conclude that the present finding is not a false positive.

A recent report showed that HLA-DPB1*02:01, *05:01, *04:01, *04:01, *09:01, and *14:01 were significantly associated with response to booster HB vaccination in Taiwan neonatally vaccinated adolescents [18]. The HLA-DPB1*02:01, *02:02, *03:01, *04:01, and *14:01 were significantly more frequent in recipients whose post-booster titers of antibodies against HBV surface antigen (anti-HBs) were detectable, on the other hand, HLA-DPB1*05:01 and *09:01 were significantly more frequent in recipients who were undetectable. Moreover, the HLA-DPB1*05:01 and *09:01 significantly increase the likelihoods of undetectable pre-booster anti-HBs titers. These results seem consistent with our findings, in which HLA-DPB1*05:01 and *09:01 are associated with susceptibility to chronic hepatitis B infection.

We also identified a protective effect of HLA-DPB1*02:01 allele on disease progression in Asian populations. Previous studies identified the association of HLA class II genes including HLA-DQ and HLA-DR with development of HBV related hepatocellular carcinoma in the Chinese population [6,19,20]. In this study using Japanese and Korean samples, we identified significant associations between HLA-DPB1*02:01 and disease progression in CHB patients (P = 4.26 × 10^{-3}; OR = 0.45; 95% CI, 0.30–0.67, for Japanese and P = 8.74 × 10^{-4}; OR = 0.47; 95% CI, 0.29–0.75 for Korean) (Table S4). Although the association of HLA-DPB1*02:01 with disease progression was weaker after adjustment for age and gender in Korean subjects (P = 2.54 × 10^{-2}; OR = 0.55; 95% CI, 0.33–0.93), the same direction of association was observed (i.e. protective effect on disease progression) (Table 2). The protective effects of HLA-DPB1*02:01 on disease progression showed a significant association after adjustment for age and gender in the Japanese population (P = 1.77 × 10^{-3}; OR = 0.47; 95% CI, 0.32–0.70); moreover, a significant association between HLA-DPB1*02:01 was observed among four Asian populations, under which population was adjusted by using dummy variables in a multivariate logistic regression analysis (P = 1.55 × 10^{-7}; OR = 0.50; 95% CI, 0.39–0.65) (Table 2).

The HLA-DPA1 and HLA-DPB1 belong to the HLA class II alpha and beta chain paralogues, which make a heterodimer consisting of an alpha and a beta chain on the surface of antigen presenting cells. This HLA class II molecule plays a central role in the immune system by presenting peptides derived from extracellular proteins. We identified two susceptible haplotypes (DPA1*02:02-DPB1*05:01 and DPA1*02:01-DPB1*09:01) and three protective haplotypes (DPA1*01:03-DPB1*04:01, DPA1*01:03-DPB1*04:02, and DPA1*01:03-DPB1*02:01) to chronic hepatitis B infection, which may result in different binding interactions with the immune system by presenting peptides derived from extracellular proteins. We identified two susceptible haplotypes (DPA1*02:02-DPB1*05:01 and DPA1*02:01-DPB1*09:01) and three protective haplotypes (DPA1*01:03-DPB1*04:01, DPA1*01:03-DPB1*04:02, and DPA1*01:03-DPB1*02:01) to chronic hepatitis B infection, which may result in different binding interactions with the immune system by presenting peptides derived from extracellular proteins.
affinities between HLA-DP subtypes and extracellular antigens. Although functional analyses of HLA-DP subtypes to identify HBV-related peptides are not fully completed, identification of susceptible and protective haplotypes as host genetic factors would lead us to understand the pathogenesis of HBV infection including viral factors.

In summary, we identified a new risk allele HLA-DPB1*09:01, which was specifically observed in Northeast Asian populations: Japanese, Korean, Hong Kong and Thai. The protective allele HLA-DPB1*02:01 was associated with both chronic HBV infection and disease progression in chronic HBV patients. Identification of a total of five alleles, including two risk alleles (dpb1*09:01 and dpb1*05:01) and three protective alleles (dpb1*04:01, dpb1*04:02 and dpb1*02:01), would enable HBV-infected individuals to be classified into groups according to the treatment requirements. Moreover, the risk and protective alleles for HBV infection and disease progression, identified in this study by means of trans-ethnic association analyses, would be key host factors to recognize HBV-derived antigen peptides. The present results may lead to subsequent functional studies into HLA-DP molecules and viral factors in order to understand the pathogenesis of HBV infection and development of hepatocellular carcinoma.

Materials and Methods

Ethics Statement

All study protocols conform to the relevant ethical guidelines, as reflected in the a priori approval by the ethics committee of all participating universities and hospitals, including The University of Tokyo, Japanese Red Cross Kanto-Koshinetsu Blood Center, The University of Hong Kong, Chulalongkorn University, Yonsei University College of Medicine, Nagoya City University Graduate School of Medical Sciences, Musashino Red Cross Hospital, Tokyo Medical and Dental University, Trine Keijinkai Hospital, Hokkaido University Graduate School of Medicine, Kurume University School of Medicine, Okayama University Graduate School of Medicine, Yamaguchi University Graduate School of Medicine, Tottori University, Kyoto Prefectural University of Medicine, Osaka City University Graduate School of Medicine, Nagoya Daini Red Cross Hospital, Ehime University Graduate School of Medicine, Kanazawa University Graduate School of Medicine, National Hospital Organization Osaka National Hospital, Iwate Medical University, Kawasaki Medical College, Shinshu University School of Medicine, Saitama Medical University, Kitasato University School of Medicine, Saga Medical School, and University of Tsukuba.

Written informed consent was obtained from each patient who participated in this study and all samples were anonymized. For Japanese healthy controls, 419 individuals were de-identified with information about gender, and all were recruited after obtaining verbal informed consent in Tokyo prior to 1990. For the 419 Japanese healthy individuals, written informed consent was not obtained because the blood sampling was conducted before the “Ethical Guidelines for Human Genome and Genetic Sequencing Research” were established in Japan. Under the condition that DNA sample is permanently de-linked from the individual, this study was approved by the Research Ethics Committee of National Center for Global Health and Medicine.

Characteristics of studied subjects

All of the 3,167 genomic DNA samples were collected from individuals with HBV, HBV-resolved individuals (HBsAg-negative and anti-HBc-positive) and healthy controls at 26 multi-center hospitals throughout Japan, Korea, Hong Kong, and Thailand (Table 1). In a total of 1,291 Japanese and 586 Korean samples, 1,191 Japanese individuals and all 586 Korean individuals were included in our previous study [9]. With regard to additional Japanese individuals, we collected samples from 48 healthy controls at Kohnozai Hospital, and 32 HBV patients at Okayama University Hospital and Ehime University Hospital, including 26 individuals with LC and 26 individuals with HCC. A total of 661 Hong Kong samples and 629 Thai samples were collected at Queen Mary Hospital and Chulalongkorn University, respectively.

HBV status was measured based on serological results for HBsAg and anti-HBe with a fully automated chemiluminescent enzyme immunoassay system (Abbott ARCHITECT; Abbott Japan, Tokyo, Japan, or LUMIPULSE f or G1200; Fujirebio, Inc., Tokyo, Japan). For clinical staging, inactive carrier (IC) state was defined by the presence of HBsAg with normal ALT levels over 1 year (examined at least four times at 3-month intervals) and without evidence of liver cirrhosis. Chronic hepatitis (CH) was defined by elevated ALT levels (>1.5 times the upper limit of normal [35 IU/L]) persisting over 6 months (by at least 3 bimonthly tests). Acute exacerbation (AE) of chronic hepatitis B was defined as an elevation of ALT to more than 10 times the upper limit of normal (ULN, 58 IU/L) and bilirubin to at least three times ULN (15 μmol/L). LC was diagnosed principally by ultrasonography (coarse liver architecture, nodular liver surface, blunted liver edges and hypersplenism), platelet counts<100,000/ cm³, or a combination thereof. Histological confirmation by fine-needle biopsy of the liver was performed as required. HCC was diagnosed by ultrasonography, computerized tomography, magnetic resonance imaging, angiography, tumor biopsy or a combination thereof.

The Japanese control samples from HBV-resolved subjects (HBsAg-negative and anti-HBc-positive) at Nagoya City University-affiliated healthcare center were used by comprehensive agreement (anonymization in a de-identified manner) in this study. Some of the unrelated and anonymized Japanese healthy controls were purchased from the Japan Health Science Research Resources Bank (Osaka, Japan). One microgram of purified genomic DNA was dissolved in 100 μl of TE buffer (pH 8.0) (Wako, Osaka, Japan), followed by storage at −20°C until use.

Genotyping of HLA-DPA1 and HLA-DPB1 alleles

High resolution (4-digit) genotyping of HLA-DPA1 and -DPB1 alleles was performed for HBV patients, resolved individuals, and healthy controls in Japan, Korea, Hong Kong, and Thailand. LABType SSO HLA DPA1/DPB1 kit (One Lambda, CA) and a Luminex Multi-Analyte Profiling system (xMAP; Luminex, Austin, TX) were used for genotyping, in accordance with the manufacturer’s protocol. Because of the small quantity of genomic DNA in some Korean samples, we performed whole genome amplification for a total of 486 samples using GenomiPhi v2 DNA Amplification kit (GE Healthcare Life Sciences, UK), in accordance with the manufacturer’s instruction.

A total of 2,895 samples were successfully genotyped and characteristics of these samples are summarized in Table S1.

Statistical analysis

Fisher’s exact test in two-by-two cross tables was used to examine the associations between HLA-DP allele and chronic HBV infection or disease progression in chronic HBV patients,
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using statistical software R 2.9. To avoid false-positive results due to multiple testing, significance levels were adjusted based on the number of observed alleles at each locus in each population. For HLA-DPA1 alleles, the number of observed alleles was 3 in Japanese, 4 in Korean, 5 in Hong Kong, and 5 in Thai subjects. Therefore, the significant levels for α were set as α = 0.05/5 in Japanese, α = 0.05/4 in Korean, α = 0.05/5 in Hong Kong, and α = 0.05/5 in Thai subjects. In the same way, significant levels for HLA-DPB1 alleles were α = 0.05/10, 0.05/11, 0.05/12, and 0.05/16, respectively. Multivariate logistic regression analysis adjusted for age and sex (used as independent variables) was applied to assess associations between the number of DPB1*02:01 alleles (i.e., 0, 1, or 2) and disease progression in CHB patients. To examine the effect of DPB1*02:01 allele on disease progression in all populations, population was further adjusted by using three dummy variables (i.e., (c1, c2, c3) = (0, 0, 0) for Japanese, (1, 0, 0) for Korean, (0, 1, 0) for Hong Kong, and (0, 0, 1) for Thai) in a multivariate logistic regression analysis. We obtained the following regression equation: logit(p) = −3.905+0.083*age+(−0.929)*sex+(−0.684)*DPB1*02:01+1.314*1+c1+(−0.478)*c2+0.748*c3. Significance levels in the analysis of disease progression in CHB patients were set as α = 0.05/10 in Japanese, α = 0.05/11 in Korean, α = 0.05/15 in Hong Kong, and α = 0.05/15 in Thai subjects. The phase of each individual (i.e., a combination of two DPA1-DPB1 haplotypes) was estimated using PHASE software [21], assuming samples are selected randomly from a general population. In comparison of the estimated DPA1-DPB1 haplotype frequencies, significant levels were set as α = 0.05/14 in Japanese, α = 0.05/17 in Korean, α = 0.05/17 in Hong Kong, and α = 0.05/18 in Thai subjects. Meta-analysis was performed using the DerSimonian-Laird method (random-effects model) in order to calculate pooled OR and its 95% confidence interval (95% CI). Meta-analysis was performed using the DerSimonian-Laird method (random-effects model) to calculate pooled OR and its 95% confidence interval (95% CI). Bold depicts a statistically significant association after correction of significance level. (DOCX)

Table S1 Individuals with successfully genotyped for HLA-DPA1 and HLA-DPB1.

(DOCX)

Table S2 Frequencies of HLA-DP alleles in HBV patients and healthy controls among Asian populations.

(MLSX)

Table S3 Frequencies of HLA-DP alleles in HBV patients and resolved individuals among Asian populations.

(MLSX)

Table S4 Associations of HLA-DPB1 alleles with disease progression in CHB patients among Asian populations.

(MLSX)

Table S5 Estimated frequencies of HLA DPA1-DPB1 haplotypes in HBV patients and healthy controls among Asian populations.

(MLSX)

Acknowledgments

We would like to thank all the patients and families who contributed to the study. We are also grateful to Ms. Mayumi Ishii (National Center for Global Health and Medicine), Ms. Megumi Sageshima, Yuko Hirano, Natsumi Baba, Rieko Shirahashi, Ayumi Nakayama (University of Tokoyo), and Yuko Ohara (Japanese Red Cross Kanto-Koshinetsu Block Blood Center) for technical assistance.

Author Contributions

Conceived and designed the experiments: NN HS MS KT M. Mizokami. Performed the experiments: NN HS KK Y. Mawatari M. Kawashima M. Minami. Analyzed the data: NN HS M. Kawashima JO. Contributed reagents/materials/analysis tools: W-KS M-FY NP YP SHA K-HH K. Matsuura YT M. Kurosaki YA NI J-HK SH TI KY IS Y. Murawaki YI AT EO YH MH SK EM KS KH ET SM MW YE NM K. Murata M. Korenaga KT M. Mizokami. Wrote the paper: NN HS JO KT M. Mizokami.

Supporting Information

Figure S1 Comparison of odds ratios in association analyses for HLA-DP with chronic HBV infection among four Asian populations: (A) HLA-DPA1 alleles; (B) HLA-DPB1 alleles; and (C) HLA-DPA1-DPB1 haplotypes. Meta-

analysis was performed using the DerSimonian-Laird method (random-effects model) to calculate pooled OR and its 95% confidence interval (95% CI). Bold depicts a statistically significant association after correction of significance level.

References