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Transmission of hepatitis B virus (HBV) genotypes among Japanese immigrants and natives in Bolivia

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Abstract

Hepatitis B virus genotypes are associated with transmission pattern, virological and clinical features and outcome of the chronic infection course. HBV genotypes other than Genotype F (HBV/F) are considered a reflection of human migration into South America. A total of 487 individuals in Bolivia, including Japanese immigrants ($n = 287$) and natives ($n = 200$), were screened for HBV serological markers. Overall 22/487 (4.5%) of the subjects were positive for HBsAg, 217/487 (44.5%) for anti-HBc and 162/487 (33.3%) for anti-HBs. Genotypes were determinable in 22 cases by EIA, followed by sequencing and phylogenetic analysis in 17 cases. HBV genotype distribution in Japanese and Bolivians was HBV/F (4 and 8); HBV/C (5 and 3); and HBV/B (1 and 1), respectively. Phylogenetic analyses of nine complete and eight partial (HBsAg/pre-core/core region) genomes, revealed that HBV/F strains cluster with previously reported regional strains, whereas HBV/B and HBV/C strains belonged to Asian subgenotype B2 (Ba) and C2 (Ce), respectively. Japanese immigrants might have introduced HBV/B and HBV/C to natives in Bolivia, conversely, exposed to the indigenous HBV/F. This report provides evidence of an inter-communities transmission of HBV revealed by its genotypes. Further study is required to investigate peculiarities of the genotypes in different ethnic groups in Bolivia.

Keywords: Bolivians; Japanese immigrants; HBV; Genotypes; Transmission

1. Introduction

Reports indicate that about two billion people are exposed to HBV and 350 million of them have chronic infection around the world. Morbidity and mortality in chronic HBV infection is associated with development of liver cirrhosis (LC) and hepatocellular carcinoma (HCC). Populations is South and East Asia, sub-Saharan Africa, and Central and South America show particularly high frequencies of HBV infection that may be maintained through mother to child perinatal transmission (Chen et al., 2004) or horizontal transmission in childhood (Dumpis et al., 2001). Knowledge of hepatitis B infection and genotype distribution is necessary to design and evaluate the preventive measures, such as universal immunization.

HBV strains infecting humans show antigenic and genetic heterogeneity and are currently classified into eight genotypes that differ in nucleotide sequence by >8% and subgenotypes by >4%. These genotypes have geographical distribution: A and D have global distributions; genotypes B and C are found predominantly in East and Southeast Asia; genotype E in West Africa; and genotypes F and H are considered indigenous to Central and South America (Miyakawa and Mizokami, 2003; Norder et

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Table 1
Prevalence of hepatitis B virus (HBV) markers among 487 residents in Eastern Bolivia

Features	Total ($n=487$)	Japanese immigrants ($n=287$)	Native Bolivians ($n=200$)	P[a]
Sex (M/F)	193/294	120/167	72/128	NS
Median age[b]	51 (8–95)	63 (8–95)	37 (8–67)	<0.0001
Anti-HBc[c]	217 (44.5)	162 (56.4)	55 (27.5)	<0.0001
Anti-HBs[c]	162 (33.3)	108 (37.6)	53 (26.5)	0.011
HBsAg[c]	22 (4.5)	10 (3.4)	12 (6)	NS
HBV DNA[c]	17 (3.5)	9 (3.1)	8 (4)	NS

[a] p-value, Japanese immigrants vs. native Bolivians.
[b] Years (range).
[c] n (%).

al., 2004) The genetic diversity of HBV and the geographical distribution of its subgenotypes provide a tool to reconstruct the evolutionary history of HBV (Norder et al., 2004). The eight genotypes of HBV have also been divided into subgenotypes with distinct ethnic or geographical origin (Campos et al., 2005; Sakamoto et al., 2006). The most prevalent genotype of Central and South America, genotype F is subdivided into two subgenotypes, F1 and F2 (Norder et al., 2003) and a total of five clusters. Subgenotype F1 includes two clusters, 1a and 1b, with strains isolated mainly in Central America and Argentina, respectively. Subgenotype F2 including three clusters with strains found in Nicaragua, Venezuela and Brazil (cluster II), in Panama, Venezuela, and Columbia (cluster III) and in Argentina and Bolivia (Cluster IV) (Huy et al., 2006; Mbayed et al., 2001).

Although HBV/F is the most prevalent genotype of Central and South America, other HBV genotypes found in different Latin American countries are considered a reflection of migration of human population from other geographical areas into the region (Campos et al., 2005). It is thought that the first Japanese who arrived at the Bolivian territory came by the way of Peru and passing through Andean mountains settled in Amazonas. In 1950s the Japanese community in Bolivia began to grow composed of Colonia Okinawa and Colonia San Juan, both in Santa Cruz (Eastern Bolivia). Keeping in view the inter-marital and cultural contacts with native Bolivians, the inter-communities transmission of HBV genotypes seems a natural phenomenon.

The present study was conducted to examine Japanese immigrants and natives in Bolivia for HBV infection and distribution of HBV genotypes in both communities.

2. Methods

2.1. Subjects

Sera were collected from 487 residents in Eastern Bolivia (randomly selected healthy carriers), these included Japanese immigrants ($n=287$) and native population ($n=200$). Japanese immigrants and native Bolivian were defined according to their birth place; Japan and Bolivia, respectively. After isolation of the serum fraction from whole blood, the samples were stored at −40 °C until use. The number of subjects studied, their ages and sexes are summarized in Table 1.

2.2. Serological analysis

HBV serological markers (HBsAg, anti-HBc, and anti-HBs) were examined by chemiluminescence with commercial assay kits (Fujirebio Inc., Tokyo, Japan) (Table 1). Serum samples

Table 2
HBV DNA oligonucleotide primers for complete genomes of genotype F

Primer	Nucleotide sequence (5′–3′)	Position	Polarity
(1) Fragment A			
HBVH55F	TCCTGCTGGTGGCTCC	55–70	Sense
HBVH1801R	GTTGCATGGTGCTGGTGAAC	1820–1801	Antisense
HB6R	AACAGACCAATTTATGCCTA	1803–1784	Antisense
(2) Fragment B			
HBVH1611F	GAGACCACCGTGAACGCCC	1611–1629	Sense
HBVH285R	GCCAGGACACCCGGGTGGTA	304–285	Antisense
HBVH229R	CGAGTCTAGACTCTGTGGTATTGTGAGG	256–229	Antisense
(3) Sequencing primers			
HB2F	TGCTGCTATGCCTCATCTTC	414–433	Sense
HBVH760F	GCCAAATCTGTGCAGCATCTTGAG	760–783	Sense
HB5F	CTCTGCCGATCCATACTGCGGAA	1256–1278	Sense
HBVH1859F	ACTGTTCAAGCCTCCAAGCTGT	1859–1880	Sense
HBVH2415F	GTCGCAGAAGATCTCAATCTC	2415–2435	Sense
HBVH2814F	GGGTCACCATATTCCTGGGAA	2814–2834	Sense