

みなさまにお伺いします。

G-4 病名はどのように説明されていますか。あてはまるもの一つを選んでください。

1. 無症候性キャリア
2. 慢性肝炎
3. 肝硬変
4. その他（ ）

G-5 肝がんと診断を受けたことはありますか。

1. はい
2. いいえ

G-6 肝臓病の治療のために支払った、平成24年（1月～12月）の医療費を教えてください。

1. 5万円未満
2. 5万円以上10万円未満
3. 10万円以上20万円未満
4. 20万円以上30万円未満
5. 30万円以上50万円未満
6. 50万円以上100万円未満
7. 100万円以上

G-7 肝炎治療医療費助成制度を利用していますか。

1. はい
2. いいえ

G-8 加入している医療保険について教えてください。

1. 国民健康保険
2. 後期高齢者医療
3. 協会けんぽ
4. 健康保険組合
5. 共済組合
6. その他（ ）

G-9 B型肝炎以外による、定期的な通院はありますか。

1. はい
2. いいえ（いはいに○をした方はH-1へ）

G-9-1 はいの場合、その病名を教えてください。

--

みなさまにお伺いします。

H-1 あなたの年齢を教えてください。

_____歳

H-2 あなたの性別を教えてください。

1. 男性 2. 女性

H-3 あなたのお住まいの地域を教えてください。

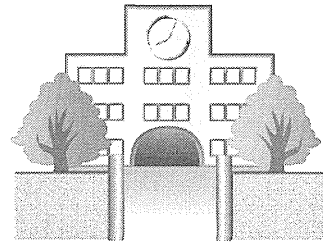
_____（都・道・府・県） _____（市・区・郡）

H-4 あなたの仕事の内容について教えてください。

- | | |
|-----------------------|---------------------------------------------|
| 1. 会社員（管理職以外の正社員） | 9. 自営業（農林漁業を除く） |
| 2. 会社員（管理職） | 10. フリーター |
| 3. 会社役員・経営者 | 11. 専業主婦・主夫（パートあり） |
| 4. 派遣・契約社員 | 12. 専業主婦・主夫（パートなし） |
| 5. 公務員・非営利団体職員 | 13. 学生（アルバイトあり） |
| 6. 教職員講師 | 14. 学生（アルバイトなし） |
| 7. 専門職（弁護士、会計士、税理士など） | 15. 無職、定年退職 |
| 8. 農林漁業 | 16. その他（ ） |

H-5 あなたの最終学歴を教えてください。

1. 高校卒業まで
2. 短期大学・専門学校卒業まで
3. 大学卒業以上
4. その他（ ）



H-6 あなたの世帯の平成24年（1月～12月）の所得額*を教えてください。

- | | |
|----------------|-----------------|
| 1. 100万円未満 | 4. 600～1000万円未満 |
| 2. 100～300万円未満 | 5. 1000万円以上 |
| 3. 300～600万円未満 | 6. 答えたくない |

*なお、所得額とは、

給与所得のみの方は、事業主が発行する給与所得の源泉徴収票の支払金額欄に記載された金額です。確定申告をされた方は、所得税の確定申告書の所得金額合計欄に記載された金額です。

みなさまにお伺いします。

H-7 あなたの世帯で、ふだん一緒にお住まいで生計を共にしている方は、あなたを含めて何人ですか。

_____人

H-8 現在お住まいの住居について教えてください。

- | | |
|------------------|----------------------|
| 1. 持ち家 | 4. 都市再生機構・公社等の公営賃貸住宅 |
| 2. 民間賃貸住宅 | 5. 間借り |
| 3. 社宅・公務員住宅等給与住宅 | 6. その他（ _____ ） |

H-9 毎日、何時頃に起きていますか。

午前・午後_____時頃

H-10 毎日、何時頃に就寝していますか。

午前・午後_____時頃

H-11 1日の食事の回数は何回ですか。

_____回

H-12 就寝時間は不規則なほうですか（床に就く時間が2時間以上変化する日が、1週間に3日以上ありますか）。

- | | |
|-------|--------|
| 1. はい | 2. いいえ |
|-------|--------|

H-13 食事時間は不規則なほうですか（毎日の食事時間が2時間以上変化するか、1日の食事回数に変化する日が、1週間のうち3日以上ありますか）。

- | | |
|-------|--------|
| 1. はい | 2. いいえ |
|-------|--------|

H-14 1日の排尿の回数はどのくらいですか。

約_____回

H-15 排便の回数はどのくらいですか。

- | | |
|-------------|-----------------|
| 1. 1日に3回以上 | 4. 1週間に1回以下 |
| 2. 1日に1~2回 | 5. その他（ _____ ） |
| 3. 1週間に2~3回 | |

みなさまにお伺いします。

H-16 一日のうち、仕事や家事、ボランティアなどに費やす時間をお答えください。
約_____時間

H-17 現在、喫煙していますか。
1. はい 2. いいえ

H-18 1週間に、1回以上飲酒しますか。
1. はい 2. いいえ

H-19 日常生活で、他の人の介助が必要なことはありますか。
あてはまるものすべてに○をつけてください。
1. 食事 6. トイレ
2. 服薬・通院 7. 歩行・移動
3. 歯磨き・洗顔 8. 会話・視覚・聴覚・判断
4. 入浴 9. その他 ()
5. 更衣 10. なし

H-20 前問(H-19)で2に○をした方にお尋ねします。(2以外に○をした方はH-21へ)
あなたの服薬・通院について介助をしてくださる方はいらっしゃいますか。
1. はい 2. いいえ (いいえに○をした方はH-21へ)

H-20-1 はいの場合、それはどなたですか。あてはまるものすべてに○をつけてください。
1. 配偶者
2. 家族
3. 親族
4. 介護ヘルパー
5. 介護施設の人
6. その他 ()

みなさまにお伺いします。

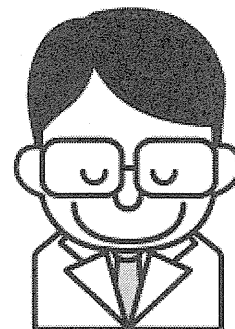
H-21 こんな薬、こんな治療法があったらいいなと思うことがありましたら、
自由にお書きください。

みなさまにお伺いします。

H-22 下記のうち、正しいと思うものすべてに○をつけてください。この質問は、B 型肝炎に関する情報をきちんとお伝えできているかを見るものですので、気楽にお答えください。

1. B型肝炎ウイルスは、血液を介して感染する
2. B型肝炎ウイルスは、血液が付着したものを介して感染する可能性がある
3. 感染を防ぐために、生活上の注意すべき事柄がある
4. ワクチンで感染を予防することができる
5. 従来型のB型肝炎ウイルスは、乳幼児期に初めて感染すると慢性化しやすい
6. 最近日本に増えてきているB型肝炎ウイルスのタイプは、成人で初めて感染しても慢性化することがある
7. B型肝炎の病気の進行の程度は、個人により差が大きい
8. B型肝炎ウイルスは、C型肝炎ウイルスとウイルスの性質が異なる
9. B型肝炎は、C型肝炎と治療方法が異なる
10. B型肝炎は、C型肝炎と治療効果の判断方法が異なる

以上で質問はすべて終了です。



長時間ご協力くださいましてありがとうございました。

本調査票は同封の返信用封筒に入れて、平成 25 年 11 月 30 日

(当日消印有効)までに、本調査用紙および返信用封筒にも無記名

の状態で（お名前や住所を記入せずに）郵送をお願いします。

Ⅲ. 研究成果の刊行に関する一覧表

【書籍】

関連	著者氏名	論文タイトル名	書籍全体の編集者名	書籍名	出版社名	出版地	出版年	ページ
	正木尚彦	急性肝炎サーベイランスの現状	山本和秀監修、考田雅彦・能祖一裕編集	わが国における急性肝炎の現状 全国調査2008-2011	中外医学社	東京	2012	20-25
	正木尚彦	第XVIII章 肝疾患診療に関する病診連携 1. 肝疾患診療連携拠点病院ならびに肝疾患診療連携ネットワーク. 第XIX章 肝疾患診療に関連する法律、制度 2. 肝炎対策基本法、3. 肝炎治療特別促進事業（医療費助成制度）	日本肝臓学会編	肝臓専門医テキスト	南江堂	東京	2013	460-464、472-473、474-479

【雑誌】

関連	発表者氏名	論文タイトル名	発表誌名	巻号	ページ	出版年
	Tamada Y, Yatsunami H, <u>Masaki N</u> , Nakamura M, Mita E, Komatsu T, Watanabe Y, Shimada M, Hijioka T, Satoh T, Mano Y, Komeda T, Takahashi M, Kohno H, Ota H, Hayashi S, Miyakawa Y.	Hepatitis B virus strains of subgenotype A2 with an identical sequence spreading rapidly from the capital region to all over Japan in patients with acute hepatitis B.	Gut	61(5)	765-773	2012
	<u>正木尚彦</u>	肝炎をめぐる政策医療	医学のあ ゆみ	240(12)	997-999	2012

IV. 研究成果の刊行物・別刷

ORIGINAL ARTICLE

Hepatitis B virus strains of subgenotype A2 with an identical sequence spreading rapidly from the capital region to all over Japan in patients with acute hepatitis B

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ABSTRACT

Objective To examine recent trends of acute infection with hepatitis B virus (HBV) in Japan by nationwide surveillance and phylogenetic analyses.

Methods During 1991 through 2009, a sentinel surveillance was conducted in 28 national hospitals in a prospective cohort study. Genotypes of HBV were determined in 547 patients with acute hepatitis B. Nucleotide sequences in the preS1/S2/S gene of genotype A and B isolates were determined for phylogenetic analyses.

Results HBV genotype A was detected in 137 (25% (accompanied by genotype G in one)) patients, B in 48 (9%), C in 359 (66%), and other genotypes in the remaining three (0.5%). HBV persisted in five with genotype A including the one accompanied by genotype G; another was co-infected with HIV type 1. The genotype was A in 4.8% of patients during 1991–1996, 29.3% during 1997–2002, and 50.0% during 2003–2008 in the capital region, as against 6.5%, 8.5% and 33.1%, respectively, in other regions. Of the 114 genotype A isolates, 13 (11.4%) were subgenotype A1, and 101 (88.6%) were A2, whereas of the 43 genotype B isolates, 10 (23.3%) were subgenotype B1, 28 (65.1%) were B2, two (4.7%) were B3, and three (7.0%) were B4. Sequences of 65 (64%) isolates of A2 were identical, as were three (23%) of A1, and five (18%) of B2, but none of the B1, B3 and B4 isolates shared a sequence.

Conclusions Acute infection with HBV of genotype A, subgenotype A2 in particular, appear to be increasing, mainly through sexual contact, and spreading from the capital region to other regions in Japan nationwide. Infection persisted in 4% of the patients with genotype A, and HBV strains with an identical sequence prevailed in subgenotype A2 infections. This study indicates the need for universal vaccination of young people to prevent increases in HBV infection in Japan.

Significance of this study

What is already known about this subject?

- ▶ In Japan, a national prevention programme was started in 1986 with selective vaccination of babies born to mothers who carry hepatitis B virus (HBV). Since then, the prevalence of hepatitis B surface antigen among younger generations has decreased sharply.
- ▶ However, retrospective studies indicate that the frequency of HBV genotype A is increasing among patients with acute hepatitis B (AHB) within the capital region of Japan.
- ▶ Infection with genotype A more often persists than infection with other genotypes.
- ▶ Because there is no reliable and comprehensive surveillance system for AHB in Japan, the incidence of AHB and factors responsible for changes over many years are not known.

What are the new findings?

- ▶ This is a prospective cohort study for surveillance of AHB throughout Japan in a national research programme.
- ▶ The incidence of AHB in Japan has not decreased, because genotype A infections have increased over time.
- ▶ Genotype A infections started to increase in the capital region of Japan, and then spread to other regions 5–6 years later.
- ▶ About 90% of genotype A found in AHB patients in Japan is subgenotype A2.
- ▶ Subgenotype A2 isolates from patients with AHB tend to preserve sequence identity over time, indicating that particular subgenotype A2 strains have been transmitted without undergoing mutations.

Hepatitis B virus (HBV) has been classified into 10 genotypes, designated A–J, based on a >8% divergence in the full-genome sequence.^{1–7} Different genotypes are associated with distinct clinical manifestations, such as severity and progression of

liver disease, as well as response to antiviral treatments.^{8–10} Some genotypes are subclassified: genotype A into at least two subgenotypes, A1 (Asian/African type) and A2 (European type)^{11–13};

Significance of this study

How might it impact on clinical practice in the foreseeable future?

- ▶ It needs to be noted that subgenotype A2 infections are spreading among sexually active generations in Japan.
- ▶ Although selective vaccination has prevented mother-to-baby transmission of HBV since 1986, it does not contain sporadic infections in Japan.
- ▶ Herd vaccination of younger generations needs to be considered in Japan.

B into B1 (Japanese type) and B2 (Asian type)^{14 15}; and C into C1 (Southeast-Asian type) and C2 (East-Asian type).¹⁶ Subgenotypes also influence the replication of HBV and clinical manifestation.^{15 17 18}

According to a report from Japan in 2001,¹⁹ genotype C was the most prevalent (84.7%), followed by genotype B (12.2%) and A (1.7%), among patients with chronic hepatitis B. In 2002, genotype A became the most prevalent in patients with acute hepatitis B (AHB) around Tokyo, the capital region of Japan.^{20 21} Several reports have shown that infection with HBV genotype A is associated with particular sexual behaviours, such as homosexual activity and promiscuous sexual contacts, and tends to persist longer than that with HBV genotype C.^{22 23} These reports have raised concerns about the horizontal HBV infection in adults, which, in general, is considered to resolve spontaneously. However, adult-acquired HBV infection may result in chronic HBV infection in some instances.

Information on changes in genotype distribution over time, as well as genotype-specific clinical manifestations, may help in planning preventive measures and antiviral therapy strategies. Therefore it is important to examine how genotype A infection has spread in Japan, and what clinical and virological characteristics it possesses.

We have been conducting a nationwide, sentinel surveillance on acute viral hepatitis for more than 30 years. As part of this surveillance, a prospective cohort study has been conducted on 547 patients with AHB in 28 medical centres over the 19 years from 1991 to 2009. Geographical and longitudinal distributions of HBV genotypes/subgenotypes were surveyed, and their influence on clinical outcome was evaluated.

PATIENTS AND METHODS

Patients

A total of 681 patients with sporadic AHB were enrolled consecutively in a survey carried out by the Japan National Hospital Acute Hepatitis Study Group (JNHAHSG). They were admitted to 28 national hospitals from January 1991 to the end of December 2009. They were grouped geographically into two areas: the capital region (Gunma, Saitama, Tokyo and Kanagawa) and other regions (figure 1). Patients were also longitudinally categorised into three periods: 1st (1991–1996), 2nd (1997–2002) and 3rd (2003–2008). In addition, the year 2009 provided the most recent data. Of the 681 patients, 547 (80.3%) entered the study, for whom serum samples were available on admission and had been stored at -20°C .

The diagnosis of AHB was based on the following criteria: (1) acute onset of liver injury without a history of liver dysfunction; (2) detection of hepatitis B surface antigen (HBsAg) in the

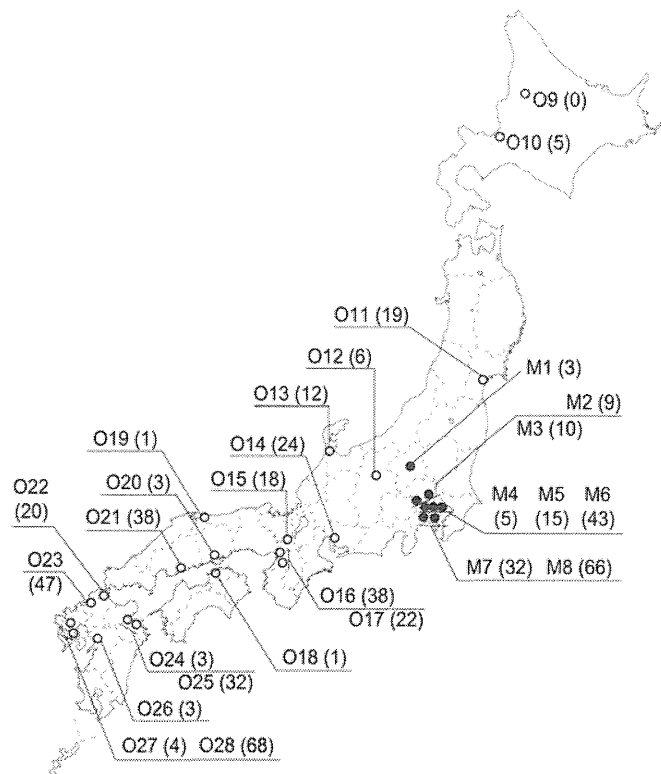


Figure 1 Locations of participating hospitals in Japan. Hospitals in the capital region (M1–M8) are indicated by eight closed circles, and those in other regions (O9–O28) by 20 open circles. Numbers in parentheses indicate the total number of enrolled subjects for each site. The hospitals are: M1, Nishigunma Hospital, Gunma; M2, Nishisaitama-Chuo Hospital, Saitama; M3, National Disaster Medical Center, Tokyo; M4, Tokyo Hospital, Tokyo; M5, Tokyo Medical Center, Tokyo; M6, National Center for Global Health and Medicine, Tokyo; M7, Sagami Hospital, Kanagawa; M8, Yokohama Medical Center, Kanagawa; O9, Asahikawa Medical Center, Hokkaido; O10, Hokkaido Medical Center, Hokkaido; O11, Sendai Medical Center, Miyagi; O12, Matsumoto Medical Center, Nagano; O13, Kanazawa Medical Center, Ishikawa; O14, Nagoya Medical Center, Aichi; O15, Kyoto Medical Center, Kyoto; O16, Osaka National Hospital, Osaka; O17, Osaka-Minami Medical Center, Osaka; O18, Zentsuji Hospital, Kagawa; O19, Yonago Medical Center, Tottori; O20, Okayama Medical Center, Okayama; O21, Kure Medical Center and Chugoku Cancer Center, Hiroshima; O22, Kokura Medical Center, Fukuoka; O23, Kyushu Medical Center, Fukuoka; O24, Beppu Medical Center, Oita; O25, Oita Medical Center, Oita; O26, Kumamoto Medical Center, Kumamoto; O27, Ureshino Medical Center, Saga; and O28, Nagasaki Medical Center, Nagasaki.

serum; (3) positivity for IgM antibody to HBV-core antigen (IgM anti-HBc) in high titres (detectable in sera diluted 10-fold); and (4) absence of past or family history of chronic HBV infection. Severe acute hepatitis (SAH) was defined as prothrombin time (PT) $\leq 40\%$ and hepatic encephalopathy of grade $\leq I$. Fulminant hepatitis (FH) was diagnosed from PT $\leq 40\%$ and hepatic encephalopathy of grade $\geq II$. Patients in whom HBsAg remained in the serum for >6 months after onset were considered to have acquired chronic HBV infection. The following information was collected from each patient: year and age at onset, gender, residential area, HBsAg, IgM anti-HBc, alanine aminotransferase, total bilirubin, PT, severity of liver disease, mortality, routes of transmission, sexual behaviours, travelling abroad in recent past, HBV genotype, mutations in precore (PreC) and core promoter (CP) regions, and RNA of hepatitis D virus. Antibody to HIV type 1 (anti-HIV) was

determined in patients who were at high risk and gave consent to testing.

Informed consent was obtained from each patient. The study protocol conforms to the ethical guidelines of the 1975 Declaration of Helsinki and the Ministry of Education, Culture, Sports Science and Technology of Japan, and was approved by the ethics committee of each institution.

Extraction of HBV DNA

HBV DNA was extracted from serum (100 μ l) by the SMITEST EX-R&D Nucleic Acid Extraction Kit (MBL Co, Nagoya, Japan) and used for genotyping/subgenotyping and detecting mutations in PreC and CP regions.

HBV genotypes

Genotypes were determined in Nagasaki Medical Center with the SMITEST HBV Genotyping Kit (MBL) by hybridisation with type-specific probes immobilised on a solid-phase support.²⁴

Determination of HBV subgenotypes

For subgenotyping, HBV DNA was amplified by PCR with TaKaRa Ex Taq (Takara Bio, Shiga, Japan). PCR was performed with appropriate nested primers to amplify a ~1.2 kb sequence in the preS1/S2/S gene (nucleotides 2854–835 in the reference isolate (AB116077)). PCR products were purified, subjected to cycle sequencing reaction with the BigDye Terminator v1.1 (Applied Biosystems, Tokyo, Japan), and applied to the DNA sequencer (3100-Avant; Applied Biosystems).

Mutations in the PreC and CP regions

The A1896 mutation in the PreC region was detected by the enzyme-linked minisequence assay (SMITEST HBV PreC ELMA; Roche Diagnostics, Tokyo, Japan), and mutations in the CP region for T1762/A1764 by the enzyme-linked specific probe assay (SMITEST HBV Core Promoter Mutation Detection Kit; Roche Diagnostics). The results were recorded as 'wild-type' and 'mutant types' dominantly expressed by HBV isolates.²⁵

Phylogenetic analyses

Nucleotide sequences were aligned, and phylogenetic trees were constructed by the CLUSTAL W program v1.83 (DDBJ homepage: <http://clustalw.ddbj.nig.ac.jp/top-j.html>). The statistical validity was assessed by bootstrap resampling with 1000 replicates. Reference HBV strains were retrieved from the GenBank database.

Statistical analysis

Results were expressed as percentage or mean \pm SD. Statistical differences were evaluated by χ^2 and Fisher exact tests for categorical variables, and analysis of variance and Scheffe's test for quantitative variables, using the SPSS software. The 95% CI, for the difference in means, was calculated in analyses for quantitative variables. $p < 0.05$ was considered significant.

RESULTS

Distribution of HV genotypes

HBV genotypes were determined in the 547 patients with AHB. The genotype was A in 137 (25.0%) patients (accompanied by G in one (0.2%)), B in 48 (8.8%), C in 359 (65.6%), D in one (0.2%), E in one (0.2%), and H in one (0.2%). Because HBV genotype G is a defective virus and cannot replicate by itself,^{26, 27} the single patient with mixed genotypes A and G was included in the 137 patients with genotype A in further analyses. RNA of hepatitis

D virus was detected in three of the 453 (0.7%) patients. Anti-HIV was examined in patients at high risk of infection and detected in 14 of the 53 (26.4%) who gave consent to testing.

Demographic and clinical differences among patients infected with HBV of distinct genotypes

Demographic and clinical characteristics of patients with different genotypes are compared in table 1. There was no difference in mean age among patients with genotypes A, B and C. The proportion of men was higher in patients with genotype A than B or C (94.2% vs 79.2%, $p < 0.05$; or 56.0%, $p < 0.0001$), and in those with genotype B than C (79.2% vs 56.0%, $p < 0.05$).

Maximum levels of total bilirubin were higher in patients with genotype A than C (9.6 ± 7.6 vs 7.1 ± 6.2 mg/dl, $p < 0.05$), with a difference of 2.5 mg/dl (95% CI 0.93 to 4.08), whereas the highest alanine aminotransferase activity and lowest PT values did not differ among patients with distinct genotypes.

SAH developed in four (2.9%) patients with genotype A, four (8.3%) with genotype B, and 26 (7.2%) with genotype C. FH developed in one (2.1%) patient with genotype B and eight (2.2%) with genotype C; no patients with genotype A developed FH. Eight (1.5%) patients died, including one with genotype B and seven with genotype C. There were no significant differences among patients with different genotypes in the frequency of SAH or FH or mortality.

The outcome of AHB was traceable in 514 of the 547 (94.0%) patients. Chronic infection with persistence of HBsAg for >6 months developed in five of the 123 (4.1%) patients with genotype A (including the one accompanied by genotype G), none of the 46 (0%) with genotype B, and none of the 342 (0%) with genotype C; it was more common in patients with genotype A than C ($p < 0.05$). HBV infection persisted exclusively in the patients with genotype A, either alone (four patients) or together with genotype G (one).

Among the five patients who acquired chronic HBV infection, four (three with genotype A and one with mixed genotypes A and G) were examined for anti-HIV, and one with genotype A was found to be positive. HBV infection persisted in three (including the one with anti-HIV) of the five patients for >1 year after the onset, and the remaining two (both without anti-HIV) cleared HBsAg from the serum after retaining it for >6 months.

Mutations in the PreC and/or CP region were detected in 3.7% (4/109) of patients with genotype A, 15.4% (6/39) of those with genotype B, and 25.5% (79/310) of those with genotype C. They were significantly less common in patients with genotype A than B or C (A vs B, $p < 0.05$; A vs C, $p < 0.0001$). The only patient with genotype A who had the PreC mutation was simultaneously infected with genotype G.

Routes of transmission were identifiable in 275 of the 547 (50%) patients, and the main route was heterosexual contacts; those in the remaining patients could not be disclosed. The frequency of heterosexual activity did not differ among patients with distinct genotypes. However, homosexual activity was more common in patients with genotype A than B or C (21.2%, 0% and 0.8%, respectively (A vs B, $p < 0.001$; A vs C, $p < 0.0001$)). Among the 32 homosexual men, HBV genotype A was detected in 29 (91%). Consent to anti-HIV testing was given by 10 of the 29 patients, and four of these (40%) were positive.

Longitudinal changes in the distribution of genotypes

Figure 2 illustrates changes in the distribution of HBV genotypes through three 6-year periods over 18 years (1991–2008). In addition, data from 2009 are shown. HBV genotype A accounted

Table 1 Demographic and clinical characteristics of patients with acute hepatitis who were infected with HBV of different genotypes (1991–2009)

Feature	Total (n=547)	HBV genotypes			
		A (n=137)† (25.0%)	B (n=48) (8.8%)	C (n=359) (65.6%)	Others (n=3)‡ (0.5%)
Age (years)	35.6±14.8	35.2±12.2	39.6±15.6	35.1±15.5	49.7±13.6
Male	367 (67.1%)	129 (94.2%)¶ * †† ***	38 (79.2%)†† *	201 (56.0%)	3 (100%)
ALT (IU/l)§	2553±1563	2289±1069	2557±1412	2342±1728	3333±2406
T-Bil (mg/dl)§	7.8±6.7	9.6±7.6††*	7.7±7.4	7.1±6.2	9.0±2.5
PT (%)§	74.6±22.6	75.2±15.9	73.8±24.5	74.7±24.5	15.8‡‡
Severe hepatitis	34 (6.2%)	4 (2.9%)	4 (8.3%)	26 (7.2%)	0 (0.0%)
Fulminant hepatitis	10 (1.8%)	0 (0.0%)	1 (2.1%)	8 (2.2%)	1 (33.3%)
Mortality	8 (1.5%)	0 (0.0%)	1 (2.1%)	7 (1.9%)	0 (0.0%)
HBsAg persisting >6 months	5/514 (1.0%)	5/123 (4.1%)††† *	0/46 (0.0%)	0/342 (0%)	0/3 (0.0%)
PreC/CP mutations					
PreC	43/461 (9.3%)	1/109 (0.9%)¶ * †† *	6/39 (15.4%)	34/310 (11.0%)	2/3 (66.7%)
CP	69/461 (15.0%)	3/109 (2.8%)†† ***	0/39 (0.0%)††† *	63/310 (20.3%)	3/3 (100%)
PreC and/or CP	92/461 (20.0%)	4/109 (3.7%)¶ * ††† ***	6/39 (15.4%)	79/310 (25.5%)	3/3 (100%)
Transmission route					
Homosexual	32 (5.9%)	29 (21.2%)¶ ** ††† ***	0 (0.0%)	3 (0.8%)	0 (0.0%)
Heterosexual	217 (39.5%)	52 (38.0%)	25 (52.1%)	139 (39.6%)	1 (33.3%)
Medical procedure	16 (2.9%)	2 (1.5%)	2 (4.2%)	12 (3.3%)	0 (0.0%)
Other	10 (1.8%)	1 (0.7%)	1 (2.1%)	7 (1.9%)	1 (33.3%)
Undetermined	272 (49.7%)	53 (38.7%)††† *	20 (41.7%)	198 (55.2%)	1 (33.3%)
Anti-HIV	14/53 (26.4%)	11/35 (31.4%)	0/3 (0.0%)	3/15 (20.0%)	0/0

Values are mean±SD or number (%).

†One patient with genotype A was simultaneously infected with genotype G.

‡Each patient was infected with genotype D, E or H.

§Highest values during the clinical course are shown for ALT and T-Bil, and lowest values for PT.

Statistical analysis was performed to compare genotypes A, B and C.

¶Significantly different compared with genotype B.

††Significantly different compared with genotype C.

*p<0.05, **p<0.001, ***p<0.0001.

‡‡Data from the patient with genotype E only.

ALT, alanine aminotransferase; CP, core promoter; HBsAg, hepatitis B surface antigen; HBV, hepatitis B virus; PreC, precore; PT, prothrombin time; T-Bil, total bilirubin.

for 6% (9/150) in the 1st period, 15.4% (19/123) in the 2nd, and 39.4% (89/226) in the 3rd, with significant differences between 1st and 2nd ($p<0.05$), 2nd and 3rd ($p<0.0001$), and 1st and 3rd ($p<0.0001$). Conversely, AHB associated with genotype C decreased through three periods with significant differences, while AHB associated with genotype B did not change appreciably.

On the basis of these results, the yearly incidence in each of the three 6-year periods is calculated to be: 25.0 cases including 1.5 with genotype A in the 1st period; 20.5 cases including 3.2 with genotype A in the 2nd; and 37.7 cases including 14.8 with genotype A in the 3rd. Hence, the incidence of AHB had not changed markedly over the 12 years from 1991 to 2002, but increased thereafter until 2008. Of the increment in the 3rd period of 17.2 (37.7 minus 20.5) cases, there were 11.6 (14.8 minus 3.2) with genotype A; they accounted for 67% (11.6/17.2) of the recent increase in AHB.

Regional distributions and longitudinal changes in genotype A

Among the 183 patients from the capital region, the genotype was A in 65 (35.5%), B in 22 (12.0%), C in 94 (51.4%), E in one (0.5%), and H in one (0.5%) (table 2). Of the remaining 364 (66.5%) patients from other regions, by contrast, the genotype was A in 72 (19.8%), B in 26 (7.1%), C in 265 (72.8%), and D in one (0.3%). Genotype A was significantly more common in the capital than in other regions (35.5% vs 19.8%, $p<0.0001$). In the capital region, genotype A accounted for 4.8% (2/42) in the 1st period, 29.3% (12/41) in the 2nd, and 50.0% (42/84) in the 3rd. There were significant differences between the 1st and 2nd periods ($p<0.05$), 2nd and 3rd ($p<0.05$), and 1st and 3rd ($p<0.0001$). In other regions, by contrast, genotype A accounted for 6.5% (7/108) in the 1st period, 8.5% (7/182) in the 2nd, and

33.1% (47/142) in the 3rd. For the first time in other regions, genotype A increased in the 3rd period, in comparison with the 1st and 2nd (1st vs 3rd, $p<0.0001$; 2nd vs 3rd, $p<0.0001$).

Subgenotypes of genotype A

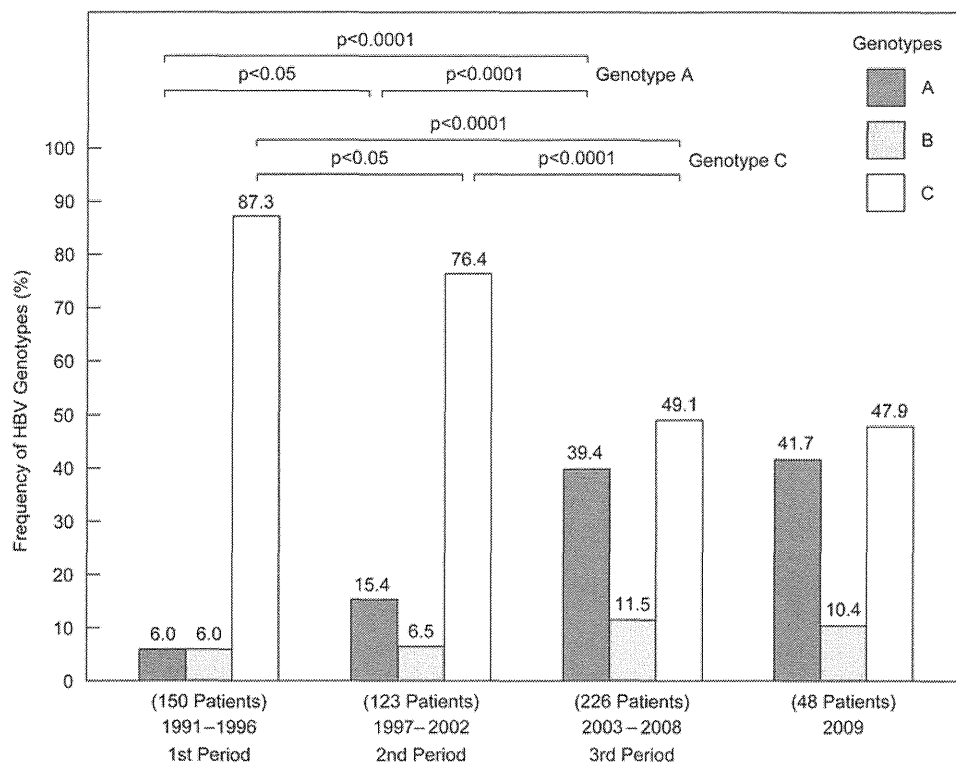
Of the 137 genotype A isolates, amplification and sequencing of HBV DNA were feasible in 114 (83.2%); the isolate from the single patient with genotypes A and G was excluded. A phylogenetic tree was constructed, on the entire preS1/S2/S genes of ~1.2 kb, for these 114 isolates along with 34 genotype A isolates retrieved from the database (figure 3).

Of the 114 isolates in this study, 101 (88.6%) were subgenotype A2, and the remaining 13 (11.4%) were subgenotype A1. In a pair-wise comparison, the sequence divergence among the 101 subgenotype A2 isolates was 0–1.3%, and that among the 13 subgenotype A1 isolates spanned 0% to 2.3%. The sequence divergence between subgenotype A2 and A1 isolates ranged from 2.6% to 4.7%.

A sequence of 1203 nucleotides was possessed in common by three of the 101 (3%) isolates of subgenotype A2. For convenience, the group comprising these three isolates was labelled 'identical group I'. Likewise, an additional six 'identical groups' were found, and numbered from 'II' to 'VII'. They comprised 35 (35%), seven (7%), two (2%), three (3%), 12 (12%) and three (3%) of the 101 isolates of subgenotype A2. In contrast, only one identical group, designated 'VIII', was constructed by three of the 13 (23%) isolates of subgenotype A1.

Some isolates of subgenotype A1 and A2 were obtained from patients who had travelled to foreign countries in the recent past (5/13 (38.5%) patients with A1 to Africa, Philippines, Myanmar and China; and 5/101 (5.0%) patients with A2 to Europe, Thailand, Brazil and the USA).

Figure 2 Distribution of hepatitis B virus (HBV) genotypes in three periods.



Subgenotypes of genotype B

Of the 48 isolates of genotype B, subgenotyping was feasible in 43 (90.0%). A phylogenetic tree was constructed on preS1/S2/S-gene sequences from these 43 isolates, along with those from 25 isolates of genotype B retrieved from the database (figure 4). Of the 43 isolates in this study, 10 (23.3%) were subgenotype B1, 28 (65.1%) were B2, two (4.7%) were B3, and three (7.0%) were B4. In a pair-wise comparison, the sequence divergence among 10 subgenotype B1 isolates ranged from 0.4% to 1.4%, and that among 28, two and three isolates of subgenotypes B2, B3 and B4 spanned 0–1.7%, 0.5% and 0.6–0.8%, respectively. The inter-subgenotype divergence among B1–B4 ranged from 0.6% to 4.4%.

One 'identical group' made up of five isolates was detected among the 28 of subgenotype B2; it was named 'IX'. In contrast, no 'identical group' was found in 10, two or three isolates of subgenotype B1, B3 or B4.

Some isolates of subgenotypes B2, B3 and B4 were obtained from patients who had travelled to foreign countries in the recent past (7/28 (25.0%) patients with B2 to China and other countries; 1/2 (50.0%) patients with B3 to a country unknown; and 1/3 (33.3%) patients with B4 to Vietnam). However, none of the 10 subgenotype B1 isolates was associated with travel to foreign countries.

Identical groups

The proportion of isolates that shared a sequence in identical groups was higher for subgenotype A2 (64.4%) than for A1, B1, B2, B3 or B4 (23.1%, 0%, 17.9%, 0% or 0%, respectively (A2 vs A1, $p < 0.001$; A2 vs B1, $p < 0.0001$; A2 vs B2, $p < 0.0001$)).

Homosexual activity was more common in patients belonging to the seven identical groups than the non-identical group of subgenotype A2 (17/65 (26.2%) vs 3/36 (8.3%), $p < 0.05$). Among the isolates in the seven identical groups of subgenotype A2, those in groups I, III and VII clustered locally during short periods of 2–7 years. In contrast, subgenotype A2 isolates in groups II and VI were scattered widely over longer periods of 11–16 years.

DISCUSSION

In Japan, as in most Asian countries, the persistent HBV carrier state had been established mainly through perinatal transmission from mother to baby and horizontal infection during infancy. In 1986, a national prevention programme was launched in Japan with selective vaccination of babies born to carrier mothers with hepatitis B e antigen (HBeAg). In 1995, this was extended to babies born to HBeAg-negative carrier mothers. As a result, the prevalence of HBsAg among younger people born since 1986 has decreased dramatically.^{28 29} However, there are an

Table 2 Changes in the distribution of genotype A compared between the capital region and other regions over three periods

Area	n	1st Period (1991–1996)	2nd Period (1997–2002)	3rd Period (2003–2008)	2009
Capital region	65/183 (35.5%) †***	2/42 (4.8%) †* §***	12/41 (29.3%) †* §*	42/84 (50.0%) †*	9/16 (56.3%)
Other regions	72/364 (19.8%)	7/108 (6.5%) §***	7/82 (8.5%) §***	47/142 (33.1%)	11/32 (34.4%)
Total	137/547 (25.0%)	9/150 (6.0%) †* §***	19/123 (15.4%) §***	89/226 (39.4%)	20/48 (41.7%)

Statistical analysis of the differences between the capital and other regions was performed, as well as through the 1st, 2nd and 3rd periods.

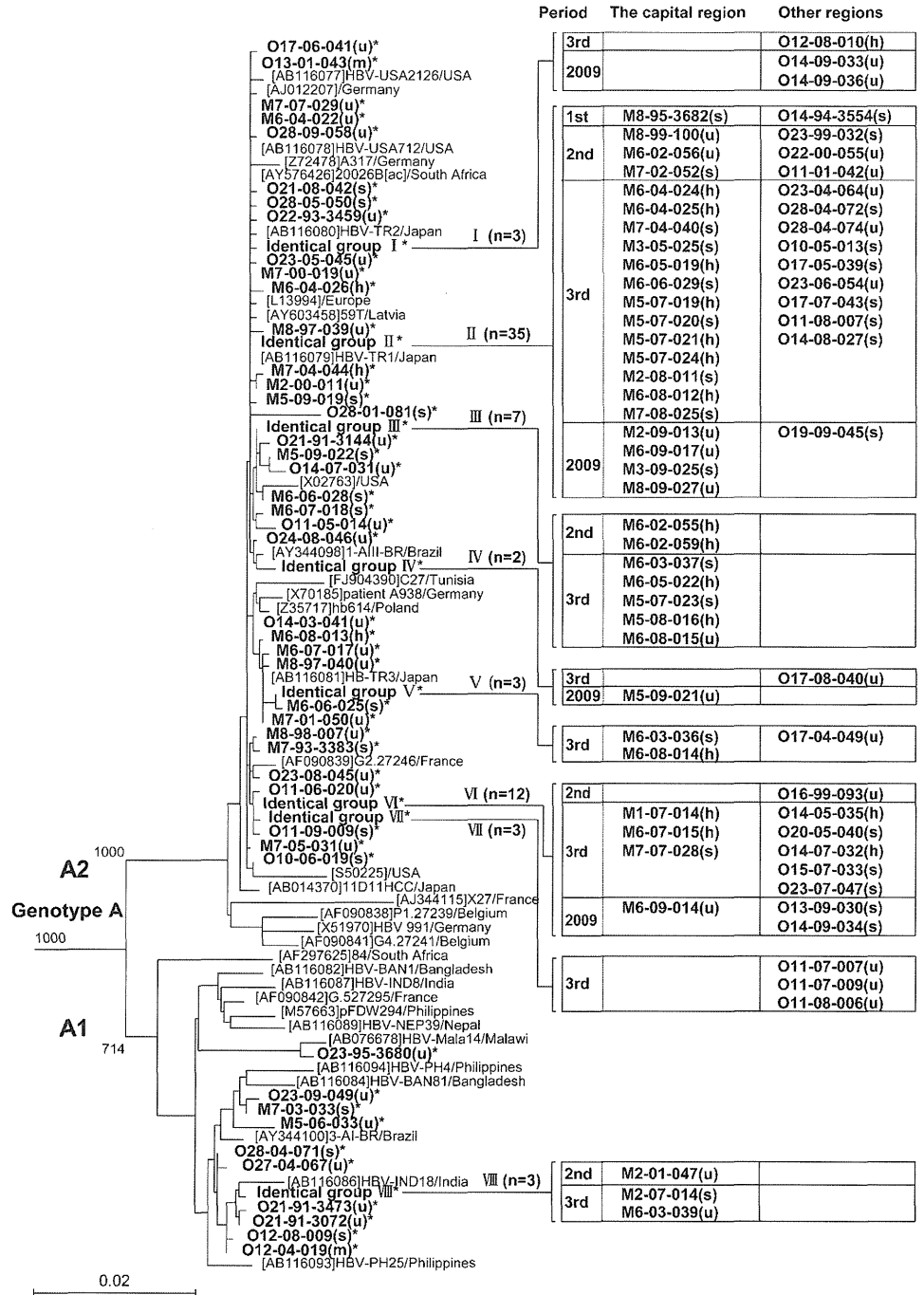
†Significantly different compared with other regions.

‡Significantly different compared with the 2nd period.

§Significantly different compared with the 3rd period.

* $p < 0.05$, *** $p < 0.0001$.

Figure 3 Phylogenetic analysis of genotype A strains by the neighbour-joining method. Isolates obtained in this study are shown in bold with asterisks. Hospitals in the capital region are labelled M1–M8 and those in other regions O9–O28 (corresponding to those in figure 1). Year of onset is indicated by the last two digits after the first hyphen. Numbers after the second hyphen represent the identification numbers of patients in each year (not always consecutive). Transmission routes are shown in lower-case letters in parentheses: h, homosexual; s, heterosexual; m, medical procedure; o, others; and u, undetermined. Isolates with identical sequences are bracketed in 'Identical groups I through VIII' on the tree. Each bracket is divided by areas and periods. Reference hepatitis B virus (HBV) isolates, including 12 of subgenotype A1 and 22 of subgenotype A2, were obtained from the database and specified by their accession numbers, isolate names and countries of origin. Bootstrap values are indicated on major phylogenetic branches.



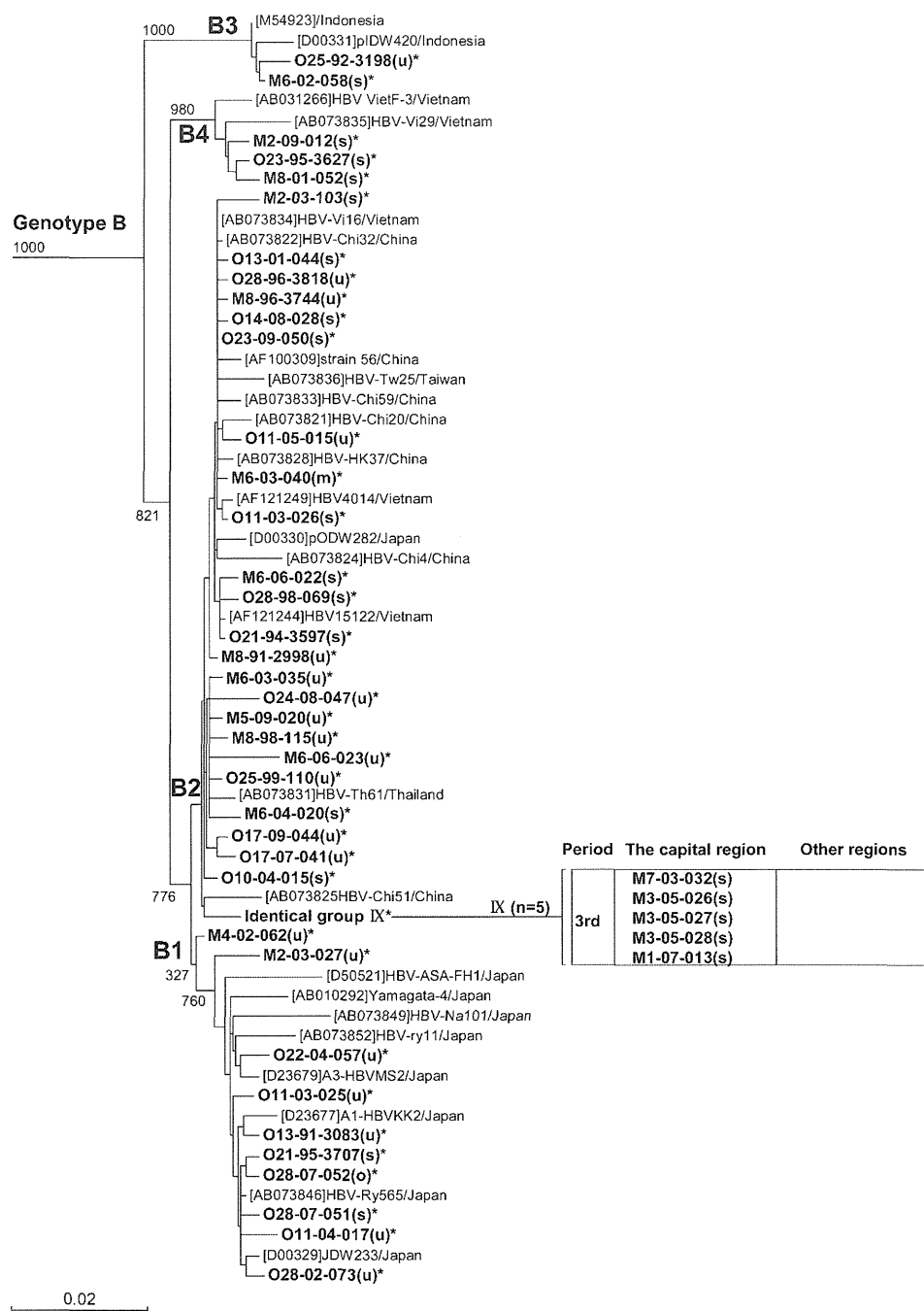
estimated one million HBV carriers in Japan at present.³⁰ Furthermore, many Japanese remain at increased risk of horizontal infection with HBV, because they have not received selective vaccination and therefore do not have the antibody to HBsAg. Because AHB is extremely under-reported and no national surveillance data are available in Japan, the incidence has not been determined accurately. In the USA, the incidence of AHB has decreased markedly since the adoption of a comprehensive immunisation strategy in 1991.^{31 32}

In the present study over 1991–2009, we conducted a nationwide, sentinel surveillance on AHB in Japan. In the 547 patients recruited over 19 years, genotype C was the most prevalent (65.6%), followed by genotype A (25.0%) and genotype B (8.8%). Demographic and clinical differences were observed among patients with genotypes A, B and C (table 1).

The proportion of men reached 94.2% for genotype A infection, higher than that for genotype B (79.2%) or C (56.0%) infection. In the analysis of the route of transmission, homosexual activity was reported by 21.2% of patients with genotype A; all were male. In general, sexual activity tends to be higher in men than women. The predominance of genotype A in men may be attributable to a high frequency of homosexual activity among men.

Although adult-acquired HBV infection persists at a high frequency of ~10% in European countries and the USA,³³ it rarely, if ever, becomes chronic in Japan. Recent studies suggest that the chance of a chronic outcome of AHB may differ by HBV genotype^{21 34}; it is more common for genotype A than other genotypes.^{22 35 36} In the present study, HBV infection persisted in 4.1% of patients with genotype A, in comparison with 0% of

Figure 4 Phylogenetic analysis of genotype B strains by the neighbour-joining method. Hepatitis B virus (HBV) isolates obtained in the present study are specified in the same manner as in figure 3, and isolates with an identical sequence are bracketed in 'Identical group IX' on the tree. Of them, 10 reference isolates of subgenotype B1 and 13, two and two of those of B2, B3 and B4, respectively, were retrieved from the database; they are specified as in figure 3.



those with genotype C. Remarkably, all five patients with AHB who acquired chronic infection possessed HBV genotype A, either alone (four patients) or together with HBV genotype G (one). Increasing genotype A infections may have changed the genotype distribution in patients with AHB and those with chronic HBV infection. In Japanese patients with chronic hepatitis B, the proportion of genotype A has doubled, from 1.7% in 1999–2000 to 3.5% in 2005–2006.³⁷

The genotype was A in 29 of the 32 (91%) homosexual men. Of the 29 homosexuals with genotype A, 10 gave consent to anti-HIV testing, and four of these (40%) were found to be positive. Of the five patients who acquired chronic HBV infection, anti-HIV was tested in four (three with genotype A and one with genotypes A and G), and one with genotype A was found to be positive. There is a possibility that co-infecting HIV in this patient with genotype A may have promoted chronic

HBV infection; HIV is known to prolong and aggravate HBV infection by compromising immune responses.³⁸

Patients with FH in this study were infected with either HBV genotype B (1/48 (2.1%)) or C (8/359 (2.2%)); no patients with genotype A developed FH. PreC and/or CP mutations were significantly less common in genotype A (1/109 (3.7%)) than B (6/39 (15.4%)) or C (279/310 (5.5%)) infection. The single patient with genotype A who had PreC mutation was simultaneously infected with HBV genotype G. There is a possibility that the PreC mutation in this patient was from HBV genotype G.²⁶ FH did not develop in any patients with genotype A, which may be attributable, at least in part, to the lack of PreC mutation in genotype A infections.³⁹

Previous reports have shown that genotype A is common in patients with AHB in Metropolitan Tokyo,^{20 21 40} as well as around Aichi located in the middle of Mainland Japan.²²

Yotsuyanagi *et al*²³ reported that genotype A is more common in patients with AHB in the metropolitan region than in other regions. Sugauchi *et al*⁴¹ found that, in patients with AHB, the proportion with genotype A has increased over time. The present study indicates that the number of patients with AHB in Japan would not have decreased. We found that the proportion of patients with genotype A infection is increasing in the 28 national hospitals in Japan (6.0% in the 1st period, 15.4% in the 2nd, and 39.4% in the 3rd (figure 2)), with the prevalence much higher in the capital than other regions (35.5% vs 19.8% (table 2)).

In this study, there was a time lag in the increase in genotype A infection between the capital region and other regions of Japan (table 2). In the capital region, the prevalence of genotype A started to increase in the late 1990s, and kept increasing through the early 2000s (4.8% in the 1st period, 29.3% in the 2nd, 50.0% in the 3rd, and 56.3% in 2009). In other regions, by contrast, the frequency of genotype A did not change during the late 1990s, and increased significantly in the 2000s (6.5% in the 1st period, 8.5% in the 2nd, 33.1% in the 3rd, and 34.4% in 2009). Thus infiltration of genotype A infection into other regions occurred 5–6 years behind the epidemic in the capital region. This indicates that genotype A infection originated in the capital region and then spread to other areas of Japan.

Some genotypes are classified into several subgenotypes, and they have distinct geographical distributions.⁴² Hence, subgenotypes are useful in tracing the route of HBV infection. By phylogenetic analysis (figures 3 and 4), 88.6% of genotype A isolates had the European–American type (A2), and the remaining 11.4% possessed the Asian–African type (A1). Likewise, 76.7% of genotype B isolates had Asian types (B2–B4), and the remaining 23.3% possessed the type endemic to Japan (B1). Of the 157 HBV isolates of genotype A or B, 147 (93.6%) had subgenotypes foreign to Japan. They are thought to have been transmitted from foreign sex workers, and spread among certain populations who share particular sexual behaviours in Japan.⁴¹

Of note, some HBV isolates of distinct subgenotypes possessed an identical sequence in the preS1/S2/S gene. The isolates of subgenotype A2 were prominent in this regard, and more often had the same sequence than those of other subgenotypes, such as A1, B1 and B2. The high prevalence of subgenotype A2 isolates with an identical sequence would not have been caused by cross-contamination. If cross-contamination had occurred, it would have affected isolates of all subgenotypes, and not influenced subgenotype A2 isolates preferentially. As many as 35% of subgenotype A2 isolates had an identical sequence, and those with the same sequence increased to 56.3% in the recent 2009 survey in Metropolitan Tokyo. Furthermore, some subgenotype A2 isolates in groups I, III and VII clustered locally within short periods, whereas others in groups II and VI were scattered widely over a long period of time. On the basis of these results, it is tempting to speculate that some subgenotype A2 strains would have been transmitted from person to person without undergoing mutations for many years.

In summary, the present study indicates the following. (1) AHB in the 28 national hospitals in Japan has not decreased, because genotype A infections are increasing. (2) Genotype A infections started to increase in the capital region, and then spread to local areas 5–6 years later. (3) Approximately 90% of genotype A in patients with AHB is subgenotype A2. (4) Subgenotype A2 strains with an identical sequence are spreading among younger generations with high sexual activity. (5) On the basis of the results obtained, AHB in Japan is not decreasing, because HBV of subgenotype A2 is prevailing in particular

subpopulations at high risk. Finally, in order to prevent further increases in AHB in Japan, universal vaccination of young people deserves consideration.

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Ethics approval Approved by the ethics committee of each institution.

Contributors YT, HY and HI designed data collection tools, monitored data collection for the whole study, wrote the statistical analysis plan, cleaned and analysed the data. YT, HY and YM drafted and revised the paper. HY, NM, MN, EM, TK, YW, TM, MS, TH, TS, YM, TK, MT, HK, HD, SH and SA collaborated in data and sample collection.

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Correction

Eapen CE, et al. Gut tutorial, *Copper and liver disease*. *Gut* 2012;**61**:63. doi:10.1136/gutjnl-2011-301743. The following author names should have been included in the author list:

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肝炎をめぐる医療政策

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わが国には肝炎ウイルスキャリアが約 350 万人存在すると推定されており、その内訳は B 型肝炎 110～140 万人、C 型肝炎 190～230 万人である。まさに“ウイルス肝炎は国民病である”との認識が妥当であり、国の医療政策の原点となっている。とくに 2010 年 1 月に“肝炎対策基本法”が施行されたことにより、現行の肝炎総合対策に対してこれまで以上の俊敏さ、具体的実効性が求められる。

■肝炎対策基本法

さて、この法律の前文には「B 型肝炎及び C 型肝炎に係るウイルスへの感染については、国の責めに帰すべき事由によりもたらされ、又はその原因が解明されていなかったことによりもたらされたものがある。特定の血液凝固因子製剤に C 型肝炎ウイルスが混入することによって不特定多数の者に感染被害を出した薬害肝炎事件では、感染被害者の方々に甚大な被害が生じ、その被害の拡大

を防止し得なかったことについて国が責任を認め、集団予防接種の際の注射器の連続使用によって B 型肝炎ウイルスの感染被害を出した予防接種禍事件では、最終の司法判断において国の責任が確定している(下線は著者による追加)」と明記されていることからわかるように、ウイルス肝炎蔓延の原因の一部にわが国固有の事案が存在する。誌幅の都合上、詳細は割愛するが、薬害肝炎事件は凝固因子製剤(フィブリノゲン、第Ⅸ因子)への C 型肝炎ウイルスの混入に起因し(推定患者数 1 万人以上)、一方、予防接種禍事件は、集団予防接種など(予防接種およびツベルクリン反応検査)の際の注射器の連続使用によって B 型肝炎ウイルスの水平感染を招いたとされる事案(推定患者数 40 万人以上)である。前者では患者・国・製薬会社の 3 者間、後者では患者・国の 2 者間での和解が成立し、補償が進められているところである。

■都道府県肝疾患診療ネットワークの構築

国がこれまで行ってきたさまざまな肝炎対策のなかで、もっとも画期的な施策の一つが 2002～2006 年度の 5 年間全国で展開された節目検診、節目外検診である。B 型肝炎ウイルス検診受診者はのべ 8,704,587 人で、うち 100,983 人(1.16%)が“陽性”と判定された。一方、C 型肝炎ウイルス検診

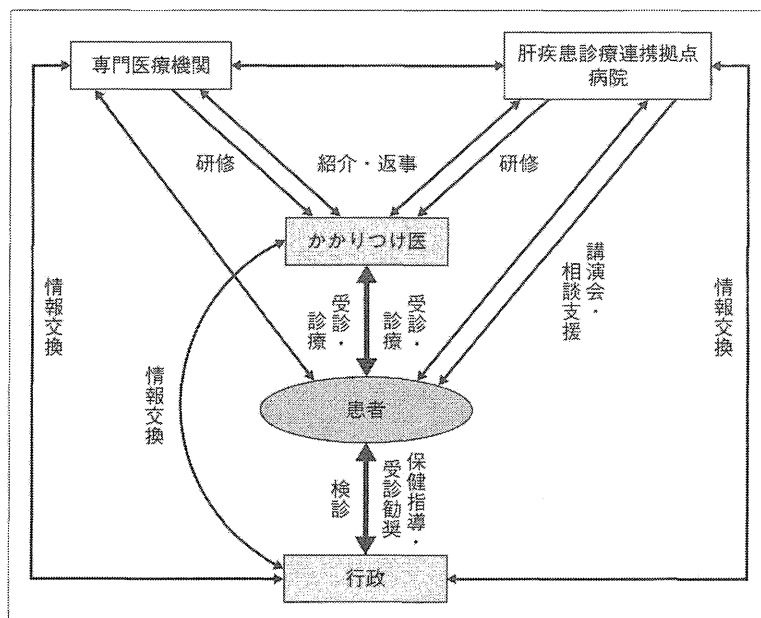


図 1 都道府県における肝疾患診療ネットワーク構築(2007年1月厚生労働省)