TABLE II. Comparison of Hepatitis B Serological Markers in Vaccinated Versus Unvaccinated Family Members Group

	Total (N = 230)	Vaccinated group (N = 142)	Unvaccinated group (N = 88)	*P*-value
Age[a]	20.6 ± 14.6	13.3 ± 10.4	32.5 ± 51.7	<0.0001
Gender (Male)[b]	96(41.7)	64 (45.1)	32 (36.4)	NS
Anti-HBc (+)[b]	53 (23)	20 (14.1)	33 (37.5)	<0.0001
HBsAg (+)[b]	28 (12.2)	15 (10.6)	13 (14.8)	NS
Anti-HBs (+)[b]	128 (55.7)	99 (69.8)	29(33)	<0.0001
HBV-DNA (+)[b]	14 (50)	8 (53.3)	6 (46.2)	NS

[a]Mean ± SD.
[b]N (%).

In the present study, 12.1% of the family members were infected with HBV. This incidence was much higher than that detected among the blood donors (1.4%) resident in the same area in Egypt (data not shown). Clustering of the HBV infection within the families has been described in nearby countries located within the same zone of the HBV endemicity but with different incidences; 30% in Turkey, 15.8% in Greece, and 11.9% in Iran [Alizadeh et al., 2005; Zervou et al., 2005; Ucmak et al., 2007]. An important risk factor was found to be implicated in acquiring the infection among the family was the presence of female infected with HBV. Furthermore, the higher incidence of HBsAg positive rate among the offspring of the females' index cases than that of males index cases illustrates clearly the role of the mother in the transmission of HBV. Similarly, Salkic et al. [2007] reported the same observation in his study from Bosnia [Salkic et al., 2007]. However, in Taiwan no significant difference was found in the HBsAg positivity among the offspring of the two groups, suggesting the importance of the paternal as well as the maternal transmission for the HBV intra-familial spread in Taiwan [Lin et al., 2005].

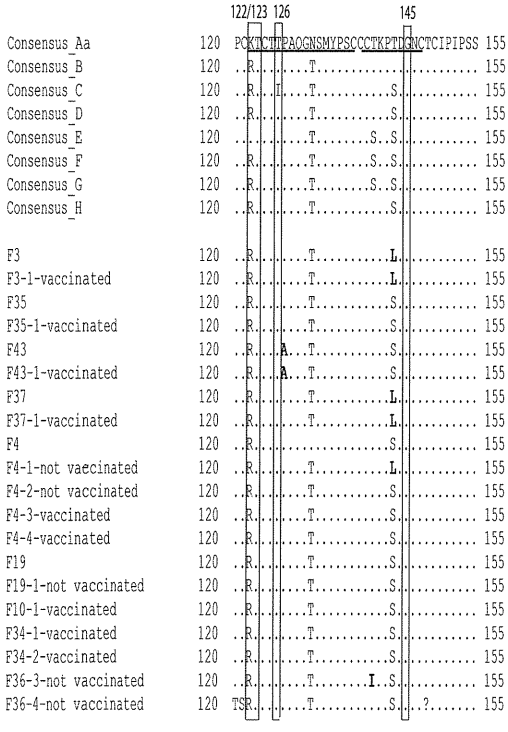

Fig. 4. The alignment of amino acid sequences of the HBV partial surface gene encompassing the "a" determinant region in the HBsAg positive family members. The upper eight sequences are consensus of the corresponding HBV genotypes Aa/A1, B, C, D, E, F, G, and H reference strain retrieved from DDBJ/GenBank database. Dots in alignment indicate identity of amino acids to the consensus sequence of genotype Aa/A1. First and second loop positions are underlined in the consensus sequence of the genotype Aa/A1 and positions of previously reported vaccine escape mutants are indicated in numbers and included in boxes.

Despite being a tedious and labor-intensive method, sequencing of the viral genomes isolated from different individuals, with the subsequent homology comparison and the phylogenetic analysis remains the golden approach for demonstrating the HBV transmission in a given population [Dumpis et al., 2001; Zampino et al., 2002; Tajiri et al., 2007].

The full length HBV sequence analysis is the gold standard for this purpose but remains a cost approach [Datta et al., 2007]. Highly variable HBV genomic region is recommended by some investigators to study the transmission event. Variability of the genomic region is affected by several factors one of which is the clinical characteristics of the studied cohort [Wu et al., 2005]. PreC/C region exhibit high variability in the cases of acute or fulminant hepatitis and thus analysis of this region is preferable for investigating the chain of recent/nosocomial fulminant cases [Bracho et al., 2006; Ozasa et al., 2006]. However, a high S gene variability is documented among the chronic hepatitis B carriers and their families, thus investigating the genotype, subgenotype, subtypes, and mutations by the sequence analysis of the S gene with further analysis by testing the constructed phylogenetic tree with the bootstrap resampling maximum-likelihood test, may provide enough confidence to prove the transmission event in the case of chronic HBV carriers [Thakur et al., 2003]. Hence, in the present study, the phylogenetic analysis of the HBV nucleotide sequences spanning the entire preS2 and S HBV genomic regions and isolated from chronic hepatitis B carriers which include index cases and their family members revealed the infection with HBV genotype D which coincides with the previous

data regarding the predominance of infection with HBV genotype D in Egypt [Saudy et al., 2003]. In addition, the phylogenetic analysis documented the presence of three different patterns of HBV genotype D transmission within the families in Egypt; maternal transmission (from mother to child as in the family 4), paternal transmission (from father to child as in family 35 and family 43) and spousal transmission (between spouses as in family 19 and family 37). This was different from the transmission pattern characteristics of genotype D in Uzbekistan where the horizontal transmission was the predominant route of infection with HBV genotype D within a family [Avazova et al., 2008].

The Data regarding the difference of transmission routes of HBV infection between different genotypes are controversial and scarce. Based on the findings that the patients infected with HBV genotype C may exhibit delayed HBeAg seroconversion decades later than the patients infected with other genotypes, Livingston et al. [2007] speculated that genotype C is the most responsible for the perinatal transmission and that the other genotypes (A, B, D, and F) are mainly transmitted horizontally [Livingston et al., 2007]. A recent study has shown a different data through exploring that both genotypes B and C can be transmitted by maternal and horizontal routes [Wen et al., 2011]. Whether different HBV genotypes have different transmission routes remains a question, which needs further global studies to clarify this interesting and important issue.

In an attempt to evaluate the influence of the universal vaccination on the intra-familial HBV infection, it was surprising to find a high prevalence rate of HBsAg among the vaccinated members with no significant difference when compared to the unvaccinated group. In an agreement with the present data, El Sherbini et al. [2006] reported the unchangeable prevalence of HBsAg among the vaccinated school children across a decade despite the significant decrease of the anti-HBc rate [El Sherbini et al., 2006]. The possible explanation for this vaccine failure is the acquiring of the HBV infection in the lag period between the birth and the time of receiving the first HBV vaccine dose at the age of 2 months. Supporting our explanation is the recent data coming from Taiwan where a different HBV infection prophylactic strategy is applied by administrating the first dose of the HBV vaccine at birth with the administration of the hepatitis B immunoglobulin to the infants born to the HBeAg positive mother within 24 hr after birth. The recent study has clearly demonstrated that the current HBV prophylactic strategy in Taiwan was capable of reducing the intra-familial HBV transmission and reducing the overall HBsAg positive rate among the infants [Mu et al., 2011]. In Japan, the extension of the active and passive immunization to the babies born to HBeAg negative mother had greatly reduced the HBsAg prevalence to 0.2% of blood donors younger than 19 years old [Noto et al., 2003; Matsuura et al., 2009]. The present study recommends the changing of the current HBV prophylactic policy in Egypt. It would be needed to provide the first dose of the HBV vaccine at birth together with screening for HBV infection markers prenatally and administration of the HBIG to the infants born from HBeAg-positive mothers. The documented role of the HBV spousal transmission in the present study by the phylogenetic analysis (Family 19 and Family 37), coincides with the recent data conducted in Egypt that the first sexual contact with an infected spouse was a significant risk factor for infection with HBV among females and may further emphasize the importance of the premarital screening for HBV in Egypt [Paez Jimenez et al., 2009]. Investigating the " a" determinant region of viral isolates retrieved from the vaccinated members infected with HBV provides no evidence of breakthrough infection by previously reported vaccine escape mutant virus [Carman et al., 1990].

In conclusion, the present study has clearly explored the role of the HBV intra-familial transmission and spread in north Eastern Egypt. Three patterns of HBV transmission were determined in the current cohort infected with HBV genotype D; maternal, paternal, and spousal. The present study recommends the change of the current prophylactic policy against the HBV infection in Egypt by including the first dose of HBV vaccine at birth, screening of pregnant women for HBsAg and the administration of HBIG to the infants born from HBeAg positive mothers within 24 hr after birth. Further studies are needed globally to determine the transmission patterns of different HBV genotypes and locally in different districts in Egypt to explore the impact of familial transmission in HBV infection in Egypt.

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Novel Evidence of HBV Recombination in Family Cluster Infections in Western China

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Abstract

Two hepatitis B virus (HBV) C/D recombinants were isolated from western China. No direct evidence indicates that these new viruses arose as a result of recombination between genotype C and D or a result of convergence. In this study, we search for evidence of intra-individual recombination in the family cluster cases with co-circulation of genotype C, D and C/D recombinants. We studied 68 individuals from 15 families with HBV infections in 2006, identified individuals with mixed HBV genotype co-infections by restriction fragment length polymorphism and proceeded with cloning and DNA sequencing. Recombination signals were detected by RDP3 software and confirmed by split phylogenetic trees. Families with mixed HBV genotype co-infections were resampled in 2007. Three of 15 families had individuals with different HBV genotype co-infections in 2006. One individual (Y2) had a triple infection of HBV genotype C, D and C/D recombinant in 2006, but only genotype D in 2007. Further clonal analysis of this patient indicated that the C/D recombinant was not identical to previously isolated CD1 or CD2, but many novel recombinants with C2, D1 and CD1 were simultaneously found. All parental strains could recombine with each other to form new recombinant in this patient. This indicates that the detectable mixed infection and recombination have a limited time window. Also, as the recombinant nature of HBV precludes the possibility of a simple phylogenetic taxonomy, a new standard may be required for classifying HBV sequences.

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Introduction

Not all viruses are equally prone to recombination. Recombination has not been detected in several viruses despite repeated searches [1]. Whether recombination does or does not exist is important for understanding the evolution and replication mechanism of a specific kind of virus. Hepatitis B virus (HBV), a major human pathogen, has been classified into 10 genotypes and several sub-genotypes [2,3]. Many sub-genotypes were identified by polygenetic analysis as recombinants. But there is no direct evidence to indicate that these subgenotypes arose as a result of recombination or perhaps a result of convergence.

Coinfection with different HBV genotype strains is a prerequisite for recombination. As more than one genotype is predominant in most of the geographic regions, coinfection between the predominating HBV genotypes is not a rare finding, especially for B and C, or A and D. The prevalence of mixed HBV genotype infections has been reported using varied genotyping methods [4,5,6].

Our previous study found two kinds of HBV C/D recombinants in northwest China [7]. In a further study of ethnic groups of five provinces, we confirmed the geographic and ethnic distribution of the HBV C/D recombinant in northwest China [8], and found that family-cluster HBV infections were common in these endemic areas. We hypothesize that infected members of HBV family clusters would gain exposure to various genotypes through marriage, while at the same time; competent strains would be selected through vertical transmission. It would be useful to observe the mixed infection in family-cluster cases, especially in patients infected with C/D recombinants.

The aim of this study was to evaluate the possibility of recombination between two HBV genotypes within an individual by finding cluster-infected families in which individual members were infected with different HBV genotypes. We would then look for individuals within these families with multiple-genotypes that were likely to have been obtained from other family members as a result of vertical or horizontal transmission. Novel viral genomes within an individual with a multiple genotype infection that were mosaics of the known viral genotypes in the family, but not present in any of the other family members, would be consistent with the hypothesis that they arose within the individual with multiple genotype infections.

Methods

Subjects

We enrolled 68 patients with a chronic HBV infection from 15 families. All the families were from a district located at the boundary of Gansu and Qinghai provinces, where the prevalence of genotype C2, D1 and C/D recombinant HBV were known to be high [8]. The families were initially identified with cluster HBV infection in an epidemiological survey in 2002. Sixty-eight individuals were sampled in June 2006 and December 2007 for the purpose of assigning HBV genotypes to chronically infected individuals and finding individuals with multiple HBV genotype co-infections. None of the patients received anti-viral therapy or immunosuppressant drugs. A written, informed consent was obtained from each family, and the study protocol was approved by the Southern Medical University Ethics Committee.

HBV DNA Extraction and HBV Genotyping

HBV DNA was extracted from 400 μL of serum by QIAamp UltraSens Virus Kit (Qiagen GmbH, Germany), then re-suspended in 50 μL water and stored at −20°C until analysis. HBV genotypes, including C/D recombinant, were initially assigned using the PCR based restriction fragment length polymorphism (RFLP) methods described previously [9], [8].

Cloning of Mixed Infection Samples

For samples with mixed genotype infections, PCR cover HBV S gene (nt136-1110) was performed using the primers and thermocycling conditions described by Sugauchi et al [10]. For samples needing further recombination analysis, PCR was performed using the primers and thermocycling conditions described by Günther to obtain full-length HBV genome [11]. Alternatively, a nested PCR was used to produce two overlapping fragments in subjects with low HBV DNA levels as described by Sugauchi et al [12]. The spanning of fragment A cover nucleotides 2813 to 1824, and fragment B included nucleotides 1821 to 237. LA-Taq (TAKARA, Japan) and high-fidelity polymerase COD-FX (TOYOBO, Japan) were used to produce amplimers for cloning and direct sequencing respectively. Finally, Fragment C (HBV nt56-nt1824) was obtained from a PCR amplification of Y2 HBV-DNA to which an aliquot of genotype B HBV-DNA had been added. The purpose of this experiment with in-tube control of genotype B was to determine if the recombinant clones were being generated during the PCR amplification. PCR products were gel-purified and cloned into the PMD19-T vector (TAKARA, Japan) according to the manufacturer's instructions, and used to transform JM109 competent cells (TAKARA, Japan). A minimum of 15 clones were sequenced from subjects with a mixed-strain infection and three clones were sequenced from family members with a single-strain infection. All sequencing of clones and PCR products was performed by Invitrogen Ltd. (Shanghai, China).

Phylogenetic and Recombination Analysis

Genotypes of clones were determined by phylogenetic tree analysis and recombination analysis. The sequences were assembled using SeqMan II software (DNAStar Inc.). Sequence alignments were performed using ClustalW and confirmed by visual inspection. Phylogenetic trees were constructed by the neighbour-joining (NJ) method (Saitou & Nei, 1987). To confirm the reliability of the phylogenetic tree analysis, bootstrap resampling and reconstruction were carried out 1000 times. A phylogenetic tree analysis of HBV strains isolated from the mixed infection family was compared with reference strains from GenBank. Accession numbers are indicated on the tree. Bootstrap values are shown along each main branch. The lengths of the horizontal bars indicate the number of nucleotide substitutions per site. The regions included in the analysis were the same with fragment A, B and C or a little shorter. Phylogenetic and molecular evolutionary analyses were conducted using MEGA version 5 (Tamura, Peterson, Stecher, Nei, and Kumar 2011).

Recombination signals were initially detected by RDP3.β.4 software [13,14]. Bootscan, Geneconv and Siscan were used. The highest acceptable P-value was 0.05. Bootscan and Siscan window sizes were 300 bp, step size was 30, replicates for 100 times. A genotype F sequence (GenBank accession numbers is X75658 and X75663) was used as external reference. The precise map of recombination was determined by split phylogenetic tree and alignment. Split phylogenetic trees were constructed by the method same as above. In alignment, each clone was compared to reference C2, D1 and CD1 consensus sequences. We then inspected the alignments to determine the identical crossover sequences around the breakpoint within which the recombination occurred.

Accession Number of the Sequences

GenBank accession number of reference sequences of HBV genotype C2, D1, CD1 and CD2 are indicated in phylogenetic tree. Accession Numbers of Y2 clones are JX036326-JX036359.

Results

Mixed-genotype Infections in HBV Cluster Families

Different HBV genotypes were found in three families among 15 families. The flow of participants in the study and family trees of families with mixed genotypes/subgenotypes of HBV infection are shown (Figure 1).

Family V had infected members across two generations and two genotypes: In 2006, the mother (V1W) and daughter (V2F) were infected with subgenotype D1 while the son (V2M) had a CD1 recombinant. In 2007, the daughter (V2F) had subgenotype D1 while other family members had HBV DNA levels below the detection limit of the nested PCR assay.

Family Q had infected members across three generations and two genotypes/subgenotypes. In 2006, the grandmother (Q1W) and grandson (Q3M) were infected with CD1 recombinant while father (Q2) and granddaughter (Q3F) had mixed infections of genotype C2 and CD1 recombinants. In 2007, the same genotypes were detected in all family members except that the granddaughter (Q3F) had an HBV DNA level below the detection limit of the nested PCR assay.

Family Y had affected members across three generations and three genotypes/subgenotypes. In 2006, the grandfather of family Y (Y1) was infected with genotype C2 while grandmother (Y1W) had mixed infections of CD1 and C2. Mother (Y2W) and granddaughter (Y3F) were infected with the CD1 recombinant. Father (Y2) had triplicate infections of genotype C2, D1 and CD recombinant. Grandson's (Y3M) serum was unavailable. In 2007, the grandfather (Y1) and mother (Y2W) had HBV DNA levels below the detection limit while the grandmother (Y1W) and granddaughter (Y3F) had genotype CD1. Father (Y2) and grandson (Y3M) had genotype D1.

Phylogenetic Analysis of Family Y, Family Q and Family V

A phylogenetic tree constructed from HBV nt 36-1110 from the clones of family Y is given (Figure 2A). The clones (dotted) of family Y exhibits three clusters on genotype C2, D1 and CD1.

The phylogenetic tree construct from HBV nt136-1110 from the clones of families Q and V is given (Figure 2B). The clones of

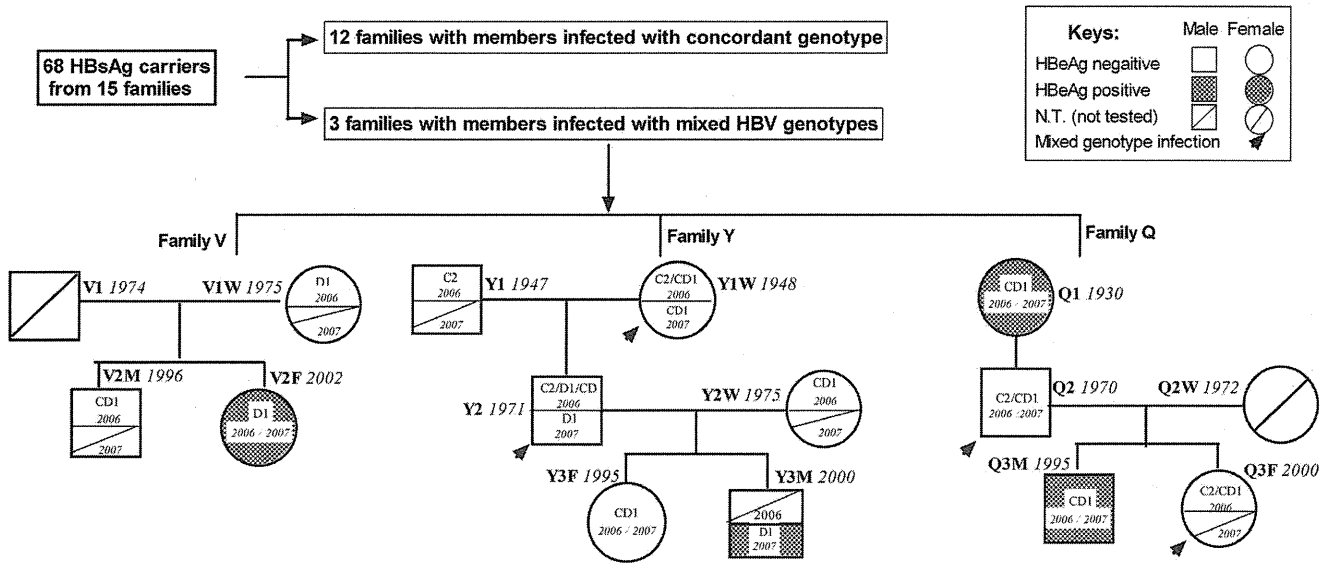

Figure 1. Flow of participants in the study and family trees of family with mixed genotypes/subgenotypes HBV infection. Circles and rectangles correspond to female and male individuals, respectively. Family name and birth date of the patients are indicated beside the circles and rectangles. Subgenotype and the year of blood sampling are indicated inside the circles and rectangles. Family V with affected members across two generations and two genotypes/subgenotypes. Family Q with affected members across three generations and two genotypes/subgenotypes. Family Y with affected members across three generations and three genotypes/subgenotypes. Specially, father (Y2) of family Y with triplicate infection of genotype C, D and CD recombinant in 2006. N.T: Not tested for HBV DNA level below the detection limit of the nested PCR assay or no serum was available.
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family Q (indicated by black dots) exhibit two clusters of subgenotypes C2, and CD1. The clones (indicated by black triangles) from family V exhibit two clusters of subgenotypes D1 and CD1.

A phylogenetic tree constructed from HBV nt 36-1110 of novel recombinants clones of Y2 is given in Figure 2C. The dotted clones are from Y2. The topology of phylogenetic tree with recombinants is totally different from typical trees. Recombinant sequences blurred the typical branch,in other words, blurred the typical genotype.

Recombination and Crossover Analysis of Quasi-species of Y2

Results of recombination analysis of Y2 clones are as bellow: Three kinds of analytical methods certificated the same recombination map. The initial pictures of the three methods were all provided as supplemental figures. Recombination events detected by RDP software are shown in Figure S1, S2, and S3. Split phylogenetic trees constructed by MEGA software are shown in Figure S4, S5, and S6, (clone number and fragment used to construct tree are indicated beside each tree). Sequence alignments are shown in Figure S7, S8, and S9.

The region where recombination breakpoints had the highest probabilities was recognized as crossover region, which is a region that one parental genotype switches to another. Upstream sequence of crossover region will have specific mutation of one genotype but with no specific mutation of another, downstream just opposite. At the same time, these two genotypes should share same sequence at crossover region. We indicated the crossover region in direct alignment by black bars in Figure S3 initially and marked it in recombination map by colorful bars in Figure 3A and black bars in Figure 3B. The clonal sequences of 2006 showed 17 unique crossover regions in fragments A, B and C. We could not identify any common motif within these sequences that might suggest a common mechanism for crossovers in the HBV. The size of switch region share the same sequence are different in different strains, from 6–174 bp (6 bp for Y2M-2 clone in Figure S7 and 174 bp for Y2M-29 clone in Figure S8).

To illustrate the recombination map in a simple way. An abbreviated alignment of fragment A, B and C are shown in Figure 3B. Green and pink bars indicated the genotype C2 and D1 respectively. Black bars showed the crossover region. The aligned sequences provide a snapshot of the recombinant HBV strains. Genotype C2, D1 and CD1 recombinant clones of Y2 were all used as parental sequences to recombine with each other to form new recombinants. A series of novel recombinants were found in three fragments.

In 15 clones of fragment A, there were five genotype C (Y2-6,9,13,14,15,); two genotype D (Y2-11,12); one CD1 (Y2-10) and seven novel different C/D recombination (Y2-1,2,4,7,8,3,5).

In 16 clones of fragment B, there were four genotype C (Y2-23,71,78,75); seven genotype D (Y2-25, 27,79,76,72,22,210); one CD1 (Y2-29) and four novel C/D recombinants (Y2-212,21 73,77).

Of the 56 clones of fragment C(in which genotype B HBVDNA were added as an in-tube control to exclude the recombination by PCR procedure), there were 32 pure genotype B clones; nine genotype C clones(Y2-B10,B5,B8,B9,B13,B16.B17.B18,B24); five genotype D clones(Y2-B22,B3,B4,B21,B23), two CD1 clones (Y2-B1,B11) and eight novel C/D recombinants (Y2-B6,B7,B14,B15,B19,B2,B12,B20). No recombinants of genotype B were found.

Discussion

Recombination is one of the major mechanisms contributing to the evolution of retroviruses [15]. Since the HBV has a reverse transcription step in its life cycle, it is conceivable that recombination also contributes to diversity in HBV genomes. Although just four cases were observed with mixed genotype

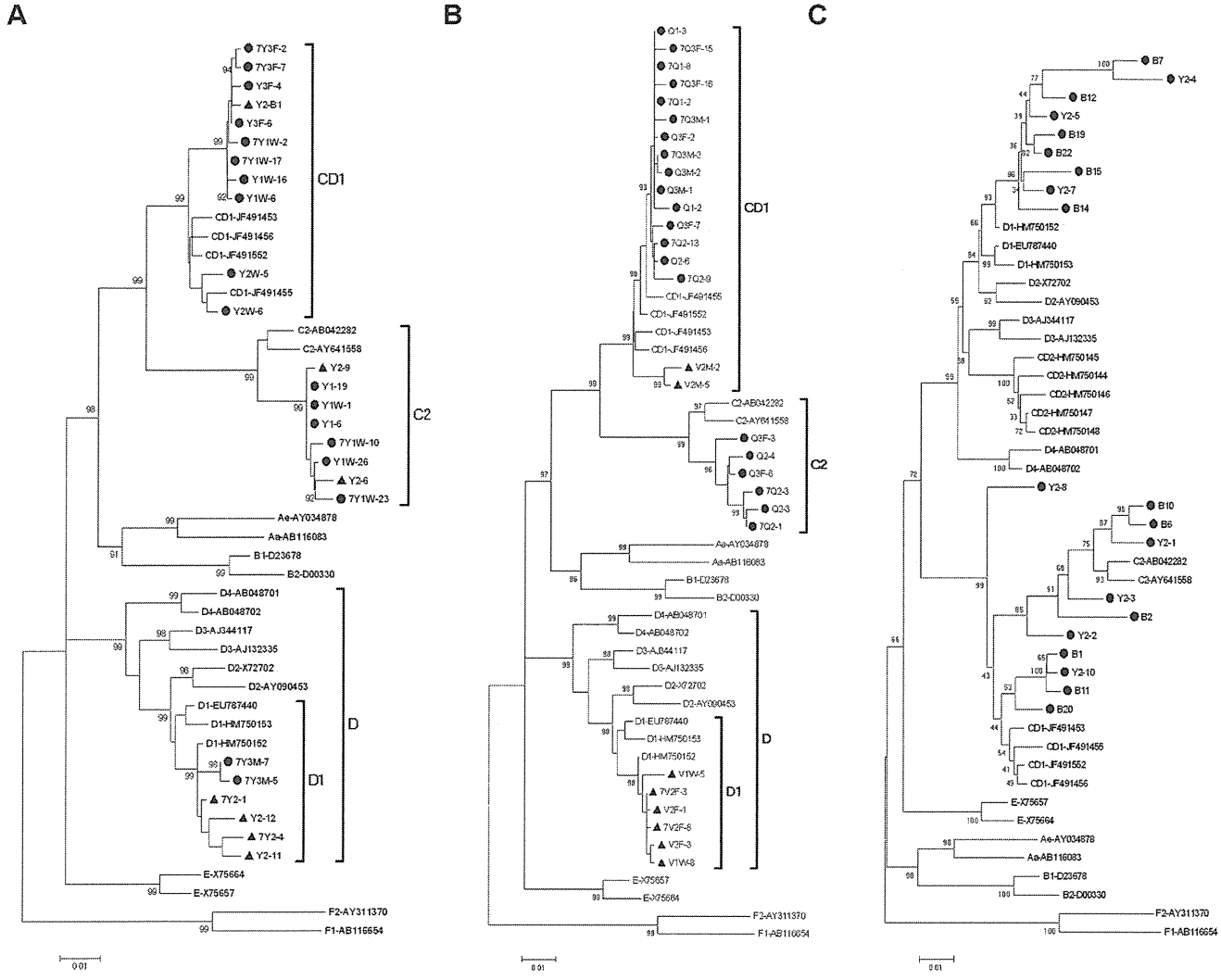

Figure 2. Phylogenetic tree construct by HBV nt 136-1110. (**A**) clones of family Y. Solid dots indicate the clones from Y1,Y1W,Y2W,Y3F and Y3M; Solid triangles indicate the clones from Y2. Family names starting with number 7 means the samples collected in 2007 otherwise in 2006. Novel recombinants of Y2 were excluded from the phylogenetic tree. (**B**) clones of family Q and family V. Solid dots indicate the clones from family Q; Solid triangles indicate the clones from family V. A family name starting with number 7 means the samples collected in 2007, otherwise, in 2006. (**C**) Novel recombinant clones of Y2. Solid dots indicate the clones from Y2.
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infections, we obtained a snapshot of naturally occurring HBV recombinants generated in the absence of selection and after selection. Our result showed direct evidence of HBV recombination, with new information of recombining crossovers compared with similar studies [16,17,18,19].

The recombination analysis of Y2 quasi-species showed variable types of recombinant between genotype C2, D1 and CD1 in 2006. Some studies show that hotspots of recombination most on the boundary of ORFs [12,20]. Our results showed that two or more strains of HBV can recombine with each other at any region along the genome. Crossover regions can be hundreds or just several base pairs, The length of crossover region is depends on the location of it on HBV genome. If it is located in a conserved HBV region, for another word, where many different genotypes share the same sequence, the length of crossover region may be long. If it is located in a non-conserved region, it may be very short. At the same time, we found that the crossover region distributed totally at random on HBV genome. Consistent with our results, *in vitro* evidence showed the initial recombination events in a laboratory system of MHV were almost entirely randomly distributed along the sequence [21]. It was only after passage through cell culture, with the opportunity for selection to remove less fit variants, that crossover sites became "localized" to just a small area of the region examined. Crucially, they also suggested initial products of recombination may go undetected because of the action of strong purifying selection which will remove new, deleterious combinations of mutations. The conclusion is therefore an interpretation for the genotype change of Y2. The Y2 presented multiple strain infections of C2/D1/CD1 and many new recombinants with no obvious dominant genotype strain in 2006. After 18 months, however, all the type C2 and CD recombinant strains disappeared while the D strain became dominant. A similar case of mixed HBV genotype infection in which one genotype was lost and another prevailed was previously described in patients with HBeAg seroconversion [4,22].

Epidemiologically, HBV genotype CD1 and C2 are the most common strains in ethnic minorities of northwest China with CD2 and D1 as minor strains. Precise mapping of recombination

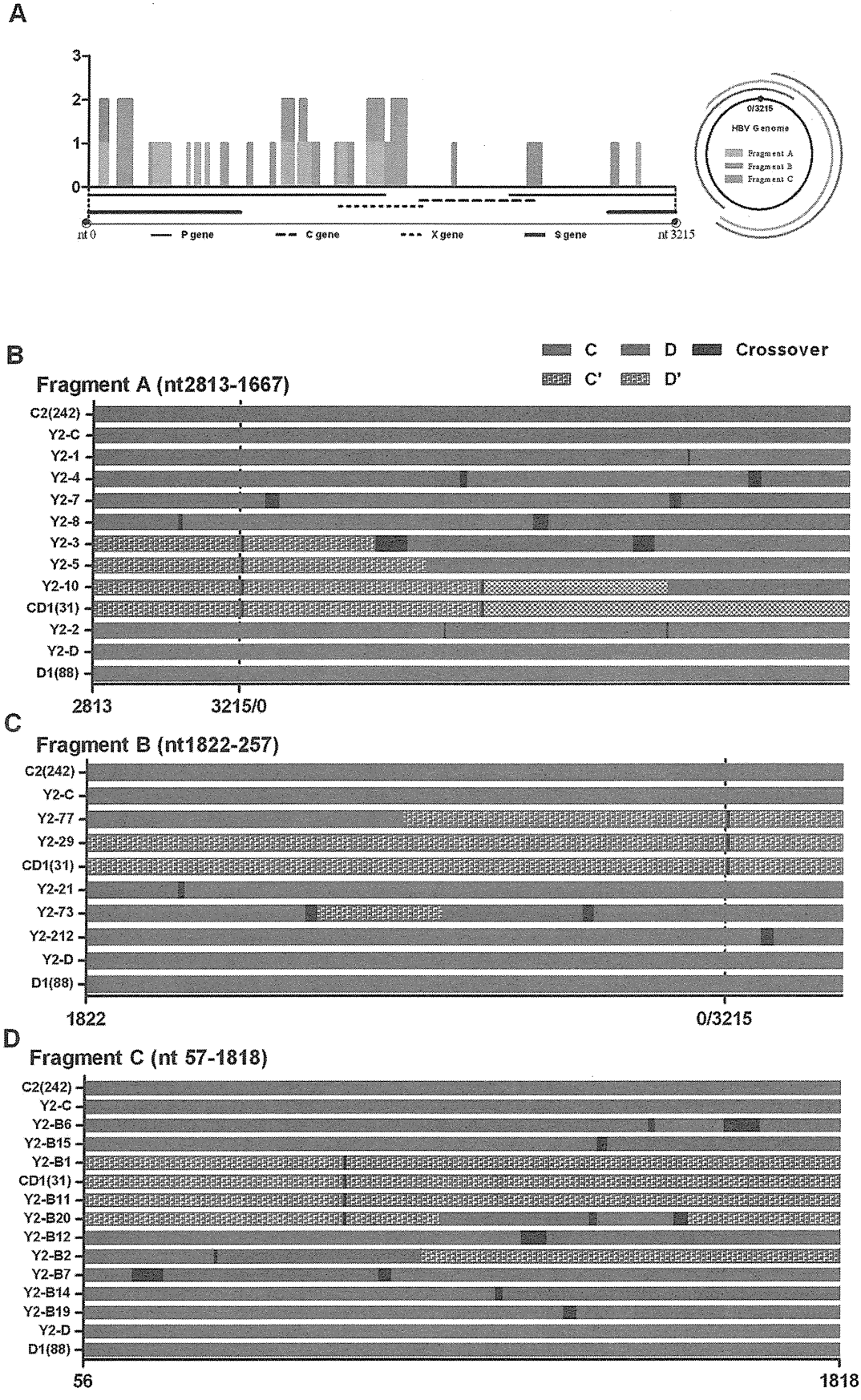
A
3
2
1
0
nt 0
P gene
C gene
X gene
S gene
nt 3215
0/3215
HBV Genome
Fragment A
Fragment B
Fragment C
B
C
D
Crossover
C'
D'
Fragment A (nt2813-1667)
C2(242)
Y2-C
Y2-1
Y2-4
Y2-7
Y2-8
Y2-3
Y2-5
Y2-10
CD1(31)
Y2-2
Y2-D
D1(88)
2813
3215/0
Fragment B (nt1822-257)
C2(242)
Y2-C
Y2-77
Y2-29
CD1(31)
Y2-21
Y2-73
Y2-212
Y2-D
D1(88)
1822
0/3215
Fragment C (nt 57-1818)
C2(242)
Y2-C
Y2-B6
Y2-B15
Y2-B1
CD1(31)
Y2-B11
Y2-B20
Y2-B12
Y2-B2
Y2-B7
Y2-B14
Y2-B19
Y2-D
D1(88)
56
1818

Figure 3. Alignment and recombination crossover regions found in Y2 clones. (**A**) Frequency and distribution of the recombination crossover regions found in Y2 clones along the HBV genome. The bars indicate the number of clones (y axis) showing recombination crossover regions at each site. The 1-3215 of x axis was consistent with the nt1-3215 of HBV genome. Different colors represent the sites find from clones of different PCR region: pink bars for fragment A, grey bars for fragment B and green bars for fragment C. (**B**) Alignment of fragment A (HBV nt 2813-0-1667). Y2-1'12: clones from fragment A of Y2 patients. (**C**) Alignment of fragment B (HBV nt 1822-0-257). Y2-21'212: clones from fragment B of Y2 patients. (**D**) Alignment of fragment C (HBV nt 57-1818) of Y2 clones. Y2-B1'B22: clones from fragment C of Y2 patients. The number on the x axis was consistent with the site of nucleotides of HBV genome. Solid green lines are genotype C2, solid pink lines are genotype D1, speckled green lines are the C2 component of genotype recombinant CD1 and speckled pink lines are the D1 component of recombinant genotype CD1. The black lines are sequence that is common to the recombining genotypes, and within which the recombination probably occurred. C2 (242) is the consensus sequence formed by 242 subgenotype C2 sequences from GenBank. D1 (88) is the consensus sequence formed by 88 subgenotype D1 sequences from GenBank. CD1 (33) is the consensus sequence formed by CD1 recombinant sequences from GenBank.
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suggests C2 and D1 are parental sequences of CD1 and CD2 recombinants. Virological differences among HBV genotypes were demonstrated in vitroand in CHiM mice, with genotype C having a higher replication capacity than D [23]. Why does the replication-deficient genotype D virus predominate over replication-competent genotype C? As mixed HBV infections together with recombination are rare, we have little knowledge about i this situation. On the one hand, we know little about host impact on different genotypes and recombinants. On the other hand, we know little about interference and competition in the quasi-species of mixed infection. In vitro results showed the replication capacity of individual clone, exclude the influence of host and other strains of quasi-species. An example from a ChiM mice study showed that monoinfection of HBV/G in ChiM mice display a very slow replication while coinfection with HBV/A remarkably enhanced the replication of HBV/G. The replication of HBV/G is heavily dependent on coinfection with other genotypes. When HBV/G superinfected on other genotypes, a rapidly takes over of HBV/G from original genotype were observed, though they are indispensable [24]. This study confirms that in a mixed infection system of different genotypes, the replication capacity of a genotype may be different from that of monoinfection. At the same time, replication capacity is not the only factor to influence which strain will become dominant. Variable recombinants found in our study may be mechanistically capable of genetic exchange, but strong selection guaranteed the elimination of hybrid genomes. The mechanism of selection in mixed infection also needs more investigation.

We found mixed HBV genotypes infection with many novel recombinants at one point in time, but just one genotype was found 18 months later. This may indicate that the detectable mixed infection and recombination has a limited time window due to the sensitivity of detection or strong selection power of the host. That's why in most studies, we can identify a major genotype in one patient. Even so, evolutionarily visible and invisible recombination of HBV could occur and play an important role by generating genetic variation or reducing mutational load. However, this study had limitation, because recombination signals were detected by RDP3 software and confirmed by split phylogenetic tree and alignment, indicating the recombinant or recombinant-like form should depend on the software. If we use another software, the results might be different.

Studies of HBV in endemic areas throughout the world have resulted in large numbers of full genome sequences available for phylogenetic analysis enabling the identification of novel, mosaic HBV genomes that appear to be the result of recombination between previously known sequences [7,25,26]. One of the most comprehensive analyses of putative HBV inter-genotype recombinants showed the existence of 24 phylogenetically independent HBV genomes involving all known human genotypes [27]. Some of these recombinants are unique to individual subjects, but some undergo expansion in specific populations and become recognized as new genotypes or subgenotypes [12,28,29,30]. Four stages in the process of generating popular HBV recombinant genomes should be recognized. The first stage is the co-circulation of different HBV strains or genotypes in the same geographic area. The second is the existence of individuals who have been infected with more than one strain of HBV. The third is the generation of a novel recombinant strain(s) within an individual. The fourth is the selection of a recombined strain with the ability to replicate and be transmitted. Our data show the natural process of the formation and selection of recombination though the recombinant strains of Y2 that appeared in 2006 that were all removed from samples in 2007.

By using phylogenetic trees and homology calculations, HBV variants infecting humans are currently classified into ten genotypes that differ from each other in nucleotide sequence by 7.5 to 13% [2,3]. There are some characteristic length differences between the genotypes that facilitates their detection and discrimination. However, as shown in Figure 2, existence of a recombinant makes the topology of the phylogenetic tree totally different from one with no recombinant. Recombinant strains obscured the definition of genotypes. Based on the algorithm creating a phylogenetic tree, sequences with high homologues cluster together. With the same logic, recombinants always clustered with the backbone parental sequence, in other words, with which they have high similarity with the larger proportion of the recombination region. Therefore, recombinants always seem to be a subgenotype of their backbone parental sequence. Similar to Y2-8 clone in Figure 2C, for recombinants with similar proportion of both parental genotypes, the sequence shows a divergent trend different from both parental genotypes.

Based on phylogenetic topology changes of different regions of HBV, it was hypothesized that some of the genotypes that are conventionally regarded as "pure," actually were recombinant. Genotype E strains show evidence of recombination with genotype D at 1950–2500. new reported genotype "I" actually belongs to genotype C. Furthermore, Subgenotype Ba possesses the recombination with genotype C at 1740 to 2485 [31,32,33]. Recombinants comprising regions with different histories have important implications for the way we think about HBV evolution. It means that there is no single phylogenetic tree that can describe the evolutionary relationships between genotypes.

In conclusion, mixed HBV genotypes infection with many novel recombinants at one point in time ended up with just one genotype 18 months later in this study. This may indicate that the detectable mixed infection and recombination have a limited time window due to the sensitivity of detection or strong selection power of the host. Also, as the recombinant or recombinant-like nature of HBV precludes the possibility of a "true" phylogenetic taxonomy, a new standard may be required for classifying HBV sequences.

Supporting Information

Figure S1 Recombination map of fragment A created by RDP software.
(TIF)

Figure S2 Recombination map of fragment B created by RDP software.
(TIF)

Figure S3 Recombination map of fragment C created by RDP software.
(TIF)

Figure S4 Split phylogenetic trees constructed by MEGA software. clone number and fragment used to construct trees are indicated beside each tree.
(TIF)

Figure S5 Split phylogenetic trees constructed by MEGA software. clone number and fragment used to construct trees are indicated beside each tree.
(TIF)

Figure S6 Split phylogenetic trees constructed by MEGA software. clone number and fragment used to construct trees are indicated beside each tree.
(TIF)

Figure S7 Alignment of fragment A(HBV nt 2813-0-1667)of Y2 clones. Deep green lines are genotype C2, deep pink lines are genotype D1, light green lines are the C2 component of genotype recombinant CD1 and light pink lines are the D1 component of recombinant genotype CD1. The black lines are sequence that is common to the recombining genotypes, and within which the recombination probably occurred. C2 (242): consensus sequence formed by 242 subgenotype C2 sequences from GenBank. D1 (88): consensus sequence formed by 88 subgenotype D1 sequences from GenBank. CD1 (33): consensus sequence formed by CD1 recombinant sequences from GenBank. Y2-1′12: clones from fragment A of Y2 patients.
(DOC)

Figure S8 Alignment of fragment B(HBV nt 1822-0-257) of Y2 clones. Deep green lines are genotype C2, deep pink lines are genotype D1, light green lines are the C2 component of genotype recombinant CD1, light pink lines are the D1 component of recombinant genotype CD1. The black lines are sequence that is common to the recombining genotypes, and within which the recombination probably occurred. C2 (242): consensus sequence formed by 242 subgenotype C2 sequences from GenBank. D1 (88): consensus sequence formed by 88 subgenotype D1 sequences from GenBank. CD1 (33): consensus sequence formed by CD1 recombinant sequences from GenBank. Y2-21′212: clones from fragment B of Y2 patients.
(DOC)

Figure S9 Alignment of fragment C(HBV nt 57-1818) of Y2 clones. Deep green lines are genotype C2, deep pink lines are genotype D1, light green lines are the C2 component of genotype recombinant CD1, light pink lines are the D1 component of recombinant genotype CD1. The black lines are sequence that is common to the recombining genotypes, and within which the recombination probably occurred. C2 (242): consensus sequence formed by 242 subgenotype C2 sequences from GenBank. D1 (88): consensus sequence formed by 88 subgenotype D1 sequences from GenBank. CD1 (33): consensus sequence formed by CD1 recombinant sequences from GenBank. B1B22: clones from fragment C of Y2 patients.
(DOC)

Author Contributions

Conceived and designed the experiments: ZW MM JH. Performed the experiments: BZ ZW. Analyzed the data: BZ JY JS. Contributed reagents/materials/analysis tools: HL YT. Wrote the paper: BZ YT.

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Special Report

Etiology and prognosis of fulminant hepatitis and late-onset hepatic failure in Japan: Summary of the annual nationwide survey between 2004 and 2009

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Aim: To summarize the annual nationwide survey on fulminant hepatitis (FH) and late-onset hepatic failure (LOHF) between 2004 and 2009 in Japan.

Methods: The annual survey was performed in a two-step questionnaire process to detail the clinical profile and prognosis of patients in special hospitals.

Results: Four hundred and sixty ($n = 227$ acute type; $n = 233$ subacute type) patients had FH and 28 patients had LOHF. The mean age of patients with FH and LOHF were 51.1 ± 17.0 and 58.0 ± 14.4 years, respectively. The causes of FH were hepatitis A virus in 3.0%, hepatitis B virus (HBV) in 40.2%, other viruses in 2.0%, autoimmune hepatitis in 8.3%, drug allergy-induced in 14.6% and indeterminate etiology in 29.6% of patients. HBV reactivation due to immunosuppressive therapy was observed in 6.8% of FH patients. The short-term survival rates of patients without liver transplantation (LT) were 48.7% and 24.2% for the acute and subacute type, respectively, and 13.0% for LOHF. The prognosis was poor in patients with HBV reactivation. The implementation rate for LT in FH patients was equivalent to that in the previous survey. The short-term survival rates of total patients, including LT patients, were 54.2% and 40.8% for the acute and subacute type, respectively, and 28.6% for LOHF.

Conclusion: The demographic features and etiology of FH patients has gradually changed. HBV reactivation due to immunosuppressive therapy is problematic. Despite advances in therapeutic approaches, the prognosis of patients without LT has not improved.

Key words: acute liver failure, fulminant hepatitis, Japan, liver transplantation, viral hepatitis

INTRODUCTION

IN JAPAN, FULMINANT hepatitis (FH) is defined as having hepatitis, when grade II or worse hepatic encephalopathy develops within 8 weeks of the onset of disease symptoms, with a prothrombin time of 40% or less.[1,2] FH is further classified into two subtypes, acute and subacute types, in which encephalopathy occurs within 10 days and later than 11 days, respectively, of the onset of the disease symptoms. Patients showing a prothrombin time of 40% or less, with hepatic encephalopathy developing between 8 and 24 weeks of disease onset are classified as having late-onset hepatic failure (LOHF).[3] Etiologies with hepatitis present in the histology, such as viral infection, autoimmune hepatitis and drug allergy-induced liver injury are defined as causes of

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FH and LOHF. In contrast, acute liver failure due to other causes with the absence of hepatitis in the histology, such as drug toxicity, circulatory disturbance and metabolic disease, are excluded as causes of FH and LOHF. Recently, a novel diagnostic criteria for acute liver failure in Japan was established by the Intractable Hepato-Biliary Disease Study Group.[4,5] These criteria included other causes with liver damage without the absence of hepatitis in the histology in addition to the present criteria.

Among viral infection, hepatitis B virus (HBV) is a major cause of FH in Japan.[6,7] HBV infection is classified into transient HBV infection type and acute exacerbation in an HBV inactive carrier. With advances in cytotoxic chemotherapy and immunosuppressive therapy, reactivation of hepatitis B is becoming a clinical problem.[8] Moreover, recent introduction of rituximab plus steroid combination therapy for non-Hodgkin's lymphoma has been associated with HBV reactivation in transiently infected patients, namely, de novo hepatitis. However, the prevalence of HBV reactivation in patients with FH and LOHF is unknown.

Advances in therapeutic strategies for FH and LOHF have improved the prognosis. Since 1988, living-donor liver transplantation (LT) has been adopted in patients who are beyond the supportive care of a critical unit.[6] Recently, artificial liver support with high-flow or on-line hemodiafiltration (HDF) has been used. Since 2006, a nucleoside analog, entecavir, has been used as a substitute for lamivudine, as an antiviral agent for HBV. However, it is unknown whether these new treatments improve the prognosis of FH.

The Intractable Hepato-Biliary Diseases Study Group has annually performed a nationwide survey of patients with FH and LOHF since 1983.[6] Since 2000, approximately 600 hospitals have been enrolled in the survey. This report summarizes the results of the survey between 2004 and 2009 to addresses the trends in the etiology and prognosis of patients with FH and LOHF and compares them with the previous survey.[7]

METHODS

THE NATIONWIDE SURVEY was performed annually. The number of hospitals for survey has changed in each year. Maximum (608) was in 2007 and minimum (544) was in 2006, with active members of the Japan Society of Hepatology and the Japanese Society of Gastroenterology between 2005 and 2010. The survey was performed in a two-step questionnaire process to detail the clinical profile and prognosis of patients who were diagnosed as FH or LOHF in the previous year. The recovery rate of the first and second questionnaire was 39–59% and 60–100%, respectively. Patients who met the diagnostic criteria for FH or LOHF were entered into the survey. Patients under 1 year of age, those with alcoholic hepatitis, those with chronic liver diseases and those with acute liver failure with no histological features of hepatitis were excluded from the analysis.

According to criteria described in previous reports,[7,9] the etiology of FH and LOHF was classified into five categories: (i) viral infection; (ii) autoimmune hepatitis; (iii) drug allergy-induced liver injury; (iv) indeterminate etiology despite sufficient examinations; and (v) unclassified due to insufficient examinations. Patients with viral infection consisted of those with hepatitis A virus (HAV), HBV, hepatitis C virus (HCV), hepatitis E virus (HEV) and other viruses. The patients with HBV infection were classified into three subgroups according to serum markers of HBV, hepatitis B core antibody (HBcAb) and immunoglobulin (Ig)M-HBcAb: (i) transient HBV infection; (ii) acute exacerbation in HBV carriers; and (iii) indeterminate infection patterns. In the present study, we classified acute exacerbation in HBV carriers into three subgroups according to the new criteria:[4,5] (i) inactive carriers, without drug exposure; (ii) reactivation in inactive carriers by immunosuppressant and/or anticancer drugs; and (iii) reactivation in transiently infected patients by immunosuppressant and/or anticancer drugs (i.e. de novo hepatitis). Because not every patient was examined for serological markers of transient HBV infection before the onset of FH and LOHF (with HBcAb and/or hepatitis B surface antigen [HBsAg] in serum), we defined HBV reactivation as that occurring in transiently infected patients when they developed HBV-related hepatitis due to immunosuppressive therapy or cytotoxic chemotherapy with reappearance of HBsAg in the serum and did not conform to the criteria of transient HBV infection.

The statistical significance of differences between groups was assessed using Student's *t*-test, Fisher's exact test or Kruskal–Wallis one-way ANOVA. Data are shown as mean ± standard deviation. The study was conducted with the approval of the Ethical Committee of Kagoshima University Graduate School of Medical and Dental Sciences.

RESULTS

Demographic features and survival rates

FROM 2004–2009, 582 PATIENTS were enrolled in the survey. Ninety-four patients were excluded from

the survey according to the exclusion criteria. Consequently, 460 patients ($n = 227$ acute type; $n = 233$ subacute type) were classified as having FH and 28 as having LOHF (Table 1). The incidence of the acute and subacute types of FH was similar and the incidence of LOHF was one-sixteenth of FH. The male : female ratio was higher for the acute type and lower for the subacute type of FH and LOHF. The mean age of patients was significantly higher for the subacute type of FH and LOHF than that for the acute type of FH. Almost half of the patients with FH and LOHF had complications which preceded the onset of acute liver failure. Furthermore, approximately 60% of patients with FH had received daily medication. This tendency for receiving medication was more obvious in patients with the subacute type of FH and LOHF.

The survival rates of patients without LT were 48.7% for the acute type and 24.2% for the subacute type of FH, and 13.0% for LOHF. The survival rates of the subacute type of FH and LOHF was worse than that of the acute type. The prognosis of both the acute type and the subacute type of FH appeared to be equivalent annually. The survival rates of patients with LT were 79.6% for FH and 100% for LOHF, with no difference in these rates among the disease types.

Clinical profile

Symptoms, imaging findings and complications are shown in Table 2. Since 2006, diagnostic criteria of systemic inflammatory response syndrome (SIRS) for fever, tachycardia and tachypnea have been adopted in the survey.[10] Icterus, flapping tremor, ascites, hepatic fetor, tachycardia, tachypnea and pretibial edema were frequently found. The frequency of patients with ascites and pretibial edema was significantly greater in the subacute type of FH and LOHF than in the acute type of FH. In contrast, fever appeared more frequently in patients with the acute type of FH. The frequency of liver atrophy was greater in the subacute type of FH, and even higher in LOHF, than in the acute type of FH.

With regard to complications, disseminated intravascular coagulation, renal failure and bacterial infection were found in more than 30% of patients with FH and LOHF. Brain edema was less frequent in the subacute type than in the acute type of FH.

Causes of FH and LOHF

The cause of FH was identified as viral infection in 46.1% of the patients (Table 3). The frequencies of viral infection were highest for the acute type of FH. HAV infection was found in 3% of patients with FH. HBV infection was found in 40.2% of patients with FH and 32.1% of patients with LOHF. Transient HBV infection was more frequent in the acute type than in the subacute type of FH, whereas the frequency of acute exacerbation in HBV carriers was greater in the subacute type than in the acute type of FH. HBV reactivation in inactive carriers and in transiently infected patients were found in 3.3% and 3.5% of patients with FH, respectively. With regard to underlying diseases in patients with HBV reactivation, non-Hodgkin's lymphoma/mucosa-associated lymphoid tissue lymphoma was most prevalent in 50% of inactive carriers and in 76% of those with transiently infected patients. Among patients with HBV

Table 1 Demographic features and survival rates of patients with fulminant hepatitis (FH) and late-onset hepatic failure (LOHF)

	FH			LOHF ($n = 28$)
	Total ($n = 460$)	Acute type ($n = 227$)	Subacute type ($n = 233$)	
Male/female	227/233	127/100	100/133**	9/19*
Age (years; mean ± SD)	51.1 ± 17.0	48.8 ± 16.9	53.4 ± 16.7**	58.0 ± 14.4**
HBV carrier (%)	13.1 (52/397)	10.5 (19/181)	15.3 (33/216)	22.2 (6/27)
Complications preceding acute liver failure (%)†	46.4 (208/448)	40.0 (88/220)	52.6 (120/228)**	50.0 (14/28)
History of medication (%)	59.9 (260/434)	51.2 (108/211)	68.2 (152/223)**	71.4 (20/28)*
Survival rates				
All patients	47.4 (218/460)	54.2 (123/227)	40.8 (95/233)**	28.6 (8/28)*
No LT	37.5 (132/352)	48.7 (93/191)	24.2 (39/161)**	13.0 (3/23)**
LT	79.6 (86/108)	83.3 (30/36)	77.8 (56/72)	100 (5/5)

*$P < 0.05$, **$P < 0.01$ vs acute type.
†Diseases such as metabolic syndrome, malignancy and psychiatric disorders.
Data in parenthesis indicate patient numbers.
HBV, hepatitis B virus; LT, liver transplantation; SD, standard deviation.

Table 2 Symptoms, imaging findings and complications of patients with fulminant hepatitis (FH) and late-onset hepatic failure (LOHF)

	FH			LOHF ($n = 28$)
	Total ($n = 460$)	Acute type ($n = 227$)	Subacute type ($n = 233$)	
(a) Symptoms at diagnosis				
Fever†	13.0 (42/322)	17.5 (28/160)	8.6 (14/162)*	0 (0/23)*
Icterus	96.8 (427/441)	95.0 (208/219)	98.6 (219/222)*	96.4 (27/28)
Ascites	57.2 (237/414)	45.2 (88/204)	71.0 (149/210)**	81.5 (22/27)**
Convulsion	5.2 (22/422)	6.7 (14/210)	3.8 (8/212)	0 (0/27)
Tachycardia‡	36.7 (117/319)	39.5 (62/157)	34.0 (55/162)	47.8 (11/23)
Tachypnea§	34.5 (87/252)	39.1 (52/133)	29.4 (35/119)	31.6 (6/19)
Flapping tremor	79.0 (309/391)	75.8 (144/190)	82.1 (165/201)	80.8 (21/26)
Hepatic fetor	46.6 (146/313)	49.0 (73/149)	44.5 (73/164)	42.1 (8/19)
Pretibial edema	35.5 (127/358)	24.1 (42/174)	46.2 (85/184)**	75.0 (15/20)**,***
(b) Imaging findings				
Liver atrophy¶	58.8 (255/434)	45.6 (98/215)	71.7 (157/219)**	92.6 (25/27)**,***
(c) Complications				
Infection	34.8 (149/428)	32.9 (68/207)	36.7 (81/221)	51.9 (14/27)
Brain edema	18.5 (71/384)	24.1 (46/191)	13.0 (25/193)**	22.7 (5/22)
Gastrointestinal bleeding	13.2 (59/446)	11.0 (24/219)	15.4 (35/227)	20.0 (5/25)
Renal failure	38.9 (177/455)	40.9 (92/225)	37.0 (85/230)	39.3 (11/28)
DIC	34.6 (150/433)	35.7 (76/213)	33.6 (74/220)	53.8 (14/26)
Congestive heart failure	7.3 (31/427)	8.9 (19/214)	5.6 (12/213)	12.0 (3/25)

*$P < 0.05$, **$P < 0.01$ vs acute type, ***$P < 0.05$ vs subacute type.
†Temperature: >38°C or <36°C.
‡Heart rate: >90 beats/min.
§Respiratory rate: >20 breaths/min or $PaCO_2$: <32 Torr.
† ‡ § Cases between 2005 and 2009.
¶Liver atrophy detected by ultrasound and/or computed tomography imaging.
Data in parentheses indicate patient numbers.
DIC, disseminated intravascular coagulation.

reactivation, rituximab plus steroid combination chemotherapy was administrated to 35% of patients in inactive carriers and to 59% of those with transiently infected patients. HCV and HEV infection were less frequently found. In the survey, Epstein–Barr virus, herpes simplex virus and human herpes virus type-6 were found as other causes of viral hepatitis.

Autoimmune hepatitis was frequently observed in patients with the subacute type of FH and LOHF. Drug allergy-induced liver injury was observed in approximately 10–20% of patients irrespective of disease types. Anti-tuberculosis agents, non-steroidal anti-inflammatory drugs, anticancer agents, drugs for metabolic syndrome, and various herbal and natural remedies were the probable causative agents for this liver injury in the survey. Notably, the etiology was indeterminate in approximately 40% of patients with the subacute type of FH.

Therapies

For artificial liver support, plasma exchange and HDF were performed in most patients with FH (Table 4). Conventional HDF and continuous HDF (CHDF) were performed in 22.5% and 51.8% of patients with FH, respectively. A more powerful method, high-flow HDF (HF-HDF), high-flow CHDF (HF-CHDF) and on-line HDF were performed in 2.6%, 11.7% and 1.8% of the patients, respectively. The nucleoside analogs lamivudine and entecavir were used in approximately a quarter of patients with FH. Entecavir were used more frequently than lamivudine since 2007. Glucocorticosteroid, mainly as steroid pulse therapy, were administrated in more than 70% of patients with FH and LOHF. Anticoagulation therapy were performed in approximately 40–50% of patients with FH and LOHF. Glucagon/insulin, branched-chain amino acid-rich solution,

Table 3 Causes of fulminant hepatitis (FH) and late-onset hepatic failure (LOHF)

	FH			LOHF ($n = 28$)
	Total ($n = 460$)	Acute type ($n = 227$)	Subacute type ($n = 233$)	
Viral infection	46.1 (212)	62.6 (142)	30.0 (70)	32.1 (9)
HAV	3.0 (14)	5.7 (13)	0.4 (1)	0 (0)
HBV	40.2 (185)	54.2 (123)	26.6 (62)	32.1 (9)
(1) Transient infection	19.6 (90)	35.2 (80)	4.3 (10)	3.6 (1)
(2) Acute exacerbation in HBV carrier	14.1 (65)	7.9 (18)	20.2 (47)	25.0 (7)
(i) Inactive carrier, without drug exposure	7.4 (34)	6.2 (14)	8.6 (20)	3.6 (1)
(ii) Reactivation in inactive carrier†	3.3 (15)	1.8 (4)	4.7 (11)	17.9 (5)
(iii) Reactivation in transiently infected patient‡	3.5 (16)	0 (0)	6.9 (16)	3.6 (1)
(3) Indeterminate infection patterns	6.5 (30)	11.0 (25)	2.1 (5)	3.6 (1)
HCV	1.1 (5)	0.9 (2)	1.3 (3)	0 (0)
HEV	0.9 (4)	0.9 (2)	0.9 (2)	0 (0)
Other viruses	0.9 (4)	0.9 (2)	0.9 (2)	0 (0)
Autoimmune hepatitis	8.3 (38)	2.2 (5)	14.2 (33)	32.1 (9)
Drug allergy-induced liver injury	14.6 (67)	13.7 (31)	15.5 (36)	17.9 (5)
Indeterminate§	29.6 (136)	19.4 (44)	39.5 (92)	17.9 (5)
Unclassified¶	1.5 (7)	2.2 (5)	0.9 (2)	0 (0)

†Reactivation in inactive carrier by immunosuppressant and/or anticancer drugs.
‡Reactivation in transiently infected patients by immunosuppressant and/or anticancer drugs (de novo hepatitis).
§Indeterminate etiology despite sufficient examinations.
¶Unclassified due to insufficient examinations.
Data in parentheses indicate patient numbers.
HAV, hepatitis A virus; HBV, hepatitis B virus; HCV, hepatitis C virus; HEV, hepatitis E virus.

cyclosporin A and prostaglandin E_1 therapy were administrated less frequently compared with the previous survey.

Liver transplantation was performed in 23.5% and 17.9% of patients with FH and LOHF, respectively. Two patients received deceased-donor LT and 111 patients received living-donor LT. The frequency of LT was significantly greater in the subacute type than in the acute type of FH.

Prognosis

The prognosis of patients with FH and LOHF differed depending on the etiology (Table 5). Prognosis was good in patients with HAV infection. The prognosis was fair in patients with transient HBV infection. In contrast, the prognosis was poor in acute exacerbation in HBV carriers. The prognosis was extremely poor in patients with HBV reactivation, either from inactive carriers or transiently infected patients. Patients with the subacute type of FH and LOHF caused by autoimmune hepatitis, drug allergy-induced liver injury and indeterminate etiology also showed a poor prognosis.

The clinical features of the patients appeared to be associated with the prognosis. In the acute type of FH with no LT, the frequency of patients with SIRS (tachycardia or tachypnea) was greater in patients who died than in surviving patients ($P < 0.05$). Liver atrophy on ultrasound and/or computed tomography imaging was an important factor in predicting the prognosis of FH and LOHF with no LT. The frequencies were 25.0% and 64.5% in patients with the acute type ($P < 0.01$) and 55.6% and 78.1% in those with the subacute type of FH in surviving patients and those who died, respectively ($P < 0.05$).

Prognosis also appeared to be affected by complications. Any of the complications significantly decreased survival rate (data not shown). Furthermore, the number of these complications affected the prognosis. The survival rate of patients with the acute type of FH was greater than 80% in those with no complications, while it was less than 30% in those with two or more complications. The survival rate of patients with the subacute type of FH was decreased in proportion to the number of complications.

Table 4 Therapies for patients with fulminant hepatitis (FH) and late-onset hepatic failure (LOHF)

	FH			LOHF ($n = 28$)
	Total ($n = 460$)	Acute type ($n = 227$)	Subacute type ($n = 233$)	
Plasma exchange	90.9 (418/460)	92.5 (210/227)	89.3 (208/233)	71.4 (20/28)**,***
Hemodiafiltration	75.0 (342/456)	75.1 (169/225)	74.9 (173/231)	57.1 (16/28)
Glucocorticosteroids	72.4 (333/460)	68.3 (155/227)	76.4 (178/233)	89.3 (25/28)*
Glucagon/insulin	14.6 (67/459)	13.7 (31/227)	14.7 (34/232)	17.9 (5/28)
BCAA-rich solution	19.1 (87/456)	14.3 (32/223)	23.6 (55/233)*	39.3 (11/28)**
Prostaglandin E_1	7.0 (32/458)	6.7 (15/225)	7.3 (17/233)	3.6 (1/28)
Cyclosporin A	10.0 (46/460)	7.0 (16/227)	12.9 (30/233)*	10.7 (3/28)
Interferon	14.1 (65/460)	15.4 (35/227)	12.9 (30/233)	10.7 (3/28)
Nucleoside analog	38.9 (179/460)	50.9 (115/226)	27.5 (64/233)**	32.1 (9/28)
Lamivudine	25.5 (116/455)	40.0 (76/224)	30.4 (40/231)	12.5 (6/28)
Entecavir†	22.4 (70/312)	27.7 (41/148)	17.7 (29/164)	33.3 (5/15)
Anticoagulation therapy‡	47.2 (216/458)	43.2 (98/227)	51.1 (118/231)	39.3 (11/28)
Liver transplantation	23.5 (108/460)	15.9 (36/227)	30.9 (72/233)	17.9 (5/28)

*$P < 0.05$, **$P < 0.01$ vs acute type, ***$P < 0.05$ vs subacute type.
†Cases between 2006 and 2009.
‡Drugs such as antithrombin III concentrate and protease inhibitor compounds, gabexate mesylate and nafamostat mesilate.
Data in parentheses indicate patient numbers.
BCAA, branched-chain amino acid.

DISCUSSION

IN THIS SURVEY, 488 patients were enrolled over 6 years. In the previous 6-year survey, 697 patients (634 for FH and 64 for LOHF) were enrolled.[7] The incidence ratio of LOHF to FH was decreased from 9:1 to 16:1. In national epidemiology research, the annual incidence of FH was estimated at 1050 cases in 1996 and 429 cases in 2004.[11] Therefore, the incidence of FH and LOHF could be decreasing longitudinally. In this survey, the mean age of patients with FH and LOHF was older than that in the previous survey. More patients with complications received daily medication compared with the previous survey. Changes in demographic features of the patients may affect the etiology and prognosis of FH. A relationship between daily dose of oral medication and idiosyncratic drug-induced liver injury has been reported.[12] Additionally, older age is considered a poor prognostic factor in acute liver failure and may be considered a relative contraindication for LT.[13,14]

The current study showed that HBV still remains a major cause of FH and LOHF. Notably, almost half of acute exacerbations in HBV carriers occurred in patients with HBV reactivation owing to immunosuppressive or cytotoxic therapy. Approximately 80% of patients with transiently infected patients had received rituximab plus steroid combination therapy for non-Hodgkin's lymphoma. This combination therapy has been identified as a risk factor for HBV reactivation in HBsAg positive/negative patients with non-Hodgkin's lymphoma.[15,16] Our survey revealed that careful attention is necessary for transiently infected patients, as well as for inactive HBV carriers using intensive immunosuppressive agents.

The frequency of HAV infection in patients with FH was decreased compared with the previous survey. This result is compatible with no occurrence of outbreak of acute hepatitis A during this period. In Japan, zoonotic transmission from pigs, wild boar and deer, either foodborne or otherwise, is the cause of HEV infection.[17,18] In the currently studied survey, two-thirds of the patients were from endemic areas (Hokkaido Island and the northern part of mainland Honshu) in Japan.

The other principal finding in this survey was that the etiology was indeterminate in approximately 40% of patients with FH. One of the reasons for this result may be the failure of diagnosis for autoimmune hepatitis or drug-induced liver injury. Although the diagnosis of autoimmune hepatitis relies on the presence of serum autoantibodies, with higher IgG levels (>2 g/dL), acute-onset autoimmune hepatitis does not always show typical clinical features.[19–21] Additionally, the sensitivity of the drug-induced lymphocyte stimulation test for diagnosis is not completely reliable.

Table 5 Survival rates and etiology of patients with fulminant hepatitis (FH) and late-onset hepatic failure (LOHF) who did not have liver transplantation

	FH			LOHF ($n = 23$)
	Total ($n = 352$)	Acute type ($n = 191$)	Subacute type ($n = 161$)	
Viral infection	39.8 (70/176)	49.2 (58/118)	20.7 (12/58)**	14.3 (1/7)
HAV	57.1 (8/14)	61.5 (8/13)	0 (0/1)	–
HBV	36.2 (55/152)	46.1 (47/102)	16.0 (8/50)**	14.3 (1/7)
(1) Transient infection	52.6 (40/76)	54.4 (37/68)	37.5 (3/8)	–
(2) Acute exacerbation in HBV carrier	15.1 (8/53)	21.4 (3/14)	12.8 (5/39)	14.3 (1/7)
(i) Inactive carrier, without drug exposure	29.2 (7/24)	27.3 (3/11)	30.8 (4/13)	0 (0/1)
(ii) Reactivation in inactive carrier†	7.7 (1/13)	0 (0/3)	10.0 (1/10)	20.0 (1/5)
(iii) Reactivation in transiently infected patients‡	0 (0/16)	–	0 (0/16)	0 (0/1)
(3) Indeterminate infection patterns	30.4 (7/23)	35.0 (7/20)	0 (0/3)	–
HCV	50.0 (2/4)	100 (1/1)	33.3 (1/3)	–
HEV	75.0 (3/4)	100 (2/2)	50 (1/2)	–
Other viruses	100 (2/2)	–	100 (2/2)	–
Autoimmune hepatitis	32.4 (9/28)	40.0 (2/5)	30.4 (7/23)	12.5 (1/8)
Drug allergy-induced	32.8 (19/58)	43.3 (13/30)	21.4 (6/28)	0 (0/3)
Indeterminate§	37.6 (32/85)	54.5 (18/33)	26.9 (14/52)*	20.0 (1/5)
Unclassified¶	1.5 (7)	40.0 (2/5)	–	–

**$P < 0.01$ vs acute type.
†Reactivation in inactive carrier by immunosuppressant and/or anticancer drugs.
‡Reactivation in transiently infected patients by immunosuppressant and/or anticancer drugs (de novo hepatitis).
§Indeterminate etiology despite sufficient examinations.
¶Unclassified due to insufficient examinations.
Data in parentheses indicate patient numbers.
HAV, hepatitis A virus; HBV, hepatitis B virus; HCV, hepatitis C virus; HEV, hepatitis E virus.

Recently, powerful HDF using large buffer volumes (HF-HDF or HF-CHDF), or on-line HDF has been used. HF-HDF or HF-CHDF has a high recovery rate from a coma.[22–24] On-line HDF has an excellent recovery rate from a coma and is useful as a liver support system.[25] However, only 16% of patients with FH received these powerful HDF in the survey examined in the current study. The frequency of brain edema, gastrointestinal bleeding and congestive heart failure was decreased compared with that in the previous survey. Advances in artificial liver support and management may contribute to prevent these complications. Further evaluation is required to determine whether a new powerful support system can improve the prognosis of FH. The survival rate for FH patients with autoimmune hepatitis improved 17.1% in the previous survey to 32.4% in the 2004–2009 survey. Early commencement of corticosteroids may improve the prognosis. However, the efficacy of these drugs has not been evaluated statistically.

Recently, in patients with acute liver failure due to HBV, entecavir has been used more frequently than lamivudine because of its high potency and extremely low rates of drug resistance.[26] Entecavir beneficially affects the course of acute liver failure as lamivudine.[27,28] Despite the use of entecavir, the prognosis of HBV-infected patients, especially in HBV carriers, has not improved. In the case of HBV reactivation, it is difficult to prevent development of liver failure, even when nucleoside analogs are administrated after the onset of hepatitis. Because these agents require a certain amount of time to decrease HBV DNA in serum, they need to be administrated in the early phase of hepatitis. Guidelines for preventing HBV reactivation recommend the administration of nucleoside analogs before the start of immunosuppressive therapy in inactive carriers and at an early stage of HBV reactivation during or after immunosuppressive therapy in transiently infected patients.[29]

Despite new therapeutic approaches and intensive care, the prognosis of patients without LT with both types of FH and LOHF appeared similar to that in the previous survey. In contrast, the prognosis of patients receiving LT was good in the present survey. Yamashiki

et al. reported that the short-term and long-term outcomes of living-donor LT for acute liver failure were good, irrespective of the etiology and disease types.[30] In the current survey, the implementation rate of receiving LT was almost equivalent to that in the previous survey, irrespective of disease type. Notably, only two patients received deceased-donor LT in the current survey. Recently, patients with FH who received deceased-donor LT have been increasing since the new organ transplant bill passed in 2009. Hepatologists should realize that more donor action to increase deceased-donor LT is necessary to improve the prognosis of patients with FH or LOHF. Determining appropriate judgment to move forward to LT is the most important step. The indications for LT in cases of FH are determined according to the 1996 Guidelines of the Acute Liver Failure Study Group of Japan.[31] To improve the low sensitivity and specificity of assessment in patients with acute and subacute types,[32] new guidelines for using a scoring system have been established by the Intractable Hepato-Biliary Disease Study Group of Japan.[33] This novel scoring system showed sensitivity and specificity of 0.80 and 0.76, respectively, and greater than those in the previous guideline.[33] Recently, new prediction methods using data-mining analysis has been established.[34,35]

In conclusion, the demographic features and etiology of FH and LOHF have been gradually changing. HBV reactivation due to immunosuppressive therapy is a particular problem because of poor prognosis. The subacute types of FH and LOHF have a poor prognosis, irrespective of the etiology. Despite recent advances in therapeutic approaches, the implementation rate for LT and survival rates of patients without LT are similar to those in the previous survey.

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