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## Molecular Evolution of Hepatitis Viruses

Flor H. Pujol, Rossana Jaspe and Héctor R. Rangel  
*Laboratorio de Virología Molecular, CMBC, IVIC, Caracas, Venezuela*

### 1. Introduction

Five hepatitis viruses (HV) are known to date. Infection by enterically-transmitted viruses (HAV and HEV) causes acute hepatitis and is generally benign compared to the disease caused by parenterally-transmitted viruses (HBV, HCV and HDV), for which chronic infection may lead to hepatocellular carcinoma (HCC). Some types of HDV have also been associated to a high frequency of fulminant hepatitis (Table 1). In addition to these viruses, other viruses have been discovered and initially proposed as causative agents of hepatitis, like GBV-C, TTV and SenV. The association with hepatitis was later discarded.

This chapter addresses the molecular evolution of these viruses. An overview on molecular biology and replication of each HV, with emphasis on aspects leading to generation of diversity, is discussed. The diversity of each HV, both at the intrahost and the population level, and the implication of HV diversity on pathogenicity is described. In addition, the possible origin of these viruses is discussed. The chapter also covers how co-infection with HIV may modulate the diversity of HV, in terms of genotypic variability and intrahost evolution.

Hepatitis Virus	Genome and size	Chronicity and HCC	Genotypes	Salient molecular feature
A	sRNA 7.5 Kb <sup>1</sup>	No	7: 4 in humans	Codon usage
B	dDNA 3.2 Kb	Yes	8 and simian genotypes	Reverse transcriptase
C	sRNA 9.5 Kb	Yes	7	Quasispecies
D	spRNA 1.7 Kb	Yes	8	Ribozyme, viroid-like genome
E	sRNA 7.2 Kb	No <sup>2</sup>	4	Zoonotic transmission of some genotypes

<sup>1</sup>: s for single stranded, d for partially double stranded, sp for single stranded with intrapairing as a viroid structure. <sup>2</sup>: HEV has not been associated to chronicity, except in immunocompromised patients (Kaba et al., 2011).

Table 1. Molecular characteristics of hepatitis viruses

### 2. Molecular biology and replication of hepatitis viruses

All but one (HBV) of the HV are RNA viruses. This fact implies that they use RNA polymerases - and for HBV a retrotranscriptase - for replication, which lack proofreading

capacity, leading to generation of mutations  $10^4$  more frequently than human DNA polymerase, for example.

## 2.1 Enterically transmitted viruses

HAV is a non-enveloped virus which belongs to the genus *Hepatovirus*, of the family *Picornaviridae* (Cristina & Costa-Mattioli, 2007). As an RNA virus, replication occurs entirely in the cytoplasm. HAV genome is a single positive stranded ARN of 7.5 Kb, with an Internal Ribosome Entry Side (IRES) at its 5' non-coding region. It encodes for a polyprotein of approximately 2.200 aminoacids (Figure 1) (Cristina & Costa-Mattioli, 2007). This polyprotein is cleaved by cellular and viral proteases to produce 11 proteins and among them the viral RNA-dependent RNA polymerase. This polymerase produces the antigenomic negative strand RNA which serves as template for generation of genomic positive strand RNAs, which will be inserted into the assembling viral capsids to be liberated by exocytosis throughout the cell (Cuthbert, 2001).

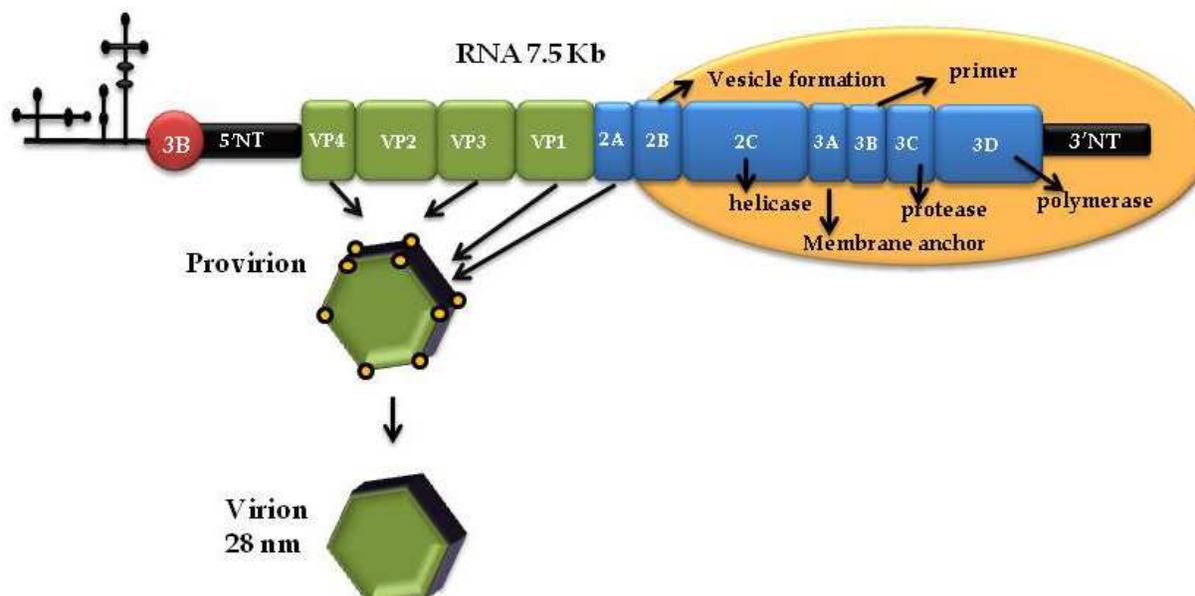


Fig. 1. HAV virion and genome organization. The positive-strand RNA genome contains a single open reading frame which encodes a polyprotein proteolytically processed by a cellular protease and the viral protease 3Cpro. Structural proteins (VP) are indicated in green, and nonstructural proteins in blue. The RNA secondary structure of the IRES is shown in the 5' end.

HEV is a non-enveloped virus classified as a *Hepevirus*, in the family *Hepeviridae* (Jameel, 1999). Infection with HEV is responsible for a high percentage of fulminant hepatitis in pregnant women (Dalton et al., 2008). The HEV genome is a positive single-stranded RNA of approximately 7.2 kb, with a 5'-methylguanine cap and a 3'- polyA stretch. It contains three partially overlapping open reading frames (ORFs) (Figure 2):

- ORF1, coding for non structural proteins including the RNA-dependent RNA polymerase,
- ORF2, coding for the viral capsid protein,

- and ORF3, which might function as a viral accessory protein affecting the host response to infection. (Ahmad et al., 2011).

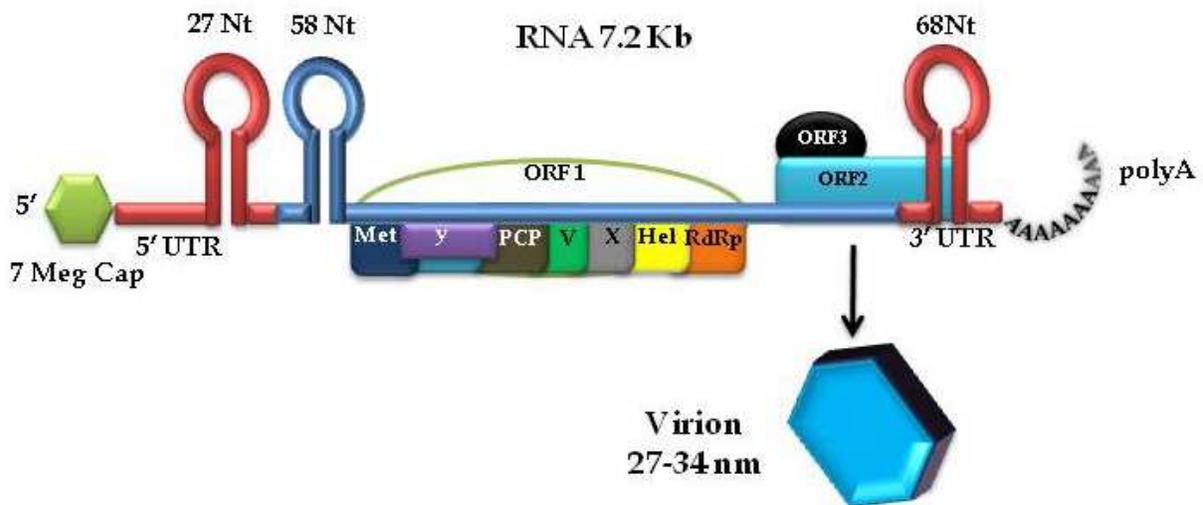


Fig. 2. **HEV virion and genome organization.** The positive strand RNA genome is capped at the 5' end and polyadenylated at the 3' end. The three open reading frames (ORFs) are shown. ORF1 encodes the nonstructural polyprotein with various functional units - methyltransferase (MeT), papain-like cysteine protease (PCP), RNA helicase (Hel) and RNA dependent RNA polymerase (RdRp). ORF2 encodes the viral core protein. ORF3 encodes a small regulatory phosphoprotein.

HEV replication is not completely known. After releasing of viral RNA in the cytosol, ORF1 is translated into the polyprotein, generating the replication complex. It is believed that negative RNA intermediates are then produced, for the synthesis of genomic as well as subgenomic positive RNAs, these latter translated into the capsid and ORF3 proteins. Positive genomic RNA is package in the capsids for liberation of HEV through exocytosis (Ahmad et al., 2011).

## 2.2 Hepatitis B virus

HBV is an enveloped virus belonging to the genus *Hepadnavirus*, in the family *Hepadnaviridae*. This family includes several genera of partially double stranded DNA generated from an intermediate RNA through reverse transcription (Ganem, 1991). HBV genome is around 3,200 bases long (Figure 3), the smallest of all known animal viruses. The viral genome encodes four overlapping ORFs:

- S, coding for the viral surface envelope proteins,
- C, coding for the capsid and e antigen proteins,
- P, coding for the polymerase, functionally divided into the terminal protein domain, which is involved in encapsidation and initiation of minus-strand synthesis; the reverse transcriptase (RT) domain, which catalyzes genome synthesis; and the ribonuclease H domain, which degrades pregenomic RNA.
- X, coding for a protein with multiple functions, including signal transduction, transcriptional activation, DNA repair, and inhibition of protein degradation (Liang, 2009).

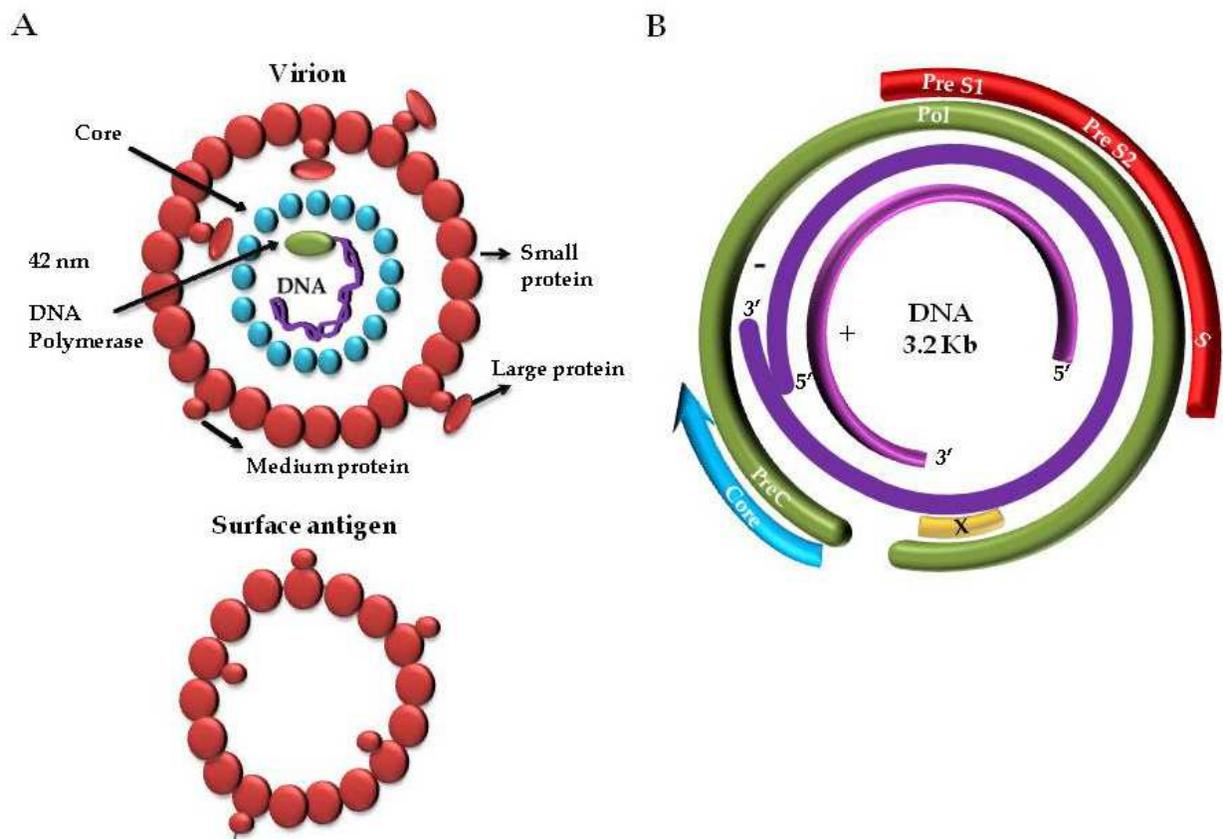


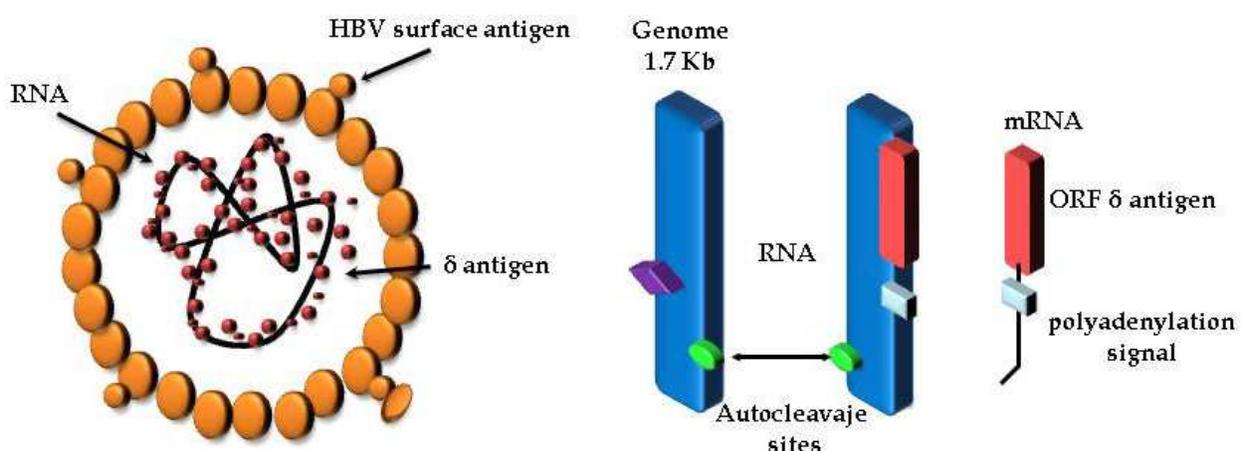
Fig. 3. **HBV virion and genome organization.** **A.** Enveloped virion of 42 nm. The 3 forms of HBV surface antigen (small, medium and large) are embedded in the lipid envelope which covers the core which interacts with the partially double stranded DNA, which is covalently linked to the polymerase. Cellular heat shock proteins inside the virion are not shown. In addition to the virion, HBV surface antigen empty particles are secreted both as spherical or cylindrical particles. **B.** The DNA genome and the 4 ORFs are shown, describing the compact nature of this genome.

After entry into the cell, the viral capsids are directed to the nucleus. The single-stranded gap region in the viral genome is repaired and circularized to a covalently closed circular form. This circular DNA is the template for transcription of the pregenomic and several subgenomic messenger RNAs. Pregenomic RNA is retrotranscribed inside the capsids by the HBV polymerase. The nucleocapsids are then directed to the endoplasmic reticulum to interact with the envelope proteins and assemble into mature virions, which are then secreted outside the cell (Liang, 2009).

### 2.3 Hepatitis D virus

HDV, genus *deltavirus*, is the smallest animal RNA virus (1,700 bases), and is related to plant viroids and satellite viruses (Figure 4). In contrast to plant satellite viruses, HDV is able to

perform autonomous replication, but depends on coinfection with HBV, since it uses its viral surface antigen for assembling its virion (Taylor, 2009). Unlike other RNA viruses, HDV lacks an RNA-dependent RNA polymerase, by using the cellular RNA polymerases of the host, which recognize its genome because of its folded, rod-like structure. Three forms of RNA are made in the host during replication: circular genomic and antigenomic RNA, and polyadenylated antigenomic mRNA, which codes for the only protein coded in this genome, the HDag. Two forms of HDag are produced by RNA editing. Replication of the circular HDV RNA template occurs via a rolling mechanism similar to that of plant viroids. A viral ribozyme selfcleaves the linear HDV RNA. These monomers are then ligated to form circular RNA, which interacts with HDag and uses HBV empty surface antigen particles for assembling the HDV virions (Hugues et al., 2011; Taylor, 2009).



**Fig. 4. HDV virion and genome organization.** HDV RNA is packed through interaction with HDV antigen, who presents in two forms, large (with an N-terminal stretch of amino acids interacting with RNA) and small form. HDV RNA and antigens are inside HBV surface antigen empty particles, provided by HBV replication. During replication, 3 HDV RNAs accumulate in the cell: the single negative strand genome and the antigenome, each possessing a ribozyme, with cleavage sites indicated by green circles, and the 800-nucleotide mRNA, that has a 5'-cap and a 3'-poly(A) tail.

## 2.4 Hepatitis C virus

HCV belongs to the genus *Hepacivirus*, in the family *Flaviviridae*. It is an enveloped virus with a positive RNA of around 9.5 Kb, which codes for a polyprotein of around 3,000 amino acids, including an RNA-dependent RNA polymerase (Figure 5). HCV interacts with a series of receptor to enter the cell via endocytosis, from which the capsid released the viral RNA in a membranous web close to the Endoplasmic reticulum, where replication takes place. The translated polyprotein is co- and post-translationally modified to produce mature viral proteins which can form replication complexes and assemble into new virions. These progeny virions bud into the lumen of the ER and leave the host cell through the secretory pathway (Poenisch & Bartenschlager, 2010; Tang & Grise, 2009).

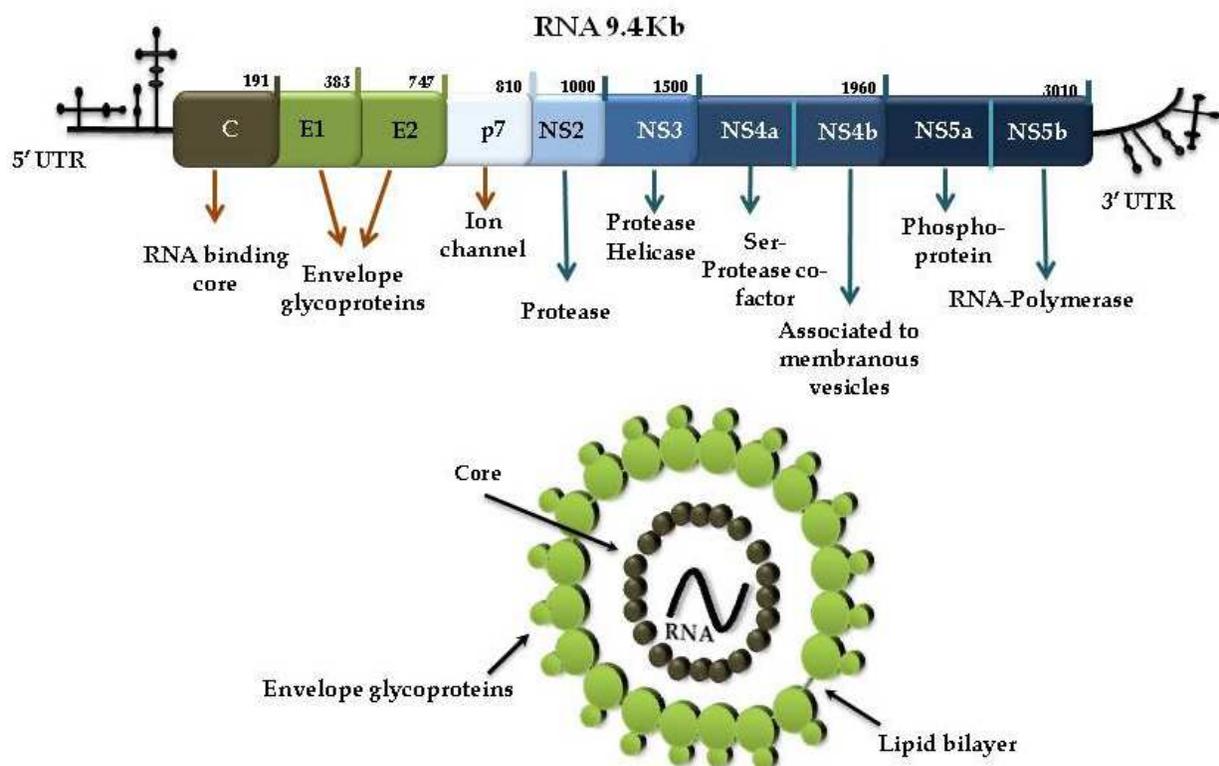


Fig. 5. **HCV virion and genome organization.** The positive-strand RNA genome contains a single open reading frame which encodes a polyprotein proteolytically processed by cellular and viral proteases. Structural proteins (VP) are indicated in green and nonstructural proteins in blue. The RNA secondary structure of the IRES is shown in the 5' end. At the 3' end, the RNA exhibit also a secondary structure involved in replication.

## 2.5 Other parenterally-transmitted viruses historically associated with hepatitis

In addition to the well established hepatitis viruses, 3 other parenterally-transmitted viruses have been identified, GBV-C (formerly known as HGV), TTV and SEN-V (Figure 6). However, the real role of these new viruses as causative agents of hepatitis is uncertain. There is no evidence at the present that these viruses cause any pathology in humans (Allain et al., 2002). A tentative genus has been proposed for GBV-C, *Pegivirus*, and 6 genotypes of GBV-C have been described (Smith et al., 2000; Stapleton et al., 2011). Genotype 1 is more prevalent in Africa, genotype 2 in Europe and North America, and genotypes 3, 4 and 5 are found mainly in Asia. GBV-C genotype 3 circulates among Central and South American population groups, a finding that may be related to the Asiatic origin of the American man (Loureiro et al., 2002; Smith et al., 2000). These findings suggest an old origin of GBV-C.

TTV is a single-stranded DNA virus, of around 3.8 Kb, distantly related to circoviruses and classified in the genus *Arnellovirus* (Biagini, 2009; Hino & Miyata, 2007). TTV represents in fact a swarm of viruses, which chronically infects human and other animals, and was originally thought to be associated with hepatitis. However, there does not seem to be any link between TTV infection and HCC or chronic hepatitis. Up to 23 genotypes of TTV have been described, which are grouped in 5 genogroups. One of these genogroups comprises SEN-V, another virus initially associated with hepatitis. Preliminary evidence suggests that some SEN-

V types may be associated to hepatitis, although this association could be a casual event, and then not meaning that SEN-V is actually a true hepatotropic virus (Hino & Miyata, 2007).

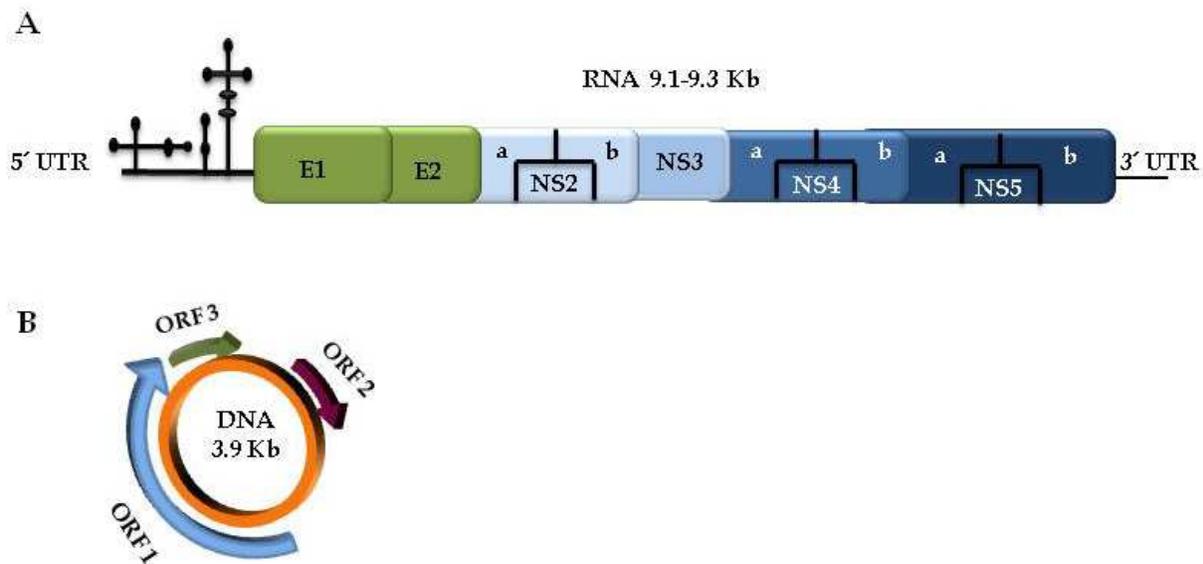


Fig. 6. **Genome organization of GBV-C and Arnellovirus.** **A: GBV-C genome.** The positive-strand RNA genome contains a single open reading frame which encodes a polyprotein proteolytically processed by cellular and viral proteases. Structural proteins (VP) are indicated in green and nonstructural proteins in blue. A core coding region is absent in the GBV-C genome. The RNA secondary structure of the IRES is shown in the 5' end. **B. Arnellovirus genome.** TTV and Sen-V single-stranded DNA viruses of negative polarity. ORF1 (DNA polymerase), ORF2 (non-structural protein), and ORF3 (core), all present in the plus strand complementary to the virion, are displayed in colours.

### 3. Genetic diversity of hepatitis viruses

#### 3.1 Enterically transmitted viruses

HAV variants can be classified in 6 genotypes, 3 of them infecting humans and the other 3 other primates from the Old World (Cristina & Costa-Mattioli, 2007; Robertson, 2001) (Table 1). Genotype I, and particularly subgenotype IA, is the most prevalent around the world (Cristina & Costa-Mattioli, 2007). Interestingly, in countries with intermediate to high prevalence of HAV infection, like Latin America and Africa, HAV genotype I is highly predominant, being exclusively found in several countries from South America, where a higher diversity would be expected due to the high frequency of infection (Cristina & Costa-Mattioli, 2007; Sulbarán et al., 2010). A founder effect, like observed for human immunodeficiency virus (HIV) subtype B in the Americas, may account for this situation (Y. Sulbarán et al., 2010; Tebit et al., 2007). In addition, HAV has adopted a naturally highly deoptimized codon usage with respect to that of its cellular host. This characteristic suggests a fine-tuning translation kinetics selection as the underlying mechanism of the codon usage bias in this specific genome region (Aragones et al., 2010). Moreover, significant differences in codon usage are found among the different genotypes (D'Andrea et al., 2011). These differences might be a factor that might bring some adaptive advantage to HAV genotype I and particularly subgenotype IA.

Four genotypes have been reported for HEV (Purcell & Emerson, 2008) (Table 1). Two of these genotypes are endemic among swines and other mammals. An interesting feature of this disease is that two modes of transmission seem to prevail in different geographic regions:

- human to human transmission in highly endemic regions, like Central and Southeast Asia, the Middle East and North Africa, where the most common genotypes are 1 and 2, the human ones, and
- a zoonotic transmission linked to contact and/or consumption of swines and other susceptible mammals, in non-endemic regions, like Europe, Japan and the Americas, with a more frequent circulation of the animal genotypes 3 and 4 (Purcell & Emerson, 2008). These zoonotic reservoirs might explain the presence of HEV infection in non-endemic areas and in isolated populations, like Amerindians, where evidence of exposure to HEV has been documented (Pujol et al., 1994).

### 3.2 HBV

The absence of proof reading capacity of the HBV reverse transcriptase leads to a high mutation rate. On the other hand, the extreme overlapping of the open reading frames of this small viral genome reduces the viability of many of these mutations (Torresi, 2002). For these opposite characteristics, the substitution rate of HBV is intermediate between RNA and DNA viruses (Kidd-Ljunggren et al., 2002). Another implication of this enhanced potential variability is the generation of a quasispecies-like viral population (Gunther et al., 1999), harboring viral mutations that can be eventually selected under particular selection pressures (Pawlotsky, 2005). The quasispecies complexity is however modulated by the compact genome organization of this virus (Pawlotsky, 2005).

In addition to the diversity which occurs during the natural course of infection, another degree of variability is displayed by HBV strains circulating worldwide. This variability includes the vaccine escape mutants and the genotypic and subtypic variability.

Vaccine escape mutants occur by point mutations in the "a" determinant of the surface antigen, the main immunogenic region, induce conformational changes that prevent the binding of neutralizing antibodies. The most frequent substitutions observed with these characteristics are G145R and D144A (Pawlotsky, 2005; Torresi, 2002). In addition to their transmission between individuals, vaccine escape mutants might be selected under the pressure of neutralizing antibodies or antiretroviral drugs (Lada et al., 2006).

Eight human HBV genotypes (A–H) have been described, based on a minimum divergence of 8% of the complete genome sequences (Table 1) (Figure 7) (Araujo et al., 2011; Norder et al., 2004). Genotypes A and D are predominant in the Old World but are also widely distributed in all the continents. Genotypes B and C are found mainly in South East Asia and the Far East, while genotype E circulates in sub-Saharan West Africa (Norder et al., 2004; Pujol & Devesa, 2005). HBV genotype E might be a recent genotype, exhibiting a low intragenotypic variation not being introduced to the Americas during slave trade (Kramvis et al., 2005; Quintero et al., 2002).

The distribution of genotype G is not fully known. This genotype exhibits several interesting characteristics. A low intragenotypic variability has been found among different isolates

from different countries (Lindh, 2005). A high frequency of mutations in the core and precore regions and a frequent association of co-circulation with HBV genotype A have also been reported. This last finding has led even to the suggestion that the genotype G represents an impaired virus which needs a helper virus for effective replication (Lindh, 2005). However, transmission and infection with exclusively HBV genotype G has recently been documented (Chudy et al., 2006). On the other hand, a segment of the preS region is identical in genotype E and G strains, suggesting an eventual recombination between these two genotypes. This last assumption might also suggest an African origin for genotype G, although this genotype has not been found yet circulating in Africa (Lindh, 2005). This genotype is might be found more frequently in co-infection with HIV (Dao et al., 2011). Alternatively, HBV genotype G is found frequently infecting men who have sex with men (MSM) (Bottechia et al., 2008; Osioy et al., 2008; Sanchez et al., 2007). The core variability displayed by HBV genotype G (a 12 amino acid insertion at the N-terminal end) has been shown recently that might be affecting the ability of assembly and secretion of the viral particle (Cotelesage et al., 2011), which supports the assumption for the need of a co-infecting strain for an efficient replication of this genotype.

Some of the HBV genotypes are divided into subgenotypes, based on a divergence of more than 4%. Seven subgenotypes are described at the moment for genotype A, 9 for genotype B (Thedja et al., 2011), 12 for genotype C (Mulyanto et al., 2011), 7 for genotype D (Meldal et al., 2009) and 4 for genotype F (Devesa et al., 2008). No subgenotypes have been found at present inside genotypes E, G and H. This fact might be due to the fact that these genotypes might be more recent than the other ones.

HBV genotype F is the most divergent of the HBV genotypes, is autochthonous to and highly predominant in some countries of South America (Devesa & Pujol, 2007). HBV genotype H is closely related to genotype F and seems to be restricted to Central and North America (Arauz-Ruiz et al., 2002). In addition to human HBV genotypes, several simian genotypes have also been identified, one in a monkey from the New World (woolly monkey), while the others have been found infecting simians from the Old World (Figure 7) (Devesa & Pujol, 2007).

In addition, a new genotype I has been proposed for a recombinant of genotypes A, C, and G mainly found in Laos and Vietnam (Tran et al., 2008), genotype J for a recombinant strain between human and ape viruses (Tatematsu et al., 2009). Indeed, several studies have pointed that recombination seems to play an important role in shaping the evolution of HBV (Fares & Holmes, 2002; Simmonds & Midgley, 2005). The exact mechanism of recombination of HBV genomes is not clear, but it seems more likely to occur in the nucleus, by illegitimate replication (Yang & Summers, 1998), or by recombination with integrated HBV DNA (Bowyer & Sim, 2000).

HBV variability seems to play a role in HCC development. Pathogenic differences in causing HCC have been reported among hepatitis B virus (HBV) variants, but also genotypes. HBV genotype C is associated with a more severe disease. (Yang et al., 2008; Yu et al., 2005), and genotype D seems to evolve worse than genotype A (Thakur et al., 2002). HBV genotype F was associated to a higher frequency of HCC development at younger age in Alaskan individuals (Livingston et al., 2007). However, the risk of HCC may differ among subgenotypes (Pujol et al., 2009).

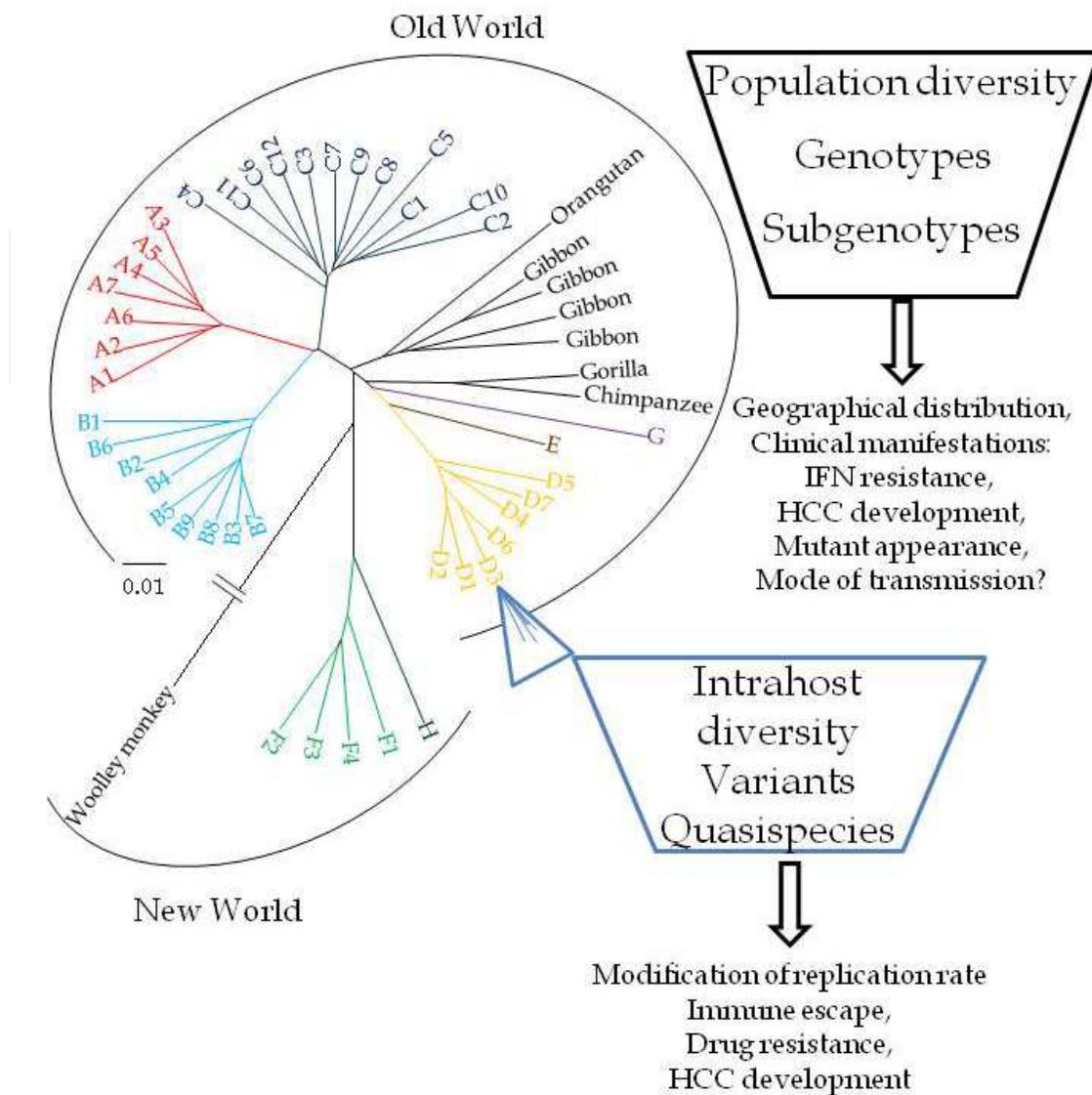


Fig. 7. **HBV molecular evolution.** Human and non-human primates HBV genotypes and subgenotypes are shown in the phylogenetic tree. Intrahost diversity is shown in blue. The implication of HBV variability is also shown.

Several variants are generated during the course of the chronic infection in response to the host or exogenous immune pressures and drug therapy. Mutations in the Precore, Core, X, Pre-S, S and Pol gen, have been reported. Particular interest has been directed toward the generation of translational stop codon mutation at the precore region (mostly G1896A) inside the  $\epsilon$  structure, and mutations in the basal core promoter region (especially A1762T, G1764A) and the upstream regulatory sequences (nt1643-1742). The selection of the G1896A seems to be genotype-dependent (Devesa & Pujol, 2007). The basal core promoter overlaps with the X region of the HBV genome, and mutations in the amino acid sequences at positions 130 and 131 in this region (K130M and V131I) has been proposed as prognostic markers for the development of liver cancer (Kuang et al., 2004, Pujol et al., 2009). Some genotypic variability may also occur in terms of interferon sensitivity and development of drug resistance (Kramvis & Kew, 2005; Ramos et al., 2007).

The current treatment for HBV involves the use of Interferon (IFN) and/or antiretroviral drugs, since some of the anti-HIV reverse transcriptase drugs can also inhibit the HBV polymerase. Although no specific mutations have been associated to IFN resistance, some genotypes are more susceptible to this immunomodulator, like genotypes A and B, compared to D and C (Lin & Kao, 2011). Five nucleoside and nucleotide analogues inhibit HBV reverse transcriptase: Adefovir, Entecavir, Lamivudine, Telbivudine and Tenofovir. Drug resistance mutations emerge during treatment with these drugs, consisting of point mutation in one of the 5 domains of the HBV polymerase (Table 2) (Yuen et al., 2009).

The origin of HBV is still an unsolved question (Jazayeri et al., 2009). The reduced size of HBV genome, together with the high degree of overlapping of its open reading frames, has impaired the drawing of an evolutionary picture of this virus. With the advent of sequences from several HBV strains circulating in non human primates (Figure 7), an alternative hypothesis has been proposed: human HBV genotypes might have emerged through several zoonotic introductions from simian strains, both at the Old and New World (Devesa & Pujol, 2007).

### 3.3 HDV

Eight genotypes of HDV have been identified (Table 1) (Deny, 2006). HDV genotype 1 is present worldwide. Genotype 2 is found in Japan, Taiwan, Russia. Genotype 3 is the most divergent genotype and is found in the Amazon Basin, and has been shown to infect individuals from Peru, Venezuela and Colombia, where severe cases have been documented. This genotype is actually the most frequently associated to fulminant hepatitis. Genotype 4 circulates in Taiwan and Japan. The remaining HDV genotypes (5–8) are found Africa (Deny, 2006).

As other RNA viruses, HDV circulates as a quasispecies distribution of variants, in which defective mutants have been described (Wu et al., 2005). In addition mutants appearing under the immune pressure, as detected by the presence of amino acids under positive selection, target of cytotoxic T lymphocytes, have also been described (Wang et al., 2007).

### 3.4 HCV

HCV has been classified in 7 genotypes, according to a genetic divergence of more than 30–35% in the complete genome and in several subtypes inside each genotype, according to divergences of more than 20% (Figure 8) (Le Guillou-Guillemette et al., 2007; Chayama & Hayes, 2011). Infections with HCV genotype 1 are associated with the lowest therapeutic success (Zeuzem et al., 2000). HCV genotypes 1, 2, and 3 have a worldwide distribution. HCV subtypes 1a and 1b are the most common genotypes in the US and are also predominant in Europe, while in Japan, subtype 1b is predominant. Although HCV subtypes 2a and 2b are relatively common in America, Europe, and Japan, subtype 2c is found commonly in northern Italy. HCV genotype 3a is frequent in intravenous drug abusers in Europe and the United States. HCV genotype 4 is prevalent in Africa and the Middle East, and genotypes 5 and 6 seem to be confined to South Africa and Asia, respectively (Simonds, 2001; Zein, 2000). HCV genotype 7 was more recently identified in Canada, in an emigrant from the Democratic Republic of Congo.

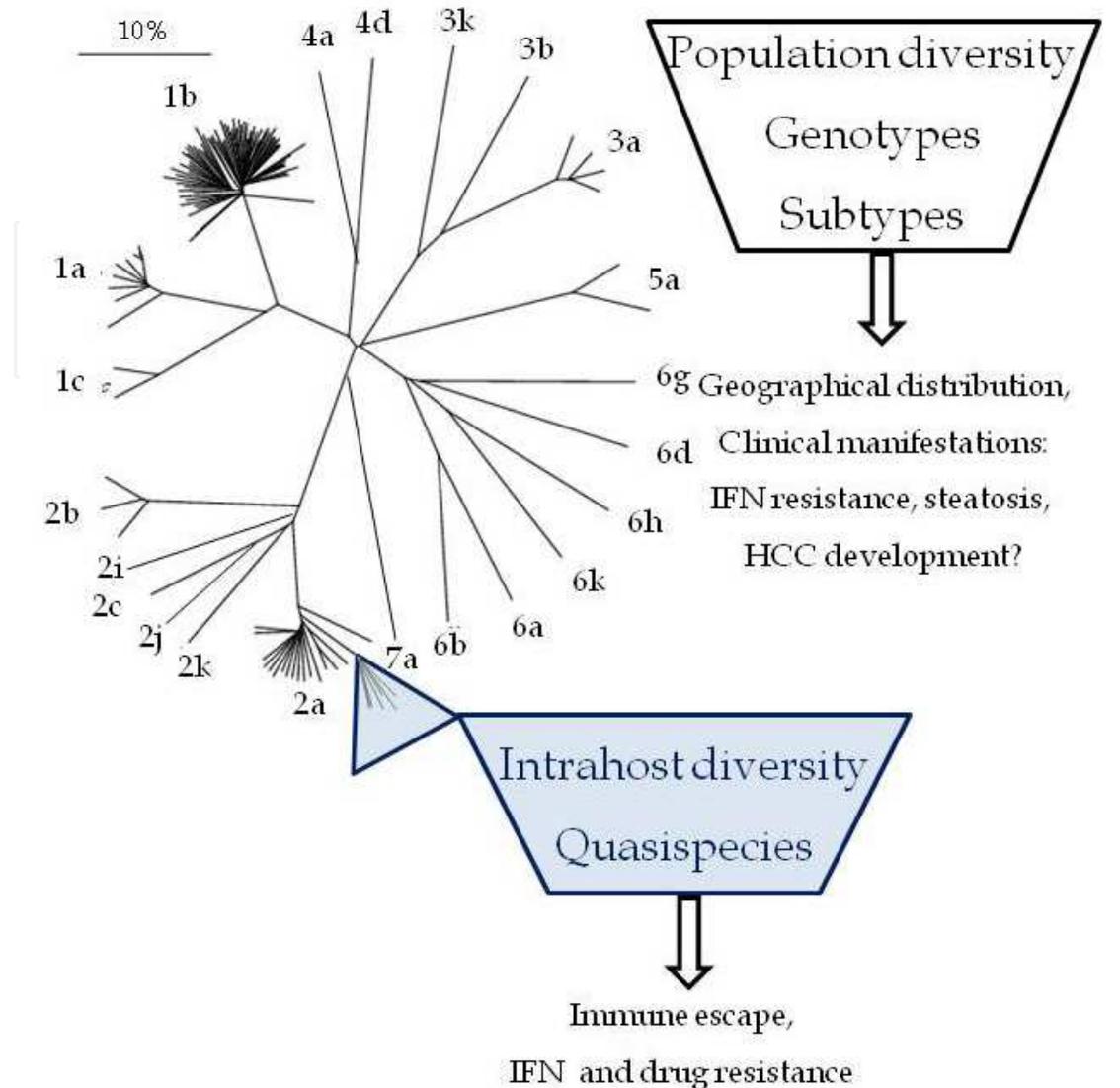


Fig. 8. **HCV molecular evolution.** HCV genotypes and subtypes for which at least one complete genome has been sequenced, are shown in the phylogenetic tree. Intrahost diversity inside each subtype is shown in blue. The implication of HCV variability is also shown.

In contrast with HBV, recombination between HCV genotypes seems to be a rare event. *In vitro* studies suggest a low frequency of recombination for this virus (Reiter et al., 2011), in agreement with the low number of recombinant strains identified so far (Morel et al., 2011). However, intergenotypic incompatibility might be a factor involved in the low frequency of recombinants observed, and intragenotypic recombination might be more frequent than expected (Mes & Doornum, 2011).

Changes in hepatitis C virus (HCV) genotype distribution with time have been reported in several countries. In Venezuela, for example, a significant reduction of the circulation of HCV genotype 1b was observed in the last decade, with the increase of circulation of genotype 2j (Pujol & Loureiro, 2007; M.Z. Sulbaran et al., 2010). Several subtypes of HCV genotype 2 and 4 were introduced in some countries of the Americas during slave trade in

Martinique (Martial et al., 2004) and of HCV genotype 2 in Venezuela (Sulbarán M.Z. et al., 2010). It is difficult to estimate for how long HCV has been present in human populations. HCV may have been endemic in Asia and Africa for a considerably longer time than in Western countries. HCV subtypes might have diverged around 200-250 years ago and genotypes around 500-2000 years ago (Bostan & Mahmood, 2010; Cantaloube et al., 2003; Smith et al., 1997).

HCV genotype 1b has been frequently associated with a more severe liver disease. Nevertheless, this association might be due to the fact that individuals infected with this genotype have a longer mean duration of infection (Zein, 2000). A recent meta-analysis showed however HCV subtype 1b associated to a higher risk factor for HCC development (Raimondi et al., 2009). Hepatic steatosis is a common consequence of HCV infection, has been recently associated with the development of HCC, and is more frequently found among HCV genotype 3 infected patients (Monto et al., 2002). More studies are needed to confirm the correlation between HCV genotype 3, the presence of steatosis and progression to HCC (Zhu & Chung, 2003).

Within an infected individual, HCV circulates as a collection of closely related variants named quasispecies (Fishman & Branch, 2009). HCV like others RNA virus has a high level of genetic variability, especially in the E1 and E2 genes (envelope glycoproteins). Humoral pressure on the hypervariably region of E2 has been associated with quasispecies diversification through immune escape mechanisms (Weiner et al., 1992). The quasispecies nature of HCV populations in an infected individual might contribute to the viral persistence in the host, IFN and drug resistance (Fishman & Branch, 2009) (Figure 8).

#### 4. HIV co-infection

HIV co-infection with HCV and/or HBV is frequent, since these viruses share many modes of transmission, and exacerbates the natural history of these viral infections. A decreased immune clearance and more rapid progression of liver disease has been documented, leading to an increased incidence of cirrhosis, risk of drug-related hepatotoxicity, HCC development, and death. On the other hand, liver disease has emerged as a major cause of morbidity and mortality in HIV-infected patients. Viral hepatitis co-infection increases the risk of drug-related hepatotoxicity of highly active antiretroviral therapy (HAART), impacting the selection of specific agents (Sulkowski, 2008).

HIV-1 co-infection increases HCV viral load in dually infected patients. This effect seems to be both related to the acquired immunodeficiency and to a direct interaction between the viruses (Rotman & Liang, 2009). In addition, HIV-1 co-infection seems to impact the quasispecies complexity exhibited by HCV. Both an increase and a decrease of quasispecies heterogeneity has been described, when compared to HCV mono-infected patients (Sherman et al., 1996; Toyoda et al., 1997). In spite of the conflicting results, many reports suggest a relatively low level of HCV quasispecies diversity before HAART, and an increase in diversity after prolonged treatment, principally due to a significant increase in both synonymous and non-synonymous substitution rates in the hypervariable region 1 of HCV E2 (Bernini, et al, 2011). This exponential growth of the quasispecies populations in immunological responders coincides with a peak in CD4 cell counts, positive selection in several proteins of HCV, and a frequent increase in HCV viral load (Bernini, et al, 2011).

Patients co-infected with HBV and HIV-1 have a higher likelihood of chronicity after acute HBV infection compared with HIV-negative patients (Lacombe et al., 2010). The natural history of HBV-related disease is modified by HIV infection in several ways. Co-infected patients have higher HBV DNA levels, lower aminotransferase levels, decreased spontaneous loss of hepatitis B early antigen (HBeAg), accelerated progression to cirrhosis, and increased risk of liver-related morbidity and mortality compared with HBV mono-infection (Lacombe et al., 2010). As previously mentioned, a number of clinically significant HBV genome mutations have been reported in HBV mono-infection, and differences in disease evolution and treatment response have been associated to a particular genotype and to some of these mutations. Many of these mutations appears during the long term evolution of infection and during exposure to nucleos(t)ides analogs, used to treat HIV (Lacombe et al., 2010). In HIV-1/HBV co-infected individuals, a novel -1G mutation in the HBV core and precore gene was found to be more frequent compared to mono-infected patients. This mutation results in premature termination of the deduced HBV precore and core genes and was associated with high HBV viral load. PreS2 deletions were observed more frequently in co-infection (Audsley et al., 2010).

An interesting observation is that the natural course of HIV-1 might be modulated by the presence of GBV-C. GBV-C co-infection seems to exert a beneficial effect on HIV disease progression (Maidana et al., 2005), although this evidence has not been consistently corroborated (Baggio-Zappia et al., 2009). The mechanism by which GBV-C interferes with AIDS progression is not yet fully understood. *In vitro* studies have shown that the inhibitory effect of GBV-C on HIV-1 replication might be related to soluble factors induced by GBV-C (Jung, 2005), and specifically with chemokines, Rantes, MIP-1 and SDF-1, which may compete with HIV-1 envelop glycoprotein 120 for the coreceptor CCR5 and CXCR4 in CD4 cells. This effect may reduce a successful HIV-1 interaction with infected cell (Xiang, 2004). Several lines of evidence suggest a possible inhibition of HIV-1 by GBV-C through increase in soluble ligands for HIV-1 coreceptor and activation of innate immunity (Lalle, 2008; Mohr & Stapleton, 2009). In addition, the beneficial effect of GBV-C on survival of HIV-1 infected patients might be genotype specific (Schwarze-Zander et al., 2006). Two GBV-C proteins, E2 and NS5A, have been shown to modulate CD4+ T-lymphocyte chemokine receptor expression and chemokine release *in vitro*, then inhibiting HIV replication. The inhibitory effect of GBV-C NS5A on HIV-1 replication was exercised *in vitro* by the non structural proteins from all the genotypes tested (Chang et al., 2007), failing then to describe a genotype specific inhibition of this protein in HIV-1 replication. More studies are needed to clarify the exact role of GBV-C co-infection on HIV-1 replication.

## 5. Conclusions

There are still 5 viral entities named hepatitis viruses, which share only their tropism for the hepatocyte. Parenterally transmitted viruses are normally the ones associated to chronicity and to more severe sequela, like cirrhosis and HCC. Due to the error prone nature of their polymerases, these viruses display a substantial degree of genetic diversity. Within these 5 viral entities, viral variants (genotypes, subgenotypes, diversity of quasispecies, mutants) might exhibit particular characteristics in term of pathogenesis and mode of transmission. Thus, instead of 5 viruses, we are in fact dealing with a multiplicity of viral variants with different consequences and evolution inside the infected host. Vaccines are not available for

all these entities, only for HAV and HBV, and partially for HDV. The significant degree of variability exhibited by these viruses is an unresolved limitation for the development of effective vaccines against them. Some of these variants might have originated separately in the New and the Old World, as for HBV and HDV, for example. Some of these viruses may have a long time of co-evolution with human host, as for GBV-C, while others might have been introduced more recently, like HCV.

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## 7. References

- Ahmad, I., Holla, R.P. & Jameel, S. (2011). Molecular virology of hepatitis E virus. *Virus Research*, in press. ISSN: 0168-1702
- Allain, J.P., Thomas, I. & Sauleda, S. (2002). Nucleic acid testing for emerging viral infections. *Transfusion Medicine*, 12(4): 275-283. ISSN: 1365-3148
- Aragonès, L., Guix, S., Ribes, E., Bosch, A. & Pintó, R.M. (2010). Fine-tuning translation kinetics selection as the driving force of codon usage bias in the hepatitis A virus capsid. *PLoS Pathogen*, 6: e1000797. ISSN: 1553-7374
- Araujo, N.M., Waizbort, R. & Kay, A. (2011). Hepatitis B virus infection from an evolutionary point of view: How viral, host, and environmental factors shape genotypes and subgenotypes. *Infection Genetics and Evolution*, 11(6): 1199-1207. ISSN: 1567-1348
- Arauz-Ruiz, P., Norder, H., Robertson, B.H. & Magnus, L.O. (2002). Genotype H: a new Amerindian genotype of hepatitis B virus revealed in Central America. *Journal of General Virology*, 83(Pt 8): 2059-2073. ISSN: 1465-2099
- Audsley, J., Littlejohn, M., Yuen, L., Sasadeusz, J., Ayres, A., Desmond, C., Spelman, T., Lau, G., Matthews, G.V., Avihingsanon, A., Seaberg, E., Philp, F., Saulynas, M., Ruxrungtham, K., Dore, G.J., Locarnini, S.A., Thio, C.L., Lewin, S.R. & Revill, P.A. (2010). HBV mutations in untreated HIV-HBV co-infection using genomic length sequencing. *Virology*, 405(2): 539-547. ISSN: 0042-6822
- Baggio-Zappia, G.L. & Hernandez Granato, C.F. (2009). HIV-GB virus C co-infection: an overview. *Clinical Chemistry and Laboratory Medicine*, 47: 12-19. ISSN: 1437- 4331
- Biagini, P. (2009). Classification of TTV and related viruses (anelloviruses). *Current Topics in Microbiology and Immunology*, 331: 21-33. ISSN: 0070-217X
- Bernini, F., Ebranati, E., De Maddalena, C., Shkjezi, R., Milazzo, L., Lo Presti, A., Ciccozzi, M., Galli, M. & Zehender, G. (2011). Within-host dynamics of the hepatitis C virus quasispecies population in HIV-1/HCV coinfecting patients. *PLoS One*. 6(1): e16551. ISSN: 1932-6203
- Bostan, N. & Mahmood, T. (2010). An overview about hepatitis C: a devastating virus. *Critical Reviews in Microbiology*, 36(2): 91-133. ISSN: 1549-7828
- Bottecchia, M., Souto, F.J., O, K.M., Amendola, M., Brandão, C.E., Niel, C. & Gomes, S.A. (2008). Hepatitis B virus genotypes and resistance mutations in patients under long term lamivudine therapy: characterization of genotype G in Brazil. *BMC Microbiology*, 8: 11. ISSN 1471-2180

- Bowyer, S.M. & Sim, J.G. (2000). Relationships within and between genotypes of hepatitis B virus at points across the genome: footprints of recombination in certain isolates. *Journal of General Virology*, 81(Pt 2): 379-392. ISSN: 1465-2099
- Cantaloube, J.F., Biagini, P., Attoui, H., Gallian, P., de Micco, P. & de Lamballerie, X. (2003). Evolution of hepatitis C virus in blood donors and their respective recipients *Journal of General Virology*, 84(Pt 2): 441-446. ISSN: 1465-2099
- Chang, Q., McLinden, J.H., Stapleton, J.T., Sathar, M.A. & Xiang, J. (2007). Expression of GB virus C NS5A protein from genotypes 1, 2, 3 and 5 and a 30 aa NS5A fragment inhibit human immunodeficiency virus type 1 replication in a CD4+ T-lymphocyte cell line. *Journal of General Virology*, 88(Pt 12):3341-3346. ISSN: 1465-2099
- Chayama, K. & Hayes, C.N. (2011). Hepatitis C virus: How genetic variability affects pathobiology of disease. *Journal of Gastroenterology and Hepatology*, 26(Suppl 1): 83-95. ISSN: 1440-1746
- Chudy, M., Schmidt, M., Czudai, V., Scheiblauber, H., Nick, S., Mosebach, M., Hourfar, M.K., Seifried, E., Roth, W.K., Grünelt, E. & Nübling, C.M. (2006). Hepatitis B virus genotype G monoinfection and its transmission by blood components. *Hepatology*, 44(1): 99-107. ISSN: 1527-3350
- Cotelesage, J.J., Osiowy, C., Lawrence, C., DeVarennes, S.L., Teow, S., Beniac, D.R. & Booth, T.F. (2011). Hepatitis B Virus Genotype G forms core-like particles with unique structural properties. *Journal of Viral Hepatitis*, 18(6): 443-448. ISSN: 1365-2893
- Cristina, J. & Costa-Mattioli, M. (2007). Genetic variability and molecular evolution of hepatitis A virus. *Virus Research*, 127(2): 151-157. ISSN: 0168-1702
- Cuthbert, J.A. (2001). Hepatitis A: old and new. *Clinical Microbiology Reviews*, 14(1): 38-58. ISSN: 1098-6618
- Dao, D.Y., Balko, J., Attar, N., Neak, E., Yuan, H.J., Lee, W.M. & Jain, M.K. (2011). Hepatitis B virus genotype G: prevalence and impact in patients co-infected with human immunodeficiency virus. *Journal of Medical Virology*, 83(9): 1551-1558. ISSN: 1096-9071
- Dalton, H.R., Bendall, R., Ijaz, S. & Banks, M. (2008). Hepatitis E: an emerging infection in developed countries. *Lancet Infectious Diseases*, 8(11): 698-709. ISSN: 1473-3099
- D' Andrea, L., Pintó, R.M., Bosch, A., Musto, H. & Cristina, J. (2011). A detailed comparative analysis on the overall codon usage patterns in hepatitis A virus. *Virus Research*, 157(1): 19-24. ISSN: 0168-1702
- Dény, P. (2006). Hepatitis delta virus genetic variability: from genotypes I, II, III to eight major clades? *Current Topics in Microbiology and Immunology*, 307: 151-171. ISSN: 0070-217X
- Devesa, M. & Pujol, F.H. (2007). Hepatitis B virus genetic diversity in Latin America. *Virus Research*, 127(2): 177-184. ISSN: 0168-1702
- Devesa, M., Loureiro, C.L., Rivas, Y., Monsalve, F., Cardona, N., Duarte, M.C., Poblete, F., Gutierrez, M.F., Botto, C. & Pujol, F.H. (2008). Subgenotype diversity of hepatitis B virus American genotype F in Amerindians from Venezuela and the general population of Colombia *Journal of Medical Virology*, 80(1): 20-26. ISSN: 1096-9071
- Fares, M.A. & Holmes, E.C. (2002). A revised evolutionary history of hepatitis B virus (HBV). *Journal of Molecular Evolution*, 54(6): 807-814. ISSN: 1432-1432

- Fishman, S.L. & Branch, A.D. (2009). The quasispecies nature and biological implications of the hepatitis C virus. *Infection Genetics and Evolution*, 9(6): 1158-1167. ISSN: 1567-1348
- Ganem, D. (1991). Assembly of hepadnaviral virions and subviral particles. *Current Topics in Microbiology and Immunology*, 168: 61-83. ISSN: 0070-217X
- Gunther, S., Fischer, L., Pult, I., Sterneck, M. & Will, H. (1999). Naturally occurring variants of hepatitis B virus. *Advances in Virus Research*, 52: 25-137. ISSN: 0065-3527
- Hino, S. & Miyata, H. (2007). Torque teno virus (TTV): current status. *Reviews in Medical Virology*, 17(1): 45-57. ISSN: 1099-1654
- Hughes, S.A., Wedemeyer, H. & Harrison, P.M. (2011). Hepatitis delta virus. *Lancet*, 378(9785): 73-85. ISSN: 0140-6736
- Jameel, S. (1999). Molecular biology and pathogenesis of hepatitis E virus. *Expert Reviews in Molecular Medicine*, 1999: 1-16. ISSN:1462-3994
- Jazayeri, S.M., Alavian, S.M. & Carman, W.F. (2010). Hepatitis B virus: origin and evolution. *Journal of Viral Hepatitis*, 17(4): 229-235. ISSN: 1365-2893
- Jung, S., Knauer, O., Donhauser, N., Eichenmüller, M., Helm, M., Fleckenstein, B. & Reil, H. (2005). Inhibition of HIV strains by GB virus C in cell culture can be mediated by CD4 and CD8 T-lymphocyte derived soluble factors. *AIDS*, 19(12): 1267-1272. ISSN: 1473-5571
- Kaba, M., Richet, H., Ravaux, I., Moreau, J., Poizot-Martin, I., Motte, A., Nicolino-Brunet, C., Dignat-George, F., Ménard, A., Dhiver, C., Brouqui, P. & Colson, P. (2011). Hepatitis E virus infection in patients infected with the human immunodeficiency virus. *Journal of Medical Virology*, 83(10): 1704-1716. ISSN: 1096- 9071
- Kidd-Ljunggren, K., Miyakawa, Y. & Kidd, A.H. (2002). Genetic variability in hepatitis B viruses. *Journal of General Virology*, 83(Pt 6): 1267-1280. ISSN: 1465-2099
- Kramvis, A. & Kew, M.C. (2005). Relationship of genotypes of hepatitis B virus to mutations, disease progression and response to antiviral therapy *Journal of Viral Hepatitis*, 12(5): 456-464. ISSN: 1365-2893
- Kramvis, A., Restorp, K., Norder, H., Botha, J.F., Magnus, L.O. & Kew, M.C. (2005). Full genome analysis of hepatitis B virus genotype E strains from South-Western Africa and Madagascar reveals low genetic variability. *Journal of Medical Virology*, 77(1): 47-52. ISSN: 1096- 9071
- Kuang, S.Y., Jackson, P.E., Wang, J.B., Lu, P.X., Muñoz, A., Qian, G.S., Kensler, T.W. & Groopman, J.D. (2004). Specific mutations of hepatitis B virus in plasma predict liver cancer development. *Proceedings of the National Academy of Sciences USA*, 101(10): 3575-3580. ISSN: 1091- 6490
- Lacombe, K., Bottero, J., Lemoine, M., Boyd, A. & Girard, P.M. (2010). HIV/hepatitis B virus co-infection: current challenges and new strategies. *Journal of Antimicrobial Chemotherapy*, 65(1): 10-17. ISSN: 0305-7453
- Lada, O., Benhamou, Y., Poynard, T. & Thibault, V. (2006). Coexistence of hepatitis B surface antigen (HBs Ag) and anti-HBs antibodies in chronic hepatitis B virus carriers: influence of "a" determinant variants. *Journal of Virology*, 80(6): 2968-2975. ISSN: 1098-5514
- Lalle, E., Sacchi, A., Abbate, I., Vitale, A., Martini, F., D'Offizi, G., Antonucci, G., Castilletti, C., Poccia, F. & Capobianchi, M.R. (2008). Activation of interferon response genes and of plasmacytoid dendritic cells in HIV-1 positive subjects with GB virus C co-

- infection. *International Journal of Immunopathology & Pharmacology*, 21(1): 161-171. ISSN: 0394-6320
- Le Guillou-Guillemette, H., Vallet, S., Gaudy-Graffin, C., Payan, C., Pivert, A., Goudeau, A. & Lunel-Fabiani, F. (2007). Genetic diversity of the hepatitis C virus: impact and issues in the antiviral therapy. *World Journal of Gastroenterology*, 13(17): 2416-2426. ISSN: 1007-9327
- Liang, T.J. (2009). Hepatitis B: the virus and disease. *Hepatology*, 49(5 Suppl): S13-S21. ISSN: 1527-3350
- Lin, C.L. & Kao, J.H. (2011). Recent advances in the treatment of chronic hepatitis B. *Expert Opinion on Pharmacotherapy*, 12(13): 2025-2040. ISSN: 1744-7666
- Lindh, M. (2005). HBV genotype G-an odd genotype of unknown origin. *Journal of Clinical Virology*, 34(4): 315-316. ISSN : 1386-6532
- Livingston, S.E., Simonetti, J.P., McMahon, B.J., Bulkow, L.R., Hurlburt, K.J., Homan, C.E., Snowball, M.M., Cagle, H.H., Williams, J.L. & Chulanov, V.P. (2007). Hepatitis B virus genotypes in Alaska Native people with hepatocellular carcinoma: preponderance of genotype F. *Journal of Infectious Diseases*, 195(1): 5-11. ISSN: 1537-6613
- Loureiro, C.L., Alonso, R., Pacheco, B.A., Uzcátegui, M.G., Villegas, L., León, G., De Saéz, A., Liprandi, F., López, J.L. & Pujol, F.H. (2002). High prevalence of GB virus C/hepatitis G virus genotype 3 among autochthonous Venezuelan populations. *Journal of Medical Virology*, 68(3): 357-362. ISSN: 1096- 9071
- Maidana, M.T., Sabino, E.C. & Kallas, E.G. (2005). GBV-C/HGV and HIV-1 coinfection. *Brazilian Journal of Infectious Diseases*, 9(2): 122-125. ISSN 1413-8670
- Martial, J., Morice, Y., Abel, S., Cabié, A., Rat, C., Lombard, F., Edouard, A., Pierre-Louis, S., Garsaud, P., Béra, O., Chout, R., Gordien, E., Deny, P. & Césaire, R. (2004). Hepatitis C virus (HCV) genotypes in the Caribbean island of Martinique: evidence for a large radiation of HCV-2 and for a recent introduction from Europe of HCV-4. *Journal of Clinical Microbiology*, 42(2): 784-791. ISSN: 1098-660X
- Meldal, B.H., Moula, N.M., Barnes, I.H., Boukef, K. & Allain, J.P. (2009). A novel hepatitis B virus subgenotype, D7, in Tunisian blood donors. *Journal of General Virology*, 90(Pt 7): 1622-1628. . ISSN: 1465-2099
- Mes, T.H. & van Doornum, G.J. (2011). Recombination in hepatitis C virus genotype 1 evaluated by phylogenetic and population-genetic methods *Journal of General Virology*, 92(Pt 2): 279-286. . ISSN: 1465-2099
- Mohr, E.L. & Stapleton, J.T. (2009). GB virus type C interaction with HOV: the role of envelope glycoproteins. *Journal of Viral Hepatitis*, 16(11): 757-768. ISSN: 1365-2893
- Monto, A. (2002). Hepatitis C and steatosis. *Seminars in gastrointestinal disease*, 13(1): 40-46. ISSN:1049-5118
- Morel, V., Fournier, C., François, C., Brochot, E., Helle, F., Duverlie, G. & Castelain, S. (2011). Genetic recombination of the hepatitis C virus: clinical implications. *Journal of Viral Hepatitis*, 18(2): 77-83. ISSN: 1365-2893
- Mulyanto, Depamede, S.N., Wahyono, A., Jirintai, Nagashima, S., Takahashi, M, & Okamoto, H. (2011). Analysis of the full-length genomes of novel hepatitis B virus subgenotypes C11 and C12 in Papua, Indonesia. *Journal of Medical Virology*, 83(1): 54-64. . ISSN: 1096- 9071

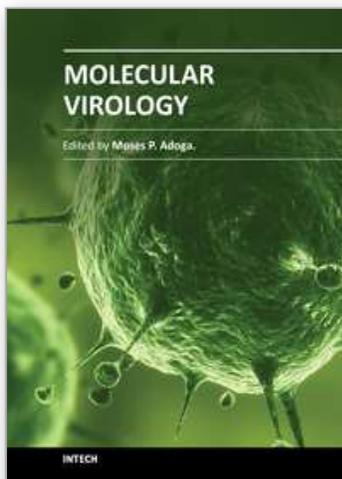
- Norder, H., Courouce, A.M., Coursaget, P., Echevarria, J.M., Lee, S.D., Mushahwar, I.K., Robertson, B.H., Locarnini, S. & Magnius, L.O. (2004). Genetic diversity of hepatitis B virus strains derived worldwide: genotypes, subgenotypes, and HBsAg subtypes. *Interferology*, 47(6): 289-309. ISSN: 1423-0100
- Osiowy, C., Gordon, D., Borlang, J., Giles, E. & Villeneuve, J.P. (2008). Hepatitis B virus genotype G epidemiology and co-infection with genotype A in Canada *Journal of General Virology*, 89(Pt 12): 3009-3015. ISSN: 1465-2099
- Pawlotsky, J.M. (2005). The concept of hepatitis B virus mutant escape. *Journal of Clinical Virology*, 34(Suppl 1): S125-S129. ISSN : 1386-6532
- Poenisch, M. & Bartenschlager, R. (2010). New insights into structure and replication of the hepatitis C virus and clinical implications. *Seminars in Liver Disease*, 30(4): 333-347. ISSN: 0272-8087
- Pujol, F.H., Favorov, M.O., Marcano, T., Esté, J.A., Magris, M., Liprandi, F., Khudyakov, Y.E., Khudyakova, N.S. & Fields, H.A. (1994). Prevalence of antibodies against hepatitis E virus among urban and rural population in Venezuela. *Journal of Medical Virology*, 42(3): 234-236. ISSN: 1096- 907
- Pujol, F.H. & Devesa, M. (2005). Genotypic variability of hepatitis viruses associated with chronic infection and the development of hepatocellular carcinoma. *Journal of Clinical Gastroenterology*, 39(7): 611-618. ISSN: 0192-0790
- Pujol, F.H. & Loureiro, C.L. (2007). Replacement of hepatitis C virus genotype 1b by genotype 2 over a 10-year period in Venezuela. *Journal of Clinical Gastroenterology*, 41(5): 518-520. ISSN: 0192-0790
- Pujol, F.H., Navas, M.C., Hainaut, P. & Chemin, I. (2009) Worldwide genetic diversity of HBV genotypes and risk of hepatocellular carcinoma. *Cancer Letters*, 286(1): 80-88. ISSN: 0304-3835
- Purcell, R.H. & Emerson, S.U. (2008). Hepatitis E: an emerging awareness of an old disease. *Journal of Hepatology*, 48(3): 494-503. ISSN: 0168-8278
- Quintero, A., Martinez, D., Alarcon De Noya, B., Costagliola, A., Urbina, L., Gonzalez, N., Liprandi, F., Castro De Guerra, D. & Pujol, F.H. (2002). Molecular epidemiology of hepatitis B virus in Afro-Venezuelan populations. *Archives of Virology*, 147(9): 1829-1836. ISSN:0304-8608
- Raimondi, S., Bruno, S., Mondelli, M.U. & Maisonneuve, P. (2009). Hepatitis C virus genotype 1b as a risk factor for hepatocellular carcinoma development: a meta-analysis. *Journal of Hepatology*, 50(6): 1142-1154. ISSN: 0168-8278
- Ramos, B., Núñez, M., Martín-Carbonero, L., Sheldon, J., Rios, P., Labarga, P., Romero, M., Barreiro, P., García-Samaniego, J. & Soriano, V. (2007). Hepatitis B virus genotypes and lamivudine resistance mutations in HIV/hepatitis B virus-coinfected patients. *Journal of Acquired Immune Deficiency Syndromes*, 44(5): 557-561. ISSN: 1525-4135
- Reiter, J., Pérez-Vilaró, G., Scheller, N., Mina, L.B., Díez, J. & Meyerhans, A. (2011). Hepatitis C virus RNA recombination in cell culture. *Journal of Hepatology*, in press. ISSN: 0168-8278
- Robertson, B.H. (2001). Viral hepatitis and primates: historical and molecular analysis of human and nonhuman primate hepatitis A, B, and the GB-related viruses. *Journal of Viral Hepatitis*, 8(4): 233-242. ISSN: 1365-2893

- Rotman, Y. & Liang, T.J. (2009). Coinfection with hepatitis C virus and human immunodeficiency virus: virological, immunological, and clinical outcomes. *Journal of Virology*, 83(15): 7366-7374. ISSN: 1098-5514
- Sánchez, L.V., Tanaka, Y., Maldonado, M., Mizokami, M. & Panduro, A. (2007). Difference of hepatitis B virus genotype distribution in two groups of mexican patients with different risk factors. High prevalence of genotype H and G. *Intervirology*, 50(1): 9-15. ISSN: 1423-0100
- Schwarze-Zander, C., Blackard, J.T., Zheng, H., Addo, M.M., Lin, W., Robbins, G.K., Sherman, K.E., Zdunek, D., Hess, G., Chung, R.T. & AIDS Clinical Trial Group A5071 Study Team. (2006). GB virus C (GBV-C) infection in hepatitis C virus (HCV)/HIV-coinfected patients receiving HCV treatment: importance of the GBV-C genotype. *Journal of Infectious Diseases*, 194(4): 410-419. ISSN: 0022-1899
- Sherman, K.E., Andreatta, C., O'Brien, J., Gutierrez, A. & Harris, R. (1996). Hepatitis C in human immunodeficiency virus-coinfected patients: increased variability in the hypervariable envelope coding domain. *Hepatology*, 23(4): 688-694. ISSN: 1527-3350
- Simmonds, P. (2001). Reconstructing the origins of human hepatitis viruses. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences*, 356(1411): 1013-1026. ISSN:0022-5193
- Simmonds, P. & Midgley, S. (2005). Recombination in the genesis and evolution of hepatitis B virus genotypes. *Journal of Virology*, 79(24): 15467-15476. ISSN: 1098-5514
- Smith, D.B., Pathirana, S., Davidson, F., Lawlor, E., Power, J., Yap, P.L. & Simmonds, P. (1997). The origin of hepatitis C virus genotypes. *Journal of General Virology*, 78(Pt 2): 321-328. ISSN: 1465-2099
- Smith, D.B., Basaras, M., Frost, S., Haydon, D., Cuceanu, N., Prescott, L., Kamenka, C., Millband, D., Sathar, M.A. & Simmonds, P. (2000). Phylogenetic analysis of GBV-C/hepatitis G virus. *Journal of General Virology*, 81(Pt 3): 769-780. ISSN: 1465-2099
- Stapleton, J.T., Fong, S., Muerhoff, A.S., Bukh, J. & Simmonds, P. (2011). The GB viruses: a review and proposed classification of GBV-A, GBV-C (HGV), and GBV-D in genus Pegivirus within the family Flaviviridae. *Journal of General Virology*, 92(Pt 2): 233-246. ISSN: 1465-2099
- Sulbarán, M.Z., Di Lello, F.A., Sulbarán, Y., Cosson, C., Loureiro, C.L., Rangel, H.R., Cantaloube, J.F., Campos, R.H., Moratorio, G., Cristina, J. & Pujol, F.H. (2010). Genetic history of hepatitis C virus in Venezuela: high diversity and long time of evolution of HCV genotype 2. *PLoS One*. 5(12): e14315. ISSN: 1932-6203
- Sulbaran, Y., Gutierrez, C.R., Marquez, B., Rojas, D., Sanchez, D., Navas, J., Rovallo, E. & Pujol, F.H. (2010). Hepatitis A virus genetic diversity in Venezuela: exclusive circulation of subgenotype IA and evidence of quasispecies distribution in the isolates. *Journal of Medical Virology*, 82(11): 1829-1834. ISSN: 1096- 907
- Sulkowski, M.S. (2008). Viral hepatitis and HIV coinfection. *Journal of Hepatology*, 48(2): 353-367. ISSN: 0168-8278
- Tatematsu, K., Tanaka, Y., Kurbanov, F., Sugauchi, F., Mano, S., Maeshiro, T., Nakayoshi, T., Wakuta, M., Miyakawa, Y. & Mizokami, M., (2009). A genetic variant of hepatitis B virus divergent 1 from known human and ape genotypes 2 isolated from a Japanese patient and provisionally assigned to new genotype J. *Journal of Virology*, 83(20): 10538-10547. ISSN: 1098-5514

- Tang, H. & Grisé, H. (2009). Cellular and molecular biology of HCV infection and hepatitis. *Clinical Science*, 117(2): 49-65. ISSN: 0143-5221
- Taylor, J.M. (2009). Replication of the hepatitis delta virus RNA genome. *Advances in Virus Research*, 74: 103-121. ISSN: 0065-3527
- Tebit, D.M., Nankya, I., Arts, E.J. & Gao, Y. (2007). HIV diversity, recombination and disease progression: how does fitness "fit" into the puzzle? *AIDS Reviews*, 9(2): 75-87. ISSN:1139-6121
- Thakur, V., Guptan, R.C., Kazim, S.N., Malhotra, V. & Sarin, S.K. (2002). Profile, spectrum and significance of HBV genotypes in chronic liver disease patients in the Indian subcontinent. *Journal of Gastroenterology and Hepatology*, 17(2): 165-70. ISSN: 1440-1746
- Theджа, M.D., Muljono, D.H., Nurainy, N., Sukowati, C.H., Verhoef, J. & Marzuki, S. (2011). Ethnogeographical structure of hepatitis B virus genotype distribution in Indonesia and discovery of a new subgenotype, B9. *Archives of Virology*, 156(5): 855-868. ISSN:0304-8608
- Torresi, J. (2002). The virological and clinical significance of mutations in the overlapping envelope and polymerase genes of hepatitis B virus. *Journal of Clinical Virology*, 25(2): 97-106. ISSN: 1386-6532
- Toyoda, H., Fukuda, Y., Koyama, Y., Takamatsu, J., Saito, H. & Hayakawa, T. (1997). Effect of immunosuppression on composition of quasispecies population of hepatitis C virus in patients with chronic hepatitis C coinfecting with human immunodeficiency virus. *Journal of Hepatology*, 26(5): 975-982. ISSN: 0168-8278
- Tran, T.T., Trinh, T.N. & Abe, K., 2008. New complex recombinant genotype of hepatitis B virus identified in Vietnam. *Journal of Virology*, 82(11): 5657-5663. ISSN: 1098-5514
- Wang, S.Y., Wu, J.C., Chiang, T.Y., Huang, Y.H., Su, C.W. & Sheen, I.J. (2007). Positive selection of hepatitis delta antigen in chronic hepatitis D patients. *Journal of Virology*, 81(9): 4438-4444. ISSN: 1098-5514
- Weiner, A.J., Geysen, H.M., Christopherson, C., Hall, J.E., Mason, T.J., Saracco, G., Bonino, F., Crawford, K., Marion, C.D., Crawford, K.A., Brunetto, M., Barrt, P.J., Miyamura, T., Mchutchinson, J. & Houghton, M. (1992). Evidence for immune selection of hepatitis C virus (HCV) putative envelope glycoprotein. *Proceedings of the National Academy of Sciences USA*, 89(8): 3468-3472. ISSN: 1091- 6490
- Wu, J.C., Hsu, S.C., Wang, S.Y., Huang, Y.H., Sheen, I.J., Shih, H.H. & Syu, W.J. (2005). "Defective" mutations of hepatitis D viruses in chronic hepatitis D patients. *World Journal of Gastroenterology*, 11(11): 1658-1662. ISSN: 1007-9327
- Xiang, J., George, S.L., Wunschmann, S., Chnag, Q., Klinzman, D. & Stapleton, J.T. (2004). Inhibition of HIV-1 replication by GB virus C infection through increases in Rantes, MIP-1 $\alpha$ , MIP-1 $\beta$ , and SDF-1. *Lancet*, 363(9426): 2040-2046. ISSN: 1474-547X
- Yang, H.I., Yeh, S.H., Chen, P.J., Iloeje, U.H., Jen, C.L., Su, J., Wang, L.Y., Lu, S.N., You, S.L., Chen, D.S., Liaw, Y.F., Chen, C.J. & REVEAL-HBV Study Group. (2008). Associations between hepatitis B virus genotype and mutants and the risk of hepatocellular carcinoma. *Journal of the National Cancer Institute*, 100(16): 1134-1143. ISSN: 0027-8874
- Yang, W. & Summers, J. (1998). Infection of ducklings with virus particles containing linear double-stranded duck hepatitis B virus DNA: illegitimate replication and reversion. *Journal of Virology*, 72(11): 8710-8717. ISSN: 1098-5514

- Yu, M.W., Yeh, S.H., Chen, P.J., Liaw, Y.F., Lin, C.L., Liu, C.J., Shih, W.L., Kao, J.H., Chen, D.S. & Chen, C.J. (2005). Hepatitis B virus genotype and DNA level and hepatocellular carcinoma: a prospective study in men. *Journal of the National Cancer Institute*, 97(4): 265-272. ISSN: 0027-8874
- Yuen, M.F., Fung, J., Wong, D.K. & Lai, C.L. (2009). Prevention and management of drug resistance for antihepatitis B treatment. *The Lancet Infectious Diseases*, 9(4): 256-264. ISSN: 1473-3099
- Zein, N.N. (2000). Clinical significance of hepatitis C virus genotypes. *Clinical Microbiology Reviews*, 13(2): 223-235. ISSN: 1098-6618
- Zeuzem, S., Feinman, S.V., Rasenack, J., Heathcote, E.J., Lai, M.Y., Gane, E., O'Grady, J., Reichen, J., Diago, M., Lin, A., Hoffman, J. & Brunda, M.J. (2000). Peginterferon alfa-2a in patients with chronic hepatitis C. *The New England Journal of Medicine*, 343(23): 1666-1672. ISSN: 1533-4406
- Zhu, A.X. & Chung, R.T. (2003). Hepatic steatosis in patients with chronic hepatitis C virus infection. Another risk factor for hepatocellular carcinoma? *Cancer*, 97: 2948-2950. ISSN: 1097-0142

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This book covers various aspects of Molecular Virology. The first chapter discusses HIV-1 reservoirs and latency and how these twin phenomena have remained a challenge to eradication. Aspects regarding the molecular evolution of hepatitis viruses including their genetic diversities with implications for vaccine development are treated in the second chapter. Metabolic disorders that are a consequence of hepatitis C virus infection are discussed in the succeeding chapter. The following two chapters discuss influenza C virus and the applications of viral vectors in therapeutic research. Avian influenza is handled in the sixth chapter and the therapeutic potential of belladonna-200 against japanese encephalitis virus infection is discussed in the succeeding chapter. The last two chapters discuss baculoviruses and their interaction with polydnviruses. Researchers, lecturers and students will find this book an indispensable companion.

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Unit 405, Office Block, Hotel Equatorial Shanghai  
No.65, Yan An Road (West), Shanghai, 200040, China  
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Phone: +86-21-62489820  
Fax: +86-21-62489821

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