showed a prevalence of 14.8 per cent (12/81) in all GT1 infected patients, and were only detected in GT1b, being mainly represented by C316N with 38.5 per cent (10/26) of GT1b infected patients. The combined NS5A RASs (Q30H + Y93H), causing high level resistance to all NS5A inhibitors, were detected at baseline in one HIV/HCV GT1a co-infected patient who later failed a treatment with SOF + LDV for 12 weeks. Finally, an isolated Y93H mutation was also detected at baseline in a GT1b mono0-infected patient experiencing recurrence. Overall 38.3 per cent (31/81) of all GT1 HCV infected patients presented NS5 RASs at baseline, in which 58.1 per cent (18/31) were co-infected with HIV/HCV whereas only 38.7 per cent (12/31) of HCV monoinfected patients showed baseline RASs. Moreover, 27.3 per cent (15/55) of GT1a infected patients presented NS5 RASs at baseline, whereas patients infected with GT1b showed the highest prevalence of natural RASs, namely 61.5 per cent (16/26). These data support the usefulness of resistance testing prior to treatment initiation, thus preventing relapses associated to the presence of baseline RASs, as a statistical significant association was found between treatment failure and the presence of major NS5 RASs, namely Y93C/H ($P = 0.04$). However, this reduced sampling can constitute a limiting factor since it may underestimate the statistical analysis, and lead to relatively higher RASs rates when comparing to other previous studies.

A42 Genetic variability and phylogeography of hepatitis B virus genotype D in Brazil

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Hepatitis B virus (HBV) has been classified into ten genotypes (A–J), some of which are divided into subgenotypes. Genotype D (HBV/D) has a worldwide distribution, and ten subgenotypes (D1–D10) have been described so far. Brazil has received different migratory flows over time. The evolutionary history of HBV/D in Brazil is not well understood and few HBV/D complete genome sequences are available. The aim of this study was (1) to examine the distribution of HBV/D subgenotypes in Brazil, (2) to determine the full-length genomic sequences of HBV/D isolates from different regions, and (3) to investigate the origin and spread of HBV/D subgenotypes in the country. All Brazilian HBV/D sequences with known subgenotype ($n = 215$) were retrieved from GenBank. HBV/D3 was the most prevalent (56 per cent) subgenotype, followed by HBV/D4 (25 per cent), HBV/D2 (17 per cent), and HBV/D1 (2 per cent). Although HBV/D was circulating countrywide, most (57 per cent) isolates were from the South region, which was the only region where all four subgenotypes were found. In addition, forty-five new full-length sequences (one D1, eleven D2, thirty-two D3 and one D4) were determined. To investigate the origin and spread of HBV/D in Brazil, we compiled different datasets of complete genomes for HBV/D1–D4, using Brazilian and worldwide sequences. Phylogeographic analysis, performed using BEAST v.1.8.2, indicated that the most probable origins of HBV/D1 and HBV/D2 were Syria and Eastern Europe, respectively, with times of the most recent common ancestor (tMRCA) in the early nineteenth century for HBV/D1 and the second half of the twentieth for HBV/D2, corroborating historical data on migrations to Brazil. Martinique was found to be the origin of Brazilian HBV/D4, probably reflecting the population of African slaves brought to the Americas. However, the methodology used was not able to determine from where and when HBV/D3 was introduced in Brazil, possibly due to different introduction routes.

A43 Molecular epidemiology of hepatitis B virus in South Kivu, an eastern province of the Democratic Republic of Congo

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Hepatitis B virus (HBV) is characterized by a wide genomic variability that could play a role in different clinical manifestations and response to therapy. The ten HBV genotypes show a distinctive geographical distribution worldwide and genotypes A, D, and E are the most frequently found in Africa. There are only limited studies on HBV genotype distribution in Democratic Republic of Congo (DRC), all performed in the western part and showing a vast majority of genotype E. We performed a study to determine the genotype distribution of HBV in South Kivu (DRC). Blood screening was performed during 2014–2015 at the Hospital Provincial General de Reference of Bukavu where serum samples of newly detected Ag HBs positive subjects were collected. These samples were sent and analysed at the Cliniques Universitaires Saint Luc, Belgium. We undertook HBV DNA load measurement by Abbott RealTime HBV assay on the m2000 system, genome sequencing using an in-house method targeting the S and P overlapping region, phylogenetic analysis using Geneious 4.0 software, and additional mutational analysis focused on the identification of mutations (P region) associated with antiviral resistance using the online HBVseq tool (Stanford University). Genotype determination was performed in forty-one patients. HBV genotype A was detected in 40/41 (97.6 per cent) and HBV genotype E in 1/41 (2.4 per cent). Only two mutations were observed and concerned the I169T nucleotide substitution, both in genotype A samples. The phylogenetic analysis showed that nearly all South Kivu genotypes A (39/40) are closely related to A1 subgenotype strains found in Rwanda, Haiti, and Martinique while only one single strain attached to the A2 subgenotype cluster was isolated. The only remaining genotype E case was linked to the western African E crescent. HBV genotype A seems to be the most predominant genotype in eastern DRC with the majority belonging to the Afro-Asian subgenotype (A1). This contrasts with the western part of RDC where genotype E is the most frequently found genotype. These results support the hypothesis of an East–West genotypic demarcation. Moreover, the low genetic variability of HBV in South-Kivu is suggestive of strong local endemicity.

A44 Complete HPV genomes from cervical samples using next-generation sequencing in Luxembourg

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While next-generation sequencing using rolling circle amplification (NGS-RCA) of human papillomavirus (HPV) has been conducted in HIV-HPV co-infected women, we performed a pilot