

**O1031 Molecular epidemiology and resistance mutations of hepatitis B virus in the last few years**

Genoveva Santillana\*<sup>1</sup>, Isabel Viciano<sup>1</sup>, Cristina García<sup>1</sup>, Juan Carlos Gavilan<sup>2</sup>, Inmaculada Moreno<sup>3</sup>, Paula Bardon<sup>1</sup>, Encarnacion Clavijo<sup>1</sup>

<sup>1</sup> Servicio de Microbiología, Hospital Universitario Virgen de la Victoria, Málaga, Spain, <sup>2</sup> Unidad de Hepatitis, Hospital Universitario Virgen de la Victoria, Málaga, Spain, <sup>3</sup> Servicio Digestivo, Hospital Universitario Virgen de la Victoria, Málaga, Spain

**Background:** Infection with HBV is one of the problems with the greatest impact on public health, due to its wide distribution and direct relationship with the development of cirrhosis and hepatocellular carcinoma. Ten genotypes (A-J) have been characterized, which have been linked to the epidemiology and possible response to treatment.

**Materials/methods:** Patients with chronic HBV infection in the period 2016-2018 have been included, who underwent detection of genotype and resistance mutations with the HBV Sequencing kit (Abbott) in our Hospital. Data on sex, age, coinfection with HCV and HDV, genotype, subtypes, clinical data and mutations of treatment resistance have been analysed.

**Results:** 109 patients, 63 (57%) men, with average age of 45 years (IQR 15-85) and median viral load of 3.68 log(IU/mL) (IQR 1.89 -8.53 log). 57(52%) were Spanish patients. Other sources: 17(15%) China, 11(10%) Africa and 12(11%) Eastern Europe. Coinfection with HCV 2% and VHD 1%. 58% of patients had negative HBeAg. Genotype distribution: A: 22(20%); A1 6(5.7%) A2 14(12%). B: 8(7%); B2 5(4.7%) B3 2(1.9%). C: 10(9%); C1 10 (9%). D: 59(54%); D1 9(8.5%) D2 28(25.5%) D3 8(7.5%) D4 5(4.7%). E: 7(6%), H: 2(1%) and F: 1(1%); F2 1(1%). Genotypes A and D were more frequent in patients from Europe and Africa; B and C in patients of China ( $p < 0.005$ ). The most prevalent genotypes with negative HBeAg were D, A and E ( $p < 0.005$ ) while C was HBeAg positive ( $p < 0.005$ ). Genotypes D(76%), A(58.8%) and E(100%) had a viral load  $< 20000$  IU/mL. Subtypes A2 and D2 were the most common with 12.3% and 25.5% respectively. 10(9.4%) patients had some resistance mutation of the polymerase gene. The L180M+T184I+M204V+S202G(2.8%) mutations that confer resistance to Lamivudine, Telbivudine and Entecavir were noteworthy due to their frequency. In relation to resistance mutations for Adefovir, we detected 2 patients(1.8%) who had the 181V/T mutation and another 2(1.8%) the 236T mutation.

**Conclusions:** The distribution of HBV genotypes changes according to age and country of origin. The presence of coinfection with HCV and VHD in our population has been low. Tenofovir maintains sensitivity in 100% of patients with resistance mutations, so it should be considered the treatment of choice.