

## **HEPATITIS C VIRUS GENOTYPE PREVALENCE AMONG BLOOD DONORS FROM CENTRAL PORTUGAL (P-185)**

M.R. Caldeira, M.J.N. Teixeira, F.J.F.C. Henggeler, N.F. Mateus, R.C.A. Diniz, M.H. Gonçalves (Coimbra, Portugal)

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### **BACKGROUND**

Hepatitis C Virus (HCV) is the principal etiological factor in post transfusional hepatitis infections. HCV is of the Flaviviridae family and is characterised by a high genomic diversity expressed in six major genotypes with numerous subtypes. Evidence has emerged indicating that typing and subtyping for HCV is clinically important in understanding HCV disease and therapy options. The Portuguese Blood Institute Regional Centre of Coimbra has been performing Nucleic Acid Testing in random blood donations since July 2000. Routine testing of all donations has been carried out as of January 2005. With the implementation of NAT testing the Institute has performed genotypingtests on all HCV RNA positive samples as part of the established algorithm.

### **METHODS**

The study looked at blood donations from 2000 to 2006. There were found 76 HCV RNA positive samples detected by Transcription Mediated Amplification (TMA) technology (Chiron Corporation, USA). The genotype was investigated with the Versant HCV Genotype Assay (LiPA) utilizing reverse hybridization of the 5' untranslated region of the genome.

### **RESULTS**

Of the 76 HCV RNA positive samples identified 23 as belonging to the genotype 1a (30.3%) followed by the genotype 3a (22.3%) and 1b (21.0%). There was one case of co-infection with genotype 1 and 4 (1.3%) identified. The remaining identified genotypes showed a much lower prevalence 1a/1b (10.5%), 4 (3.9%), 4c/4d (2.6%), 2a/2c (2.6%) and genotype 1 (5.3%) of which we could not obtain a subtype.

### **CONCLUSION**

The prevalence of Genotype 1a within our population is concordant with epidemiological data from West Europe. Hepatitis C Virus genotyping permits the analysis of the distribution of the different virus types contributing the knowledge of its epidemiology. The clinical importance of the genotype has been clearly evidenced in numerous studies and strict algorithms have been implemented with focus on the genotype for treatment options and durations.