HEPATITIS C VIRUS GENOTYPE 3H: THE PROBLEM OF THE MISDIAGNOSIS

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Hepatitis C Virus (HCV) is a positive-sense single-stranded RNA virus of the Flaviviridae family. Globally, about 130–150 million people have chronic Hepatitis C infection (1).

Since 2011 new specific drugs called Direct-Acting Antivirals (DAAs) have been commercialized. These DAAs target specific nonstructural proteins of the virus, resulting in disruption of viral replication and infection. The international guidelines for HCV management specifically recommends specific therapies related to the different HCV genotypes (2). A particular focus is on genotype HCV 3. Available data suggest that fibrosis progression occurs most rapidly in patients with HCV genotype 3 infection (3)(4). In particular, subtype HCV 3h shows characteristic polymorphisms at positions -99, -108 and -138 in the 5'UTR region. The major part of HCV genotyping assays has difficulties to recognize it (5), leading to misdiagnosis.

Two HCV 3h clinical samples were found in two laboratories in Naples. Different diagnostic devices for HCV genotyping were used to analyze the samples: VERSANT HCV Genotype 2.0 (LiPA) (Siemens), PCR Real time HCV Genotype Plus Real-TM (Sacace), HCV RNA REAL TIME QUALITATIVE 2.0 (Nuclear Laser Medicine) and AMPLIQUALITY HCV TYPE PLUS (AB ANALITICA). Results were confirmed with the NS5B sequencing and the phylogenetic analysis of the sequences, the Gold Standard method for HCV genotyping.

The first sample was defined as not determinable both with Siemens and Sacace devices. The second one was identified as HCV 6m with Nuclear Laser Medicine product. Both were recognized as genotype HCV 3h with AMPLIQUALITY HCV TYPE PLUS. The NS5B phylogenetic analysis confirmed HCV 3h genotype for both samples.

These cases underline the difficulty on genotyping HCV 3h (6) (7) because of the presence of several polymorphisms in 5'UTR region (5). The success of AMPLIQUALITY HCV TYPE PLUS, is due to a probe specifically drawn for the HCV 3h 5'UTR polymorphisms. In this way, it is possible to distinguish this subtype without any possibilities of misinterpretations. This mistake could lead to therapeutic failure and to the onset of new viral pharmaceutical resistances.

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