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VIROLOGIA

HCV SEROPREVALENCE AND GENOTYPES EVOLUTION IN CATANZARO TEACHING HOSPITAL, SOUTHERN ITALY, FROM 2008 TO 2018.

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INTRODUZIONE

HCV chronic infection is estimated to affect 103 million people worldwide, while antibodies prevalence is estimated at 2.5% globally. HCV genotypes distribution is related to epidemiological parameters and risk factors. Aim of this study was to assess seroprevalence and genotypes distribution of HCV among patients attending at our Hospital from 2008 to 2018.

METODI

Serum samples from 5,877 new consecutive anti-HCV positive patients were test to detect viral load. HCV RNA was performed using Cobas AmpliPrep/Cobas TaqMan HCV v.2.0 (Roche). Viral genotype on RNA positive samples was identified by Versant HCV genotype 2.0 assay (Siemens). The $\chi 2$ analysis was used to evaluate association between HCV genotypes and demographic parameters ($p < 0.05$ was considered significant).

RISULTATI

Among anti-HCV positive patients we detected 1,525 chronic patients (25,9%). Antibodies prevalence increased from 2008 (8,72%) to 2010 (13,2%), while decreased from 2013 (8,88%) to 2016 (6,5%). Additionally, it did not vary significantly in the last 2 years. HCV1b was the most prevalent subtype (47.2%) followed by HCV2a/2c (20.2%). HCV1b decreased starting from 2010 (43.6%) to 2013 (39.5%), then a constant prevalence until 2018 (48,8%) was reported, while HCV 2a/2c did not vary significantly over the time. HCV3 showed a peak of 13.3% during 2014, and a progressive increase from 2015 (7.0%) to 2018 (10.2%). HCV4 increased between 2010 and 2013 reaching the peak in 2013 (9.3%). HCV3 was the third most frequent (9.6%) and was significantly more common in male patients (86.9% vs 13.0% female). HCV4 showed a rate of 6.1%, with significant gender differences (62.3% male vs 37.6% female). HCV1b and HCV2a/2c positive patients were older (born before 1959) than those infected by HCV3 and HCV1a (born before 1977). Overall most of infected patients was born before 1949. HIV positive patients were mainly intravenous drug users and co-infected by HCV3.

CONCLUSIONI

During 10 years, the study showed a low anti-HCV prevalence in the last 3 years and a significant association of types and epidemiological parameters. Male gender was related to HCV3 and HCV4 genotypes, while the oldest patients were infected by HCV1b or HCV2a/2c. Transmission route was documented only in a few patients. However, epidemiological studies are important to identify prevalence of current difficult-to-treat types, such as HCV3 infected or HIV co-infected patients, to optimize therapy design as well as screening policy.