Title: Two Single Nucleotide Polymorphisms in the MICA Gene and Smica Plasma Levels Are Associated with Hepatocellular Carcinoma Development in an Italian Population of HCV Related Liver Cirrhosis

Dr. Lydia Giannitrapani, Giuseppa Augello, Daniele Balasus, Caterina Fusilli, Tommaso Mazza, Maria Rita Emma, Rosalia Agliastro, Melchiorre Cervello, and Giuseppe Montalto
Researcher
Biomedical Department of Internal Medicine and Specialties
University of Palermo
Italy

Abstract

Background & Aims: We investigated the relationships between MICA polymorphisms, sMICA levels and hepatocellular carcinoma (HCC) risk in HCC patients with chronic hepatitis C virus (HCV) infection.

Methods: 154 HCV-related HCC cases, 93 HCV-related liver cirrhosis (LC) cases and 244 healthy controls were genotyped using KASP™ SNP method. Levels of plasma soluble MICA (sMICA) were measured in 132 HCC, 90 LC patients and in 78 controls.

Results: Genotyping of MICA rs2596542 showed that G/G genotype was significantly more frequent in HCC than in controls and in LC than in LC patients. As for MICA rs2596538 allele C and C/C genotype were significantly more frequent in HCC than in controls and in HCC than in LC cases. These results demonstrate that MICA rs2596542 and rs2596538 are associated with the risk of developing HCV-related HCC in a Sicilian population. The presence of both rs2596542 and rs2596538 among LC patients raised the risk of HCC by 3.94 times. In addition, by a machine learning classifier, we found that age coupled with either rs2596542 or rs2596538 was an important discriminating factor between LC and HCC patients. Finally, sMICA levels significantly increased during HCV-related liver disease progression, and a significant relationship with either rs2596542 and rs2596538 genotypes and sMICA plasma levels was found between LC and HCC patients.

Conclusions: MICA rs2596542 and rs2596538 variants are associated with the risk of developing HCV-related HCC in an Italian population.