Role of *IL-10* polymorphisms in susceptibility to hepatitis B virus-related hepatocellular carcinoma

M.W. Peng[1], S.Q. Lu[2], J. Liu[1] and C.Y. Dong[1]

[1]Laboratory of Molecular Virus & Cancer, State Key Laboratory of Virology, Wuhan University School of Basic Medicine, Wuhan University, Wuhan, China
[2]Department of Anesthesiology, Hubei Cancer Hospital, Hongshan, Wuhan, China

Corresponding author: C.Y. Dong
E-mail: changydyd@163.com

Genet. Mol. Res. 15 (1): gmr.15017984
Received November 4, 2015
Accepted January 15, 2016
Published March 18, 2016
DOI http://dx.doi.org/10.4238/gmr.15017984

ABSTRACT. We conducted a case-control study to investigate the role of three common single nucleotide polymorphisms of *IL-10* (-592G/A, -819T/C, and -1082A/C) in the development of hepatitis B virus (HBV)-related hepatocellular carcinoma (HCC). The study included 173 HBV-related HCC patients and 182 healthy controls. A polymerase chain reaction-restriction fragment length polymorphism assay was applied to assess the sequence variants of interest. Compared with control subjects, HCC patients were more likely to be older (t = 1.94, P = 0.03), have a family history of cancer (chi square = 17.86, P < 0.001), and exhibit higher alanine transaminase (t = 13.32, P < 0.001) and aspartate transaminase (t = 12.63, P < 0.001) levels. Using unconditional logistic regression analyses, we found that the GG genotype of -592G/A was associated with increased risk of HCC [odds ratio (OR) = 2.20, 95% confidence interval (CI) = 1.12-4.38], compared to the AA genotype. Under a dominant model, the AG+GG genotype correlated with HBV-related HCC susceptibility compared to the AA genotype, with an OR (95%CI) of 1.56 (1.02-2.48). Moreover, a recessive model showed the GG genotype to be associated with elevated risk of HCC compared to the

AA+AG genotype (OR = 1.85, 95%CI = 1.01-3.47). However, no significant association between the -819T/C and -1082A/C variants and development of HBV-related HCC was observed under codominant, dominant, and recessive models. We conclude that the *IL-10* -592G/A polymorphism does play a role in susceptibility to HBV-related HCC under codominant, dominant, and recessive models.

Key words: *IL-10*; Polymorphism; Hepatitis B virus; Hepatocellular carcinoma

