Association of Autophagy Gene Atg16L1 Variant rs2241879 and Chronic Hepatitis B in North Indian Population

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Abstract—*Autophagy related gene 16L1 (Atg16L1), a part of ubiquitin conjugation system like enzyme E3 (Atg5-Atg12/Atg16L1), plays an important role in autophagosome formation in autophagy. Involvement of Atg16L1 gene variants in susceptibility to various diseases has been demonstrated but no such information is available for hepatitis B. In this study we targeted Atg16L1 rs2241879(C/T) in North Indian population to assess its association in Hepatitis B infection. We genotyped rs2241879 in 200 healthy control individuals and 279 hepatitis B infected individuals at different infection stages using PCR-RFLP technique. Genotypic frequencies in healthy controls were CC=17.43% (n=16), CT=48.64% (n=135) and TT=33.93% (n=49) with allele frequencies C=41.75% and T=58.25% while in infected individuals CC=14.57% (n=30), CT=47.2% (n=153), and TT=38.23% (n=96) with allele frequencies C=38.17% and T=61.83%, respectively. We did not find significant association when healthy group were compared with the total infected samples (OR = 1.1609, 95%CI = 0.8933-1.5087, P = 0.2644). On categorizing patients based on the stage of infection, we found no significant association of rs2241879 with acute (OR = 0.5921, 95%CI = 0.3688-0.9506, P = 0.0300) and asymptomatic (OR = 1.0970, 95%CI = 0.7272 -1.6551, P = 0.6589) groups but in the patients with chronic hepatitis B (CHB) infection significant association was observed (OR = 1.4092, 95%CI = 1.0464-1.8978, P = 0.0239). In conclusion, our data suggest that Atg16L1 rs2241879 may predispose HBV infected individuals to the risk of chronic infection. We are further collecting samples to analyze these data in more number of samples.*