Abstract

Hepatocellular carcinoma (HCC) is one of the most prevalent forms of liver cancer and remains a significant global health challenge. *Tp53* and *CTNNB1* gene mutations are the most frequently altered genetic variants that lead towards the HCC. Single nucleotide polymorphism (SNPs) in these genes can be very useful to predict the risk of development of HCC. Our research was started with the goal of determining how single nucleotide polymorphism in the human *TP53* and *CTNNB1* genes affected the stability, subcellular localization, half-life, isoelectric point, instability index, aliphatic index, extinction coefficient, 2-D and 3-D structures, validation of the 3D structure and docking among other characteristics of encoded mutated proteins. To achieve this purpose coding sequence (CDS) and single nucleotide polymorphism of the desired gene were first obtained from Ensemble data set. Then these CDS was translated by using EXPASY Translate tool. Protein sequences of mutated genes were subjected to Prot Param, I-MUTANT, CELLO2, SOPMA (secondary structure prediction method), SWISS (tertiary structure prediction method), SAVES v6.0 (Structure Validation Server) and HDOCK Server tool. Three SNPs of *TP53* named rs1555526997 (case 9) in exon 15, rs1567556784 (case 26) in exon 59 and rs869054324 (case 29) in exon 66 among 30 and one SNPs rs1553631845 (case 29) in exon 452 of *CTNNB1* among 51 cases showed complete alteration in physiochemical structure, subcellular localization, 2D structure, 3D structure, validation of 3D structures and docking high energy values. There are twenty-one missense, three frameshift and six stop gained mutations of *TP53* while forty missense, one frameshift and ten stop gained mutations of *CTNNB1* in the present study. Our study demonstrated that how an in-silico methods is used to predict hepatocellular carcinoma associated biomarkers in *Tp53* and *CTNNB1* gene.

Keywords: Hepatocellular carcinoma, *TP53*, *CTNNB*1, Single nucleotide polymorphism