ABSTRACT

In the current research molecular analysis of total sixty breast cancer biopsy samples were carried out after isolation of DNA. In 38 samples amplification of human interferon alpha 2b gene was observed out of 60 samples indicating that there may be some deletion at the ends of this gene in breast cancer patients. The amplified gene fragments were subjected to sequencing displaying frequent alterations mostly after 400 bp. Homology modeling tools were applied on frequently observed mutated amino acids sequence showed no significant structural changes in protein fold except some local changes after superimposed models variants. The *in silico* docked complexes of IFN α 2b variants with IFNAR1 revealed different binding patterns including without binding (such as in 46F and 47F) with receptor, binding with receptor (all variants except 46F, 47F and 49F) just like normal sample and even a more strong binding (such as 49F) containing new binding contacts with sugar moiety of receptor in addition to protein-protein contacts. Therefore it is suggested that only few mutational variants of interferon α 2b can be the risk factor alongwith other genetic and environmental risk factors that may be associated with carcinoma of breast among females.