In silico identification, analysis and Docking of SNP in human FGF20 Gene for Parkinson Disease

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From National Conference on Natural Products as therapeutics, Medical Microbiology, Nanobiology and System biology: Current Scenario & Emerging Trends, 'NATCON-2014'.
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18-19 September 2014.

American J of Bio-pharm Biochem and Life Sci 2014 September, Vol. 4 (Suppl 1): P 21

ABSTRACT

Parkinson Disease is the second most spreading neurodegenerative disease which occurs due to the depletion of dopamine level in the brain. Recent studies on this disease revealed that it can also be occurred by some genetic factor. In the current study of genetic Parkinson disease it was identified that, there was some mutation occurred in the gene encoded protein FGF20 which is responsible for the depletion of dopamine level. An attempt was made, to correct the presence of mutation in the gene using SNP analysis and Prediction tools to make the gene function normally. SNP tools predicted that D206N SNP present in protein sequence is not only affecting the protein structure, but also alter gene function when compared with other SNP's present in the gene. The SNP 3Dstructure structure of FGF20 was retrieved. Using mutation tool the SNP was altered on the 206th position of the protein sequence (Aspartic Acid was replaced for Asparagine). Then energy minimization was carried out. Further Molecular docking were done for this normalized protein against currently used 5 drugs for Parkinson disease which will usually increase the Dopamine level. Finally the drug shows highest binding affinity of -259.90 kcal/mol with normal FGF20 protein was reported. This study can be further executed for *in vitro* clinical trials.

Published: September 2014.