Computational Analysis of Single Nucleotide Polymorphisms (SNPs) in human *ATP1-A2*gene

Afra.M.Bkrye(1)Mona. M.Khaier(2) Hind Elnasri(3)
(1,2,3)Department of Biochemistry and Molecular Biology, College of Veterinary Medicine- University of Bahri – Khartoum- Sudan

Abstract:

BACKGROUND: In this study we analyzed the effect of genetic mutations mainly Single nucleotide polymorphisms (SNPs) mutations that can alter the expression and functions of *ATP1A2* gene as gene had been candidate to cause Migraine

METHODS: ATP1A2 gene was investigated in dbSNP/NCBI database in June 2016 and we used different computational analysis approach. Deleterious nsSNPs were predicted by SIFT and Polyphen-2 softwares. Then the damaging nsSNPs were submitted to I- mutant to Predict the change in stability due to mutation and PHD-SNP and SNPS&GO software used to demonstrate the relationship between SNP and related Migraine Protein structural analysis of amino acid variants was performed by Project Hope .To highlight genetic interactions of ATP1A2 we used Gene MANIA software.

RESULTS: Gena mania revealed that ATP1A2Gene encodes for the α2 subunit of ATPase Na+/ K. The SNPs sequence of ATP1A2 gene was collected from NCBI; 2576of them [Homo sapiens] only From sift and polyphen-2 software the high score deleterious SNPs were found as following: (rs28933401),) rs368405677), (rs121918612), (rs121918614), (rs121918615),(rs121918618), (rs121918619),(rs200425518), (rs181618883)and (rs149144720) Which analysis in Project HOPE software to analyzed the changing in amino acid properties and domains, , which found among these (rs). (rs28933401),) rs368405677), (rs121918612)have 100% mutation. Additionally, I-Mutant and PHD-SNPs and SNP&GO showed decrease instability for these nsSNP sup on mutation. Protein structural analysis with these amino acid variants was performed by using I-Mutant, Swiss PDB viewer, to check their molecular dynamics and energy minimization calculations.

CONCLUSION: in this study we found R689Q,T378N,G301R, D718N, P979L, T415M, R171W, A688P,A297T and G855E mutations in ATP1A2gene could directly or indirectly destabilize the amino acid interactions and hydrogen bonds networks thus explaining the functional deviations of protein To some extent mutations in ATP1A2 gene could directly or indirectly destabilize the amino acid interactions and hydrogen bonds networks thus explaining the functional deviations of protein to some extent.

Keywords: ATP1A2, SNP, nsSNPs. miRNA site