EuroSciCon

EuroScicon Joint event on

Genetics, Cell and Gene Therapy

August 20-21, 2018
Amsterdam, Netherlands

Biochem Mol biol 2018 Volume: 4
DOI: 10.21767/2471-8084-C3-015

IN SILICO STUDIES OF DRD2 GENE STRUCTURAL VARIANT (SER311CYS) BINDING TO RISPERIDONE FOR SCHIZOPHRENIA TREATMENT

Alireza Sharafshah[1] and Mohammad Raad[2]

[1]Guilan University of Medical Sciences, Iran
[2]University of Guilan, Iran

As an antipsychotic drug which has been increasingly used for treatment and maintenance therapy in schizophrenia, Risperidone has potent antagonistic properties for the dopamine D2 receptor. As a complex and severe disorder affecting 1% of the population, with high heritability nearly 80%, schizophrenia is strongly involved with genetic factors including functional polymorphisms. The tertiary structures of human DRD2 protein in wild-type (Ser311) and mutant (Cys311) alleles of *rs1801028* (C>G) were modeled by the chosen template (PDB ID: 6CM4) through SWISS-MODEL. Then, opted models were built after energy minimization by Swiss-PdbViewer ver. 4.1.0 software. The structures of dominant and recessive models were then validated using ERRAT (Errat value: 94.97 and 90.35, respectively), RAMPAGE (Number of residue in favored region: 93.8 and 93.3, respectively) and ProSA (z-score: -6 and -2.48, respectively) online softwares. To prepare Risperidone, energy minimization was performed using Hyperchem professional tool ver. 8.0.8. Active site of DRD2 was predicted by COACH. By Autodock ver. 1.5.6., best conformation was opted based on the lowest binding energy and H-Bonds in cluster. *In silico* analyses of DRD2 protein with Risperidone represented that the best conformation of Risperidone had more binding affinity to Ser311 (binding Energy=-11.23 kcal/mol with 2 Hydrogen bonds formation) compared to Cys311 model (binding Energy=-10.78 kcal/mol with 1 H-bond formation). Considering clinical response and side effects of Risperidone, optimizing drug treatment for patient is often by trial and error which costs a lot of time and money, so genotyping of Ser311Cys might be a novel SNP marker to predict Risperidone response and C allele carriers (Ser311) could receive lower doses compared to G allele carriers.

alirezasharafshah@yahoo.com