24th International Conference on
CANCER RESEARCH AND PHARMACOLOGY
&
International Congress on
STRUCTURAL BIOCHEMISTRY, STEM CELLS AND MOLECULAR BIOLOGY
August 5-6, 2019 | Singapore

Bioinsilico analysis of c-MYC gene association with Burkitt's Lymphoma

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Background: MYC gene is an important proto-oncogene transcriptional factor encodes a nuclear phosphoprotein for central cellular processes. Dysregulated expression or function of c-MYC is one of the most common abnormalities in human malignancies. The normal c-MYC gene is encoded in three separate exons divided by two large intervening sequences in this study we focused on detection of single nucleotide polymorphisms SNPs in MYC gene associated with formation of Burkitt's lymphoma, and to confirm or exclude most reported SNPs relationship with the disease, and detect novel mutations associated with the disorder.

Materials and methods: MYC gene was investigated in NCBI database http://www.ncbi.nlm.nih.gov/) and SNPs were analysed by computational softwares. SNPs in the coding region (exonal SNPs) that are non-synonymous (nsSNP) were analysed by (sift, polyphen2, I-mutant, SNPs&GO and PHD-SNP softwares.

Result: we analysed 2868 SNPs from(NCBI) 286 of them found in Homo sapiens,48 of them deleterious furtherly investigated.

Conclusion: eight SNPs were considered most disease causing (rs4645959, rs4645959, rs141095253, rs141095253, rs150308400, rs150308400, rs150308400, rs150308400) according to the four softwares used. Two ofwhich have not been reported previously[rs4645959 (N25S), rs141095253 (P396L)].

Biography

Enas Abdalla Mohammed Ahmedon is a student. Currently pursuing her master's in University of Khartoum, Sudan and she is interested in hematology and immunohematology. She is good learner, interested in knowing, learning and developing skills, knowledge and competencies. And she works as Scientist at Jafar IBin Auf Specialized Hospital for Children – Khartou.

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