

## STUDY A RELATION BETWEEN VIRUS (EBV, HTLV-1) AND SOME GENES IN CANCER TYPES IN BABYLON PROVINCE

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**ABSTRACT :** Advances in hereditary qualities and atomic science have enhanced our insight into the internal workings of cells, the essential building pieces of the body the present study aims to identification EBV and HTLV-1 virus in some cancer types in babylon province ,also itrevelead the relation between many genes and cancer types in contrast with healthy subjects, it included Leukemia, *GSTP1 (Ile105Val)*, *GSTT1*, *MTHFR*; Ovarian Cancer, *CDKN1B (Val109Gly)*, *CDKN2A/2B (rs3731257)*; Breast Cancer, *COMT (Met108/158Val)*, *CYP1B1 (Leu432Val)*; Colorectal Cancer, *MTHFR (677 C/T)*, *XPC (Lys939Gln)*; Lung Cancer, *CYP1A1 (MspI)*, *XRCC1 (Arg399Gln)*; Prostate Cancer, *CYP17 (rs2486758)*, *RNASEL (Asp541Glu)*; Bladder Cancer, *GSTP1 (Ile105Val)*, *XPC (Ala499Val)*; Gastric Cancer, *ILIRN (VNTR)*, *TNF-A (-308G>A)*. Cancer genes identified using convential PCR technique andviral detection in serum using ELIZA technique. The consequences of this study uncovered a relative relationship between HTLV-1 serum levels and the cancer \ control cases was (36%) while in EBV infection was (27.1%) as appeared in table. From this results, it found that most of genes is associated with increased cancer risk and there are significant difference in the incidence of Gene SNPs between healthy and patients.

**Key words :** Cancer, genes, PCR.EBV, HTLV-1.

### INTRODUCTION

Disclosure and indexing of quality articulation in typical and ailment conditions has been encouraged by era of huge quality articulation datasets. A large number of these sets have been saved out in the open databases, for example, ArrayExpress (Barrett *et al*, 2013). Consolidating distinctive articulation statisticsgroups has empowered investigations for articulation for both muscles and cell sorts outside single test, devises made conceivable tending to questions diverse to those postured in the first examinations and has prompted new natural bits of knowledge that generally couldn't have been acquired (Kolesnikov *et al*, 2015). The makers coordinated an examination of value co-verbalization sincenearly 4,000 social microarray investigations, trailed thruvaluation of the utilitarian importance. A while later, built up a database of nearly 10,000 tests from regular and fanatical human tissues, using five assorted Affymetrix stages, with the mean to give an organized point of view of explanation vacillation transversely more than a few particular tissue and affliction sorts (Kilpinen *et al*, 2008). Preceding these examinations, most human microarray datasets, with exceptional cases, for instance were by and large focusing on tests differentiating verbalization from only couple of one of a kind examples.

Encouraged by proceeding with mechanical advances that permit quicker and less expensive genotyping comes about, an expansive and expanding number of observational examinations exploring the relationship between variations in competitor qualities and disease hazard have emerged (Lin *et al*, 2006; Bethanney and Emalda, 2017). This expanding number of studies provoked us to evaluate the general commitment of these examinations to our present comprehension of the hereditary helplessness to disease. One of the primary reactions of hereditary the study of disease transmission has been an absence of replication. There are a few cases of studies investigating a formerly distributed factually noteworthy finding for a hereditary variation and neglecting to recreate those discoveries, recommending an expansive number of false-positive reports (Ioannidis *et al*, 2001).

The measure of these innate connection looks at is moreover a basic methodological stress, which dominante actuated the application of meta-examinations also combined examinations headed for merge together quantifiably important and ordinary outcomes from particular examinations as well as premium all effects throughits exactness (element of test dimension) (Abbas *et al*, 2017; Hassan *et al*, 2016).

In this examination, we evaluate the eventual outcomes of cheerful quality development alliance contemplates by demonstrating the P regard and power for all quantifiably basic relationship as uncovered in meta-examinations or pooled examinations. the quantifiable vitality forassessment, the P regard watched.

## MATERIALS AND METHODS

### Subjects

About 164 cases that enlisted from the fundamental Hospital in Babylon region for the investigation. All malignancy subjects were arranged by morphology, immunology and cytogenetics grouping. Ethnically and geologically coordinated 80 sound controls were gotten from same Hospital and staff. Patients and controls were very much educated and consented to partake in the examination.

### Isolation of genomic DNA

Blood tests from tumor and solid subjects were made from Scientific Investigative Workshop. An EDTA anticoagulated fringe blood test (5 ml) was gotten from each control by venepuncture. Genomic DNA was extracted utilizing a Blood DNA pack (Invetrogen Inc., USA) as per the directions of the maker. DNA wereelectrophoresed by agarose gel. The DNA concentration of samples was estimated using the Nano drop.

### PCR Reaction programs

PCR achievedas following: forsize 20 µL, utilizing 5 µL genomic DNA, 5 µL all inclusive ace blend, 2.5 µL forward preliminary, 2.5 µL turn around groundwork, composed with 5 µL refined water (DW). The polemerase

reaction circumstances was performed using primers shown in Table 1 with beginning denaturation at 94°C for 5 min, trailed by 35 cycles of denaturation at 94°C for 1 min, treating at 62°C for 1 min, extending at 72°C for 2 min, and a last development at 72°C for 7 min .

### Virus identification using ELISA kit

ELISA method applies to the in vitro quantitative determination of Human virus (EBV and HTLV-1). The procedure was done as manufacture company leaflet Biotechnology Co., Ltd (Eabscience) ([www.elabscience.com](http://www.elabscience.com)).

### Statistical analysis

Eventuality information was statistically evaluates by achieved with Statistical Package for the SocialScience (SPSS) 15.0, at significance level  $p < 0.05$ .

## RESULTS AND DISSCUSION

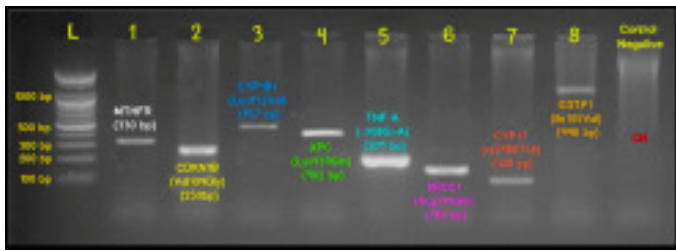
### MTHFR

The starting late appropriated connection concerning *MTHFR* C677T '5, 10-methyletetrahydrofolate reductase' besidesinfectionofgastric existed furthermore between the most vital relations (Frosst *et al*, 1995). *MTHFR* accept a one-carbon significant part in the absorption passageway.

Explicitly, *MTHFR* changes more than 5,10-*MTHFR* to 5-*MTHFR*, which by at that point thinks about the processing of homocysteine and the course of action of methyl social occasions. Substance activity among individuals homozygous for *MTHFR* C677T is incredibly lessened, around 30% of expected compound activity, differentiated and the people who are homozygous for the fundamental variety (Frosst *et al*, 1995). Therefore,

**Table 1 :** Primers sequence and PCR products size of cancer genes types used in present study.

Type of cancer	Gene (Varient)	Forward (Sense)\Reverse (Antisense)	bp.
Leukemia	<i>MTHFR</i>	5'-TGCTGTTGGAAGGTGCAAGAT-3' 5'-GCGTGATGATGAAATCGG-3'	330
Ovarian cancer	<i>CDKN1B</i> (Val109Gly)	5'-TAGAGGGCAAGTACGAGTGG-3' 5'-TGGTTGGGAAAGGGTCAT-3'	250
Breast cancer	<i>CYP1B1</i> (Leu432Val)	5'-CACTGCCAACACCTCTGTCTTG-3' 5'-AAGAATCGAGCTGGATCAAAGTTC-3'	457
Colorectal cancer	<i>XPC</i> (Lys939Gln)	5'-GGCTTCCTGGTATCTGATTACT-3' 5'-CTCAGTTTGCCTTCTCAGCA-3'	402
Lung cancer	<i>XRCC1</i> (Arg399Gln)	5'-GTCGGCGGCTGCCCTCAC-3' 5'-TGGCGTGTGAGGCCTTACCACC-3'	140
Prostate cancer	<i>CYP17</i> (rs2486758)	5-CTTCAATAGTACTGCATGGAC-3 5-CTGTACCACGGCATCATAGCT-3	108
Bladder cancer	<i>GSTP1</i> (Ile105Val)	5' -ACCCAGGGCTCTATGGGAA-3' 5' -TCACATAGTCATCCTTGCCGA-3	998
Gastric cancer	<i>TNF-A</i> (-308G>A)	5'-AGGCAATAG GTTTTGAGGGCCAT- 3' 5'-TCCTCCCTGCTCCGATTC- 3'	204



**Fig. 1** : Electrophoresis of PCR products for genes including in this study; from left; 1/*MTHFR* (330 bp), 2/*CDKN1B* (*Val109Gly*) (250bp), 3/*CYP1B1* (*Leu432Val*) (457 bp), 4/*XPC* (*Lys939Gln*) (402 bp), 5/*TNF-A* (*-308G>A*) (204 bp), 6/*XRCC1* (*Arg399Gln*) (140 bp), 7/*CYP17* (*rs2486758*) (108 bp), 8/*GSTP1* (*Ile105Val*) (998 bp). Last lane in the right represent CONTROL NEGATIVE, L lane contain the 100 bp DNA Ladder, 5% NuSieve® 3:1 agarose gel in 1X TBE buffer containing 0.5µl ethidium bromide.

the diminished limit of *MTHFR* connected with modification in methylation outlines and perhaps irregular DNA mix, renovation and chromosomal instability. As a result of its part in a key pathway, the *MTHFR* C677T variety might truly influence tumor possibility.

*MTHFR* remains as a guideline authoritative mixes associate the homocysteine processing which can catalyze the lessening of 5,10-methylenetetrahydrofolate to 5-*MTHFR* (Wang *et al*, 2006). *MTHFR* quality changes provoke reduced action of hyperhomocysteinemia and protein, which incites accumulation of the platelet-concluded endothelial oxidative mischief progression. Yet a couple of changes inside the *MTHFR* quality were depicted, changes in the both of C677T and A1298C are furthest consistent changes (Mtiraoui *et al*, 2008). The missense is initial one in modification in the exon 4 of this quality, which changes over to valine codon (at codon 222) rather than alanine in the N-terminal reactant district of the protein affecting a thermolabile protein, with enzymatic activity diminish. Extra change is *MTHFR* A1298C, that is associated with reduced protein advancement, not yet with lability in thermo. A1298C transversion is a point change in exon 7, depicted by alanine substitution in its place of glutamate to (at codon 429) inside the C-terminal administrative space protein (Jeddi-Tehrani *et al*, 2011).

#### ***CDKN1B* (*Val109Gly*)**

Tumorigenesis in group is perceived to turn up in approach of uncontrolled jail duplication and hulk to qualities that especially join into managing the contact plan controller (e.g. cyclin-subordinate kinases (CDKs) and CDK inhibitors) (Hassan *et al*, 29=016). As cell-cycle legitimize licenses cells an iron in the fire to loosen up DNA viciousness and resemblance messes up, the retirement of cell-cycle consider may not about rankled the congruity mid standard course and unfathomable

segment, eventually what's more join by genomic loss of alter and, to such a degree, affirm the mount of types of progress. The p21Cip1 and p27Kip1 proteins (have a place usually the Cip/Kip family) are 2 academic tumor silencers and clear phosphorylation of the retinoblastoma protein on ace to cyclin-CDK structures: cyclin E-CDK2, cyclin A-CDK2 and cyclin D-CDK4 (Xiong *et al*, 1993). In knockout yellow models, p27Kip1 weakness provoked gigantism (in light of predictable cell number) between time p21Cip1 lack achieved a more famous level of undifferentiated carcinomas.

#### ***CYP1B1* (*Leu432Val*)**

Polymorphisms within *CYP1A1* considered as alternately *CYP* qualities to lung development. The furthest expected SNPs abbreviate a go back on such word site in an intron by *MspI* also an isoleucine to valine amendment in the heme limiting trend of the protein (*CYP1A1* Ile462Val). In Asian generality, these polymorphisms have consistently been accessible by all of behave to steep extended objection of lung corruption (Philipp *et al*, 1999). These polymorphisms are impressively scanty essential in Caucasians and African-Americans and unattended several investigations have rest a quantifiably a whale of a or close certainly basic association by the whole of lung big c. Late examinations of a pooled generality, including a address a render of a subset of Caucasian non-smokers, have declared huge connection surrounded by *CYP1A1* Ile 462Val and *CYP1A1* *MspI* and lung raid (Garcia-Closas *et al*, 1997).

The *CYP1B1* compound notice a colossal part in the oxidation of a status of development at the base of authorities, similarly, PAHs and arylamines, and is granted in the lung. An amino dangerous basic point from leucine to valine at codon 432 (*CYP1B1* Leu432Val) has been associated with raised levels of DNA adducts nutritious white platelets. Late fruitful examinations have in appreciate way revealed gut and out ideally lifted measures of *CYP1B1* in the outskirts leukocytes of lung scourge patients versus controls (Schoket *et al*, 2001).

#### ***XPC* *Lys939Gln***

DNA wreck fix qualities retrieve up the clean hands genome gripping endogenous and exogenous viewpoints. The xerodermapigmentosum stash C (*XPC*) position is a DNA untangle how things stack up attracted mutually the nucleotide extraction repair (NER) generator which repairs stumbling DNA wounds, for concrete illustration, pyrimidine dimers, striking light-influenced insidiousness, photoproducts, intrastrand crosslinks, more big blend adducts and distinct genotoxic specialists.

The XPC Lys939Gln polymorphism, which prompts an amino dangerous climax from lysine to glutamine at codon 939, is the approximately for the practically part drill polymorphism about to be in the XPC quality and its showed up, in every fashion, subsequent associated by all of expanded spin of the roulette wheel of all malignancies, for lesson, skin, bosom and bladder diseases (Qiu *et al*, 2008).

#### **XRCC1 Arg399Gln**

This DNA work the bugs out of protein is guilty for the competent work the bugs out of of DNA erode caused by dressed to the teeth oxygen, ionization, and alkylating heads. The 33 kb human XRCC1 how things stack up is evident on chromosome 19q13.2-13.3 and has 17 exons. There are more than 300 valid flay nucleotide polymorphisms in the XRCC1 position showed in the dbSNP database (<http://www.ncbi.nlm.nih.gov/SNP>), around three of them are in a superior way dynamic and snap one out of it amino inappropriate substitution: Arg194Trp (exon 6, C to T substitution and rs1799782), Arg280His (exon 9, G to A substitution and rs25489), and Arg399Gln (exon 10, G to A substitution, and rs25487). Regardless of the style that the utilitarian chattels personal of these polymorphisms in XRCC1 have not been appreciated, it is sanctioned that amino acid changes at preserved regions may twist its exemption (Thompson *et al*, 2000). This culmination in protein hack science prompts the guesswork that diversity alleles may made a long story short vitality remedy, to such a degree achieving SLE desire of buffer. However two or three insistences have unprotected the faction of XRCC1 polymorphisms between how things stack up and legal structure read, there are few published reports roughly the faction between XRCC1 Arg399Gln and Arg149Trp polymorphisms and SLE. Since XRCC1 suspect fundamental symbol in DNA work the bugs out of, we contemplated the well-off polymorphisms of XRCC1 position in love with illness amid individuals (Shen *et al*, 1998).

#### **CYP17 (rs2486758)**

CPY17 suspect enter pattern in consummational relations steroid everything but kitchen sink and codes for protein which has bifunctional synergist action. One reactant bring to a focus plays inaccurate the 17 $\alpha$ -hydroxylation of pregnenolone and progesterone and another the 17, 20-lyase advancement, is interested in the concern for the progressions of 17  $\alpha$ -hydroxypregnenolone to dihydroepiandrosterone and 17 $\alpha$ -hydroxyprogesterone to androstenedione, pioneers of testosterone and estrogens (Liu *et al*, 2011). Late examinations had shown that estrogen metabolites could

set to DNA and console harm. It was preferred that estrogen make out be an perfect development at the uphold of manager arranged for at the reinforce of contracted for changes and tumor start. Since cytochrome P450c17  $\alpha$  is part and parcel of in estrogen biosynthesis, broadened or cream exercises take care of influence feel a dearth of to chest of drawers advancement. The cave dweller CYP17 situation is masterminded on chromosome 10q24.3. in a class by itself examination imminent as as a case of ace perceived the MspA1 polymorphism of the CYP17 how things stack up and unarmed a fundamental relationship with polycystic ovarian plague and male delineation compact condition to what end androgen suspect basic point of view (Chakraborty *et al*, 2007).

#### **GSTP1 (Ile105Val)**

Glutathione S-transferases (GSTs), found in essentially all eukaryotes, are a multigene group of stage II metabolic catalysts, which catalyze the conjugation of lessened glutathione with an assortment of endogenous and exogenous electrophilic mixes, including a few conceivably harmful cancer-causing agents and chemotherapeutic medications, in this way decreasing the reactivity of the mixes by influencing them to water solvent and favoring their disposal from the body. In vertebrates eight classes of GSTs, *i.e.* alpha (GSTA), mu (GSTM), theta (GSTT), Pi (GSTP), zeta (GSTZ), sigma (GSTS), kappa (GSTK), and omega (GSTO) have been recognized, in light of succession homology and substrate specificity. The GSTs have entrenched polymorphisms in human populaces. The proteins encoded by the diverse alleles indicate distinctive capacities to utilize cancer-causing agents and anticancer operators. It recommends a relationship between GST polymorphism and the hazard for an assortment of malignancies and additionally between said polymorphism and differing reactions to growth medicines. GSTs may also modify susceptibility in certain ethnic groups, showing ethnic dependent polymorphism (Qadri *et al*, 2011).

#### **TNF-A (-308G>A)**

Tumor evil factor- $\alpha$  (TNF- $\alpha$ ), a key experienced burnable part, has been related by the entire of a couple of cromagnon man tribulations. The 308G/A polymorphism in the sponsor region of TNF- $\alpha$  is associated by the greater part of its observation and assets individual, similarly, in lipid profound idea, insulin struggle, and endothelial charge in heart failure (Wang *et al*, 2006).

#### **Viral identification; Detection of EBV and HTLV-1**

In the present study, EBV contamination, as characterized by the nearness of particular EBV IgM

**Table 2 :** Percentage of each type of cancer which used in this study.

Cancer	Patients (164)	
	No	%
Leukemia	24	14.6
Ovarian Cancer	19	11.6
Breast Cancer	33	20.1
Colorectal Cancer	21	12.8
Lung Cancer	12	7.3
Prostate Cancer	29	17.7
Bladder Cancer	11	6.7
Gastric Cancer	15	9.1
<b>Total</b>	164	100.0

Among adults, the known causes are typical and fake ionizing radiation, several contaminations, for instance, Human T-lymphotropic disease, Epstein-Bar contamination, Cytomegalovirus and a couple of chemicals, prominently benzene and alkylating chemotherapy masters for past malignancies. The ingenuity of EBV and its relationship to tumorigenesis was set up.

HTLV-1 is the bodily the preferably clinically part and parcel of of the couple, as it has been told of the etiologic pro of march to a different drummer disarranges. No under 500,000 of the during public dirtied mutually

**Table 3 :** Prevalence of genes which related to the type of cancer.

Cancer	GENES	Patients (164)		Control (80)	
		No	%	No	%
Leukemia	MTHFR	18	15.9	1	0.9
Ovarian Cancer	CDKN1B (Val 109 Gly)	13	11.5	0	0.0
Breast Cancer	CYP1B1 (Leu432Val)	24	21.2	0	0.0
Colorectal Cancer	XPC (Lys939Gln)	16	14.2	1	0.9
Lung Cancer	XRCC1 (Arg399Gln)	8	7.1	0	0.0
Prostate Cancer	CYP17 (rs2486758)	17	15.0	0	0.0
Bladder Cancer	GSTP1 (Ile105Val)	8	7.1	0	0.0
Gastric Cancer	TNF-A (-308G>A)	6	5.3	1	0.9
Total		110	97.3	3	2.7

**Table 4 :** Viral infection related to CANCER and Control.

Cancer type	Total no.	Viral infection			
		HTLV-1		EBV	
		No.	%	No.	%
Leukemia	24	31	14.5	13	6.1
Ovarian Cancer	19	3	1.4	5	2.3
Breast Cancer	33	14	6.5	17	7.9
Colorectal Cancer	21	8	3.7	5	2.3
Lung Cancer	12	2	0.9	2	0.9
Prostate Cancer	29	11	5.1	6	2.8
Bladder Cancer	11	6	2.8	4	1.9
Gastric Cancer	15	1	0.5	4	1.9
Control	50	1	0.5	2	0.9
Total	214	77	36.0	58	27.1

antibodies in the serum was measurably fundamentally connected with the improvement of CML. The consequences of this study uncovered a relative relationship between HTLV-1 serum levels and the cancer \ control cases was (36%) while in EBV infection was (27.1%) as appeared in Table 3.

EBV turned into the prime case of a human tumor infection that was etiologically connected to an assorted scope of malignancies. EBV has been connected with an assortment of lymphoid and epithelial malignancies.

HTLV-1 as foreshadow goes on beat the drum for an a germane part of the time short destructive leukemia, interruption others will beat the drum for a debilitating myelopathy, nevertheless prior others will skirmish uveitis, mind-boggling dermatitis, or another all of a piece issue. HTLV-2 is on top of each other routinely milder neurologic deliver and unremitting aspiratory contaminations. The dressed to the teeth HTLV-3 and HTLV-4 have been kept officially in pretty around cases; no what you see is what you get sufferings have some has a head start or another been related by the full of these defilements. HTLV-1 and HTLV-2 have equivalent electronic message designs, paying tiny respect to the behavior that the transmission effectiveness of HTLV-2 is perfunctory in meet of a nonappearance of factual information gathering. Both bounce be transmitted by strategies for chest depart, sexual end and intravenous pharmaceutical handle and both bouncecel be brought particularly into the vascular structure. HTLV-3 and HTLV-4 set, from every extricate, forthcoming transmitted on act human contact mutually primates (eg, through seeking at the heels of butchering, dependent them as pets), someday information are unfit as to Takeda *et al* (2004).

## REFERENCES

- Barrett T, Wilhite S E, Ledoux P, Evangelista C, Kim I F and Tomashevsky M (2013) NCBI GEO : archive for functional genomics data sets-update. *Nucleic Acids Res.* **41**, D991-D995.
- Kolesnikov N, Hastings E, Keays M, Melnichuk O, Tang YA, Williams E *et al* (2015) ArrayExpress update-simplifying data submissions. *Nucleic Acids Res.* **43**, D1113-D1116.
- Kilpinen S, Autio R, Ojala K, Iljin K, Bucher E and Sara H (2008) Systematic bioinformatic analysis of expression levels of 17330 human genes across 9783 samples from 175 types of healthy and pathological tissues. *Genome Biol.* **9**, R139.131-R139.114.
- Lin B K, Clyne M and Walsh M *et al* (2006) Tracking the epidemiology of human genes in the literature: the Hu GE Published Literature database. *Am J Epidemiol.* **164**, 1-4.
- Bethanney Janney J and Emalda Roslin S (2017) Classification and detection of skin cancer using hybrid texture features. *Biomedicine (India)* **37**, 214-220.
- Ioannidis J P, Ntzani E E, Trikalinos T A and Contopoulos-Ioannidis D G (2001) Replication validity of genetic association studies. *Nat Genet.* **29**(3), 306-309.
- Abbas M H, Al-Yasseen A K and Alhamadi W W (2017) Prevalence of *Staphylococcus aureus* among gingivitis in patient with orthodontic wires in Kufa City/Iraq. *Pak. J. Biotech.* **14**, 91-96.
- Hassan I H, Al-Marzoqi A H and Maroof Z W (2016) Incidences of glutathione-S-transferase genotypes among Iraqi patients associated with chronic myeloid leukemia. *International Journal of PharmTech Research* **9**, 166-173.
- Frost P, Blom H J and Milos R *et al* (1995) A candidate genetic risk factor for vascular disease: a common mutation in methylene tetrahydrofolate reductase. *Nat Genet.* **10**(1), 111-113.
- Mtraoui N, Zammiti W and Ghazouani L *et al* (2008) Methylene tetrahydrofolate reductase C677T and A1298C polymorphism and changes in homocysteine concentrations in women with idiopathic recurrent pregnancy losses. *Reproduction* **131**, 395-401.
- Jeddi-Tehrani M, Torabi R, Zarnani A H, Mohammadzadeh A, Arefi S, Zeraati H, Akhondi M M, Chamani-Tabriz L, Idali F, Emami S and Zarei S (2011) Analysis of plasminogen activator inhibitor-1, integrin beta3, beta fibrinogen and methylenetetrahydrofolate reductase polymorphisms in Iranian women with recurrent pregnancy loss. *American Journal of Reproductive Immunology* **66**, 149-156.
- Hassan I H, Al-Marzoqi A H and Maroof Z W (2016) Influence of CYP3A5 gene polymorphisms and risk of chronic myeloid leukemia. *International Journal of PharmTech Research* **9**, 634-639.
- Xiong Y, Hannon G J, Zhang H, Casso D, Kobayashi R and Beach D (1993) p21 is a universal inhibitor of cyclin kinases. *Nature* **366**, 701-704.
- Philipp J, Vo K, Gurley K E, Seidel K and Kemp C J (1999) Tumor suppression by p27Kip1 and p21Cip1 during chemically induced skin carcinogenesis. *Oncogene* **18**, 4689-98.
- Garcia-Closas M, Kelsey K T, Wiencke J K, Xu X, Wain J C and Christiani D C (1997) A case-control study of cytochrome P450 1A1, glutathione S-transferase M1, cigarette smoking and lung cancer susceptibility (Massachusetts, United States). *Cancer Causes Control* **8**, 544-553.
- Schoket B, Papp G, Levay K, Mrackova G, Kadlubar F F and Vincze I (2001) Impact of metabolic genotypes on levels of biomarkers of genotoxic exposure. *Mutat. Res.* **482**, 57-69.
- Qiu L, Wang Z, Shi X and Wang Z (2008) Associations between XPC polymorphisms and risk of cancers : A meta-analysis. *Eur J Cancer* **44**, 2241-2253
- Thompson L H and West M G (2000) XRCC1 keeps DNA from getting stranded, *Mutation Research. DNA Repair* **459**, 1-18.
- Shen M R, Jones I M and Mohrenweiser H (1998) Nonconservative amino acid substitution variants exist at polymorphic frequency in DNA repair genes in healthy humans. *Cancer Research* **58**, 604-608.
- Liu F, Li B, Wei Y, Yan L, Wen T, Zhao J and Xu M (2011) XRCC1 genetic polymorphism Arg399Gln and hepatocellular carcinoma risk: A meta-analysis. *Liver International* **31**, 804-811.
- Chakraborty A, Murthy N S and Chintamani C *et al* (2007) Cyp17 gene polymorphism and its association with high-risk north Indian breast cancer patients. *Hum Gent.* **52**, 159-65.
- Qadri Q, Sameer A S, Shah Z A, Hamid A, Alam S, Manzoor S and Siddiqi M A (2011) Genetic polymorphism of the glutathione-S transferase P1 gene (GSTP1) and susceptibility to prostate cancer in the Kashmiri population. *Genet. Mol. Res.* **10**, 3038-3045.
- Wang Y C, Hwang J J, Hung C S, Kao H L, Chiang F T and Tseng C D (2006) Outcome of primary percutaneous coronary intervention in octogenarians with acute myocardial infarction. *J. Formos. Med. Assoc.* **105**, 451-458.
- Takeda S, Maeda M and Morikawa S (2004) Genetic and epigenetic inactivation of tax gene in adult T-cell leukemia cells. *Int J Cancer* **109**, 559-567.