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Application of the yeast comet assay in testing some food additives for genotoxicity by comet assay in yeast

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Abstract

Food additives of various types are frequently used in the food sector. Their use is justified by the need to preserve, color, or sweeten a variety of foods. Despite the fact that some additives have been demonstrated to be cytotoxic, they are nevertheless utilized in practice. The effects of monosodium glutamate (MSG), sodium benzoate (SB), and saffron on several yeast haploid knockout strains were studied in this study (YKO). We used the Comet test method to find the optimum amounts at which this set of dietary additives could cause DNA damage. Three regularly used dietary additives were found to efficiently damage DNA. We also evaluated the sensitivity of higher eukaryotic cells to the genotoxic effects of these chemicals with yeast. The comet assay exhibited a better sensitivity of yeast cells, which was undeniably confirmed. The genotypes of haploid (knockout) yeast strains were chosen based on the (Clustal Omega Multiple Sequence Alignment EMBL-EBI) alignment of human and yeast gene sequence homology.

Keywords: YKO, MSG; saffron, SB, Comet assay, genotoxic

1. Introduction

Yeast is a type of organism that lives Saccharomyces cerevisiae is an essential microbial bioreactor for the generation of added-value compounds and biofuels, and it remains a highly relevant experimental model in toxicogenomics. Purir is at the forefront of systems and synthetic biology, as an instrumental tool for obtaining mechanistic insights into the response to multiple toxicants and in the event of strong industrial strains, thanks to its deep functional characterization combined with the straightforward exploitation of Omic approaches and metabolic engineering.

Various additives have been used in the food industry for hundreds of years. Originally, they were only used to preserve food by pickling (with vinegar), salting, or adding sulphur dioxide (as in some wines). After that, some chemicals and supplements are used to improve the style and appearance of the dish. Several chemicals have been shown to be harmful and have been banned from use as food preservatives, such as furylfuramide (AF-2), which has been banned since 1974 after being found to be carcinogenic in both experimental animals [10] and humans [25]. Similarly, numerous radical chemicals, including Butter yellow, were discovered to have undeniable genotoxic and carcinogenic activity in experimental animals [6]. Despite the fact that food additives are dangerous, they are still used.

Surprisingly, several chemicals and prescription medications have modest toxicity, but at low doses, they can cause certain genotoxicity [18]. Genotoxins may alter DNA through direct cleavage or chemical group modifications in DNA. The majority of polymer damages are unquestionably harmful to both the cell and the organism as a whole. They have the potential to cause cell death or to enhance carcinogenic processes [1].

Several approaches for detecting genotoxicity have been developed [12,13]. However, none of them found any damage to the DNA structure per se. Furthermore, many of these procedures are timeconsuming, costly, and necessitate a large number of cells.

Single Cell Gel Electrophoresis (SCGE), often known as the Comet Assay, has grown in popularity

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as a genotoxicity test [17, 21]. The technique allows imaging and measurement the for of deoxyribonucleic acid damage at the single-cell level in a simple, rapid, and repeatable manner [5]. Wherever fragmented deoxyribonucleic acid exits the remaining nucleoid and produces an extraterrestrial comet tail, electrical is applied to cells implanted in agarose during this assay. The resulting can be easily quantified using either visual scoring of the comets or software [27].

The Comet Assay method was modified to work with yeast cells. Saccharomyces cerevisiae cells were shown to be more sensitive to the action of alkyl paraffin salt and oxide than class cells [16]. The Comet Assay's findings of increased sensitivity of S. cerevisiae to irradiation [4], oxidative damage during replicative ageing [15], and Cr-(III)-organic compounds [3] were further confirmed [20, 2].

The goal of this study was to see if three food additives (mono sodium glutamate (MSG), sodium benzoate (SB), and saffron) had any mutagenic or carcinogenic effects on yeast haploid knockout strains (YKO).

2. Materials and Methods 2.1. Materials

2.1.1. Yeast Saccharomyces cerevisiae (haploid strain)

Knock out haploid yeast strains (Mat-A) Complete Set (Cat. no. 95401.H2), were bought from Invitrogen company (1600 Faraday Avenue PO Box 6482, Carlsbad CA, 92008 United States).

2.1.2. Food additives

Three differing kinds of food additives MSG, SB and Saffron were employed in this study [obtained from Sigma Chemical Company, St. Louis, USA].

2.2. Methods

2.2.1. Yeast Comet assay (YCA)

The in vitro Comet assay was performed using the first procedure published by [23]. We used yeast culture media with the optimal MSG dosage of 0.5 mg/ml. SB was added in triplicates at the optimal dosage of 0.05 mg/ml, and saffron was added at the optimum concentration of 1 mg/ml. A medium without chemical components was also employed as

an untreated control. 1 g of crushed materials were placed in a one-cubic-centimeter container with cold PBS.

This suspension was filtered after five minutes of stirring. 100 g of cell suspension was combined with 600 g of low-melting agarose (0.8 percent in PBS). On pre-coated slides, one hundred percent of this mixture was spread out. For fifteen minutes, the coated slides were immersed in lyses buffer (0.045 M TBE, pH 8.4, containing a pair of .5% SDS). The slides were placed in an activity chamber with a same TBE buffer but no SDS. Two V/cm for two minutes and one hundred mA were the activity conditions. Ethidium bromide 20g/m1 staining at 4°C.

The polymer fragment migration patterns of one hundred cells for each exposure level were analysed with a visible radiation magnifier while the samples were still moist (With excitation filter 420-490nm [issue 510nm]). The tail lengths of extraterrestrial objects were measured from the nucleus to the top of the tail with a 40x increase to count and measure the comet's size. Observations of Gel Red-stained polymer were done using a 40x objective on a fluorescence magnifier to visualise polymer damage. By measuring the length of polymer migration and the proportion of migrated polymer, an extraterrestrial object five image analysis developed by Kinetic Imaging, code Ltd. (Liverpool,UK) connected to a CCD camera was used to assess the quantitive and qualitative extent of polymer injury within the cells. The program then estimated the tail moment. In most cases, fifty to one hundred randomly selected cells were evaluated per sample. This study looked at the effects of three popular food additives on yeast cells: MSG, SB, and saffron.

2.2.2. knockout yeast strains of choice

Two plates containing two haploid knockout strains with completely distinct genotypes were used in this investigation, and the sequences of each strain were chosen and aligned with human sequence information in NCBI (The National Center for Biotechnology Information). four genes aligned with cancer-related human genes were chosen to correspond with the yeast genes used in this investigation (Table 1).

Table (1). Selected	Table (1). Selected yeast genes which matched with cancel related human						
Selected strains	Selected genes of yeast strains (genotypes)	Homologous genes in human					
YMR035W	IMP2	IGF2BP2					
YMR190C	SGS1	RECQL					
YMR167W	MLH1	MLH1					
YER095W	RAD51	RAD51					

Table (1): Selected yeast genes which matched with cancer related human

2.2.3. selection of yeast haploid strains deficient in genes similar to human cancer genes

The genotypes of yeast haploid (knockout) strains were chosen based on (Clustal Omega Multiple Sequence Alignment EMBL-EBI) alignment between human and yeast sequence sequence similarity, as well as the question cowl and E-value Table (1).

2.2.4. Protein-protein interaction prediction

In accordance with the sequence, the interaction network was used. MANIA (http://www.genemania.org) is a flexible, userfriendly web interface for evaluating gene function hypotheses, examining sequence lists, and prioritising genes for specific experiments.

Sources of information

3. Results and Discussion

Co-expression information from the organic phenomenon Omnibus (GEO); physical and genetic interaction information from Bio GRID; foretold macromolecule interaction information supported by orthology from I2D; and pathway and molecular interaction information from Pathway Commons, which includes data from Bio GRID, Memoria, and Pathway Commons.

Yeast protein-protein interaction network, Human protein-protein interaction network

(A) (B) (C) (D) (E) (F) (F) (H)

Fig. 1: Photomicrographs showing DNA damage in yeast strains using the Comet assay and MSG at a dose of 0.5 (g/ml). Control cells A: control MLH1 gene; B: treated MLH1 gene; C: control IMP2 gene; D: treated IMP2 gene; E: control RAD51 gene; F: treated RAD51 gene; control SGS1 gene; H: treated SGS1 gene; control SGS1 gene.

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3.1. Toxicity to (YKO) strains tested with monosodium glutamate by extraterrestrial object assay

All three chemicals displayed varying degrees of yeast significant genotoxic effects on YKO in accordance with the extraterrestrial object assay. At the optimum dose of zero.5 g/ml, monosodium glutamate revealed its genotoxic effect (recommended by FDA). The genotoxic effects of the IMP2, RAD51, and SGS1 genes were severe, whereas the genotoxicity of the MLH1 sequence was low. The distribution of the share of determined comets for monosodium glutamate was shown in Table (2).

It should be noticed that the yeast predicted significantly more comets than the various management for each of the four tested genes (Fig. 1), indicating that the tested drug caused a large number of identified desoxyribonucleic acid damages. To be more precise in contrast to the strategies, we have a tendency to accept the optimal concentration as a live of sensitivity at that twice a lot of comets appear in treated culture as compared to management.

The cells that had been exposed to twenty-five metric linear units of monosodium glutamate were each given a pre-treatment with a concentration of zero.5 g/ml of monosodium glutamate. It was clear that monosodium glutamate therapy caused significant damage to each of the four genes evaluated.

Group	Tailed %	Untailed %	Tails length µm	Tail DNA%	Tail moment
Control MLH1	2.5	97.5	2.02±0.21c	1.81	3.66
MLH1	18	82	6.93±0.53 b	5	34.65
Control IMP2	2	98	1.73±0.17d	1.72	2.98
IMP2	24	76	8.37±0.79a	6.8	56.92
Control RAD51	3	97	2.19±0.23c	1.9	4.16
RAD51	26	74	8.82±0.84a	7.45	65.71
Control SGS1	1.5	98.5	1.32±0.12d	1.48	1.95
SGS1	29	71	9.5±0.90a	8.17	77.62

Table (2): Image analysis of comet assay parameters in cells of all groups after MSG therapy.

Different superscript letters in the same column of tail length showed significance difference at P < 0.05.

3.2. Toxicity of SB to (YKO) strains as determined by extraterrestrial object assay

At the optimum dose of zero.1 g/ml, SB revealed its genotoxic action. Table 1 shows that the IMP2 sequence has a significant genotoxic impact, while the MLH1, RAD51, and SGS1 genes have moderate genotoxicity (3). It was discovered that the yeast predicted significantly more comets than the various

management for each of the four examined genes, when the tested drug caused a lot of desoxyribonucleic acid damage (Fig. 2). Each of the management and treated cells that had been exposed to twenty-five metric linear units of SB received an additional pre-treatment with zero.1 g/ml of SB. It was clear that SB therapy caused significant harm to all four genes evaluated.



Fig. 1: Assay of a comet Photomicrographs demonstrating DNA damage in yeast strains after treatment with SB at a dose of 0.1 (g/ml). Control cells A: control MLH1 gene; B: treated MLH1 gene; C: control IMP2 gene; D: treated IMP2 gene; E: control RAD51 gene; F: treated RAD51 gene; control SGS1 gene; H: treated SGS1 gene; control SGS1 gene.

Group	Tailed %	Untailed %	Tails length µm	Tail DNA%	Tail moment
Control MLH1	3	97	2.21±0.21c	1.97	4.35
MLH1	15	85	6.34±0.39 b	4.42	28.02
Control IMP2	2.5	97.5	2.09±0.15c	1.86	3.89
IMP2	25	75	8.6±0.58 a	7.11	61.15
Control RAD51	1.5	98.5	1.29±0.10c	1.42	1.83
RAD51	16	84	6.51±0.42 b	4.6	29.95
Control SGS1	1	99	1.03±0.06c	1.17	1.20
SGS1	17	83	6.72±0.41 b	4.81	32.32

Table (3): Image	analysis of comet	assay parameters in	cells from all gr	oups following SB treatme	ent.
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Different superscript letters in the same column of tail length showed significance difference at P< 0.05.

3.3. Saffron revealed its genotoxic action at the optimum dose of one g/ml when tested with (YKO) strains using an extraterrestrial object assay.

The SGS1 sequence had a significant genotoxic effect, whilst the MLH1 and IMP2 sequences had mild genotoxicity and the RAD51 gene had quantifiable genotoxicity (Table 4). For each of the four genes evaluated, the yeast predicted much more comets than the various management. Moreover, Fig. (3) revealed that the tested chemical caused a

significant amount of desoxyribonucleic acid damage. To be more precise in comparison to the strategies, we have a tendency to accept the optimum concentration as a live of sensitivity at that double a lot of comets appear in treated culture compared to management, untreated culture compared to management. The cells that had been exposed to twenty-five metric linear units of Saffron and the cells that had been exposed to one (g/ml) of Saffron. It was proven that each of the four genes studied had unmasked significant harm as a result of Saffron treatment.

Table (4): Image analysis of comet	assav parameters in cells of a	all groups followin	g saffron therapy.

	9 1	7 I		<u> </u>	9
Group	Tailed %	Untailed %	Tails length µm	Tail	Tail
				DNA%	moment
Control MLH1	3.5	96.5	2.31±0.20d	2.10	4.86
MLH1	15	85	6.56±0.40b	4.51	29.59
Control IMP2	4	96	2.51±0.19d	2.13	5.35
IMP2	17	83	6.80±0.44b	4.79	32.57
Control RAD51	4	96	2.62±0.23d	2.17	5.69
RAD51	12	88	5.35±0.46c	3.93	21.03
Control SGS1	3.5	96.5	2.32±0.21d	2.17	5.03
SGS1	24	76	8.45±0.57a	6.82	57.629

Different superscript letters in the same column of tail length showed significance difference at P < 0.05.



Fig. (3): Shows a comet assay. Photomicrographs demonstrating DNA damage in yeast strains after treatment with saffron at a dose of 1 (g/ml). Control cells A: control MLH1 gene; B: treated MLH1 gene; C: control IMP2 gene; D: treated IMP2 gene; E: control RAD51 gene; F: treated RAD51 gene; control SGS1 gene; H: treated SGS1 gene; control SGS1 gene.

3.4. Selection of yeast haploid strains devoid of genes similar to specific human cancer genes in vitro.

Genotypes of yeast haploid (knockout) strains were determined based on sequence similarity results between human and yeast sequences (E-value and question covery). Figure (4) depicted the results of an alignment between the human IGF2BP2 and the yeast IMP2 sequences, with a question cowl of hour and an E-value of 3e-150. IMP2 was found to play a role in the chemical change monetary unit of the mitochondrial inner membrane enzyme complex; [14] it is required for the maturation of mitochondrial proteins in the inter membrane space; [11] it has two chemical change subunits (Imp1p and Imp2p, which differ in substrate specificity) [19].

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Score 15.8 bits(29)	Experies 3.1	ct Method Compositional matrix adjust.	Identities 55%	Positives 13/23(56%)	Gaps 1/23(4%)
X61928.1IMP2 KJ900814.1IC	2yea SF2B	GGTCGACGAACCAAAGCTGTTGC-CC GTTCGTTGCAACAAA-TTGATGAGCA	AGGTAATACT	TGCAATTCAGG TATAATGCCAA	
X61928.1IMP2 KJ900814.1IC	2yea 3F2B	GTATTCCGAGGGAAGCATTTCCTGCA GTTGGCATGAACAAGCTTTACATCG	AGCCACTGAG		TCCAGCTTGTGATG -CCGCCGACG **. * **.*
X61928.1IMP2 KJ900814.1IC	2yea SF2B	AC-CTC-CGGCA-GCT	ACCTTCTAGO	GACCAGGAAG- GGACAGGAAGC	AGGCGGTG TGCCCCTGGCGG-G
X61928.1IMP2 KJ900814.1IC	2yea SF2B	ACAGGTCCTGCTGCAAGCTTC		ACTCCCATCA	GCCCGTTAACCATG GACCAGAACTGG * ** .* * *
X61928.1IMP2 KJ900814.1IC	2yea SF2B	GCGATCGACGACGCAGTAGCGTGCGG GCCATCCG-CGCCATCGAGACCCT	GGTCGGGGGTC	AGAACAGTGCG	ATATCAACGTAGTG ATTGCATGGGAAAA
X61928.1IMP2 KJ900814.1IC	2yea 3F2B	TACTTGTGAAGATGATACTTGATTCT T-CATG-GAAGTTGATTACTCAGTCT	IGTGAATGGC ICTAAAAAGC	TAGTGACGATTO TAAGGA-GCAG	GGAAGTCCAGCGTT GAAAATTCAG *.**.*.**
X61928.1IMP2 KJ900814.1IC	2yea SF2B	GTCTGCGTATCGAAGATACGTTTCAC ATTCGAAACATCCCTCCTCAC * ** * *. * *	CGGCGTAGAG CTGCAGTG-G	GAAGGTGGCGT GGAGGTGTTGG	GCGGCCAATCTACA ATGGACTTTTGGCT
X61928.1IMP2 KJ900814.1IC	2yea 3F2B	CGATCCAGAGACACTTTCTTTGCTCGT CAAT-ATGGGACAGTGC	AGAATG-TG		CGTTCTTTTGCACT CACAGACACAGA
X61928.1IMP2 KJ900814.1IC	2yea SF2B	AACCGCCGTTGTCAACGTCACATA	TTAAGAAAG ATGCAACAAG * * ***	AGAAGAAG	CGGAAAAAAGGCTT C-AAAAATAGCCAT * _**** ** * *
X61928.1IMP2 KJ900814.1IC	2yea 5F2B	GATCAAACACAAGAGACTATTGAAAA GGAGAAGCTAAGCGGGCATCAA * ** * * * * * * * * *	GGGTGAGTACO	CAAAAGAACCA TACTCCT .* **	ACAAGAGAAACAAC TCAAGATTTCCTAC
X61928.1IMP2 KJ900814.1IC	2yea 5F2B	CAAGTACGCAATGCAGAAGAG ATCCCGGATGAAGAGGTGAGCTG .* * .*** ***.* *	CATATTGCTC CCCCTTCGCCC	GACTAAACTGA	CGGAAAACAATC CCCAGCGTGGGGAC *.* · · · · *
X61928.1IMP2 KJ900814.1IC	2yea 3F2B	GAATCTACACAGCATCAAAACGGAAA CACTCTTCCCGGGAGCAAGGCCA	ACGCCACCACG	GGTGGAGTTCG GGGGCACT	ACTCGGAGCAGATG TCTCAGGCCAGACA
X61928.1IMP2 KJ900814.1IC	2yea 3F2B	GAAAGGGGCCACAG-GGAAAGAGG GATTGATTTCCCGCTGCGGATCCTGG	TCCCCACCC	GAAGAAAAGAG AGTTTGTTGGT - · · * ·	GCGAACGAGACTCA GCCATCATCGGA
X61928.1IMP2 KJ900814.1IC	2yea 3F2B	AACGTGAGC-AGTCTGTCGCGGT AAGGAGGGCTTGACCATAAAGAACAT ** * *.** * ** *		GGGCCAGTAGC	CGCAGCAGAGTAAG CG-GGTAGATATCC
X61928.1IMP2 KJ900814.1IC	2yea 3F2B	GGAGGAAGAGTTCCTCAAGTGGACCO ATAGAAAAGAGAAACTCTGGAGCTC . **.** *** .* *	CAGAGAAGCO	AGGAC-CCCTC	GATGCGGTTGAGGG CATGCCA ****
X61928.1IMP2 KJ900814.1IC	2yea 3F2B	TCGTGGATGTGGATTCTGAAG CCCCAGAGGGGGACTTCTGAAGCATGC .*** * * . *******	AGGAAGGTGA	AGGGCAACGAC	GAAGATGACGACGA GCAGAAAGAGGCAG * *** ·· *·*··
X61928.1IMP2 KJ900814.1IC	2yea 3F2B	CGGCGACGGCGACGATATGGACGAGG ATGAGACCAAACTAGCCGAAG	AAGAGTCCG	ATGAAGAGCAA CTGAAAATCTT ****	GTGA-GCGAT GGCACACAATGGCT * * .*.**
X61928.1IMP2 KJ900814.1IC	2yea 5F2B	ATAGAGAACGATTTAGAGATTGA TGGTTGGAAGACTGATTGGAAAAGAA *.**** . ****		CCACTACGATC TTGAAGAAAAAT	TGGGCATGAAAGTG TGAACATGAAACAG
X61928.1IMP2 KJ900814.1I0	2yea GF2B	GGACCAAGATAACAATCTCATCTT-	ATGAAGTGCT	AGGATTTGAGC	AAGCCCTGGA ATATACAACCCGGA
X61928.1IMP2 KJ900814.1I0	2yea GF2B	TAGCCAAGTACGAGATCAGCATCA AAGAACCATCACTGTGAAGGGCA-CA	GTGGCC- GTTGAGGCC1	ACGAAAAC IGTGCCAGTGCI .* **	-GAAGGCGTGTCTC FGAGATAGAGATTA
X61928.1IMP2 KJ900814.1I0	2yea GF2B	TGGAGCAACTCGACG-GAGG-CTACG TGAAGAAGCTGCGTGAGGCCTTTC **.** *.** .** **** ** .*		IGC-AACTACTO IGCTGGCTGTTA	ACCAAGGGTGCCG
X61928.1IMP2 KJ900814.1I0	2yea GF2B	GCGCAGAGGCGGGGGAACCAAAGGTCC GC-CAATCTGATCCCAGGG	TTGAACCTCA	ACACGGACCTO	SAGCAGCGAGTCCA
X61928.1IMP2 KJ900814.1I0	2yea GF2B	CC-TACGCCCTGACCTATCTCATGGC CAGGACTGTCCGTGCTATCTCC4 * ** .*.* *******	CGCAGCTGTC C-CAGCAGGC	CAACCAGGGAGA GCCCCGCGGAG ** - ****	ACACCGTCTACATT -CTCCCCCCGCT * ** *. **
X61928.1IMP2 KJ900814.1I0	2yea GF2B	GTCCACTGGGAGCCC-TCGAAGCCCA GCCCCCTACCACCCCTTCACTACCCA *.** **. * *** ******	ACGGACGACTO ACT	CCAGATG-TTO CCGGATACTTO	CGCCAACGTTGCCA CTCCAGCCT * *** ***
X61928.1IMP2 KJ900814.1I0	2yea GF2B	GAATCAGAAAGCACGTCATGCACCTC GTACCCCCATCACCAC	attractact	G-TCGCGGGCGT GTTCCCGCAT	IGCTGCACGA I-CATCACTCTTAT * * *** -
X61928.1IMP2 KJ900814.1I0	2yea GF2B	CCTGCACGTCGTCGT-CCTCTCT CCAGAGCAGGAGATTGTGAATCTCT ** *** * .*.** ****.*	TGACCCAT-O	CGTACCCAAA CAGGCTGTGGG	ACACCTCCTCAACG SCGCCATCATCG .*.** *** **
X61928.1IMP2 KJ900814.1I0	2yea GF2B	AGATGATCCACGGCCTCAAGC GGAAGAAGGGGGGCAC-ACATCAAACA	CAGTCGCCC AGCTGGCGAGA	TGTGCTGCTGCTCC TTCGCCGGAG	CTCTCGGTCATCC

X61928.1IMP2yea	TGTCCACT-CTGCAGAAACTTCGTCTGC-TCTGTGCCCATCCTCG-CGGTTAGAAAG
KJ900814.1IGF2B	TTGCCCCTGCGGAAAGGCCCAGAAGGCGCAGCGAAAGGATGGTCATCATCACCGGGCCACCGG
X61928.1IMP2yea	AAGCTGAAACGTGCCAAGGCGCCAAGGGCC-ATCAGCGAGTGACCAATAATCACTGCAGTAA
KJ900814.1IGF2B	AAGCCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAA
X61928.1IMP2yea	TTCCTTTTTAGCAACACATACTTATATACAGCAACAGAC-CTTATGTCTTTTCCTGCTC
KJ900814.1IGF2B	AACTTCTTTAACCCCAAAGA-AGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTC
X61928.1IMP2yea	CGATACGTTATCCACCCAACTTTATTTCAGTTTTGGCAGGGGGGAATTTCACAA
KJ900814.1IGF2B	C-AC-AGCTGGCCGGGTGATTGGCAAAGGTGGCAAGAACCGAACCGAACTGCCAGAA
X61928.1IMP2yea	CCCGCACGCTAAAAATTGTATTTAAACTTAAAAAAGAACAGCCACAAATAGGGAAC
KJ900814.1IGF2B	CTTAACCAGTGCAGGAAGTCATCGTGCCCCGTGACCAAAC-GCCAGATGAAAATGAGGAA-
X61928.1IMP2yea KJ900814.1IGF2B	TTTGGTCTAAAGCAAGGACTCTCCCTCCCTTATCTTGACCGTGCTATTGCCATCACTGCT -GTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAG-ACTGC- ************************************
X61928.1IMP2yea	ACAAGACTAAAATACGTACTAATATATGTTTTCGGTAACGAGAAGAAGAAGACGCGCCGGTGCA
KJ900814.1IGF2B	ACAGCGCAAGATCAGGGAAAATTGT
X61928.1IMP2yea KJ900814.1IGF2B	GCTGCTGCCATGGCCACAGCCACGGGGACGCTGTACTGGATGACTAGCCAAGGTGATAGG GAAATACCCTCAGG GAGTCGCCTCAC
X61928.1IMP2yea	CCGTTAGTGCACAA-TGACCCGAGCTACATGGTGCAATTCCCCACCGCCGCTCCACCG
KJ900814.1IGF2B	CAGCAAGTGCCCCAACTTTCTTGTACAAAGTTG-GCATTATAAGAAAGCATTGCTTATCAA
X61928.1IMP2yea	CAGGTCTCTA-GA
KJ900814.1IGF2B	TTTGTTGCAACGAAC
	. **. * * **

Fig. (4): Gene alignment between human gene IGF2BP2 and yeast gene IMP2 in the Clustal Omega web site ('*' indicates identical between two aligned, '-' indicates gaps missing of one) and ('.' indicates low similarity, ':' indicates more similarity used to denote the level of similarity that are not identical) at position

Figure (5) depicted the results of an alignment between the human and yeast MLH1 sequences, with a question cowl of 99% and an E-value of 7e-170. According to its own role in the sequence, MLH1 is required for pair repair in cellular division and meiosis; it is also required for biological processes during meiosis; it forms a posh with Pms1p and Msh2p-Msh3p during pair repair; and its human homolog is linked to hereditary non-polyposis carcinoma [24]. Pair repair defects produce increased spontaneous mutation rates and parabolic instability of simple repeating sequences, whereas mutations in human pair repair genes cause hereditary nonpolyposis body part malignancies [8].

Score	Expec	t Method		Identities	Positives	Gap:s
496 bits(1278)	7e-17	0 Composition	al matrix adjust.	294/788(59%)	454/788(57%)	62/788(7%)
DQ356646.1M KR709638.1M	LH1y LH1H	GTTCGTTGCAAC	AAATTGATGAG	AATGCTTTTTA	ATGTC-TCTC TAATGCCAACTT	AGAATAAAA TGTACAAAAAAA * *.****
DQ356646.1M KR709638.1M	LH1y LH1H	TTGGCATGTCGT	TCGTGGCAGGGG	GTTATTCGGCGGC	TTGATGCATCAG TGGACGAGACAG	TGGTTAACAAAA TGGTGAACCGCA
DQ356646.1M KR709638.1M	LH1y LH1H	TTGCTGCAGGTG TCGCGGCGGGGGG *.** **.** *	AGATCATAATAT AAGTTAT	TCCCCCGT TCCAGCGGCCAGC	AAATGCTCTCAA TAATGCTATCAA	AGAAATGATGGA AGAGATGATTGA
DQ356646.1M KR709638.1M	LH1y LH1H	GAATTCCATCGA GAACTGTTTAGA	TGCGAATGCTAG	CAATGATTGATAT CAAGTATTCAAGT	TCTAGTCAAGGA GATTGTTAAAGA	AGGAGGAATTAA GGGAGGCCTGAA ·***** ***
DQ356646.1M KR709638.1M	LH1y LH1H	GGTACTTCAAAT GTTGATTCAGAT	CCAAGACAATGO	GATCTGGAATTAA GCACCGGGATCAG	TAAAGCAGACCT GAAAGAAGATCT	GCCAATCTTATO GGATATTGTATO
DQ356646.1M KR709638.1M	LH1y LH1H	TGAGCGATTCAC TGAAAGGTTCAC	GACGTCCAAATI	TACAAAAATTCGA TGCAGTCCTTTGA ***. ****	AGATTTGAGTCA	G-ATTCAAACGT GTATTTCTACCT
DQ356646.1M KR709638.1M	LH1y LH1H	ATGGATTCCGAG ATGGCTTTCGAG	GAGAAGCTTTAG GTGAGGCTTTGG	SCCAGTATCTCAC	ATGTGGCAAGAG ATGTGGCTCATG	TCACAGTAACGA TTACTATTACAA
DQ356646.1M KR709638.1M	LH1y LH1H	CAAAAGTTAAAG CGAAAACAGCTG	AAGACAGATGTC	GCATGGAGAGTTT GCATACAGAGCAA	CATATGCAGAAG GTTACTCAGATG	GTAAGATGTTGG GAAAACTG * **. *
DQ356646.1M KR709638.1M	LH1y LH1H	AAAGCCCC	AAACCTGTTGCT	IGGAAAAGACGGT IGGCAATCAAGGG	ACCACGATCCTA	GTTGAAGACCTT GTGGAGGACCTT

DQ356646.1MLH1y KR709638.1MLH1H	TTTTTCAATATTCCTTCTAGATTAAGGGCTTTGAGGTCCCATAATGATGAATACTCTAAA TTTTACAACATAGCCACGAGGAGAAAAGCTTTAAAAAATCCAAGTGAAGAATATGGGAAA
DQ356646.1MLH1y KR709638.1MLH1H	ATATTAGATGTTGTCGGGCGATACGCCATTCATTCCAAGGACATTGGCTTTTCTTGTAAA ATTTTGGAAGTTGTTGGCAGGTATTCAGTACACAATGCAGGCATTAGTTTCTCAGTTAAA ** **.** *****.** *.** ***. ·· ·*.****.**
DQ356646.1MLH1y KR709638.1MLH1H	AAGTTCGGAGACTCTAATTATTCTTTATCAGTTAAACCTTCATATACCGTCCAGGATAGG AAACAAGGAGAGACAGTAGCTGATGTTAG-GACACTACCCAATGCC-TCAACCGT ** ***** * * ** *.** * *** **.** **.
DQ356646.1MLH1y KR709638.1MLH1H	ATTAGGACTGTGTTCAATAAATCTGTGGCTTCGAATTTAATTACTTTTCATATCAG GGACAATATTCGCTCCATCTTTGGAAATGCTGTTAGTCGAGAACTGATAGAAATTG **** .*.** * **** *** .* **** *** *** *
DQ356646.1MLH1y KR709638.1MLH1H	CAAAGTAGAAGATTTAAACCTGGAAAGAGTTGATGGAAAGGTGTGTAATTTGAATTT -GATGT-GAGGATAAAACCCTAGCCTTCAAAATGAATGGTTACATATCCAATGCAAACTA .* ** **.*** ** ***.* ** ***.* *.*** * .**** * .****
DQ356646.1MLH1y KR709638.1MLH1H	CATATCCAAAAAGTCCATTTCACCAATTTTTTTCATTAATAATAGACTAGTGACATGTGA CTCAGTGAAGAAGTGCATCTTC-TTACTCTTCATCAACCATCGTCTGGTAGAATCAAC * .* . **.**** ** ** .* * .* .* .* * **.*** **
DQ356646.1MLH1y KR709638.1MLH1H	TCCTCTAAGAAGAGCTTTGAACAGTGTTTACT-CCAATTATCTGCCAAAGGGCAACAG TTCCTTGAGAAAAGCCATAGAAACAGTGTATGCAGCCTATTTGCCCAAAAAACACACA *.**.*****************
DQ356646.1MLH1y KR709638.1MLH1H	ACCTTTTATTTATTTGGGAATTGTTATAGATCCGGCGGCTGTTGATGTTAACGTTCACCC CCCATTCCTGTACCTCAGTTTAGAAATCAGTCCCCAGAATGTGGATGTTAATGTGCACCC ** **. * *** * * * ***** *. *** ******
DQ356646.1MLH1y KR709638.1MLH1H	GACAAAGAGAGAGGTTCGTTTCCTGAGCCAAGATGAGATCATAGAGAAAATCGCC CACAAAGCATGAAGTTCACTTCCTGCACGAGGAGAGCATCCTGGAGCGGGTGCAGCAGCA ****** * ****************************
DQ356646.1MLH1y KR709638.1MLH1H	AATCAATTGCACGCCAAATTATCTGCCATTGATACTTCACGTACTTTCAAGGCTTCTT CATCGAGAGCAAG-CTCCTGGGCTCCAATTCCTCCAGGATGTACTTCACCCAGACTT-TG
DQ356646.1MLH1y KR709638.1MLH1H	CAATCTCAACAAACCAAGCCAGAGTCATTGATACCATTTAATGACACCATAGAAAGTG CTACCAGGACTTGCTGGCCCCTCTGGGGAGATGGTTAAATCCACAACAAGT-
DQ356646.1MLH1y KR709638.1MLH1H	ATAGGAATAGGAAGAGTCTCCGACAAGCCCAAGTGGTAGAGAATTCATATACGACAGCCA
DQ356646.1MLH1y KR709638.1MLH1H	-ATAGTCAACTAAGGAAAGCGAAAAGACAAGAGAAT-AAACTAGTCAGAATAGATGCTTC GATGGTTCGTACAGATTCCCGGGAACAGAAGCTTGATGCATTTCTGCAGCCTCTGA ******
DQ356646.1MLH1y KR709638.1MLH1H	ACAAGCTAAAATTACGTCATTTCTATCCTCAAGTCAACAGTTCAA GCAAAACCCCTGTCCAGTCAGCCCCAGGCCATTGTCACAGAGGGATAAGACAGATATTTCTA
DQ356646.1MLH1y KR709638.1MLH1H	CTTTGAAGGATCGTCTACAAAGCGA-CAACTGAGTGAACCCAAGGTAACAAATGTAAGCC GTGGCAGGGCTAGGCAGCAAGATGAGGAGAGATGCTTGAACTCCCAGCCCCTGCTG-AAGTG
DQ356646.1MLH1y KR709638.1MLH1H	ACTCCCAAAGAGGCAGAAAAGCTGACACTAAATGAAAGCGAACAACCGCGTGATGC GCTGCCAAAAATCAGAGCTTGGAGGGGGGATACAACAAAGGGGACTTCAGAATGT
DQ356646.1MLH1y KR709638.1MLH1H	CAATACAATCAATGATAATGACTTGAAGGATCAACCTAAG-AAGAAACAAAAGTTGGGGG CAG-AGAAGAGAGGAGCTACTTCCAGCAACCCCAGAAAGAGACATCGGGAAG ******
DQ356646.1MLH1y KR709638.1MLH1H	ATTATAAAGTTCCAAGCATTGCCGATGACGAAAAGAATGCACTCCCGATTTCAAAAGACG ATTCTGATGTGGAAATGGTGGAAGATGATTCCCGAAAGGAAATGAC-
DQ356646.1MLH1y KR709638.1MLH1H	GGTATATTAGAGTA-CCTAAGGAGCGAGTTAATGTTAATCTTACGAGTATCAAGAAATTG TGCAGCTTGTACCCCCCGGAGAAGGATCATTAACCTCACTAGTGTTTTGAGTCTC *.* ** *** **. ***** * ****.** ***.**
DQ356646.1MLH1y KR709638.1MLH1H	CGTGAAAAAGTAGATGATTCGATACATCGAGAACTAACAGACATTTTTGCAAATTTGAAT CAGGAAGAAATTAATGAGCAGGGACATGAGGTTCT-CCGGGAGATGTTGCATAACCAC *. ***.**.* .**** . *. ***** ** *.*. * ***** *.
DQ356646.1MLH1y KR709638.1MLH1H	TACGTTG-GGGTTGTAGATGAGGAAAGAAGAAGAATAGCCGCTATTCAGCATGACTTAAAGCT TCCTTCGTGGGCTGTGTGAATCCTCAGTGGGCCTTGGCACAGCATCAAACCAAGTT * * *.* ****.** ** *.* * * *.* ** *.*
DQ356646.1MLH1y KR709638.1MLH1H	TTTTTTAATAGATTACGGATCTGTGTGTGCTATGAGCTATTCTATCAGATTGGTTTGACA ATACCTTCTCAACACCACCAAGCTTAGTGAAGAACTGTTCTACCAGATACTCATTTAT * **. * ** ** ** *** * ****.******
DQ356646.1MLH1y KR709638.1MLH1H	GACTTCGCAAACTTTGGTAAGATAAACCTACAGAGTACAAATGTGTCAGA GATTTTGCCAATTTTGGTGTTCTCAGGTTATCGGAGCCAGCACCGCTCTTTGACC-T ***********************************
DQ356646.1MLH1y KR709638.1MLH1H	TGATATAGTTTTGTATAATCTCCTATCAGAATTTGACGAGTTAAATGACGATGCTTC TGACATGCTTGCCTTAGATAGTCCAGAGAGTGGCTGGACAGAGAGAAGATGGTCC *********************************
DQ356646.1MLH1y KR709638.1MLH1H	CAAAGAAAAAATAATT-AGTAAAATATGGGACATGAGCAGCATGCTAAATGA CAAAGAAGGACTTGCTGAATACATTGTTGAGTTTCTGAAGAAGAAGGCTGAGATGCTTGC ********************************
DQ356646.1MLH1y KR709638.1MLH1H	GTACTATTCCATAGAATTGGTGAATGATGGTCTAGATAATGACTTAAAGTCTGTGAAGCT AGACTATTTCTCTTTGGAAATTGATGAGGAAGGGAACCT . ******.* *****
DQ356646.1MLH1y KR709638.1MLH1H	AAAATCTCTACCACTACTTTTAAAAAGGCTACATTCCATCTCTGGTCAAGTTACCATTTTT GATTGGATTACCCCTTCTGATTGACAACTATGTGCCCCCCTTTGGAGGGGACTGCCTATCTT

DQ356646.1MLH1y KR709638.1MLH1H	TATATATCGCCTGGGTAAAGAAGTTAATTGGGAGGATGAACAAGAGTGTCTAGATGGTAT CATTCTTCGACTAGCCACTGAGGTGAATTGGGACGAAGAAAAGGAATGTTTTGAAAGC .** . *** **.* .* **.** **************
DQ356646.1MLH1y KR709638.1MLH1H	TTTAAGAGAGATTGCATTACTCTATATACCTGATATGGTTCTGAAAGTCGATACATCT CTCAGTAAAGAATGCGCTATGTTCTATTCCATCCGGAAG-CAGTACATATCT .*.*. *.*** ****** *** **
DQ356646.1MLH1y KR709638.1MLH1H	GATGCATCGTTGTCAGAAGACGAAAAAAGCCCAGTTTATAAATAGAAAGGAACACATAT GAGGAGTCGACCCTCTCAGGCCAGCAGAGTGAAGTGCCTGGCTCCATT ** * .*** *** .*** .*** .*** .*** .**
DQ356646.1MLH1y KR709638.1MLH1H	CCTCATTACTAGAACACGTTCTCT-TCCCTTGTA-TCAAACGAA CCAAACTCCTGGAAGTGGACTGTGGAACACATTGTCTATAAAGCCTTGCGCTCACAC ** *.* * * * * * * * * * * * * * * * *
DQ356646.1MLH1y KR709638.1MLH1H	GGTTCCTGGCCCCTAGACACATTCTCA-AGGATGTCGTGGAAATAGCCAACCTT ATTCTGCCTCCTAAACA-TTTCACAGAAGATGGAAATATCCTGCAGCTTGCTAACCTG *.*** *.****.*** *** *.*** *** *.****
DQ356646.1MLH1y KR709638.1MLH1H	CCAGGTCTATACAAAGTTTTTGAGAGGTGTTAA CCTGATCTATACAAAGTCTTTGAGAGGTGTTACCCAACTTTCTTGTACAAAGTTGGCATT ** *.*************
DQ356646.1MLH1y KR709638.1MLH1H	ATAAGAAAGCATTGCTTATCAATTTGTTGCAACGAAC

Fig. (5): Gene alignment between human gene MLH1 and yeast gene MLH1 in the Clustal Omega web site ('*' indicates identical between two aligned, '-' indicates gaps missing of one) and ('.' indicates low similarity, ':' indicates more similarity used to denote the level of similarity that are not identical) at position.

Figure (6) shows the results of alignment between human and yeast RAD51 sequences, with an E-value of 8e-176 and a question cowl of 85. RAD51 plays a function in genetic recombination and desoxyribonucleic acid double-strand break repair, according to its own description. RAD51 further processes the product of the organic process between these desoxyribonucleic acid partners to produce nicked circular duplex desoxyribonucleic acid, indicating that RAD51 will shift state strand exchange [26]. RAD51 is involved in baker's yeast mitotic recombination and repair of desoxyribonucleic acid damage, as well as meiosis [22]. It is a homologue of recA from Escherichia coli and plays critical roles in both mitotic and cell division recombination, as well as the repair of double-strand breaks of desoxyribonucleic acid.

Score	Expect	Method		Identities	Positives	Gaps
481 bits(1239)	8e-176	Compositional	matrix adjust.	227/341(67%)	278/341(81%)	6/341(1%)
X64270.1RAD51 CR536559.1RAD	Ye GGA 51	TCCGACATTTTT	ATTTTTATGCTT ATG ***	TATTCACTGTTC	AATATTTTCACCA	CAATTCGCA GCA ***
X64270.1RAD51 CR536559.1RAD	Ye AGA 51 A	AACGCACTCTAC	TTCGAAACTAC	GGTTCAAACTTAC AGAT	GCAGCTTCC	GATTTAAT
X64270.1RAD51 CR536559.1RAD	Ye TGG 51	CCTTTCTACTAT	GCCATAAACTC	тттсттсстстс	TTTTCATCGCCCC	AGCAAATGC
X64270.1RAD51 CR536559.1RAD	Ye ACT 51 AGA *	TTTTTGCCACCG	GCAGTGCCATC	CGGTCACATGAC	FACACCACGTTAA GAAGAAGA * * .*	ATAGCGATCT
X64270.1RAD51 CR536559.1RAD	Ye GGC 51 GGC ***	TTATCATTGTCA	CAGAGTAAATT	AAAATGGACGGT	AATGTTGGAAAT	GCACCACTA
X64270.1RAD51 CR536559.1RAD	Ye CCG 51 CC- **	TTCTTCAACCAA	ATCTAGTTTAGC	TATCCTGCAACAG	GTGGCCTTCTTG	AGCATTCCC
X64270.1RAD51 CR536559.1RAD	Ye TGA 51	GCATTCCAACCO	GTTGTATCAGT	GTTTTATCACCG GT	TCTCACCATATCC	CACGACTAG
X64270.1RAD51 CR536559.1RAD	Ye GCC 51 GC- **	ACACTTCGTTAC	CCTATGCTACG	CGTCATTTCCGC	TATTTCTGTCCTG	GTTTGTTTA
X64270.1RAD51	Ye CAG	TACGCGTGGTGG	GACCATAAAGG	GGAATAGTGGGG	ACTGGAGAAAAAA	TTTTCTCAG

X64270.1RAD51Ye CR536559.1RAD51	TTACTTCTTCTATCTTCCGTAGTTTCCATATACTAGTAGTGAGTG
X64270.1RAD51Ye CR536559.1RAD51	AGACGTAGTTATTTGTTAAAGGCCTACTAATTTGTTATCGTCATATGTCTCAAGTTCAAG
X64270.1RAD51Ye CR536559.1RAD51	AACAACATATATCAGAGTCACAGCTTCAGTACGGGAACGGTTCGTTGATGTCCACTGTAC
X64270.1RAD51Ye CR536559.1RAD51	CAGCAGACCTTTCACAGTCAGTCGTTGATGGAAACGGCAACGGTAGCAGCGAAGATATTG
X64270.1RAD51Ye CR536559.1RAD51	AGGCCACCAACGGCTCCGGCGATGGTGGCGGATTGCAGGAGCAAGCGGAAGCGCAAGGTG
X64270.1RAD51Ye CR536559.1RAD51	AAATGGAGGATGAAGCATACGATGAAGCTGCCTTAGGTTCGTTTGTGCCAATAGAAAAAC
X64270.1RAD51Ye CR536559.1RAD51	TGCAAGTGAACGGGATTACTATGGCGGATGTGAAAAAACTAAGGGAGAGTGGGCTTCACA
X64270.1RAD51Ye CR536559.1RAD51	CTGCTGAAGCGGTAGCATATGCTCCCAGAAAGGATTTATTGGAAATCAAAGGTATATCGG CTGTGGAGGCTGTTGCCTATGCGCCAAAGAAGGAGCTAATAAATA
X64270.1RAD51Ye CR536559.1RAD51	AAGCTAAGGCAGATAAGTTGCTAAACGAAGCGGCAAGGCTAGTGCCTATGGGATTTGTCA AAGCCAAAGCTGATAAAATTCTGGCTGAGGCAGCTAAATTAGTTCCAATGGGTTTCACCA ****.**.**
X64270.1RAD51Ye CR536559.1RAD51	CGGCTGCTGATTTTCATATGAGAAGATCGGAGCTGATTTGTTTG
X64270.1RAD51Ye CR536559.1RAD51	ATTTGGACACTCTTTTGGGTGGTGGTGGTGGTGGGAAACTGGTTCTATTACTGAGCTTTTCGGTG AGCTTGACAAACTACTTCAAGGTGGAATTGAGACTGGATCTATCACAGAAATGTTTGGAG * .* **** ** .* .* .* **.**** *********
X64270.1RAD51Ye CR536559.1RAD51	AATTCAGGACAGGTAAGTCCCAGCTATGTCACACTTTGGCCGTGACATGCCAAATTCCAT AATTCCGAACTGGGAAGACCCAGATCTGTCATACGCTAGCTGTCACCTGCCAGCTTCCCA ***** *.** ** *** ***** * *****.** .******
X64270.1RAD51Ye CR536559.1RAD51	TGGATATTGGTGGCGGTGAAGGTAAGTGTTTGTATATCGATACCGAAGGTACTTTCAGGC TTGACCGGGGTGGAGGTGAAGGAAAGGCCATGTACATTGACACTGAGGGTACCTTTAGGC * **. ***** **************************
X64270.1RAD51Ye CR536559.1RAD51	CGGTAAGATTGGTATCCATAGCTCAGCGGTTCGGATTAGACCCGGATGATGCTTTGA CAGAACGGCTGCTGGCAGTGGCTGAGAGAGGTATGGTCTCTCTGGCAGTGATGTCCTGG *.* * *** *. *** ** *** .** .** .**
X64270.1RAD51Ye CR536559.1RAD51	ACAACGTTGCGTATGCAAGAGCCTATAACGCCGATCATCAGTTAAGACTTCTGGATG ATAATGTAGCATATGCTCGAGCGTTCAACACAGACCACAGACCCAGGCCCCTTTATCAAG *.**.** **.**** **.**** * .***** **.******
X64270.1RAD51Ye CR536559.1RAD51	CTGCTGCCCAAATGATGAGCGAGTCTCGGTTTTCCTTGATTGTGGTCGATTCTGTTATGG CATCAGCCATGATGGTAGAATCTAGGTATGCACTGCTTATTGTAGACAGTGCCACCG * * *** ****************************
X64270.1RAD51Ye CR536559.1RAD51	CTCTATACCGTACGGATTTTTTCTGGTCGTGGTGAACTAAGCGCAAGGCAAATGCATTTAG CCCTTTACAGAACAGA
X64270.1RAD51Ye CR536559.1RAD51	CCAAATTTATGCGTGCTTTGCAAAGGCTGGCCGACCAATTTGGTGTTGCAGTCGTCGT CCAGGTTTCTGCGGATGCTTCTGCGACTCGCTGATGAGTTTGGTGTAGCAGTGGTAAT ****** **** **** * . *.** **.**. *.******

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X64270.1RAD51Ye CR536559.1RAD51	TACTAACCAAGTGGTCGCCCAAGTTGATGGTGGTATGGCTTTTAATCCAGATCCAAAGAA CACTAATCAGGTGGTAGCTCAAGTGGATGGAGCAGCGATGTTTGCTGCTGATCCCAAAAA .*****.**.*********************
X64270.1RAD51Ye CR536559.1RAD51	GCCTATCGGTGGTAATATTATGGCACATTCTTCCACCACGCGATTAGGTTTCAAAAA ACCTATTGGAGGAAATATCATCGCCCATGCATCAACAACCAGATTGTATCTGAGGAAA .******.** ** *****.** ** *** ** ** ** *
X64270.1RAD51Ye CR536559.1RAD51	GGGTAAGGGATGTCAAAGATTATGCAAAGTTGTTGACTCACCTTGCTTACCAGAGGCTGA GGAAGAGGGGAAAC-CAGAATCTGCAAAATCTACGACTCTCCCTGTCTTCCTGAAGCTGA ******* * *************************
X64270.1RAD51Ye CR536559.1RAD51	ATGTGTGTTCGCGATCTATGAAGATGGTGTTGGTGACCCCAGAGAAGAAGAAGACGAGTAGGT AGCTATGTTCGCCATTAATGCAGATGGAGTGGGAGATGCCAAAGA
X64270.1RAD51Ye CR536559.1RAD51	ATTTGGTCTCTTGTCTCTATTTATTTACACAGGTTTACTTTCAATTCTCCTCTTTTTCTT
X64270.1RAD51Ye CR536559.1RAD51	AGGTTGCGTTCCGTACATTTTTATCTTCATTTCCATCCACTGTCTTAGATTTTTGCATAT
X64270.1RAD51Ye CR536559.1RAD51	ATTTTGTCATATACCTCGCAACCCTACTGCGGTCTTAACCTTTTTTTCAGTTCTTTTAA
X64270.1RAD51Ye CR536559.1RAD51	ATAACTTTCGTATTGTCTGTCACCCATGAAATATATGTATTTTTCTACTCTTCCCGA
X64270.1RAD51Ye CR536559.1RAD51	TGACTACTTCCTCCTGCAGGGTCCGCGCGCGCTTTATCCTTTTAGGGGAGTGAAGAGAAAA
X64270.1RAD51Ye CR536559.1RAD51	ATTTTCTGATATGTCGCCATCCTC CTGA ****

Figure (6): Gene alignment in the Clustal Omega web site between human gene RAD51 and yeast gene RAD51 ('*' indicates identical between two aligned, '-' indicates gaps missing of one) and ('.' indicates low similar, ':' indicates more similar used to denote the level of similarity that are not identical) at position.

With a question cowl of thirty-eight and an E-value of 6e-138, **Figure** (7) depicted the findings of alignment between human sequence SGS1 and yeast sequence RECQL. RECQL family nucleolar desoxyribonucleic acid helicase; was involved in ordering integrity maintenance, body organic process, cell division joint molecule/crossover formation; stimulates activity of Top3p; forms nuclear foci in response to desoxyribonucleic acid replication stress in a Rrd1p-dependent manner; yeast SGS1 enhances mutations in human homolog BLM Bloom and Werner syndromes, which are linked to genomic instability and cancer risk, are linked to RECQL helicases [28]. Genes in each creature performed in exactly the same way.

Score	Expect	Method	Identities	Positives	Gaps
427 bits(1097)	6e-138	Compositional matrix adjust.	229/560(70%)	341/560(60%)	35/560(6%)
U22341.1SGS1 AY157499.1RE	LYea AA ECQL TT	GCTTTGCAGGAATTAGAGTGGGA	AGCACTGATTTAA	TCCGCCTAGTGA	GTTGAAAAAA
U22341.1SGS1 AY157499.1RE	LYea AC	CTCAAAGATATAGTCATGTTAT	TCACGGCTTCTTG TCTTTCA **	GGTAAATTTGAT	ACTGGAAGTCG
U22341.1SGS1 AY157499.1RE	LYea AA ECQL	TAAGCTCTCTGCCCTAATAATCT TC-CTTCCCT	TCTTTGATGTAG	CATATTCCAGTT	GGTAAAAAGGC GCAGGC
U22341.1SGS1 AY157499.1RE	LYea CC	CTTGGGGCTCCTTTGGGCACTCT GAGGCCGGTCT *.***	TGGGAAAAGAAGC TGATGC * ** **	AAATTTACTGAC	ATTGGGAACAG
U22341.1SGS1 AY157499.1RE	LYea GT	CTGAAATGGTCAAACCTTGCGAT CTTCCTTTCG ** **** **	-CCCACACATTGG	GAGAGGAGAGATAC	CGTTAAA CGGAAAGTTAA
U22341.1SGS1 AY157499.1RE	LYea CC CQL TC	ACTTGCCCTCCTAAAAGCTGTA AC-TGCCCTGCTCTG-AG	GAAGCCTCAAATA GAA	GGCTCTTCCACC	CAAGTGCCAAA GGGCC * ***
U22341.1SGS1 AY157499.1RE	LYea AT	ATTGCGATAATATTGGTGGGAAA	AAATTCCCATGGC	ACGTTC-	GCGTTCGGTCC GCCTGCTGACC
U22341.1SGS1 AY157499.1RE	LYea AG	AGACTTCGTGATCTGCCTGAGGT GGTCTTC-TGATCT	TGGACCCGTGACA	TTCGCAGCCACA	TGCTCCAGTTA TGCAGGAGGAT
U22341.15G51 AY157499.1RE	LYea TT CQL TG	ACCACCGACAGCCATATTTCGT	GTTGGTGCTCTTC GCAGCTGCC	TATTGTGAAAGA ATTTGTTAAAGA	ACCACTTTAGA

U22341.1SGS1Yea	TCATGAAATGCGAAATGTGAAGGAAGAGAGAGCTTCTCTCCACATGTCCTTTATATTTA
AY157499.1RECQL	TTATTTTAGAAACAATTTGGAAAGAAAAAGAA
U22341.1SGS1Yea	TATAGTTCAGCCGTGCGTTTCGAAGTGGATTGCCCGGCTTCGGCTGCCAGGATTTGTTTA
AY157499.1RECQL	TGGCGTCCGTTTC
U22341.1SGS1Yea AY157499.1RECQL	TGCTTTTGCAATGCACATATAACAAGAAACTCGAGCCTGATCTAAAAGCTGATATACGGA
U22341.1SGS1Yea AY157499.1RECQL	TCAATAGAGGGGCACTTAGCAGGCTGGGTGATCATTGGTGATACATTTCGGATTTGTGGCT GGAACTGGATTCT ** ***
U22341.1SGS1Yea AY157499.1RECQL	TTACCGTTTAGTTTGTTTTTATCAGCCAGCTTGGAGTCATTGGCTAGAGGAAAGGAAAAG ATAACCAGTGAGCTACATGCAGTAGAA ** * * ****************************
U22341.1SGS1Yea	ATACAGATTATTGTTGTATATATTTAAAAAATCATACACGTACACAAAGGCGGTAATGG
AY157499.1RECQL	ATTCAAATTCAAGAAC
U22341.1SGS1Yea AY157499.1RECQL	TGACGAAGCCGTCACATAACTTAAGAAGGGAGCACAAATGGTTAAAGGAAACGGCGACTT T *
U22341.1SGS1Yea	TACAGGAAGACAAAGATTTCGTATTCCAGGCTATCCAAAAGCACATCGCGAACAAAAGGC
AY157499.1RECQL	TACGGAAAGGCAACAAGAGCTTATTC
U22341.1SGS1Yea	CTAAGACAAATTCGCCACCAACAACGCCATCCAAAGATGAATGTGGACCAGGAACAACAA
AY157499.1RECQL	CTGACAAAGAAAATAAA
U22341.1SGS1Yea AY157499.1RECQL	ACTITATAACCAGCATTCCTGCATCTGGACCAACGAATACTGCTACGAAACAACATGAAG GCAGTGTTTAGAGGATTCTTATGCCTACAGGAG- .* *.* ** **** ****
U22341.1SGS1Yea	TCATGCAAACTTTGTCGAACGATACAGAATGGCTCTCGTACACTGCCACATCGAATCAAT
AY157499.1RECQL	GTGGAAAGA
U22341.1SGS1Yea	ATGCTGACGTACCCATGGTTGATATACCAGCCAGCACAAGTGTTGTATCGAACCCGAGGA
AY157499.1RECQL	GCTTATGTTACCAGTTACCAGCATTA-TGTT
U22341.1SGS1Yea	CGCCCAATGGCTCGAAAACTCACAATTTCAATACTTTTCGACCGCACATGGCTAGTTCTC
AY157499.1RECQL	CAGATGGTTT-TACACTCGTCATTT
U22341.1SGS1Yea	TTGTCGAAAATGACAGTAGCAGAAATCTAGGTAGTAGAAATAACAATAAAAGCGTAATCG
AY157499.1RECQL	TTATGGAAGAC
U22341.1SGS1Yea AY157499.1RECQL	ATAATTCAAGTATAGGCAAACAGCTCGAAAATGATATAAAATTAGAGGTGATCCGCCTTC GTTTTAAAACAATTAGGAATTTC ** * . **** ****
U22341.1SGS1Yea	AAGGCTCCCTAATTATGGCATTGAAAGAGCAATCGAAATTATTGCTACAGAAGTGTAGTA
AY157499.1RECQL	
U22341.1SGS1Yea AY157499.1RECQL	TTATCGAATCCACATCATTGTCAGAGGACGCTAAAAGGCTACA-GTTAAGTAGGGATATA TCTAAGGAGCATGTTAAATGGGTTCATGATGAAATGGTAAATA ** **
U22341.1SGS1Yea AY157499.1RECQL	CGGCCTCAGTTATCAAATATGTCGATACGAATAGATAGTCTGGAAAAGGAGATCATAAAA AAAACTCCGAGTT-AAAG-CTGATTTATGTGA-CT *** * ** ***. * ** ***.
U22341.1SGS1Yea AY157499.1RECQL	GCCAAAAAAGATGGAATGTCAAAAGATCAAAGTAAAGGTCGCAGTCAAGTTTCTTCACAA -CCAGAGAAAATTGCAAAA-AGCAAAATGTTTATGTCAAGACTA ***.*.**** * *************************
U22341.1SG51Yea AY157499.1RECQL	GATGATAATATCATATCAAGCATTCTGCCCAGCCCCTTGGAATACAATACATTCCAGG GAGAAAGCCTATGAAGCAAGG ** .* * * *** *****
U22341.1SG51Yea	AGATTCAAACCTGACAAGTACTACTGCGACTACCG-TCACTAAGGCATTAGCCATCACTGG
AY157499.1RECQL	AGATTTACTCGAATTGCTGTGGATGAAGTTCACTGCTGTAGTCAGTGG
U22341.1SG51Yea AY157499.1RECQL	
U22341.1SGS1Yea AY157499.1RECQL	TGATTTGATTCAAGTCCTGGATGATGAGGATGATATAGACTGTGACCCTCCTGTAATATT TGATTTCAGACCT-GATTATAAAGGCACTTGGTATCTT +++++++++++++++++++++++++++++++++
U22341.1SGS1Yea	GAAGGAGGGGGGCTCCACATTCTCCCGCATTCCCGCATCTCCACATGACGTCAGAAGAACA
AY157499.1RECQL	AAAGCGGCAGT-TCCCTA-ACGCATC
U22341.1SGS1Yea AY157499.1RECQL	AGATGAACTTACAAGAAGGAGAAATATGCGTTCAAGAGAACCAGTCAACTACAGAATACC AATTGGGCTGACTGCAACTGCA *. **** ** ** ** **
U22341.1SGS1Yea	TGATAGGGATGATCCTTTTGACTATGTTATGGGTAAATCTTTGAGGGACGATTATCCGGA
AY157499.1RECQL	
U22341.15G51Yea	TG-TCGAAAGAAGAAGAAGATGAGTTAACAATGGAGGCAGAAGATGATGCCCATTCCAGCT
AY157499.1RECQL	TGCTCAGAAAATTTTGTGCATTGAAAAGTGTTTTACTTTTACAGCT

U22341.1SGS1Yea AY157499.1RECQL	ACATGACTACTAGAGATGAAGAAAAAGAAGAAGAAAACGAATTACTAAATCAAAGCGATTTTG TCTTTTAATAGGCCAAATCTAT ** *********************************
U22341.1SGS1Yea AY157499.1RECQL	ATTTTGTGGTAAACGACGACCTAGACCCAACTCAAGACACAGATTATCATGATAATATGG ATTATGAGGTTCGGCAGAAGCCCTCAA-ACACTGAAG *** ** *** *** *** *** **** **** ***
U22341.1SGS1Yea AY157499.1RECQL	ATGTTAGTGCAAATATTCAGGAAAGTTCTCAAGAAGGTGACACTAGGTCCACAATTACCT ATTTTATTGAGGATATTGTAAAGCTCATTAATGGGAGATACAAAGG
U22341.1SGS1Yea AY157499.1RECQL	TGTCGCAAAATAAAAATGTTCAAGTTATTTTATCATCTCCCACAGCACAGAGCGTTCCCT GCAATCAGG
U22341.1SGS1Yea AY157499.1RECQL	CAAATGGCCAAAATCAAATAGGCGTGGAGCATATTGACTTGTTGGAAGATGATCTGGAAA
U22341.1SGS1Yea AY157499.1RECQL	AGGACGCAATTTTGGATGATAGCATGAGTTTCTCCTTTGGCCGTCAACACATGCCCATGT
U22341.1SGS1Yea AY157499.1RECQL	CTCATTCTGATCTAGAGTTGATAGACAGCGAAAAAGAAAATGAGGATTTTGAAGAAGATA TCTGAACAAG
U22341.1SGS1Yea AY157499.1RECQL	ATAACAATAACGGTATCGAGTACCTATCAGATAGCGATTTAGAAAGATTTGACGAAGAAA TTACGGT
U22341.1SGS1Yea AY157499.1RECQL	GAGAGAATAGAACCCAAGTAGCAGATATCCAGGAACTAGACAATGACCTGAAAAATAATAA TAGTTTGCAGA-ATCTGGGAATT
U22341.1SGS1Yea AY157499.1RECQL	CAGAAAGGAAGCTTACAGGTGACAATGAACACCCACCACCACCATCTTGGTCTCCCAAAATAA CATGCAGGTGCTTACCATGCCAATTT * .***** **** * * **** *
U22341.1SGS1Yea AY157499.1RECQL	AAAGGGAGAAATCCAGTGTTAGTCAAAAGGATGAGGAAGACGATTTTGATGACGATTTTT GGAGCCAGAAGATAAGAC
U22341.1SGS1Yea AY157499.1RECQL	CATTAAGTGATATAGTGAGTAAATCCAATTTATCTTCTAAGACGAATGGTCCAACCTATC CACAGTTCATAGA-AAATGGT-CAGCC ** ** *** *** .**
U22341.1SGS1Yea AY157499.1RECQL	CTTGGTCTGATGAAGTTTTATATCGTTTACATGAAGTCTTTAAACTGCCTGGTTTTAGAC
U22341.1SGS1Yea AY157499.1RECQL	CTAACCAACTAGAGGCTGTAAATGCAACTTTGCAAGGTAAGGATGTTTTTGTTCTTATGC GGTATGGGAATTGATAAGC *.***** *** *** *** *** *** *** ***
U22341.1SGS1Yea AY157499.1RECQL	CAACAGGGGGTGGTAAATCTCTTTGCTATCAACTTCCTGCAGTGGTGAAATCGGGTAAAA CAGATGTGAGGTTTGTTATCCATCATTCAATGAGTAAATC **. * *.* * *** * ***.**. * ***
U22341.1SGS1Yea AY157499.1RECQL	CACATGGTACTACTATTGTCATCTCCCGCTAATTTCCCTGATGCAAGATCAAGTGGAAC CATGGAAGAGTGGAGAGTGGA
U22341.15G51Yea AY157499.1RECQL	ATTTATTGAATAAAAATATTAAGGCGAGCATGTTCAGTTCGAGGGGGTACTGCCGAGCAAA CGTGCAGGT
U22341.1SG51Yea AY157499.1RECQL	GACGACAAACTTTCAATTTATTTAATGGATTATTGGATTTAGTTTACATATCTCCTG
U22341.15G51Yea AY157499.1RECQL	AGATGATCAGTGCCTCAGAACAATGCAAGAGAGAGCTATCAGTAGATTATACGCAGACGGTA AGATGACATGAAAGCAGACTGTATTTTGTACTAC ****** * **. *** **.** **
U22341.15G51Yea	AGTIGGCTCGTATIGTTGTAGATGAAGCACACTTGTTGTTCTAACTGGGGCCACGATTTCA GGCTTTGGAGAT
AV157499.1RECQL	
AY157499.1RECQL	AGGAACCTGTTTTCCTAAAACAAAGTTTTAATAGAACAAATTTGTATTACGAAGTAAACA
AY157499.1RECQL	AGAAGC
AY157499.1RECQL	AAACGGGTATAATATATATTGCCACTCCAAGAAATCATGCGAGCAAACATCAGCCCAAATGC
U22341.15G51Yea	AAAGAAATGGCATCAAGTGTGCCATGCAGGCATGGAGCCTGATGAAAGATTAA
U22341.15G51Yea	GTGTACAGAAGGCATGGCAGGCGGATGAGATACAAGTCATGTGGCTACTGTTGCTTTCG TCAGAA-GCATGTAACAAAATGTGGCGATAACTGCT
	***** **** * *** * ***** * *****

U22341.1SGS1Yea AY157499.1RECQL	GAATGGGTATTGATAAACCTGATGTGAGATTTGTTTACCACTTTACCGTTCCCCGAACAT GTAAAGACAGTGCATTTGAAAGAACGAACAT *** **.*. * ** .***
U22341.1SGS1Yea AY157499.1RECQL	TAGAAGGCTATTATCAAGAAACCGGCCGTGCTGGAAGAGATGGGAACTATTCATATTGTA AACAGAGTACT-GCAGAGATCTAATC *** *. **.** * ******
U22341.1SGS1Yea AY157499.1RECQL	TTACCTACTTTCATTCAGGGACATTAGAACCATGCAGACAATGATCCAGAAGGATAAGA
U22341.15G51Yea AY157499.1RECQL	ACTTAGACAGAGAGAAAAAGGAAAAAACATCTGAATAAATTACAGCAAGTAATGGCATACT CAGGCAGAGGAACTGAATGAAAAAC
U22341.1SGS1Yea AY157499.1RECQL	GTGACAACGTTACTGACTGCAGAAGAAAGTTAGTTTTATCTTATTTCAATGAGGATTTTG
U22341.1SGS1Yea AY157499.1RECQL	ACTCCAAACTGTGTCATAAAAACTGTGATAATTGTAGAAATAGCGCCAACGTGATAAA ACTCCATTGAAACTGATTGATTCTTGGAT **** *** *** *** ***
U22341.1SGS1Yea AY157499.1RECQL	CGAGGAAAGGGATGTTACAGAACCTGCCAAGAAGATTGTAAAATTAGTGGAAAGTATCCA GGGAAAGGGTGCAGCAAAACTGAGAGTAGCAGGTGTTGTGGCTCC- **.**.**.**. **.*** *.**. * ****
U22341.1SGS1Yea AY157499.1RECQL	AAATGAAAGAGTCACAATAATTTATTGCCAAGATGTCTTTAAAGGTTCGAGAAGCTCCAA CACACTTCCTCGTGAAGATC **** * *** ***
U22341.1SGS1Yea AY157499.1RECQL	AATTGTTCAGGCTAACCATGACACCTTAGAGGAGCATGGTATTGGTAAATCCATGCAAAA TGGAGAAGATTATTGCACACTTTCTAAT *.***.** ***. *. *. *. *. * * *
U22341.15G51Yea AY157499.1RECQL	ATCAGAAATCGAAAGGATTTTCTTCCATTTGATTACGATCCGAGTTTTACAAGAGTATTC A-CAGCAGTATCTTAAAGAAGAACTACAGTTTTAC-AGCTTATGC * *** *. * **** * **.***
U22341.1SGS1Yea AY157499.1RECQL	AATAATGAACAATAGCGGTTTTGCTTCAAGCTATGTGAAAGTTGGTCCCAATGCTAAGAA TACCATTTCGTATTTGAAAATAGGACCTAAAGCTA ** ** ** ** ** ** ** ** ** ** **
U22341.15G51Yea AY157499.1RECQL	ATTGCTGACTGGAAAAATGGAGATAAAGATGCAATTTACAATATCAGCACCAAACTCCCG
U22341.1SGS1Yea AY157499.1RECQL	TCCCTCGACATCTTCT-AGCTTTCAAGCAAATGAAGATAATATACCAGTTATCGCGCAGA ATCTTCTGAACAATGAGGCACATGCTATTACTATGCAAGTGA
U22341.1SGS1Yea AY157499.1RECQL	AATCAACAACCATTGGAGGAAATGTGGCTGCTAATCCACCGCGCTTTATAAGTGCGAAGG CAAAGTCCACGCAGAACTCTTTCAGGGCTGA *** . *** * ** .* * ** .*
U22341.1SGS1Yea AY157499.1RECQL	AACACCTAAGATCGTATACATACGGCGGGTTCGACCATGGGTAGCTCACATCCGATCACTT
U22341.1SGS1Yea AY157499.1RECQL	TGAAAAACACAAGCGATTTACGCTCGACACAAGAACTTAATAATCTGCGAATGACATACG TGAACAAGGTGATAAAAAGATG *** *****. *** **
U22341.1SGS1Yea AY157499.1RECQL	AACGTCTGAGGGAATTATCTTTAAATTTAGGAAATAGAATGGTTCCTCCAGTTGGGAACT GAGGAAAAAAATTCAGGCAACTTCCAG *****.**
U22341.1SGS1Yea AY157499.1RECQL	TTATGCCTGACAGTATTTTAAAAAAGATGGCAGCAATATTACCAATGAATG
U22341.15G51Yea AY157499.1RECQL	TTGCAACTTTAGGCACAGTGGAGGACAAATATCGCCGAAGGTTCAAGTACTTTAAAGCCA CAGCAATCTGGTTCTAAGAATACA
U22341.1SG51Yea AY157499.1RECQL	CGATAGCAGATCTTAGCAAAAAGAGATCAAGCGAGGATCATGAAAAATACGACACAATAC
U22341.15G51Yea AY157499.1RECQL	TAAATGATGAATTTGTGAACAGGGCCGCGGCTTCCAGCAATGGGATTGCCCAAAGTACTG TAAATTTTCTAATTAAAGATGGTTTATGC-ATGTATATGCCATTATTTTTG
U22341.15G51Yea AY157499.1RECQL	GAACAAAATCTAAGTTTTTTGGCGCCCAATTTAAACGAAGCCAAAGAAAATGAACAAATTA TAGTTAGACAATAGTTTTTAAAAG-AATTTCATAGATATTTTATATGTATGGA
U22341.15G51Yea AY157499.1RECQL	TCAATCAAATCAGACAAAGCCAATTACCCAAAAATACCACAAGCAGCAAATCAGGTACAA TCTATATTTTCAG
U22341.15G51Yea AY157499.1RECQL	GGTCCATCAGTAAGTCGTCCAAGAAGTCTGCTAATGGGAGACGAGGTTTTAGAAATTACC TCTGAAGATC
U22341.15G51Yea AY157499.1RECQL	GAGGTCACTACAGAGGAAGAAAGTGAAGAGTGAAGAAAAAAAA
U22341.15G51Yea AY157499.1RECQL	ACGACACCATTCGCCAAGCATTCTTTTTGGGCACTTTTTTAGCTTCTTTACCTCTTATAC -AACAAGGGAAAAATTTTTATGTAAAAACCCTT
U22341.15G51Yea AY157499.1RECQL	TAATTGCATACACAATAACATAGCATATAAAAAAGGCGAATCATAAAAATTTTAAATC TAAATGTAAAATATTTGAGAATAAGTTCATACAATCGTCTTAAGTTTTTTATGC

U22341.1SGS1Yea AY157499.1RECQL	AACCACGACATATTGTGGTGTGG CTTTATAT	ACTTAGCTATATT	AACTTCGAATT	TTCTCTCGTA
U22341.1SGS1Yea AY157499.1RECQL	AACTTTTAACTTTTCTTTGACC	IGAATATTTTATATTAT ATAAC ** *.	CTACATATGTO CATCTTTT	CATAAATGCG
U22341.1SGS1Yea AY157499.1RECQL	TCAACTAATATACAATATACAACA	ATAATGGGTATGTACTC	ATTCAGTTTCG	TTCGCTAATT
U22341.1SGS1Yea AY157499.1RECQL	TCTTCTACAGAAGGGCATGTACA GATACT	ATATTAAATTCATGTCA TTAAGTT ****.**	CCATAAGTGTC	ATCCAGCTAG GATCAG
U22341.1SGS1Yea AY157499.1RECQL	CGACAGTAGGCCAGAATTTATTC	GTATCTCAAAAAGGGTA	ATGGGTAAGCG	GCTTCTTCAC
U22341.1SGS1Yea AY157499.1RECOL	GGGTATAACCTCTCGTATCCCA/	ATTGGAGGAAGTAATAA	GATCT	

Figure (7): Gene alignment in the Clustal Omega web site between human gene RECQL and yeast gene SGS1 ('*' indicates identical between two aligned, '-' indicates gaps missing of one) and ('.' indicates low similar, ':' indicates more similar used to denote the level of similarity that are not identical) at position.

3.5. Yeast protein-protein interaction prediction (Networking).

Predicting protein-protein interactions in yeast and humans could lead to a determination of the degree of deliberate resemblance between two animals' genes linked to cancer (Figures eight,9).

Gene MANIA displays the prognostic value of each data set selected for the inquiry. Currently, two organisms (Homo sapiens and Saccharomyces cerevisiae) are supported in addition to or above distinct sequencing execute prediction methodologies on yeast and humans. The GeneMANIA prediction algorithmic program's excellent accuracy, Associate in Nursing intuitive computer programme, and vast knowledge make sequence MANIA a helpful tool for any scientist [7].

The results of four yeast inquiries are displayed in Gene MANIA (8A, B). The resulting networks are completely different, with various totally different

absolutely different relationships and four separate relevant genes in yeast that are linked by a pathway to the query list. Physical interaction (44.06 percent), Genetic interaction (40.80 percent), Co-expression (9.10 percent), Co-localization (2.41 percent), foretold interaction (1.79 percent), other (1.51 percent), and Shared macromolecule domains were the other degrees of question customization (0.31 percent). The impact of knowledge set selection on topology. The results of gene queries are displayed in GeneMANIA. (A) The default inquiry about the yeast cell cycle, with all default parameters mistreated. (B) Mistreatment default network weight methodology for the yeast cell cycle default inquiry. On yeast and mouse benchmarks, the GeneMANIA algorithmic programme outperforms or outperforms alternative sequence perform prediction algorithms, according to [7]. GeneMANIA is a beneficial gadget for any man of science because of the high accuracy of the GeneMANIA prediction algorithmic programme, Associate in Nursing intuitive computer programme, and enormous information.



Figures (8A and B): (A) The yeast cell-cycle default query with all default parameters. (B) The yeast cell-cycle default query with all default parameters. (B) Using the default network weighting approach, the yeast cell-cycle default query.

Four yeast inquiries are being displayed by GeneMANIA (Fig. 8A, B). The networks that result are completely distinct, with various totally different absolutely different relationships and four separate relevant genes in yeast that are linked by a pathway to the query list. Physical interaction (67.64%), co-expression (13.50%), foretold interaction (6.35%), co-localization (6.17%), route (4.35%), genetic interaction (1.40%), and common macromolecule domains are some of the other levels of question customisation (0.59 percent). GeneMANIA displays

the results of gene queries in Effects of Knowledge Set Choice on Topology. (A) Mistreatment of all default parameters in the human default question. (B) Mistreatment default network weight approach, which is a human default question. YKOs lacking genes that are similar to cancer genes in humans were chosen. The ability to predict protein-protein interactions in yeast and humans could lead to an assessment of the degree of deliberate similarity of some cancer-related genes between the two organisms.



Figures (9A and B): (A) The human default query, using all default parameters. (B) The human default query, using default network weighting method.

4. Conclusions

Extraterrestrial object assay was used to assess desoxyribonucleic acid harm in yeast deletion strains when treatment with suggested concentrations of food additives to YKO strains resulted in a significant increase in desoxyribonucleic acid harm (P zero.05) as measured by a rise in tail length, tail microchip, and tail moment when compared to traditional management strains. These data indicated that food additives MSG, SB and saffron decreased cell viability in malignant and non-malignant cells as well as confirmed the occurrence of their cytotoxic effects according to a pervious study [22] and determine the possible genotoxic effects of three food additives (MSG, SB and Saffron) on human cell lines by Flow cytometric and RT-pcr to a pervious study [23].

5. Conflicts of interest

"There are no conflicts to declare".

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