

## Electrophoretic and Molecular Dynamic Evaluation of Mutagenicity Induced by Toxic Factors Affecting Testicular Tissue in Rats

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### ABSTRACT

The testes contain many proteins including testis-specific protein kinase 1 (TESK1) expressed predominantly and ubiquitously in mature testis. They exhibited a vital role in spermatogenesis process. Lithium is an effective drug for the treatment of psychiatric disorders. Lead acetate (Pb<sub>2</sub>COOH) and Carbon tetrachloride (CCl<sub>4</sub>) which is used as an insecticide in agriculture are considered as environmental pollutants. The prolonged exposure to these (toxic) substances exhibited adverse effect on male reproductive organs. Doxorubicin (DXR) and cyclophosphamide (CYP) are effective chemotherapeutic drugs. They exhibited toxicity on testicular proteins. Irradiation caused disruption of normal cyclic spermatogenesis through radiotherapy. During the present study, these toxic factors affect all electrophoretic patterns at qualitative level through their effect on number and arrangement of the bands and at the quantitative effect through changing the band quantity. In the electrophoretic protein pattern, the lowest similarity index (SI) value (0.42) was recorded with CYP-treated group and the highest SI value (0.79) noticed with Pb<sub>2</sub>COOH-treated group. In the electrophoretic lipoprotein pattern, the lowest SI values (0.44) was observed with Pb<sub>2</sub>COOH-treated group and the highest SI values (0.73 and 0.80) observed with CCl<sub>4</sub>-treated and irradiated groups. In catalase (CAT) pattern, the lowest SI value (0.69) was noticed in DXR-treated, CYP-treated and irradiated groups. The highest SI value (0.91) was observed with Pb<sub>2</sub>COOH-treated, Li<sub>2</sub>CO<sub>3</sub>-treated and CCl<sub>4</sub>-treated groups. In peroxidase (Gpx) pattern, the lowest SI value (0.25) was noticed with irradiated group and the highest value (0.75) observed with CCl<sub>4</sub>-treated group. In esterase (EST) pattern, the lowest SI value (0.44) was observed with irradiated group and the highest SI value (0.86) noticed with DXR-treated group. The 3D model of TESK1 was built by means of restraint-based comparative modeling. It was noted that model of the TESK1 was quite big and no available template for the whole sequence and its first half (Up to residue 333).

**Keywords:** Lithium Toxicity, Carbon Tetrachloride, Lead Toxicity, Doxorubicin, Cyclophosphamide, Irradiation, Testis-specific protein kinase.

### INTRODUCTION

The testes contain various proteins necessary for spermatogenesis and development of the reproductive system. These proteins and their mRNA are expressed widely in the mature testes. The protein content was considered as a marker of testicular tissue injury<sup>1</sup>. Lithium is alkali element. It is used as an effective drug for the treatment of several psychiatric disorders in human. The prolonged exposure to lithium during the therapeutic use has several toxic effects leading to various undesirable side effects. It was found that lithium carbonate promoted toxicity and showed adverse effect on male reproductive organs through lowering the fertility index of male rats to 50%<sup>2</sup>. Injection of lithium at the therapeutic doses caused destruction of leydig cells followed by remarkable reduction of sperm viability and motility<sup>3</sup>. This might lead to reducing steroidogenic activity and efficiency of spermatogenesis process in a dose-dependent manner<sup>2,4</sup>.

Carbon tetrachloride (CCl<sub>4</sub>) is a colorless liquid organic compound. It is well known that it exhibits hepatotoxic and nephrotoxic activities<sup>5</sup>. It is used as an insecticide in agriculture for fumigation of the grains. The industrial workers are susceptible to the particular tissue injury induced by CCl<sub>4</sub> toxicity during their life. It enhance the oxidative stress through generation of the free radicals and oxidation of the macromolecules such as lipids and proteins<sup>5,6</sup>. Lead is a heavy metal belongs to common environmental and occupational pollutants. It is considered an important cause of infertility among occupational workers. It affects the male reproductive organs at the biochemical<sup>7</sup> and physiological level<sup>8</sup>. Low dose of lead was sufficient to arrest spermatogenesis process<sup>9</sup>. Cancer treatment by mean of chemotherapy is not found to be safe due to the side effects of the chemotherapeutic drugs on the healthy tissues<sup>10</sup>. The testicular cells are most sensitive to the chemotherapeutic drugs which influence severely on

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spermatogenesis process<sup>11</sup>. Doxorubicin (DXR) and cyclophosphamide (CYP) belong to numerous chemotherapeutic drugs<sup>12</sup>. The treatment with CYP affects testicular cells through depletion of the differentiated cells in the testis<sup>13</sup>. This results in depletion of germ cells maturation and hence reduction in sperm counts<sup>14,15</sup>. DXR is very active against wide spectrum of cancerous tumors and is mainly used in the treatment of lymphomas, leukemias and other solid tumors<sup>16</sup>. It exhibits dose-dependent toxic effect on different organs<sup>17</sup>. It affected the male reproduction ability through changing the testicular proteins<sup>18</sup>. Also, it influences the testicular lipids which are consisting of very long chain polyunsaturated fatty acids<sup>19</sup>. The radiation exposure by mean of radiotherapy leads to serious systemic damage to various cellular structures<sup>20</sup>. It affected the testicular tissue which represents the most radiosensitive organ through disruption of normal cyclic spermatogenesis process and therefore, impairment of fertility<sup>21,22</sup>. Testis-specific protein kinase 1 (TESK1) is a 626 amino acid serine/threonine kinase. It is a protein kinase with a unique structure consisting of an N-terminal protein kinase domain and a C-terminal proline-rich domain<sup>23</sup>. It was revealed that TESK1 protein exhibited a vital role in spermatogenesis. Its mRNA is expressed predominantly and ubiquitously in the testicular germ cells and it may play an important role in spermatogenesis process<sup>24,25</sup>. TESK1 is a dual specificity protein kinase. It is capable of phosphorylating both serine/threonine and tyrosine residues in its sequence. The autophosphorylation plays a role in regulating the kinase activity of TESK1<sup>26</sup>. The present framework aimed to investigate the different mutagenicity induced by selected toxic substances in the testicular tissue in rats. Various electrophoretic patterns were monitored and compared with control group. The 3D models of the TESK1 were built using homology modeling to give a first insight about the structural characteristics of the activated regions in this protein kinase.

## MATERIALS AND METHODS

### Materials: Chemicals and Reagents

Acrylamide, Bis-acrylamide, Ammonium persulfate (APS), N, N,N,N-Tetramethylethylenediamine (TEMED), Tris buffer, Coomassie Brilliant Blue G-250 (CBBR-250) and Sudan Black B (SBB) were procured from Sigma-Aldrich. The chemicals used for in-gel esterase staining including  $\alpha$ - and  $\beta$ -naphthylacetate, Fast Blue RR were purchased from Qualigens Fine Chemicals, India. Cyclophosphamide (CYP), Doxorubicin (DXR), Lead Acetate Trihydrate ( $Pb_2COOH$ ), Carbon Tetrachloride ( $CCl_4$ ), Lithium Carbonate ( $Li_2CO_3$ ) and Benzidine were purchased from Sigma Chemicals Company (London, UK). All other chemicals and reagents used were of analytical grade and of highest purity.

### Animals and Treatment

Healthy seventy adult male Wistar rats (weighing 150–170 g) were housed as 7 groups. The animals were kept under normal conditions at  $25 \pm 2^\circ C$ . All the experimental procedures were carried out according to the ethical guidelines and protocol approved by the institutional animal care of National Research Centre, Egypt.

### Experimental Design

The rats were randomly divided into 7 groups each containing 10 rats. Group I (Control group): Rats were fed with normal diet as *ad libitum* and received distilled water for 60 days. Group II ( $Pb_2COOH$ -treated group): Rats received  $Pb_2COOH$  at concentration of 30 mg/kg body weight orally by gavage tube for 60 days by gavage tube<sup>27</sup>. Group III ( $Li_2CO_3$ -treated group): Rats were treated with  $Li_2CO_3$  solution interperitoneally (i.p.) at the dose 25 mg/kg B.W./day for 31 days<sup>28</sup>. Group IV (DXR-treated group): Rats received DXR at dose level of 25mg/kg b.wt for three times per week for two weeks<sup>29</sup>. Group V ( $CCl_4$ -treated group): Rats were injected with  $CCl_4$  (i.p.) at the dose 0.5 ml/kg b.w. (50 %  $CCl_4$  in olive oil) twice a week for 28 days<sup>30</sup>. Group VI (CYP-treated group): Rats received CYP (i.p.) at 40 mg/kg b.w. twice a week for 15 days<sup>31</sup>. Group VII (Irradiated group): Rats were exposed to single dose of 7 Gy delivered at the dose rate of 1.167 Rad / Sec. at Middle Eastern Regional Radioisotope Centre for the Arab Countries, Dokki, Egypt using Cobalt 60 ( $Co^{60}$ )<sup>32</sup>.

### Testicular protein extraction

All the animals were anaesthetized and killed by decapitation. Testes were quickly dissected and carefully cleaned of superficial fatty layer, weighed and then washed in ice-cold saline. As mentioned in Elshawi *et al.*<sup>33</sup>, the testes were freezed with liquid nitrogen and homogenized in 1 ml water-soluble extraction buffer. The homogenates left in refrigerator

overnight and vortexed for 15 seconds then centrifuged at 10,000 rpm at  $4^\circ C$  for 15 min. The supernatants containing water-soluble proteins were transferred to new eppendorf tubes and kept at deep-freeze until the different electrophoretic patterns.

### Protein Determination

All samples of each group were pooled together and used as one sample. Protein concentration was estimated in the tissue homogenates according to the method suggested by Bradford<sup>34</sup> using bovine serum albumin as standard. The protein concentration in each well should be in the range between 60–80  $\mu g$  protein.

### Electrophoretic protein pattern

To determine the relative molecular weight of isolated proteins, vertical slab, non-denaturing 10 % polyacrylamide gel electrophoresis of samples was carried out according to method suggested by Laemmli<sup>35</sup> using Mini-gel electrophoresis (BioRad, USA), with the modification that samples, gels and running buffers were lacking SDS. The gels contained Acrylamide/Bis (30% T, 2.67% C) (Acrylamide: bis-acrylamide = 29.2:0.8) and 10% glycerol. Equal quantities of protein were loaded in each well. The gel

was run in buffer containing Tris (24 mM) and glycine (194 mM) at room temperature. After completing the electrophoretic run, protein bands were visualized by staining with Coomassie Brilliant Blue G-250 and destained overnight with 7% (v/v) glacial acetic acid after documentation<sup>36</sup>. The molecular weight of the separated proteins was estimated in comparison to marker of standard molecular weights with regularly spaced bands ranging from 6.458 to 195.755 KDa. 5 $\mu l$  of the marker

loaded in the first well with the samples each run. The native gels were also stained for lipid with Sudan Black B (SBB)<sup>37</sup>. Relative mobilities (Rf) and band percent (B %) of protein and lipoprotein bands were determined.

#### *Electrophoretic localization of in-gel enzyme activity*

The native gel was stained for catalase (CAT) pattern according to method described by Siciliano and Shaw<sup>38</sup>. It was stained for peroxidase (Gpx) pattern using benzidine stain prepared according to method of Rescigno *et al.*<sup>39</sup>. The native gel was processed for localization of in-gel esterases (EST) pattern according to method suggested by Ahmad *et al.*<sup>40</sup> who reported that the gel was incubated in reaction mixture containing  $\alpha$ ,  $\beta$ -naphthyl acetate ( $5.58 \times 10^{-3}$  mM, pH 7.5) as substrates along with dye coupler Fast Blue RR at 25°C in dark. After developing the dark brown bands of EST activity, the reaction was stopped by fixing the gels in 7% glacial acetic acid for 30 min, followed by preserving the gel in 5% acetic acid prepared in 10% methanol.

#### *Computational Methods*

##### *Protein Structure Prediction*

Prediction of protein structure is considered as one of the most important and advanced technologies used by computational structural biology and theoretical chemistry. It aims to determine the three-dimensional structure of proteins from sequences of their amino acid. By this technology, it was expressed that the tertiary structure of protein predicted from its primary structure.

##### *Comparative Protein Modeling*

The solved structures were used as starting points or templates by the comparative protein modeling. This technology is effective because it shows that there is a limited set of tertiary structural motifs to which most proteins belong although number of actual proteins is vast. Furthermore, it was suggested that there are only around 2000 distinct protein folds in nature, though there are many millions of different proteins. Sequence-based methods for identifying protein homology compare sequences to find similarities that are unlikely to occur by chance. Essentially all methods employ some sort of scheme to judge amino acid substitutions, insertions and deletions. Based on the scoring scheme a query sequence is aligned to another sequence or to a profile that represents a set of sequences. In an alignment equivalent amino acids are set side-by-side so that insertions and deletions become apparent as shown in Fig. 1. The score of the sequence, which is used to detect homology, is directly related to the alignment. Profile-profile sequence-based homology detection was used. Sequences can be scored globally or locally. In the former case, the alignment is over the entire length of the sequences. From a biological point of view this is not always desired because related proteins may not have recognizable homology along their entire length. Proteins may share only one out of several domains. Local scoring aligns subsequences only and can be better for finding local similarities. It is also possible to align a global domain model locally to a sequence, (global/local scoring) or to align part of a domain model locally to a sequence (local/local scoring). Based on the amount of information

built into the scoring scheme, existing methods for sequence-based homology detection can broadly be divided into three categories. pair-wise methods that compare sequences one by one, profile methods that compare one sequence to a family of sequences and profile-profile methods that compare families of sequence. It has been shown that at comparable levels of misclassifications, profile based methods are more sensitive than pair-wise methods<sup>41,42</sup> and that profile-profile methods are even more sensitive<sup>43</sup>. All the modeling methods belong to one of the following groups: Homology modeling depends on the reasonable assumption that the two homologous proteins will involve in very similar structures. Due to a protein's fold is more evolutionarily conserved than sequence of its amino acids, comparative modeling of

a target sequence can be carried out with reasonable accuracy on a very distantly related template. This provided with evidence that there is relationship between target and template discerned through alignment of the sequence. Based on study of the comparative modeling, it was suggested that the primary bottleneck arises from difficulties in alignment rather than from errors in prediction of structure given a known-good alignment<sup>44</sup>. When the target and template have identical sequences, the homology modeling becomes the most accurate unsurprisingly. Protein threading is used for scanning sequence of the amino acid in an unknown structure against solved structures in a database<sup>45</sup>. Assessment of compatibility of the sequence to the structure in each case is carried out by a scoring function, thus yielding possible three-dimensional models. Also, this type of the technological method is known as 3D-1D fold recognition due to its compatibility analysis between three-dimensional structures and sequences of linear protein. Moreover, this method has given rise to methods performing an inverse folding search through evaluating compatibility of a given structure with a large sequences in database, thus it is possible to predict which sequences have the potential to produce a given fold<sup>46,47</sup>.

##### *Molecular Dynamic Simulations*

Concepts of the molecular dynamic simulations are quite simple. In these simulations, it is possible to follow the trajectories of N particles interacting via a many-body potential  $U(r_1, r_2, \dots, r_N)$  using Newton's equation of motion<sup>48</sup>:

$$m_i \frac{d^2 r_i}{dt^2} = -\nabla_i U(r_1, \dots, r_N) \quad ; \quad i = 1, \dots, N$$

Where  $m_i$  and  $r_i$  indicate the mass and position of the particle. On the other hand, the force on it is given by the potential gradient  $U$ . Otherwise, in Brownian dynamic simulations, only the ions are simulated explicitly, all the atoms (ions, water, protein and lipid) can be included in the molecular dynamics. At every time step, the potential function is recalculated using new positions of the particles to determine their positions a short time later, and this process is iterated for a large number of steps until a statistically satisfactory data set is generated. The success of molecular dynamics simulations in capturing the

dynamics of the real system hinges critically on how accurately the potential functions or force fields are selected. In the past two decades, numerous studies have been carried out to develop force fields for biomolecular applications, and these are incorporated into several user-friendly computer programs for simulation of biomolecular systems<sup>49,50</sup>. In these programs, the non-bonded interactions between atoms are represented by Coulomb and Lennard-Jones potentials. Pairwise interactions are used for all the atoms in the system, and the potential parameters are determined empirically from spectroscopic data and fits to bulk properties. Most atoms in the system are also covalently bonded to other atoms, and these bonds are represented in molecular dynamics by a set of force parameters. For a geometry in Fig. 2 the bonds will typically involve the separation  $r_{12} = |r_1 - r_2|$  between adjacent pairs of atoms in a molecular framework. The bend angles  $\theta_{123}$  is between successive bond vectors ( $r_2 - r_1$ ) and ( $r_3 - r_2$ ). Usually this bending term is taken to be quadratic in the angular displacement from the equilibrium value. The torsion angles  $\Phi_{1234}$  are defined in terms of three connected bonds, hence four atomic coordinates:

$$\cos \phi_{1234} = -\hat{n}_{123} \cdot \hat{n}_{234}$$

Where  $\hat{n}_{123} = r_{12} \times r_{23}$ ,  $\hat{n}_{234} = r_{23} \times r_{34}$ .

The normal unit defined by each pair of bonds. Usually the torsional potential involves an expansion in periodic functions<sup>51</sup>.

## RESULTS

Electrophoretic protein pattern in the testicular tissue of healthy rats produced 15 bands with Rfs ranged between 0.10 - 0.98 (Mwts 6.70 - 216.96 KDa and B % 0.39 - 16.70). There was only one common bands noticed with Rf 0.98 (Mwt 6.70 KDa and B % 1.96). There was only one characteristic band appeared in irradiated group with Rf 0.64 (Mwt 17.85 KDa and B % 10.07). As compared to control, the 1<sup>st</sup> normal band (Rf 0.10, Mwt 216.96 KDa and B % 16.70) disappeared from CCl<sub>4</sub>-treated and irradiated groups. The 3<sup>rd</sup> normal band (Rf 0.27, Mwt 93.75 KDa and B % 3.82) disappeared from CYP-treated group. The 4<sup>th</sup> band (Rf 0.33, Mwt 58.49 KDa and B % 1.36) disappeared from Pb<sub>2</sub>COOH-treated and Li<sub>2</sub>CO<sub>3</sub>-treated groups. The 6<sup>th</sup> band (Rf 0.45, Mwt 29.85 KDa and B % 6.78) disappeared from irradiated group. Several normal bands (Rfs 0.49, 0.79, 0.84, 0.87 and 0.91, Mwts 26.29, 14.36, 12.81, 11.38 and 9.96 KDa and B % values 7.64, 5.10, 3.73, 3.33 and 10.08) disappeared from CYP-treated group. As shown in Table 1 and illustrated in Fig. 3a, Pb<sub>2</sub>COOH caused quantitative mutation represented by decreasing B % of the 1<sup>st</sup>, 5<sup>th</sup>, 8<sup>th</sup> and 14<sup>th</sup> bands (Rfs 0.11, 0.42, 0.55 and 0.92, Mwts 205.15, 34.04, 21.61 and 9.25 KDa and B % 8.94, 3.00, 0.63 and 6.68 respectively) and by increasing B % of the 11<sup>th</sup> band (Rf 0.80, Mwt 14.16 KDa and B % 38.85). Li<sub>2</sub>CO<sub>3</sub> administration caused disappearance of 2 normal bands with appearance of 2 abnormal bands with Rfs 0.14 and 0.53 (Mwts 187.26 and 23.13 KDa and B % 8.44 and 2.39) respectively. It was

PTSX-----PQTQG---LAKD-----AWEIPRESL

PT + PQ+ GL + AE + S

PTRRTFLDPQSCGDLQAVHLFAKELDAKSV

Figure 1: An alignment between two sequences. Conserved amino acids are aligned and insertions are marked with dashes.

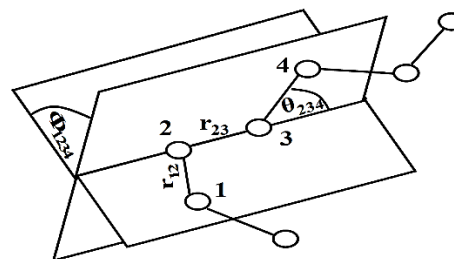


Figure 2: Geometry of a simple chain molecule, illustrating the definition of interatomic distance  $r_{23}$ , bend angle  $\theta_{234}$ , and torsion angle  $\Phi_{1234}$ .

probable that the 2<sup>nd</sup> band was deviated to be appeared with Rf 0.23 (Mwt 120.81 KDa and B % 3.76). This was in association with the quantitative mutation represented by decreasing B % of the 1<sup>st</sup>, 4<sup>th</sup>, 7<sup>th</sup> and 12<sup>th</sup> bands (Rfs 0.10, 0.33, 0.50 and 0.85, Mwts 215.78, 55.78, 25.29 and 12.27 KDa and B % values 9.62, 0.31, 0.53 and 8.64 respectively)

and by increasing B % of the 3<sup>rd</sup>, 6<sup>th</sup> and 9<sup>th</sup> bands (Rfs 0.28, 0.45 and 0.68, Mwts 87.32, 30.40 and 16.78 KDa and B % 5.30, 14.33 and 30.03 respectively). From the SI values, the lowest SI value (0.42) was recorded with CYP-treated group and the highest SI value (0.79) was recorded with Pb<sub>2</sub>COOH-treated group (Fig. 3b). Lipoprotein pattern in healthy testicular tissue produced 5 bands with Rfs 0.05, 0.14, 0.26, 0.38 and 0.85 (B % 6.07, 19.62, 29.75, 12.60 and 31.97) respectively. There was one common band appeared with Rf 0.05 (B % 6.07) (Table 2 and illustrated in Fig. 4a). As compared to control, CYP administration and irradiation caused disappearance of the 5<sup>th</sup> normal band. Pb<sub>2</sub>COOH administration caused qualitative alterations represented by disappearance of the 2<sup>nd</sup> band with deviation of the 3<sup>rd</sup> and 4<sup>th</sup> bands to be appeared with Rfs 0.28 and 0.44 (B % 14.01 and 41.10). Li<sub>2</sub>CO<sub>3</sub> administration caused qualitative alterations represented by disappearance of 2 normal bands with appearance of one abnormal band (Rf 0.07, B % 22.88). In the DXR-treated group, the qualitative alterations were represented by disappearance of 2 normal bands with deviation of the 3<sup>rd</sup> normal band to be appeared with Rf 0.25 (B % 47.00). This was in addition to the quantitative mutation which was represented by increasing B % of the 1<sup>st</sup> band (Rf 0.04, B % 21.45). In the CCl<sub>4</sub>-treated group, the qualitative alterations were represented by disappearance of one normal bands with appearance of one abnormal band with Rf 0.06 (B % 7.33). This was in addition to the quantitative mutation which was

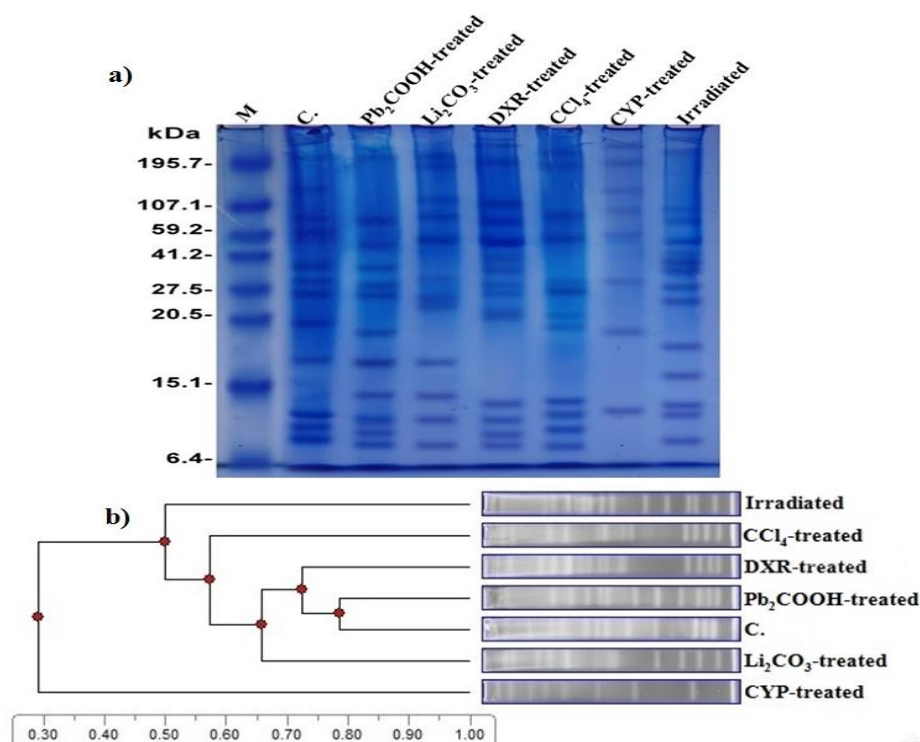


Figure 3: (a) Electrophoretic protein pattern showing toxic effect of  $Pb_2COOH$ ,  $Li_2CO_3$ , DXR,  $CCl_4$ , CYP and irradiation on protein pattern in testicular tissue of male rats, (b) Dendrogram showing the similarity and relationship among  $Pb_2COOH$ -treated,  $Li_2CO_3$ -treated, DXR-treated,  $CCl_4$ -treated, CYP-treated and Irradiated groups in male rats as compared to control.

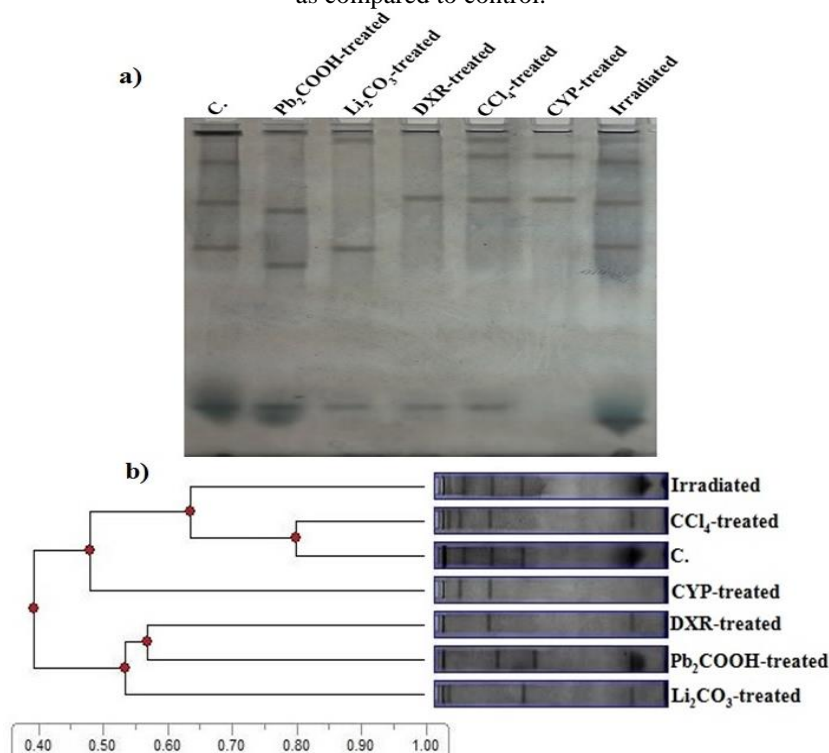


Figure 4: (a) Electrophoretic lipoprotein pattern showing toxic effect of  $Pb_2COOH$ ,  $Li_2CO_3$ , DXR,  $CCl_4$ , CYP and irradiation on lipoprotein pattern in testicular tissue of male rats, (b) Dendrogram showing the similarity and relationship among  $Pb_2COOH$ -treated,  $Li_2CO_3$ -treated, DXR-treated,  $CCl_4$ -treated, CYP-treated and Irradiated groups in male rats as compared to control.

represented by increasing B % of the 3<sup>rd</sup> band (Rf 0.26, B % 48.22). In the CYP-treated group, the qualitative

alterations were represented by disappearance of 2 normal bands with deviation of the 3<sup>rd</sup> normal band to be appeared

with Rf 0.24 (B % 52.36). The quantitative mutation was represented by increasing B % of the 2<sup>nd</sup> band (Rf 0.12, B

% 41.47). In the irradiated group, the qualitative alterations were represented by appearance of one abnormal band (Rf

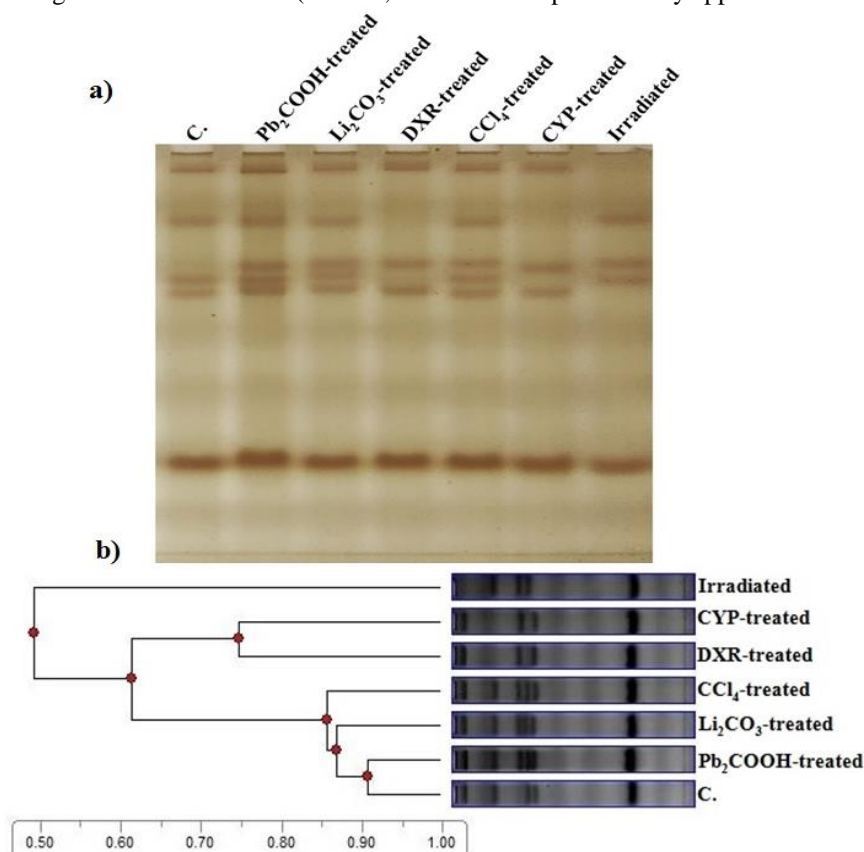


Figure 5: (a) Electrophoretic CAT pattern showing toxic effect of Pb<sub>2</sub>COOH, Li<sub>2</sub>CO<sub>3</sub>, DXR, CCl<sub>4</sub>, CYP and irradiation on CAT pattern in testicular tissue of male rats, (b) Dendrogram showing the similarity and relationship among Pb<sub>2</sub>COOH-treated, Li<sub>2</sub>CO<sub>3</sub>-treated, DXR-treated, CCl<sub>4</sub>-treated, CYP-treated and Irradiated groups in male rats as compared to control.

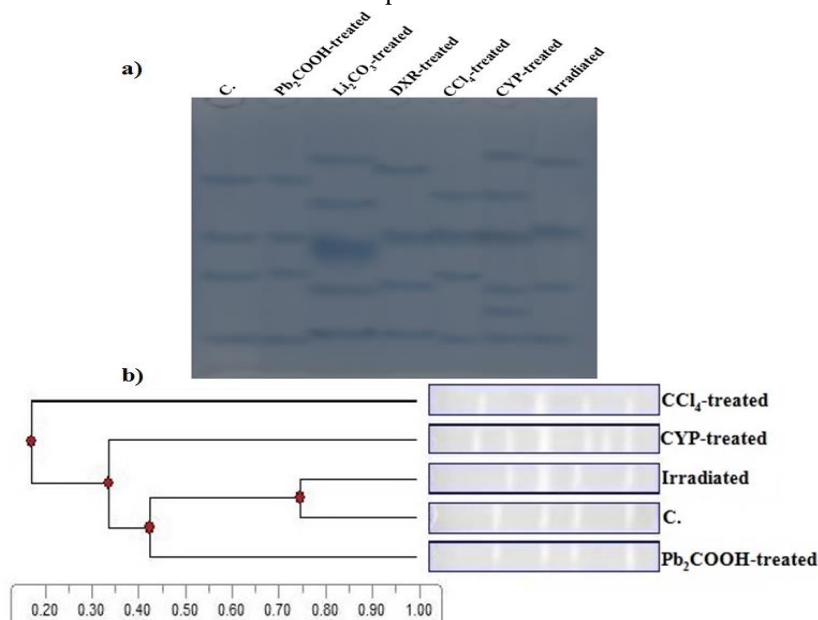


Figure 6: (a) Electrophoretic Gpx pattern showing toxic effect of Pb<sub>2</sub>COOH, Li<sub>2</sub>CO<sub>3</sub>, DXR, CCl<sub>4</sub>, CYP and irradiation on Gpx pattern in testicular tissue of male rats, (b) Dendrogram showing the similarity and relationship among Pb<sub>2</sub>COOH-treated, Li<sub>2</sub>CO<sub>3</sub>-treated, DXR-treated, CCl<sub>4</sub>-treated, CYP-treated and Irradiated groups in male rats as compared to control.

0.07, B % 4.65) with deviation of the 5<sup>th</sup> normal band to be appeared with Rf 0.90 (B % 32.28). There was no quantitative mutation. The lowest SI value (0.44) was observed with Pb<sub>2</sub>COOH-treated group and the highest SI

0.28 (B % 13.01) in irradiated group. On the other hand, there was quantitative mutation occurred through increasing B % severely in the 1<sup>st</sup> type of the enzyme appeared in the DXR-treated group (Rf 0.06 and B %

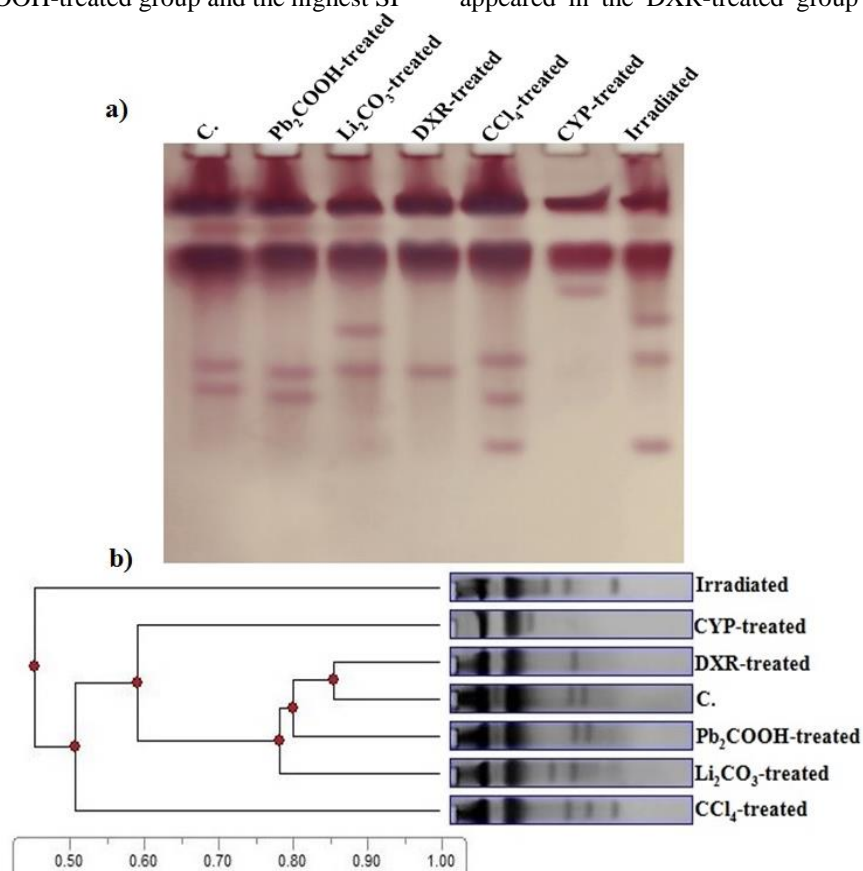


Figure 7: (a) Electrophoretic EST pattern showing toxic effect of Pb<sub>2</sub>COOH, Li<sub>2</sub>CO<sub>3</sub>, DXR, CCl<sub>4</sub>, CYP and irradiation on EST pattern in testicular tissue of male rats, (b) Dendrogram showing the similarity and relationship among Pb<sub>2</sub>COOH-treated, Li<sub>2</sub>CO<sub>3</sub>-treated, DXR-treated, CCl<sub>4</sub>-treated, CYP-treated and Irradiated groups in male rats as compared to control.

values (0.73 and 0.80) were observed with CCl<sub>4</sub>-treated and irradiated groups (Fig. 4b). There was complete similarity between DXR-treated and CYP-treated groups in number and arrangement of the bands. As revealed in Table 3 and illustrated in Fig. 5a, 5 types of CAT enzyme were produced in healthy testicular tissue with Rfs 0.07, 0.19, 0.31, 0.35 and 0.75 (B % values 14.31, 25.65, 15.14, 22.13 and 22.78). There was only one common band appeared with Rf 0.75 (B % 22.78). As compared to control group, Pb<sub>2</sub>COOH administration caused obvious qualitative alterations represented by existence of one abnormal band with Rf 0.28 (B % 10.22). Irradiation caused disappearance of the 1<sup>st</sup> and 4<sup>th</sup> normal types of the enzyme. Li<sub>2</sub>CO<sub>3</sub> caused qualitative alterations represented by appearance of one abnormal type with Rf 0.27 (B % 9.74). This was in addition to the quantitative mutation occurred by decreasing B % in the band appeared with Rf 0.33 (B % 9.85). In all treated groups, there was one abnormal band appeared with different data. This band was appeared with Rf 0.28 (B % 16.19) in DXR-treated group, with Rf 0.28 (B % 8.39) in CCl<sub>4</sub>-treated group, with Rf 0.29 (B % 13.11) in CYP-treated group and with Rf

47.65) and CYP-treated group (Rf 0.05 and B % 43.20). The lowest SI value (0.69) was noticed in DXR-treated, CYP-treated and irradiated groups. There was complete similarity between the Li<sub>2</sub>CO<sub>3</sub>-treated and irradiated groups (Fig. 5b). The highest SI value (0.91) was observed with Pb<sub>2</sub>COOH, Li<sub>2</sub>CO<sub>3</sub>-treated and CCl<sub>4</sub>-treated groups. Four types of Gpx enzyme were produced in healthy testicular tissue with Rfs 0.30, 0.51, 0.66 and 0.88 (B % values 29.11, 19.44, 32.41 and 19.04) respectively. There were no common bands. As shown in Table 4 and illustrated in Fig. 6a, it was found that Pb<sub>2</sub>COOH administration caused qualitative alterations represented by disappearance of the 4<sup>th</sup> type with deviation of the 3<sup>rd</sup> type to be appeared with Rf 0.64 (B % 41.28). Li<sub>2</sub>CO<sub>3</sub> administration caused qualitative abnormalities represented by disappearance of the 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>th</sup> types with deviation of the 4<sup>th</sup> type to be appeared with Rf 0.86 (B % 19.75). In addition, there were 4 abnormal bands appeared with Rfs 0.23, 0.39, 0.55 and 0.70 (B % values 21.18, 19.17, 1.41 and 38.49) respectively. The abnormalities occurred with the same degree in DXR-

treated and irradiated groups. These alterations were represented by disappearance of the 1<sup>st</sup> type of the enzyme and appearance of one abnormal band with deviation of the other types of enzyme to be appeared with different data. In the DXR-treated group, the abnormal band was appeared with Rf 0.26 (B % 33.12). The 2<sup>nd</sup>, 3<sup>rd</sup> and 4<sup>th</sup>

qualitative alteration was represented by disappearance of the 1<sup>st</sup> type with appearance of one abnormal band (Rf 0.36, B % 22.48). The quantitative mutation occurred by decreasing B % of the 2<sup>nd</sup> type (Rf 0.51 and B % 0.89) and increasing B % of the 3<sup>rd</sup> type (Rf 0.65 and B % 56.37). The lowest SI value (0.25) was noted with irradiated group

and  
the

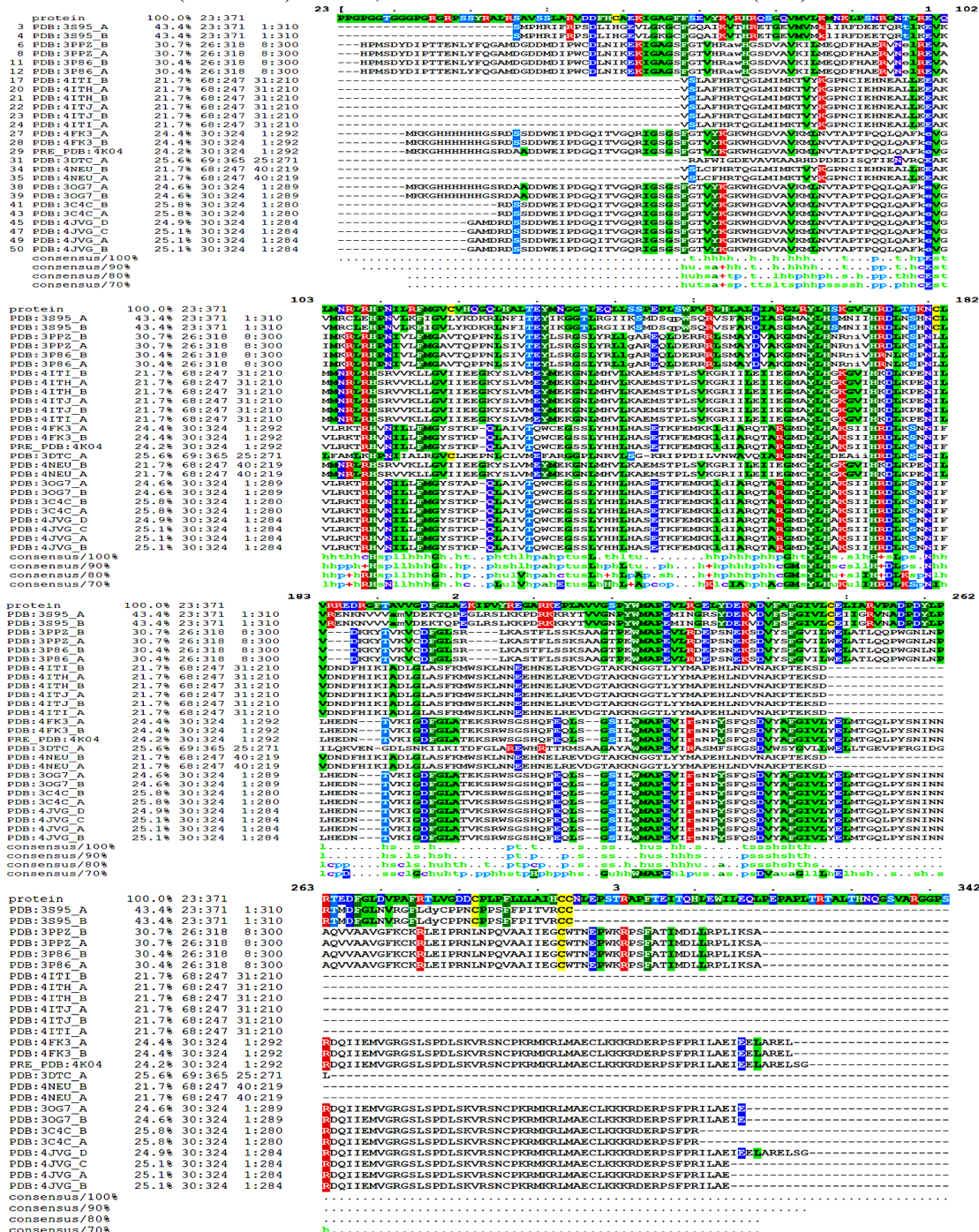


Figure 8: Sequence alignments of TESK1 protein kinases and its homolog structures extracted from the protein data bank (PDB) database. Amino acids are colored based on their properties.

types deviated to be appeared with Rfs 0.52 and 0.68 (B % values 23.19 and 23.54). While in irradiated group, the abnormal band appeared with Rf 0.23 (B % 33.28). The normal types were deviated to be appeared with Rfs 0.49 and 0.69 (B % 0.58 and 49.70). In CCl<sub>4</sub>-treated group, the

highest value (0.75) was observed with CCl<sub>4</sub>-treated group. In the Li<sub>2</sub>CO<sub>3</sub>-treated and DXR-treated groups, it was observed that all the bands were not matched with all bands of the other groups (Fig. 6b). Four types of EST enzyme were produced in testicular tissue of control rats

with Rfs 0.14, 0.26, 0.50 and 0.57 (B % values 38.78, 33.44, 8.12 and 19.66) respectively (Table 5 and illustrated in Fig. 7a). There were 2 common bands appeared with Rfs 0.14 and 0.26 (B % 38.78 and 33.44). Administration of  $\text{Pb}_2\text{COOH}$  caused no obvious qualitative or quantitative mutations as compared to control sample.  $\text{Li}_2\text{CO}_3$  administration caused qualitative mutation represented by disappearance of the 4<sup>th</sup> normal type with appearance of

model of the TESK1 was quite big and no available template for the whole sequence and its first half (up to residue 333) was synthesized with a very good homology model. For the rest of the model (334 - 626), a draft structure was carried out using residue addition algorithm but its 3D structure is not good. The current framework concerns to obtain 3D model of TESK1 using homology and threading techniques. The 3D model was

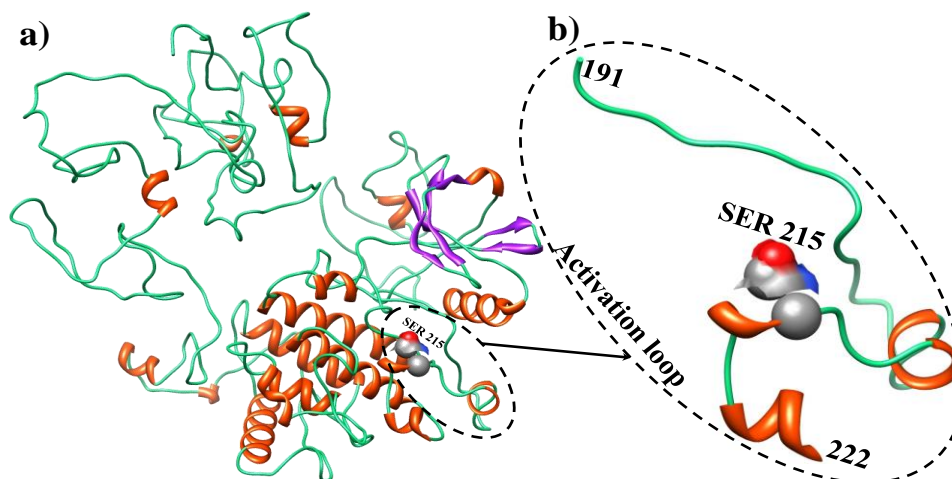


Figure 9: 3D-Homology model of TESK1 predicted by I-TASSER platform, a) The full length protein structure and b) the activation loop subdomain. Residues are colored based on the secondary structure (helix in orange, strand in purple and coil loop in cyan).

one abnormal band with Rf 0.42 (B % 9.90). This was in addition to increasing B % of the 3<sup>rd</sup> normal band (Rf 0.52 and B % 29.28). In the DXR-treated group, the alterations were represented by disappearance of the 4<sup>th</sup> type with increasing B % of the 3<sup>rd</sup> type (Rf 0.51 and B % 23.86). In the  $\text{CCl}_4$ -treated group, the alterations occurred qualitatively by appearance of one abnormal band (Rf 0.69 and B % 7.79) without disappearance of the normal types of enzymes. In the CYP-treated group, the alterations occurred qualitatively by disappearance of the 3<sup>rd</sup> and 4<sup>th</sup> types of enzyme with appearance of one abnormal band (Rf 0.33 and B % 19.70). In the irradiated group, the qualitative alterations occurred through disappearance of the 4<sup>th</sup> type of enzyme with appearance of 2 abnormal bands with Rf 0.40 and 0.68 (B % 8.51 and 8.14) respectively. There was complete similarity between  $\text{Pb}_2\text{COOH}$ -treated and  $\text{Li}_2\text{CO}_3$ -treated groups (equal SI values 0.75). The lowest SI value (0.44) was observed with irradiated group. The highest SI value (0.86) was noticed with DXR-treated group (Fig. 7b). Although the genome expression of TESK1 protein as well as its one dimension sequence were identified previously [Jiro Toshima, Tomoko Tanaka, Kensaku Mizuno, THE JOURNAL OF BIOLOGICAL CHEMISTRY, 274, 12171-12176 (1999) - S. Davila, F. E. Froeling, A. Tan, C. Bonnard, G. J. Boland, H. Snippe, M. L. Hibberd, M. Seielstad, Genes Immun. 11, 232-238 (2010)], however its crystal structure is not known yet. Structural data has vital role not only in comparative analysis between TESK1 and other kinase protein but also for structural activity relationship (SAR) investigation. During the current work, it was noted that

built by means of restraint-based comparative modeling. Sequence identity percentages between the target TESK1 and templates obtained from FASTA and BLAST databases [H. McWilliam H, W. Li, M. Uludag, S. Squizzato, Y. M. Park, N. Buso, A. P. Cowley, R. Lopez, Analysis Tool Web Services from the EMBL-EBI, Nucleic acids research 41 (Web Server issue) :W597-600 (2013 Jul) - A. Morgulis, G. Coulouris, Y. Raytselis, T. L. Madden, R. Agarwala, A. A. Schäffer, "Database indexing for production MegaBLAST searches." Bioinformatics 15: 1757-1764 (2008)]. Templates were selected according to the similarity with the query sequence (with similarity percent of  $43.0 \pm 2\%$ ). The model was construct using multiple alignment by means of restraint-based comparative modeling, using the X-ray crystallographic structures of human LIMK1 kinase (PDB ID: 3s95), Tank-binding kinase I (PDB ID: 4iw0), tyrosine-protein kinase (PDB: 2fo0), and G protein coupled receptor kinases (PDB ID: 3c4w, 2acx and 3NYN) as templates. Finally the hydrogen atoms were added. [Y. Zhang. I-TASSER server for protein 3D structure prediction. BMC Bioinformatics, 9:40 (2008) - A. Roy, A. Kucukural, Y. Zhang. I-TASSER: a unified platform for automated protein structure and function prediction. Nature Protocols, vol 5, 725-738 (2010) - A. Roy, J. Yang, Y. Zhang. COFACTOR: an accurate comparative algorithm for structure-based protein function annotation. Nucleic Acids Research, vol 40, W471-W477 (2012)]. Fig. 9 shows the constructed 3D model of TESK1 model where high similarity domains (from residue 23 to residue 341) were constructed by threading and the other domains (1~23 and 341~626) were

Table 1: Electrophoretic pattern showing effect of Pb<sub>2</sub>COOH, Li<sub>2</sub>CO<sub>3</sub>, DXR, CCl<sub>4</sub>, CYP and irradiation on protein pattern in testicular tissue of male rats.

Control						Toxic substances											
						Pb <sub>2</sub> COOH-treated				Li <sub>2</sub> CO <sub>3</sub> -treated				DXR-treated			
Rf.	Mwt	B. %	Rf.	Mwt	B. %	Rf.	Mwt	B. %	Rf.	Mwt	B. %	Rf.	Mwt	B. %	Rf.	Mwt	B. %
0.10	216.96	16.70	0.10	216.96	25.60	0.10	215.78	9.62	0.06	245.32	8.04	0.09	221.69	8.58	0.06	245.32	4.78
0.19	146.54	6.54	0.28	84.20	0.69	0.14	187.26	8.44	0.11	205.15	8.94	0.13	194.49	11.86	0.12	200.43	5.81
0.27	93.75	3.82	0.35	49.39	5.82	0.23	120.81	3.76	0.24	115.06	3.33	0.27	88.38	5.36	0.20	142.99	13.54
0.33	58.49	1.36	0.41	35.85	5.56	0.28	87.32	5.30	0.28	83.17	3.86	0.35	51.55	1.51	0.25	107.10	8.11
0.41	36.12	7.03	0.46	29.14	7.37	0.33	55.78	0.31	0.35	48.88	3.59	0.44	30.98	13.16	0.33	55.78	15.76
0.45	29.85	6.78	0.49	25.85	0.53	0.45	30.40	14.33	0.39	40.14	0.40	0.49	25.85	7.37	0.60	19.16	29.98
0.49	26.29	7.64	0.60	19.23	19.18	0.50	25.29	0.53	0.42	34.04	3.00	0.56	21.31	3.53	0.83	13.21	19.69
0.57	20.59	0.39	0.68	16.88	0.54	0.53	23.13	2.39	0.46	28.97	6.16	0.58	19.79	26.15	0.98	6.84	2.33
0.68	16.88	11.46	0.78	14.72	18.37	0.68	16.78	30.03	0.49	26.14	6.22	0.80	14.06	4.07	0.98	6.84	0.00
0.74	15.58	14.09	0.85	12.33	4.11	0.78	14.59	8.01	0.55	21.61	0.63	0.83	12.98	4.81	—	—	—
0.79	14.36	5.10	0.89	10.91	3.53	0.85	12.27	8.64	0.80	14.16	38.85	0.88	11.25	5.44	—	—	—
0.84	12.81	3.73	0.92	9.46	7.26	0.92	9.25	7.05	0.85	12.20	4.67	0.94	8.68	6.07	—	—	—
0.87	11.38	3.33	0.99	6.47	1.44	0.98	6.70	1.58	0.89	10.85	3.73	0.98	6.84	2.09	—	—	—
0.91	9.96	10.08	—	—	—	—	—	—	0.92	9.25	6.68	—	—	—	—	—	—
0.98	6.70	1.96	—	—	—	—	—	—	0.98	6.70	1.90	—	—	—	—	—	—
Rf.: Relative Mobility, Mwt.: Molecular Weight, B. %: Band Percent.						Irradiated											
In each lane, arrangement of the bands is not correlated to arrangement of the bands in the other lanes.						Rf.	Mwt	B. %	Rf.	Mwt	B. %	Rf.	Mwt	B. %	Rf.	Mwt	B. %
						0.10	216.96	16.70	0.08	229.96	5.65	0.08	229.96	5.65	0.08	229.96	5.65
						0.19	146.54	6.54	0.25	108.23	16.78	0.25	108.23	16.78	0.25	108.23	16.78
						0.27	93.75	3.82	0.29	80.13	5.27	0.29	80.13	5.27	0.29	80.13	5.27
						0.33	58.49	1.36	0.34	53.89	0.36	0.34	53.89	0.36	0.34	53.89	0.36
						0.41	36.12	7.03	0.38	41.93	4.62	0.38	41.93	4.62	0.38	41.93	4.62
						0.45	29.85	6.78	0.40	38.50	0.25	0.40	38.50	0.25	0.40	38.50	0.25
						0.49	26.29	7.64	0.43	32.87	6.16	0.43	32.87	6.16	0.43	32.87	6.16
						0.57	20.59	0.39	0.47	27.66	3.94	0.47	27.66	3.94	0.47	27.66	3.94
						0.68	16.88	11.46	0.52	24.10	14.89	0.52	24.10	14.89	0.52	24.10	14.89
						0.74	15.58	14.09	0.64	17.85	10.07	0.64	17.85	10.07	0.64	17.85	10.07
						0.79	14.36	5.10	0.73	15.85	8.98	0.73	15.85	8.98	0.73	15.85	8.98
						0.84	12.81	3.73	0.79	14.31	1.22	0.79	14.31	1.22	0.79	14.31	1.22
						0.87	11.38	3.33	0.83	12.98	11.69	0.83	12.98	11.69	0.83	12.98	11.69
						0.91	9.96	10.08	0.91	10.03	7.47	0.91	10.03	7.47	0.91	10.03	7.47
						0.98	6.70	1.96	0.98	6.77	2.65	0.98	6.77	2.65	0.98	6.77	2.65

constructed through insertion algorithms. The activation loop (191~222) has flexible coil shape attached to short helix at the end. This subdomain consists of the SER215 that is known to be phosphorylated within kinase activation loop reaction [Jiro Toshima, Tomoko Tanaka, Kensaku Mizuno, The Journal of Biological Chemistry, 274 : 12171-12176 (1999)].

## DISCUSSION

The difference in protein pattern acts as a tool to identify the physiological state of the testicular tissue in the treated groups as compared to control. It was reported that electrophoresis used to detect the mutations reflected as quantitative changes in the protein expression<sup>52</sup>. The SI value is inversely proportional to the genetic distance. When the SI value between the control and all the treated groups recorded low values, this indicates to toxic effect of these substances and the differences in number and arrangement of the protein bands<sup>53,54</sup>. The alterations in protein pattern can be detected electrophoretically due to the chemical changes which may be represented by fragmentation, cross-linking, aggregation and oxidation by oxygen radicals. These disturbances lead to variation of the different biological processes due to activation of the genes which are responsible for synthesis of different types of proteins not produced in the healthy group<sup>55</sup>. During the present study, all the toxic factors exhibited different mutagenic effects and caused irreversible changes at the molecular level. The protein bands in testicular tissue of treated rats may differ qualitatively through disappearance in some normal bands or appearance of new abnormal ones. Disappearance of the normal bands in treated rats may be attributed to effects of toxic substances which inhibit expression of the genes responsible for synthesis of these deleted proteins. In addition, the alterations may occur quantitatively through remaining the bands but with different quantity. This may be explained by effect of the toxic substances which could not inhibit expression of the genes which are responsible for synthesis of this protein type, but it may be affected only at the quantitative level. The quantitative mutation may occur due to disturbances in the golgi apparatus which subsequently leads to accumulation of protein due to impairment of glycosylation and glycoprotein trafficking<sup>56</sup>. During the present study, lithium caused alterations in the protein pattern. This was in accordance with Mathur *et al.*<sup>57</sup> who reported that the toxicity may occur due to presence of the reactive oxygen species (ROS). These radicals prevent the spin restriction of O<sub>2</sub> giving rise to generation of ROS and chain reaction. This leads to structural alterations in the native the proteins. The abnormalities in the different electrophoretic patterns as a result of lithium exposure may refer to elevation of lipid peroxidation reaction<sup>58</sup>. During another recent point of view, it was suggested that the disturbances occurred as a result of lithium administration may not be caused due to the oxidative stress or lipid peroxidation. The toxicity may occur as a result of other possible

mechanism due to lithium toxicity<sup>59</sup>. In the current experiment, administration of CCl<sub>4</sub> induced testis toxicity through by altering the protein pattern. This was in agreement with Terzi *et al.*<sup>60</sup> who postulated that CCl<sub>4</sub> caused generation of the ROS leading to loss of germ cells, inhibition of structural deterioration of the sertoli cells in seminiferous tubules of testicular tissue in rat<sup>61</sup>. DXR administration induced testicular toxicity. This was in accordance with Patil and Balaraman<sup>62</sup> who reported that DXR induced a significant decline in testes weight, sperm count, serum testosterone, increase in serum lactate dehydrogenase and increases lipid peroxidation in that tissue. The injury in this organ may occur due the oxidative stress induced by the reactive intermediates

semiquinone formed from DXR. The semiquinone radical intermediates react with molecular oxygen to form ROS that interact with cellular macromolecules causing cytological damage<sup>63</sup>. Irradiation caused differences in protein pattern. This was in agreement with Moon and Song<sup>64</sup> who suggested that irradiation caused initial fragmentation of polypeptide chains and leads to lowering the ordered protein structure as a result of subsequent aggregation and degeneration of proteins. The alterations in protein pattern may occur as a result of the DNA damage after irradiation, resulting in subsegment changes in mRNA. Subsequently, this leads to impairment in transcription of the genes and hence inhibition of protein synthesis<sup>65</sup>.

Table 2: Electrophoretic pattern showing effect of Pb<sub>2</sub>COOH, Li<sub>2</sub>CO<sub>3</sub>, DXR, CCl<sub>4</sub>, CYP and irradiation on lipoprotein pattern in testicular tissue of male rats.

Pattern in testicular tissue of male rats.													
Control				Toxic substances									
		Pb <sub>2</sub> COOH-treated		Li <sub>2</sub> CO <sub>3</sub> -treated		DXR-treated		CCl <sub>4</sub> -treated		CYP-treated		Irradiated	
Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %
0.05	6.07	0.04	10.25	0.04	9.55	0.04	21.45	0.04	3.37	0.04	6.17	0.04	2.70
0.14	19.62	0.28	14.01	0.07	22.88	0.25	47.00	0.06	7.33	0.12	41.47	0.07	4.65
0.26	29.75	0.44	41.10	0.39	38.40	0.86	31.56	0.12	12.66	0.24	52.36	0.13	20.11
0.38	12.60	0.85	34.64	0.86	29.17	—	—	0.26	48.22	—	—	0.26	20.66
0.85	31.97	—	—	—	—	—	—	0.86	28.42	—	—	0.38	19.59
—	—	—	—	—	—	—	—	—	—	—	—	0.90	32.28

Rf.: Relative Mobility, B.%: Band Percent.

In each lane, arrangement of the bands is not correlated to arrangement of the bands in the other lanes.

Table 3: Electrophoretic pattern showing effect of Pb<sub>2</sub>COOH, Li<sub>2</sub>CO<sub>3</sub>, DXR, CCl<sub>4</sub>, CYP and irradiation on CAT pattern in testicular tissue of male rats.

Control		Toxic substances											
		Pb <sub>2</sub> COOH-treated		Li <sub>2</sub> CO <sub>3</sub> -treated		DXR-treated		CCl <sub>4</sub> -treated		CYP-treated		Irradiated	
Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %
0.07	14.31	0.07	15.35	0.06	21.60	0.06	47.65	0.06	17.98	0.05	43.20	0.17	55.44
0.19	25.65	0.19	24.45	0.18	26.05	0.28	16.19	0.19	23.35	0.29	13.11	0.28	13.01
0.31	15.14	0.28	10.22	0.27	9.74	0.34	10.95	0.28	8.39	0.35	24.17	0.32	12.91
0.35	22.13	0.32	7.49	0.30	6.40	0.76	25.22	0.32	7.47	0.75	19.51	0.76	18.64
0.75	22.78	0.34	21.22	0.33	9.85	—	—	0.35	25.14	—	—	—	—
—	—	0.74	21.27	0.75	26.36	—	—	0.76	17.67	—	—	—	—

Rf.: Relative Mobility, B.%: Band Percent.

In each lane, arrangement of the bands is not correlated to arrangement of the bands in the other lanes.

In addition, the formation of free radicals can cause breakage of chemical bonds and destruction of protein molecules<sup>66</sup>. The testes are susceptible to oxidative stress caused by free radicals. ROS-scavenging enzymes play a vital role in the testicular tissue. The CAT and Gpx are particularly important during the testicular regression<sup>67</sup>. The oxidative stress leads to changes in activities of CAT and Gpx and hence leading to impairment of the spermatogenesis process<sup>68</sup>. During the present work, it was found that irradiation caused alterations in the electrophoretic isoenzymes. This was in accordance with finding of Manciluae *et al.*<sup>69</sup> who reported that irradiation

affected activity of the enzymes due to inhibition in synthesis of the DNA and RNA which are responsible for biosynthesis of these enzymes. Moreover, the abnormalities might refer to the lesions induced by radiation and these lesions repair may occur at sites non-specific for synthesis of these enzymes<sup>70</sup>. It is well known that the testes are a comparatively rich source of EST enzyme. The pubertal growth is correlated with the increase of testicular EST in the gonads<sup>71</sup>. So, EST enzyme selected to be under the present study. According to results of the current study, all the toxic factors caused qualitative and quantitative alterations in the electrophoretic EST

Table 4: Electrophoretic pattern showing effect of Pb<sub>2</sub>COOH, Li<sub>2</sub>CO<sub>3</sub>, DXR, CCl<sub>4</sub>, CYP and irradiation on Gpx pattern in testicular tissue of male rats.

Control		Toxic substances											
		Pb <sub>2</sub> COOH-treated		Li <sub>2</sub> CO <sub>3</sub> -treated		DXR-treated		CCl <sub>4</sub> -treated		CYP-treated		Irradiated	
Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %
0.30	29.11	0.30	36.94	0.23	21.18	0.26	33.12	0.36	22.48	0.22	17.93	0.23	33.28
0.51	19.44	0.51	21.78	0.39	19.17	0.52	23.19	0.51	0.89	0.35	18.65	0.49	0.58
0.66	32.41	0.64	41.28	0.55	1.41	0.68	23.54	0.65	56.37	0.51	0.92	0.69	49.70
0.88	19.04	—	—	0.70	38.49	0.86	20.15	0.88	20.26	0.70	33.92	0.88	16.45
—	—	—	—	0.86	19.75	—	—	—	—	0.78	11.47	—	—
—	—	—	—	—	—	—	—	—	—	0.88	17.11	—	—

Table 5: Electrophoretic pattern showing effect of Pb<sub>2</sub>COOH, Li<sub>2</sub>CO<sub>3</sub>, DXR, CCl<sub>4</sub>, CYP and irradiation on EST pattern in testicular tissue of male rats.

Control		Toxic substances											
		Pb <sub>2</sub> COOH-treated		Li <sub>2</sub> CO <sub>3</sub> -treated		DXR-treated		CCl <sub>4</sub> -treated		CYP-treated		Irradiated	
Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %	Rf.	B. %
0.14	38.78	0.14	38.77	0.14	35.04	0.14	42.32	0.14	38.17	0.14	35.27	0.14	36.70
0.26	33.44	0.26	27.85	0.25	25.78	0.26	33.82	0.27	29.72	0.26	45.04	0.26	32.85
0.50	8.12	0.51	8.00	0.42	9.90	0.51	23.86	0.49	11.79	0.33	19.70	0.40	8.51
0.57	19.66	0.58	25.39	0.52	29.28	—	—	0.58	12.53	—	—	0.49	13.80
—	—	—	—	—	—	—	—	0.69	7.79	—	—	0.68	8.14

Rf.: Relative Mobility, B. %: Band Percent.

Arrangement of the bands at each lane is not correlated with the bands in the other lanes.

pattern in the testicular tissue. This may refer to inhibition in expression of the genes which are responsible for synthesis of the testicular EST. This caused structural changes of leydig and sertoli cells and hence inhibition of spermatogenesis<sup>72</sup>. It was reported that the 3.6-kb TESK1 mRNA was expressed predominantly in rat testicular germ cells at stages of pachytene spermatocytes to round spermatids<sup>24,25</sup>. Several protein kinases are phosphorylated on residues located in the activation loop. The exposure to the external deleterious factors like irradiation and the other toxic substances exhibited mutagenic effect on this protein kinase. According to the site-specific mutation analyses, it was demonstrated that TESK1 autophosphorylates Ser-215, which lies in the activation loop. The TESK1 mutant with replacement of Ser-215 by alanine has no activity to phosphorylate histone H3, which suggests that autophosphorylation of Ser-215 is required to exhibit the kinase activity of TESK1<sup>73,74</sup>.

## CONFLICTS OF INTEREST

There are none declared conflicts of interest by authors

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