

## Research Article

### DNA Interaction Study of Some Symmetrical 1,2-Phenylenediamine Schiff's Base Derivatives as New Potential DNA Intercalators using Ethidium Bromide Competition Fluorescent Assay

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#### Abstract

A series of novel potential DNA intercalators of symmetrical 1,2-phenylenediamine Schiff's base derivatives were synthesized. The binding properties of these compounds to Genomic DNA (G-DNA) have been investigated by fluorescence spectroscopy. Ethidium binding to DNA significantly enhanced its fluorescence making it a convenient probe to evaluate DNA binding of many drugs. The addition of a DNA binding agent induces a progressive decrease in fluorescence of ethidium due to its displacement from the duplex. This also allows distinguishing non-intercalative binding agents from intercalating agents: Agents having a huge site size groove binders need correspondingly smaller concentrations to saturate the sites. The results indicate that all the targeted compounds can interact with G-DNA, and among them, SW7 (1,1'-((1E,1'E)-(1,2-phenylenebis (azanylylidene)) bis (methanylylidene)) bis (naphthalen-2-ol)), showed the highest key selection vector (KSV) value, suggest that compound SW7, binds most strongly to G-DNA.

**Keywords:** Fluorescence; DNA intercalation; Key selection vector

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#### Introduction

Several biological experiments proposed that DNA is one of the principal cellular targets for numerous anticancer agents. Mainly, in cancer cells, DNA could be selectively damaged, as a result of interactions with anticancer agents, consequently blocking of cell division leads to cell death [1,2]. The molecules that interact with DNA are generally bound to DNA through non-covalent bonds by three main mechanisms: Groove binding, intercalation or static electronic interactions. Static electronic interactions could be related to molecules that bind to the negatively charged DNA double helix at external sites through non-specific interaction. The second mode of interaction is called groove binding in which the targeting molecules interact with DNA in base edges of minor or major grooves [3-6]. The third mode of interaction is intercalation that is closely related to the antitumor ability of several anticancer drugs [7-9].

Intercalators are ligands interacting with the DNA double helix in a reversible manner. Many of them are currently used as powerful drugs for the treatment of breast and ovarian cancers, acute leukemia, and many others are still in clinical trials. Intercalating agents have several universal structural features; the most important is a planar polyaromatic system that inserts between DNA base-pairs with a marked preference for the purine-3'-pyrimidine-5' sequence [10-12]. Ethidium bromide is frequently utilized as a fluorescent tag (nucleic acid stain) in molecular biology for many procedures such as agarose gel electrophoresis. It intercalates with double-stranded DNA and leads to the deformation of the DNA which could affect biological processes, such as DNA transcription and replication [13,14]. Schiff's bases (imines) are compounds that contain azomethine groups [-HC=N-] in their structure. They are formed by condensation of a dynamic carbonyl compound with a primary amine [15,16]. Schiff's bases show a large range of biological activities including anti-viral, anti-bacterial, anti-inflammatory, anti-proliferative, antifungal, anti-malarial and antipyretic pharmacological activities [17-21]. We have recently reported on using microwave assisted synthesis and antimicrobial evaluation of symmetrical 1,2-Phenylenediamine Schiff's base derivatives finding that some of the synthesized compounds showed antibacterial and antifungal activity [22]. Now our aim is to explore how different structural features of 1,2-Phenylenediamine Schiff's base derivatives can affect the DNA binding capability using molecular modeling and key selection vector studies which may serve as a basis for understanding the molecular mechanism of action of the 1,2-Phenylenediamine Schiff's base derivatives and can help to design of new chemotherapeutic molecules.

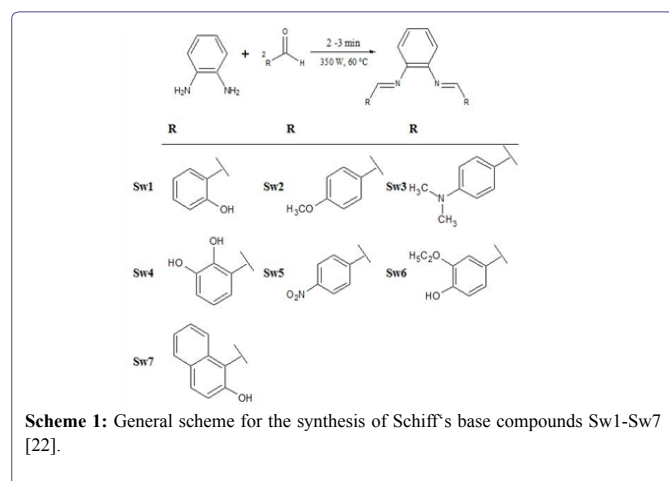
#### Material and Methods

##### Chemistry

##### General procedure for Synthesis of Schiff's bases (Sw1-Sw7)

Schiff's bases were prepared according to our previously reported procedure by reacting of one mole of phenylenediamine and two moles of substituted aromatic aldehydes [22]. All reactants were

mixed together and small amount of ethanol (5-6 ml) was added. This mixture was subjected to microwave irradiation at 350 watt for 2-3 minutes at a maximum of 60°C. After the reaction was completed (2-3 minutes), the mixture was left for cooling and the solid product (crude) was gathered by filtration and washed several times (5-6 washes) with ethanol and then vacuum dried. The gained product was recrystallized in ethanol and after drying that gave the clean pure product (Scheme 1). The crystalline product obtained was characterized as described previously by FTIR and <sup>1</sup>H NMR [22].



### DNA Binding Properties

To study how competently our synthesized compounds interact with G-DNA, the compounds were investigated for their DNA binding ability using fluorescence emission spectroscopy. All experiments were conducted in Tris buffer (0.01M Tris, 0.1M NaCl, at pH 7.4), glass-distilled deionized water and analytical grade reagents were used throughout experiments. The pH values of all solutions were measured with a calibrated Jenway pH-meter model 3510 (Staffordshire, UK). All buffer solutions were filtered through Millipore filters (Millipore, UK) of 0.45 mm pore diameter.

### Absorbance spectra

Absorbance spectra were measured on a Jenway UV-visible spectrophotometer, model 6505 (London, UK) using quartz cells of 1.00 cm path length. The UV-Vis absorbance spectra were recorded in the 200-500nm range and a spectral bandwidth of 3.0nm. For the final spectrum of each solution analyzed baseline subtraction of the buffer solution was performed. Genomic DNA was used in a concentration of 75µg/ml. DNA was extracted from peripheral lymphocytes of anti-coagulated blood (EDTA) samples by Proteinase K digestion and phenol/chloroform extraction [23]. The purity was determined by measuring the absorbance at 260/280nm indicating that the sample is free from protein contamination [23]. The concentration was assayed spectrophotometrically using 6600M<sup>-1</sup>cm<sup>-1</sup> as a molar extinction coefficient at 260nm.

### Fluorescence spectra and DNA-binding studies

Fluorescence emission and excitation spectra were measured using Jasco FP-6200 spectrofluorometer (Tokyo, Japan) using fluorescence 4-sided quartz cuvettes of 1.00cm path length. The automatic shutter-on function was used to minimize photo bleaching of the

sample. The selected excitation wavelength for ethidium bromide was 480nm. The emission spectrum was corrected for background fluorescence of the buffer. The Ethidium Bromide (EB) fluorescence displacement experiment was performed by sequential addition of aliquots of 1790µl Tris buffer, 10µl EB (final concentration of 72µM), 100µl G-DNA from stock solutions (1.5mg/ml) and finally 10µl of compounds (SW1 to SW7, final concentration of 30µM). Emission spectra were recorded for each system using excitation wavelengths of maximum fluorescence intensity determined for the systems to be 480nm using a slit width of 5nm to examine alterations in emission spectra resulting from the complex construction of both systems. On construction of the full systems, the system was allowed to equilibrate for 30 minutes at room a temperature and emission spectra (500-730nm) were recorded to monitor changes in EB intensity.

### Prediction of ADMET properties and drug-likeness

To verify drug-likeness, canonical SMILES format of the synthesized molecules SW compounds were used in swiss ADME (<http://www.swissadme.ch/index.php>) [24]. The main bioavailability parameters were molecular weight (g/mol), lipophilicity (XlogP3), solubility (log S), polarity (Topological Polar Surface Area-TPSA in Å<sup>2</sup>), saturation (fraction of carbon atoms in Sp<sup>3</sup> hybridization-Csp<sup>3</sup>) and flexibility (No of rotatable bonds). Absorption parameters such as Human Intestinal Absorption, Blood Brain Barrier, P-glycoprotein interaction (substrate or inhibitor) and metabolism (inhibitor or substrate) of the bio-active molecules with different cytochrome P450 enzymes were also estimated using admetSAR, which is based on QSAR data for prediction of Absorption, Distribution, Metabolism, Excretion and Toxicity (ADMET) [25,26]. Drug-like molecules considering Ghose, Veber, Egan, Muegge and Lipinski rules and good ADMET properties were chosen as ligands in a consequent molecular docking procedure.

### Molecular docking

The starting geometry of the synthesized SW compounds (SW1 to SW7) was constructed using chem3D Ultra (version 8.0, Cambridge soft Com., USA). The optimized geometry of SW compound with the lowest energy was used for molecular docking. Crystal structures of the DNA fragment with the B-form 1bna, 102d, 1k2j and 102d were downloaded from the Protein Data Bank (<https://www.rcsb.org/structure/102D>). Molecular dockings of SW compounds with B-DNAs were accomplished by Auto Dock 4.2 software from The Scripps Research Institute (TSRI) (<http://autodock.scripps.edu/>). Firstly, polar hydrogen atoms were added into B-DNA molecules. Then, partial atomic charges of the B-DNA and SW molecules were calculated using Kollman methods [27]. In the process of molecular docking, the grid maps of dimensions (62Å × 62Å × 62Å) with a grid-point spacing of 0.376Å and the grid boxes are centered. The number of genetic algorithm runs and the number of evaluations were set to 100. All other parameters were default settings. Cluster analysis was performed on the results of docking by using a Root Mean Square (RMS) tolerance of 2.0Å, which was dependent on the binding free energy. Lastly, the dominating configuration of the binding complex of SW compounds and B-DNA fragments with minimum energy of binding were determined which relied strongly on the information of 3D structures of the DNA binding site and ultimately generated a series of DNA binding complex.

## Results and Discussion

### Synthesis

The targeted compounds, symmetrical 1,2-phenylenediamine Schiff's base derivatives, have been successfully synthesized using previously reported synthetic procedures [22]. Their chemical structures were confirmed by means of spectroscopic analysis as described previously [22].

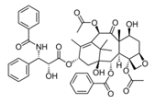
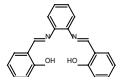
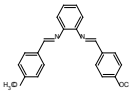
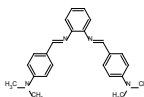
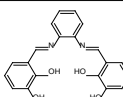
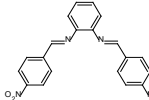
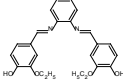
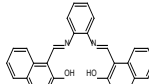
### ADMET properties

The pharmacokinetic properties, Lipinski's rule of 5 and toxicity of all synthesized SW compounds were studied. Lipinski's rule of five (L. Ro5) for drug-likeness includes i) molecular mass should be below 500 kDa ii) logP value should be below 5 iii) hydrogen bond donor sites should be 5 or below iv) hydrogen bond acceptor sites should be 10 or below. An orally active compound should not have more than 2 violations of the Lipinski rule and have rotatable bonds (0-15) and polar surface area (7-200 Å). All the synthesized compounds reported in this paper were not found to violate the rule more than the maximum permissible limits and have rotatable bonds and polar surface area within the range thus proving their drug likeness properties.

Lipophilicity (LogP o/w) values of all synthesized compounds were in range from 2.50 to 6.98 (Table 1), while their molecular weights are within the range 316.35-416.47 gram/mole. The compounds were found with optimum number of hydrogen bonding donors (0-4) and acceptors (2-6) as shown in Table 1. The achieved results of this part of our study indicate that most of the compounds follow Lipinski rules and have a good partition coefficient. Swiss ADME predictions suggested that symmetrical phenylenediamine Schiff's base derivatives have optimum parameters for anti-cancer activity and can be considered as lead molecules for further modifications.

### Molecular docking analysis

Table 2 shows the binding energies of the SW compounds and the DNAs-fragments obtained by docking the investigated compounds within the DNA molecule. In this part of the current study, the molecular dockings of SW compounds with four B-DNA fragments were performed using Auto Dock 4.2 to understand the possible binding mode of SW compounds with B-DNA and to obtain information about interaction forces between ethidium bromide and DNA. Ethidium bromide and DNA were kept as flexible molecules and were docked into four forms of rigid B-DNA fragments to obtain the preferential binding site to SW compounds on B-DNAs. The molecular docking results are shown in Table 2.

Compounds (M Wt) g/mol	Chemical structure	Log P*	Hydrogen bonds**		KSV (M <sup>-1</sup> )	R <sup>2</sup> (5 points)
		Calculated	donors	acceptors		
Taxol (853.92)		2.5	4	14	$5.90 \times 10^3$	0.999
SW1 (316.35)		4.99	2	4	$3.17 \times 10^3$	0.968
SW2 (344.4)		5.52	0	4	$1.10 \times 10^3$	0.995
SW3 (370.49)		6.34	0	2	$1.20 \times 10^3$	0.987
SW4 (348.35)		4.21	4	6	$6.10 \times 10^3$	0.996
SW5 (374.34)		5.84	0	6	$6.02 \times 10^3$	0.988
SW6 (404.45)		5.41	2	6	$4.7 \times 10^3$	0.996
SW7 (416.47)		6.98	2	4	$7.31 \times 10^3$	0.998

**Table 1:** Some chemical, physical properties and the key selection vector (KSV) values of compounds (SW1-SW7).

**Note:** \*Log P values were calculated using ChemDraw Ultra 8.0 software. \*\*Numbers and type of hydrogen bonds involved in the interaction between SW compounds and DNA were determined using swiss ADME website [24].

Compounds (Ligands)	DNA PBD ID (1bna)	DNA PBD ID (102d)	DNA PBD ID (1k2j)	DNA PBD ID (102d)
	$\Delta G_a$	$\Delta G_a$	$\Delta G_a$	$\Delta G_a$
Sw1	-7.8	-5.73	-5.03	-5.61
Sw2	-6.4	-6.67	-7.57	-5.2
Sw3	-6.7	-5.03	-5.23	-6.19
Sw4	-8.0	-5.73	-6.0	-5.51
Sw5	-7.4	-3.29	-6.78	-3.21
Sw6	-6.8	-4.58	-4.92	-5.27
Sw7	-7.9	-6.02	-5.39	-6.94
Taxol	-1.16	-3.24	-12.38	-3.65

**Table 2:** Various energies in the binding process of the SW compounds with DNAs obtained from molecular docking. The unit of all energies was kcal/mol.

**Note:** (1bna): d(CGCGAASSCGCG)2, (102d): d(CGCAAATTTGCG)2, (1k2j), d(CGTACG)2, (102d): d(CGCGATATCGCG)2,  $\Delta G^*$  is the binding free energy change.

The molecular modeling results showed that there are *van der Waals*, hydrogen bonds and electrostatic interactions between ethidium bromide, SW compounds and DNA. The contribution of van der Waals and hydrogen bond interaction is much greater than that of the electrostatic interaction because the sum of van der Waals energy, hydrogen bonding energy and desolvation free energy is larger than the electrostatic energy, which is consistent with the experimental results shown in Table 1. As indicated in the literature, the binding mode of ethidium bromide on DNA is intercalating binding [28]. The fluorescence emission intensity of ethidium bromide decreased on addition of SW compounds suggesting that there is competitive binding between ethidium bromide and SW compounds on G-DNA. Therefore, it can be concluded that the binding mode of ethidium bromide on G-DNA is intercalating binding which is consistent with our modeling and fluorescence results.

### DNA Binding Properties

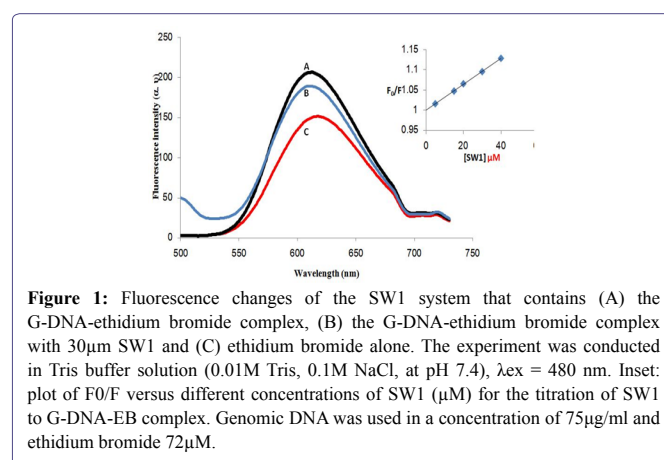
To study how proficiently the synthesized compounds interact with G-DNA, the DNA binding primary properties were explored by using fluorescence emission spectroscopy. Fluorescence emission experiments have been extensively used to study the synthesized compound-DNA interactions, in which the fluorescence emissions of compounds (SW1 to SW7) were increased significantly in the presence of the G-DNA. This is in good agreement with the fluorescence behavior of other intercalators reported in the literature [29]. The results indicated that all the compounds can interact with G-DNA.

### Ethidium bromide (EB) Competition Assay

The structural properties of the complex formed between genomic DNA were studied using Raman microscopy equipped with near-infrared laser excitation [30]. The study showed that the phenanthridinium plane is tilted by  $35 \pm 5^\circ$  from the plane perpendicular to the fiber (DNA helix) axis. The study also indicated that the co planarity of the phenanthridinium ring and its immediate base neighbors at the intercalation site have a tilt angle closer A-DNA ( $20^\circ$ ) than to B-DNA ( $6^\circ$ ) and the average base tilt in stretches of DNA between intercalation sites remains to that of B-DNA [30]. The entrenched quenching assay based on the displacement of the intercalating dye, ethidium bromide, from G-DNA was utilized to explore the interaction mode between the complexes and G-DNA. EB is an extremely helpful DNA structural probe, which shows an important increase in fluorescence intensity when intercalating into the base pair of DNA. However, the increased fluorescence can be quenched obviously when there is a second

complex that can replace the bound EB or break the secondary structure of DNA [31,32]. It has been shown that groove DNA binders can cause a decrease in EB emission intensity [33,34]. The entire compounds do not fluoresce with an excitation at 612nm. The EB competition assay results are shown in Figure 1. The fluorescence intensity of DNA-bound EB at 612nm decreased outstandingly with an increase of the compound (SW1-SW7) concentration. This decrease in fluorescence intensity may be due to the quenching of some EB molecules that were released from DNA into the solution after being substituted by the SW1-SW7 compounds. The phenomenon that the fluorescence of DNA-bound EB was quenched as a result of DNA and compound interactions is a typical sign of intercalation [33,34].

According to the literature the fluorescence quenching of DNA-bound EB can be well described by the linear Stern-Volmer equation [35-37] in which the synthesized (SW1-SW7) compounds were the quenchers:  $I_0/I = 1 + K_{SV} [Q]$ .  $I_0$  and  $I$  represent the fluorescence intensities in the absence and presence of quencher, respectively;  $K_{SV}$  is a linear Stern-Volmer quenching constant;  $Q$  is the concentration of quencher. The  $K_{SV}$  values were given by the ratio of the slope to intercept. The  $K_{SV}$  values for the (SW1-SW7) compounds are summarized in Table 1. As shown is Table 1, compound SW7 had the highest  $K_{SV}$  value, which suggests that compound SW7 binds most strongly to G-DNA-even more than taxol.



**Figure 1:** Fluorescence changes of the SW1 system that contains (A) the G-DNA-ethidium bromide complex, (B) the G-DNA-ethidium bromide complex with  $30\mu\text{M}$  SW1 and (C) ethidium bromide alone. The experiment was conducted in Tris buffer solution (0.01M Tris, 0.1M NaCl, at pH 7.4),  $\lambda_{\text{exc}} = 480 \text{ nm}$ . Inset: plot of  $F_0/F$  versus different concentrations of SW1 ( $\mu\text{M}$ ) for the titration of SW1 to G-DNA-EB complex. Genomic DNA was used in a concentration of  $75\mu\text{g/ml}$  and ethidium bromide  $72\mu\text{M}$ .

### Conclusion

We have synthesized seven symmetrical 1,2-phenylenediamine compounds and characterized using various spectroscopic techniques.

DNA binding with SW compounds was investigated by fluorescence spectral techniques and revealed an intercalative interaction between the synthesized compounds and G-DNA. Among the investigated SW compounds, SW7 showed the highest binding affinity.

### Author Contribution

A.S., I.A.S. and N.H. M. designed the study. A.S.A., S.A.A. and A.A.I. performed the DNA binding studies and docking. S.M. B and A.H. performed analysed the data. A.M., G. wrote the paper with input from all authors. All authors read and approved the manuscript.

### Acknowledgement

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### Conflict of Interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest and it is compliance with ethical standards.

### Ethical Approval

This article does not contain any studies with human participants performed by any of the authors.

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