

## Antibacterial Activity of Schiff Bases Derived from Ortho-Diaminocyclohexane, Meta-Phenylenediamine and 1,6-Diaminohexane: Qsar Study with Quantum Descriptors

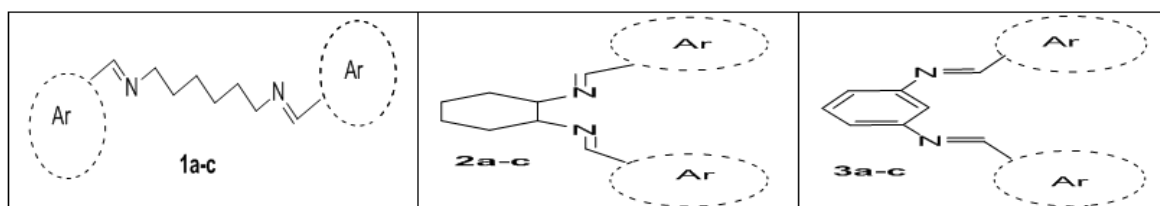
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**Abstract:** Schiff bases (SBs) are known to possess many biological activities. In this paper we will be interested in nine SBs derived from ortho-diaminocyclohexane, meta-phenylenediamine, 1,6-diaminohexane and benzaldehydes variously substituted by nitro group. We had synthesized, characterized and tested these molecules for their antibacterial properties. Herein our study focuses in particular on the determination of quantum descriptors on which observed antibacterial activity depends, in order to be able to predict biological activities in analogue molecule series. Using quantum chemistry methods at B3LYP / 6-31G (d, p) level, we determined for each molecules, theoretical antibacterial potentials that we correlated to the experimental ones. Calculation results showed that, the energy of the Highest Occupied Molecular Orbital ( $E_{HOMO}$ ), electronegativity ( $\chi$ ) and electronic energy ( $E$ ), are the best quantum descriptors related to the antibacterial activity values of studied molecules. The correlation coefficient  $R^2$  indicates that 92.1% of the molecular descriptors defining this model are taken into account with a standard deviation of 0.152. The model significance is reflected by Fischer coefficient  $F = 7.721$ : Correlation coefficient of cross-validation  $Q_{CV}^2 = 0.88$ . This model is acceptable with  $R^2 - Q_{CV}^2 = 0.921 - 0.88 = 0.041 < 0.3$ . The values of the  $pCE_{50theo}/pCE_{50exp}$  values of the validation set tend to unity.

**Keywords:** Schiff base, Quantum chemistry, QSAR, Quantum Descriptors, Antibacterial activity

### I. Introduction

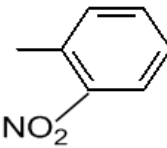
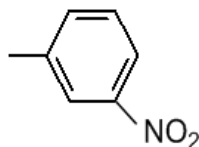
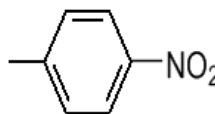
Organic Schiff base (SB) molecules, discovered by Hugo Schiff in 1864 are condensation products of primary amines with carbonyl compounds [1,2]. The common structural feature of these compounds is the azomethine group with the general formula  $R_1HC=N-R_2$ , where  $R_1$  and  $R_2$  are alkyl, aryl, cycloalkyl, or heterocyclic groups. Imine or azomethine function present in various natural compounds and non-natural derivatives has been found to be critical for their biological activities [3-5]. For this reason, SBs, which are very easy to synthesize, are inexhaustible source of promising multipurpose pharmacophores for design and development of new biologically important molecules. SBs are in reality known to have a wide range of biological properties such as antibacterial [6-12], anticancer [13-15], antiviral [16], antifungal [8,12,17,18], antiparasitic [8] in addition to other biological performances [19,20]. As several authors [21-23], our systematic research on SBs has enabled us to synthesize many diimines. In this work we are interested in three types of diimine. We have recently synthesized, characterized and tested these compounds for their biological properties against bacterial strain *Staphylococcus aureus* [24]. The molecules used in this study are shown in Figure 1.



**Figure 1:** Molecular structures of the types of Schiff bases studied

These derivatives differ from each other by the aryl groups (Ar). These aryl groups are shown in the table below.

**Table 1:** The different aryl groups and molecule codes corresponding

Molecule code	Ar Group
<b>1a-3a</b>	
<b>1b-3b</b>	
<b>1c-3c</b>	

These synthesized molecules have shown, among other things, promising antibacterial activity for several of them. On the other hand, their structures offer a high probability of structural change, implying high degree of molecular diversity, which remains very useful for the development of new, less toxic and potent therapeutic agents. Our research work up to now has been limited to the synthesis and the research of activities of these molecules. By implementing the methods of quantum chemistry, this work focus on determining the quantum descriptors whose antibacterial activities observed depend on, in order to be able to predict biological activities in analogue molecule series taking into account these important theoretical results.

## II. Experimental Section

### 2. Materials and methods of calculation

#### 2.1. The calculation level

The six molecules of the training set and the three other validation set molecules used in this study, have various antibacterial concentrations ranging from 48.87 to 375 µg/mL. This range of concentrations makes it possible to define a quantitative relationship between the antibacterial activity and the theoretical descriptors. Biological data are generally expressed as the opposite of the log 10 base of activity ( $-\log_{10}(C)$ ) in order to obtain higher mathematical values when the structures are biologically very efficient [25,26]. The antibacterial activity is expressed by the antibacterial potential  $pCE_{50}$ . The antibacterial potential is defined from equation (1):

$$pCE_{50} = -\log_{10} \left( \frac{CE_{50}}{M} * 10^{-3} \right) \quad (1)$$

Where M is the molecular weight (g/mol) and  $CE_{50}$  is the potential concentration 50 in bacteria, it gives the concentration of substance required to destroy 50% bacteria in a population of bacteria under the conditions of the experiment (µg/mL).

The performance of a mathematical model, for Eriksson *et al.* [27], is characterized by a value of  $Q_{cv}^2 > 0.5$  for a satisfactory model when for the excellent model  $Q_{cv}^2 > 0.9$ . According to them, from a given test set, a model will be performant if the acceptance criterion  $R^2 - Q_{cv}^2 < 0.3$  is respected.

In order to find a link between the values of antibacterial activity of the molecules studied and their molecular structures, calculations of quantum chemistry were carried out using the software Gaussian 03 [28]. DFT methods are generally known to generate a variety of molecular properties [29-36] in Quantitative Structure Activity Relationship (QSAR) studies that increase predictability, reduce calculation time and cost implications in the design of new drugs [37, 38]. The theory level B3LYP/6-31G (d, p) was used to determine the molecular descriptors. As for the choice of the split-valence and double-dzeta bases, they are sufficiently wide and the diffuse and polarization functions are to be taken into account in the quantification of the

molecular descriptors obtained. The modeling was done using the multilinear regression method implemented in Excel and XLSTAT spreadsheets.

## 2.2. Quantum descriptors used

For the development of QSAR models, some theoretical descriptors related to conceptual DFT have been determined. In particular, the energy of the Highest Occupied Molecular Orbital ( $E_{HOMO}$ ), electronegativity ( $\chi$ ) and electronic energy ( $E$ ), which are determined from the optimized molecules. It should be noted that the descriptors related to the boundary molecular orbitals ( $E_{HOMO}$ ,  $\chi$ ) were calculated very simply in the framework of the Koopmans approximation [39] and the electronic energy ( $E$ ). The lowest molecular orbital energy ( $E_{HOMO}$ ) is obtained after optimization of the molecules. As for electronegativity, it is obtained from equation (2):

$$\chi = -1/2 (\epsilon_{LUMO} + \epsilon_{HOMO}) \quad (2)$$

For all the descriptors studied, bivariate data analysis, that is to say the calculation of the linear correlation coefficient R between each of the pairs of the set of descriptors is less than 0.95 ( $R < 0.95$ ), Which means that these different descriptors are independent of each other [40-45].

## III. Results And Discussion

### 3.1. Results

The test set of the six (6) SBs molecules and the three (3) molecules of the validation set (Table 2) are shown in Table 2. Subsequently, the values of the bivariate linear correlation coefficients R of the descriptors are also presented in Table 3.

**Table 2:** Quantum descriptors and experimental antibacterial activities of the test and validation set

Code	$E_{HOMO}(eV)$	$\chi(eV)$	$E(U.a)$	$CE_{50\ exp}(\mu g/mL)$	$pCE_{50\ exp}$
<b>Training Set</b>					
1a	-0.092	0.172	-1295.085	375	3.008
1c	-0.100	0.181	-1295.104	375	3.008
2b	-0.095	0.177	-1293.901	375	3.006
2c	-0.105	0.185	-1293.905	187.5	3.307
3b	-0.097	0.164	-1290.278	187.5	3.299
3c	-0.108	0.173	-1290.278	48.87	3.884
<b>Validation Set</b>					
1b	-0.093	0.176	-1295.105	187.5	3.309
2a	-0.095	0.176	-1293.890	93.75	3.608
3a	-0.097	0.160	-1290.263	375	2.999

**Table 3:** Values of the bivariate linear correlation coefficients of the descriptors

	$E_{HOMO}(eV)$	$\chi(eV)$	$E(U.a)$
$E_{HOMO}(eV)$	1		
$\chi(eV)$	0.272	1	
$E(U.a)$	0.42	0.718	1

For all the descriptors used, the analysis of the data two by two, that is to say the calculation of the linear correlation coefficient R between each of the pairs of the set of descriptors is less than 0.95 ( $R < 0.95$ ).

### 3.2. Quantitative Structure Activity Relationship (QSAR) model and contribution of descriptors

It should be noted that the negative or positive sign of the coefficient of a descriptor of the model reflects the effect of proportionality between the evolution of the biological activity of interest and this parameter of the regression equation. Thus, the negative sign indicates that when the value of the descriptor is high, the biological activity decreases while the positive sign translates the opposite effect. The model equation (3) obtained using the theoretical descriptors related to the optimized molecules and the statistical indicators are presented below:

$$pCE_{50} = -7.949 - 58.869E_{HOMO} - 28.168\chi - 0.008E \quad (3)$$

$$N = 6 \quad R^2 = 0.921 \quad Q_{CV}^2 = 0.88 \quad S = 0.152 \quad F = 7.721$$

The negative signs of the different coefficients of the model parameters indicate that the antibacterial activity ( $pCE_{50}$ ) evolves inversely with ( $E_{HOMO}$ ,  $\chi$  and  $E$ ). The correlation coefficient  $R^2$  indicates that 92.1% of the molecular descriptors that define this model are taken into account at a standard deviation of 0.152. The significance of the model is reflected by the Fischer coefficient  $F = 7.721$ : The correlation coefficient of cross-validation  $Q_{CV}^2 = 0.88$ . This model is acceptable with  $R^2 - Q_{CV}^2 = 0.921 - 0.88 = 0.041 < 0.3$ .

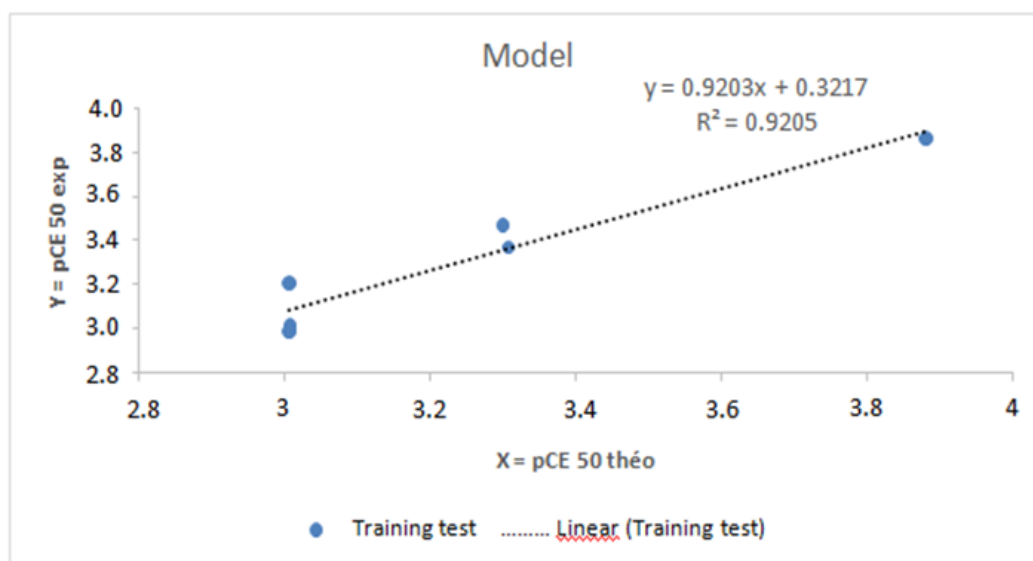


Figure 2: The regression line of the model

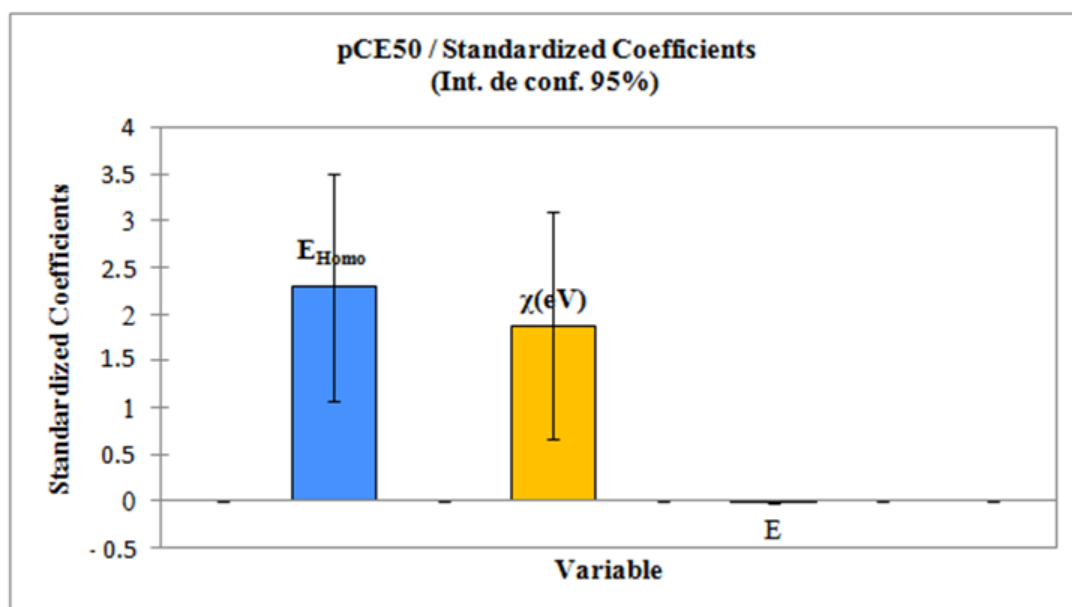
The values of the ratio  $pCE_{50}^{theo}/pCE_{50}^{exp}$  of the validation set which tend to unity (Table 4) reflect the good correlation between the theoretical and experimental potentials of the molecules studied.

Table 4: Values of the relationship between theoretical and experimental antibacterial potentials of the validation set.

Validation Set		
$pCE_{50}^{theo}$	$pCE_{50}^{exp}$	$pCE_{50}^{theo}/pCE_{50}^{exp}$
3.037	3.608	0.842
2.929	3.309	0.885
3.577	2.999	1.193

The study of the contribution of each of the three parameters in the prediction of antibacterial activity was made. The various contributions are illustrated by Figure 3.

The energy of the Highest Occupied Molecular Orbital ( $E_{HOMO}$ ) shows a large proportion followed by electro negativity ( $\chi$ ) and finally the lowest proportion is attributed to the electron energy (E). Thus it is clear that the Highest Occupied Molecular Orbital energy ( $E_{HOMO}$ ) is the priority descriptor in the prediction of antibacterial activity in the molecule series studied.



**Figure 3:** Contribution of descriptors in the model**IV. Conclusion**

This study made it possible to demonstrate a relationship between the antibacterial activity pCE<sub>50</sub> (µg/mL) and the quantum descriptors. Thus, we have established a multilinear regression equation between the antibacterial activity and the descriptors of the optimized molecules. The descriptors of the optimized molecules ( $E_{\text{HOMO}}$ ,  $\square$  and  $E$ ) make it possible to explain and predict the behavior of the molecules studied because there is a strong correlation between the calculated and experimental values of the antibacterial activity. This model presents good statistical indicators ( $R^2 = 0.921$ ,  $S = 0.152$ ,  $F = 7.721$ ). The model QSAR obtained allows us to predict the activity of new molecules on the one hand and on the other hand, to identify descriptors that improve the antibacterial activity thus giving guidance to design new molecules more active against bacteria. The Highest Occupied Molecular Orbital ( $E_{\text{HOMO}}$ ) energy is the priority descriptor in the prediction of antibacterial activity in the studied molecule series. The model obtained was validated using a test set comprising three molecules.

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