Conformational Analysis of an Arylazo Phosphate Dimer by Molecular and Quantum Mechanics Approaches

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Abstract: The phosphorous, halogen and nitrogen-containing polymers have excellent thermal stability and good flame retardant properties**.** In this paper the structure of a diarylazo phosphate was simulated by molecular mechanics methods using the MM+, AMBER and MMFF94s force fields included in the Hyperchem, respectively Omega software. Structures of minimum energy were generated using the RMS gradient value of 0.01 kcal/Å·mol as criterion to choose an optimized conformation, in case of the Hyperchem program and a RMSD deviation value of 2.0 Å for the duplicate removal, in case of the Omega software. The conformations of minimum energy obtained by Omega were further minimized by the semiempirical RM1 method included in the MOPAC 2009 software. Structural dimer features which characterize the most stable energetically conformations obtained by molecular and quantum mechanics methods were compared, yielding a unified dimer structure.

Keywords: arylazo phosphate; conformational analysis; Hyperchem; Omega; MOPAC 2009

1. Introduction

The phosphorous, halogen and nitrogen-containing polymers are the most widely used as commercial fire-retardant polymers [1].

The arylazo polymers have excellent thermal stability and good flame retardant properties [2]. They have been modelled in a first approximation by their monomers, which were studied by molecular mechanics and quantum chemical (semiempirical AM1) methods [3-5]. Structural parameters were derived from the structures of minimum energy thus obtained. The influence of calculated structural descriptors of arylazo polymers on their flammability (expressed by the limiting oxygen index) was accomplished by the multiple linear regression [4], principal component regression [5] and partial least squares methods [3].

In this paper the structure of a diarylazo phosphate (Fig. 1) was simulated by conformational analysis using molecular mechanics and quantum methods, in vacuum. The conformations of minimum energy thus obtained were analyzed in order to elucidate the possible dimer structure.
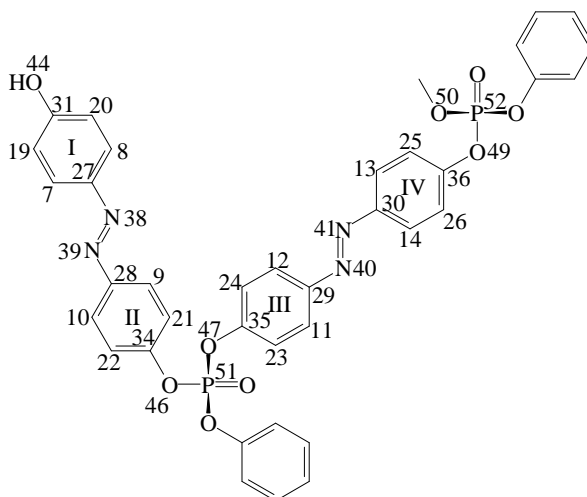

Figure 1. Structure of the studied diarylazo phosphate

2. Methods

2.1. Dimer structure simulation by OMEGA software

The molecular structure of the diarylazo phosphate was modelled by the conformational search ability of the Omega v.2.3.2 [6] program. Isomeric SMILES notation was used as program input in order to avoid any influences on conformational model generation by presenting 3D seed structures. Omega employs a rule-based algorithm [7] in combination with variants of the Merck force field 94 [8].

For the dimer generation of conformers, following parameters were used: a maximum of 200 conformers per compound, an energy cutoff of 10 kcal/mol relative to global minimum identified from the search. The force field used was the 94s variant of the MMFF (Merck Molecular force field) [8] with coulomb interactions and the attractive part of the van der Waals interactions. The RMSD fit value 2.0 Å was used to avoid redundant conformers.

2.2. Dimer structure simulation by HYPERCHEM

Dimer structure was built by the Hyperchem software [9] and conformational analysis was performed by molecular mechanics calculations, using the MM+ and AMBER force fields, with the RMS gradient value of 0.01 kcal/Å·mol as criterion to choose an optimized conformation, an acceptance energy cutoff of 20 kcal/mol above the minimum energy, a maximum number of conformers to be generated was set to 5000 and 100 conformers over the minimum energy conformer were kept. All flexible bonds were considered in the conformational search.

2.3. Quantum chemical calculations

Structures of minimum energy obtained by molecular mechanics calculations were further minimized by quantum chemical calculations. Taking into account the big number of flexible bonds present in the dimer skeleton, around which the rotation is quasi free, the semiempirical RM1 method [10] included in the MOPAC 2009 software [11]

was employed, with SCF convergence of 10^{-10}, RMS gradient value of 0.01 kcal/Å·mol as criterion to choose an optimized conformation and the EF and PRECISE keywords.

3. Results and Discussion

247 conformers and 16 types of stereoisomers were found by Omega. The minimum energy conformer obtained for each type is presented in Table 1. Four stereoisomer types of the diarylazo phosphate molecular structure, with respect to the phosphorus atoms (P51 and P52, in Fig. 1) more stable were obtained: *38E,51R,40E,52R*; *38E,51S,40E,52S*; *38E,51R,40E,52S* and *38E,51S,40E,52R*. Lowest molecular energy was noticed in case of the *38E,51S,40E,52S* conformer (see Table 1). The energy minimized structure of the *38E,51S,40E,52S* conformer is presented in Fig. 2.

TABLE 1. Minimum energy of different stereoisomer types obtained by Omega

Conformer	Energy (kcal/mol)
38Z,51S,40Z,52R	174.41
38E,51S,40Z,52R	117.57
38Z,51S,40E,52R	119.43
38E,51S,40E,52R	62.41
38Z,51R,40Z,52R	173.39
38E,51R,40Z,52R	116.48
38Z,51R,40E,52R	119.68
38E,51R,40E,52R	62.60
38Z,51S,40Z,52S	174.54
38E,51S,40Z,52S	117.17
38Z,51S,40E,52S	119.37
38E,51S,40E,52S	62.35
38Z,51R,40Z,52S	172.95
38E,51R,40Z,52S	117.24
38Z,51R,40E,52S	119.63
38E,51R,40E,52S	62.54

Conformational analysis performed by the MM+ and by the Amber force fields included in the Hyperchem software yielded only the *38E,51S,40E,52R* conformation. Tables 2 and 3 present the skeleton torsion angles of minimum energy conformations obtained by different methods.
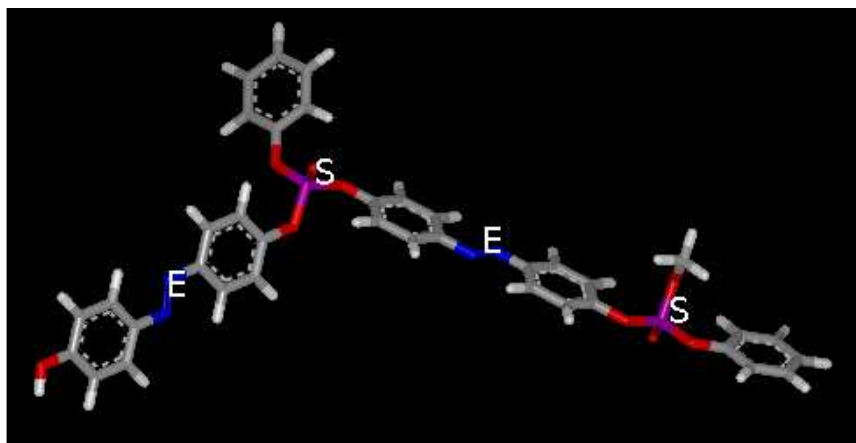

Figure 2. The structure of the minimum energy *38E,51S,40E,52S* conformer obtained by Omega

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TABLE 2. Torsion angles of macromolecule skeleton around the P-O bonds of minimum energy conformer obtained by different approaches

Optimization method	C22-C34-O46-P51	C34-O46-P51-O47	O46-P51-O47-C35	P51-O47-C35-C23	C26-C36-O49-P52	C36-O49-P52-O50	O49-P52-O50-C37
MM+	+ac (127.1°)	-sc (-54.3°)	+sc (57.01°)	-ac (-111.1°)	ap (178.4°)	ap (trans) (-178.3°)	-sc (-61.7°)
Amber	+sc (66.2°)	+sc (61.3°)	-sc (-54.8°)	+ac (130.3°)	-ac (90.4°)	ap (trans) (176.9°)	-sc (-59.7°)
MMFF94s	sp (0.001°)	ap (-173.6°)	-sc (-66.4°)	ap (-179.99°)	sp (-0.003°)	+sc (66.7°)	+sc (53.8°)
RM1*	-ac (-98.47°)	-sc (-72.2°)	-sc (-89.5°)	ap (177.9°)	sp (-6.6°)	+ac (101.8°)	+sc (61.1°)

* minimum energy conformation derived by Omega and semiempirically minimized

TABLE 3. Other torsion angles of the macromolecule skeleton of minimum energy conformer obtained by different approaches

Optimization method	C34-O46-O47-C35	C22-C34-C35-C23	C8-C27-N38-N39	N38-N39-C28-C9	C12-C29-N40-N41	N40-N41-C30-C13
MM+	sp (3.1°)	sp (6.2°)	ap (179.2°)	sp (4.2°)	ap (-172.3°)	ap (-179.3°)
Amber	sp (6.4°)	+ac (130.2°)	sp (2.6°)	ap (177.1°)	sp (3.05°)	ap (-178.8°)
MMFF94s	+ac (147.6°)	+sc (43.5°)	ap (-179.99°)	sp (0.004°)	ap (-180.0°)	sp (-0.004°)
RM1*	-ac (-108°)	-ac (-124.9°)	ap (-173.9°)	sp (16.4°)	ap (-175.2°)	sp (3.4°)

* minimum energy conformation derived by Omega and semiempirically minimized

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Following general structural features were derived from the inspection of the dimer minimized energy structures:

- The N38=N39 azo group is situated in the same plane with the I and II phenyl rings and the N40=N41 azo group is placed in the same plane with the III and IV phenyl rings in conformations obtained by molecular mechanics calculations (with small deviation in case of structures minimized by the RM1 semiempirical hamiltonian).

- In case of conformers minimized by the MM+ and Amber force fields the phenyl skeleton rings I and II are situated in parallel planes with the III and IV rings, suggesting an intramolecular self-assembly by main chain folding (explained by possible hydrophobic forces, van der Waals forces, or π-π interactions between the phenyl chain nuclei).

- Dimers built by the MMFFs94s force field inside Omega and further minimized by the RM1 semiempirical hamiltonian suggest an intermolecular macromolecular self-assembly. Stereodescriptor *E* is assigned to both azo groups in the minimum energy chosen stereoisomer.

- No hydrogen bonds were noticed in all conformations of minimum energy.

Only conformations having the torsion angles around the P-O bonds in the ± gauche, ± eclipsed, or trans forms were finally considered to be acceptable, in accordance to X-ray experimental data of some organo-phosphorus compounds [12]. Thus, the *38E,51S,40E,52S,* conformation obtained by Omega fulfilled this condition, being considered most reliable dimer structure.

4. Conclusions

Several optimization procedures were studied to obtain a consistent diarylazo phosphate molecular structure. Conformational analysis was performed by molecular mechanics calculations employing the MM+, Amber and MMFF94s force fields and by the semiempirical RM1 approach. Omega software employing the MMFF94s force field gave the most reliable structure, the torsion angles of the macromolecular skeleton around the P-O bonds of the *38E,51S,40E,52S* chosen conformation of minimum energy thus obtained being closer to the X-ray experimental data.

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