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Abstract
Architectures of the molecules and their behavior in the clustered system are important for various consequence functions in the realistic environment. In order to gain detailed knowledge of the phenol–water clusters, 1–nano second (ns) the molecular dynamic (MD) simulation has been performed. The various structural parameters have been obtained from the MD trajectories. MD simulation reveals the presence of well–defined hydrogen–bonded network of water molecules around the phenol molecule and their dynamics. The existence of cooperativity in the hydrogen bonding and high dynamics nature of hydrogen–bonded network are evident from the present study. The calculated mutual diffusion coefficient is in close agreement with the experimental value of the phenol–water system.

Keywords. Molecular dynamics; solvation; phenol–water cluster; hydrogen bonding.

Abbreviations and notations

MD, Molecular dynamics	ps, Pico seconds
ns, nano second	PBC, Periodic boundary conditions
CASSCF, Complete Active Space Self Consistent Field	MC, Monte Carlo
CVFF, consistent valence force field	RDF, Radial Distribution Function

1 INTRODUCTION

Hydrogen bonding determines the structure and dynamics of protic liquid and biopolymers like protein and nucleic acids. Structure, energetics and dynamics of different types of molecular clusters have received much attention, since the information of such complexes could lead to the understanding of the interaction in biological systems [1–5]. Significant advancement in the various spectroscopic techniques allowed probing the structure and energetics of small van der Waals complexes in the gas phase with reasonable accuracy [6,7]. Similarly development of new computer hardware and algorithms has also helped us to look at small hydrogen bonded and van der Waals complexes with higher accuracy. A variety of experimental and theoretical techniques have been employed to probe the solvation of molecules and biomolecules in order to gain insight into the nature of hydrogen bonding and solvation process as a whole [8]. Recently femto second mid

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infrared photon echo study on intermolecular hydrogen bonded systems have been made to investigate the vibrational dephasing dynamics of O–H stretching excitations [9]. Frequency dependent vibrational population relaxation time of the O–H stretching mode in liquid has been investigated [10]. It is now possible to look at the importance of hydrogen–bonded bridges in the flexible biomolecules using laser spectroscopy of jet–cooled biomolecules and their water clusters [6–9].

Computer simulation of SPC/E model of water has been performed at various thermodynamic conditions. The n–folded hydrogen bonded coordination of single molecule and the lifetime of such coordination have been determined from correlation time [11]. Numerous studies based on dielectric continuum models in the framework of classical and quantum chemical approaches have been used to probe the bulk effect of solvent molecules on solute [4,5]. Although, bulk effect of solvation is important factor in determining the solvation properties of solute, the local interactions present in the first solvation sphere need to be addressed more critically. This can be achieved using classical mechanics/quantum mechanics based methods to compute the interaction of individual solvent molecules with solute molecules. Several theoretical calculations have been made to understand the micro solvation of various solute molecules using *ab initio* and density functional methods [8,12]. It is evident from the previous studies that the computational resources limit the number of solvent molecules included in the quantum chemical calculation. On the other hand the classical molecular dynamics simulation strategies based on force field approach helps to realistically investigate solvation as well as the local nature of the solute–solvent interaction. It is also possible to include several hundreds of solvent molecules in probing solvation of various solute molecules using classical molecular dynamics methods.

Phenols are widely used as synthetic organic materials and also as antioxidants in living organisms. Phenol is the simplest aromatic alcohol and special interest in organic chemistry since their acid–base equilibria have often been used as reference values in establishing linear free energy relationships. Phenoxyl radicals are known as important intermediates in many biological and industrial applications. The structure of phenol in the electronically excited S_1 state have been examined theoretically by different groups using the Complete Active Space Self Consistent Field (CASSCF) method. Since phenol resembles aromatic amino acids, hydration of phenol molecule in aqueous solution has been studied, as a natural step which is a prototypical intermolecular hydrogen–bonding that demonstrates solute–solvent and acid–base interaction on a microscopic scale for understanding the molecular interactions in organic and bioorganic molecules. Several theoretical studies have been made on the interaction of phenol with water [13–18]. Various theoretical and experimental studies revealed that the hydrogen bonding of phenol in water is similar to that of water [19]. This implies that phenol takes part in the formation of mixed cyclic clusters where the phenyl ring is not interacting significantly with any water molecules. The presence of the phenyl ring in phenol should lead to the formation of a π–hydrogen bond with one of the surrounding molecule when the cluster is flexible enough for the bond energy to compensate for the steric strain induced by the deformation of the hydrogen bonded network. Structure and stabilization of the hydrogen bonded complexes of phenol with 1–4 water molecules have been investigated at various levels of *ab initio* method by Dimitrova [20]. Above studies revealed that for complexes with two, three and four water molecules, the most stable structure were planar ring structure with deepest minimum in the total energy and strength of hydrogen bonds. The MP2 method with interaction–optimized DZPi basis set has been used to probe the structure and stability of phenol–water complex [21]. This study has revealed the existence of three distinct minima in the phenol–water complex. Recently, Benoit and Clary have studied phenol–water clusters using rigid–body diffusion quantum Monte Carlo method [16]. Previous studies demonstrated that interactions involved in the phenol–water complexes are similar to π–hydrogen bond type. *Ab initio* calculations have been carried for the electronic ground state and lowest excited states of phenol, the complexes of phenol with water and ammonia and the corresponding cations. From the above study it is possible to understand the electron and proton transfer process in phenol–water complexes [22,23]. In this present investigation classical MD simulations have been performed for 1 ns on phenol–water systems with view to gain information about the dynamics of hydrogen bonding network.

2 COMPUTATIONAL DETAILS

Using molecular building tools, molecular model of phenol molecule has been constructed and the geometry of the phenol has been minimized using consistent valence force field (CVFF). Phenol has been soaked in a cubic box of edge 14 A°. The soaking of phenol introduces 86 water molecules in the box. The geometry of phenol–water cluster has been minimized using DISCOVER [24] molecular minimization/dynamics package employing CVFF. The energy–minimized structure has been subjected to molecular dynamics simulations using NVT ensemble at 298 K. Phenol–water system has been equilibrated for 100 Pico seconds (ps) and dynamics simulation has been carried out for 1 nanoseconds (ns). Periodic boundary conditions (PBC) have been employed to evaluate the non–bonded interactions. Cut off distance of 9.5 A° has been used in the calculation. Distance dependent dielectric constant has been used in the MD simulation. From the trajectories collected for 1 ns, various snapshots of cluster at different time intervals, average structure, and fluctuation in energy contribution with time and radial distribution function and other parameters have been computed.

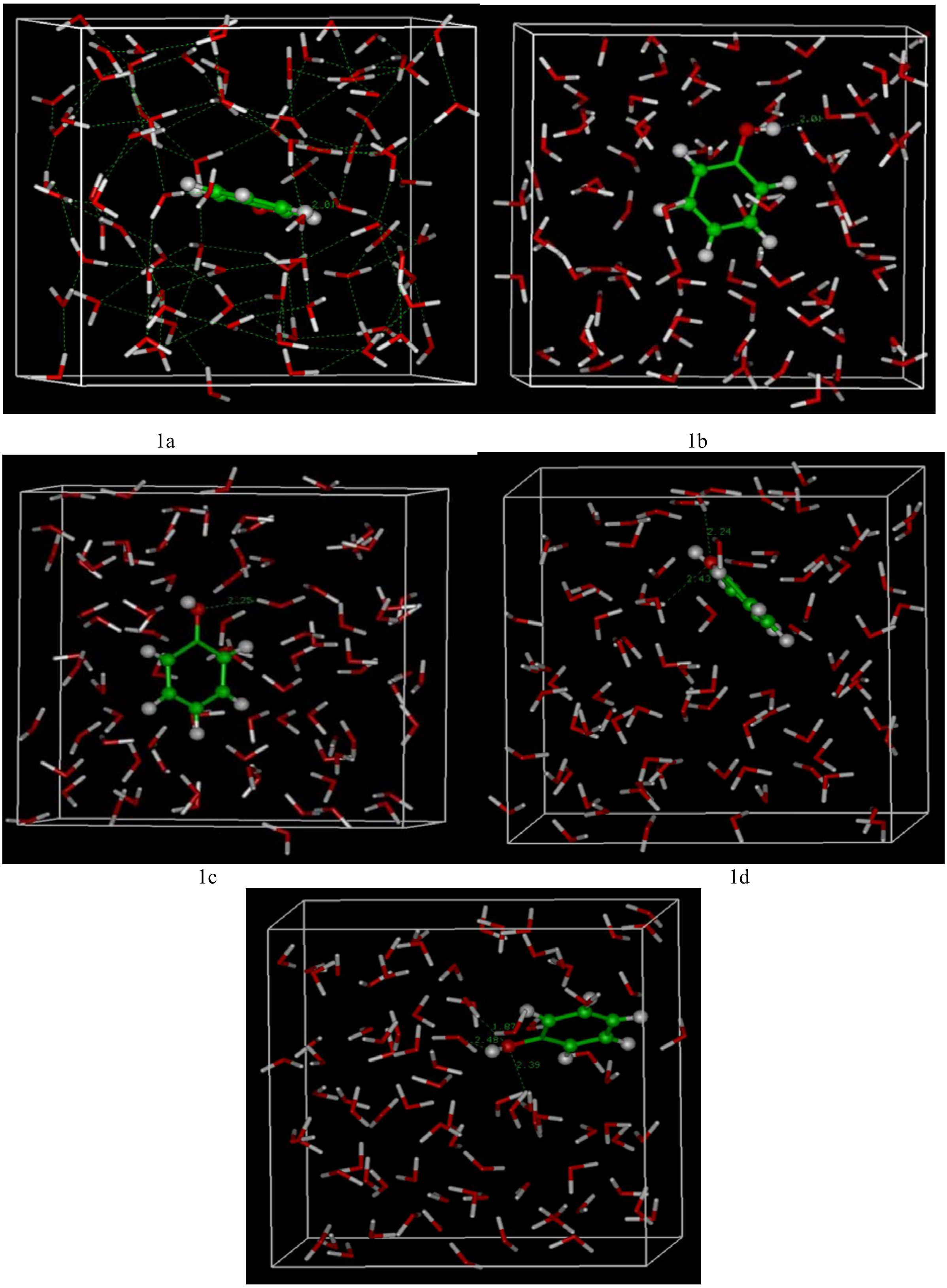
3 RESULTS AND DISCUSSION

The molecular structures of phenol–water cluster generated during molecular dynamics simulation are depicted in Figure 1. Figure 1a corresponds to initial molecular structure with a single hydrogen bond in which phenol donates proton to water molecule. The Figure 1b shows that the water molecules tend to concentrate themselves on the plane parallel to the molecular plane of the phenol. Previous Monte Carlo (MC) study rendered the probability of water finding sites in the phenol–water complex [18]. The MC generated pattern is in close agreement with the present observations. Figures 1c, 1d and 1e depict the molecular structures obtained after 400, 600 and 1000 ps of time evolution respectively.

It is possible to see from figure 1e that two water molecules can be hydrogen bonded to phenol. Similarly the molecular structure of phenol–water cluster shown in Figure 1d reveals the proton accepting nature of phenol molecule. Figure 1e illustrate that more than three water molecule can be coordinated to phenol molecule. The time evolution of the phenol–water cluster for 1 ns revealed that presence of both proton donor and proton acceptor interaction were present in the phenol–water complexes. The present molecular dynamics calculations have also revealed the presence of closed ring structure in which the water molecule hydrogen bonded to phenol behaves like proton donor and acceptor. The existence of cooperativity in the hydrogen bonding of water molecules is also evident from the molecular structure presented in figure 1.

The structure of the phenol–water cluster obtained after molecular dynamics simulation is highly similar to the one found by *ab initio* calculation on interaction of phenol with water molecules [16, 20]. Water can interact with phenol in number of different ways. It can bind to hydroxyl group as proton acceptor as well as proton donor. Three different modes of interaction of water molecules with phenol have been identified by earlier studies [16,20,21]. The most stable minima have been found to be the one in which phenol acts like proton donor. The second minima correspond to the interaction in which phenol molecule behaves like proton acceptor. The third type of minima exhibits π–OH type of hydrogen bonding. The most stable structure of interaction of two, three and four water molecules with phenol molecule have been obtained from previous *ab initio* calculations. It is clear from that study that the phenol–water molecules exhibited planar ring structures, which exemplified both proton acceptor and donor natures of water molecules. These structures are also in accordance with the cluster chemistry IR spectroscopy on hydrated phenol clusters [13,25].

The variations in the total energy, potential energy and kinetic energy during the 1 ns molecular dynamics have been represented in Figure 2. The fluctuation in the potential energy confirms the proper equilibration of the phenol–water system and hence assures the quality of the trajectories collected during the molecular dynamics simulation. Though there is a drastic fluctuation in the phenol–water cluster in the first 200 ps, the system becomes stable after 500 ps. In order to probe the changes in the various components of potential energy during MD simulation, bond energy, angle energy, torsional energy, and van der Waals attractive energy, van der Waals repulsive energy and coulombs energy calculation have been computed and are presented in Figure 3. The bond energy, angle energy and van der Waals energy significantly vary during the molecular dynamics of the phenol–water cluster. This clearly indicates that hydrogen–bonded network is weak and undergoes fast orientational reordering.



1a 1b

1c 1d

1e

Figure 1. (a) Molecular structure of phenol–water cluster. (b) Molecular plane of the phenol with hydrogen bonded network of whole system. (c) Molecular structures obtained after 400 ps. (d) Molecular structures obtained after 600 ps. (e) Molecular structures obtained after 1000 ps.

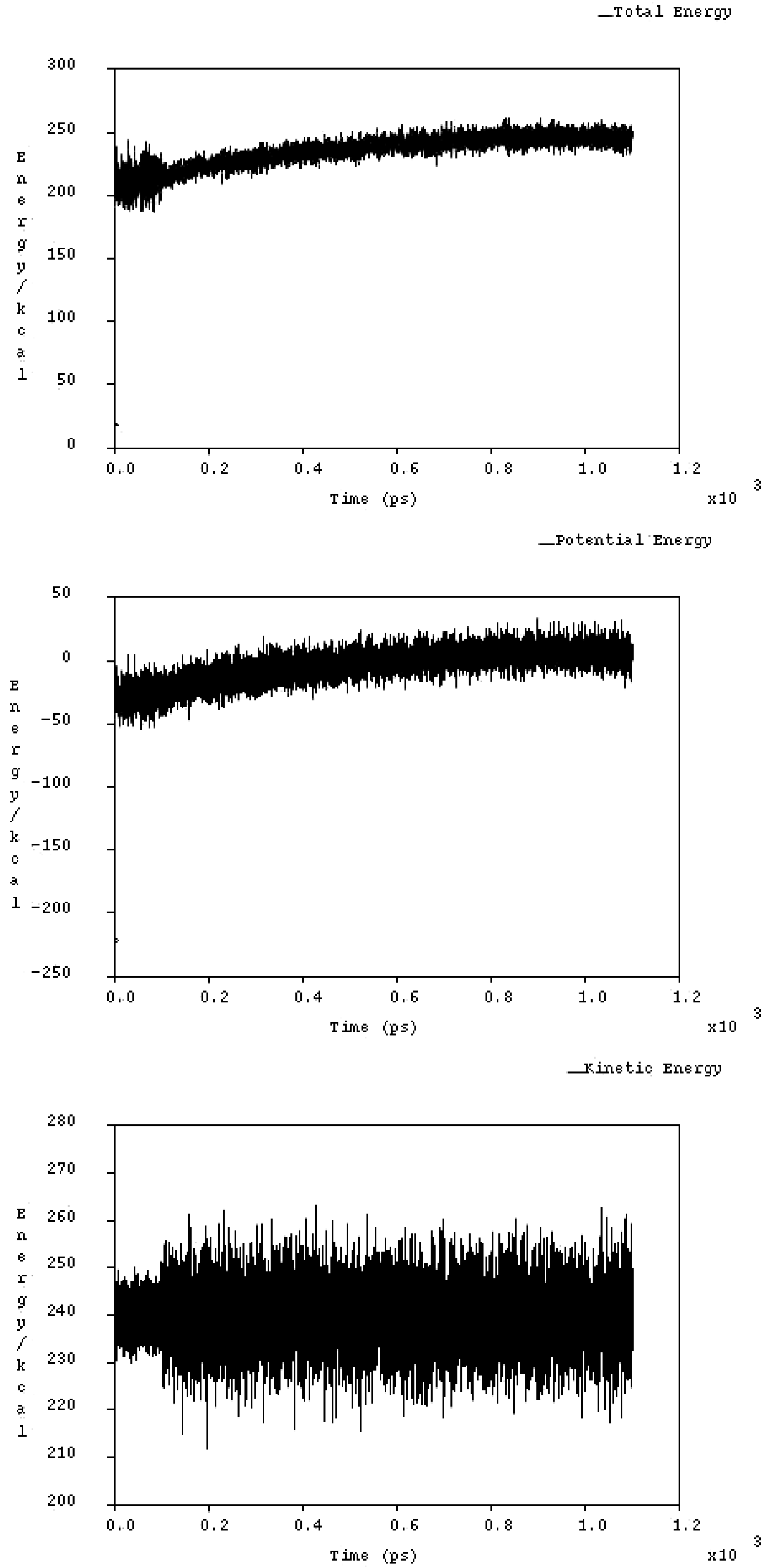


Figure 2. The variation of total energy, potential energy and kinetic energy during molecular dynamics.

By tagging the water molecule, which is hydrogen bonded to phenol in the geometry minimized using molecular mechanics, the variation of hydrogen bonding distance with time, *i.e.*, the fluctuation in the hydrogen bonding distance for 1 ns have been plotted against time in Figure 4.

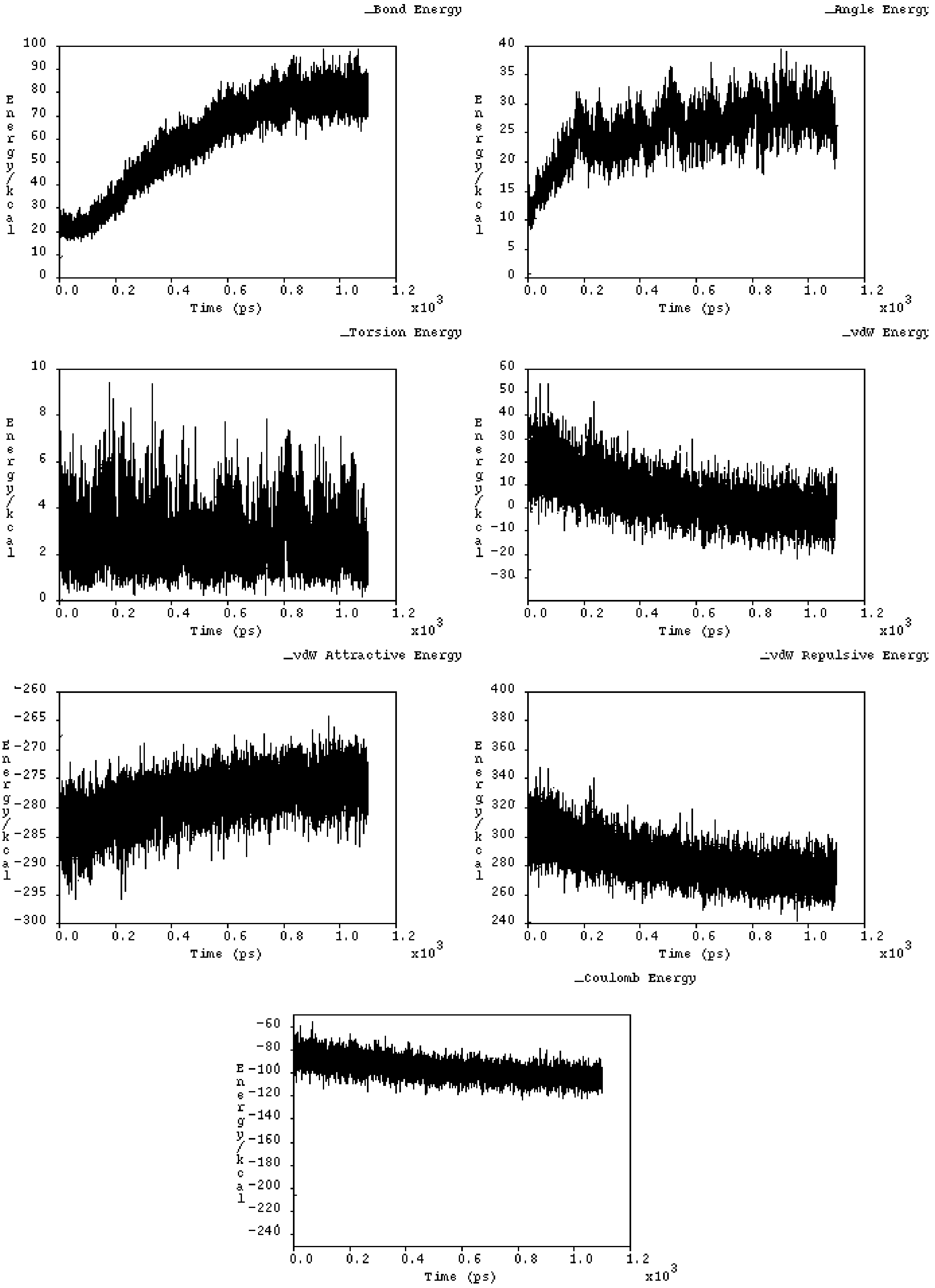


Figure 3. Variations of bond energy, angle energy, torsion energy, vdw energy, vdw attractive energy, vdw repulsive energy and Coulomb energy with time during MD simulation.

In the starting geometry, the phenol acts as proton donor. The fluctuation in the hydrogen bonded distance ranges from 2.0 to 24.0 Å. The changes in the distance with time provide direct information on the fast orientational reordering of water molecules and their respective interaction with phenol.

The high dynamic nature of the interaction is evident from the MD fluctuations. This is also supported by the various snap shots collected for different time periods presented in Figure 1. Due to possibility of proton accepting and donating nature, water molecules forms hydrogen bonded network with phenol as well with itself. In this respect, the phenol OH group donates and accepts proton and the interaction is highly similar to water molecules. In addition to the interaction of water molecule with phenol, the network structure formed by water molecules is also interesting.

It is well known from experimental and computer simulation; water is arranged in a tetrahedral structure. Each water molecule has four nearest neighbors, two of them can act as donors and other two can accept the hydrogen bonds. In a realistic situation coordination number of water molecule is slightly larger than four due to temperature fluctuations and reordering of water molecules during dynamics, thereby leading to a making and breaking of the hydrogen bonded structure.

Present MD simulation reinforces the above fact that the water molecules have coordination number four. The five coordinated water molecules can also be seen from the snapshots collected during the time interval. The water molecule hydrogen bonded to the phenol molecule is again hydrogen bonded to other water molecules to derive stable arrangement during the dynamics. The displacement of the entire phenol–water cluster has been obtained from the MD trajectory and presented in Figure 5. High dynamic nature of the entire system is evident from the fluctuations.

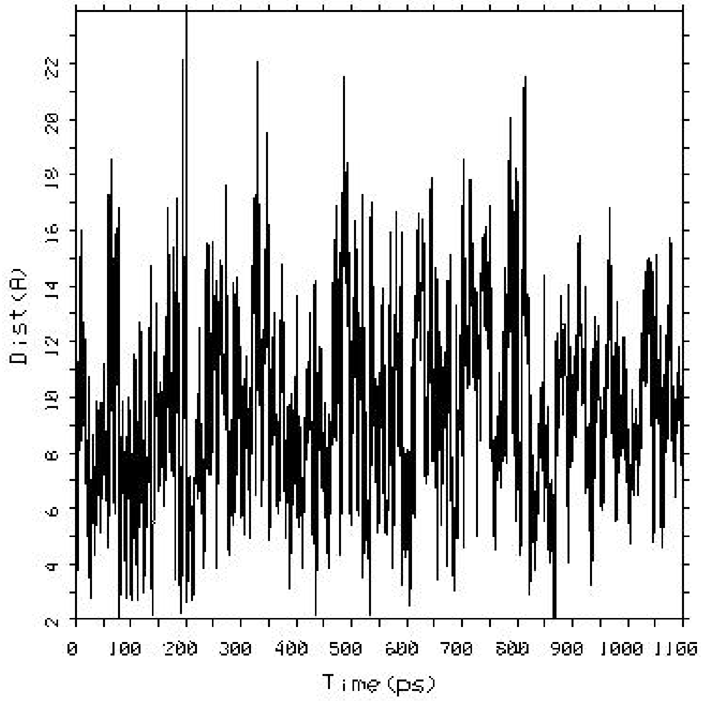


Figure 4. MD trajectories of the hydrogen bond distance between phenol and water molecule.

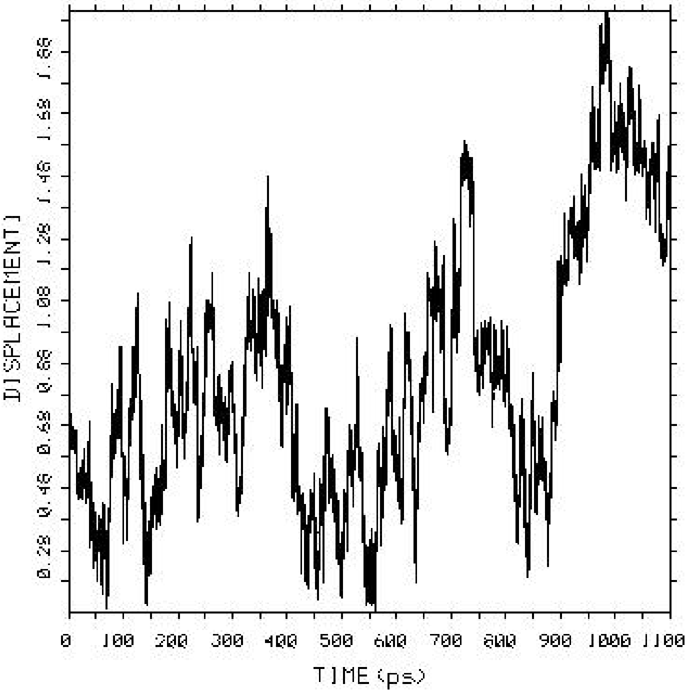
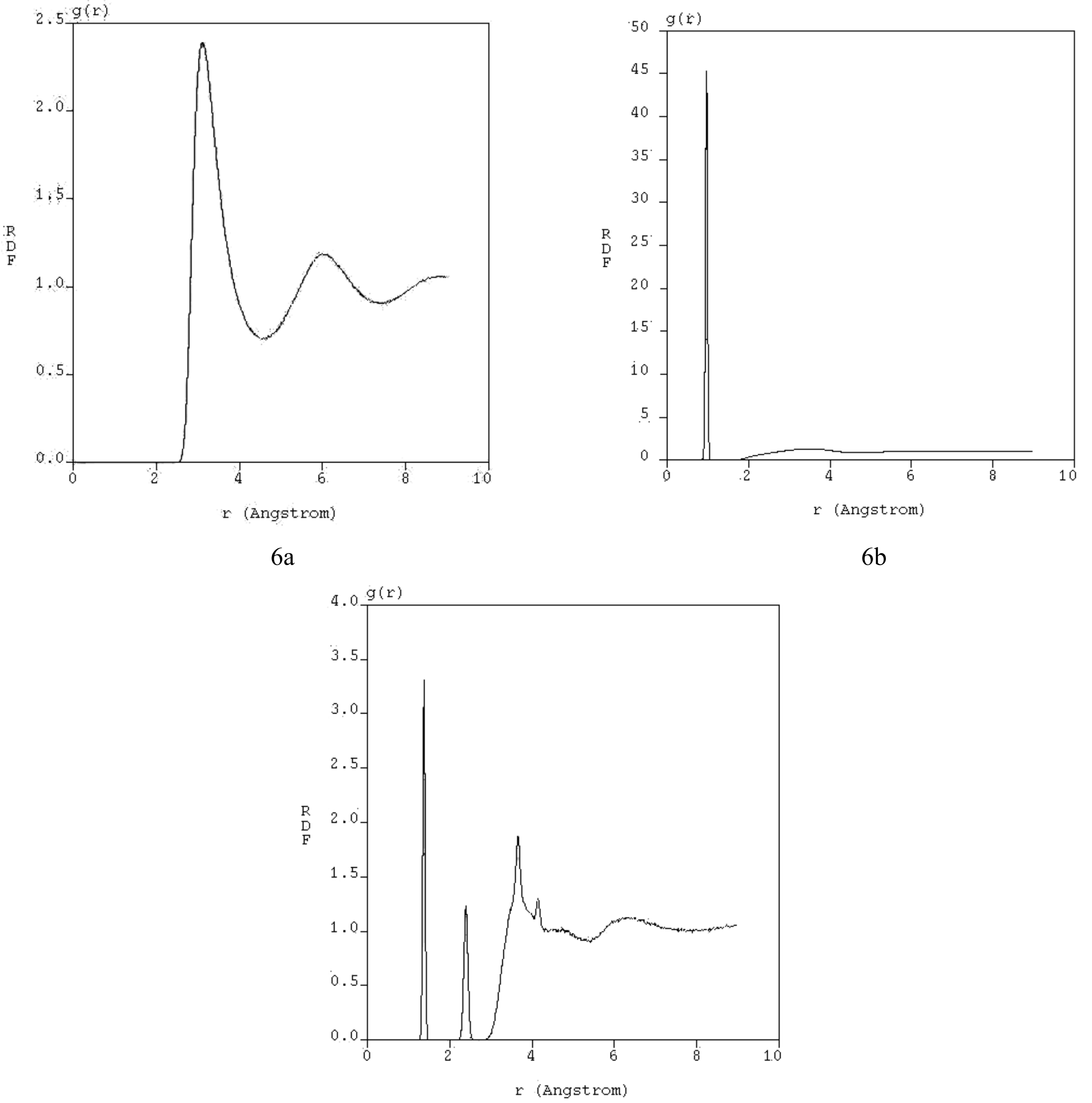


Figure 5. Displacement of phenol–water cluster during 1 ns.

The radial distribution is a measure of the probability of finding a particle as a function of distance from a typical particle, relative to that expected from a completely uniform distribution. In order to get information of the time averaged coordination of water molecule with phenol and itself, various radial distribution functions have been calculated. The calculated radial distribution functions for $g(R_{CO})$, $g(R_{OO})$ and $g(R_{OH})$ for 1ns seconds time duration are presented in Figure 6. All the distribution function rises to a sharp value and then levels off to a value of 1 implying that molecules no longer sense each other and behaves as in an ideal gas conditions.

The peak maximum for $g(R_{CO})$ distribution corresponds to the typical C–O distance in the phenol molecules. Similarly the peak maximum of $g(R_{OH})$ correspond to the O–H distance. The broad band present in the radial distribution functions for $g(R_{CO})$, $g(R_{OH})$ and $g(R_{O\text{–}O})$ show the possible interaction of water molecules with phenol and range of interaction present in the phenol–water cluster. The main peak at 2.7 Å for $g(R_{OO})$ corresponds to the O–H…H bond distance found in the phenol–water cluster.

Similarly $g(R_{OC})$ indicates the interaction between phenol and water molecules. The mutual diffusion coefficient in water–phenol mixture was calculated by fitting mean square displacement. The calculated value of the mutual diffusion coefficient is 0.73×10^{-5} cm^2/second. The experimental value of the diffusion coefficient for phenol–water complexes ranges from 1.75×10^{-5} to 0.85×10^{-5} cm^2/second [18]. The present value is in close agreement with the experimental value thereby ensuring the quality of simulation.



6a

6b

6c

Figure 6. (a) Radial distribution function (RDF) O–O atoms. (b) RDF for O–H atoms. (c) RDF for C–O atoms.

4 CONCLUSIONS

The analysis of MD simulation results shows clearly the existence of well–defined hydrogen bonded networks of water molecules as well as their interaction with phenol. Water molecule can act as proton donor and acceptor, the possible interaction as proton donor/acceptor is evident from the present MD simulation. Similarly the hydroxyl group of phenol behaves like water molecules in the sense that it donates as well as accepts proton and hence its interaction with water molecules. The variation in the hydrogen bonding distance between phenol and water molecules, fluctuation in the overall displacement of the molecule during the time evolution and various structures obtained at different time periods clearly provides information on the high dynamics nature of the entire system and presence of fast orientation reordering of water molecules. The calculated mutual diffusion coefficient is in concurrence with the experimental value.

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