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STRUCTURIZATION OF COUNTERIONS AROUND DNA DOUBLE HELIX: A MOLECULAR DYNAMICS STUDY

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The structurization of DNA counterions around the double helix has been studied by the molecular dynamics method. A DNA dodecamer d(CGCGAATTCGCG) in a water solution with alkali metal counterions Na^+, K^+, and Cs^+ has been simulated. The systems have been considered in the regimes without excess salt and with different added salts (0.5 M of NaCl, KCl, or CsCl). The results have shown that the Na^+ counterions interact with the phosphate groups directly from outside of the double helix and via water molecules at the top edge of the DNA minor groove. The potassium ions are mostly localized in the grooves of the double helix, and the cesium ions penetrate deeply inside the minor groove, being bonded directly to atoms of the nucleic bases. Due to the electrostatic repulsion, the chlorine ions tend to be localized at large distances from the DNA polyanion, but some Cl^- anions have been detected near atomic groups of the double helix, by forming electrically neutral pairs with counterions already condensed on DNA. The DNA sites, where counterions are incorporated, are characterized by local changes in the double helix structure. The lifetime of Na^+ and K^+ in the complex with DNA atomic groups is less than 0.5 ns, while it can reach several nanoseconds in the case of cesium ions. On this time scale, the Cs^+ counterions form a structured system of charges in the DNA minor groove that can be considered as ionic lattice.

K e y w o r d s: DNA, macromolecule, structure counterions, molecular dynamics.

1. Introduction

Under the natural conditions, the DNA double helix is surrounded by water molecules and positively charged ions (counterions). The counterions (usually, Na^+, K^+, or Mg^{2+}) condense on the DNA polyanion, by neutralizing the negatively charged atomic groups of the macromolecule [1–5]. The neutralization of a negative charge by counterions is the key point in the stability of the DNA double helix. The relative disposition of counterions on the macromolecule is modulated by the double helical structure of DNA. The structurization of counterions around a DNA macromolecule is a necessary stage in many mechanisms of conformational transformation of the double helix, such as the DNA condensation, formation of microscopic textures on the surface, *etc.* [6–11]. The study of a dynamical structure of counterions is important for understanding the molecular level of biological processes, where the DNA macromolecule is involved.

The localization of counterions on the macromolecule can be determined definitely only in the case of solid samples of DNA [12–14]. In solution, the counterions are mobile. Therefore, they are detected experimentally as a cloud that they form around the DNA double helix [15–18]. At the same time, the molecular dynamics method (MD) can provide a detailed information about the interaction of counterions with DNA and about the changes in the double helix structure [19–22]. In this regard, the MD study of DNA systems is indispensable for understanding the organization of counterions around the double helix.

Starting with the early MD simulations, the counterions are known to interact to the phosphate groups

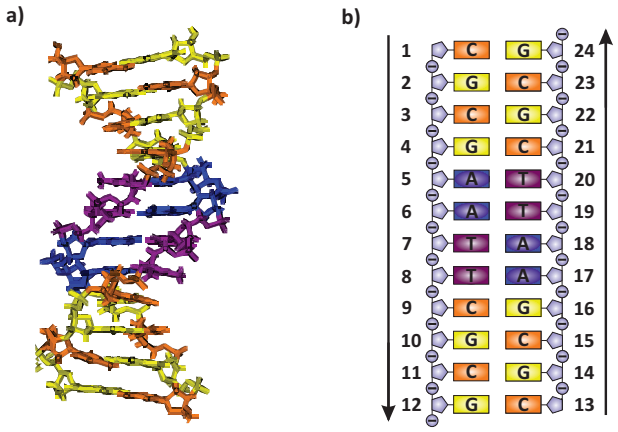

Fig. 1. (*Color online*) Modeled DNA fragment d(CGCGAATTCGCG). The color corresponds to the type of a nucleic base: adenine (A) – dark blue, thymine (T) – purple, guanine (G) – yellow, cytosine (C) – orange. Atomic structure of the fragment [46] (*a*). Schematic structure of the DNA fragment (*b*). The numeration of nucleotides is shown

of the double helix backbone, atoms of nucleic bases, and the oxygen atom of deoxyribose [23–26]. The character of the counterion interaction essentially depends on the counterion type, concentration, and sequence of nucleic bases [27–35]. The results for alkali metal ions (Li^+, Na^+, K^+, Rb^+, and Cs^+) show that the sodium ions interact mostly with the phosphate groups [29, 30]. They can be also localized at the top edge of the minor groove and interact with phosphates via water molecules. The potassium ions are usually localized in the groves of the double helix close to the negative base sites [22]. The heavy ions of Rb^+ and Cs^+ penetrate deeply inside the minor groove and interact directly with the atoms of nucleic bases and the oxygen atoms of deoxyribose [27, 34, 35]. The smallest ions Li^+ squeeze through water molecules surrounding the phosphate group and form stable complexes with phosphate groups of the DNA backbone [27]. The counterion organization around a DNA macromolecule induces different structure changes that are the key factors in the conformational transitions between *A*-, *B*-, and *Z*-forms of the double helix [36–38].

Due to a regularity of the DNA structure, the counterions should form a regular structure around the double helix. In the previous studies, the counterions tethered to the phosphate groups of the DNA backbone have been shown to form a structure resembling an ionic crystal lattice (ion-phosphate lattice) [39–43].The existence of the ion-phosphate lattice has been confirmed by the modes of counterion vibrations with respect to the phosphate groups observed in the Cs-DNA low-frequency spectra (<200 cm^{-1}) [44]. Effects of counterion ordering have been also observed in the experiments on the conductivity of DNA water solutions with a KCl salt [45]. To elucidate the lattice arrangement of counterions around the DNA double helix, it is necessary to conduct molecular dynamics studies.

The goal of the present research is to study a counterion structuring around the DNA double helix, by using the molecular dynamics method. To solve this problem, the MD simulations of DNA with Na^+, K^+, and Cs^+ counterions have been made. The description of the modeled systems and the MD simulation procedure is given in the second section. In the third section, the typical positions of counterions have been determined by analyzing the calculated radial distribution functions. The influence of counterions on the double helix structure has been studied in the fourth section. In the fifth section, the features of the structuring of counterions around a DNA macromolecule have been discussed.

2. Model and Methods

The DNA fragment d(CGCGAATTCGCG) known as a Drew–Dickerson dodecamer [46] has been simulated. The atomic and schematic structures of the modeled DNA dodecamer are shown in Fig. 1.

The counterions Na^+, K^+, and Cs^+ are added to the system. The ions are considered in two concentration regimes: i) the number of positively charged ions equals the number of negatively charged phosphate groups of the DNA backbone; ii) the chloride salt (NaCl, KCl, or CsCl) with a concentration of 0.5 M is added to the system consisting of DNA with counterions neutralizing phosphate groups of the double helix. The oligomer is emersed into a rectangular box (42 Å $\times$ 42 Å $\times$ 62 Å) with about 2,990 TIP3P water molecules. The periodic boundary conditions in all directions are used. Thus, three systems without added salt (Na0, K0, and Cs0) and three systems with an added salt (Na05, K05, and Cs05) have been modeled. The parameters of these systems are shown in Table 1.

The computer simulations are performed within the framework of the NAMD software package [47] and

the CHARMM27 force field parameter set [48]. The integration time step equals 2 fs. All bond lengths are fixed using the SHAKE algorithm [49]. The long-range electrostatic interactions are treated, by using the particle meshed Ewald method [50]. The switching and cutoff distances for the long-range interactions are taken to be equal to 8 Å and 10 Å, respectively. The simulations are performed at the constant pressure 101,325 Pa and a temperature of 300 °K. For the pressure and temperature control, the Langevin dynamics is used for all heavy atoms (damping constant is 5 ps^{-1}). The oscillation time and damping time constants for the Langevin piston are 100 fs and 50 fs, respectively.

The simulation protocol analogous to [29] is used. At the first stage of simulation, the minimization is made for the system with fixed heavy atoms (1,000 steps). Then the system is minimized with fixed DNA atoms (2,000 steps). At the second stage, the solvent is heated to a temperature of 300 K (15 ps) and equilibrated during 100 ps. At the third stage, the minimization is performed for the system with restrained DNA atoms by a harmonic potential (2,000 steps). The restrain coefficient is equaled to $k = 5$ kcal/mol $Å^2$. Then the system is heated to a temperature of 300 K (30 ps) and equilibrated during 100 ps. After that, the atoms of DNA are set free, and the system is equilibrated during 1 ns. The total duration of the MD trajectory is 12 ns. The first nanosecond is not taken into consideration in the further analysis of modeled systems.

To perform the complete characterization of the counterion dynamics around the DNA double helix, the length of an MD trajectory should be about several hundreds of nanoseconds [21, 22, 34]. However, for the comparative study of the dynamics of counterions of different types (in our case Na^+, K^+, and Cs^+), the length of a MD trajectory may be shorter. Taking into consideration that the characteristic residence time of a counterion in complex with DNA atomic groups is usually about 1 ns [19–21], the MD trajectory of about 10 ns in length may be appropriate. Thus, in the present study, the lengths of MD trajectories for the modeled systems are taken equal to 12 ns.

To characterize the equilibrium state of the systems, the deviation of the DNA structure from the initial structure is analyzed, by using a root mean square deviation (RMSD). The RMSD is defined as

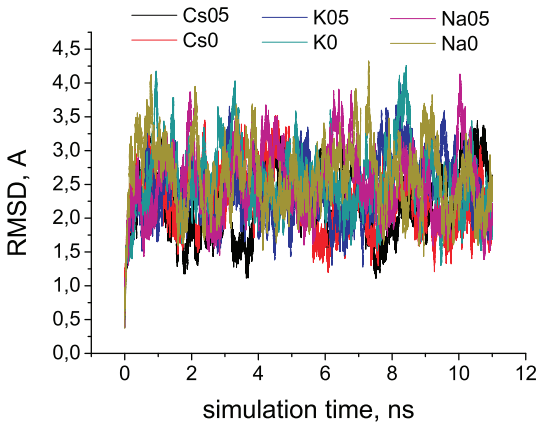

Fig. 2. (*Color online*) Root-mean-square deviation (RMSD) of DNA atoms from the initial structure as a function of the time. RMSDs for different systems are shown by different colors

$\Delta R(t) = \sqrt{\frac{1}{N}\sum_{\alpha=1}^{N}\left[\mathbf{r}_\alpha(t) - \mathbf{r}_\alpha(0)\right]^2}$, where N is the number of considered atoms, $\mathbf{r}_\alpha(t)$ and $\mathbf{r}_\alpha(0)$ are the coordinates of atom α at the time moments t and $t = 0$, respectively. RMSD of systems is derived using the VMD program [51]. The obtained dependence of RMSD on the time for all simulated systems is shown in Fig. 2. One can see that, for the first nanosecond, the RMSD values increase from 0 to about 2 Å and then fluctuate with respect to the average value. The amplitude of RMSD fluctuations is about 1 Å during the whole simulation trajectory. The obtained RMSD are appropriate for equilibrated systems on the nanosecond time scale.

3. Distribution of Ions around DNA Double Helix

To analyze the distribution of counterions with respect to the DNA double helix, the radial distribu-

Table 1. **Parameters of the modeled systems. Mt^+ denotes the counterion type (Na^+, K^+, or Cs^+). N_{Mt+} and N_{Cl-} are the numbers of metal and chlorine ions in the system. C is the concentration of an added salt. N_W is the number of water molecules**

System	Mt^+	N_{Mt+}	N_{Cl-}	C (M)	N_W
Na0	Na^+	22	0	0.0	2988
Na05	Na^+	50	28	0.5	2932
K0	K^+	22	0	0.0	2988
K05	K^+	50	28	0.5	2932
Cs0	Cs^+	20	0	0.0	2990
Cs05	Cs^+	50	28	0.5	2932

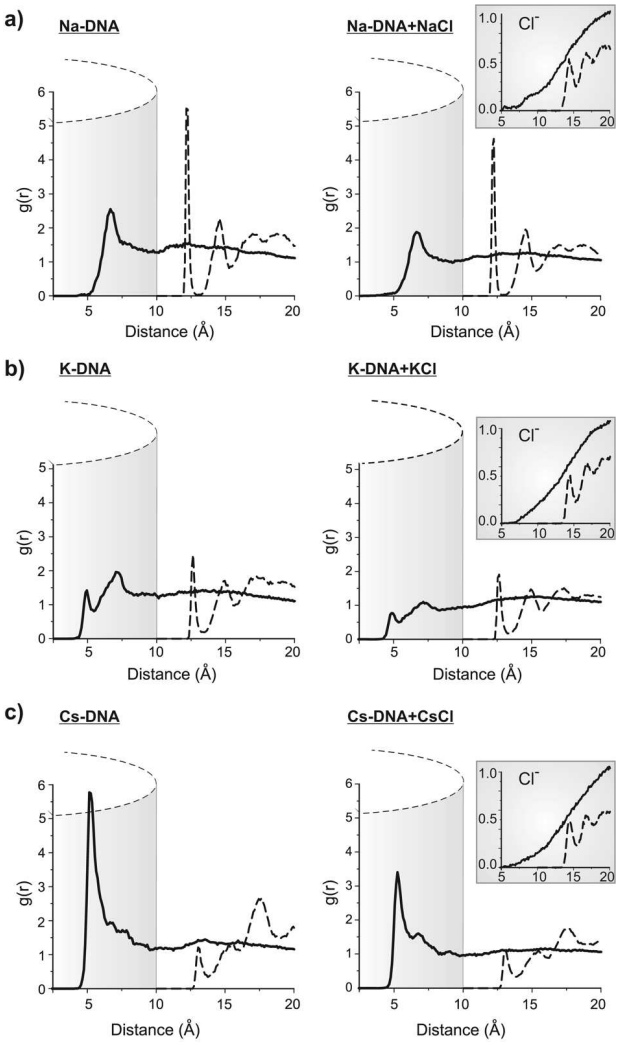

Fig. 3. Averaged radial distribution functions (RDFs). Central RDFs (solid lines) and phosphate RDFs (dashed lines) describe the distribution of ions with respect to the double helix axis and backbone phosphates, respectively. The phosphate RDFs are shifted by 10 Å to illustrate the characteristic radius of *B*-DNA. The cylinder schematically shows the surface of the double helix. The RDFs of Na^+ counterions in Na0 and Na05 systems (*a*). The RDFs of K^+ counterions in K0 and K05 systems (*b*). The RDFs of Cs^+ counterions in Cs0 and Cs05 systems (*c*). In the insets, the RDFs for Cl^- ions are shown

tion functions (RDFs) of two type have been calculated with the use of the VMD program [51]. The first RDF type (phosphate RDF) characterizes the distribution of ions with respect to oxygen atoms O1 and O2 of the phosphate groups. The second RDF type (central RDF) characterizes the distribution of ions with respect to the atoms that are localized close to the center of *B*-DNA double helix (atoms N3 of purine and N1 of pyrimidine bases). The RDFs are calculated for all nucleotide pairs except that belonging to the ends of DNA fragment. To avoid the end effects, 1-21, 2-23, 12-13, and 11-14 nucleotide pairs (Fig. 1, *b*) (ends of the dodecamer) are not considered. Using the obtained series of functions, the averaged RDFs of each type have been defined. The averaged RDFs are shown in Fig. 3.

The phosphate RDFs describe the distribution of counterions outside the double helix. The obtained phosphate RDFs usually have two prominent maxima and one weak maximum. The position of the first maximum is within the distance range (2.2÷3.1) Å (Table 2), which correlates with the ion size. The first peak characterizes the direct binding of ions to the oxygen atoms of the phosphate groups of the DNA backbone. The second maximum at about (4.5÷7.3) Å characterizes the localization of ions in the grooves of the double helix and in the ion-hydrate shell of the macromolecule. The third weak peak (at about 10 Å) characterizes the ions in the ion-hydrate shell of DNA.

The central RDFs feature the localization of counterions with respect to the double helix axis. The obtained central RDFs may have one or two peaks. The first peak is at about the distance 5 Å, while the second peak is at about 7 Å from the helix center. These peaks characterize the localization of counterions in the grooves of the double helix. The first peak arises due to the ions contacting with the atoms of bases directly at the bottom of the grooves. The second peak characterizes the localization of ions at the top edge of the grooves.

Our results have shown that the distribution of Na^+ counterions in the both Na0 and Na05 systems is

Table 2. **Positions of maxima of the radial distribution functions (Å)**

System	Na0	Na05	K0	K05	Cs0	Cs05
Phosphate RDF						
I-peak	2.2	2.2	2.6	2.6	3.1	3.1
II-peak	4.5	4.6	4.9	5.0	7.3	7.1
Central RDF						
I-peak	–	–	4.9	4.9	5.2	5.3
II-peak	6.7	6.7	7.1	6.7	7.3	7.1

characterized by the first intense and the second small maxima in the phosphate RDF (Fig. 3, *a*). The positions of these peaks are at about 2.2 Å and 4.5 Å from the phosphate group, respectively (Table 2). The central RDF has a low-intensity band at about 7 Å from the double helix center. The first intense peak in the phosphate RDF and the band in the central RDF indicate that the sodium counterions interact with the phosphate groups and do not enter the grooves deeply. The Na^+ ions with water molecules of its hydration shell may be localized at the top edges of the grooves.

In the case of K0 and K05 systems, the maxima of phosphate RDFs are not as intense as in the systems with sodium ions (Fig. 3, *b*). At the same time, the central RDF has two peaks at the distances about 5 Å and 7 Å (Table 2) characterizing a direct interaction of the ions with the atoms of bases and the localization of an ion at the top edge of a groove, respectively. The interaction of K^+ with the phosphate groups is not dominant.

The radial distribution functions of Cs0 and Cs05 systems are characterized by an intense peak in the central RDF at the distance about 5 Å and by a shoulder at about 7 Å (Fig. 3, *c*). The phosphate RDFs are characterized by the low-intensity first and second peaks and a rather strong band at about 7 Å (Table 2). Such structures of RDFs indicate that Cs^+ ions are localized mostly in the grooves of the double helix and interact directly with the atoms of bases.

The distributions of Cl^- ions in Na05, K05, and Cs05 systems are rather similar. The central RDFs have no maxima and gradually increase with the distance from the double helix center. The phosphate RDFs are characterized by a low maximum at a distance of about 5 Å, which is more than twice greater than the ion radius (insets in Fig. 3). Thus, the chlorine anions tend to be localized at large distances from the DNA double helix.

The analysis of the radial distribution functions shows that the counterions usually interact with atoms O1 and O2 of phosphates, atoms N3, N7, and O2 of nucleic bases, and atom O4′ of deoxyribose. The snapshots illustrating the localization of Na^+, K^+, and Cs^+ counterions on the DNA double helix are shown in Fig. 4. A visual examination has showed that, in the case of the salt-free system, the sodium counterions are localized near the phosphate groups from the outside of the double helix and

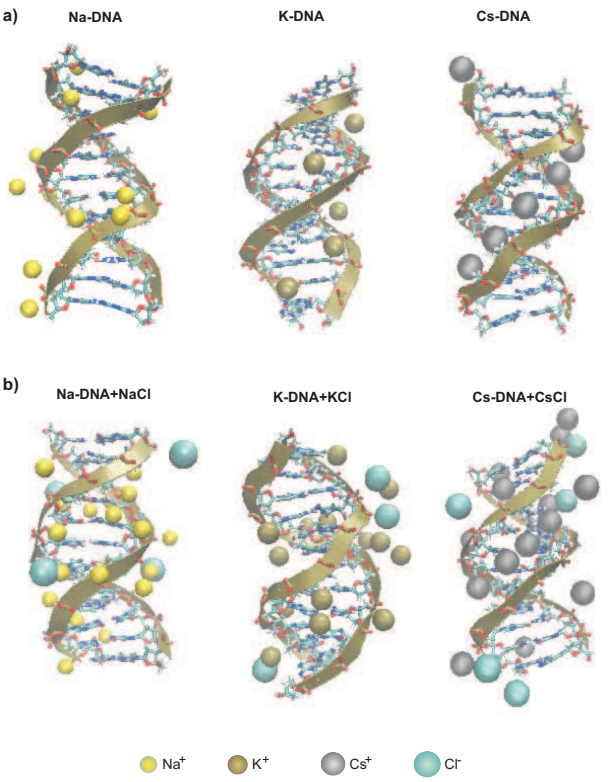

Fig. 4. (*Color online*) Snapshots of DNA double helix with counterions. DNA with Na^+, K^+, and Cs^+ counterions in Na0, K0, and Cs0 systems, respectively (*a*). DNA with added NaCl, KCl, and CsCl salts in Na05, K05, and Cs05 systems (*b*)

in the grooves of the macromolecule (Fig. 4, *a*). In the minor groove of the double helix, the Na^+ ions can be localized between phosphate groups of different strands at the top edge of the groove. The interaction of sodium ions with the atoms of nucleic bases occurs via water molecules. The potassium ions in K0 system can interact mostly to the phosphate groups from the grooves side of macromolecule. In contrast to the Na^+ ions, the K^+ ions can also interact directly with the atoms of nucleic bases. The cesium counterions in Cs0 system can penetrate deeply into grooves. In the minor groove, they interact with N3 and O2 atoms of purine and pyrimidine bases. From time to time, the regular structure of Cs^+ counterions are observed in the minor groove of the double helix. The distance between structured Cs^+ ions in the minor groove of the double helix is about 7 Å.

In the systems with added Mt^+Cl^- salt (Na05, K05, and Cs05), the interaction sites of counterions

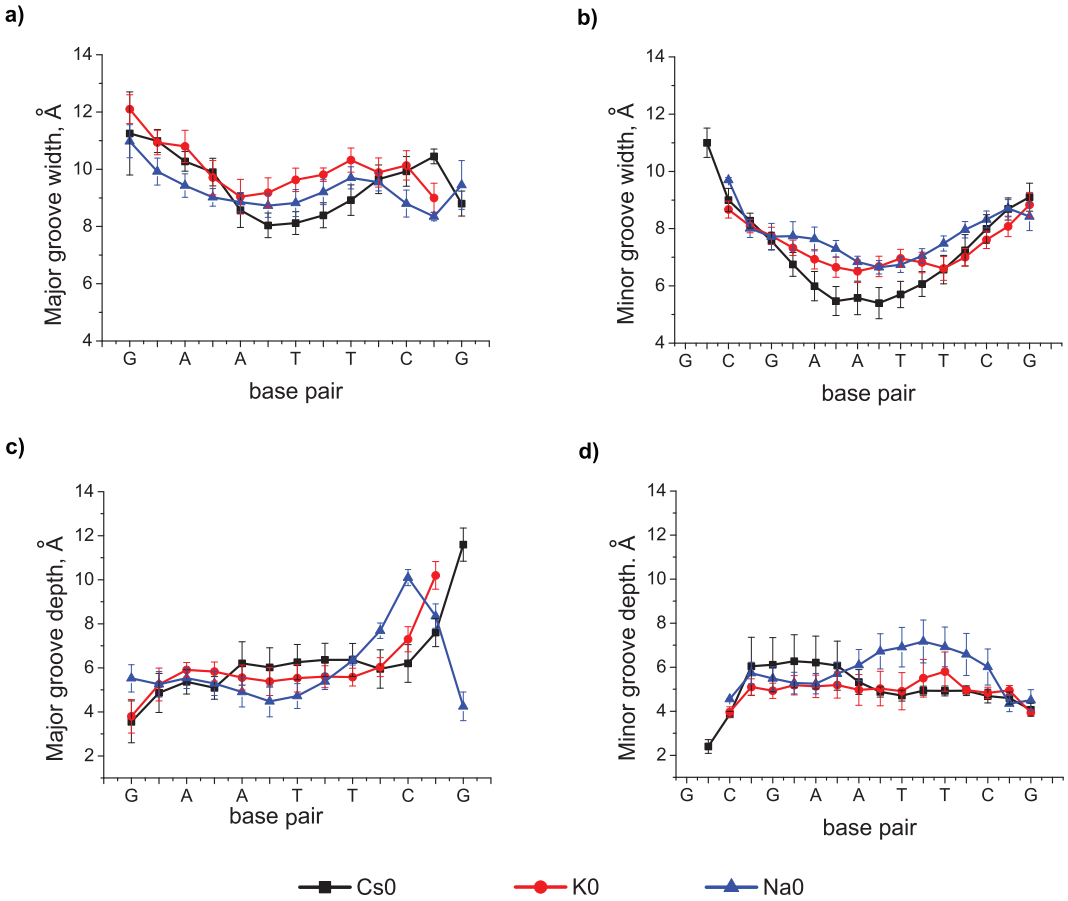

Fig. 5. (*Color online*) Average grooves parameters for Na0, K0, and Cs0 systems. Major groove width (*a*). Minor groove width (*b*). Major groove depth (*c*). Minor groove depth (*d*)

with the DNA double helix are the same as in salt-free solutions. The chlorine ions form the associates with the metal ions. The cation-anion pairs can approach rather close the macromolecule and even be incorporated into the double helix (Fig. 4, *b*). The interaction of cations with the central base pairs of DNA fragment is more intense, while the anions more often come to the ends of the double helix.

The analysis of the obtained results shows that the derived RDFs have shape similar to that obtained in MD studies with a much longer simulation trajectory [21, 22, 28, 30, 34], but the intensities of RDFs maxima are slightly different. The detected DNA-counterion contacts and their lifetimes correlate with the values obtained earlier [21, 28–30]. Thus, the conducted MD research describes well (at least, in qualitative aspects) the features of the counterion structurization around the DNA double helix.

4. Transformations of the Double Helix Structure under the Influence of Counterions

The counterions interacting with DNA atoms induce the conformational changes of the double helix. To analyze the influence of counterions on a conformational state of the macromolecule, the structure parameters of the double helix have been calculated. The DNA conformational parameters have been derived with the help of the Curves+ program [52]. Using the obtained data, the parameters, which were averaged over the time, of the double helix grooves have been calculated. The dependences of groove widths and depths on the base pair level are shown in Figs. 5 and 6.

The obtained dependence of the groove parameters on the base pair level and the influence of counterions correlates with the results of early molecular dynam-

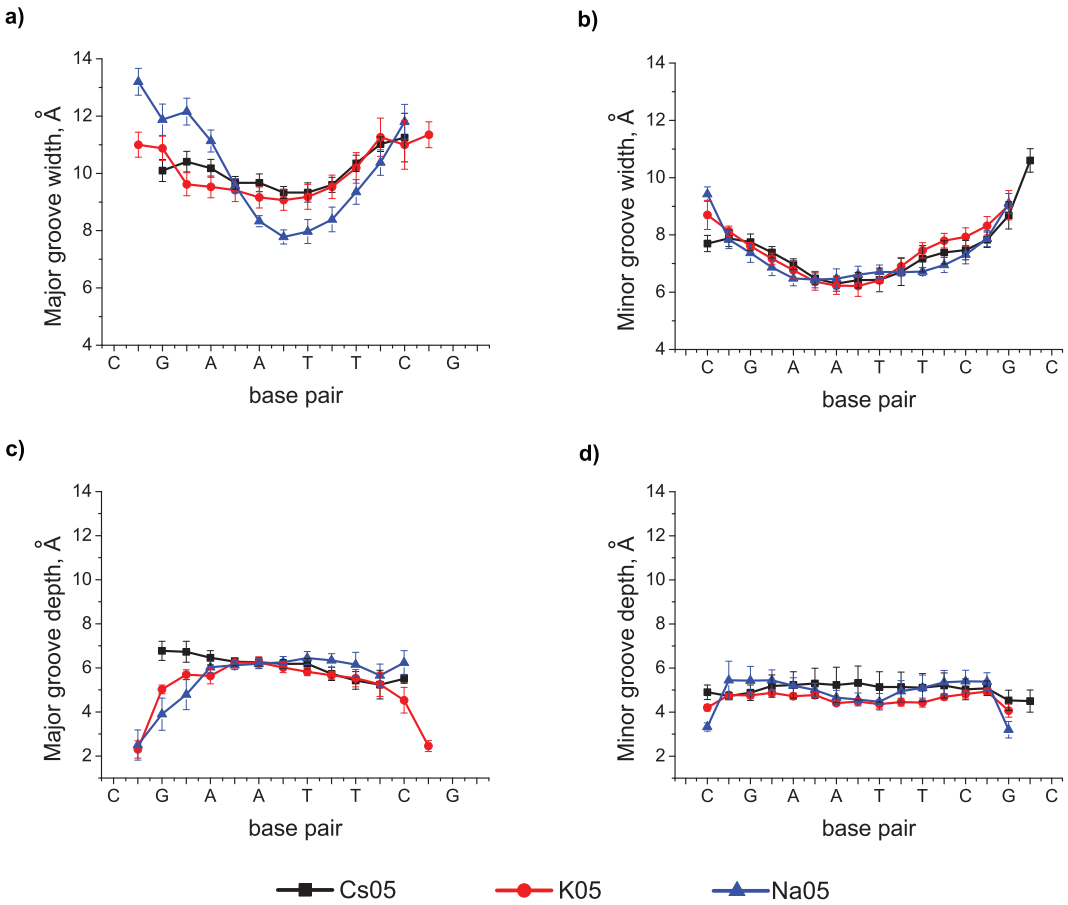

Fig. 6. (*Color online*) Average grooves parameters for Na05, K05, and Cs05 systems. Major groove width (*a*). Minor groove width (*b*). Major groove depth (*c*). Minor groove depth (*d*)

ics simulations [27, 29–32, 34]. In the case of salt-free systems, the widths of the major and minor grooves change within the range (8÷12) Å and (5.5÷11) Å, respectively (Fig. 5, *a*, 6, *b*). The minimal values of groove width correspond to the central base pairs, while the largest values are characteristic of the ends of the DNA fragment. For the central base pairs, the values of groove width are the lowest in the case of Cs^+ ions. In the case of Na^+ and K^+ ions, the widths of the grooves are almost similar.

The widths of grooves in the case of the systems with added salt vary within the range (6÷13) Å and have the same dependence on the base pair level, as that in the salt-free systems (Figs. 6, *a*, 6, *b*). The groove depth is approximately constant in the central part of the dodecamer (about 6 Å) and changes on its ends for all systems (Figs. 5, *c*, 5, *d* and Figs. 6, *c*, 6, *d*).

To characterize the macromolecule elasticity, the time-averaged angle of the double helix bending has been calculated for DNA in the modeled systems (Table 3). One can see that the average angle values are rather large and vary within the range (10÷21)°. The bending angle is especially large in the case of K05 and Cs0 systems, while, in the case of Na0 and K0 systems, it has the lowest value. The bending angle is related to the persistence length of the macromolecules. Increasing the double helix bending angle should induce a decrease in the persistence length of DNA. The dependence of the persistence length on

Table 3. **Values of total bend of DNA macromolecules for different systems**

System	Na0	Na05	K0	K05	Cs0	Cs05
Angle (°)	11±4	15±7	11±7	21±9	21±5	12±7

the counterion type and the concentration has been observed experimentally [4].

Our analysis of DNA structure parameters has shown that the conformational changes of the double helix are the most prominent in the center of the modeled DNA dodecamer, where the localization of counterions is the most often. At the same time, the conformational changes may occur due to the length effects of the polynucleotide and due to the intrinsic properties of the AATT sequence of DNA that is in the central part of Drew–Dickerson dodecamer (Fig. 1). All these factors of the double helix structural transformations may be interrelated.

5. Discussion

The results of the conducted MD study have shown that Na^+, K^+, and Cs^+ counterions interact with DNA in different manners, and the relative positions of ions on the double helix are essentially different. Sodium ions are bound mostly to the phosphate groups of the DNA backbone and may enter the grooves of the double helix with water molecules of the hydration shell. The potassium ions are localized mostly in the grooves of the double helix. The interaction of K^+ with the phosphates is not so essential, as in the case of Na^+. The cesium ions penetrate deeply into the grooves of the double helix and interact directly with the atoms of bases.

The reason for such different interactions of alkali metal ions with DNA is considered due to different sizes of ions and their different solvation types [19]. The radii of alkali metal ions are known to increase in the following order: $Li^+ < Na^+ < K^+ < Rb^+ < Cs^+$, while their hydration radii have opposite gradation [53]. As a result, the energy of hydration is positive in the case of Li^+ and Na^+ ions and is negative in the case of K^+, Rb^+, and Cs^+ ions [54]. That is why the water molecules of the hydration shells of sodium and lithium ions are constrained, which does not allow the ions to enter the grooves of the double helix deeply and to interact directly with the atoms of bases. The smallest alkali metal ion Li^+ interacts with the oxygen atoms of DNA phosphates and forms the common hydration shell, which provides a long living complex with the double helix [19]. In contrast, the water molecules around cesium ions are not so constrained by ions, and Cs^+ can be easily dehydrated and pass to the bottom of DNA grooves. The properties of rubidium ions in DNA solutions have been shown to be rather similar to Cs^+ ions [19, 34, 35].

Due to the electrostatic repulsion, the negatively charged chlorine ions tend to be localized at large distances from the DNA polyanion. However, some Cl^- ions have been detected close to the DNA surface and even inside the grooves of the macromolecule. The intrusion of Cl^- into the double helix occurs due to the formation of neutral cation-anion pairs with the counterions already condensed on DNA. A recent MD study of ionic aggregates in DNA solutions has shown that the formation of large ionic clusters is characteristic of different force fields, but not of the CHARMM force field used in the present work [55]. Thus, the formation of cation-anion pairs in our MD simulations is not an artifact of the method.

The structure of the DNA double helix is not uniform for all base pairs. The grooves of the double helix shrink at the center of the macromolecule fragment, and the double helix is bent as a whole. The observed conformational transformations of the macromolecule occur due to both intrinsic properties of the AATT sequence of the DNA fragment and the influence of the counterions interacting with the double helix. The length effects of the DNA fragment may be also essential.

The relative disposition of Na^+ and K^+ ions on DNA macromolecules changes dynamically. The lifetime of these ions tethered to the phosphate groups of the double helix is equal or less than 0.5 ns. The cesium ions can spend a rather long time in complex with DNA atomic groups (about several nanoseconds) and, from time to time, form a regular structure in the minor groove of the double helix. The characteristic distance between structured Cs^+ ions is about 7 Å. The structure of Cs^+ counterions with DNA may be considered as the ionic lattice. The existence of such lattice structure for DNA with alkali metal ions was predicted in the previous works [39–43].

6. Conclusions

In the present research, the dynamical and structural features of the DNA-counterion system have been studied by the molecular dynamics method. The MD simulations have been made for different systems consisting of the molecular fragment d(CGCGAATTCGCG) and counterions of some type

(Na^+, K^+, or Cs^+). The systems have been considered in the regimes without excess salt and with different added salts (0.5 M of NaCl, KCl, or CsCl). The results have shown that the Na^+ ions interact mostly with phosphate groups of the DNA backbone. The K^+ ions are localized mostly in grooves of the double helix, while the Cs^+ ions penetrate deeply inside the grooves of the double helix and interact directly with atoms of the bases. The difference in counterion interactions with DNA is considered as a consequence of the different ion hydrations. The addition of an extra salt to the system does not change the character of interaction of counterions with DNA. The chlorine anions are usually localized at large distances from the DNA polyanion, but some Cl^- ions have been detected near atomic groups of the double helix that is due to the formation of neutral pairs with the counterions already condensed on DNA. The interactions of counterions with DNA induce local changes in the double helix structure. The counterions dynamically change their positions on the DNA macromolecule. The lifetime of Na^+ and K^+ ions near phosphate groups of the double helix is equal to or less than 0.5 ns. In contrast, the lifetime of cesium ions in the DNA minor groove may reach several nanoseconds. On this time scale, the regular structure of Cs^+ in the DNA double helix is formed, which may be considered as an ionic lattice.

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СТРУКТУРУВАННЯ ПРОТИІОНІВ НАВКОЛО ПОДВІЙНОЇ СПІРАЛІ ДНК: ДОСЛІДЖЕННЯ МЕТОДОМ МОЛЕКУЛЯРНОЇ ДИНАМІКИ

Р е з ю м е

Структурування протиіонів навколо подвійної спіралі ДНК досліджувалося за допомогою методу молекулярної динаміки. Моделювання проводилося для додекамера ДНК d(CGCGAATTCGCG) з протиіонами лужних металів Na^+, K^+ та Cs^+ у водному середовищі. Розглядалися системи без надлишкової солі та з додаванням різних солей (NaCl, KCl або CsCl з концентрацією 0,5 М). Результати показали, що протиіони Na^+ взаємодіють з фосфатними групами безпосередньо з зовнішньої сторони подвійної спіралі і через молекули води на поверхні мінорного жолоба ДНК. Іони калію локалізуються переважно в жолобах подвійної спіралі, а іони цезію проникають глибоко всередину мінорного жолоба, безпосередньо зв'язуючись з нуклеїновими основами. За рахунок електростатичного відштовхування іони хлору, зазвичай, знаходяться на великих відстанях від ДНК, проте деякі аніони Cl^- спостерігалися поблизу атомних груп подвійної спіралі, формуючи електрично нейтральні пари з протиіонами, які вже сконденсувалися на поліаніоні ДНК. В місцях зв'язування протиіонів з ДНК спостерігалися зміни локальної структури подвійної спіралі. Час життя Na^+ та K^+ менший за 0,5 нс, а у випадку іонів цезію може сягати декількох наносекунд. У цьому масштабі часу протиіони Cs^+ формують впорядковану систему зарядів в мінорному жолобі ДНК, яку можна розглядати як іонну ґратку.