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Low-Frequency Intra- and Intermolecular Vibration Modes of H-Bonded Nucleobases in Oligonucleotide Double Helixes and Hydrated Nucleotide Duplex: Application of the PM3 Method

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ABSTRACT: To understand the physical mechanisms of the structural–dynamic organization of the DNA double helix, it is important to investigate the spectrum of vibration modes of Watson–Crick base pairs with different models of H-bonding complexes. Using the PM3 technique, we calculate the energy of low-frequency intra- and inter-molecular vibration modes of isolated canonical nucleoside and nucleotide pairs and analyze the dependence on the elongation of oligonucleotide double helix. The vibration spectrum of hydrated duplex $[d(ApA) \cdot d(TpT)]^{-2} \cdot 47H_2O$ was also calculated to elucidate the role of water in formation of the DNA spectrum. The results are compared with the available experimental data and analytical estimations. Int J Quantum Chem 100: 595–609, 2004

Key words: DNA; oligonucleotide duplexes; normal modes; intra- and intermolecular vibrations; hydrate effect; PM3 calculations

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Introduction

Vibration dynamics of the double helix polynucleotides is an important factor in the structural–functional organization of the nucleic acid molecules. The stability of DNA structure in different polymorphic states, the flexibility of the double helix when forming protein–DNA complexes, and the velocity of some enzyme regulated processes of transcription of genetic information are substantially dependent on the vibration properties of the molecular system [1].

In recent years, due to the perfection of experimental spectroscopic methods, mainly of the terahertz Fourier-transform infrared (FT-IR) spectroscopy technique [2], the low-frequency dynamics of DNA in the region 100 cm^{-1} has been intensively developed. This region includes collective modes of hydrogen-bonded nucleotide chains and local modes of constituent components of DNA molecule. The spectrum of these modes is the most sensitive both to the conformation of the complex as a whole and to the composition and state of surrounding (i.e., to the existence of different types counterions, to the changing of the degree of hydration, to the change of the temperature of the environment) [1, 3–5].

Several estimations of the vibration characteristics of lengthy double chains of nucleotides are known [6–10]. According to these estimations, IR active low-frequency collective modes of DNA molecule are localized mainly in the regions 20–30 cm^{-1} and 60–100 cm^{-1} of the absorption spectrum, and they are conditioned by interbase H-bond breathing modes [7, 9], chains twist-like motions [6], plasmon excitations [10], and nucleoside torsion vibrations [8].

At the same time, some examples of more rigorous, quantum chemical calculations on the vibration structure of different complexes of H-bonded nucleobases are known in the literature [11–18]. The results, for example, of HF/MINI-1 normal mode calculations [18] point out that in the case of simple dinucleotides, the low-frequency spectrum of interbase (collective) vibration modes is located in the far-IR region, namely in the region of $\sim$5 cm^{-1}. It remains unclear what behavior of the spectrum of collective vibrations in the long double polynucleotide helixes could be expected.

It is also well known that real DNA molecules are hydrated complexes [1], and the stability of the double helical structure is dependent on the number of water molecules in the surrounding Watson–Crick nucleotide pairs. Therefore, to understand physical mechanisms of structural–dynamic organization of the DNA molecule correctly, it is important to investigate the behavior of low frequency spectrum of inter- and intra-molecular vibrations of H-bonded nucleotides not only in the structure of isolated lengthening double chains of oligonucleotides, but in the structure of hydrated duplexes as well.

In this context, the use of semi-empirical quantum chemical methods in the electronic structure calculations of double chain complexes could be rather effective. The methods require substantially smaller resources, and they quite satisfactorily describe structural, spectral and thermodynamical properties of the molecules with rather ramified system of valent bonds.

Earlier in our publications [19, 20], and in the work of other investigators [11, 21] the applicability of semi-empirical PM3 approach [22] to electronic structure calculations of H-bonded nucleobases and small nucleotide duplexes was demonstrated. In the present work, the same quantum chemical technique was used to analysis of the spectrum of normal modes in short double helices of DNA molecules. Using as examples of isolated oligonucleotide duplexes: d(ApA) · d(TpT), d(ApApA) · d(TpTpT), d(ApApApA) · d(TpTpTpT), d(ApTpApT) · d(ApTpApT), d(GpGpGpG) · d(CpCpCpC), and d(GpCpGpC) · d(GpCpGpC), we investigated the dependence of low-frequency vibrations of H-bonded double chains on the length of the helix.

The influence of water surrounding on the changing of vibration spectrum of duplex is also studied, and the spectrum of normal vibrations of H-bonded dinucleotide $[d(ApA) \cdot d(TpT)]^{-2}$, which is surrounded by a double layer of H_2O molecules, was calculated.

The aim of given work is to show that (i) the lower bound of the harmonic vibrational spectrum of isolated oligonicleotide double helixes is located in the rather far IR region, of about several cm^{-1}, and low-frequency modes are forming mainly by intermolecular vibrations of H-bonded nucleotide pairs; and (ii) in the hydrated nucleotide complex because of the large amount of hydrogen bonds with the participation of water molecules, the spectrum of low normal modes of the duplex is highly condensed by intermolecular modes of water shells.

Method

Supermolecule and harmonic force field approximations were used in PM3 geometry optimization calculations and vibration spectrum simulations of both the isolated H-bonded DNA duplexes and H-bonded hydrate nucleotide complex. We considered the oligonucleotide duplexes of the composition: d(ApA) · d(TpT), d(ApApA) · d(TpTpT), d(ApApApA) · d(TpTpTpT), d(ApTpApT) · d(ApTpApT), d(GpGpGpG) · d(CpCpCpC), and d(GpCpGpC) · d(GpCpGpC). 3′-5′ antiparallel double chains in the B-form are designed as neutral species. The charge neutrality of sugar-phosphate backbone was modelled by placing protons (H^+) on the appropriate anionic oxygen (=O^-) of the phosphate groups. The nucleotides were built in the *anti*-orientation about glycosyl $C_{1'}$ (sugar) -- N_1 (Pyr) (or $C_{1'}$ (sugar) -- N_9 (Purt) bond.

The solvate effect in vibration spectrum of hydrated nucleotide duplex was modeled by normal mode calculation of the complex with charged $[d(ApA) \cdot d(TpT)]^{-2}$ duplex surrounded by 47 molecules of H_2O.

Some comments are needed to clarify the manner of hydrated complex forming.

1. The initial coordinates of all atoms of the hydrated duplex were chosen similar to the theoretical scheme designed early by A. V. Teplukhin et al. [23] especially for the systems "DNA + water environment." For single complementary nucleotide pairs, the coordinates of atoms were taken from an appropriate molecular mechanics calculation [24] of the double-spiral fragment of B-form of a poly(dA) · poly(dT) oligonucleotide. Then, the Monte-Carlo simulation of water distribution (~1,600 molecules) around the duplex was carried out. A simulated cell represented a rectangular parallelepiped by sizes 41.5 × 37.5 × 31.5 Å^3. For elimination of surface effects at the system the periodic boundary conditions were imposed. The size of the system provides normal density of water, and selected sizes of edges yield an optimal layout of the dinucleotide pair in relation to limiting surfaces of simulated cell. In this size, there was enough space for creation not less than three nonperturbed water shells.
2. Orientation of water molecules was evaluated by minimization of energy of intermolecular interactions on the basis of empirical atom–atomic potential functions for hydrogen-bonded systems with the parameters presented in the paper [25]. For the approach of the system to thermodynamic equilibrium, 3,000,000 configurations (in calculation per one molecule of water) were generated at temperature 300 K. After that, through every 100,000 trials (per one molecule of water) some sets of coordinates of all atoms were selected. For each of these sets, we obtained by Monte Carlo simulation the molecular configurations appropriate to local minima of potential energy at 5 K.
3. From a rather major set of almost equienergetic configurations revealed for water shells around the duplex under study the patterns with two water shells were left. Thus, the molecules of the first water shells were formed the hydrogen bonds with atoms of the duplex, while the molecules of the second water shells were considered to be involved not less than in two hydrogen bonds with water molecules of the first shell. Finally, after the comprehensive analysis of a grid of hydrogen bridges in the obtained variants of aqueous shells one configuration which includes 47 water molecules was selected. The result is in correspondence with the most probable distribution of aqueous bridges between hydrophylic atoms of dinucleotide pair [23] in poly(dA) · poly(dT) oligonucleotide of B-form.

This model structure of hydrated d(ApA) · d(TpT) duplex was used for our subsequent, more detailed PM3 optimization calculations and for normal modes analysis.

For comparison, a vibration spectrum of two different configurations of isolated water cluster consisting of 47 molecules H2O was also calculated. One configuration was chosen and optimized close to a compact sphere-like shape, and another—close to the shape of ellipsoid of gyration.

In PM3 calculations, the gradient norm was minimised by Eigenvector Following routine (EF) with the use of DMAX = 0.1 keyword of MOPAC6.0 package [36]. Termination criteria of geometry optimization was chosen by specifying GNORM = 0.01 keyword. The SCF criteria was also defined by SCF = 1.D-12. The Hessian matrix was calculated numerically. All fully geometry-optimized structures were considered in stationary

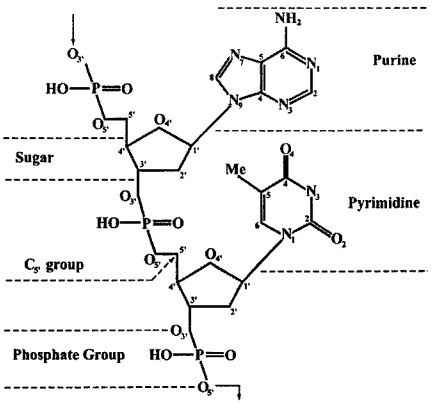

FIGURE 1. pApTp fragment of the DNA chain with the names of the components.

states and in the true minima of potential energy surfaces. Reaching the optimal geometry was checked by the extremeness of calculated heat of formation and the lack of imaginary frequencies in the spectrum of normal modes of a complex. Input geometries of B-forms of isolated duplexes were taken from the crystallographic data-base, NDB [26]. Standard nomenclature of atoms numeration in 3′-5′ nucleotide chain structure was used [1]. Figure 1 presents an example of a pApTp fragment of the chain with the names of the components.

Results and Discussion

LOW-FREQUENCY VIBRATION MODES OF NUCLEOBASES, THEIR DERIVATIVES, AND HYDROGEN-BONDED PAIRS

Before discussing the character of intra- and intermolecular vibration modes in oligonucleotide double chains we shall consider, in the beginning, some features of vibration spectrum of single nucleobases, their sugar and phosphate derivatives, and also of their isolated H-bonded pairs. Tables I and II represent the results of our PM3 calculations, which illustrate the spectrum evolution of harmonic frequencies in the row of isolated molecules (nitrous bases–nucleosides–nucleotides) and in the row of their complementary H-bonded pairs. Because in the present work we discuss low-frequency vibration dynamics of nucleic acids, the tables represent characteristics of only the lowermost normal modes of these compounds.

The data reported in the literature data [27] and in our previous PM3 theoretical studies [19] show that vibration modes in spectrum of initial, unsubstituted molecules of nitrous bases start with frequencies about 100 cm^{-1}. In this spectral region, deformation vibrations of exocyclic amino and methyl groups, and also of purine and pyrimidine parts of the molecules, are localized. Adding a sugar and phosphate group to the molecules of bases results in the shift of vibration spectrum of these molecules to far infrared region [18]. The data presented in Table I describe spectral changes from this structure complication.

It is shown that transition from the nitrous bases to nucleotides is accompanied by long-wave shift of its low vibration modes to the region of 10 cm^{-1}. For these compounds, with a mass twice exceeding the mass of initial nucleobases, it is a natural result. It is also seen that the spectrum of vibrations becomes rather dense. The activity of the low-frequency nucleotide modes, which is determined through the values of transition dipole moments μ'_{tr}, appears not high in the region near 100 cm^{-1}. It is known, prominent feature of deformation vibrations [14–16]. Contrary to many intensive characteristic modes of middle and high frequencies with large values of the transition dipole moments, reaching sometimes up to several units of D/Å, these low-frequency deformations have the values of the transition moments, according to Table I, not higher than 0.3 D/Å.

A description of group vibrations is not presented in Table I because of its bulky volume. We note only that in the case of nucleotides, the lowest modes are formed mainly by the deformations of phosphate and sugar groups. Only in the molecule of monophosphate-deoxythymidine (pdT), torsion vibrations of methyl group also appear in low-frequency region of the spectrum. With increasing the energy, torsion vibrations of amino group (in nucleotides pdA, pdG, pdC) and mixed vibrations with the participation of sugar-phosphate fragment begin to appear. Vibrations of a more complex nature, with the participation of purine and pyrimidine parts of nucleotides, also become active.

For the structure of isolated hydrogen-bonded base pairs [11–17], nucleosides, and nucleotides [18], it is a natural further downturn of the energy of lowest normal modes and the appearance of intermolecular character of some modes [4, 18]. Note that the process of H-bonding of the bases, as shown in our previous reports [19, 20], is accompanied by an ambiguity of the spatial form of their complementary pairing. It is caused by the bistability of a pyramidal structure of exocyclic amino

TABLE I

PM3 calculated low-frequency spectrum of normal modes of single nitrous bases, adenine (A), thymine (T), guanine (G), cytosine (C), and of their nucleoside dA, dT, dG, dC and nucleotide pdA, pdT, pdG, pdC derivatives.

	A		**T**		**G**		**C**		**dA**		**dT**		**dG**		**dC**		**pdA**		**pdT**		**pdG**		**pdC**	
ΔH_f^o	55.969		−76.48		7.37		−13.92		−73.37		−203.06		−121.29		−140.28		−278.10		−406.85		−326.51		−346.04	
N	ν	μ'_{tr}	ν	μ'_{tr}	ν	μ'_{tr}	ν	μ'_{tr}	ν	μ'_{tr}	ν	μ'_{tr}	ν	μ'_{tr}	ν	μ'_{tr}	ν	μ'_{tr}	ν	μ'_{tr}	ν	μ'_{tr}	ν	μ'_{tr}
1	151	0.4	74	0.0	112	0.3	120	0.2	23	0.1	28	0.1	20	0.1	25	0.1	8	0.3	18	0.1	12	0.3	17	0.2
2	200	0.4	85	0.0	117	0.3	184	0.5	33	0.1	35	0.1	27	0.2	37	0.3	20	0.1	22	0.3	16	0.3	19	0.2
3	254	0.7	88	0.1	185	0.6	273	0.9	52	0.2	49	0.2	47	0.2	51	0.2	29	0.1	36	0.1	28	0.1	35	0.3
4	298	0.4	268	0.4	248	0.6	314	0.3	65	0.2	70	0.1	70	0.2	96	0.2	37	0.2	41	0.1	34	0.3	42	0.4
5	324	0.7	303	0.2	306	0.2	353	0.5	103	0.2	85	0.1	102	0.3	126	0.2	59	0.2	51	0.1	56	0.2	54	0.2
6	375	0.3	341	1.0	316	0.3	451	0.6	144	0.3	88	0.0	119	0.2	164	0.2	70	0.2	68	0.1	65	0.2	70	0.4
7	491	0.6	373	0.7	317	0.3	452	0.7	149	0.2	102	0.2	127	0.4	182	0.4	95	0.3	70	0.2	88	0.3	103	0.1
8	496	0.5	413	0.5	390	0.9	491	0.8	199	0.3	146	0.2	132	0.1	213	0.4	120	0.5	77	0.0	114	0.3	127	0.2
9	504	0.5	450	0.7	431	1.0	544	0.7	212	0.3	206	0.3	175	0.6	221	0.5	136	0.5	85	0.1	118	0.3	138	0.2
10	559	0.4	467	1.4	457	0.2	611	0.8	226	0.8	221	0.5	205	0.7	235	0.6	148	0.5	106	0.2	120	0.3	159	0.2
11	601	0.6	506	0.9	485	0.3	678	0.7	257	0.4	233	0.6	211	0.8	248	1.0	168	0.4	138	0.5	123	0.4	183	0.2
12	602	1.0	554	0.6	548	0.1	759	1.5	261	0.3	245	0.6	251	0.6	289	0.3	174	0.4	147	0.1	154	0.5	198	0.2
13	716	2.1	620	1.2	582	0.9	795	0.9	280	0.2	256	1.0	262	0.2	384	0.2	200	0.3	179	0.2	166	0.6	209	0.4
14	756	1.7	716	1.2	620	1.4	839	1.6	300	0.4	288	0.2	280	0.3	327	0.2	220	0.6	193	0.1	179	0.3	224	0.8
15	792	2.3	751	0.3	632	0.7	943	0.8	330	0.3	307	0.3	302	0.0	340	0.4	225	0.8	217	0.8	224	0.7	240	0.4

ΔH_f^o (298°K), heat of formation (kcal/mol); *N*, number of normal mode; ν, frequency of the mode (cm^{-1}); μ'_{tr}, value of transition moment (D/Å).

TABLE II

PM3 calculated low-frequency normal modes of base, nucleoside, and nucleotide canonical pairs.

ΔH_f^0	AT −26.21				GC −18.42			d(AT) −279.12		d(GC) −271.61		pd(AT) −688.02			pd(GC) −681.87		
N	ν	μ'_{tr}	ν^a	ν^b	ν	μ'_{tr}	ν^a	ν	μ'_{tr}	ν	μ'_{tr}	ν	μ'_{tr}	Description	ν	μ'_{tr}	Description
1	**21**	0.4	22	25	**25**	0.4	25	**8**	0.3	**8**	0.3	**5**	0.3	**(PhosGr(dpA), PhosGr(pdT)) def**	3	0.3	(PhosGr(dpG)) def
2	**26**	0.1	30	37	**42**	0.4	34	**13**	0.1	**17**	0.1	**8**	0.1	**(Sugar, Pur(dpA), Sugar, Pyr(dpT)) def**	**6**	0.2	**(PhosGr(dpG), PhosGr, C'_5Gr, Pur(dpC)) def**
3	**55**	0.3	53	41	63	0.3	69	**19**	0.1	**20**	0.1	**10**	0.2	**(PhosGr(dpA), PhosGr(dpT)) def**	**9**	0.1	**(Sugar, Pyr(dpC), Pur(dpG)) def**
4	77	0.1	65	74	**101**	0.1	84	**20**	0.1	**26**	0.3	**16**	0.1	**(Sugar, Pur(dpA), Me, Pyr(dpT)) def**	**14**	0.2	**(PhosGr(dpG), PhosGr(dpC)) def**
5	86	0.1	122	91	120	0.3	116	**23**	0.2	29	0.1	**17**	0.1	**(PhosGr(dpA), Me, PhosGr(dpT)) def**	17	0.1	(PhosGr, Sugar(dpC)) def
6	90	0.2	169	93	132	0.2	123	35	0.2	36	0.1	20	0.3	(PhosGr, Sugar(dpT)) def	23	0.1	(Sugar, Pyr(dpC)) def
7	101	0.1			145	0.2		45	0.2	48	0.1	**25**	0.1	**(PhosGr, Sugar(dpT), Sugar(dpA))def**	**28**	0.2	**(PhosGr(dpC), Sugar, Pur(dpG)) def**
8	119	0.2			171	0.3		48	0.1	**57**	0.4	33	0.2	(PhosGr, Sugar, Pur(dpA)) def	32	0.2	(Sugar, Pyr(dpC)) def
9	156	0.3			188	0.7		53	0.1	65	0.3	36	0.3	(Sugar, Pyr(dpT)) def	**34**	0.3	**(PhosGr(dpC), Sugar, Pur(dpG)) def**
10	**177**	0.2			**194**	0.7		63	0.2	72	0.2	**38**	0.1	**(Sugar, Pur(dpA), Me, Pyr(dpT)) def**	35	0.1	(Sugar, Pyr(dpC)) def
11	212	0.5			**224**	0.5		**70**	0.1	**80**	0.1	**43**	0.2	-------//-------	44	0.3	(PhosGr, C'_5Gr(dpG)) def
12	258	0.4			183	0.8		77	0.2	**93**	0.1	49	0.1	(Sugar, Pyr(dpT)) def	**53**	0.3	**(Sugar, Pur(dpG), Pyr(dpC)) def**
13	261	0.7			297	0.3		88	0	97	0.1	53	0.1	-------//-------	61	0.4	(Sugar, Pyr(dpC) def
14	**305**	0.9			**342**	0.4		92	0.2	128	0.3	59	0.2	(PhosGr, C'_5Gr(dpT)) def	67	0.4	(C'_5Gr, Sugar, Pur(dpG)) def
15	337	0.8			354	0.6		96	0.1	130	0.1	61	0.2	(SugarPhosGr, Pur(dpA)) def	**69**	0.2	**(C'_5Gr, Pyr(dpC), Sugar, Pur(dpG)) def**

ΔH_f^0 (298°K), heat of formation (kcal/mol); *N*, number of normal mode; ν, frequency of the mode (cm^{-1}); μ'_{tr}, value of transition moment (D/Å); ν^a, HF/6-31G** results [12]; ν^b, HF/MINI-1 results, with anharmonic corrections [13].
Inter-molecular modes are marked by bold font.

groups involved in base H-bonding. Two steady orientations of N—H bonds of amino group are possible: "up" and "down" relative to the base plane. Bistability of the structure of the NH_2-group in the Watson–Crick AT(WC) pair leads to two symmetric and equal in energy, propeller-like configurations of coupling: AT(WC)u and AT(WC)d. While for Watson–Crick GC(WC) pair the existence of four nonplanar forms of pairing is possible (two symmetric propeller-like forms GC(WC)uu, GC-(WC)uu and two symmetric step-like forms of H-bonding GC(WC)du and GC(WC)ud) with close values of energy.

No direct experimental data on gas-phase vibrational spectrum of base pairs, nucleosides, and nucleotides are yet available. However, X-ray data do specify the existence of variety of nonplanar forms of pairing of the bases both in separate pairs and in structure of double chains of polynucleotides [1, 28]. Thus, in the strict sense, consideration of features of a spectrum of normal modes of the H-bonded pairs should occur in view of distinction of force fields of different polymorphic forms for each base pair.

Earlier, we pointed out [19] that nonplanar character of the pairs "mixes up" their vibration modes. Sometimes it is difficult to allocate the characteristic vibrations of those or another group. Nevertheless, spectral differences, for example, of step-like (GC-(WC)du and GC(WC)ud) and propeller-like (GC-(WC)dd and GC(WC)uu) forms of H-bonding of canonical GC(WC) pair, reduce mainly to differences in intensity of characteristic frequencies of some vibration modes of the bases. Therefore, Table II presents only the results of normal modes calculations for propeller-like configurations of Watson–Crick pairs. This type of base pairing is most frequently observed in the structure of nucleic acids molecules and molecular complexes [1, 28]. For comparison, some ab initio quantum-chemical estimations by use of usual harmonic approach [12], and with anharmonic corrections [13] are also displayed.

Tables I and II display a significant lowering, up to several cm^{-1} (in the case of nucleotide pairs), of the long-wave border of the spectrum of normal modes when passing from the structure of single molecules to the structure of the H-bonded complexes. On the whole, we have well correlation of our semiempirical estimations of energy of low vibration modes of nitrous base pairs with the results of more rigorous, HF/6-31G** and HF/MINI-1 calculations, based on the usual harmonic approach [12], and on the inclusion of anharmonic corrections [13]. And this emphasizes high enough reliability of used standard PM3 technique in the decision of the given type of spectral problem. Some difference between our PM3 results and the results of HF/6-31G** calculation [12] on 6th oscillatory mode in the Watson–Crick A-T pair is, more probably, the consequence of the technique used when the valence-force field scaling of the A-T complex. If we look, however, at other ab initio estimations [15] made by modern technique of density functional theory (DFT) with hybrid exchange-correlation functional B3PW91/6-311G approach, such discrepancy is not observed any more. So, as presented in [15], the first six frequencies of a spectrum of normal oscillations A-T pair ($\nu_1 = 27\ cm^{-1}$, $\nu_2 = 38\ cm^{-1}$, $\nu_3 = 67\ cm^{-1}$, $\nu_4 = 83\ cm^{-1}$, $\nu_5 = 115\ cm^{-1}$, $\nu_6 = 117\ cm^{-1}$) are rather close to our PM3 findings presented in Table II.

The obtained location, close to 20–50 cm^{-1}, of intermolecular modes with out-of-plane movements of the bases are in accordance with findings of another investigators [11–16].

The data presented in Table II also specify that in the most interesting case for us, namely in the case of dinucleotides, the density of low vibration modes becomes large enough. This density exceeds density of vibration modes in single pairs of nitrous bases counting upon the same interval of frequencies. Intermolecular types of normal modes are dominating in this far-IR region. These vibrations are marked in boldface in Table II.

With the purpose of compact description of character of arising modes, we used a little bit simplified classification of group vibrations. Table III presents the specification of the basic groups of nucleotides which atoms involved in formation of the nature of low-frequency vibrations of a hydrogen-bonded complex. Contributions greater than 2% for the potential energy distributions (PED) are taken into account.

According to this description of vibration modes for the spectrum of nucleotide pairs, it is possible to draw the following conclusions.

Watson–Crick pd(AT) Nucleotide Pair

As shown in Table II, the most long-wave region of vibration spectrum is formed from five intermolecular modes. Here, the nonplanar character of hydrogen bonding of the bases, as mentioned above, appreciably "mixes up" the normal vibrations. The character of these modes becomes com-

TABLE III

Specification of the local vibrations of nucleotide components determining the form of low-frequency modes of H-bonded complexes.

N	Abbreviation	Localization
1	Me	Methyl (thymine) group deformation
2	Pur	Purine (adenine or guanine) deformation
3	Pyr	Pyridine (thymine or cytosine) deformation
4	NH_2	NH_2-group (adenine, guanine, or cytosine) deformation
5	$C_5'Gr$	C_5'—group deformation
6	Sugar	Sugar deformation
7	PhosGr	Phosphate group deformation

plicated and affects the deformations of sugar-phosphate groups of both nucleotides, their purine and pyrimidine parts, and also the deformations of methyl group. Close to intermolecular modes the group of intramolecular vibrations in the region 20–36 cm^1, corresponding to some local deformations of the sugar-phosphate group, adjoins. The activity of intermolecular vibrations, with participation of deformations of furanose rings of dpA, and deformations of the dpT methyl group, is marked for higher frequencies.

Further, with the energy increasing, the intramolecular modes localized on these or those nucleotide are dominating in a spectrum of hydrogen-bonded dinucleotide. Only a few deformation modes, located in the area of 108, 178, 321, 362, and 562 cm^{-1}, can be assigned as the intermolecular vibrations.

The intensity of all low-frequency intra- and intermolecular modes, arising from their deformational nature and having large mass of groups involved in vibrations, is not high. According to our calculations, appropriated values of their transition dipole moments, μ'_{tr}, do not exceed 0,4 · D/Å.

Vibration Spectrum of Watson–Crick dp(GC) Pair

Initiated from the region of 3 cm^{-1}, we obtained practically the same dense filling of far-infrared region by inter- and intra-molecular vibration modes. Intensities of low-frequency modes are not high. As well as in the case of dp(TA) pair, the values of the transition dipole moments, μ'_{tr}, do not exceed 0,4 · D/Å.

In the region above 100 cm^{-1} intermolecular vibration modes less often participate in formation of a spectrum of normal vibrations of the H-bonded complex. These modes are located near 155, 189, 268, 376, 422, and 462 cm^{-1}.

It is possible to conclude that the mixed intermolecular modes, with the active contribution of vibration movements of end sugar-phosphate groups, play the dominant role in the formation of the most low-frequency area of vibration spectrum of hydrogen-bonded nucleotide pairs.

PECULIARITIES OF LOW-FREQUENCY VIBRATION SPECTRUM OF OLIGONUCLEOTIDE DUPLEXES

The resulting spectrum of low-frequency modes of oligonucleotide duplexes is presented in Table IV. As we describe a specificity of far-infrared spectrum in elongating hydrogen-bonded double chains, the data for 20 lowest normal modes are only displayed in Table IV. For brevity, the description of modes in accordance with Table III is presented only for the dimer complex, d(ApA) · d(TpT). Intermolecular modes, as earlier, are marked in bold. Typical base pairs nonplanarity, which appeared in structure of isolated duplexes, is displayed in Figure 2. PM3 optimized conformations of only two oligonucleotide duplexes, d(ApA) · d(TpT) and d(ApApApA) · d(TpTpTpT), are presented.

Taking into account the heterogeneity of geometrical parameters of nucleotide steps in double helices of oligonucleotides [20], it is natural to expect the "mixed" character of vibrations of all low-frequency modes, both intermolecular and intramolecular. For the simplest duplex d(ApA) · d(TpT), 16 of 20 low modes presented in Table IV appear to be intermolecular. Most of them, especially modes in the region of 10, 14, 20, 22, 24, 28, 37, 39, 43, 47, 54, and 56 cm^{-1} have a collective character. Vibrations of different functional groups of both hydrogen-bonded pairs take part in their formation.

The intramolecular low-frequency modes concerning the vibrations of groups in one chain also appear to have a rather complex, mixed nature. Local vibrations of individual groups become more precise only for rather high frequencies.

The spectra of harmonic vibrations of more elongated trimer and tetramer duplexes are rather strongly leveled. The similarity of many vibration modes makes spectra almost continuous. In spite of different thermodynamic stability of homo- and

TABLE IV

PM3 calculated low-frequency normal modes of isolated oligonucleotide duplexes: d(ApA) · d(TpT), d(ApApA) · d(TpTpT), d(ApApApA) · d(TpTpTpT), d(ApTpApT) · d(ApTpApT), d(GpGpGpG) · d(CpCpCpC) and d(GpCpGpC) · d(GpCpGpC).

ΔH_f^0	d(ApA) · d(TpT) −844.80			d(ApApA) · d(TpTpT) −1405.69		d(ApApApA) d(TpTpTpT) −1965.37		d(ApTpApT) d(ApTpApT) −1968.74		d(GpGpGpG) d(CpCpCpC) −1933.85		d(GpCpGpC) d(GpCpGpC) −1937.21	
N	ν	μ'_{tr}	Description	ν	μ'_{tr}	ν	μ'_{tr}	ν	μ'_{tr}	ν	μ'_{tr}	ν	μ'_{tr}
1	**6**	0.1	**(Sugar(dpA)$_1$, Sugar(dpT)$_1$) def**	**3**	0.2	**3**	0.1	**3**	0.2	**6**	0.1	**4**	0.1
2	8	0.1	(Me(dpT), C$'_5$Gr(dpT), PhosGr(dpT)$_2$) def	**6**	0.1	**5**	0.1	**4**	0.1	**7**	0.2	**5**	0.2
3	**10**	0.1	**Sugar(dpT)$_1$, (Pur(dpA)$_1$, Me, Pyr(dpT)$_2$, PhosGr(dpT)$_2$, PhosGr(dpA)$_2$) def**	8	0.0	7	0.1	**5**	0.1	8	0.1	6	0.1
4	11	0.1	(Pyr(dpT)$_2$, Pyr(dpT)$_1$, C$'_5$Gr(dpT)$_2$) def	**11**	0.1	**9**	0	7	0.1	**10**	0.1	**7**	0.1
5	**14**	0.2	**(PhosGr(pdA)$_2$, PhosGr(pdT)$_2$, Me(pdT)$_1$, Me(dpT)$_2$) def**	**12**	0.1	**11**	0.1	**7**	0.1	**11**	0.1	**8**	0.1
6	15	0.2	(Pur, Sugar(dpA)$_1$) def	**12.5**	0.1	**12**	0.1	**9**	0.1	12	0.1	9	0.2
7	**18**	0.1	**(C$'_5$Gr(dpA)$_2$, PhosGr(dpT)$_2$, Me(dpT)$_2$, C$'_5$Gr(dpT)$_2$) def**	13	0	14	0.2	**10**	0.2	**13**	0.1	**10**	0.1
8	**20**	0.1	**(Sugar(dpT)$_1$, Sugar(dpA)$_1$, Me(dpT)$_2$, C$'_5$Gr, Sugar(dpT)$_2$) def**	14	0.2	**14**	0.1	11	0.1	**14**	0.1	**11**	0.1
9	**22**	0.1	**(Sugar(dpT)$_1$, Pyr(dpT)$_1$, C$'_5$Gr(dpA)$_2$, Sugar(dpT)$_2$, Pur(dpA)$_1$) def**	**16**	0	**16**	0.2	**12**	0.1	**16**	0.2	**12**	0.1
10	**24**	0.1	**(Sugar(dpT)$_1$, C$'_5$Gr(dpA)$_2$, PhosGr(dpT)$_2$) def**	**18**	0.2	**16**	0.1	13	0.2	17	0.1	**13**	0.1
11	**28**	0.2	**(Me(dpT)$_1$, Me(dpT)$_2$, PhosGr(dpA)$_2$, Pur(dpA)$_1$) def**	**19**	0.1	**17**	0.1	**14**	0.1	**18**	0.1	**13**	0.2
12	**30**	0.1	**(Sugar(dpA)$_1$, C$'_5$Gr(dpT)$_2$) def**	**20**	0.1	**18**	0.1	**17**	0.1	19	0.1	**15**	0.1
13	34	0	(Sugar(dpA)$_2$, Pur(dpA)$_2$) def	21	0.2	19	0.2	**18**	0.1	19	0.2	**17**	0.1
14	**37**	0.1	**(C$'_5$Gr(dpA)$_1$, PhosGr(dpA)$_2$, Sugar(dpT)$_1$, Sugar(dpA)$_1$) def**	**22**	0.1	**20**	0.1	20	0.2	21	0.1	19	0.2
15	**39**	0.3	**(PhosGr, Pur(dpA)$_2$, C$'_5$Gr(dpA)$_1$, Sugar(dpT)$_1$, Pyr(dpT)$_1$) def**	**24**	0.1	**21**	0.2	**21**	0.1	**22**	0.1	**21**	0.1
16	**43**	0.1	**(C$'_5$Gr(dpT)$_1$, PhosGr(dpT)$_2$, Pyr(dpT)$_2$, Me(dpT)$_2$, Pur(dpA)$_1$) def**	**26**	0.2	**24**	0.2	**23**	0.1	**23**	0.1	**22**	0.1
17	**47**	0.3	**(Sugar Pur(dpA)$_1$, Pur(dpA)$_1$, Pyr(dpT)$_2$, C$'_5$Gr(dpT)$_2$) def**	28	0.3	24	0.3	**24**	0.1	**24**	0.3	**23**	0.3
18	**48**	0.1	**(Sugar(dpA)$_2$, Me(dpT)$_1$) def**	29	0.4	25	0.3	**25**	0.2	**25**	0.2	**24**	0.2
19	**54**	0.2	**(Sugar(dpT)$_1$, PhosGr(dpT)$_2$, C$'_5$Gr(dpT)$_1$, Sugar(dpA)$_2$) def**	**30**	0.2	**26**	0.2	26	0.3	**26**	0.3	25	0.3
20	**56**	0.3	**(Me(dpT)$_1$, Sugar(dpT)$_1$, Sugar(dpT)$_2$, Sugar(dpA)$_2$) def**	31	0.2	**27**	0.3	**27**	0.2	**27**	0.2	**26**	0.2

ΔH_f^0 (298°K), heat of formation (kcal/mol); *N*, number of normal mode; ν, frequency of the mode (cm^{-1}); μ'_{tr}, value of transition moment (D/Å).

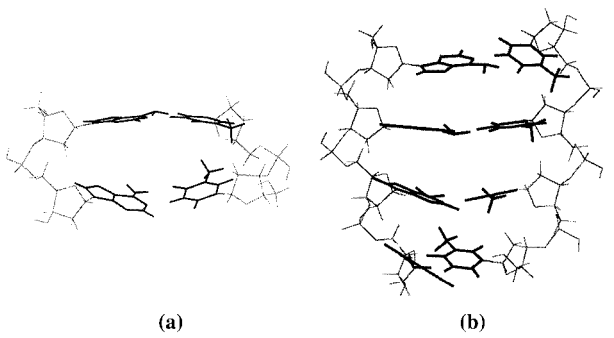

FIGURE 2. PM3 optimized structure of isolated dimer duplexes (**a**) d(ApA) · d(TpT), and (**b**) d(ApApApA) · d(TpTpTpT).

heteronucleotide double sequences (heats of formation, ΔH_f^0 (298°K) differ) their low-frequency vibrational spectra are similar. Vibration frequencies fill rather densely, through 1 cm^{-1}, all far-IR region of the spectrum. Such a quasi-continuum of normal modes reaches up to the frequency of 400 cm^{-1}. Above this origin, vibrational modes, through intervals of 3–10 cm^{-1}, completely fill in the rest of the IR spectrum reaching frequencies of $\leqslant$3,900 cm^{-1}, where characteristic stretching vibrations hydroxyl, O—H groups are located.

Intensities of all low-frequency modes are small, as shown by the calculations. As well as in single pairs of bases, nucleosides, and nucleotides, the deformation type of these vibrations determines here again small sizes of transition dipole moments, μ'_{tr}. According to Table IV, their values do not exceed the value of 0,4 · D/Å.

The results presented do not contradict experimental data on far-IR pulsed terahertz spectroscopy of DNA molecules [2], and correlate well with theoretical estimations of vibrational modes in small duplexes made by other investigators on the basis of the method of molecular mechanics [18].

ANALYTICAL ESTIMATIONS OF BORDER OF LOW-FREQUENCY VIBRATION MODES IN LONG DOUBLE CHAINS OF DNA

PM3 estimations within 3 cm^{-1} of border of low-frequency of normal modes in duplexes of different length allow us to suggest that the lowest frequency of vibration mode for very long isolated double nucleotide chains should be close to zero. Carrying out quantum chemical calculations of such structures now is not possible. At the same time in the literature successful examples of analytical estimations of vibrational characteristics of various dynamic models for extended structures of DNA molecules are known [29, 30].

In the study presented, we have tried to estimate the frequency of a low vibration motion of bases around sugar-phosphate chains. Calculations were made on the basis of the approach developed in [29], and only the case of isolated double stranded DNA was considered. As a model of nucleic acid, the model of complementary oligonucleotide double chain of infinite length was examined. Harmonic approximation for the description of vibrations was used.

The hamiltonian of the model has the form [30]:

$$H = T + V_{\parallel} + V_{\perp}; \tag{1}$$

where the kinetic energy (T), the energy of interactions along chains ($V_{\parallel}$) and the energy of interactions between bases in pairs ($V_{\perp}$) is determined by formulas

$$T = \sum_n [(m_1 r_1^2/2)(d\varphi_{n,1}/dt)^2 + (m_2 r_2^2/2)(d\varphi_{n,2}/dt)^2], \tag{2}$$

$$V_{\parallel} = \sum_n [(K_1 r_1^2/2)(\varphi_{n,1} - \varphi_{n-1,1})^2 + (K_2 r_2^2/2)(\varphi_{n,2} - \varphi_{n-1,2})^2], \tag{3}$$

$$V_{\perp} = \sum_n (k_{1-2}/2)[r_1(r_1 + r_2)(\varphi_{n,1})^2 + r_2(r_1 + r_2)(\varphi_{n,2})^2 - r_1 r_2(\varphi_{n,1} - \varphi_{n,2})^2] \tag{4}$$

where $\varphi_{n,i}$ is the angular displacement of the *n*th base of the *i*th chain from its equilibrium position; r_i, is the distance between the center of mass of the *i*th base and the nearest sugar-phosphate chain; a is the distance between neighboring bases along the chains; m_i is mass of bases of the *i*th chain; K_i is the coupling constant along the sugar-phosphate chain; and k_{1-2} is the force constant that characterizes interactions between bases in pairs; $n = 1, 2, \cdots N$; $i = 1, 2$. We suggest that N is rather large integer, so the end effects can be neglected.

The dynamic equations corresponding to hamiltonian (1) are

$$m_1 r_1^2(d^2\varphi_{n,1}/dt^2) = K_1 r_1^2[(\varphi_{n-1,1} - 2\varphi_{n,1} + \varphi_{n+1,1})] - k_{1-2} r_2 r_1(\varphi_{n,1} + \varphi_{n,2}), \tag{5}$$

$$m_2 r_2^2 (d^2\varphi_{n,2}/dt^2) = K_2 r_2^2[(\varphi_{n-1,2} - 2\varphi_{n,2} + \varphi_{n+1,2})] - k_{1-2} r_2 r_1 (\varphi_{n,1} + \varphi_{n,2}). \quad (6)$$

To find the values of the low frequencies, it is suggested that the solutions of the linear equations have the form of plane waves

$$\varphi_{n,1} = \varphi_{0,1}\exp[i(qz - wt)]; \varphi_{n,2} = \varphi_{0,2}\exp[i(qz - wt)], \quad (7)$$

where $\varphi_{0,1}$ and $\varphi_{0,2}$ are the amplitudes, w is the frequency, and q is the wave vector.

After inserting (7) into (5)–(6), we obtain the algebraic equations

$$\{-w^2 m_1 r_1^2 + 2K_1 r_1^2[1 - \cos(qa)] + k_{1-2} r_1 (r_1 + r_2) - k_{1-2} r_2 r_1\}\varphi_{0,1} + \{k_{1-2} r_2 r_1\}\varphi_{0,2} = 0; \quad (8)$$

$$\{-w^2 m_2 r_2^2 + 2K_2 r_2^2[1 - \cos(qa)] + k_{1-2} r_2 (r_1 + r_2) - k_{1-2} r_2 r_1\}\varphi_{0,2} + \{k_{1-2} r_2 r_1\}\varphi_{0,1} = 0. \quad (9)$$

Algebraic equations (8)–(9) have nontrivial solutions if

$$[-m_1 r_1^2 w^2 + \lambda_1(q) r_1^2][-m_2 r_2^2 w^2 + \lambda_2(q) r_2^2] - [k_{1-2} r_2 r_1]^2 = 0.$$

$$\lambda_1(q) = 2K_1[1 - \cos(qa)] + k_{1-2}; \lambda_2(q) = 2K_2[1 - \cos(qa)] + k_{1-2}. \quad (10)$$

For small values of the wave vector q, the solutions of equations (10) are

$$w_1(\text{small q}) = (qa)(c_1/2b_0)^{1/2} = (qa)[(K_1 + K_2)/(m_1 + m_2)]^{1/2}; \quad (11)$$

$$w_2(\text{small q}) \cong (b_0/a_0)^{1/2}\{1 + (1/2) \times [(b_1/2b_0) - (a_0/2b_0^2)c_1](qa)^2\}; \quad (12)$$

where

$$b_0 = k_{1-2}(m_1 + m_2); b_1 = 2(K_1 m_2 + K_2 m_1);$$

$$b = [m_1\lambda_2(q) + m_2\lambda_1(q)] = b_0 + b_1[1 - \cos(qa)];$$

$$c = [\lambda_1(q)\lambda_2(q) - (k_{1-2})^2] = c_1[1 - \cos(qa)] + c_2[1 - \cos(qa)]^2;$$

$$c_1 = 2k_{1-2}(K_1 + K_2); c_2 = 4K_1 K_2.$$

Formula (10) describes the acoustic branch in the spectrum of DNA molecule, and formula (12) describes the optical branch. If q = 0, the acoustic frequency is equal to zero

$$w_1^{AT}(q = 0) = w_1^{GC}(q = 0) = 0 \quad (13)$$

and the value of optical frequency is not equal to zero.

We used the obtained formula (12) to estimate the value of low-frequency vibration mode for different type of hydrogen-bonded nucleotide chains.

For the AT chain, we have

$$w_2^{AT}(q = 0) = [k_{AT}(m_A + m_T)/m_A m_T]^{1/2} \cong 0{,}75 \times 10^{+12}\ s^{-1}; \quad (14)$$

and for the GC chain, we obtain

$$w_2^{GC}(q = 0) = [k_{GC}(m_G + m_C)/m_G m_C]^{1/2} \cong 0{,}94 \times 10^{+12}\ s^{-1}. \quad (15)$$

These values correspond to the energies $\hbar w_1^{AT} = 3.9$ cm^{-1} and $\hbar w_2^{GC} = 5.0$ cm^{-1}, which correlate well with the results of our PM3 estimations, described above, for the structure of lengthened olygonucleotide duplexes, d(ApApApA) · d(TpTpTpT) and d(GpGpGpG) · d(CpCpCpC).

Thus, analysis the carried out gives us the possibility to conclude that vibrational dynamics of isolated short double chains of DNA should appear starting from far IR area of a spectrum, namely from area approximately close to a few cm^{-1}. Collective intermolecular modes strongly correlated by joint deformation movements of components of nucleotides in the different hydrogen-bonded pairs are the basis of these dynamics.

INFLUENCE OF HYDRATE SHELL ON LOW-FREQUENCY VIBRATION SPECTRUM OF OLIGONUCLEOTIDE DUPLEX

Hydration of nucleotides, which is an important factor in the structural and dynamical organization of molecules of nucleic acids, is not homogeneous in DNA. Two discrete stratums representing primary and secondary hydrated shells are identified. It is agreed that double helix stability, mobility of its separate fragments, and vibrational properties of

DNA molecule as a whole rather strongly depend on concentration of water in these water shells. At the same time, the physical mechanism of influence of water environment on formation of vibrational properties of nucleic acids remains unclear.

Theoretical quantum chemical consideration of the role of structural water in vibration spectra of DNA components is a rather labor-consuming problem because rigorous calculation of harmonic frequencies of complexes with explicit inclusion of water molecules demands the enormous computational and time resources, especially when ab initio techniques are applied. As a consequence, continual models of water environment [5, 31] are commonly used in the analysis of hydration effects in vibration spectra of molecules. But even within the framework of this simple approximation the role of water environment is usually examined only for hydrogen-bonded pairs of nitrous bases.

In this work, we have calculated a spectrum of harmonic vibrations of hydrate complex consisting negatively charged duplex $[d(ApA) \cdot d(TpT)]^{-2}$ in an environment of 47 molecules of water. The calculations were made by using PM3 semiempirical technique and within the framework of supermolecule approximation. Initial structure of the complex, and also the choice of number of water molecules in hydrate environment are in detail described in the Method section. Note that the number of water molecules in hydrate shells, per 1 nucleotide, agrees with known estimations on the nominal concentration of water molecules in real structure of DNA [1].

Figure 3 illustrates the result of PM3 optimization of hydrated complex conformation. Table V presents some calculated vibration characteristics of this complex. The full spectrum of normal vibrations involves 783 modes, without taking into account translation and rotation modes. Because we discuss low-frequency vibrational dynamics, in Table V the characteristics of only the 30 lowest normal vibrations are displayed. Collective, intermolecular modes are bolded.

For comparison, in Table V, we present the spectrum of the low vibration frequencies of isolated water cluster, consisting of 47 water molecules, i.e., the same number of molecules, as in the hydrate environment of a duplex. Two different structures of a water cluster have been considered: the compact ball-shaped and deformed ellipsoidal form. In the calculated low-frequency spectra, there are no negative frequencies. This allows us to discuss the tolerance of conformations for all complexes examined. The obtained heightened value of the heat of formation, ΔH_f^0 (298°K) = −2837 kcal/mol, for a ball-shaped structure, specifies that the given frame is the most stable and compact form of a single water cluster.

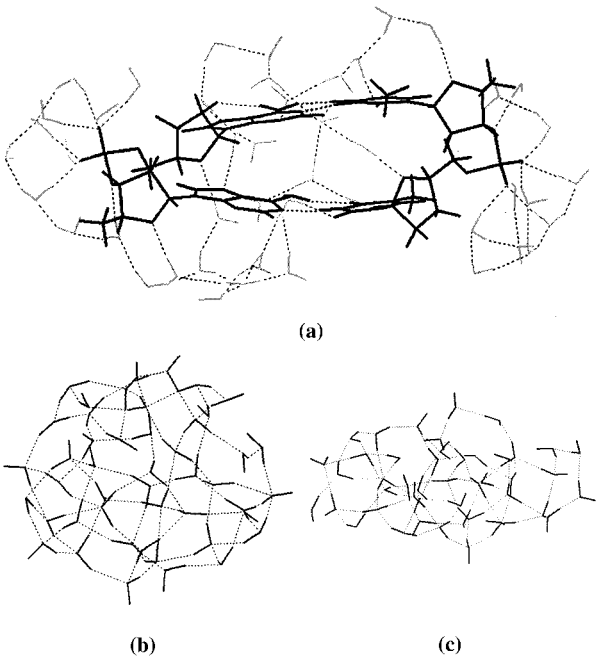

FIGURE 3. PM3 optimized conformations of (**a**) hydrate duplex $[d(ApA) \cdot d(TpT)]^{-2} \cdot 47H_2O$, (**b**) ball-shaped configuration of $47H_2O$ and (**c**) ellipsoidal configuration of $47H_2O$.

First, the analysis of the character of the water environment of hydrated complex presented in Figure 3 permits to mark out 3 types of the allocated water. The first type, designated BW (bounded water), characterizes molecules of water directly hydrogen-bonded with nucleotides in active places of linkage (with phosphate, sugar and bases). The second type, designated W1 (water of the first hydration shell), characterizes the water molecules which forming bridges between molecules of bounded water, and also with the water participating in hydrogen bonding with molecules of an external shell of water. The third type, designated W2 (water of the second hydration shell), designates the remaining water molecules.

Water concentrates differently on the surface of a duplex. Predictably, according to the well-known data on hydration of DNA [1], the region near phosphate groups is most "occupied" by water molecules. Sugar groups and nitrous bases are less populated. Actually, this distribution reflects the common character of electrostatic potential distribution around negatively charged nucleotide duplex in the field of which the formation of hydration shells takes place.

TABLE V

PM3 calculated low-frequency normal modes of hydrated duplex [d(ApA) · d(TpT)]$^{-2}$ · 47 H_2O and water cluster (47H_2O).

ΔH_f^0	[d(ApA) · d(TpT)]$^{-2}$ · 47 H_2O −3569.331			47 H_2O (ball-shaped) −2837.981		47 H_2O (ellipsoidal) −2824.062	
N	ν	μ'_{tr}	Description	ν	μ'_{tr}	ν	μ'_{tr}
1	**7**	**0.1**	**(W2) def**	**16**	0.1	**13**	0.1
2	**9**	**0.2**	-------//-------	**22**	0.1	**16**	0.1
3	**11**	**0.1**	**(W1) def**	**23**	0.1	**18**	0.2
4	**12**	**0.05**	**(W1, Sugar(dpA)$_1$, Sugar(dpT)$_1$) def**	**25**	0.1	**19**	0.1
5	**13**	**0.2**	**(W2) def**	**27**	0.2	**21**	0.2
6	**13.5**	**0.2**	-------//-------	**29**	0.1	**23**	0
7	**14**	**0.1**	-------//-------	**30**	0.1	**24**	0.2
8	**15**	**0.2**	-------//-------	**31**	0.2	**25**	0
9	**17**	**0.1**	-------//-------	**31.8**	0.2	**27**	0.2
10	**18**	**0.15**	**(W2, C$'_5$Gr(dpT)$_2$, Me(dpT)$_1$) def**	**34**	0.1	**28**	0.1
11	**19**	**0.04**	**(W2) def**	**35**	0	**28.7**	0.2
12	**20**	**0.15**	**(W2, Sugar(dpT)$_1$) def**	**38**	0.1	**30.6**	0.2
13	**21**	**0.25**	**(W2, Pyr(dpT)$_1$) def**	**38.4**	0.1	**32**	0.1
14	**21.2**	**0.3**	**(W2, C$'_5$Gr, Pur(dpA)$_2$) def**	**41**	0.1	**34**	0.1
15	**23**	**0.15**	**(W2) def**	**42**	0.2	**35**	0.1
16	**24**	**0.0**	-------//-------	**43**	0.1	**37**	0.3
17	**24.2**	**0.1**	**(W2, Me(dpT)$_2$) def**	**45**	0.2	**38**	0.2
18	**25**	**0.2**	**(W2) def**	**46**	0	**39**	0.1
19	**26**	**0.3**	**(BW, C$'_5$Gr, Me(pdT)$_2$) def**	**47**	0	**39.8**	0.3
20	**27**	**0.3**	**(BW, Sugar(pdT)$_1$) def**	**48**	0.1	**40.2**	0.2
21	**28**	**0.4**	**(BW, Sugar(pdT)$_1$) def**	**50**	0.3	**42**	0
22	**28.6**	**0.1**	**(W1) def**	**52**	0.1	**43**	0.1
23	**29**	**0.5**	**(W1, W2) def**	**52.5**	0.2	**44.8**	0.25
24	**30**	**0.2**	-------//-------	**54**	0.2	**45.5**	0
25	**31**	**0.25**	-------//-------	**55.8**	0.1	**46.6**	0.1
26	**32**	**0.1**	**(W1, W2, Sugar(dpA)$_1$) def**	**56.5**	0.2	**47.6**	0.2
27	**32.2**	**0.15**	**(W1, W2) def**	**58.9**	0.2	**49.8**	0.1
28	**33**	**0.1**	**(W1, W2, C$'_5$Gr(dpT)$_2$) def**	**59.4**	0.2	**50.6**	0.16
29	**34**	**0.25**	**(BW, Sugar(dpA)$_1$) def**	**60.6**	0.1	**52.9**	0.14
30	**36**	**0.2**	**(W1, W2, Sugar(dpT)$_2$, Me(dpT$_1$) def**	**61**	0.1	**53.5**	0.1

ΔH_f^0 (298°K), heat of formation (kcal/mol); *N*, number of normal mode; **ν**, the frequency of the mode (cm^{-1}); **μ'_{tr}**, value of transition moment (D/Å).

We are aware of some conventional character of shell classification entered by us. Nevertheless, our calculations, which show that different low-frequency modes of hydrated duplex are formed by different water shells, speak in favor of this classification.

As for the concrete features of low-frequency normal modes in a hydrated complex, it is possible to make some remarks:

1. Comparison of frequency spectra of a duplex d(ApA) · d(TpT) in an isolated condition and in hydrated phase reveals their qualitative differences. So, in an isolated duplex the majority of low-frequency vibration modes, as it were pointed above, are intermolecular modes of hydrogen-bonded nucleotides. In the case of a hydrated duplex, the basis of a spectrum, in accordance with data presented in Table V, is formed by mixed intermolecular vibrations of water molecules and of functional groups of nucleotides. Different water shells (BW, W1, and W2) participate in the formation of different vibration modes. The spectrum of normal modes of such a complex

is practically quasi-continuous in the calculated range of frequencies of 7–3,990 cm^{-1}. Many of these modes are pure intermolecular vibrations of a water grid of hydrogen bonds.

2. The calculated spectrum of water cluster ($47H_2O$), which has the volume of the hydrate shell, is in itself rather peculiar. First, in contrast to single water molecules, the H-bounded water cluster, even though it has such small size, already possess a quasi-continuum sort of spectrum initiated at very low frequencies in far-IR region (Table V, the last four columns). It is possible to assume that the vibration spectrum of more massive water formation should start practically from the beginning of IR range, i.e., from a few cm^{-1}. Recent experimental data on terahertz Fourier-transform infrared (FT-IR) spectroscopy of water [32] confirm this possibility.

   Second, the spectrum of low-frequency vibrations $\leqslant$800 cm^{-1} is rather densely filled with intermolecular modes. It is generally accepted [33] that vibration frequencies of liquid water (frequencies near 50 cm^{-1}) are determined by O···O···O bending modes. Higher in the area of 200 cm^{-1}, there should be stretch vibrations of these bonds and, at last, in the field of frequencies ~500 cm^{-1} libration modes of O···O···O bonds of water are concentrated. Our results indicate that such partition of water low-frequency spectrum is rather conventional. The calculated spectrum of water cluster proves to be continuous up to rather high frequencies, and all vibrations have a complex collective nature.

   Third, middle- and high-frequency regions of IR spectrum of water cluster are almost quasi-continuous. They densely fill in the area from 1,680 cm^{-1} up to 1,800 cm^{-1}. Here, bend H—O—H movements of water molecules are concentrated. The high-frequency area from 3,690 cm^{-1} up to 4,000 cm^{-1}, where the most active normal modes of symmetric and antisymmetric stretch vibrations of O—H bonds are distributed, is also densely filled.

3. The obtained high lability of vibrations of H-bonded water molecules and almost continuous character of a spectrum of their normal modes show that, actually, the vibrational dynamics of the hydrated oligonucleotide duplex is strongly limited (even more than was expected), by vibrations of water environment. On the one hand, as is evident from Table V, there is a dislodgment of many low-frequency intermolecular and intramolecular vibrations of duplex by collective vibrations of water molecules. On the other hand, the growth of some modes intensity is observed. It is especially visible in the case of intermolecular collective modes in the region of 20, 25–28, and 31–34 cm^{-1}. So, if the intensities of these modes in a single duplex have been comparable with the neighboring ones, then after hydration their intensities (values of their transition moment, μ'_{tr}) are increased considerably. Modes are grouped, and the activity of separate vibrations is strengthened. Improvement of IR bands resolution along with their increase of absorption in the structure of nucleic acids under hydration is also an observable experimental fact as has been repeatedly noted in the literature [35].

Thus, hydrate water in structure of DNA double helixes carries out the role of a universal solution matrix with different structural-dynamical consequences. One of them, by analogy with "effect of Shpolsky matrixes" [34], consists of "freezing" of many low-frequency deformation vibrations of nucleotide chains and in amplification of activity of vibration modes only in some regions of the DNA IR spectrum. Now, it is clear why we noted the low-frequency band near 20 cm^{-1} in the IR spectrum of hydrated oligonucleotide duplex is experimentally identified as the basic low frequency of a DNA collective vibration.

Conclusions

The theoretical analysis of a low-frequency vibration spectrum of double chains of oligonucleotides has shown, that (i) in isolated oligonicleotide duplexes, the lower bound of harmonic vibration spectra is located in the rather far-IR region, of several cm^{-1}. And low-frequency modes are forming mainly by intermolecular vibrations of H-bonded nucleotide pairs; and (ii) in the hydrated oligonucleotide complex, the spectrum of low normal modes of the duplex is highly condensed by intermolecular modes of water. The lower bound of vibration frequencies of the hydrated duplex lies in the same region of a few cm^{-1}. However, many low-frequency intermolecular modes of H-bonded nucleotides are "frozen" by hydrogen bonds of water molecules. In addition, the water environment increases the activity

of collective vibration modes in some regions of the IR spectrum. The band near 20 cm^{-1} is the lowest active band of collective modes of nucleotide deformations.

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