Molecular Crystals and Liquid Crystals
Publication details, including instructions for authors and subscription information:
http://www.tandfonline.com/loi/gmcl20

The Study of Lyotropic Liquid Crystal Structure Using the Molecular Dynamics Simulation Method

A. A. Shahinyan [a] , P. K. Hakobyan [b] , L. H. Arsenyan [b] & A. H. Poghosyan [a]

[a] The International Scientific-Educational Center of NASRA

[b] Institute for Applied Problems of Physics of NASRA

Version of record first published: 13 Jun 2012.

To cite this article: A. A. Shahinyan , P. K. Hakobyan , L. H. Arsenyan & A. H. Poghosyan (2012): The Study of Lyotropic Liquid Crystal Structure Using the Molecular Dynamics Simulation Method, Molecular Crystals and Liquid Crystals, 561:1, 155-169

To link to this article: http://dx.doi.org/10.1080/15421406.2012.687174

Mol. Cryst. Liq. Cryst., Vol. 561: pp. 155–169, 2012

ISSN: 1542-1406 print/1563-5287 online
DOI: 10.1080/15421406.2012.687174

Taylor & Francis
Taylor & Francis Group

The Study of Lyotropic Liquid Crystal Structure Using the Molecular Dynamics Simulation Method

A. A. SHAHINYAN,[1,*] P. K. HAKOBYAN,[2] L. H. ARSENYAN,[2] AND A. H. POGHOSYAN[1]

[1]The International Scientific-Educational Center of NASRA,
[2]Institute for Applied Problems of Physics of NASRA

We have performed a 500 ns Molecular Dynamics (MD) to study the lamellar phase of lyotropic liquid crystasl consisting of more or less hydrophobic lamellas. As more hydrophobic lamellas were used lamellas of biological origin, in this case, asymmetric human erythrocyte membrane and as less hydrophobic lamellas—planar micelles of sodium pentadecylsulfonate (SPDS), representing a commercial interest. Some important parameters have been obtained which characterize the dynamic structure of lyotropic liquid crystal's lamella. A good correspondence is established for the results of computer and physical experiments.

Keywords Molecular dynamics simulation; liquid crystal; erythrocyte membrane

Introduction

Currently the computational research and study of liquid crystals is widely spread and is very actual. There are different types of simulation methods for research of these systems and one of them is MD method [1–4]. The MD simulation, which is intensively used for the study of biological systems can be used also for studying of lyotropic liquid crystalsis and is an important tool to understand the intra- and intermolecular interactions properly in such complex multimolecular systems [3, 4]. During the last decade a lot of research was done using MD investigation of the structure and behavior of biological membranes [5–9] which are very close to the lamellas of lyotropic liquid crystals. Most of the investigated membranes were exclusively represented as the phospholipid bilayers in water environment.

The main objective of this work is to study the dynamic structure of the lamellar phase of lyotropic liquid crystals consisting of amphiphilic compounds which differ from each other with the degree of hydrophobicity. As a more hydrophobic lamella a fragment of human erythrocyte asymmertic membrane was taken, as well as a less hydrophobic lamella bimolecular layer of commercially important surfactant—sodium pentadecyl sulphonate (SPDS) in water.

*Address correspondence to A. A. Shahinyan, The International Scientific-Educational Center of NASRA, 24, Marshall Baghramian Avenue, 0019 Yerevan, Armenia. E-mail: artsha@sci.am

Construction and Simulation Details

The construction of lamella model of biological origin was implemented by using Hyperchem (Hypercube Inc.) software and MDesigner [10, 11] on the grounds of experimental data of molecular composition of human erythrocyte asymmetric membrane [15] (Table 1).

For the construction of human erythrocyte membrane the molecules of phosphaditylethanolamine (PE), phosphaditylcholine (PC), phosphaditylserine (PS), sphingomyelin(SM) and cholesterol were created and we have received a system consisting of 252 molecules of phospholipids, cholesterol and 27 Sodium counterions by random replication making allowance for asymmetry of model membrane and final concentration of phospholipids and cholesterol.The transmembrane part of the protein GpA of erythrocyte consising of from 62 to 101 amino acid residues and representing two helicese were inserted into the model of phospholipid bilayer from the previous simulation. The investigated model was solvated by inserting into water bulk with 8572 water molecules of TIP3P [12]. The membrane model was hydrated at about 33 water molecules per phospholipid molecule so in order to assure that the system is in fully hydrated state. The initial lamella (membrane) model size was about $10.5 \times 9 \times 9$ nm^3 so the rough estimation for area per phospholipid was about 0.89 nm^2. The initial configuration of lamella was determined by energy minimization using conjugate gradient method for 15000 steps and was subjected to short (about 1000 ps) MD simulation in NVT ensemble .The Langevin dynamics [13] with 5ps^{-1} damping coefficient was used. The constant temperature and pressure were set correspondingly to 310K and normal 1 atm. The constant temperature and pressure were controlled by using the Langevin piston Nose-Hoover method [14]. For the non bonded full electrostatic interactions between atom pairs cutoff parameter was set to 14A^o. The coordinates and velocities were saved with 2 stages first- each 0.001 ns for the calculation of MSD and diffusion coefficient values of phospholipids and cholesterol and second-0.01 ns for the calculation of other parameters of the system. The visual representation was performed by using VMD package. System's MD simulation run (in NPT ensemble) was done with 2 fs time step, using NAMD software code with CHARMM27 all-atom force field on parallel Linux cluster. The simulation was performed for 80 ns on 12 nodes (24 Intel Xeon 3.06 GHz processors) of the cluster with the duration of about 60 days. The force field parameters of Cholesterol molecule were generated using Dundee PRODRG server. The system ready for MD simulation consisted of 57640 atoms.

For the SPDS-water lyotropic system construction molecules of SPDS compounds were created using Hyperchem (Hypercube Inc.) software. By random rotation and translation of each molecule using MDesigner program package, lamella was received consisting of 512 SPDS molecules.

The temperature and pressure were controlled in the same way as the lamellas of biological origin (erythrocyte membranes). The system energy minimization and simulation run were done in the presence of 512 SPDS and 8887 water molecules, with 1fs timestep, using GROMACS software code with CHARMM27 all-atom force field on parallel Linux cluster. The system consisted of 55333 atoms.

The force field parameters of molecules were generated using Dundee PRODRG server. 500 ns (0.5) overall parallel Molecular Dynamics (MD) run in NPT ensemble was done correspondingly 300ns for T = 300K, 100ns for T = 323K and 100ns for T = 323K The parallel MD simulation was performed on ArmGrid sites (http://www.grid.am) using 48 processors.

Minimization of free energy of the system was performed, for having the lamella model in thermodynamic equilibrium state.

Table 1. Proportion of phospholipids, cholesterol and sphingomyelin in the phospholipid bilayer of asymmetric erythrocyte membrane

		Amount of molecules in Top layer of membrane		Amount of molecules in Bottom layer of membrane			
Name	Acyl Chains	number of molecules in model	con. (%)	number of molecules in model	con. (%)	Average Consistence in all membrane, (%)	Chem. Symbol
Lignoceroyl Sphingomyelin	24:0–14:0	24	19.8%	3	2.3%	21.8%	*LSM*
Hexadecanoyl Sphingomyelin	16:0–14:0	25	20.6%	3	2.3%		*HSM*
1-stearoyl-2-arachidonoyl-sn-glycero-3-Phosphatidylserine	18:0–20:4w6	0	0%	13	9.9%	10.7%	*SAPS*
1-stearoyl-2-docosahexaenoyl-sn-glycero-3-Phosphatidylserine	18:0–22:6w3	0	0%	14	10.8%		*SDPS*
1-stearoyl-2-arachidonoyl-sn-glycero-3-phosphoethanolamine	18:0–20:4	4	3.3%	24	18.3%	21.4%	*SAPE*
1-stearoyl-2-oleoyl-sn-glycero-3-phosphoethanolamine	16:0–18:1	2	1.6%	24	18.3%		*SOPE*
1-palmitoyl-2-oleoyl-*sn*-glycero-3-phosphocholine	16:0–18:1	18	14.9%	10	7.6%	22.6%	*POPC*
1-stearoyl-2-oleoyl-*sn*-glycero-3-phosphocholine	18:0–18:1	19	15.7%	100	7.6%		*SOPC*
Cholesterol	-	29	24.1%	30	22.9%	23.5%	Chol

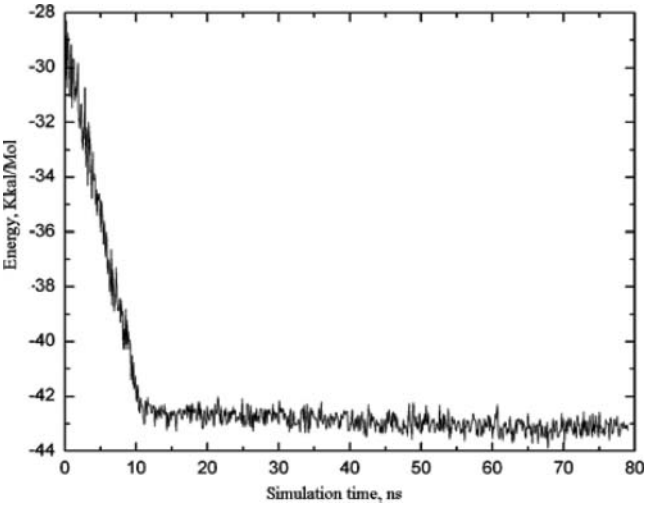

Figure 1. Dependence of value of the energy of lamella (erythrocyte membrane) on the time of simulation.

Results and Discussion

As it has been mentioned above the model of lamella of biological origin has been constructed, based on the experimental data of the molecular composition of human erythrocyte membrane [15] (see Table 1). The table shows the basic phospholipid molecules of human erythrocyte membrane which differ from each other with length of hydrocarbon chains and their degree of saturation.

For obtaining the thermodynamic equilibrium model of lamella consisting of alternating fragments of erythrocyte membranes and layers of water, the minimizing of energy of the system was carried out. In a simulation using the software package NAMD, at each step of the simulation, the energy stored in a special OUT file.

Fig. 1 shows the change of energy of asymmetric phospholipid bilayer, the structure-forming component of human erythrocyte membrane in the process of simulation using the molecular dynamics method.

It's known from the literature that in equilibrium state the free energy of biological membranes takes values 89.7 ± 35.4 kcal / mol [16]. On the other hand from the data obtained by the computer experiment (Fig. 1) it appears that after 12–14 ns simulation lamella (erythrocyte membrane) is already in equilibrium state with the energy of -43 ± 0.5 kcal /mol.

Assuming that the lamella is in equilibrium state, it becomes important to study the structural features and dynamical properties of the lamella. It's a well-known fact that one of most important structural parameters characterizing the lamella and defined by physical methods is the thickness of lamella. Figure 3 shows the variation of thickness of lamella depending on the time of simulation. As it can be seen from Fig. 3 in the process of simulation (up to 60 ns) the growth of the lamella thickness is observed after which it remains practically unchanged equal to 51.5 ± 0.5Å. This result is comparable with the experimental data obtained for the thickness of the erythrocyte membrane - 55 ± 0.5Å [17].

One of the main structural parameters of lamella is also the average area per phospholipid molecule polar group on the surface of lamella. The average area per molecule for

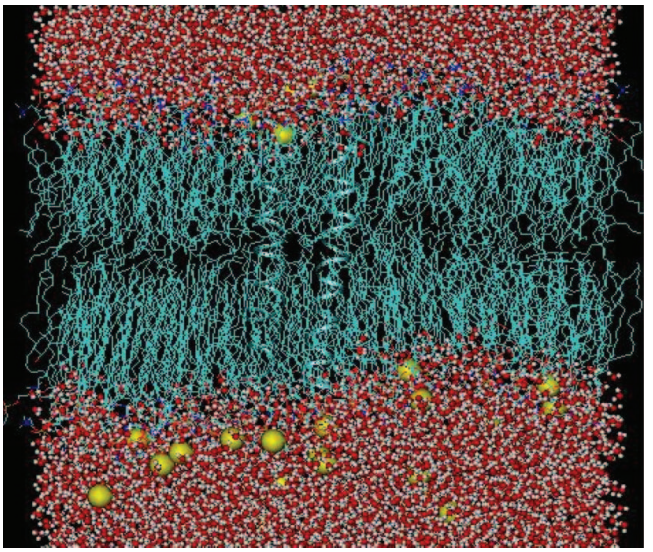

Figure 2. Model of lamella (erythrocyte membrane) after 14 ns MD simulation.

individual phospholipids (SAPS, SDPS, POPE, SAPE, LSM, HSM, POPC and SOPC) was obtained by the Voronoi algorithm. As the lamella is asymmetric, it would be more correct to represent the values of the average area per molecule of phospholipids for the top and bottom halves of lamella separately. Figure 4 (a,b,c,d) represents the values of the average area per phospholipid molecules on the surface of lamella depending on the MD simulation time. Each figure displays the change of the value of average area separately for the top and bottom halves of the lamella.

As it is evident from these figures the value of average area per molecule for the upper and lower halves of the lamella are different: for the LPC we have values of about 67 $Å^2$ and

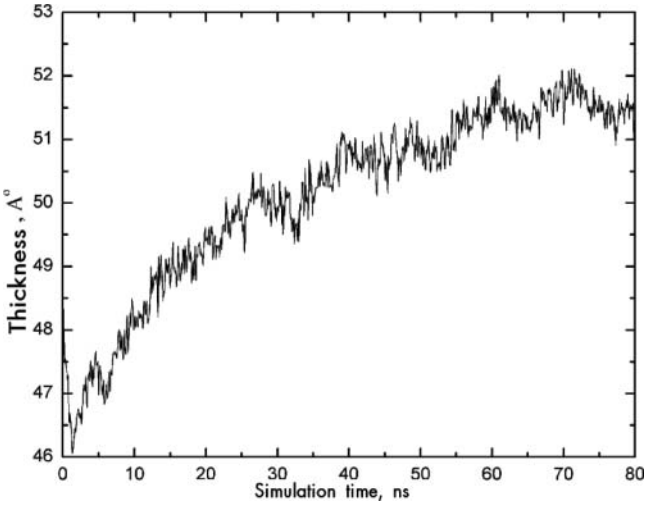

Figure 3. The thickness of lamella, depending on the simulation time.

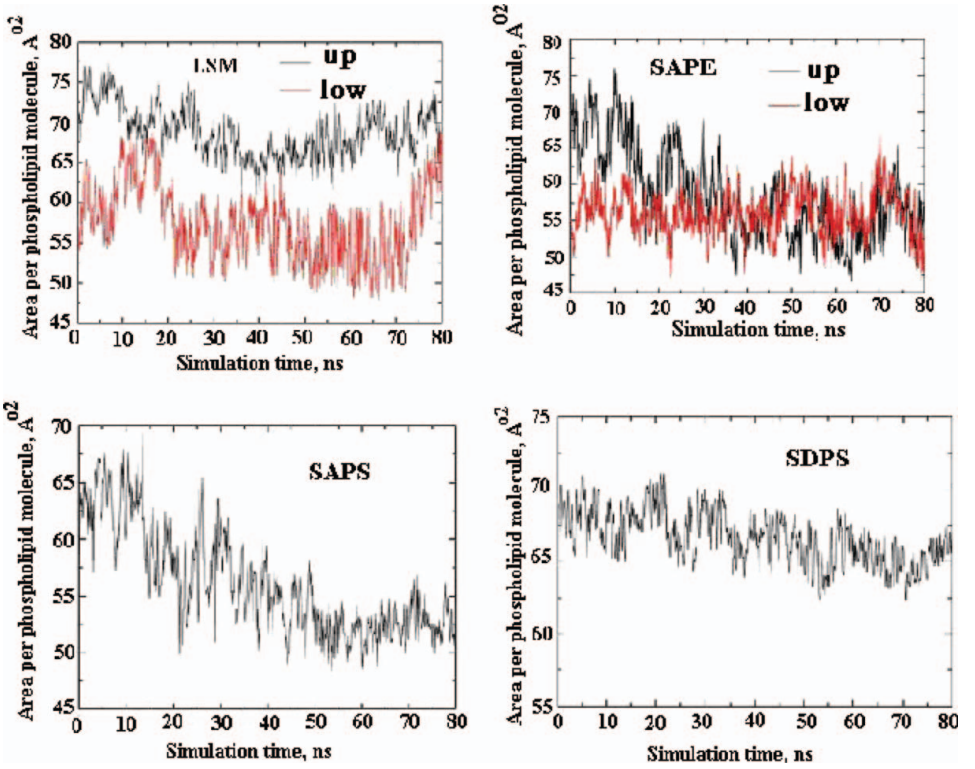

Figure 4. Area per phospholipid molecules on the surface of lamella, depending on MD simulation time. a) LSM, b) SAPE, c) SAPS, d) SDPS.

57 Å^2 and for the HSM 65 Å^2 and 55 Å^2, respectively. Such a difference can be explained by the asymmetry of lamella in which the phospholipid and cholesterol composition of the upper and lower layers of lamella are different.

In the case of sphingomyelin a difference in the concentrations of the upper and lower halves of the lamella is also observed. Its content in the upper layer is much larger than that of the lower one. From this data we see that the molecular environment also affects the value of average area per molecule of certain phospholipid. For example, the average area per molecule of sphingomyelin in the phospholipid bilayer which consists of only these molecules is the order of 52 Å^2 [18] while for multi-component lamellae we have obtained a value of about 60 Å^2. All these features should be considered when studying the structure of the transmembrane part of protein GPA. It is also known that the molecules of phosphaditylserine are absent in the upper half of the erythrocyte plasma membrane. For this reason in constructing the model of the lamellae the molecules of phosphaditylserine were introduced only in the lower half of the lamella. From Figure 4 it is clear that the average area per molecule of phosphaditylserine (SDPS and SAPS) decreases with the time of simulation and becomes constant after 60 ns. The average area per molecule of SDPS and the SAPS are $\cong$ 68 Å^2 and 53 Å^2 correspondingly. Average area per molecule of phosphaditylserine for the membrane as a whole is $\cong$61Å^2. These findings correspond to data ($\cong$58 Å^2), received for the symmetric bilayers consisting of only three types of phospholipids (Phosphotydilcholine, Phosphotidylethanolamine, Phosphatidylserine). All the results of computer simulations are comparable with the experimental data.

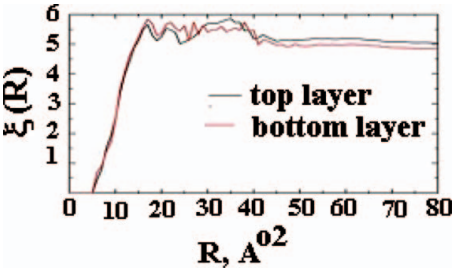

Figure 5. Surface roughness function of lamella.

An important parameter characterizing the dynamic structure of lamella is the roughness of its surface. For visualization of the surface structure of lamella its roughness is submitted as a sum of vertical displacements of molecules to the surface of the lamella. Calculations were carried out according to the following formula [19]:

$$\xi(R) = \sqrt{< (z(r) - z(r+R))^2 >}$$

where z (r) and z(r+R) are the coordinates of phospholipid molecules polar groups phosphorus atoms on the surface of the lamella. In Fig. 5 and 6 the dependence of the roughness for both surfaces of the lamella as well as the general view of the surfaces at the end of the simulation are shown. As it is evident from figures the depth of roughness for the two surfaces of lamella on average reaches up to $\sim$ 5,5 Å and then remains constant.

It's also important to study the dynamic properties of the protein macromolecule within the lamella. To solve this problem the transmembrane part of GpA has been introduced into the model of lamella and then to investigate its behavior depending on the dynamic properties of lamella.

One of the main structural parameters that characterizes GpA within the lamellae is the angle between α and β helices of macromolecule.

The angle between α and β helices of GpA was calculated as follows: in each step of the simulation each of the helices was examined as a vector from the center of mass of the last amino acid to the center of the mass of the first amino acid and the angle between the helices was considered as an angle between these vectors. As it's seen from Fig. 7 the angle among α and β helices of the molecule GPA ranged from $33\ ^{O} \pm 2$ to $42\ ^{O} \pm 2$ passing through a maximum at around $53\ ^{O}$ and after 60 ns simulation remains practically unchanged.

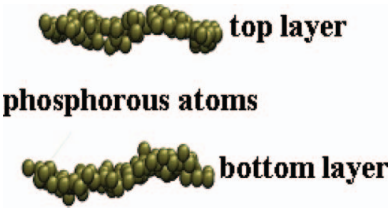

Figure 6. Snapshot of phosphorus atoms of phospholipid molecules at the surface of lamella after 80 ns MD simulation.

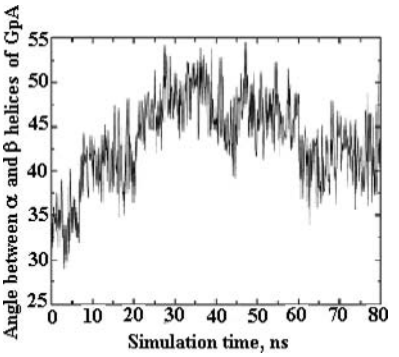

Figure 7. Angle between α and β helices of GpA in lamella.

NMR studies showed that increasing the degree of instauration of hydrocarbon chains of phospholipid molecules in bilayer leads to the increase of the angle between the helices in the GpA molecule in bilayer [20]. As the length of hydrocarbon chains of phospholipid molecules increases from 14 to 20 of CH2 groups, the difference of the angle between the helices is equal to 12 ^{O}.

In our case when instead of homogeneous mono phospholipid bilayer there is a lamella asymmetric to the content of phospholipids and cholesterol in the upper and lower halves of the lamella and that of the transmembrane protein molecule GpA, to determine the effect of the surrounding molecules on the conformation of the protein it is necessary to clarify the behavior of molecules of phospholipids and cholesterol in the immediate surrounding of the protein molecule.

For this the protein was placed in the cylinder with the radius of 10 Å and was calculated the number of molecules of phospholipids and cholesterol in the virtual volume, between cylinders of 10 and 20 Å radii (Fig. 8).

To determine the composition of the molecules in the immediate surroundings of GPa the concentration of phospholipid molecules and cholesterol in the above mentioned volume at the end of MD simulation was calculated (Table 2)

The table demonstrates that during the simulation the accumulation of some and the removal of other molecules from the surrounding of protein take place. The concentration of phosphatidylserine is growing around the upper half of lamella is entirely absent.

The investigations of the distribution of phospholipids and cholesterol in the lamellae show the following features: there is a significant decrease of cholesterol molecules around the protein and about two times increase of phosphatidylserine molecules around the GpA in the upper layer of lamella is observed. While this type of phospholipid is absent in the lower half of the lamella, sphingomyelin and phosphatidylcholine are located mainly in the lower half of lamella.

It was established experimentally that the formation of separate phases of lyotropic liquid crystals of amphiphilic compounds was carried out in accordance with the phase diagram presented below (Fig. 9) [21].

At the temperatures above the point of Krafft (T_K) depending on the temperature and concentration of amphiphilic compounds the system can undergo structural changes from the state of molecular solution to the liquid-crystalline phases and at temperatures below T_c the system will be in more ordered gel or coagel phases.

Table 2. Concentration (%) of phospholipids molecules and cholesterol in the immediate surroundings of the GpA in the upper and lower halves of lamella at the end of simulation

Location of molecules	Chol.	Phosphotydilchol.	Phosphotidylethanol.	Phosphatidylser.	Sphingomyel.
Upper layer of lamella, in 10–20 Å shell	13%	13%	21.7%	47.8%	4.5%
Average of upper layer of lamella	22.9%	15.1%	36.6%	20.6%	4.8%
Lower layer of lamella, in 10–20Å shell	20%	30.5%	10%	0%	40%
Average of lower layer of lamella	24.1%	30.6%	4.8%	0%	40.5%

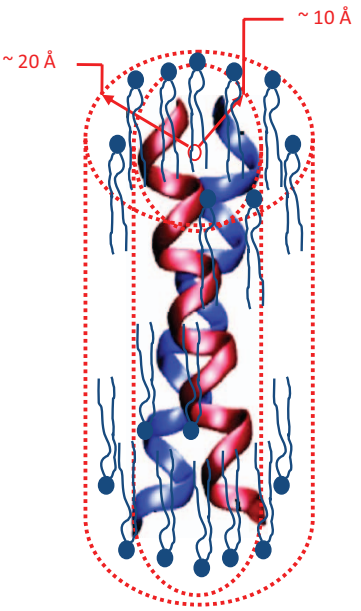

Figure 8. The scheme to measure the concentration of phospholipids and cholesterol In immediate surrounding s of GpA.

In the present paper by the method of MD simulation a less hydrophobic lamella of the lamellar liquid crystalline phase of SPDS/water system at temperatures below and above of Krafft point was investigated.

For the detailed analysis of SPDS / water system the value of some structural parameters of the system has been determined. An important parameter that describes the structure of lamellar liquid crystalline phase is the average interplane distance (Fig. 10).

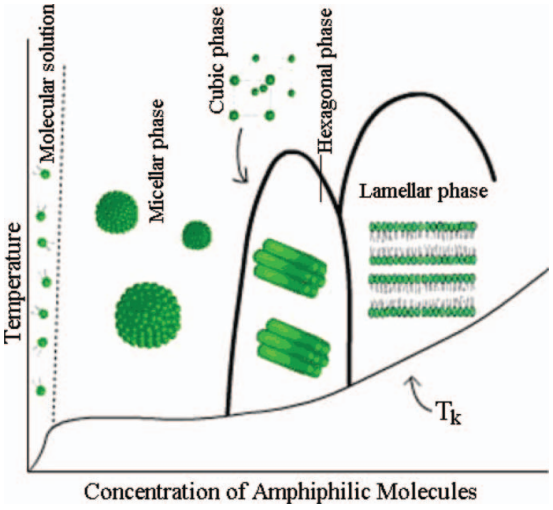

Figure 9. Phase diagram of aqueous solution of amphiphilic molecules.

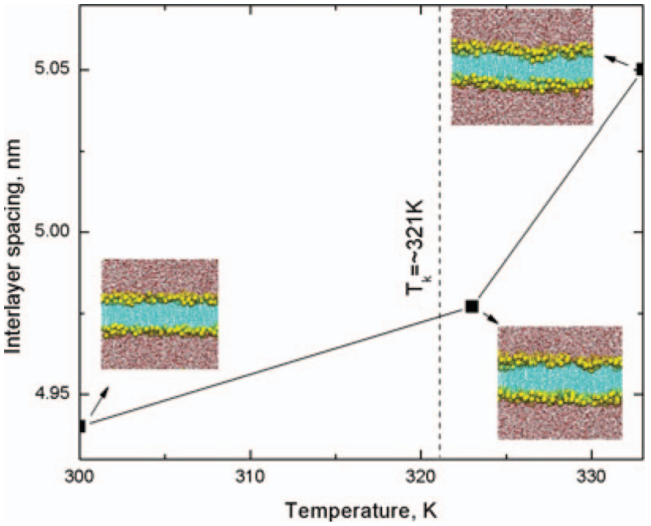

Figure 10. The average interlayer spacing of the system depending on temperature.

As we can see from the figure the increase of the temperature leads to the growth of average interlayer spacing. After increasing of the temperature from 300K (below Krafft point - the coagel phase) to 323K (above Krafft point- the bottom border of lamellar phase) this parameter grows slightly from ~4.94 nm to ~4.97 nm, meanwhile the further increase of the temperature up to 333K (in lamellar phase) influences more significantly and, finally, the average interlayer spacing reaches 5.05 nm. According to [22] the value of interlayer spacing for this type of surfactants is in the range of 2.7–5.3 nm. Thus, at temperatures above Kraft point the sharper growth of interlayer spacing is observed.

As it's seen in the figure the increase of temperature leads to the increase in average interlayer spacing. After increasing of the temperature from 300 K (below the Krafft point-

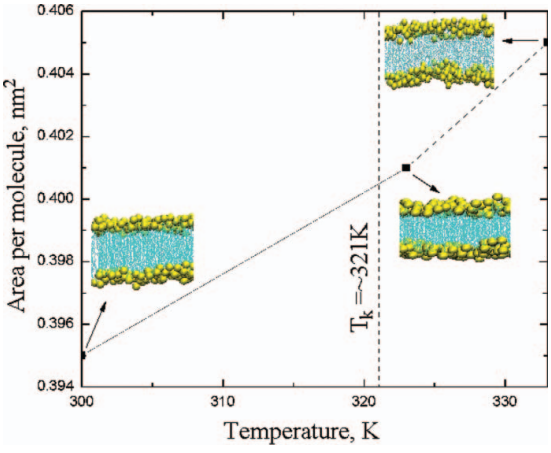

Figure 11. The average area per SPDS molecule polar head group on the surface of lamella depending on temperature.

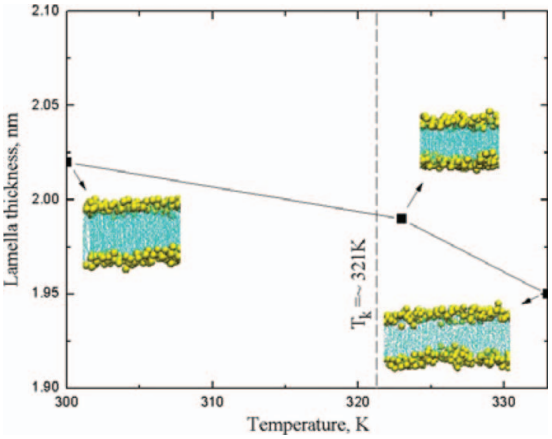

Figure 12. The lamella average thickness depending on temperature.

the coagel phase) to the 323K (above Krafft point, but near the lower boundary of lamellar phase), this parameter is growing slightly from ∼ 4.94 to ∼ 4.97 nm, meanwhile the further increase of temperatures up to 333K (in lamellar phase) affects more significantly, and finally the average interlayer spacing reaches is in the range of 5.05 nm. According to [22], the value of the interlayer spacing for this type of surfactants changes between 2.7–5.3 nm. Thus, at temperatures above the Krafft point the sharper growth of interlayer spacing is observed.

The following parameter that may be obtained from real experiments is average area per polar group of surfactant molecule at the surface of the lamella. Figure 11 shows the dependence of the mean area per polar group of the molecule of SPDS on the temperature. As it can be seen from the figure, the value of this parameter increases with the temperature, reaching ∼ 0.405 nm 2, which is in good agreement with the real experiment [23]. The growth of the average area per molecule of the polar group of SPDS means that

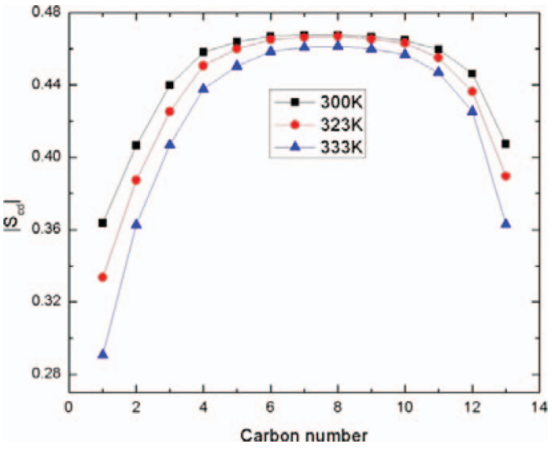

Figure 13. The orientation order parameter of SPDS molecules alkyl chains.

with increasing of temperature, the surface of the lamella increases and consequently the compactness of SPDS molecules arrangement in the lamella is reduced.

Figure 12 shows the dependence of the average thickness of lamella on the temperature change. As it's evident from the figure, temperature increase leads to the insignificant decrease of lamella's thickness from 2.02nm at 300 K to 1.95nm for 333K. In this case also above the Krafft point lamella thickness is decreasing rapidly.

Comparing this data with the values of interplanar spacing shows that the decrease in the interplanar spacing occurs mainly because of the out-flow of the water molecules from interlamellar water layer, while the decrease in the thickness of lamella is more likely due to the conformational changes of the hydrocarbon chains of SPDS molecules inside the lamella. To clarify this question the orientation order parameters of alkyl chains of SPDS molecules have been defined (Fig. 13). The calculations were performed using the following formula:

$$S_{zz}^{mol} = \frac{3}{2} < \cos^2\alpha_i > -\frac{1}{2} \tag{1}$$

assuming

$$-S_{CD} = S_{zz}^{mol} \tag{2}$$

where α_i is the angle between z-axis of the simulation box and the molecular axis is defined as a vector from C_{i-1} to C_{i+1} carbon atom and the brackets denote the ensemble and time average. As it can be seen from the plot at 300K (below the Kraft temperature) the order parameter value shows the plateau region for C_4 to C_{11} carbon atom, which refers to strongly ordered conformation of the mentioned atoms, while at 333K (above the Kraft temperature) after simulation the strongly ordered conformation was observed only for C_6 to C_{10} atoms. Hence, one can see that the increase of temperature leads to the disordering of SPDS molecules hydrocarbon chains.

Another parameter describing the conformation of alkyl chains inside the lamella is the degree of interpenetration of SPDS molecules hydrocarbon chains of up and down parts of lamella (Fig. 14) which represents the mean distance between C_{15} terminal atoms of

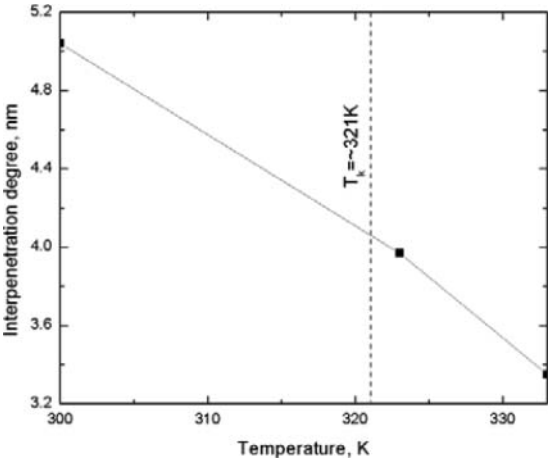

Figure 14. The interpenetration degree of SPDS molecules alkyl chains.

SPDS molecules of two halves of lamella. Due to the higher temperature the interpenetration degree decreases from ∼5.05 nm to 3.35 nm which also shows that the packing of hydrocarbon chains inside the lamella becomes more disordered above Kraft temperature.

Conclusion

Thus, with the help of molecular dynamics the lamellar phases of lyotropic liquid crystals were investigated containing more or less hydrophobic lamellas. As a more hydrophobic lamella the most realistic model of the asymmetric human erythrocyte membrane has been studied, and as a less hydrophobic - plane micelles sodium pentadecyl sulphonate of commercial interest. It is established that the dynamic parameters, characterizing the lamella, such as the thickness and the compactness of the lamella, the conformation of the hydrocarbon chains of amphiphilic molecules within the lamella, the selective interaction of the hydrophobic fragment of the protein molecule in erythrocyte membrane with the surrounding molecules, the influence of the temperature in a less hydrophobic lamellae on the structural parameters of the latter, etc. give important information about the dynamic state of the investigated structures. The main achievement of this work lies in the fact that many of the data obtained by dynamic simulations show good agreement with the results of real experiment. At the same time, a lot of data concerning the dynamics of the processes at the molecular level is not yet available to the existing methods of physical experiment.

Acknowledgement

The authors express their gratitude to the team of ArmGrid for making it possible to carry out the computer experiments.

References

[1] Poghosyan, A. H., Gharabekyan, H. H., & Shahinyan, A. A. (2007). *IJMPC 18*(1), 73.
[2] Mori, K., Hata, M., Neya, S., & Hoshino, T. (2004). *Chem-Bio Inf. J.*, *4*, 15.
[3] Robinson, A. J., Richards, W. G., Thomas, P. J., & Hann, M. M. (1994). *Biophys. J. 67*(6), 2345.
[4] Berkowitz, M. L. (2009). Biochimica et biophysica acta. *Biomembranes*, *1788*, 86.
[5] Soumana, O. S., Garnier, N., & Genest, M. (2007). *Eur.Biophys. J. 36*, 1071.
[6] Zhang, J., & Lazaridis, T. (2009). *Biophys. J. 96* (11), 4418.
[7] Eilers, M., Patel, A. B., Liu, W., & Smith, S. O. (2002). *Biophys. J. 82*, 2720.
[8] Smith, S. O., Song, D., Shekar, S., Groesbeek, M., Ziliox, M., & Aimoto, S. (2001). *Biochemistry*, *40* (22), 6553.
[9] Smith, S. O., Eilers, M., Song, D., Crocker, E., Ying, W., Groesbeek, M., Metz, G., Zilox, M., & Aimoto, S. (2002). *Biophys. J. 82*, 2476.
[10] Shahinyan, A. A., Poghosyan, A. H., Yeghiazaryan, G. A., & Gharabekyan, H. H. (2004). *Elec J. Nat. Sci. 1*, 56.
[11] Jorgensen, W. L., Chandrasekhar, J., Medura, J. D., Impey, R. W., & Klein, M. L. (1983). *J. Chem. Phys. 79*, 926.
[12] *Hypercube Inc.* URL: http://www.hyper.com/
[13] Levy, R. M., McCammon, J. A., & Karplus, M. (1979). *Chem. Phys. Lett. 64*, 4.
[14] Feller, S. E., Zeng, Y. H., Pastor, R. W., & Brooks, B. R. (1995). *J. Comp. Phys. 103*, 926.
[15] Jaim, T. Dodge, & Gerald, B. Phillips (1967). *Journal of Lipid Research*, *8*, 667–675.
[16] Sandermann, H. Jr. (2002). *FEBBS Letters*, *514* (2–3) 340–342.
[17] Sackmann, E.. Biological Membranes.Architecture and Function. *Handbook of Biological Physics*. 1, edited by R. Lipowsky and E. Sackmann. Elsevier Science B.V. (1995).

[18] Petrache, H. I., Grossfield, A., MacKenzie, K. R., Engelman, D. M., & Woolf, T. B. (2000). *J. Mol. Biol. 302*, 727.
[19] Belorgey, O., & Benatter, J.J., (1991). *Phys. Rev. Letter*, *66*, 313.
[20] White, S. H., & Wimley, W. C. (1999). *Annu. Rev. Biophys. Biomol. Struct. 28*, 319.
[21] http://plc.cwru.edu/tutorial/enhanced/files/llc/Phase/phasehtm *Structure and Properties of Lyotropic Liquid Crystals*.
[22] Yeghiazaryan, G. A., Poghosyan, A. H., Shahinyan A. A.. (2006). *Physica A.*, *362*, 197.
[23] A. A. Shahinyan. *The role of structural organization of ionic micelles in the mechanism of macromolecules formation in the emulsions (in Russian)*. Phblishing House "GITUTIUN" NAS RA, (1985).