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Polarity and Chirality in NCP Mesophases and Chromatin Fibers

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We propose a unified mechanism of phase transitions in the high density solutions of Nucleosomal Core Particles. We demonstrate its relation with the high shape and charge anisotropy of the NCP due to the DNA wrapping around the histone protein core. Hexagonal-to-lamellar transition in the solution of NCP columnar aggregates is shown to be driven by the condensation of the periodic antiparallel polar vector field. The transition results in the polar dyadic axes correlations. Fine structure of the NCP organization is also explained, namely the correlated tilting of NCP with respect to the column axis.

Keywords: chirality; chromatin fiber; condensed mesophases; NCP; polarity

I. INTRODUCTION

Chromatin fiber is one of the essential elements of eukaryotic cells [1]. It has two fundamental functions in the living matter: it compacts DNA and orders it to allow targeted genetic operations. The structure,

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density and dynamics of the chromatin fiber affect accessibility of proteins that regulate genes transcription, replication, repair and recombination and influence the gene expression or silencing [2–4]. Recently it was even shown that the irreversible growth arrest in normal cells (which is perturbed in cancer cells) was accompanied by profound changes in chromatin structure [5] and that the defects in chromatin assembly contribute to genome instability and cancer [6].

Chromatin fiber permits to compact eukaryotic DNA approximately 50000 times and to make it fit into the microns sized nuclei. On the very elementary level of the chromatin structure DNA is packaged at 10 nm scale into a more or less regular array of repeating units that are folded into a higher-order structure at the greater scale. The elementary particle of the chromatin fiber called nucleosome comprises 147 base pairs (bp) of DNA wrapped in 1.7 left-handed superhelical turns around an octameric core of histone proteins (two copies each of four histones) H2A, H2B, H3 and H4. The structural properties of each nucleosome are also ensured by the H1 histone protein which fixes the exit-entry point of the wrapped DNA. Successive nucleosomes are connected by stretches of linker DNA which are about 20 to 60 bp long.

Despite more than twenty years of research, the structure of the chromatin fiber and its molecular elements remain enigmatic. For a long time no clearcut conclusion could be made about its precise structural organization even at the 30 nm scale. Recent progress in physical approach to the problem which involves modern methods in high-resolution structural technique and cryomicroscopy together with the theoretical modeling have given some new insight into the structure and its determinant ingredients. However, very little is known about molecular mechanisms that organize nucleosomes into a condensed three-dimensional fibers. Each histone protein contains domains responsible on histone-histone and on histone-DNA interactions and N-terminal tails which are external to the nucleosome and highly flexible. The role of the tails in high-order structure assembly has not yet been rigorously elucidated [7]. To fulfill their biological function nucleosomes should be able to interact with each other in an efficient way using for this purpose various external parameters. Post-translational modification of the histones along their tails and variation of ionic conditions are among the most important of them [8,9]. However, a great number of the X-ray diffraction investigations of the native chromatin structure [10–12] could not discriminate between several structural models, like «solenoid» model or «two-start-helix» model, for example (for a review, see [13]). In such a situation, the information can be completed by a study of simplified or mimetic systems. Along this way, a great progress has been achieved by the study of a

closed nucleosomal oligomers like a tetranucleosome which comprises four nucleosomes connected by linker DNA in a closed loop [14].

Another promising way to get an insight into the interactions between nucleosomes and the chromatin structure is the study of the condensed states formed by isolated nucleosomal core particles (NCP) resulting from a digestion of the linker DNA in the native chromatin. Under osmotic pressure and in presence of a certain amount of monovalent salt the NCP form a whole series of mesophases which can be studied by standard optical, X-ray diffraction and electron microscopy methods together with specific biophysical techniques. Corresponding structures can be analyzed in a usual for the liquid crystal science way, paying the main attention to the mesogenic factors of individual NCP particles. Resulting information on the nucleosomes organization and interactions could be very useful for the precise study of the native chromatin.

An isolated NCP particle is stable in aqueous solutions up to 750 mM monovalent salt ionic strength [15]. Even in absence of the H1 histone protein it conserves typical for a nucleosome nearly cylindrical shape (Fig. 1), of height 5.5 nm and diameter about 11 nm. Its structural charge attains -165 . Dilute solutions of the NCP,

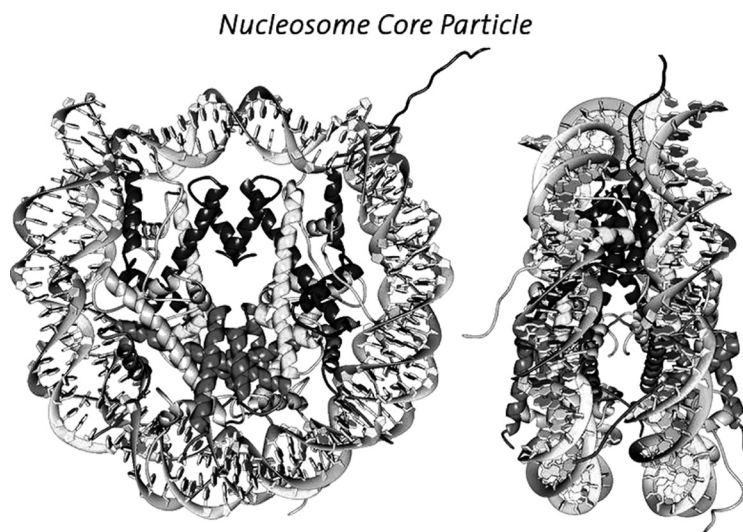


FIGURE 1 Nucleosomal core particle: Biochemical view. Histone proteins and DNA are shown using ribbon presentation. Side view of the particle has a typical V-like shape which can be clearly distinguished in the electron microscopy experiments.

prepared in the presence of monovalent ions, may be progressively concentrated, either by controlled drying of the sample, or by exerting an osmotic pressure with polyethylene glycol (PEG) [16]. At low salt concentrations and sufficiently high osmotic pressure NCP aggregate into almost ideal cylindrical columns which contain dozens of individual particles (Fig. 4). Columns formed by the stacked NCP can be clearly seen in the freeze-fracture experiments [17]. These columns then form a whole series of complex mesophases due to competing interactions mainly of the electrostatic origin [18,19] and to the excluded volume effects. Note that these interactions are extremely complex and still poorly understood. In the present work we perform structural analysis and thermodynamical study of the NCP mesophases which is free of model assumptions on the nature of the interactions. We establish the relation between the properties of polarity and chirality of individual particles and the mechanism of phase transitions between the experimentally observed liquid crystalline phases. In addition we make several remarks about the possible mesophases which can be induced by the same physical mechanism.

II. SHAPE AND CHARGE ANISOTROPY OF THE NUCLEOSOMAL CORE PARTICLES AND ORDERED MESOPHASES

We start with the analysis of mesogenic properties of the nucleosomal particles. The NCP are characterized by a high shape and charge anisotropy (Fig. 1) [20] due to the DNA wrapping around the histone core. A short (1.7 turns) well-defined superhelix provides the NCP with non-zero chirality. Asymmetry of the wrapping results in the polarity of the particle. Indeed, the entry-exit point of the DNA free ends marks a polar axis which passes just in the middle of the superhelix and is usually called dyadic (or dyad) axis in the biochemical literature (Fig. 2). Polar dyadic axis of a particle, which can be conventionally called transverse «polarization» [21] determines the orientation of the NCP. Density difference in the DNA crown and in the histone core (Fig. 1) makes the orientation of the dyadic axis visible on cryoelectron micrographs [17]. Thus, it is possible to determine experimentally the orientation of the NCP inside each column or their relative orientation from one column to another. This remarkable property has allowed us to analyze in detail the structural peculiarities of the main NCP mesophases and to propose the mechanism of the phase transitions between them. Note that this topological «polarization» vector is accompanied, in principal, by a polarization in a usual physical sense. Indeed, the main positive charge of the NCP complex is carried by the

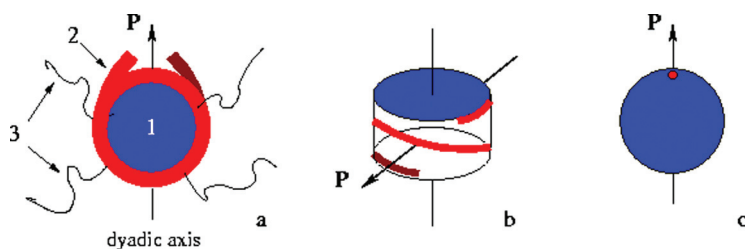


FIGURE 2 Nucleosomal core particle: Biophysical view. DNA is wrapped around the cylindrical core formed by the octamer of four histone proteins. Superhelix DNA twisting around the histone core makes the particle chiral. The entry-exit point of the DNA free ends marks a polar dyadic axis **P**. a – Top view. 1 – histone core; 2 – 1.7 superhelical turns of the DNA; 3 – histone tails. b – Side view. c – Schematic notation of the NCP and its polar dyadic axis.

octamer protein core, while the negative charge is mainly concentrated on the DNA. However, in this complex system in water solution with a rather high ions concentration no direct conclusion about the electric polarization can be made without a profound analysis of all electrostatic interactions.

Under rather high salt conditions (above 50 mM) and for the particles concentration of the order of 500 mg/ml the NCP aggregates form a columnar hexagonal phase, leading at still higher salt concentration to 3D hexagonal crystal or to the orthorhombic columnar phase. At low salt concentration (under 25 mM) and for the particles concentration ~300 mg/ml NCP columns form a lamellar phase. In this region of the phase diagram the main electrostatic interactions are not screened and the resulting mesophase should have structural organization rather close to the local structure of the chromatin fiber. The structure of the lamellar phase has been analyzed by means of cryoelectron microscopy (Fig. 3) [17]. Each lamella is formed by a bilayer of parallel columns. A layer of solvent with the thickness dependent on the NCP concentration separates the lamellae, the total period of the structure varying from 27 to 42 nm [16,17]. Inside each bilayer the columns are arranged in slightly distorted close packing of two rows of cylinders. The structural analysis of the bilayer phase and its comparison with the hexagonal one allowed us to indicate the key property of the bilayer phase, which is related to the orientation of the polar dyadic axes of the particles. In the lamellar phase the polar axes of individual particles are strongly correlated along the column. Consequently, each column carries a non-zero average transverse polarization vector **P** of the column (Fig. 4c). Polarization vectors **P** of columns situated in the

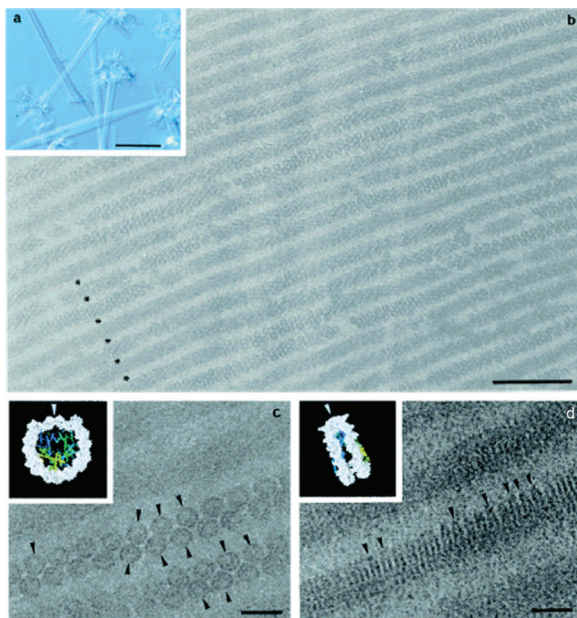


FIGURE 3 Structure of the lamellar phase [17]. a – Tubules observed by optical microscopy. b – d – Lamellar structure of the NCP columns revealed by cryoelectron microscopy. b, c – Images perpendicular to the columns axes. d – Image parallel to the columns axes. The orientations of the dyadic axes of individual NCP are shown in d. The orientations of the average polar axes directions are shown in c.

two layers of the same lamella are in antiparallel direction, with the DNA exit point facing the solvent (Figs. 3b, c). The average direction of the dyadic axes in each layer is normal to the lamella, though the directions of individual particles are fluctuating around the average one. The state of the dyadic axes is quite different in the 2D columnar hexagonal phase stable at high salt concentrations. The cryomicroscopy shows that the polar axes of the NCP are orientationally disordered along each column (Fig. 4b). Consequently, the average polarization vector \mathbf{P} of the column is zero. By contrast, this phase has the well-defined 2D positional order.

III. PHASE TRANSITIONS BETWEEN THE CONDENSED NCP MESOPHASES

In what follows we are interested in the factors (order parameters) which drive the phase transitions between the hexagonal and lamellar

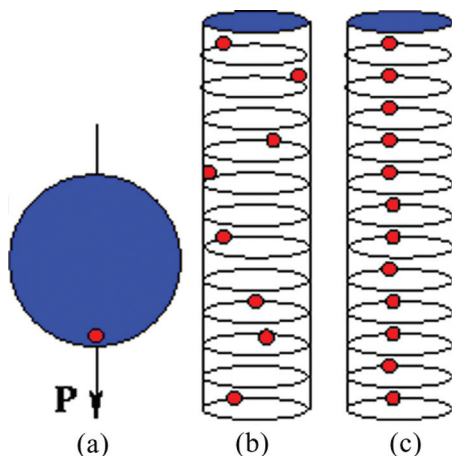


FIGURE 4 Dyadic axes orientation. a – Red point marks the entry-exit point of the DNA superhelix; the arrow indicates the orientation of the axis. b – dyadic axes orientations disordered along the column in the hexagonal phase. c – dyadic axes are correlated along the column in the lamellar phase; each column carries a non-zero polarization vector \mathbf{P} .

phases in the condensed NCP solutions. We also propose that the transitions to other phases in this system (for the recent experimental progress see [22]), namely orthorhombic and inverted hexagonal ones, can be understood in the framework of the same mechanism. We argue that the main factor influencing the bilayer phase formation (and probably, the chromatin fiber structure) is the polar interaction due to the shape and charge anisotropy of the NCP. Group theory analysis of the hexagonal and bilayer structure shows that the order parameter of the transitions from the columnar hexagonal phase (taken as a parent state) is a periodic polar vector field. It is related to the simultaneous ordering of the dyadic axis along the column and between the columns, accompanied by the collective displacement of the columns. For the most important hexagonal-to-lamellar transition the order parameter is reduced to a simple antiparallel ordering of the average polarization vectors \mathbf{P} of the columns in neighboring rows of the hexagonal structure (Fig. 5). This result is obtained in the framework of a Landau theory [23] which reveals to be efficient for the analysis of complex systems with a big number of competing interactions. Its evident advantage is weak sensibility to model assumptions which explains its wide application in numerous domains of condensed matter physics (see for example, [24–26]). The principle scheme of the

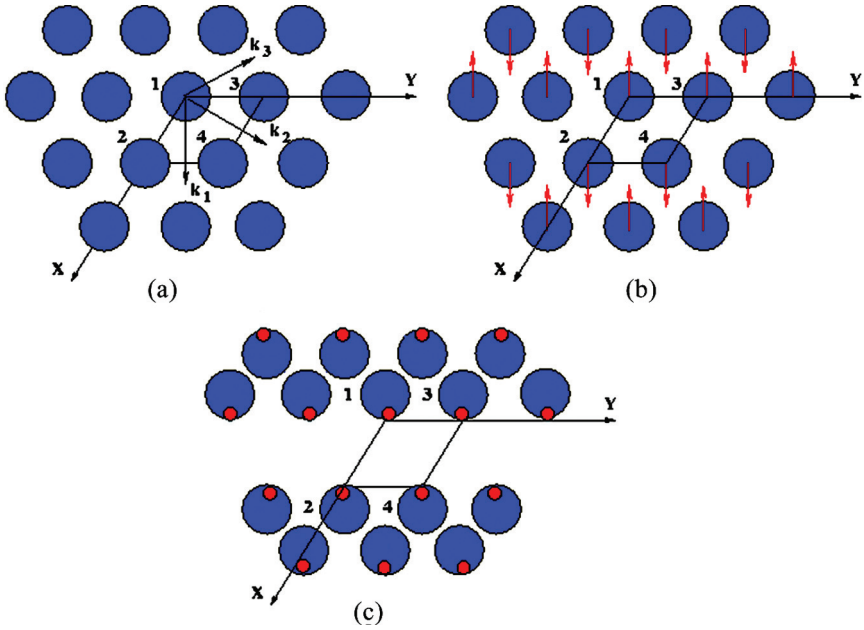


FIGURE 5 Hexagonal and lamellar structures. a – Hexagonal parent structure: columns noted as 1, 2, 3, and 4 indicate the nodes of a unit cell in the 2D hexagonal structure; \mathbf{k}_1 , \mathbf{k}_2 , and \mathbf{k}_3 are the wave vectors of the periodic polar vector field which drives the transition; X and Y are the hexagonal coordinates. b – Antiparallel displacement field $\mathbf{D}(\mathbf{k}_1)$ of the columns (indicated by the arrows). c – Resulting columns positions and the antiparallel field $\mathbf{P}(\mathbf{k}_1)$ of the dyadic axes orientations in the lamellar phase (indicated by the red points).

approach is the following. The system in the parent phase (in the present case we take the hexagonal structure as a parent one) is characterized by the probability density function $\rho_0(\mathbf{x}, \mathbf{y}, \mathbf{z}) = \rho_{\text{hex}}(\mathbf{x}, \mathbf{y}, \mathbf{z})$. In the phases with the ordered orientations of the dyadic axes (like bilayer lamellar one) the probability density function $\rho(\mathbf{x}, \mathbf{y}, \mathbf{z})$ can be presented in the form:

$$\rho(\mathbf{x}, \mathbf{y}, \mathbf{z}) = \rho_{\text{hex}}(\mathbf{x}, \mathbf{y}, \mathbf{z}) + \sum \eta_i \Psi_i(\mathbf{x}, \mathbf{y}, \mathbf{z}) \quad (1)$$

where $\Psi_i(\mathbf{x}, \mathbf{y}, \mathbf{z})$ are the basic functions responsible on the phase transition, and η_i are the corresponding order parameter components. $\Psi_i(\mathbf{x}, \mathbf{y}, \mathbf{z})$ (and consequently η_i) span the irreducible representation of the symmetry group of the parent phase responsible on the symmetry

breaking through the phase transition: $G_\alpha \Psi_i(\mathbf{x}, \mathbf{y}, \mathbf{z}) = \Psi_j(\mathbf{x}, \mathbf{y}, \mathbf{z})$, where $G_\alpha \in G_{\text{hex}}$ are the elements of the symmetry group of the parent hexagonal structure. When the order parameter components η_i are different from zero the symmetry of the probability density function is that of the ordered phase while for vanishing η_i the density function is equal to that of the parent structure. According to Landau the thermodynamics of the system of phases is described by a free energy invariant with respect to all symmetry operations of the parent structure. Both parent and ordered states of the system are obtained as the minima of the free energy functional:

$$F = \int [f(\eta_i \Psi_i(\mathbf{x}, \mathbf{y}, \mathbf{z})) + g(\nabla \eta, (\nabla \eta)^2)] d\mathbf{x} d\mathbf{y} d\mathbf{z} \quad (2)$$

In the present consideration we will also use the peculiarity of the colloidal systems with polar-like order which results from the Curie principle [23–26]: duality between the average polarization vectors \mathbf{P} of the column and its displacement vector \mathbf{D} . Indeed, both polarization vector \mathbf{P} and the displacement vector \mathbf{D} have the same symmetry in the chiral cylindrical aggregate. Thus, in any phase with the ordered polar vector \mathbf{P} the column should shift in the direction of the average polarization, the displacement \mathbf{D} being proportional to \mathbf{P} . In our study of the order parameter and of the mechanism of the phase transition we will follow only the vectors of the average column polarization \mathbf{P} , and then add the displacement \mathbf{D} in the same direction. We apply a standard group theory analysis to the structures of the hexagonal and bilayer phases. The results are resumed in Figure 5. The columns with disordered dyadic axes (zero polarization \mathbf{P}) and positionally equivalent in the unit cell of the hexagonal phase become ordered and different in the bilayer and in the other ordered phases. To follow this changes we note the columns in a function of their hexagonal coordinates in the same unit cell as follows: column 1 has the coordinates (0,0), column 2 \rightarrow (1,0); 3 \rightarrow (0,1), and 4 \rightarrow (1,1). We express then the order parameter of the phase transition in terms of four vectors \mathbf{P}_i ($i = 1, 2, 3, 4$) of polarizations carried by these four columns in the ordered state. For that purpose we find the irreducible representation of the hexagonal symmetry group responsible on the symmetry breaking during the transition to the bilayer phase. It is three-dimensional and is spanned by the three basic functions: $\Psi_1 = (2\hat{e}_x + \hat{e}_y) \exp(i \mathbf{k}_1 \mathbf{r})$; $\Psi_2 = (\hat{e}_x + 2\hat{e}_y) \exp(i \mathbf{k}_2 \mathbf{r})$; $\Psi_3 = (-\hat{e}_x + \hat{e}_y) \exp(i \mathbf{k}_3 \mathbf{r})$. Here \hat{e}_x and \hat{e}_y are the unit vectors along the hexagonal axes; $\mathbf{k}_1 = \mathbf{b}_1/2$;

$\mathbf{k}_2 = \mathbf{b}_2/2$; $\mathbf{k}_3 = (-\mathbf{b}_1 + \mathbf{b}_2)/2$, are the three arms of the star of the wave vector associated with the order parameter, and \mathbf{b}_1 and \mathbf{b}_2 are the reciprocal basic vectors of the 2D hexagonal lattice. Corresponding order parameter components can be presented in the form:

$$\begin{aligned}\eta_1 &= P_{x1} - P_{x2} + P_{x3} - P_{x4} + (P_{y1} - P_{y2} + P_{y3} - P_{y4})/2 \\ \eta_2 &= (P_{x1} + P_{x2} - P_{x3} - P_{x4})/2 + P_{y1} + P_{y2} - P_{y3} - P_{y4} \\ \eta_3 &= (-P_{x1} + P_{x2} + P_{x3} - P_{x4} + P_{y1} - P_{y2} - P_{y3} + P_{y4})/2\end{aligned}\quad (3)$$

By studying the invariant subspaces of the order parameter space [23–26] it is easy to enumerate all possible ordered phases induced by order parameter (3). They are the solutions of the equations of state obtained by the minimization of the free energy invariant with respect to the considered group representation. In our case the free energy of the system $F(I_1, I_2, I_3)$ is dependent on the three basic invariants: $I_1 = \eta_1^2 + \eta_2^2 + \eta_3^2$; $I_2 = \eta_1^2\eta_2^2 + \eta_2^2\eta_3^2 + \eta_3^2\eta_1^2$; $I_3 = \eta_1^2\eta_2^2\eta_3^2$. Its minimization gives six different solutions [21]. The symmetry of the solutions can be found using the invariant properties of the free energy and studying the equations: $\partial F/\partial \eta_i = (\partial F/\partial I_k)(\partial I_k/\partial \eta_i) = 0$. Among the solutions of the equations of state, the most important from the thermodynamics point of view are those dependent on only one component: the bilayer phase ($\eta_1 \neq 0$; $\eta_2 = 0$; $\eta_3 = 0$); orthorhombic phase ($\eta_1 = \eta_2 \neq 0$; $\eta_3 = 0$); and the inverted hexagonal phase ($\eta_1 = \eta_2 = \eta_3 \neq 0$). Using these results we illustrate the mechanism of the hexagonal-to-lamellar phase transition in Figure 5. Indeed, the polarization vectors carried by the columns 1 and 3 are equal in this state: $\mathbf{P}_1 = \mathbf{P}_3$; the same concerns the columns 2 and 4: $\mathbf{P}_2 = \mathbf{P}_4$. Due to the duality discussed above, the same relations exist between the displacements of the columns: $\mathbf{D}_1 = \mathbf{D}_3$; and $\mathbf{D}_2 = \mathbf{D}_4$. Thus, the mechanism of the hexagonal-to-lamellar transition is reduced to a simple antiparallel vector field. In the final structure of the lamellar phase the positions of the columns are the results of the antiparallel displacements and the average dyadic axes orientations are the result of the antiparallel orientation field. The only non-zero component of the order parameter has in this phase the form:

$$\eta_1 = (2P_{x1} + P_{y1}) - (2P_{x2} + P_{y2}) \quad (4)$$

Analogously, one can find the directions of the displacements and of the dyadic axes orientations in the orthorhombic and inverted hexagonal phases (see [21]).

To study the thermodynamics of the system we calculate the phase diagram of the model which contains the domains of stability of the parent hexagonal phase and of the three mentioned phases.

For the sake of clarity we omit the gradient terms expressing large-scale elastic deformation and consider a homogeneous sample. In this case the free energy is a function (and not a functional) of the order parameter components. The simultaneous presence of four phases on the same 2D phase diagram and the first order of the transitions between them impose the expansion of the free energy up to at least sixth degree in η_i :

$$\begin{aligned}
 F = & a_1(C_1, C_2)(\eta_1^2 + \eta_2^2 + \eta_3^2) + a_2(\eta_1^2 + \eta_2^2 + \eta_3^2)^2 \\
 & + b_1(\eta_1^2\eta_2^2 + \eta_2^2\eta_3^2 + \eta_3^2\eta_1^2) + d_{12}(\eta_1^2 + \eta_2^2 + \eta_3^2)(\eta_1^2\eta_2^2 + \eta_2^2\eta_3^2 + \eta_3^2\eta_1^2) \\
 & + a_3(\eta_1^2 + \eta_2^2 + \eta_3^2)^3 + c_1(\eta_1^2\eta_2^2\eta_3^2) + \dots
 \end{aligned} \quad (5)$$

The phenomenological coefficients of free energy (5) are dependent on both NCP and monovalent salt concentrations (C_1, C_2). As usual in the Landau theory the stability of the parent hexagonal phase is lost when the quadratic term becomes negative. Typical two-dimensional section of the calculated phase diagram of the model is given in Figure 6. One can approximately orient the axes of the salt content and of the osmotic pressure in the plane of the (a_1, b_1) coefficients.

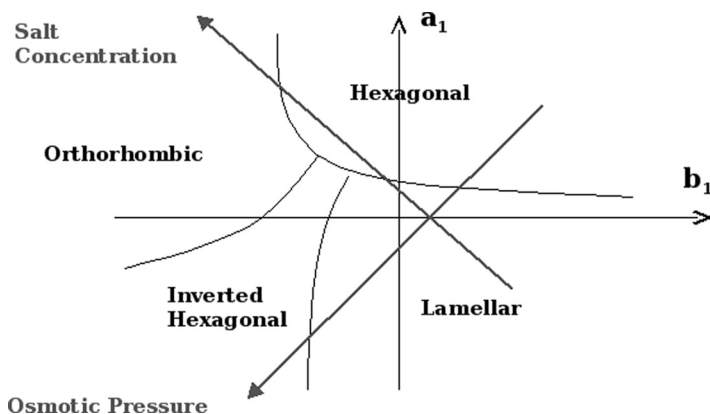


FIGURE 6 Phase diagram of model (5). Typical 2D section presenting stability regions of the parent structure and three ordered phases is given. Tentative orientation of the axes (Salt Concentration – Osmotic Pressure) is indicated.

IV. INFLUENCE OF THE NCP CHIRALITY ON THE CONDENSED NCP MESOPHASES

In the final part of our work we indicate several important consequences of the NCP chirality and its influence on the structure of the phases with the correlated dyadic axes. Let us first consider the state of an individual columnar aggregate constituted of the chiral and polar NCP particles. The point symmetry of a chiral column of this type with disordered NCP axes is D_∞ . Like in chiral smectic or chiral columnar phases of thermotropic liquid crystals the polar vector \mathbf{P} and the axial vector Θ carried by the column have exactly the same symmetry. Following the Curie principle, in such a case, Θ is proportional to \mathbf{P} and vice versa. Thus, if the polar dyadic axes become ordered along the columnar aggregate their average polarization \mathbf{P} induces a non-zero axial vector Θ . The NCP aggregation energy being rather low, the non-zero axial vector is realized as a non-zero average tilt of the individual NCP particles with respect to the column axis (Fig. 7). In biochemical literature the axis of an individual particle is usually noted as S-axis. Using this notation we can formulate this results as follows: in the phases formed by the NCP particles in the condensed aqueous solutions the correlated orientation of the dyadic axes is accompanied by the tilting of the S-axes with respect to the column axis. Note that in more rigid aggregates or in chiral biopolymers (DNA or actin, for example) the covalent bonds ensure the cohesion of the elementary parts of the molecules and a non-zero axial vector can not be realized as a tilt of the parts. In some cases the axial vector induces an additional twisting of the biomolecule instead. As for the NCP mesophases the tilting of the NCP with respect to the columnar axes is the most realistic explanation of the «monoclinicity» of the unit cell observed in the X-ray experiments [16] and by cryoelectronic microscopy [17]. In a good agreement with the predictions of our model the NCP particles are not tilted in the hexagonal phase which is characterized by the disorder of the dyadic axes orientation along each column. The zero value of the average polarization $\mathbf{P} = \mathbf{0}$ induces the zero value of the axial vector of the tilt $\Theta = \mathbf{0}$ (Fig. 7). Another important remark on the correlation between the effects of polarity, chirality and tilt order in the NCP mesophases concerns the periodicity of the tilt in the lamellar phase. As we have already stressed above the orientations of the average polarization vectors \mathbf{P}_1 in the upper and \mathbf{P}_2 in the lower layer of the same lamella are antiparallel (Fig. 5c). The tilt Θ_1 of the NCP in the columns of the upper layer is determined by the direction of the \mathbf{P}_1 while the tilt Θ_2 in lower layer is determined by the direction of the \mathbf{P}_2 . Consequently, the antiparallel orientation of

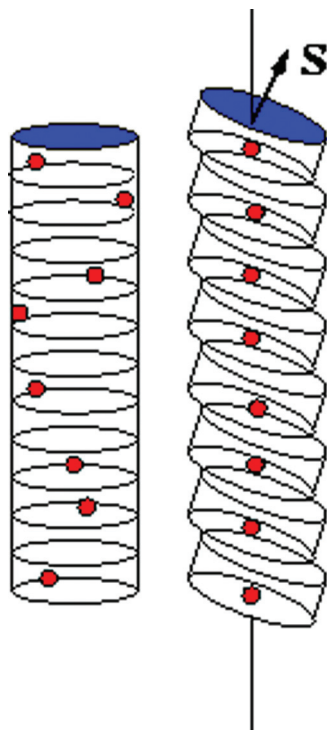


FIGURE 7 Tilting of individual NCP in the mesophases with ordered orientation of dyadic axes. Disordered orientation of polar dyadic axes with the average polarization $\mathbf{P} = \mathbf{0}$ induces the zero value of the axial vector of the tilt $\Theta = 0$ in the hexagonal phase. Ordered orientation of the polar dyadic axes leads to the non-zero average tilt of the individual NCP particles with respect to the column axis in the lamellar phase.

the average polar vectors induces the anticlinic tilting of the \mathbf{S} -axes of the NCP particles in the two different layers of each lamella in the bilayer phase (Fig. 8). This important prediction of the layers anticlinicity resulting from our model has been recently verified experimentally [27] by the refined X-ray scattering in the lamellar phase of the NCP columnar aggregates. Let us finally note that the chirality can have other important influence on the structure of the NCP mesophases, inducing namely, the helical twisting of the NCP particles along the columns. However, the cylindrical columns of the NCP are not very long with respect to the possible pitch of the helix formed by the NCP dyadic axes orientations, and the consequences of this effect are rather weak. The main manifestation of the chiral twisting

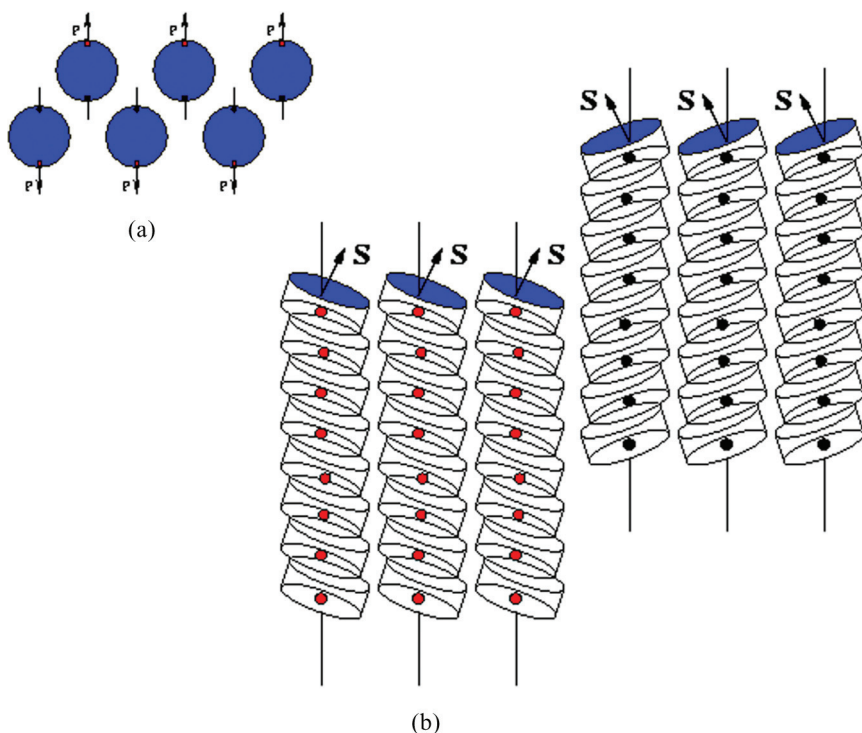


FIGURE 8 Anticlinic tilting of the NCP particles in the two different layers of each lamella in the bilayer lamellar phase. a – antiparallel orientation of the average polarization vectors P of the columns; b – anticlinic tilting of the S-axes in the two layers of the same lamella.

in the bilayer phase is a weak but visible at large distances periodic modulation of the axes of columns inside each layer [17]. It results from the competition of the chiral twisting of the NCP in each column and the high packing density of the columns in the layer. The detailed study of this effect together with the direct consequences of the main features of the proposed model on the structure of the 30 nm chromatin fiber will be reported in the forthcoming paper [28].

In summary, we have shown that one of the most important interactions which influences the structures of the condensed NCP mesophases is the polar interaction of the particles due to their shape and charge anisotropy. Polarity and chirality of the particles are the properties to take into account both for the considered simplified system and for the native chromatin fiber. The mechanism of the transitions in the condensed NCP mesophases is mainly related to the

simultaneous orientational ordering of the polar dyadic axes of individual NCP along the column and between the columns, and the correlated displacements of the columns. The periodic vector field of the dyadic axis orientations becomes antiparallel for the hexagonal-to-lamellar phase transition. Due to the chirality of the NCP particle the ordering of the polar dyadic axes induces the tilting of individual particles with respect to the column axes. In the bilayer lamellar phase the antiparallel orientation of the average polar axes in the upper and in the lower layer results in the anticlinic tilting of the particles in the columns belonging to the different layers of the same lamella.

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