BBA 71412

FURTHER ASPECTS OF THE Ca^{2+} -DEPENDENT POLYMORPHISM OF BOVINE HEART CARDIOLIPIN

B. DE KRUIJFF a, A.J. VERKLEIJ a, J. LEUNISSEN-BIJVELT b, C.J.A. VAN ECHTELD c, J. HILLE c and H. RIJNBOUT d

^a Institute of Molecular Biology, ^b Department of Molecular Cell Biology, ^c Department of Biochemistry and ^d Department of Physical Chemistry, State University of Utrecht, Padualaan 8, 3508 TB Utrecht (The Netherlands)

(Received July 21st, 1982)

Key words: Ca²⁺ dependence; Cardiolipin polymorphism; Cubic phase; ³¹P-NMR

The influence of cations on the structure of aqueous dispersions of the sodium salt of bovine heart cardiolipin was investigated using binding experiments, ³¹P-NMR, freeze-fracture electron microscopy, small angle X-ray diffraction and batch calorimetry techniques. In the 1-3 mM concentration range, Ca² induces a bilayer → hexagonal H_{II} transition for the lipid. During this transition there is a marked increase in Ca²⁺ binding from a maximum of 0.35 Ca/cardiolipin in the bilayer to 1.0 Ca/cardiolipin in the hexagonal H_{II} phase. Only when the cardiolipin liposomes are exposed to locally high Ca²⁺ concentrations is the bilayer → hexagonal H_{II} transition accompanied by the appearance of an intermediate 'isotropic' structure characterized by an isotropic 31 P-NMR signal and lipidic particles. In contrast, in mixed dioleoylphosphatidylcholine/cardiolipin (1:1) liposomes, Ca²⁺ concentrations as low as 100 μM will induce an 'isotropic' structure under conditions where no locally high Ca²⁺ concentrations can occur. In this system at higher Ca2+ concentrations (above 5 mM) the hexagonal H_{II} phase formation occurs. At least 80% of the phosphatidylcholine can be incorporated into this phase. The Ca²⁺-induced bilayer to hexagonal transition is an endothermic reaction with a ΔH of approx. 1.8 kcal/mol. Removal of Ca^{2+} from the hexagonally organized calcium-cardiolipin (1:1) complex by dialysis is an extremely slow process with a half-time in excess of 80 h. After 23 h of dialysis at a Ca/cardiolipin ratio of 0.86 an 'isotropic' structure is observed, characterized by an isotropic ³¹P-NMR signal and the presence of lipidic particles. After 70 h of dialysis (Ca/cardiolipin = 0.7) a new phase is observed. This phase which is optically isotropic and highly viscous separates from a lipid-free aqueous phase and contains 111 mM cardiolipin (15.5% by weight). The phospholipid molecules undergo rapid isotropic motion and the freeze-fracture morphology indicates the presence of a highly curved interconnected bilayer network separating various aqueous compartments. No defined X-ray diffraction bands can be observed for this phase. These characteristics are typical for cubic phases. This phase is metastable as mechanical agitation immediately induces the formation of large bilayer vesicles.

Introduction

Cardiolipin, present in eukaryotic cells, is in many respects a unique membrane lipid. Chemically, it can be defined as a 'double' phospholipid, containing four fatty acids and, at neutral pH, two charged phosphates. It is synthesized [1] and found

exclusively in the inner mitochondrial membrane, where it is the only major (20 mol% of the total lipids, thus 33% by weight) negatively charged phospholipid [2].

1

In general, cardiolipins isolated from mammalian sources are highly unsaturated and specifically enriched in linoleic acid [3]. Several studies have indicated that this lipid is involved in different inner mitochondrial membrane functions. The best documented is the absolute requirement of the activity of the cytochrome-c oxidase for cardiolipin [4,5]. Also, the activity of other mitochondrial enzymes is strongly affected by the presence of this lipid [6]. Furthermore, cardiolipin might be involved in different transport processes, in particular that of Ca²⁺ [7] and it plays an important structural role in this membrane [6]. These functional abilities must be a reflection of specific and unique structural features of the cardiolipin molecule.

One of the most remarkable properties of cardiolipin is the polymorphism of aqueous dispersions of this lipid. In excess buffer, the sodium salt of bovine heart cardiolipin is organized in extended bilayers [8-10]. Under similar conditions the Ca, Mg, Mn and Ba salts, dependent upon the temperature, can form the lamellar and hexagonal H_{II} phase [8,11,12]. At physiological temperatures the hexagonal H_{II} phase is preferred. This isothermal regulation of the macroscopic structure of cardiolipin by divalent cations and also by mitochondrial inner membrane proteins such as cytochrome c [13] forms the basis for the hypothesis [7] that non-bilayer lipid structures formed by cardiolipin account for the functional properties of this lipid. Conceptually, it is difficult to reconcile the presence of extended areas of hexagonal H_{II} phase with the barrier function of the membrane. Therefore, this hypothesis is strengthened by the observation that in mixtures of cardiolipin with bilayer forming lipids a new non-bilayer lipid structure, the 'lipidic particle' has been observed [14,15]. This structure has been interpreted by us as representing intrabilayer inverted micelles [14-17]. Although other models have been proposed [18-20] recent evidence [21] strongly supports the inverted micellar model. The presence of lipidic particles in cardiolipin containing model membranes markedly affects the dynamical properties of the system as evidenced by fast lipid flip-flop and divalent cation transport [22]. Furthermore, these structures are associated with vesicle fusion [16,23].

Despite the wealth of information on the polymorphism of bovine heart cardiolipin still several basic questions are unanswered. Such questions

include: at which Ca2+ concentration is the bilayer to hexagonal H_{II} transition induced? How much Ca²⁺ is bound to cardiolipin in the lamellar and hexagonal phase and what are the thermodynamics of the transition? Is the absolute Ca2+ concentration or the concentration difference across the bilayer determining the phase change, in particular in view of the mechanism of vesicle fusion and the occurrence of an 'isotropic' structure with associated lipidic particles upon the addition of limiting amounts of Ca²⁺ to cardiolipin liposomes [9]? Furthermore, is the bilayer → hexagonal transition reversible, are there structural intermediates and what are the kinetics of the reversed reaction? With these and related questions in mind we report in this paper ³¹P-NMR, freeze-fracture electron microscopy, small angle X-ray diffraction, batch calorimetry and ⁴⁵Ca²⁺ binding experiments on aqueous dispersions of bovine heart cardiolipin.

Materials and Methods

Lipids

The sodium salt of bovine heart cardiolipin was either purchased from Avanti (Birmingham, AL, U.S.A.) or isolated from bovine heart. In the latter case the tissue was extracted with chloroform and methanol followed by acetone and ethanol precipitations whereafter the barium salts of the negatively charged phospholipids were precipitated by the addition of barium acetate. The barium salt of cardiolipin was obtained in a pure form by quantitative high performance liquid chromatography (HPLC) on silica gel. The sodium salt was obtained by treatment with Na₂SO₄. Details of this isolation procedure will be published elsewhere. Both cardiolipin species were over 99% pure as determined by high performance thin-layer chromatography, had a cation composition of > 98% Na⁺ as determined by scanning transmission electron microscopy and gave identical results in our experiments. 1,2-Dioleoyl-sn-glycero-3-phosphocholine (dioleoylphosphatidylcholine) was synthesized as described before [24].

Chemicals

⁴⁵Ca²⁺ was obtained from the Radiochemical Centre (Amersham, U.K.) as the chloride in water

(2 mCi/ml) with a specific activity of 1.08m Ci/mg Ca. The Ca²⁺ ionophore A23187 was obtained from Boehringer (Mannheim, F.R.G.). Calcium and sodium chloride were ultrapure. All other chemicals were of analytical grade.

Preparation of model membranes

Dry phospholipid firms were prepared by evaporation from chloroform in a round-bottom flask of approx. 50 μ mol of lipid followed by storage under high vacuum. In some cases the chloroform solution of the lipids was directly evaporated in a 10 mm NMR tube under a stream of N₂ followed by storage overnight under high vacuum. The lipids were then dispersed by vortexing in 1.0-5.0 ml 100 mM NaCl, 10 mM Tris-HCl, pH 7.0 buffer in some cases containing 20% (v/v) 2 H₂O. When the Ca²⁺ ionophore A-23187 was used it was added as a 1 mg/ml solution in ethanol to the chloroform solution of the lipids (100 μ g ionophore per 50 μ mol of cardiolipin) prior to evaporation.

⁴⁵Ca²⁺ binding experiments

In order to determine both the phospholipid structure by ³¹P-NMR and the ⁴⁵Ca²⁺ binding to cardiolipin, three methods were used.

a. Addition method. In this method small aliquots of a concentrated CaCl2 solution are added to a concentrated lipid dispersion in the NMR tube. Typically, 50 µmol of cardiolipin were dispersed in 1.2 ml buffer containing 20% ²H₂O. To these liposomes 2 µl 45 CaCl₂ solution (4 µCi of ⁴⁵Ca) and aliquots of a 1 M CaCl₂ solution were added after which the 31P-NMR spectrum was recorded. After each CaCl, addition a 50-µl sample was taken which was centrifuged for 30 min at $100\,000 \times g$ in a Beckman airfuge. The amount of bound Ca was determined by measuring the ⁴⁵Ca content of the liposome-free supernatant. This method has the disadvantage that both the Ca2+/cardiolipin ratio and the total Ca2+ concentration are changing after each Ca2+ addition. Furthermore, with this method, liposomes are locally exposed to high Ca2+ concentrations.

b. Dialysis method. 50 μ mol of cardiolipin were dispersed in 5.0 ml buffer, whereafter the liposomes were pelleted by centrifugation at 4°C for 20 min at $16\,000 \times g$. The liposomal pellet was

resuspended in buffer and brought to a final volume of 0.8 ml. This suspension was transferred to a microcollodion bag (Sartorius, Göttingen, F.R.G.), which was fitted on to a 9 mm outer diameter glass tube. The collodion bag was then placed at room temperature in 500 ml 100 mM NaCl, 10 mM Tris-HCl, pH 7.0 stirred buffer containing 10% ²H₂O. 10 µl ⁴⁵CaCl₂ solution (20 μCi ⁴⁵Ca) was added to the dialysis buffer and the desired amount of CaCl₂ (from a 1 M stock solution). After 3 h of equilibration the bag was placed in a 10 mm outer diameter NMR tube containing 0.2 ml of the buffer in which the equilibration was carried out. After the ³¹P-NMR spectrum was recorded a 50-µl aliquot of the liposomal suspension was removed from the bag. 2 µl were used for lipid phosphate analysis [25], 5 μ l for LSC and the remainder of the liposomes was pelleted by centrifugation at room temperature for 20 min at $100\,000 \times g$ in a Beckman airfuge, 5 μ l of the lipid-free supernatant was collected for liquid scintillation counting (LSC). Subsequently the Ca²⁺ concentration in the 500 ml buffer was increased and the whole procedure was repeated until a. complete tritration curve was obtained. Control experiments revealed that no significant binding of ⁴⁵Ca²⁺ to the dialysis bag occurred and that the half-time of 45 Ca²⁺ equilibration across the bag was 50 min. Furthermore, no chemical degradation of cardiolipin could be detected at the end of the experiment. With this procedure it is possible to determine both the 31P-NMR spectrum of the cardiolipin liposomes and the 45 Ca2+ binding under conditions where there is always a molar excess of Ca²⁺ present. The dissociation constant K_{Ca} , defined as:

$$K_{\text{Ca}} = \frac{[\text{cardiolipin}]_{\text{free}} [\text{Ca}^{2+}]_{\text{free}}}{[\text{cardiolipin-Ca}]_{\text{complex}}}$$

was determined using a non-linear regression analysis of the experimental data points.

c. Immersion method. This method is similar to the dialysis method (b) except that the collodion bag containing the 50 μ mol of cardiolipin (made in the presence of the Ca²⁺ ionophore) was immersed in 100 μ l 1 M CaCl₂ (containing 4 μ Ci ⁴⁵Ca) present in a 10 mm NMR tube. The ³¹P-NMR spectrum and Ca²⁺ binding was determined

as a function of time. In this way a large molar excess of ca²⁺ is present in a small volume (like in the addition method (a)), but due to the rate limiting diffusion of Ca²⁺ through the semipermeable membrane of the bag, no Ca²⁺ concentration gradients are induced across the liposomal bilayers.

Reversibility of the Ca²⁺-cardiolipin complex formation

85 μ mol of cardiolipin and the Ca²⁺ ionophore were dispersed in 0.6 ml buffer. The liposomes were transferred to a microcollodion bag connected to a 9 mm tube. $100 \mu l$ 1 M CaCl₂ and 2 μl (4 μ Ci) ⁴⁵CaCl₂ was added. The bag was placed in a 10 mm NMR tube and the ³¹P-NMR spectrum was recorded. Subsequently the bag was placed in 500 ml stirred buffer at room temperature whereafter as a function of time the ⁴⁵Ca²⁺ concentration in the dialysate and the ³¹P-NMR spectrum of the cardiolipin dispersion were determined.

Techniques

36.4 MHz proton decoupled (input power 18 watt) ³¹P-NMR spectra of aqueous dispersions were recorded at 30°C as described before [26]. Signal intensities of the various spectral components were obtained by computer subtraction methods using reference spectra consisting of only one spectral component. The estimated error in the signal intensities is 10%. For freeze-fracturing the samples were quenched by jet freezing [27] without the use of cryoprotectants and subsequently worked up in a Balzer freeze-etch machine according to standard procedures. Small angle Xray diffraction was carried out at room temperature using a Kratky camera with a 10 × 0.2 mm Cu-K α beam (40 kV, 23 mA) and exposure times of 1-3 h. The aqueous sample was mounted in a slit $(12 \times 2 \times 2 \text{ mm})$ in between two sheets of cellophane. Radioactivity was determined by LSC using standard techniques. The isothermal enthalpy of reaction between Ca²⁺ and cardiolipin was measured at 25.0 ± 0.1 °C using an LKB 2107 batch microcalorimeter equipped with gold cells. In each experiment 4.0 ml of 3 mM cardiolipin in buffer was mixed with 2.0 ml of buffer containing increasing amount of Ca2+. In the reference cell 4.0 ml of buffer and 2.0 ml of Ca²⁺-containing

buffer were added. The heats of reaction were corrected for frictional heats. For each experiment two friction runs and usually one electrical calibration were done. Electrical calibration was adjusted to produce a heat effect within $\pm 20\%$ of that observed for the reaction mixture. The electrical calibration heaters were checked by measuring the heat of dilution of sucrose [28].

Results

Liposomes prepared from the sodium salt of cardiolipin are organized in extended bilayers as evidenced by the characteristic asymmetrical ³¹P-NMR lineshape with a low-field shoulder and a high-field peak [29] separated by approx. 32 ppm (Fig. 1A). As noted before [12] a small (approx. 5%) isotropic component is present in the spectrum which most likely originates from some smaller vesicles present in the preparation as can be detected by freeze-fracturing. Addition of aliquots of a concentrated CaCl₂ solution (cf. addition method) induces the formation of an iso-

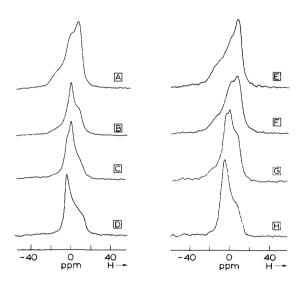


Fig. 1. 36.4 MHz ³¹P-NMR spectra of cardiolipin liposomes before (A, E) and after the addition of Ca^{2+} via the addition (B, C, D) or the dialysis method (F, G, H). Spectra B, C, D were obtained from liposomes (50 μ mol cardiolipin in 1.2 ml buffer) to which was added 15, 25 and 35 μ l 1 M CaCl₂, respectively. The free Ca^{2+} concentrations were determined to be 0.80, 1.49 and 5.3 mM, respectively. In spectra F, G, H the liposomes were dialyzed against 0.8, 1.5 and 3.0 mM Ca^{2+} , respectively.

tropic spectral component (Figs. 1B and 1C). In the presence of a molar excess of Ca²⁺ the lineshape typical of lipids in the hexagonal H_{II} phase [29] with a reversed asymmetry and reduced width is observed (Fig. 1D). These and additional data are plotted in a quantitative manner in Fig. 2. In the insert the macroscopic structure of cardiolipin is plotted versus (Ca²⁺/cardiolipin)_{total}. The intermediate structure(s) giving rise to an isotropic signal are formed at the lowest amount of Ca²⁺ added. No further change in the spectrum is observed above a (Ca2+/cardiolipin)total of approximately 1. Due to Ca²⁺ binding to cardiolipin in this experiment we are simultaneously changing (Ca/cardiolipin)_{total} and [Ca²⁺]_{free}. Since only the free Ca2+ concentration will determine the Ca2+ binding to and the structure of cardiolipin, the structural data are plotted in Fig. 2 as a function of $[Ca^{2+}]_{free}$. In the 1-5 mM $[Ca^{2+}]_{free}$ range the hexagonal phase is formed. The 'isotropic structure' already is found at a free Ca2+ concentration in excess of 200 µM. Furthermore, Fig. 2 shows that increasingly more Ca2+ is bound to cardiolipin until a limiting 1:1 binding is observed in the hexagonal H_{II} phase. Freeze-fracturing of a sample in which $(Ca^{2+}/cardiolipin)_{total} = 0.5$ revealed the presence of bilayers with associated lipidic particles and areas of hexagonal H_{II} phase (Figs. 3A and 3B). At (Ca²⁺/cardiolipin)_{total} > 1 only the pure H_{II} was observed. Inclusion of 100 µg of the Ca²⁺-ionophore A 23187 in the liposomes did not significantly affect the ³¹P-NMR and Ca²⁺binding characteristics of the system under the experimental conditions described in the legends of Figs. 1 and 2.

Since in the addition method the induction of

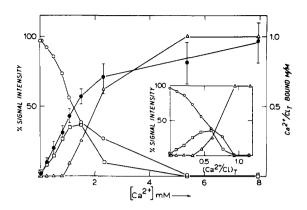


Fig. 2. Ca^{2+} binding (ullet—ullet) to and structure of cardiolipin liposomes: addition method. The amount of signal originating from lipid organized in extended bilayers (\bigcirc — \bigcirc), isotropic structures (\square — \square) or hexagonal H_{II} phase (\triangle — \triangle) were determined from 36.4 MHz 31 P-NMR spectra of the liposomes after the addition of aliquots of a 1 M CaCl_2 solution and are plotted as a function of the free Ca^{2+} concentration. The insert shows the structural data plotted versus the ratio of total amount of Ca^{2+} and cardiolipin present in the sample. The error bars represent the S.D. in the amount of Ca^{2+} bound.

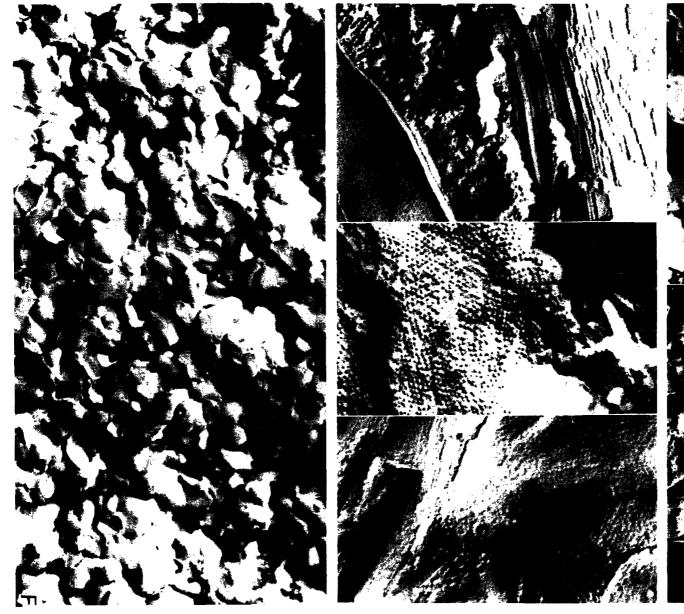
the 'isotropic' structure with associated lipidic particles might be the result of an exposure of cardiolipin to local high Ca²⁺ concentrations, the experiment was repeated with cardiolipin liposomes containing the Ca²⁺ ionophore, using the dialysis method. In this method the liposomes are incubated in a controlled way in a large volume of Ca²⁺ containing buffer, such that the liposomes are never exposed to local high Ca²⁺ concentrations and the (Ca/cardiolipin)_{total} ratio always exceeds 1. Figs. 1 E-H and 4 show that upon increasing the Ca²⁺ concentration from 1 to 3 mM a transition from a lamellar to a hexagonal H_{II}

TABLE I

CALORIMETRY OF THE Ca-CARDIOLIPIN COMPLEX FORMATION

Heat and enthalpy of reaction are corrected for the heat of dilution of Ca²⁺ caused by Ca²⁺ binding to cardiolipin. Fo details see text.

Ca ²⁺ added (mM)	Ca ²⁺ total (mM)	(Ca/cardiolipin) _{total}	Heat of reaction (mcal)	Enthalpy of reaction (kcal/mol)
3	1	0.5	2.8	0.2
15	5	2.5	15.5	1.3
100	33.3	16.7	21.4	1.8





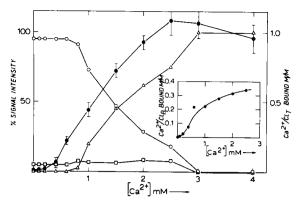


Fig. $4.\text{Ca}^{2+}$ binding (ullet—ullet) to and structure of cardiolipin liposomes: dialysis method. The amount of signal originating from lipids organized in extended bilayers (\bigcirc — \bigcirc), isotropic structures (\square — \square) or hexagonal H_{II} phase (\triangle — \triangle) were determined from 36.4 MHz ³¹P-NMR spectra of the liposomes and are plotted versus the Ca^{2+} concentration of the dialysis medium. The insert shows the Ca^{2+} binding to cardiolipin in the lamellar phase (CL_{B}) versus the Ca^{2+} concentration of the dialysis medium. The data in the 1 to 2.5 mM Ca^{2+} range are corrected for the amount of Ca^{2+} bound to that part of the structures organized in the hexagonal H_{11} phase assuming a 1:1 binding. The error bars represent the S.D. in the amount of Ca^{2+} bound.

structure is observed without the formation of a significant amount of the 'isotropic' structure. In the hexagonal $H_{\rm II}$ phase Ca is stoichiometrically bound to cardiolipin (Fig. 4). In the insert of this figure the ${\rm Ca^{2+}}$ binding to cardiolipin in the lamellar phase is shown to reach a limiting value of 0.35 Ca/cardiolipin at a free Ca²⁺ concentration of 2.5 mM, the highest concentration at which lamellar phase can still be detected. From such experimental data intrinsic Ca-cardiolipin binding constants are difficult to derive due to the complexity of non-specific ion-absorption processes [30]. Using a simple binding model and curve fitting procedures a dissociation constant $K_{\rm ca}$ of 1.5 ± 0.5 mM could be derived from these data.

When Ca²⁺ was added to the cardiolipin liposomes via the immersion method very similar results were obtained (data not shown), in that a time-dependent change from a bilayer to a hexago-

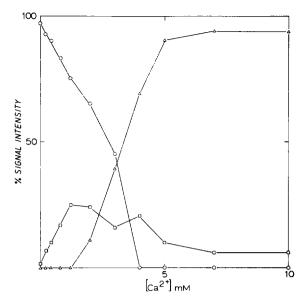


Fig. 5. Effect of Ca^{2+} on the structure of dioleoylphosphatidylcholine/cardiolipin (1:1) liposomes: dialysis method. The amount of signal originating from lipids in extended bilayers $(\bigcirc ---- \bigcirc)$, isotropic structures $(\square ----- \square)$ or hexagonal H_{II} phase $(\triangle ----- \triangle)$ were determined from 36.4 MHz ³¹P-NMR spectra of the liposomes (50 μ mol cardiolipin, 50 μ mol dioleoylphosphatidylcholine, 100 μ g A23187 in 1.0 ml buffer) and are plotted versus The Ca^{2+} concentration of the dialysis medium.

nal H_{II} phase was observed without the occurrence of the intermediate 'isotropic' structure.

Since Ca²⁺ addition from a concentrated solution to mixed phosphatidylcholine-cardiolipin systems also results in the appearance of an 'isotropic' structure in association with lipidic particles [15], we thought it of interest to see whether similar structures would be observed when the Ca²⁺ was added via the dialysis method. As shown in Fig. 5 for dioleoylphosphatidylcholine/cardiolipin (1:1) liposomes, in contrast to the pure cardiolipin system Ca²⁺ concentrations in excess of 100 µM already induces an isotropic ³¹P-NMR signal. The 'isotropic' structure occurs as intermediate between the lamellar and the hexagonal H_{II} phase. This latter phase is formed in the 1-5 mM Ca²⁺ range. Since more than 90% of the total

Fig. 3. Freeze-fracture electron microscopy of various Ca-cardiolipin systems. Cardiolipin liposomes (50 μ mol cardiolipin in 1.2 ml buffer) after the addition of 25 μ l 1 M CaCl₂ (A, B). Ca-cardiolipin (1:1) complex after dialysis against Ca²⁺-free buffer for 23 (C, D, E) and 70 h (F). Final magnification 80000×.

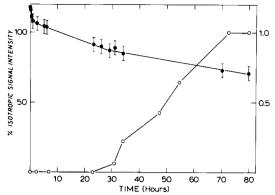


Fig. 6. Ca²⁺ binding to (•—•) and structure of (O—•), % isotropic signal) the Ca-cardiolipin complex as a function of the dialysis time against excess buffer. The error bars represent the S.D. in the amount of Ca²⁺ bound to the cardiolipin liposomes.

lipids are organized in the hexagonal $H_{\rm II}$ phase above this ${\rm Ca^{2}}^+$ concentration, it can be calculated that at least 80% of the bilayer phase preferring dioleoylphosphatidylcholine is incorporated into the hexagonal $H_{\rm II}$ phase.

The heat of reaction between cardiolipin and Ca^{2+} was measured by batch calorimetry using an experimental procedure which is comparable to the addition method except that lower cardiolipin and Ca^{2+} concentrations are used. In the presence of a limiting amount of Ca^{2+} which in the addition method induces a bilayer \rightarrow isotropic transition of 30% of the lipids and a bilayer \rightarrow hexagonal

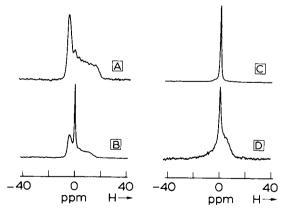


Fig. 7. Effect of Ca²⁺ removal from the Ca-cardiolipin (1:1) complex by dialysis on the 36.4 MHz ³¹P-NMR spectra of cardiolipin. (A) Before dialysis, (B) and (C) after 23 and 70 h of dialysis, respectively. (D) As (C) after 2 min vortexing.

 H_{II} transition of 10% of the lipids (Fig. 2), an endothermic reaction with a ΔH of 0.2 kcal/mol was observed (Table I). In the presence of a molar excess of Ca^{2+} the endothermic reaction has a heat content of 1.3 kcal/mol which further increased to 1.8 kcal/mol in the presence of a 16.7-fold molar excess of Ca^{2+} .

Dilution of the Ca-cardiolipin (1:1)-salt in a large excess of Ca2+-free buffer did not affect the ³¹P-NMR characteristics of the system for several hours. To get a more quantitative measure on the kinetics of the dissociation of the Ca-cardiolipin complex we dialyzed the salt against buffer and monitored both structure and Ca-binding as a function of time (Figs. 6 and 7). After an initial fast release of excess unbound Ca2+ the bound Ca2+ is exceedingly slowly released from the complex (Fig. 6). The half-time of the dissociation is in excess of 80 h. After approx. 23 h when still 86% of the Ca2+ is present a change in the 31P-NMR from hexagonal H_{II} - 'isotropic' occurs (Fig. 7). In the next 50 h when an additional 12% of Ca²⁺ is removed (Fig. 6), only a very sharp (linewidth at half-weight 13 Hz) ³¹P-NMR signal is observed (Figs. 6, 7). At this time the visual appearance of the sample has changed dramatically from a milky dispersion of lipid aggregates to a two-phase sys-

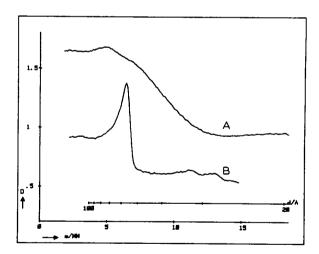


Fig. 8. Densitometer tracings of small angle X-ray diffraction patterns of the Ca-cardiolipin (1:1) complex before (B) and after (A) 70 h of dialysis against Ca^{2+} -free buffer. The intensity of the diffraction D (in arbitrary units) is plotted both versus the distance (in mm) on the film between the diffracted and the non-diffracted beam and the corresponding lattice value d (in Å).

tem consisting of a lipid-free aqueous supernatant and an optically clear, highly viscous lower phase. The isotropic phase contained 111 mM cardiolipin (15.5% by weight) which accounted for all the cardiolipin initially present. Freeze-fracturing revealed that after 23 h of dialysis the sample consisted of hexagonal H_{II} phase and lipidic particles containing bilayers (Figs. 3C, D, E). The optically clear isotropic phase consisted of an interwoven network of lipid and water fracture planes (Fig. 3F). The lipid-fracture planes appear to be interconnected with sizes of approx. 1000-2000 Å. Small angle X-ray diffraction measurements of the Ca-cardiolipin (1:1) complex revealed diffraction bands at d values of 57, 33 and 28 Å (Fig. 8), Such a diffraction pattern with a $1:1/\sqrt{3}:\frac{1}{2}$ relationship between the first and higher order diffraction bands, is characteristic for a hexagonally organized lipid phase. The distance between the tubes is 57 A. In the optically clear isotropic phase no defined diffraction bands can be observed (Fig. 8). Instead, a broad (ranging from d = 30-90 Å) diffuse band, typical [31] of an X-ray scattering profile for a liquid-like concentrated 'solution' of small aggregates is observed. Another feature of this phase is its mechanical instability. Brief vortexing results in the formation of a milky turbid dispersion and a change in the ³¹P-NMR spectrum (Fig. 6) indicating the formation of bilayer structures. This was further evidenced by freeze-fracturing, which revealed the presence of many bilayer vesicles of variable size in the preparation.

Discussion

An aqueous dispersion of the sodium salt of bovine heart cardiolipin undergoes a bilayer \rightarrow hexagonal H_{II} phase transition when the Ca^{2+} concentration is increased through the 1-3 mM range, both when Ca^{2+} is added from a concentrated solution as well as when the liposomes are dialyzed against excess Ca^{2+} containing buffer. In the hexagonal H_{II} phase Ca^{2+} is stoichiometrically bound to cardiolipin. From the cation specificity of the induction of the phase change [8,11,12] as well as from monolayer data [32] a binding of Ca^{2+} to the two phosphates of one cardiolipin molecule seems most likely. From space filling models of cardiolipin it can be estimated

that the two charged phosphates are separated by approx. 9 Å assuming an extended conformation of the connecting glycerol molecule. Such a configuration seems most likely in view of both charge repulsion arguments as well as from the similarity in the ³¹P-NMR residual effective chemical shift anisotropy of the phosphates in cardiolipin and other phospholipids such as phosphatidylcholine [9]. For these lipids an extended conformation of the base part of the polar headgroup oriented parallel to the plane of the membrane has been documented (for review see Ref. 32).

Since in the hexagonal H_{II} phase of the Cacardiolipin (1:1) complex the headgroup appears to be dehydrated [8] and the diameter of the dehydrated Ca²⁺ ion is 1.98 Å it is most likely that the two phosphates are pulled together over a considerable distance thereby reducing the headgroup's size. Molecular models reveal that this can only be accomplished when the connecting glycerol is bended. Assuming a similar configuration of the phosphatidic acid moieties of cardiolipin and other phospholipids such that the glycerol is perpendicular to the plane of the bilayer and the acyl chain at the 2-position is bent at C₂ [34], this subsequently will have to result in an increased hydrocarbon chain area. Analogous with previous suggestions [26] we consider the change in molecular shape as the main driving force behind the bilayer -> hexagonal H_{II} transition.

The heat of the Ca-cardiolipin complex formation levels off with higher Ca2+ concentrations at approximately 1.8 kcal/mol. The bilayer → hexagonal H_{II} transition thus is an endothermic reaction with an enthalpy ΔH of approx. 1.8 kcal/mol. For thermally induced bilayer → hexagonal H_{II} phase transitions in aqueous dispersions of phosphatidylethanolamine similar low energy endothermic transitions have been observed using differential scanning calorimetry [26]. The low heat content of these transitions must reflect the fluid character of both the bilayer and hexagonal H_{II} phases. The exact origin of the slight increase in ΔH at high Ca^{2+} concentrations is not understood and will be studied in more detail using flow calorimetry.

Prior to the induction of the hexagonal $H_{\rm II}$ phase ${\rm Ca^{2}}^+$ binding to cardiolipin in the lamellar phase occurs. Although the present data do not

allow for a discrimination between 'adsorbed' and bound Ca2+ it is clear that maximally 0.35 Ca2+ per cardiolipin can be bound in the lamellar phase at a free Ca²⁺ concentration of 2.5 mM. Thus at the bilayer → hexagonal transition a large increase in Ca²⁺ binding occurs. It is of interest to compare these data with those obtained for bovine brain phosphatidylserine. It is also observed with this negatively charged phospholipid that above a threshold concentration of 1-2 mM Ca²⁺ an 1:2 Ca²⁺ phosphatidylserine complex is formed resulting in a large structural change [35,36]. However, the organization of the Ca-phosphatidylserine complex is markedly different from that of the Ca-cardiolipin complex, in that the phosphatidylserine is organized in a closely packed cochleated lamellar arrangement in which the acyl chains are in the gel state [35,36]. The Ca-phosphatidylserine complex formation is an exothermic reaction with a ΔH of -4.7 ± 0.5 kcal/mol [37,38] l in agreement with a chain crystallization process. Thus, despite the similarities in effect of Ca²⁺ on phosphatidylserine and cardiolipin, the structural properties of the resulting complexes are very specific and emphasize the importance of polar headgroup Ca2+ interactions for membrane struc-

The formation of the intermediate 'isotropic' structure characterized by an isotropic ³¹P-NMR signal with associated lipidic particles was only observed when intermediate amounts of Ca2+ were added as aliquots from a concentrated solution to the cardiolipin liposomes. The formation of this structure must be the result of the transient existence of local high Ca²⁺ concentrations as inclusion of the Ca²⁺ ionophore A23187 in the liposomes did not prevent its formation. Ca²⁺ introduction via dialysis methods only caused a bilayer → hexagonal H_{II} transition. Our interpretation is that due to locally high Ca²⁺ concentrations, Cacardiolipin (1:1) complexes are formed locally in the outer monolayer of the outer bilayer of the liposomes. In this complex the molecules favour hexagonal H_{II} phase formation. However, the bilayer → hexagonal H_{II} transition must be a highly cooperative event and can occur only when extended areas of molecules would like to undergo the same phase change. Instead, rapid fusion events between destabilized areas of the Ca-cardiolipin

(1:1) complex in one or between different cardiolipin liposomes occur resulting in the formation of inverted micelles at the sites of fusion. In the dialysis experiments the gradual increase in Ca²⁺ concentration leads to increased Ca²⁺ binding and a gradual decrease in surface charge density inducing a close approximation of extended bilayer surfaces allowing a cooperative bilayer → hexagonal H_{II} transition to occur.

In mixed dioleoylphosphatidylcholine/ cardiolipin bilayers addition of Ca2+ from a concentrated solution [15] or via the dialysis method (this study) even at Ca2+ concentrations as low as 0.2 mM induces the formation of the 'isotropic' structure. In agreement with observations made in other lipid mixtures [15] lipidic particle formation must be the result of the coexistence of both bilayer and hexagonal H_{II} phase preferring lipids. It could be suggested that the presence of phosphatidylcholine interferes with the formation of extended areas of the Ca-cardiolipin (1:1) complex thereby inhibiting hexagonal H_{II} phase formation. However, it should be noted that at higher Ca2+ concentrations substantial amounts (up to 80%) of dioleoylphosphatidylcholine can be incorporated into the hexagonal H_{II} phase of cardiolipin (Ref. 11, and this study). For a better understanding of the phase changes in this system the kinetics of the various processes will have to be investigated.

The bilayer → hexagonal H_{II} phase transition can be readily reversed by dialysis of the Cacardiolipin (1:1) complex against EDTA containing buffers resulting in the formation of large bilayer vesicles [9,10]. Our experiments show that in the absence of EDTA not only the rate of this process is extremely slow but that also several structural changes occur. Below a critical amount of Ca²⁺ bound (Ca/cardiolipin = 0.86) a structure is formed, characterized by an isotropic ³¹P-NMR signal and lipidic particles thus resembling the structure induced by adding limiting amounts of Ca²⁺ to the cardiolipin liposomes. Upon further removal of Ca²⁺ (Ca/cardiolipin = 0.7) another structural change occurs, in that an optically clear, highly viscous cardiolipin-rich phase separates out of solution. The cardiolipin molecules undergo rapid isotropic motion in this phase. These characteristics are typical for cubic phases [39]. Since

this phase does not give a discrete X-ray diffraction pattern as often [39] encountered with cubic phases, the exact structure is unknown. Our freeze-fracturing data would be consistent with a cubic phase related to the 'Schwarz's primitive cubic minimal surface' structure in which the lipids are organized in a continuous highly curved bilayer which separates two independent three-dimensional systems of aqueous channels (see for instance Fig. 3 in Ref. 40). From the linewidth of the ³¹P-NMR signal it can be estimated [41] that the average radius of bilayer curvature is 180 Å assuming similar lateral diffusion rates of cardiolipin and egg phosphatidylcholine. The curbic phase is metastable as mechanical agitation immediately results in the formation of large bilayer vesicles. The mechanism(s) of the phase changes observed upon the removal of Ca²⁺ from cardiolipin are obscure at the moment. Since thermally induced bilayer → hexagonal H_{II} transitions in general are fully reversible [29] the complex phase behaviour of this system must be the result of the way the hexagonal H_{II} triggering agent Ca²⁺ is released from the structure. As the aqueous channels in the hexagonal H_{II} phases appear to be open to the surrounding aqueous phase as evidenced by the observation that paramagnetic ions broaden the entire ³¹P-NMR signal of hexagonally oriented phosphatidylethanolamines (van Echteld, C.J.A., unpublished observations) it can be expected that Ca²⁺ is relased from the ends of the tubes. At these sites cardiolipin would like to adopt a bilayer configuration but this is inhibited because these molecules are still connected to the remainder of the hexagonal H_{II} phase. In these transitional regions apparently lipidic particles are formed. After a possible reorganization the lipidic particles dissociate and the cubic phase results.

The relationship between the lipidic particles and cubic phases is of particular interest since both structures have now been observed in different mixtures of hydrated membrane lipids and both structures have been reported as intermediates between lamellar and hexagonal H_{II} phases. For instance, cubic phases have been reported for aqueous dispersions of glycolipids from *Acholeplasma laidlawii* [42], whereas lipidic particles have been observed in many other lipid systems [29]. The present study demonstrates that

one type of lipid can adopt both structures. The exact interrelationship between lipidic particles and cubic phases as well as the biological significance of this latter phase can only be speculated upon. However, it is noteworthy that the morphology of the prolamellar body [43] which is involved in the formation of thylakoid membranes of chloroplasts and which contains substantial amounts of the hexagonal H_{II} phase preferring monogalactosyl diacylglycerol [21] greatly resembles the structure of some of the cubic phases observed in model membranes [40].

Acknowledgements

Dr. M.R. Egmond is thanked for the calculation of the dissociation constants and Dr. T.F. Taraschi for correcting the English. The excellent technical assistance of W.S.M. Geurts van Kessel and Ms. M. Tieman in the synthesis and isolation of the lipids is greatfully acknowledged.

References

- 1 Hostetler, K.Y., Van den Bosch, H. and Van Deenen, L.L.M. (1971) Biochim. Biophys. Acta 239, 113-119
- 2 Krebs, I.I.R., Hansen, H. and Carafoli, E. (1979) J. Biol. Chem. 254, 5308-5316
- 3 Gray, G.M. and MacFarlane, M.G. (1958) Biochem. J. 70, 409-425
- 4 Fry, M. and Green, D.E. (1980) Biochim. Biophys. Res. Commun. 93, 1238-1246
- 5 Vik, S.B., Georgevich, G. and Capaldi, R.A. (1981) Proc. Natl. Acad. Sci. U.S.A. 78, 1456-1460
- 6 Ioannou, P.V. and Golding, B.T. (1979) Prog. Lipid Res. 17, 279-318
- 7 De Kruijff, B., Verkleij, A.J., Van Echteld, C.J.A., Gerritsen, W.J., Noordam, P.C., Mombers, C., Rietveld, A., De Gier, J., Cullis, P.R., Hope, M.J. and Nayar, R. (1981) in International Cell Biology 1980-1981 (Schweiger, H.G., ed.), Springer Verlag, Berlin
- 8 Rand, R.P. and Sengupta, S. (1972) Biochim. Biophys. Acta 255, 484-492
- 9 Cullis, P.R., Verkleij, A.J. and Ververgaert, P.H.J.T. (1978) Biochim. Biophys. Acta 513, 11-20
- 10 Vail, W.J. and Stollery, J.G. (1979) Biochim. Biophys. Acta 551, 74-85
- 11 Van Venetië, R. and Verkleij, A.J. (1981) Biochim. Biophys. Acta 645, 262-269
- 12 Vasilenko, I., De Kruijff, B. and Verkleij, A.J. (1982) Biochim. Biophys. Acta 684, 282-286
- 13 De Kruijff, B. and Cullis, P.R. (1980) Biochim. Biophys. Acta 602, 477–490
- 14 Verkleij, A.J., Mombers, C., Leunissen-Bijvelt, J. and

- Ververgaert, P.H.J.T. (1979) Nature 279, 162-163
- 15 De Kruijff, B., Verkleij, A.J., Van Echteld, C.J.A., Gerritsen, W.J., Mombers, C., Noordam, P.C. and De Gier, J. (1979) Biochim. Biophys. Acta 555, 200-209
- 16 Verkleij, A.J., Van Echteld, C.J.A., Gerritsen, W.J., Cullis, P.R. and De Kruijff, B. (1980) Biochim. Biophys. Acta 600, 620-624
- 17 Verkleij, A.J. and De Kruijff, B. (1981) Nature 290, 427-428
- 18 Hui, S.W. and Stewart, T.P. (1981) Nature 290, 427
- 19 Miller, R.O. (1980) Nature 287, 166-167
- 20 Rand, R.P., Reese, T.S. and Miller, R.G. (1981) Nature 293, 237-238
- 21 Sen, A., Williams, W.P., Brain, A.P.R., Dickens, M.J. and Quinn, P.J. (1981) Nature 293, 488-489
- 22 Gerritsen, W.J., De Kruijff, B., Verkleij, A.J., De Gier, J. and Van Deenen, L.L.M. (1980) Biochim. Biophys. Acta 598, 554-560
- 23 Verkleij, A.J., Mombers, C., Gerritsen, W.J., Leunissen-Bijvelt, J. and Cullis, P.R. (1979) Biochim. Biophys. Acta 555, 358-361
- 24 Van Deenen, L.L.M. and De Haas, G.H. (1964) Adv. Lipid Res. 2, 168-363
- 25 Fiske, C.H. and SubbaRow, J. (1925) J. Biol. Chem. 66, 375-379
- 26 Cullis, P.R. and De Kruijff, B. (1978) Biochim. Biophys. Acta 513, 31-42.
- 27 Müller, M., Meister, N. and Moor, H. (1980) Mikroskopie 36, 129-140

- 28 Gucker, F.T., Pickard, H.B. and Planck, R.W. (1939) J. Am. Chem. Soc. 61, 459-470
- 29 Cullis, P.R. and De Kruijff, B. (1979) Biochim. Biophys. Acta 559, 399-420
- 30 Nir, S., Newton, C. and Papahadjopoulos, D. (1978) Bioelectrochem. Bioenerg. 5, 116-133
- 31 Guinier, A. and Fournet, C. (1955) Small-angle scattering of X-ray, John Wiley and Sons, New York
- 32 Shaw, D.O. and Schulman, J.H. (1965) J. Lipid Res. 6, 341-349
- 33 Hauser, H., Pascher, I., Pearson, R.H. and Sundell, S. (1981) Biochim. Biophys. Acta 650, 21-51
- 34 Seelig, J. and Seelig, A. (1980) Q. Rev. Biophys. 13, 19-61
- 35 Papahadjopoulos, D., Vail, W.J., Jacobson, K. and Poste, G. (1975) Biochim. Biophys. Acta 394, 483-491
- 36 Newton, C., Pangborn, W., Nir, S. and Papahadjopoulos, D. (1978) Biochim. Biophys. Acta 506, 281-287
- 37 Portis, A., Newton, C., Pangborn, W. and Papahadjopoulos, D. (1979) Biochemistry 18, 780-790
- 38 Rehfeld, S.J., Düzgünes, N., Newton, C., Papahadjopoulos, D. and Eatough, D.J. (1981) FEBS Lett. 123, 249-251
- 39 Fontell, K. (1981) Mol. Cryst. Liq. Cryst. 63, 59-82
- 40 Larsson, K., Fontell, K. and Krog, N. (1980) Chem. Phys. Lipids 27, 321–328
- 41 Cullis, P.R. (1976) FEBS Lett. 70, 223-228
- 42 Wieslander, A., Rilfors, L., Johansson, L.B. and Lindblom, G. (1981) Biochemistry 20, 730-735
- 43 Simpson, D.J. (1978) Carlsberg Res. Commun. 43, 145-170