

ORIENTATION OF GRAMICIDIN A TRANSMEMBRANE CHANNEL

Infrared Dichroism Study of Gramicidin in Vesicles

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ABSTRACT Polarized infrared spectroscopy has been used to investigate the orientation of gramicidin A incorporated in dimyristoylphosphatidylcholine liposomes. Dichroism measurements of the major lipid (C=O ester, PO_2^- , CH_2) and peptide (amide A, I, II) bands were performed on liposomes (with or without gramicidin) oriented by air-drying. The mean orientation of the lipid groups and of the π_{LD} helix chain in the gramicidin has been determined. It can be inferred from infrared frequencies of gramicidin that the dominant conformation of the peptide in liposomes cannot be identified to the antiparallel double-helical dimer found in organic solution. No shift in lipid frequencies was observed upon incorporation of gramicidin in the liposomes. However, a slight reorganization of the lipid hydrocarbon chains which become oriented more closely to the normal to the bilayer is evidenced by a change in the dichroism of the CH_2 vibrations. The infrared dichroism results of gramicidin imply a perpendicular orientation of the gramicidin transmembrane channel with the π_{LD} helix axis at $<15^\circ$ with respect to the normal to the bilayer.

INTRODUCTION

Gramicidin A is a linear polypeptide antibiotic consisting of 15 alternating L and D amino acids (1); in natural and artificial lipid bilayer membranes it forms ion conductive channels (2–4), each of which is composed of two molecules of gramicidin (3, 5–10). Several structural models have been proposed for the conformation of the dimer gramicidin transmembrane channel (7, 11, 12). Structure-function studies of gramicidin derivatives in lipid bilayers (7, 13–18) and more recently ^{13}C and ^{19}F NMR studies of gramicidin in phosphatidylcholine liposomes (19, 20) both argue that the major conformation of the gramicidin channel in lipid vesicles consists of two π_{LD} helices joined at their NH_2 terminals, as originally proposed by Urry et al. (7, 11).

Here, we report the first infrared (IR)¹ spectroscopic investigation of gramicidin A incorporated in dimyristoylphosphatidylcholine (DMPC) vesicles. Recently, polarized IR spectroscopy has been shown to be a useful technique for studying the orientation of intrinsic proteins in biological membranes (21–24). We have used it to obtain direct information on the molecular structure and on the orientation of gramicidin in DMPC vesicles. By measuring the IR dichroism of the amide and lipid absorption bands, we have estimated that the gramicidin transmembrane channel is

tilted at $<15^\circ$ from the normal to the bilayer plane. Our data also indicate that the lipid hydrocarbon chains become oriented more closely to the normal to the bilayer in the presence of gramicidin.

MATERIALS AND METHODS

Preparation and Orientation of Liposomes

DMPC and gramicidin A were purchased from Sigma Chemical Co. (St. Louis, MO) and used without further purification; they were dissolved in CHCl_3 at a molar ratio of 30 DMPC per gramicidin and evaporated to dryness by vacuum pumping at 30°C . The dry film was resuspended in 1.5 ml H_2O and incubated at 30°C for 30 min to hydrate the lipid. The sample was then sonicated for 10 min at 35°C . After sonication, the suspension was centrifuged at 2,000 g for 30 min. The lipid suspension (100 μl) was then applied to a CaF_2 disk. Stacking of the vesicles parallel to the disk plane was achieved by air-drying at room temperature (24).

Spectroscopic Measurements

IR spectra were recorded on a Perkin-Elmer 180 double beam spectrometer (Perkin-Elmer Corp., Norwalk, CT) equipped with a common beam Perkin-Elmer wire grid polarizer and linked to a Hewlett-Packard 9825 A computer (Hewlett-Packard Co., Palo Alto, CA). IR dichroism was measured with an angle of incidence of 60° . IR light was linearly polarized either perpendicular to the normal to the disk plane (to record A_\perp) or parallel to the plane of incidence (to record A_\parallel), as described earlier (24). When recording A_\perp , the transitions parallel to the disk surface will absorb strongly, while the transitions oriented along the normal will not absorb. A blank CaF_2 disk was mounted with an identical geometry in the reference beam.

¹Abbreviations used in this paper: DMPC, dimyristoylphosphatidylcholine, DPPC, dipalmitoylphosphatidylcholine; IR, infrared.

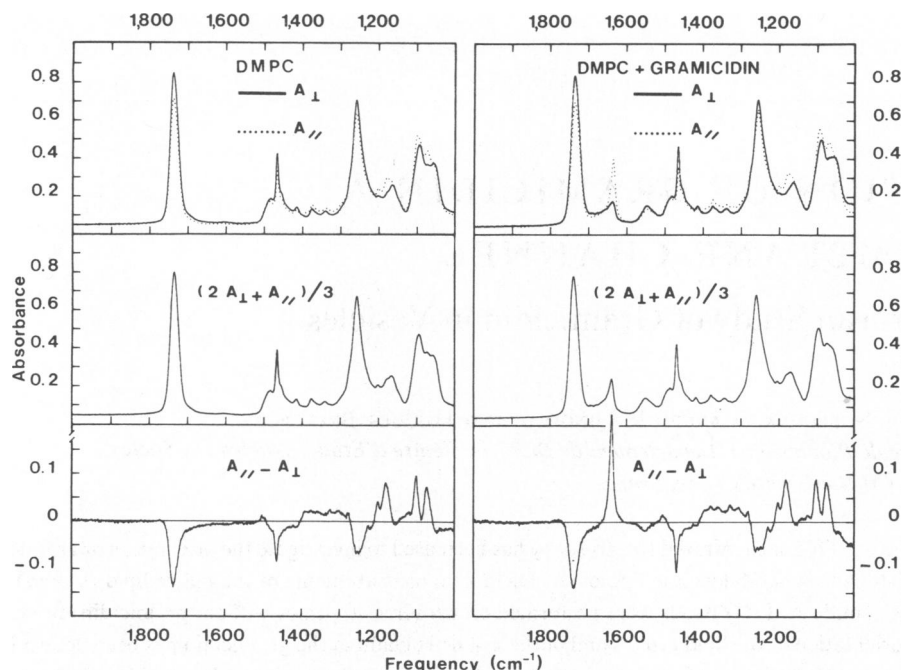


FIGURE 1 Polarized infrared spectra (A_{\parallel} , A_{\perp}), absorbance spectrum [$A = (2A_{\perp} + A_{\parallel})/3$] and difference spectrum ($A_{\parallel} - A_{\perp}$) of air-dried dimyristoylphosphatidylcholine (DMPC) liposomes from 2,000 to 1,000 cm^{-1} . The angle of incidence was 60° and the polarization direction was perpendicular (—) to the normal to the disk (A_{\perp}) or parallel (· · ·) to the plane of incidence (A_{\parallel}).

Data Analysis

The model used to estimate the orientation of the transition moments in our air-dried samples of liposomes (\pm gramicidin) has been described (24). Briefly, the distribution of a set of transition moments corresponding to a given absorption band can be characterized by an order parameter $S = (3 \cos^2 \phi - 1)/2$, where ϕ is the angle between the transition moment of the absorption peak and the normal to the disk. As described (24), S can be estimated from the band absorbance for parallel and perpendicular polarized light. The dichroic ratio $D = A_{\parallel}/A_{\perp}$ measured at a tilt angle i is related to S by applying the relation (25, 26):

$$D = \frac{3S}{1 - S} \frac{\sin^2 i}{n^2} + 1 \quad (1)$$

where n , the refractive index of the layer of air-dried lipids was taken as 1.55 (27). Then, from the measured dichroic ratio, we can calculate the mean orientation of the transition vector.

RESULTS AND DISCUSSION

Assignments of IR Absorption Bands

Fig. 1 displays typical IR spectra from 2,000 to 1,000 cm^{-1} for pure DMPC liposomes and DMPC liposomes containing gramicidin A in a 30/1 lipid-peptide mole ratio. Polarized IR spectra (A_{\parallel} and A_{\perp}), computed absorbance [$A = (2A_{\perp} + A_{\parallel})/3$] and difference spectra ($A_{\parallel} - A_{\perp}$) are shown in this figure. Many of the major peaks can be assigned to specific group vibrations, on the basis of previous IR studies of lipids and proteins (28–30). In particular, for pure DMPC, the ester carbonyl stretching vibration at 1,738 cm^{-1} , the CH_2 bending mode of hydrocarbon chains at 1,467 cm^{-1} , and the PO_2^- antisymmetric

stretching transition at 1,258 cm^{-1} are easily identified (Fig. 1). Other assignments are listed in Table I. Note that the frequencies of the PO_2^- symmetric and antisymmetric stretching vibrations depend on hydration and intermolecular interaction: a shift to lower frequencies is observed after hydrogen bonding with water molecules (31, 32). In our experimental conditions, the absorption bands due to the PO_2^- group were observed at 1,258 and 1,095 cm^{-1} , which is comparable to the frequencies reported by Fookson and Wallach (32) for various phosphatidylcholines in a dry state.

For the gramicidin peptide, Figs. 1 and 2 show the amide I ($\text{C}=\text{O}$ stretching), II ($\text{N}-\text{H}$ bending) and A ($\text{N}-\text{H}$ stretching) bands located at 1,638; 1,547; and 3,280 cm^{-1} ; respectively.

IR Dichroism of DMPC Liposomes

Several lipid bands exhibit strong dichroism with their absorption more intense in the A_{\perp} spectrum [for example, $\nu(\text{C}=\text{O})$ ester, $\delta(\text{CH}_2)$, $\nu_{\text{as}}(\text{PO}_2^-)$, $\nu_{\text{s}}(\text{CH}_2)$ and $\nu_{\text{as}}(\text{CH}_2)$] when the light is polarized perpendicular to the normal to the disk plane than in the A_{\parallel} spectrum (Fig. 1). An opposite situation is observed for other vibrations, such as the CH_2 wagging mode of the hydrocarbon chains at 1,202 cm^{-1} and $\nu_{\text{s}}(\text{PO}_2^-)$ at 1,095 cm^{-1} . Therefore, the observed dichroism for the polar head groups of DMPC qualitatively indicates that the mean orientation of the PO_2^- and $\text{C}=\text{O}$ stretching transition moments is rather parallel to the bilayer plane while the hydrocarbon chains are preferentially oriented along the normal to the bilayer plane.

TABLE I
ASSIGNMENT OF MAIN PEAKS IN IR SPECTRA OF AIR-DRIED DMPC LIPOSOMES WITH OR WITHOUT INCORPORATED GRAMICIDIN A

Frequency (cm^{-1})		Assignment	Dichroism
3,280	Amide A	N—H stretching of peptide groups	$A_{\parallel} > A_{\perp}$
2,955	$\nu_{\text{as}}(\text{CH}_3)$	Antisymmetric stretching of hydrocarbon methyl groups	$A_{\perp} > A_{\parallel}$
2,918	$\nu_{\text{as}}(\text{CH}_2)$	Antisymmetric stretching of hydrocarbon methylene groups	$A_{\perp} > A_{\parallel}$
2,849	$\nu_s(\text{CH}_2)$	Symmetric stretching of hydrocarbon methylene groups	$A_{\perp} > A_{\parallel}$
1,738	$\nu(\text{C}=\text{O})$	C=O stretching of fatty acid ester groups	$A_{\perp} > A_{\parallel}$
1,638	Amide I	C=O double bond stretching of peptide groups	$A_{\parallel} > A_{\perp}$
1,547	Amide II	N—H bending of peptide groups	$A_{\perp} > A_{\parallel}$
1,467	$\delta(\text{CH}_2)$	CH_2 bending of hydrocarbon chains	$A_{\perp} > A_{\parallel}$
1,455	$\delta(\text{CH}_2) + \delta(\text{CH}_3)$	CH_2 bending + CH_3 asymmetric deformation of hydrocarbon chains methyl groups	$A_{\perp} > A_{\parallel}$
1,415	$\delta(\text{CH}_2)$	CH_2 deformation	
1,377	$\delta_s(\text{CH}_3)$	CH_3 symmetric bending of hydrocarbon chain methyl groups	
1,258	$\nu_{\text{as}}(\text{PO}_2^-)$	Antisymmetric stretching of PO_2^- group	$A_{\perp} > A_{\parallel}$
1,202	$\gamma_w(\text{CH}_2)$	CH_2 wagging of hydrocarbon chains	$A_{\parallel} > A_{\perp}$
1,165–1,180	$\nu(\text{CO})$	C—O stretching	$A_{\parallel} > A_{\perp}$
1,095	$\nu_s(\text{PO}_2^-)$	Symmetric stretching of PO_2^- group	$A_{\parallel} > A_{\perp}$
1,075–1,060	$\nu(\text{CO})$	C—O stretching	$A_{\parallel} > A_{\perp}$

Measurements of dichroism were performed individually for six lipid vibrational modes: $\nu(\text{C}=\text{O})$ at $1,738 \text{ cm}^{-1}$; $\delta(\text{CH}_2)$ at $1,467 \text{ cm}^{-1}$; $\nu_{\text{as}}(\text{PO}_2^-)$ at $1,258 \text{ cm}^{-1}$; $\nu_w(\text{CH}_2)$ at $1,202 \text{ cm}^{-1}$; $\nu_{\text{as}}(\text{CH}_2)$ at $2,918 \text{ cm}^{-1}$; and $\nu_s(\text{CH}_2)$ at $2,849 \text{ cm}^{-1}$. Table II summarizes the IR dichroism of head groups and chain vibrations of DMPC in oriented vesicles.

First, it is shown that the transition moments of the C=O ester stretching and PO_2^- antisymmetric stretching bands are oriented nearly parallel to one another and deviate by 23° (C=O) and 27° (PO_2^-) with respect to the

bilayer plane. These values are in good agreement with those measured by Akutsu et al. (31) by IR dichroism on dry oriented multilayers: these authors calculated that the $\nu(\text{C}=\text{O})$ ester of dipalmitoylphosphatidylcholine (DPPC) deviates from the lipid film plane by 26° while the P—O bonds orient in the range $0\text{--}35^\circ$ from the film plane.

Second, analysis of the polarization of the CH_2 vibrations at $2,918$; $2,849$; $1,467$; and $1,202 \text{ cm}^{-1}$ allows calculation of the mean orientation direction of the hydrocarbon chains (perpendicular to the CH_2 plane). As shown in Table II, the hydrocarbon chains of DMPC are tilted from the bilayer normal by $\sim 20^\circ$, which is comparable to previous results on DPPC multilayers (19°). It must be

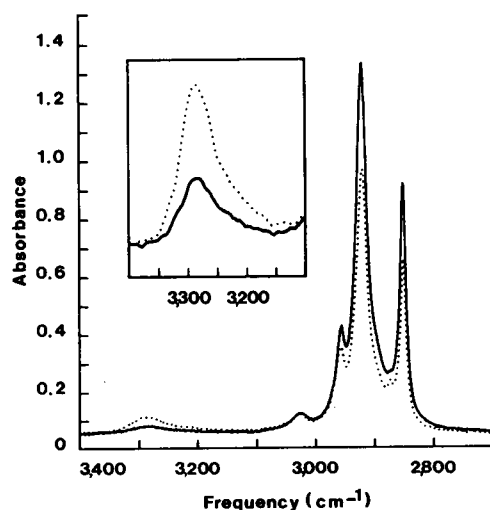


FIGURE 2 CH_2 and amide A region of air-dried DMPC liposomes with gramicidin. Inset: expansion 10 of amide A region. A_{\perp} (—); A_{\parallel} (· · ·).

TABLE II
INFLUENCE OF GRAMICIDIN A ON IR PARAMETERS OF AIR-DRIED DMPC LIPOSOMES

Assignment	DMPC		DMPC + Gramicidin A	
	D^*	ϕ	D^*	ϕ^\ddagger
$\nu(\text{C}=\text{O})$	0.80 ± 0.02	67°	0.83 ± 0.02	64°
$\nu_{\text{as}}(\text{PO}_2^-)$	0.85 ± 0.02	63°	0.85 ± 0.02	63°
$\delta(\text{CH}_2)$	0.78 ± 0.02	69°	0.74 ± 0.02	74°
$\gamma_w(\text{CH}_2)$	7 ± 1	17°	>15	$<12^\circ$
$\nu_{\text{as}}(\text{CH}_2)$	0.77 ± 0.02	70°	0.70 ± 0.02	82°
$\nu_s(\text{CH}_2)$	0.75 ± 0.02	72°	0.70 ± 0.02	82°

* D , dichroic ratio (average obtained from four different air-dried samples).

$\ddagger\phi$, angle between the transition moment of a given vibration and the normal to the disk plane.

noticed that a small (or even negligible) chain tilt was also detected in oriented multilayers of other lipids by using different techniques such as IR (33), attenuated total reflection IR (27), spin labeling (34), neutron diffraction (35), and x-ray diffraction (36–38) analysis; in particular, it was reported that in the DMPC crystal, the hydrocarbon chains tilt from the bilayer normal by 12° (36).

Incorporation of gramicidin A into DMPC liposomes does not influence significantly the IR frequencies of the lipids (Fig. 1) nor the dichroism of the polar groups (Tables I and II). However, Table II shows that the dichroic ratios of $\delta(\text{CH}_2)$, $\nu_{\text{as}}(\text{CH}_2)$ and $\nu_s(\text{CH}_2)$ vibrations are all slightly decreased while that of the $\gamma_w(\text{CH}_2)$ is greatly increased, as is also seen in Fig. 3. For this last vibration, the absorption nearly vanishes in the A_\perp spectrum of DMPC with incorporated gramicidin (Fig. 3). It therefore seems that the tilt angle between the hydrocarbon chains of DMPC and the normal to the bilayer is decreased (from 20° to $\sim 10^\circ$) in the presence of gramicidin. A similar effect was observed by Fringeli et al. (39) after incorporation of the antibiotic alamethicin in dry DPPC bilayers.

Conformation of Gramicidin A in DMPC Liposomes

Different models for the structure of the dimeric gramicidin channel have already been proposed:

(a) A head-to-head (NH_2 terminal to NH_2 terminal) association of two π_{LD} helical monomers proposed by Urry (7, 11). Dimerization occurs via six intermolecular hydrogen bonds with antiparallel hydrogen bonding.

(b) An antiparallel double helix in which all the hydrogen bonds are intermolecular. This structure isolated from nonpolar solvents, has been discussed by Veatch et al. (12).

In proteins, correlations between amide band frequen-

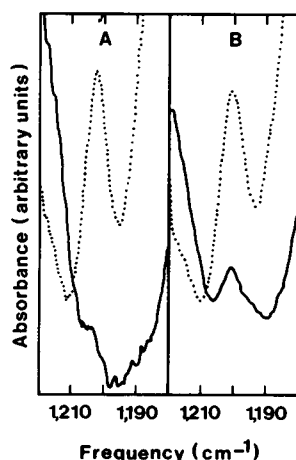


FIGURE 3 Comparison of CH_2 wagging region (expansion 20) of dried DMPC liposomes with (A) or without gramicidin (B); A_\perp (—); A_\parallel (· · ·).

cies and molecular conformation exist and have been well resolved for α -helix, β -sheets, and unordered structures (30, 40–43). However, only limited IR data are available for π_{LD} helix (44, 45). The amide I frequency of gramicidin in liposomes at $1,638\text{ cm}^{-1}$ (Fig. 1) could indicate some β -sheet structure (the π_{LD} helix is essentially a rolled parallel β -structure in its intramolecular hydrogen bonding) but the position of the amide II band at $1,547\text{ cm}^{-1}$ is out of the range characteristic for β or antiparallel pleated sheets ($\sim 1,530\text{ cm}^{-1}$) (40); furthermore, the absence of any shoulder at $1,685\text{ cm}^{-1}$ usually associated with antiparallel hydrogen bonding (40, 41, 43) seems to exclude antiparallelism of the polypeptide chain, and therefore is not consistent with the double helix model of Veatch et al. (12). In contrast, the IR spectrum of gramicidin dried from a CHCl_3 solution shows the amide I and amide II peaks at $1,632$ and $1,535\text{ cm}^{-1}$, respectively and a shoulder at $1,685\text{ cm}^{-1}$ (spectrum not shown) which indicates an antiparallel structure and is in agreement with previous IR and Raman studies in nonpolar solvents (12, 46, 47). This demonstrates that the dominant conformation of the antibiotic is different in the liposomes and in the solid state or in organic solution.

Furthermore, recent NMR studies (19, 20) of gramicidin in DMPC vesicles (same experimental conditions as ours) argue strongly for a NH_2 terminal to NH_2 terminal arrangement of the gramicidin dimer in vesicles. We therefore suggest that the observed amide I and amide II frequencies of gramicidin in liposomes at $1,638$ and $1,547\text{ cm}^{-1}$, respectively, may be characteristic of the NH_2 terminal to NH_2 terminal helical dimer, i.e., the model of Urry (7). It should be, however, noted that the calculated amide I frequency (at $1,655\text{ cm}^{-1}$) for a gramicidin dimer with a head-to-head π_{LD} helix (48) appears quite far from that observed for gramicidin in liposomes (at $1,638\text{ cm}^{-1}$). This discrepancy suggests that refinements in the calculations of IR frequencies for π_{LD} helix dimers are probably required. It is also possible that the contribution of other conformations and/or interactions between the antibiotic and the lipids have to be taken into account.

Orientation of Gramicidin Peptide Chain in DMPC Liposomes

Figs. 1 and 2 show that gramicidin in DMPC liposomes gives a high dichroism in the amide I and amide A bands with their absorption more intense in the A_\parallel spectrum than in the A_\perp spectrum; the opposite situation is found for the amide II band. Qualitatively, this argues for an alignment of the $\text{C}=\text{O}$ and $\text{N}-\text{H}$ bonds approximately parallel to the normal to the disk plane, suggesting a preferential orientation of the peptide groups with respect to the bilayer.

In a π_{LD} helix, the backbone $\text{C}=\text{O}$ groups are positioned rather parallel or antiparallel to the helix axis (7) in contrast to the usual α -helix in which the $\text{C}=\text{O}$ groups

form a parallel array. Note that parallel and antiparallel bonds are not distinguishable by IR dichroism. For the C=O stretching amide I and the N—H stretching amide A vibrations, the transition moment lies approximately parallel to the C=O or the N—H bond respectively; in contrast, for the N—H bending amide II mode, it lies rather perpendicular to the N—H bond (49). Therefore, it appears that the π_{LD} helices in the gramicidin dimer are preferentially oriented along the normal to the bilayer with the amide I transition dipole moment oriented predominantly parallel to the hydrocarbon chains of DMPC and the transition moment of amide II directed perpendicular to the lipid chains.

In order to calculate the tilt angle ϕ_r of the helix relative to the bilayer normal, we must take into account the angle ϕ_M between the transition moments of the amide vibrations and the helix axis. In a π_{LD} helix, the two peptide units of the LD repeat do not have the same orientation with respect to the helical axis. Investigations of poly- γ -benzyl-D-L-glutamate (which is regarded as a stereochemical model of gramicidin A) show that this polypeptide can adopt a great variety of conformations (44, 45) such as single-stranded π_{LD}^{44} helix and double-stranded π_{LD} π_{LD} helices (with 5.6, 7.2, 9.0, and 10.8 amino acid residues per helical turn of the helix). For each of these structures, angles between amide transition moments and the helical axis were calculated (44, 45). However, no data are available for the π_{LD}^{63} helix of gramicidin proposed by Urry (7, 11). In these conditions, we use the transition moments data available for the π_{LD}^{44} helix to calculate ϕ_r . Heitz et al. (44, 45) reported that within each LD repeat of a π_{LD}^{44} helix, the individual amide I vibration vectors make an angle ϕ_{MI} of about 21°8 and 23°4 with respect to the helical axis. In the following analysis, we calculated the average order parameter $\overline{S_{MI}} = \frac{1}{2} [S(21^\circ 8) + S(23^\circ 4)] = 0.778$ leading to the average angle $\overline{\phi_{MI}} = 22^\circ 6$; for amide II, $\phi_{MII} = 81^\circ 0$ and $46^\circ 0$ (44, 45) and $\overline{\phi_{MII}} = 59^\circ 8$; for amide A, $\phi_{MA} = 13^\circ 3$ and $30^\circ 3$ (44, 45) and $\overline{\phi_{MA}} = 23^\circ 1$. Finally, the distribution S_r of the gramicidin π_{LD} helix axis with respect to the bilayer normal can be calculated from the following equation (24):

$$S = S_r \times S_M, \quad (2)$$

where S is estimated from the amide band dichroic ratio (Eq. 1) and S_M is the average order parameter for the amide transition moment.

The IR dichroism results of gramicidin are summarized in Table III; it is shown that the dichroic ratio of the amide I band leads to $\phi_r = 15^\circ$, whereas from the dichroic ratio of the amide A band, a value $\phi_r = 24^\circ$ is obtained. It therefore appears that gramicidin polypeptide chain is approximately perpendicular to the bilayer plane and nearly parallel to the DMPC hydrocarbon chains. Notice that a ϕ_r value cannot be calculated from the amide II data ($S_r > 1$). Table III shows that the accuracy on the di-

TABLE III
ESTIMATION OF D AND ϕ_r FROM GRAMICIDIN IR
DICHROISM DATA

IR Parameters	Amide I	Amide II	Amide A
D^*	3.10 ± 0.20	0.78 ± 0.10	2.25 ± 0.20
ϕ_r^\ddagger	$15^\circ \begin{smallmatrix} +3^\circ \\ -1^\circ \end{smallmatrix}$	\S	$24^\circ \begin{smallmatrix} +3^\circ \\ -2^\circ \end{smallmatrix}$

*Average obtained from four different air-dried samples.

$\ddagger \phi_r$, calculated assuming perfect orientation of the liposomes parallel to the disk surface.

\S See Results and Discussion for explanation. Otherwise as in Table II.

chroism measurement is worse for the amide II band than for the other bands. We calculate that the amide II dichroic ratio would have to be increased to 0.91 to give a ϕ_r value of 15° . Nevertheless, the measured dichroic ratio values for the amide II band are always <0.88 . Accordingly, the possibility of some inconsistency in the choice of ϕ_M angles ought to be taken into account. For example, an average ϕ_{MII} value of 71° (instead of $59^\circ 8$) does lead to $\phi_r = 15^\circ$. It must be also emphasized that no ϕ_r value can be obtained from our IR data (for any amide band) if we use the transition moments data given for an antiparallel double π_{LD}^{56} helix model (44, 45). This again confirms that the conformation of gramicidin in liposomes cannot be identified to the model of Veatch et al. (12). Further calculations for a π_{LD}^{63} helix dimer may be required in order to improve our results on the orientation of gramicidin in liposomes.

The tilt angles for the lipid and peptide chains were calculated, assuming that the liposome membranes are oriented perfectly parallel to the disk surface. If the mosaic spread of our samples is $>0^\circ$, i.e., if the extent of orientation of the vesicles is not perfect, then the hydrocarbon chains and the helix axis would even be oriented more closely parallel to the normal to the bilayer plane. Stamatoff et al. (37) have measured by x-ray diffraction the tilt of DPPC chains in phospholipid bilayers and observed different mosaic spreads for various samples but each was $<15^\circ$. If we assume this 15° mosaic spread value, the DMPC lipid chains and the π_{LD} helix axis are calculated to be essentially perpendicular to the membrane plane.

The IR dichroism study presented here shows that addition of gramicidin to DMPC vesicles does not influence the polar regions of the lipid but seems to induce a slight reorganization of the acyl chains: the tilt angle between the hydrocarbon chains of the lipids and the normal to the bilayer (about 20° for DMPC alone) is decreased by almost 10° upon interaction with gramicidin (Table II). This result appears consistent with the hydrophobic character of gramicidin. Different types of lipid-peptide interactions were recently suggested by IR and Raman spectroscopic investigations, by monitoring the lipid thermal phase transition (50, 51) or the IR dichroism of lipid bands (39, 52). In particular, it has been shown

that melittin can influence both the polar and apolar regions of phosphatides arranged in multilayers (52), while alamethicin incorporated in dry DPPC bilayers only changes the hydrocarbon chain ordering (39).

The transmembrane orientation of the gramicidin channel has previously been inferred from functional and structural studies (7, 13–20). However, a tilt value for the axis of the channel had never been estimated. Our data quantify the transmembrane orientation of the gramicidin channel at $<15^\circ$ with respect to the normal to the bilayer.

We are indebted to Professor C. M. Gary-Bobo for helpful suggestions that initiated this work. We wish also to thank Dr. Y. Prigent for discussions, Dr. D. Tiede for a critical reading of the manuscript, P. Calvet, and C. Schneider for interfacing the Perkin-Elmer 180 infrared spectrometer with the Hewlett-Packard 9825 A computer.

Received for publication 15 December 1981.

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