

## Monitoring ion channel conformations in membranes utilizing a novel dual fluorescence quenching approach <sup>☆</sup>

Devaki A. Kelkar, Amitabha Chattopadhyay <sup>\*</sup>

*Centre for Cellular and Molecular Biology, Uppal Road, Hyderabad 500 007, India*

Received 22 February 2006

Available online 9 March 2006

### Abstract

The linear peptide gramicidin forms prototypical ion channels specific for monovalent cations and has been extensively used to study the organization, dynamics, and function of membrane-spanning channels. We have analyzed the localization of the functionally important tryptophan residues of the membrane-bound channel and non-channel conformations of gramicidin utilizing a novel dual fluorescence quenching approach [G.A. Caputo, E. London, *Biochemistry* 42 (2003) 3265–3274]. In this paper, we show for the first time that the dual quenching approach is applicable to multiple tryptophan containing functional ion channel peptides such as gramicidin. Importantly, dual quenching is found to be sensitive to the membrane-bound conformations of this important model ion channel.

© 2006 Elsevier Inc. All rights reserved.

**Keywords:** Gramicidin; Ion channel; Acrylamide quenching; Dual quenching; 10-DN; Non-channel

Ion channels are transmembrane proteins that regulate ionic permeability in cell membranes. They are crucial for normal functioning of cells and defective ion channels are implicated in a number of diseases collectively known as ‘channelopathies’ [1]. The recent successes in crystallographic analyses of ion channels starting with the KcsA potassium channel [2] have provided exciting molecular insights into ion channel structure and function. However, it is becoming increasingly clear that static crystallographic structures of membrane proteins may not always provide accurate representations of channel function [3]. Due to this ambiguity in the structural analysis of ion channel function, simple models of ion channels continue to provide useful information to understand and characterize more complex systems [4,5]. The linear peptide gramicidin forms prototypical ion channels specific for monovalent

cations and has been extensively used to study the organization, dynamics, and function of membrane-spanning channels [6,7]. Gramicidin serves as an excellent model for transmembrane channels due to its small size, ready availability, and the relative ease with which chemical modifications can be performed.

The unique sequence of alternating L- and D-chirality renders gramicidin sensitive to the environment in which it is placed [5]. Gramicidin therefore adopts a wide range of environment-dependent conformations. Two major folding motifs have been identified for gramicidin in various media: (i) the single stranded helical dimer (‘channel’ form) and (ii) the double stranded intertwined helix (collectively known as ‘non-channel’ form) [8]. Interestingly, the initial conformation adopted by gramicidin in membranes has been reported to be influenced by the nature of the solvent in which it was dissolved prior to incorporation, i.e., gramicidin conformation in membranes depends on its ‘solvent history’ [9]. However, the single stranded helical dimer conformation is the thermodynamically preferred conformation in membrane and membrane-mimetic environments [9–12].

The cation conducting gramicidin channel in membranes is formed by the head-to-head (amino terminal-to-amino

<sup>☆</sup> *Abbreviations:* 10-DN, 10-doxylnonadecane; DMPC, 1,2-dimyristoyl-*sn*-glycero-3-phosphatidylcholine; NBS, *N*-bromosuccinimide; MLV, multilamellar vesicles; SUV, small unilamellar vesicles; POPC, 1-palmitoyl-2-oleoyl-*sn*-glycero-3-phosphatidylcholine; REES, red edge excitation shift.

<sup>\*</sup> Corresponding author. Fax: +91 40 2716 0311.

*E-mail address:* [amit@ccmb.res.in](mailto:amit@ccmb.res.in) (A. Chattopadhyay).

terminal) single stranded  $\beta^{6.3}$  helical dimer [13]. In this conformation, the carboxy terminus is exposed to the membrane–water interface and the amino terminus is buried in the hydrophobic core of the membrane. This places the carboxy terminal tryptophan residues clustered at the membrane–water interface at the entrance to the channel [13–16]. This interfacial localization of the gramicidin tryptophan residues is an essential aspect of gramicidin conformation and function in membranes [7]. The membrane interface seeking properties of tryptophan [17] and the oriented dipole moments of the tryptophan side chains play an important role in gramicidin conformation and ion channel activity [18–21]. While the channel conformation in membranes has been extensively investigated [14], the dynamics of the non-channel conformation is relatively unexplored [16]. Importantly, the membrane interfacial localization of tryptophan residues is absent in ‘non-channel’ conformations and the tryptophan residues are distributed along the membrane axis [16]. Such conformations have been shown to exist in membranes with polyunsaturated lipids [22] and in membranes with increased acyl chain lengths [23,24]. We have earlier utilized wavelength-selective and other sensitive fluorescence approaches to monitor the organization and dynamics of the functionally important tryptophan residues of gramicidin in the channel and non-channel conformations [16].

In this report, we have utilized a novel dual fluorescence quenching approach [25] to analyze the distribution and depths of the tryptophan residues of gramicidin in the channel and non-channel conformations. This method is based on the differing accessibility of an aqueous and membrane-bound quencher to membrane-bound tryptophan residues. The ratio of quenching ( $Q$ -ratio) by these quenchers has been shown to be related to the average depth of the fluorophore in the membrane [25]. The advantage of this approach lies in the fact that even though information on depth may be obtained by the use of a single quencher, the use of two quenchers in the  $Q$ -ratio increases sensitivity by canceling out any non-depth related effects on quenching. This work represents the first report of the dual quenching analysis of a functional multitryptophan ion channel peptide.

## Materials and methods

**Materials.** 1-Palmitoyl-2-oleoyl-*sn*-glycero-3-phosphocholine (POPC) was obtained from Avanti Polar Lipids (Alabaster, AL). Gramicidin A' (from *Bacillus brevis*) and 1,2-dimyristoyl-*sn*-glycero-3-phosphocholine (DMPC) were purchased from Sigma Chemical Co. (St. Louis, MO). Ultra pure grade acrylamide was from Invitrogen Life Technologies (Carlsbad, CA). 10-Doxylnonadecane (10-DN) was a generous gift from Prof. Erwin London (SUNY, Stony Brook). The purity of acrylamide was checked from its absorbance using its molar extinction coefficient ( $\epsilon$ ) of  $0.23 \text{ M}^{-1} \text{ cm}^{-1}$  at 295 nm and optical transparency beyond 310 nm [26]. Gramicidin A', as obtained, is a mixture of gramicidins A, B, and C. The concentration of gramicidin was calculated from its molar extinction coefficient ( $\epsilon$ ) of  $20,700 \text{ M}^{-1} \text{ cm}^{-1}$  at 280 nm [10]. The concentration of a stock solution of 10-DN in ethanol was calculated from its molar extinction coefficient ( $\epsilon$ ) of  $12 \text{ M}^{-1} \text{ cm}^{-1}$  at 422 nm [25]. Lipids were checked for purity by thin-layer chromatography on silica gel precoated

plates (Sigma) in chloroform/methanol/water (65:35:5, v/v/v) and were found to give only one spot in all cases with a phosphate-sensitive spray and subsequent charring [27]. The concentration of phospholipids was determined by phosphate assay subsequent to total digestion by perchloric acid [28]. DMPC was used as an internal standard to assess lipid digestion. All other chemicals used were of the highest purity available. Solvents used were of spectroscopic grade. Water was purified through a Millipore (Bedford, MA) Milli-Q system and used for all experiments.

**Sample preparation.** All experiments were done using unilamellar vesicles (ULV) of POPC containing 2% (mol/mol) gramicidin A'. The channel and non-channel conformations of gramicidin were generated essentially as described earlier [16]. In general, 160 nmol of POPC in chloroform/methanol was mixed with 3.2 nmol of gramicidin in methanol. A few drops of chloroform were added to this solution. The solution was mixed well and dried under a stream of nitrogen while warming gently ( $\sim 40^\circ \text{C}$ ) and dried further under a high vacuum for at least 12 h. To prepare the channel form, the dried film was swelled in 1.5 ml of 10 mM sodium phosphate, 150 mM sodium chloride, pH 7.2 buffer, and samples were vortexed for 3 min to uniformly disperse the lipids. The samples were sonicated to clarity under argon ( $\sim 30$  min in short bursts while being cooled in an ice/water mixture) using a Branson model 250 sonifier (Dansbury, CT) fitted with a microtip. The sonicated samples were centrifuged at 15,000 rpm for 15 min to remove any titanium particles shed from the microtip during sonication and incubated for 12 h at  $65^\circ \text{C}$  with continuous shaking in order to completely convert to the channel conformation [9,10]. For the non-channel conformation, the dried film was dissolved in ethanol to give a final concentration of 40 mM lipid in ethanol. The ethanolic solution was then injected into 1.5 ml of 10 mM sodium phosphate, 150 mM sodium chloride, pH 7.2 buffer, and samples were vortexed to uniformly disperse the lipids.

For experiments involving 10-DN, 160 nmol of POPC containing 10 mol% 10-DN was mixed with 3.2 nmol gramicidin. The solution was mixed well and dried as described above. To prepare the channel form, the dried lipid film was carefully sonicated under argon to avoid any possible damage to the spin label and incubated overnight at  $65^\circ \text{C}$  as described above. All samples were incubated in dark at room temperature for 1 h before fluorescence measurements. Background samples were prepared the same way except that gramicidin was omitted. All experiments were done with multiple sets of samples at  $25^\circ \text{C}$ .

**Steady state fluorescence measurements.** Steady state fluorescence measurements were performed with a Hitachi F-4010 spectrofluorometer using 1-cm path length quartz cuvettes. Excitation and emission slits with a nominal bandpass of 5 nm were used for all measurements. Background intensities of samples in which gramicidin was omitted were negligible in most cases and were subtracted from each sample spectrum to cancel out any contribution due to the solvent Raman peak and other scattering artifacts.

**Fluorescence quenching measurements.** Quenching of gramicidin tryptophan fluorescence was estimated by measurement of fluorescence intensity in the presence and absence of 0.3 M acrylamide (taken from a freshly prepared 4 M stock solution in water) or 10 mol% 10-DN. Samples were kept in dark for at least 1 h before measuring fluorescence. The excitation wavelength used was 295 nm and emission was monitored at 334 nm. For samples containing acrylamide, corrections for inner filter effect were made using the following equation [29]:

$$F = F_{\text{obs}} \text{antilog} [(A_{\text{ex}} + A_{\text{em}})/2], \quad (1)$$

where  $F$  is the corrected fluorescence intensity and  $F_{\text{obs}}$  is the background subtracted fluorescence intensity of the sample.  $A_{\text{ex}}$  and  $A_{\text{em}}$  are the measured absorbances at the excitation and emission wavelengths. The absorbances of the samples were measured using a Hitachi U-2000 UV–visible absorption spectrophotometer. Dual quenching ratios ( $Q$ -ratio) were calculated using [25]:

$$Q\text{-ratio} = [(F_o/F_{\text{acrylamide}}) - 1]/[(F_o/F_{10\text{-DN}}) - 1], \quad (2)$$

where  $F_o$  is the fluorescence intensity in the absence of any quencher,  $F_{\text{acrylamide}}$  is the corrected fluorescence intensity in the presence of 0.3 M acrylamide, and  $F_{10\text{-DN}}$  is the fluorescence intensity in the presence of 10 mol% 10-DN.

**Circular dichroism measurements.** CD measurements were carried out at room temperature (25 °C) on a JASCO J-715 spectropolarimeter as described earlier [16]. Data are represented as mean residue ellipticities and were calculated using the formula:

$$[\theta] = \theta_{\text{obs}} / (10Cl), \quad (3)$$

where  $\theta_{\text{obs}}$  is the observed ellipticity in mdeg,  $l$  is the path length in cm, and  $C$  is the concentration of peptide bonds in mol/L.

## Results and discussion

The initial conformation that gramicidin adopts when incorporated into membranes is dependent on the nature of the solvent in which it was dissolved prior to incorporation in membranes [9,10]. Thus, when gramicidin is dissolved in solvents such as chloroform/methanol or ethanol before incorporation into membranes, it tends to adopt double helical non-channel conformations. Upon sonication and incubation at 65 °C, such conformations are converted to the characteristic channel conformation. We used the ethanol injection method [30] to generate non-channel conformations of gramicidin in POPC vesicles. Gramicidin incorporated in membrane vesicles this way has been shown to initially adopt the non-channel conformation [16]. Fig. 1A shows representative circular dichroism spectra for the channel and non-channel conformations obtained this way. The intensity-normalized fluorescence emission spectra of the channel and non-channel conformations of gramicidin are shown in Fig. 1B. When excited at 280 nm, gramicidin tryptophans in the channel form exhibit an emission maximum of 333 nm. The emission maximum of the non-channel form, on the other hand, displays a slight red shift and is at 335 nm, in agreement with previous literature [16,31]. In addition, the fluorescence intensity of the non-channel form is increased compared to the channel form (not shown). This is clearly indicative of differing average environments for the gramicidin tryptophans in the channel and non-channel conformations. Previous work from our laboratory utilizing wavelength-selective fluorescence indicated that the gramicidin tryptophans in the channel conformation are localized at the membrane interfacial region characterized by restricted motional reorientation [15,16]. In contrast, the average environment of tryptophans in the non-channel form is considerably less restricted as evidenced by the reduced magnitude of red edge excitation shift (REES) observed in this conformation [16].

Quenching of tryptophan fluorescence using aqueous quenchers such as acrylamide is a widely used tool to monitor tryptophan environments in proteins [32]. Interestingly, acrylamide quenching of gramicidin tryptophan fluorescence was found to be insensitive to the conformation of membrane-bound gramicidin as evaluated by the Stern–Volmer constant ( $K_{SV}$ ) and the bimolecular quenching constant ( $k_q$ ) [16]. Thus, while  $K_{SV}$  values indicated an increased accessibility to the aqueous environment for the non-channel tryptophans, the values for bimolecular quenching constants however did not support this interpre-

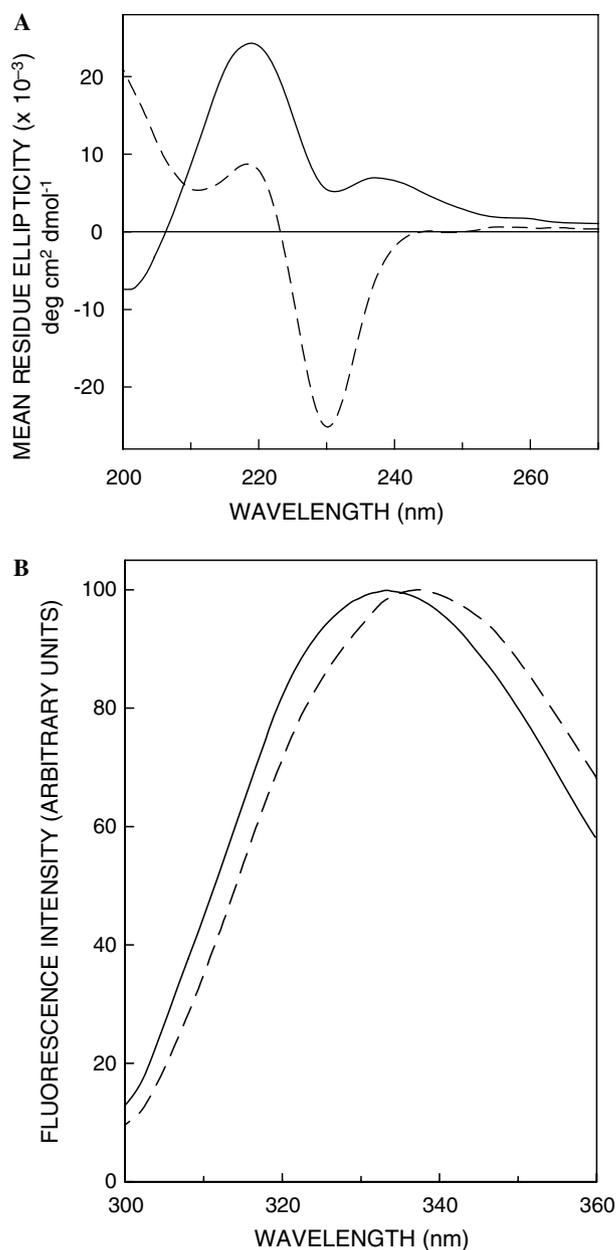


Fig. 1. (A) Far UV CD spectra of the channel (—) and non-channel (---) forms of gramicidin in vesicles of POPC. (B) Fluorescence emission spectra of the channel (—) and non-channel (---) forms of gramicidin in vesicles of POPC. The excitation wavelength was 280 nm. The spectra are intensity-normalized at the emission maximum. The two forms of gramicidin were generated as described in Materials and methods. Concentration of POPC was 0.43 mM and the ratio of gramicidin to POPC was 1:50 (mol/mol). See Materials and methods for other details.

tation. This is in contrast to other sensitive fluorescence parameters such as REES which indicated a deeper average location for gramicidin tryptophans in the non-channel conformation [16]. In addition, chemical modification of tryptophan residues using *N*-bromosuccinimide (NBS) as an oxidant also did not provide a clear picture for the distribution of tryptophan residues in these conformations [16].

In the present work, we have addressed the issue of relative depths of gramicidin tryptophans in the channel and

non-channel conformations by using a novel dual quenching approach [25] which eliminates some of the complications associated with earlier measurements. This method utilizes two quenchers, the aqueous quencher acrylamide and membrane-bound spin label quencher 10-doxylnonadecane (10-DN), to calculate a quenching ratio ( $Q$ -ratio) which has been found to have an approximate linear relationship with fluorophore depth in the membrane [25]. Even though information on depth may be obtained by the use of a single quencher (such as acrylamide), the use

of two quenchers in the  $Q$ -ratio amplifies sensitivity by canceling out any non-depth related effects on quenching. 10-DN is a derivative of the aliphatic hydrocarbon nonadecane and contains a nitroxide-bearing doxyl group (spin label). Spin labels are known to be strong quenchers of a wide range of fluorophores including tryptophans [33–36]. 10-DN is a hydrophobic molecule and does not have a polar moiety to anchor the nitroxide group in the membrane at a fixed depth, in contrast to spin-labeled phosphatidylcholines, where the spin label is known to be at a very specific location (depth) in the membrane bilayer [34,35].

Fig. 2 shows the quenchings of gramicidin tryptophan fluorescence obtained in the presence of fixed concentrations of the aqueous quencher acrylamide and the membrane-bound quencher 10-DN. As discussed above, acrylamide quenching does not exhibit appreciable sensitivity to the different conformations of gramicidin. Importantly, fluorescence quenching by 10-DN appears to be more sensitive to the channel and non-channel conformations of gramicidin. The  $Q$ -ratios calculated according to Eq. (2) are shown in Fig. 2. The  $Q$ -ratio in the non-channel conformation (0.27) is low while the  $Q$ -ratio for the channel conformation (0.69) is relatively high. The lower  $Q$ -ratio for the non-channel conformation is consistent with tryptophans embedded in the deeper regions of the membrane in this conformation, while a higher  $Q$ -ratio for the channel conformation is representative of tryptophan residues present in shallower regions of the membrane [25] (see Fig. 3). It should be noted that analysis of membrane penetration depths using the dual quenching approach does not provide absolute values for fluorophore depth in the membrane bilayer. However, the dual quenching approach has some advantages over more quantitative approaches such as parallax [34] and distribution [37]

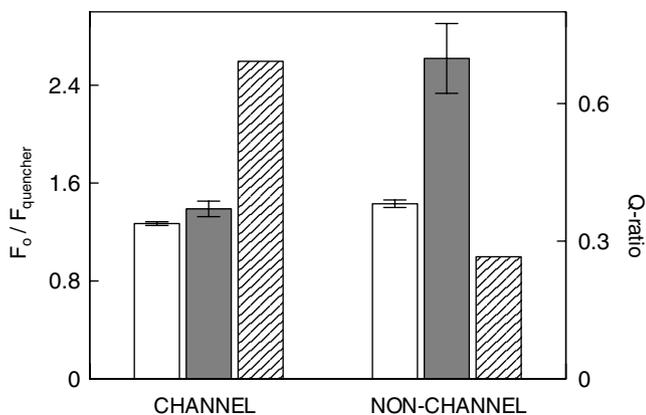


Fig. 2. Quenching and  $Q$ -ratios of gramicidin fluorescence in the non-channel and channel conformations.  $F_0$  is the fluorescence intensity in the absence of quencher (acrylamide or 10-DN), and  $F$  is the fluorescence intensity in the presence of quencher (acrylamide or 10-DN). The open bars represent quenching by 0.3 M acrylamide and the shaded bars represent quenching by 10 mol% 10-DN. Data shown represent means  $\pm$  standard error of three independent measurements. The excitation wavelength was 295 nm and emission was monitored at 334 nm. The hatched bars represent  $Q$ -ratios calculated according to Eq. (2). Concentration of POPC was 0.11 mM and the ratio of gramicidin to POPC was 1:50 (mol/mol). See Materials and methods for other details.

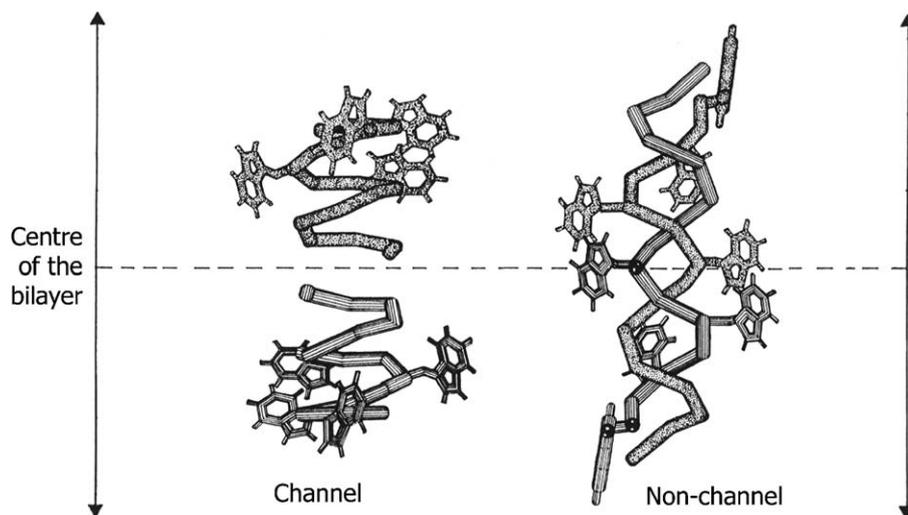


Fig. 3. Schematic representation of the channel and non-channel conformations of gramicidin indicating the location of tryptophan residues in a membrane bilayer. The membrane axis is represented by double headed arrows and the center of the bilayer is marked by a dotted line. Note that in the channel conformation tryptophan residues are clustered towards the membrane interface whereas in the non-channel conformation tryptophan residues are distributed along the membrane axis (adapted and modified from [16]).

analysis. In addition, since this approach utilizes quenchers at very different locations (aqueous and membrane-bound), the difference in quenching is large and more easily measured when compared to other methods where the quenchers (spin-labeled or brominated lipids) are placed at only slightly different depths.

The  $Q$ -ratio was originally calibrated and found to be linear for  $\alpha$ -helical peptides with a single tryptophan placed at different positions in the sequence of the transmembrane helix [25]. However, the  $Q$ -ratios obtained by us for gramicidin in the channel and non-channel conformation are for a multityryptophan peptide. Nonetheless, the overall agreement of the  $Q$ -ratios with the relative location of tryptophan residues in the membrane bilayer even for a multityryptophan peptide such as gramicidin is indeed encouraging. It would be interesting to compare  $Q$ -ratios of analogues of gramicidin containing single tryptophan residues [18,38] at defined locations in the membrane bilayer.

Importantly, 10-DN does not anchor at any specific location and can therefore be easily accommodated in membranes of different hydrophobic thicknesses [25]. This is particularly useful to study the organization and conformation of tryptophan containing peptides in cases of hydrophobic mismatch [25,39–41].  $Q$ -ratios therefore provide a relative scale for depth of the fluorophore in the membrane that can be conveniently used across different membrane systems. Dual quenching analysis has been found to be useful to analyze the membrane penetration of membrane peptides, utilizing both intrinsic tryptophan fluorescence and external fluorophores [41–43]. This report shows, for the first time, that the dual quenching analysis could be applicable to functional multityryptophan peptides such as gramicidin. Such an approach could prove especially useful to analyze the membrane thickness induced conformational response of such multiple tryptophan peptides.

## Acknowledgments

This work was supported by the Council of Scientific and Industrial Research, Government of India. A.C. is an Honorary Professor of the Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore (India). D.A.K. thanks the Council of Scientific and Industrial Research for the award of a Senior Research Fellowship. We thank members of our laboratory for critically reading the manuscript.

## References

- [1] T.J. Jentsch, C.A. Hübner, J.C. Fuhrmann, Ion channels: function unravelled by dysfunction, *Nat. Cell Biol.* 6 (2004) 1039–1047.
- [2] D.A. Doyle, J.M. Cabral, R.A. Pfuetzner, A. Kuo, J.M. Gulbis, S.L. Cohen, B.T. Chait, R. MacKinnon, The structure of the potassium channel: molecular basis of  $K^+$  conduction and selectivity, *Science* 280 (1998) 69–77.
- [3] M.B. Jackson, Advances in ion channel structure, *Trends Neurosci.* 27 (2004) 291.
- [4] G.V. Miloshevsky, P.C. Jordan, Permeation in ion channels: the interplay of structure and theory, *Trends Neurosci.* 27 (2004) 308–314.
- [5] A. Chattopadhyay, D.A. Kelkar, Ion channels and D-amino acids, *J. Biosci.* 30 (2005) 147–149.
- [6] J.A. Killian, Gramicidin and gramicidin–lipid interactions, *Biochim. Biophys. Acta* 1113 (1992) 391–425.
- [7] R.E. Koeppe, O.S. Andersen, Engineering the gramicidin channel, *Annu. Rev. Biophys. Biomol. Struct.* 25 (1996) 231–258.
- [8] W.R. Veatch, E.T. Fossel, E.R. Blout, The conformation of gramicidin A, *Biochemistry* 13 (1974) 5249–5256.
- [9] P.V. LoGrasso, F. Moll, T.A. Cross, Solvent history dependence of gramicidin A conformations in hydrated lipid bilayers, *Biophys. J.* 54 (1988) 259–267.
- [10] J.A. Killian, K.U. Prasad, D. Hains, D.W. Urry, The membrane as an environment of minimal interconversion. A circular dichroism study on the solvent dependence of the conformational behavior of gramicidin in diacylphosphatidylcholine model membranes, *Biochemistry* 27 (1988) 4848–4855.
- [11] L.E. Townsley, W.A. Tucker, S. Sham, J.F. Hinton, Structures of gramicidin A, B, and C incorporated into sodium dodecyl sulfate micelles, *Biochemistry* 40 (2001) 11676–11686.
- [12] D.A. Kelkar, A. Chattopadhyay, Effect of graded hydration on the organization and dynamics of an ion channel: a fluorescence approach, *Biophys. J.* 88 (2005) 1070–1080.
- [13] A.M. O’Connell, R.E. Koeppe, O.S. Andersen, Kinetics of gramicidin channel formation in lipid bilayers: transmembrane monomer association, *Science* 250 (1990) 1256–1259.
- [14] R.R. Ketchum, W. Hu, T.A. Cross, High-resolution conformation of gramicidin A in a lipid bilayer by solid-state NMR, *Science* 261 (1993) 1457–1460.
- [15] S. Mukherjee, A. Chattopadhyay, Motionally restricted tryptophan environments at the peptide–lipid interface of gramicidin channels, *Biochemistry* 33 (1994) 5089–5097.
- [16] S.S. Rawat, D.A. Kelkar, A. Chattopadhyay, Monitoring gramicidin conformations in membranes: a fluorescence approach, *Biophys. J.* 87 (2004) 831–843.
- [17] W.C. Wimley, S.H. White, Experimentally determined hydrophobicity scale for proteins at membrane interfaces, *Nat. Struct. Biol.* 3 (1996) 842–848.
- [18] M.D. Becker, D.V. Greathouse, R.E. Koeppe, O.S. Andersen, Amino acid sequence modulation of gramicidin channel function: effects of tryptophan-to-phenylalanine substitutions on the single-channel conductance and duration, *Biochemistry* 30 (1991) 8830–8839.
- [19] V. Fonseca, P. Daumas, L. Ranjalahy-Rasoloarijao, F. Heitz, R. Lazaro, Y. Trudelle, O.S. Andersen, Gramicidin channels that have no tryptophan residues, *Biochemistry* 31 (1992) 5340–5350.
- [20] O.S. Andersen, D.V. Greathouse, L.L. Providence, M.D. Becker, R.E. Koeppe, Importance of tryptophan dipoles for protein function: 5-fluorination of tryptophans in gramicidin A channels, *J. Am. Chem. Soc.* 120 (1998) 5142–5146.
- [21] D.G. Anderson, R.B. Shirts, T.A. Cross, D.D. Busath, Noncontact dipole effects on channel permeation. V. Computed potentials for fluorinated gramicidin, *Biophys. J.* 81 (2001) 1255–1264.
- [22] S.V. Sychev, L.I. Barsukov, V.T. Ivanov, The double  $\pi\pi$  5.6 helix of gramicidin A predominates in unsaturated lipid membranes, *Eur. Biophys. J.* 22 (1993) 279–288.
- [23] M. Zein, R. Winter, Effect of temperature, pressure and lipid acyl chain length on the structure and phase behaviour of phospholipid–gramicidin bilayers, *Phys. Chem. Chem. Phys.* 2 (2000) 4545–4551.
- [24] D.A. Kelkar, A. Chattopadhyay, Modulation of ion channel conformation and organization by hydrophobic mismatch: a fluorescence approach, *FEBS J.* 272 (Suppl. 1) (2005) 238.
- [25] G.A. Caputo, E. London, Using a novel dual fluorescence quenching assay for measurement of tryptophan depth within lipid bilayers to determine hydrophobic  $\alpha$ -helix locations within membranes, *Biochemistry* 42 (2003) 3265–3274.
- [26] M.R. Eftink, Fluorescence quenching reactions: Probing biological macromolecular structure, in: T.G. Dewey (Ed.), *Biophysical and*

- Biochemical Aspects of Fluorescence Spectroscopy, Plenum Press, New York, pp. 1–41.
- [27] J.C. Dittmer, R.L. Lester, A simple, specific spray for the detection of phospholipids on thin-layer chromatograms, *J. Lipid Res.* 5 (1964) 126–127.
- [28] C.W.F. McClare, An accurate and convenient organic phosphorus assay, *Anal. Biochem.* 39 (1971) 527–530.
- [29] J.R. Lakowicz, *Principles of Fluorescence Spectroscopy*, Kluwer-Plenum Press, New York, 1999.
- [30] J.M.H. Kremer, M.W.J. Esker, C. Pathmanathan, P.H. Wiersema, Vesicles of variable diameter prepared by a modified injection method, *Biochemistry* 16 (1977) 3932–3935.
- [31] K.J. Cox, C. Ho, J.V. Lombardi, C.D. Stubbs, Gramicidin conformational studies with mixed-chain unsaturated phospholipid bilayer systems, *Biochemistry* 31 (1992) 1112–1118.
- [32] M.R. Eftink, Fluorescence quenching: theory and applications, in: J.R. Lakowicz (Ed.), *Topics in Fluorescence Spectroscopy, Principles*, Vol. 2, Plenum Press, New York, 1991, pp. 53–126.
- [33] E. London, G.W. Feigenson, Fluorescence quenching in model membranes. I. Characterization of quenching caused by a spin-labeled phospholipid, *Biochemistry* 20 (1981) 1932–1938.
- [34] A. Chattopadhyay, E. London, Parallax method for direct measurement of membrane penetration depth utilizing fluorescence quenching by spin-labeled phospholipids, *Biochemistry* 26 (1987) 39–45.
- [35] A. Chattopadhyay, Membrane penetration depth analysis using fluorescence quenching: a critical review, in: B.P. Gaber, K.R.K. Easwaran (Eds.), *Biomembrane Structure and Function—The State of the Art*, Adenine Press, Schenectady, New York, 1992, pp. 153–163.
- [36] K. Kachel, E. Asuncion-Punzalan, E. London, Anchoring of tryptophan and tyrosine analogs at the hydrocarbon–polar boundary in model membrane vesicles: parallax analysis of fluorescence quenching induced by nitroxide-labeled phospholipids, *Biochemistry* 34 (1995) 15475–15479.
- [37] A.S. Ladokhin, Distribution analysis of depth-dependent fluorescence quenching in membranes: a practical guide, *Methods Enzymol.* 278 (1997) 462–473.
- [38] A. Chattopadhyay, Role of tryptophan residues in the functional conformation of an ion channel, *Eur. Biophys. J.* 34 (2005) 570.
- [39] G.A. Caputo, E. London, Cumulative effects of amino acid substitutions and hydrophobic mismatch upon the transmembrane stability and conformation of hydrophobic  $\alpha$ -helices, *Biochemistry* 42 (2003) 3275–3285.
- [40] G.A. Caputo, E. London, Position and ionization state of Asp in the core of membrane-inserted  $\alpha$  helices control both the equilibrium between transmembrane and nontransmembrane helix topography and transmembrane helix positioning, *Biochemistry* 43 (2004) 8794–8806.
- [41] S.S. Antollini, Y. Xu, H. Jiang, F.J. Barrantes, Fluorescence and molecular dynamics studies of the acetylcholine receptor  $\gamma$ M4 transmembrane peptide in reconstituted systems, *Mol. Membr. Biol.* 22 (2005) 471–483.
- [42] M. Hayashibara, E. London, Topography of diphtheria toxin A chain inserted into lipid vesicles, *Biochemistry* 44 (2005) 2183–2196.
- [43] A.A. Musse, J. Wang, G.P. DeLeon, G.A. Prentice, E. London, A.R. Merrill, Scanning the membrane-bound conformation of helix 1 in the colicin E1 channel domain by site-directed fluorescence labeling, *J. Biol. Chem.* 281 (2006) 885–895.