# Curcumin is a Modulator of Bilayer Material Properties<sup>†</sup>

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ABSTRACT: Curcumin (1,7-bis(4-hydroxy-3-methoxyphenyl)-1,6-heptadiene-3,5-dione) is the major bioactive compound in turmeric ( $Curcuma\ longa$ ) with antioxidant, antiinflammatory, anticarcinogenic, and antimutagenic effects. At low  $\mu\text{M}$  concentrations, curcumin modulates many structurally and functionally unrelated proteins, including membrane proteins. Because the cell membranes' lipid bilayer serves as a gate-keeper and regulator of many cell functions, we explored whether curcumin modifies general bilayer properties using channels formed by gramicidin A (gA). gA channels form when two monomers from opposing monolayers associate to form a conducting dimer with a hydrophobic length that is less than the bilayer hydrophobic thickness; gA channel formation thus causes a local bilayer thinning. The energetic cost of this bilayer deformation alters the gA monomer  $\leftrightarrow$  dimer equilibrium, which makes the channels' appearance rate and lifetime sensitive to changes in bilayer material properties, and the gA channels become probes for changes in bilayer properties. Curcumin decreases bilayer stiffness, increasing both gA channel lifetimes and appearance rates, meaning that the energetic cost of the gA-induced bilayer deformation is reduced. These results show that curcumin may exert some of its effects on a diverse range of membrane proteins through a bilayer-mediated mechanism.

Turmeric has a long history in Asian cooking and traditional Indian Ayurvedic medicine (1-3). The major active ingredient in turmeric is the polyphenol curcumin (diferuloylmethane, 1,7-bis(4-hydroxy-3-methoxyphenyl)-1,6-heptadiene-3,5-dione), Figure 1.

Curcumin has been reported to have a wide range of pharmacological effects, including antioxidant, antiinflammatory, anticarcinogenic, and antimutagenic actions (4-7). It is not clear how curcumin exerts these many different effects, nor is it clear whether curcumin exerts its effects through just one or through several mechanisms.

Indeed, curcumin modulates the function and expression of a wide range of unrelated proteins (5, 6) including transcription factors (e.g., NF- $\kappa$ B, PPAR $\gamma$ , AP-1, and STAT3); antiapoptotic proteins (e.g., cytochrome c, caspase 9, and Bcl-2); and membrane proteins such as ion pumps, receptors, and channels (see Table 1).

To date no curcumin binding site seems to have been identified on any of these "target" proteins, but curcumin accumulates in biological membranes and is a known membrane-destabilizing agent at concentrations of  $\sim 100 \, \mu M$  (25, 26). These observations raise the possibility that

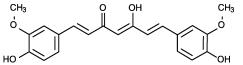


FIGURE 1: Structure of curcumin (diferuloylmethane).

curcumin at the low  $\mu M$  concentrations used in most of the studies in Table 1 could alter membrane protein function by modulating the host lipid bilayer properties, a mechanism whose feasibility we explore in this article.

Generally, bilayer-mediated alterations of membrane protein function arise because membrane-associated proteins are coupled to the bilayer through hydrophobic interactions. This hydrophobic coupling allows changes in bilayer properties to propagate to the proteins, and vice versa (27). Specifically, if membrane proteins undergo conformational changes that involve the protein/bilayer boundary, the protein conformational changes will perturb the adjacent bilayer, which would make the proteins' conformational or state preference sensitive to changes in bilayer material properties (28-31).

To explore whether curcumin alters lipid bilayer properties at pharmacologically relevant concentrations, we used gramicidin (gA<sup>1</sup>) channels to probe for curcumin-induced changes in bilayer material properties (thickness, lipid intrinsic curvature, and the bilayer compression and bending moduli).

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 $<sup>^1</sup>$  Abbreviations: DOPC, 1,2-dioleoyl-sn-glycero-3-phosphocholine; gA, gramicidin; AgA(15), gramicidin analogue [Ala¹]gA; gA^(13), gramicidin analogue des-[Val¹-Gly²]gA^; CFTR, cystic fibrosis transmembrane conductance regulator; curc, used in the context of curcumin concentration [curc], surface density {curc}, and mole mole-fraction  $m_{\rm curc}$ .

FIGURE 2: Schematic model of gA channel formation in lipid bilayers. The three panels show unassociated monomers (top, middle), a right-handed AgA(15) dimer (left), and a left-handed gA<sup>-</sup>(13) dimer (right). The characteristic electrophysiological signatures associated with each state are shown at the bottom of the figure. The hydrophobic thickness of the bilayer is denoted  $d_0$ , and the hydrophobic length of the gramicidin channels is  $l_1$  and  $l_2$  for AgA(15) and gA<sup>-</sup>(13), respectively. The gA/lipid mole-fraction is  $\sim 10^{-6}$  (47), so each gA monomer or channel should be independent of any other channel.

Table 1: Membrane Proteins That Are Modified by Curcumin curcumin activity protein refs 8, 9 epidermal growth factor receptor (EGFR) suppresses expression, inhibits tyrosine phosphorylation human epidermal growth factor receptor 2 (ErbB-2) 10 promotes degradation 9 peroxisome proliferator-activated receptor- $\gamma$  (PPAR $\gamma$ ) stimulates trans-activating activity vascular endothelial growth factor (VEGF) 11 suppresses expression cystic fibrosis transmembrane conductance regulator (CFTR) prolongs channel open time, reducing channel close time 12 - 15inositol 1,4,5-trisphosphate-sensitive Ca<sup>2+</sup> channel (InsP<sub>3</sub> receptor) inhibitor 16 Kv1.4 potassium channels inhibitor 17 mitochondrial permeability transition pore (PTP) promotes opening 18. 19 F0F1-ATPase/ATP synthase inhibitor 20 multidrug resistance-linked ATP-binding cassette transporter (ABCG2) inhibitor 21 multidrug resistance protein 1 (ABCC1) inhibitor 22

gA channels are suitable for this purpose because, first, the channels are formed by the transbilayer dimerization of two nonconducting monomers (32); second, the channels' hydrophobic length usually is less than the bilayer's hydrophobic thickness; and third, the bilayer deforms (thins) locally to adjust to the length of the channel (33); see Figure 2.

sarcoplasmic/endoplasmic reticulum Ca<sup>2+</sup>-ATPase (SERCA)

P-glycoprotein (Pgp)

This membrane deformation incurs an energetic cost that depends on bilayer material properties, which in turn are reflected in the gA channel appearance rate and average lifetime, thus allowing the channels to function as bilayer-spanning force transducers (34). This feature allows for the detection of curcumin-induced alterations in bilayer material properties, whether curcumin increases or decreases bilayer stiffness (35). A decrease in stiffness causes an increased gA channel appearance rate and lifetime; conversely, an increase in stiffness causes a decreased gA channel appearance rate and lifetime.

It is possible to extend this analysis by noting that the energetic cost of deforming the bilayer,  $\Delta G_{\text{def}}^0$ , can be expressed as (36)

$$\Delta G_{\text{def}}^0 = H_{\text{B}}(d_0 - l)^2 + H_{\text{X}}(d_0 - l)c_0 + H_{\text{C}}c_0^2$$
 (1)

The local bilayer thinning associated with channel formation thus will result in a disjoining force ( $F_{dis}$ ) that the bilayer imposes on the bilayer-spanning channel, tending to pull it apart (27):<sup>2</sup>

$$F_{\rm dis} = 2H_{\rm B}(d_0 - l) + H_{\rm X}c_0 \tag{2}$$

where the coefficients  $H_B$ ,  $H_X$ , and  $H_C$  are determined by the bilayer elastic moduli and thickness together with the

channel geometry (36),  $d_0$  is the bilayer's hydrophobic thickness, l is the channel's hydrophobic length, and  $c_0$  is the lipid intrinsic curvature. Equations 1 and 2, and the underlying theory of elastic bilayer deformations (37, 38), have been tested and calibrated by examining how the gA channel lifetimes vary as a function of lipid bilayer thickness (39).

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suppresses expression, inhibitor

inhibitor

It is, in principle, possible to distinguish between changes in the bilayer elastic moduli and intrinsic curvature by using gA analogues of different length, which will result in the formation of channels of different hydrophobic length (with different channel—bilayer hydrophobic mismatches,  $d_0 - l$ ). Changes in intrinsic curvature would alter the lifetimes of short and long channels equally, whereas changes in elastic moduli (in  $H_B$  and  $H_X$ ) would result in a greater change in  $F_{\rm dis}$  for the channel with the greater hydrophobic mismatch.

Using this approach we find that curcumin—at the concentrations at which it modifies many membrane proteins—is a modifier of lipid bilayer material properties. Curcumin thus joins an increasing number of small bioactive phytochemicals (35, 40, 41) that decrease bilayer stiffness and alter membrane protein function. The present results thus provide for a possible mechanistic basis for curcumin's modification of membrane protein function.

 $<sup>^2</sup>$  The deformation energy,  $\Delta G_{\rm def}^0$ , is determined from the local bilayer compression and bending contributions (36, 37). When solving this integral for the energy, the result can be expressed in the form of eq 1. The disjoining force is then obtained as the partial derivative of  $\Delta G_{\rm def}^0$  with respect to the hydrophobic mismatch ( $d_0 - l$ ).

## EXPERIMENTAL PROCEDURES

1,2-Dioleoyl-sn-glycero-3-phosphocholine (DOPC) from Avanti Polar Lipids (Alabaster, AL) was used without further purification. The bilayer-forming solutions were 2% (w/v) of DOPC in 99.9% pure n-decane from ChemSampCo (Trenton, NJ). Curcumin was from Sigma Chemical Co. (St. Louis, MO) and was dissolved in dimethyl sulfoxide from Burdick & Jackson (Muskegon, MI). Curcumin is susceptible to hydrolytic degradation in electrolyte solutions, especially at high pH (42), and is sensitive to light (43, 44). To minimize curcumin deterioration, individual samples were prepared for each day of experiments and kept at -40 °C; exposure to light was kept to a minimum. Because curcumin absorbs to plastics, care was taken to minimize contact with plastic materials-though the single-channel experiments were done in Teflon chambers, which resulted in a loss of 15-30% of added curcumin (data not shown). The gramicidin analogues [Ala<sup>1</sup>]gA (AgA(15)) and des-[Val<sup>1</sup>-Gly<sup>2</sup>]gA<sup>-</sup> (gA<sup>-</sup>(13)) were synthesized and purified as described previously (45).

Gramicidin single-channel experiments were done at 25  $\pm$  1 °C using the bilayer punch method (46). The electrolyte solution was 1 M NaCl, buffered to pH 7.0 using 10 mM HEPES (Sigma). The single-channel measurements where done using a Dagan 3900A Integrating patch clamp (Minneapolis, MN), with 100 or 200 mV applied potential. For some experiments, the reported gA channel lifetimes were pooled from data recorded at both 100 and 200 mV applied potential. In 1.0 M NaCl, the lifetimes of AgA(15) and gA<sup>-</sup>(13) channels vary less than 5% from experiment to experiment and are insensitive to voltage, with no systematic variation between 100 and 200 mV (results not shown). The current signal was low-pass filtered at 2 kHz, digitized at 20 kHz, and digitally filtered at 500 Hz. Single-channel current transition amplitudes and lifetimes were determined and the respective histograms constructed as described previously (46, 47). Average channel lifetimes ( $\tau$ ) were determined by fitting a single exponential distribution  $N(t)/N(0) = \exp\{-t/\tau\}$ , where N(t) is the number of channels with lifetime longer than time t (47), to the lifetime histograms.

The membrane capacitance was measured using a sawtooth potential waveform (31).

Curcumin's stability and adsorption to Teflon were determined using  $25~\mu\mathrm{M}$  curcumin and the same electrolyte solution as was used in the single-channel experiments. Measurements were taken with a Spectronic AquaMate spectrophotometer (Thermo Electron Corporation, Waltham, MA). The absorption spectra were scanned from 300 to 500 nm every 10-15 min; all comparisons were done using the absorption peak of 426 nm (48). For the curcumin stability measurements, comparisons were made between samples without or with exposure to light; for the adsorption measurements, comparisons were made between samples kept in a glass beaker and samples kept in Teflon chambers.

Curcumin's lipid bilayer/electrolyte partition coefficient  $(K_p)$  was determined from the difference between the second derivatives of the absorption spectra measured in solutions having increasing concentrations of unilamellar lipid vesicles (49). The vesicles were prepared by sonication and miniextrusion (50), using a 0.1  $\mu$ m filter (Avanti Polar Lipids). The

lipid suspension was passed though the filter 11 times, at room temperature, which gives a vesicle size distribution with 60–100 nm average diameter (50, 51). Absorption spectra were collected between 300 and 500 nm (at 25  $\pm$  1  $^{\circ}\text{C}$ ) with 25  $\mu\text{M}$  curcumin in the electrolyte solution and varying concentrations of lipid vesicles. Actual phospholipid concentrations were assayed following Chen et al. (52).

 $K_{\rm p}$  was determined as described by Kitamura et al. (49). In brief a nonlinear least-square fit of

$$\Delta D = \frac{\Delta D_{\text{max}} K_{\text{p}}[L]}{[W] + K_{\text{p}}[L]}$$
 (3)

to the results was done using MATLAB 7 (The MathWorks, Inc, Natick, MA), where [W] and [L] are molar water and lipid concentrations, respectively, and  $\Delta D$  is the difference between the second derivatives of the baseline (no phospholipid) spectrum and spectra measured at increasing phospholipid concentrations (24, 41, 63, 84, 130, 185, 276, 369, and 573  $\mu$ M; the individual determinations have less than 2% error, as judged by repeated assays). The second derivatives were obtained from a Savizky—Golay fit to the absorption spectra, and  $\Delta D$  was determined at the wavelength that gives maximal signal, in this case at  $\lambda = 423$  nm.  $\Delta D_{\text{max}}$  and  $K_{\text{p}}$  are fitted parameters with  $\Delta D_{\text{max}}$  being the estimated maximal  $\Delta D$ . The standard deviation of the  $K_{\text{p}}$  estimate was determined using the leave-one-out jackknife (53).

### RESULTS

Curcumin is a potent modifier of bilayer material properties, as evidenced by the curcumin-induced changes in gA channel function, whether it be the longer, right-handed AgA(15) channels or the shorter, left-handed gA $^-$ (13) channels. At low  $\mu$ M concentrations, curcumin increases both the appearance rates and lifetimes of both channel types as already evident from the single-channel current traces (Figure 3).

Curcumin does not alter the current transition amplitudes, as illustrated in the current transition amplitude histograms (Figure 4A), at concentrations up to 6  $\mu$ M (Figure 5A).

In contrast to the invariant current transition amplitudes, the lifetimes of both gA channel types increase as a function of the curcumin concentration ([curc]) (Figures 4B and 5B). Importantly, the lifetime of the shorter gA<sup>-</sup>(13) channels increases more than the lifetime of the longer AgA(15) channels (Figure 5B). This result shows that the effect of curcumin varies as a function of the channel—bilayer hydrophobic mismatch. That is, curcumin reduces the  $2H_B(d_0 - l)$  term in eq 2, most likely by reducing the elastic coefficient  $H_B$ , though we cannot exclude that curcumin may also alter the intrinsic curvature (see Discussion).

For a given channel length, the disjoining force also varies as a function of bilayer thickness (cf. eq 2), meaning that the curcumin-induced increases in channel lifetime could result from bilayer-thinning. Any changes in bilayer thickness, however, would be expected to affect long and short channels equally and therefore be unable to account for the results in Figure 5B. To probe whether curcumin thins the bilayer, we measured the membrane capacitance in the absence and presence of  $10 \, \mu \text{M}$  curcumin. The capacitance

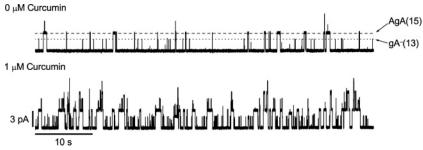


FIGURE 3: Curcumin enhances gA channel activity. Single-channel current traces recorded before and after addition of 1  $\mu$ M curcumin to a DOPC/n-decane bilayer that has been doped with gA $^-$ (13) and AgA(15). The two horizontal lines are drawn at the mean single channel current amplitude for the gA $^-$ (13) channels (dotted) and the AgA(15) channels (dashed). 1.0 M NaCl, 10 mM HEPES, pH 7.0, 25 °C, +200 mV, 500 Hz.

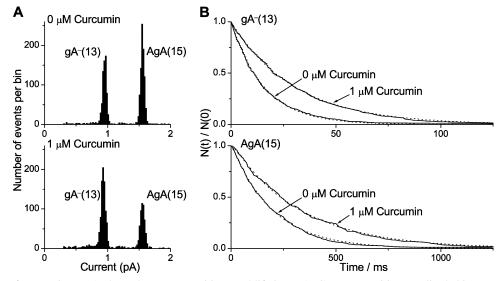


FIGURE 4: Effects of curcumin on gA channel current transitions and lifetimes. A. Current transition amplitude histograms before and after addition of 1  $\mu$ M curcumin for gA<sup>-</sup>(13) channels (left peak) and AgA(15) channels (right peak). B. Normalized single-channel survivor histograms for gA<sup>-</sup>(13) channels (top) and AgA(15) channels (bottom). Note the 10-fold difference in time scale in the lifetime histograms for the shorter gA<sup>-</sup>(13) channels and the longer AgA(15) channels. The histograms were fitted with a single exponential distribution (dotted line) given by  $N(t)/N(0) = \exp\{-t/\tau\}$ . 1.0 M NaCl, 10 mM HEPES pH 7.0, 25 °C, ±100 mV, 500 Hz.

was  $4.8 \pm 0.4 \text{ nF/mm}^2$  in the absence and  $4.4 \pm 0.2 \text{ nF/mm}^2$  in the presence of  $10 \,\mu\text{M}$  curcumin (mean  $\pm \text{SD}$ , n = 5). Curcumin does not decrease bilayer thickness; if anything it increases the thickness.

The single-channel experiments were complicated by the curcumin coloration of the electrolyte solution. Beyond 6 µM curcumin, the lack of visibility hinders the experiment. Moreover curcumin adsorbs avidly to lipid bilayers (present results) and is a bilayer destabilizing agent (25, 26). At concentrations  $\geq 3 \,\mu\text{M}$ , curcumin reduces the stability of the bilayer, meaning that the membranes break frequently and need to be re-formed. Each time a new membrane is formed, a small amount of DOPC/n-decane solution is added to the system, which will tend to deplete the aqueous solutions of curcumin. Thus, if a new membrane is formed in the presence of curcumin, the resulting decrease in [curc] will cause a reduction in the curcumin-induced effect on gA channel function (by 20-50%, as determined by measuring the lifetime before and after breaking and re-forming a membrane). To understand better the basis for the observed decrease in curcumin's apparent effect, we determined curcumin's water/bilayer partition coefficient  $(K_p)$ , which was  $6.3 \pm 1.4 \times 10^5$  (Figure 6).

Given  $K_p$ , we can estimate the curcumin adsorption to the bilayer following Bruno et al. (54). Let {curc}<sub>m</sub> denote the

[curc] in each leaflet of the membrane phase (in moles/area) and [curc]<sub>a</sub> the aqueous [curc]:

$$\{\text{curc}\}_{\text{m}} = K_{\text{p}} \frac{d_0}{2} [\text{curc}]_{\text{a}} \tag{4}$$

where  $d_0$  is the bilayer thickness. Knowing  $K_p$ , {curc}<sub>m</sub>, and [curc]<sub>a</sub>, the conservation relation for curcumin becomes

$$[\operatorname{curc}]_{\text{nom}} V_{\text{aq}} = \frac{[\operatorname{curc}]_{\text{a}} V_{\text{aq}}}{(1 - F_{\text{T}})} + [\operatorname{curc}]_{\text{m}} V_{\text{lip}}$$
 (5)

where [curc]<sub>nom</sub> is the nominal [curc] added to the aqueous solutions,  $V_{\rm aq}$  the aqueous volume,  $V_{\rm lip}$  the volume of the lipid forming solution, and  $F_{\rm T}$  the fraction of curcumin that is adsorbed to the walls of the Teflon chamber. Combining eqs 4 and 5:

$$\{\text{curc}\}_{\text{m}} = K_{\text{p}} \frac{d_0}{2} [\text{curc}]_{\text{a}} = \frac{K_{\text{p}} [\text{curc}]_{\text{nom}} V_{\text{aq}} d_0}{(V_{\text{aq}}/(1 - F_{\text{T}}) + K_{\text{p}} V_{\text{lip}}) 2}$$
 (6)

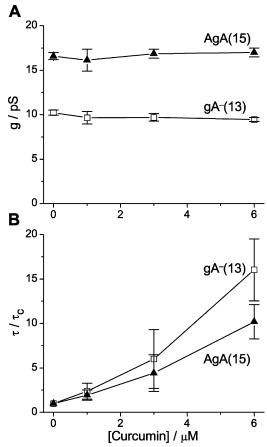


FIGURE 5: gA channel conductance (g) and lifetime ( $\tau$ ) as a function of [curc]. A. AgA(15) and gA<sup>-</sup>(13) channel conductance (mean  $\pm$  SE for n=3-4; mean  $\pm$  range for n=2). B. AgA(15) and gA<sup>-</sup>(13) channel lifetimes normalized with respect to control (0  $\mu$ M) (mean  $\pm$  SE for n=3-4; mean  $\pm$  range for n=2). 1.0 M NaCl, 10 mM HEPES pH 7.0, 25 °C,  $\pm$ 100–200 mV, 500 Hz.

In our case  $V_{\rm aq}=5$  mL,  $V_{\rm lip}\approx 2~\mu L$ ,  $F_{\rm T}\approx 0.3$ , and  $d_0\approx 4$  nm, which leads to  $[{\rm curc}]_{\rm a}\approx (4\times 10^{-3})[{\rm curc}]_{\rm nom}$  and  $\{{\rm curc}\}_{\rm m}\approx (5\times 10^{-4})[{\rm curc}]_{\rm nom}$  cm (note the difference in dimensionality: moles/area vs moles/volume). If  $V_{\rm lip}$  were 4  $\mu L$ , however, then  $[{\rm curc}]_{\rm a}$  and  $\{{\rm curc}\}_{\rm m}$  would be 2-fold less due to the depletion of curcumin from the aqueous phase!

That is, given curcumin's high  $K_{\rm p}$ , any variation in the amount of lipid in the system will alter the curcumin/lipid ratio in the bilayer, which will be reflected in the variation among different experiments (standard errors in Figure 5B). If, however, we compare the relative lifetime increases observed for gA<sup>-</sup>(13) channels against the relative lifetime increases observed for AgA(15) channels (measured in the same experiment, meaning the same curcumin/lipid ratio) the results display a tight straight line behavior (Figure 7), with a slope of 1.599  $\pm$  0.036, mean  $\pm$  SD ( $r^2 = 0.993$ , n = 16).

# DISCUSSION

Curcumin is a promiscuous modulator of many different biological functions and has been shown to alter the function of numerous proteins (5, 6), including membrane proteins (Table 1). In this study we show that curcumin modifies the function of gA channels. The present results thus add to the long list of proteins that are affected by curcumin. The results further show that curcumin, in addition to its antioxidant

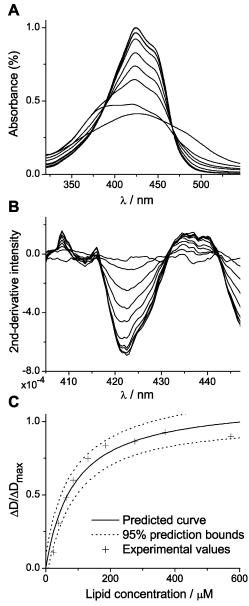


FIGURE 6: Determination of the curcumin's lipid bilayer/electrolyte partition coefficient ( $K_p$ ). A. Absorbance of curcumin at varying concentration of DOPC liposomes (0, 24, 41, 63, 84, 130, 185, 276, 369, and 573  $\mu$ M phospholipid); the results are normalized to the peak adsorption in the absence of lipid vesicles. B. Second derivative of absorbance spectra. The trough at 423 nm was used for the analysis in panel C. C. The solid line is a nonlinear least-squares fit of  $\Delta D = (\Delta D_{\text{max}} K_p[L])/([W] + K_p[L])$  to the data with  $K_p = 6.3 \pm 1.4 \times 10^5$ ; standard deviation was estimated with a leave-one-out jackknife. The dotted lines are upper and lower 95% confidence bounds for a new observation.

effects, modifies lipid bilayer properties, which provides for a novel mechanism by which curcumin could modify membrane protein function.

We discuss first the curcumin-induced changes in gA channel function. Then we consider the implications for integral membrane proteins, including the effects of curcumin on CFTR.

The changes in gA channel function could be due to specific interactions or to general lipid bilayer-mediated changes in channel function. Curcumin most likely does not bind directly to the gA channels. First, gA channels are miniproteins that are fully imbedded in the lipid bilayer with

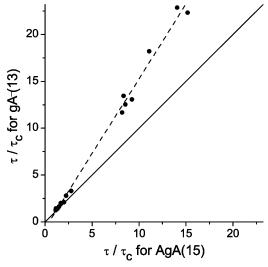


FIGURE 7: The curcumin-induced changes in gA-(13) channel lifetimes vary as a linear function of the changes in AgA(15) channel lifetimes. Each point denotes the relative change in the lifetime of gA<sup>-</sup>(13) channels as a function of the relative change in the lifetime of AgA(15) channels determined in the same experiment. The solid line has a slope of 1 and is drawn for reference, whereas the dashed line is a linear fit to the data giving a slope of 1.599  $\pm$  0.036, mean  $\pm$  SD ( $r^2 = 0.993$ , n = 16). 1.0 M NaCl, 10 mM HEPES pH 7.0, 25 °C, ±100-200 mV, 500 Hz.

no obvious binding or catalytic site. Second, curcumin had no effect on the current transition amplitudes for either channel type tested (Figure 5A) which, given the large changes in single-channel conductance when the amino acid sequence is varied (55, 56), makes direct binding unlikely. Third, both the current transition amplitude and lifetime histograms provide evidence for only one population of gA<sup>-</sup>(13) channels and one population of AgA(15) channels (Figure 4), with the channel properties varying "continuously" as a function of [curc]. Fourth, curcumin has qualitatively similar effects on the activity of two gA analogues of opposite chirality, except that the changes in channel function were more pronounced for the shorter channels (Figure 5B), similar to what has been observed with other small amphiphiles (35, 40). Fifth, there was no evidence for saturation in the changes in gA channel lifetime as a function of [curc] (Figures 5B and 6), even up to nominal concentrations of 6 µM, where we observed a 15-fold increase in  $\tau$ .

Curcumin adsorbs avidly to lipid bilayers; in our system the curcumin mole fraction ( $m_{curc}$ ) in the (unperturbed) bilayer is  $\sim$ 0.01, because curcumin not only will adsorb to the Teflon but also partition into the membrane-forming solution we added to the system. Specifically, for 3  $\mu$ M curcumin (and  $V_{\rm lip} \approx 2 \ \mu \rm L$ ), then the concentration of "free" curcumin in the aqueous solution, [curc]<sub>a</sub>  $\approx$  12 nM and {curc}<sub>m</sub>  $\approx$  1.5  $\times$  10<sup>-12</sup> moles/cm<sup>2</sup> (or 9  $\times$  10<sup>-3</sup> molecules/nm<sup>2</sup>); using an area/lipid molecule of  $\sim 0.7 \text{ nm}^2$  (57),  $m_{\text{curc}}$  is about  $6 \times 10^{-3}$ . As noted, this estimate applies to the unperturbed bilayer; the local  $m_{\rm curc}$  in the vicinity of a channel could be higher due to local accumulation of curcumin adjacent to a bilayerspanning channel in the perturbed lipid bilayer (54).

Though we cannot fully exclude direct curcumin—gramicidin interaction, we conclude that the curcumin-induced changes in gA channel function primarily are due to curcumin's modification of lipid bilayer material properties

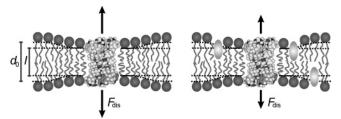


FIGURE 8: Schematic model of curcumin's effect on lipid bilayer properties and gA channel function. When a gA channel forms, the lipid bilayer responds to the local bilayer thinning by imposing a disjoining force ( $F_{\rm dis}$ ) on the channel. When curcumin adsorbs to the bilayer, the bilayer elastic moduli are reduced, leading to a reduction in the magnitude of  $F_{dis}$ , which in turn increases the gA channel lifetime (and appearance rate).

rather than direct curcumin-gramicidin interaction. That is, we can to the first approximation relate the changes in gA channel lifetime to changes in the disjoining force  $(F_{\rm dis})$  the bilayer imposes on the bilayer-spanning channels (cf. eq 2). Because the bilayer thickness is invariant, we conclude that the increase in gA channel lifetimes (Figure 5B) implies that  $F_{\rm dis}$  is reduced as [curc] is increased. This reduction in  $F_{\rm dis}$ reflects the adsorption of curcumin at the bilayer/solution interface, and the force decreases as  $m_{\text{curc}}$  increases (Figure 8). The 60% greater lifetime increase for the shorter gA<sup>-</sup>(13) channels, relative to the longer AgA(15) channels (Figure 7), further means that the change in  $F_{\rm dis}$  is greater for the shorter gA<sup>-</sup>(13) channels. The difference in  $F_{\rm dis}$  between gA<sup>-</sup>(13) and AgA(15) channels reflects the difference in hydrophobic mismatch  $(d_0 - l)$ , and we conclude that curcumin reduces the bilayer elastic moduli, making the bilayer less stiff. Similar amphiphile-dependent changes in bilayer elastic moduli have been reported previously in studies on phospholipid vesicles (58-60) and in studies using gA channels as force transducers (35, 54).

In the case of integral membrane proteins, it becomes more difficult to exclude that curcumin does not bind to the target protein, cf (15, 21). It is in this context important that unrelated membrane proteins are modified at similar nominal [curc] (but see ref 21), as this points to a general, physical mechanism rather than a more specific, chemical mechanism. (Though the nominal [curc] usually is in the  $\mu$ M range, the actual aqueous concentrations may be in the nM range; see above). The parsimonious interpretation of these results is that a major effect of curcumin is to alter bilayer elastic moduli and thus the bilayer-dependent contribution to the free energy difference between different membrane protein conformations; cf (61). Importantly, such bilayer-mediated mechanisms may show vestiges of specificity, as the relative enrichment (or depletion) of amphiphiles adjacent to a membrane protein in a perturbed bilayer may depend upon the amphiphile structure and the extent of the bilayer perturbation (54).

We finally note that curcumin, like capsaicin and genistein, two other small molecules that modify the lipid bilayer material properties (35, 40), also activate CFTR (62, 63) at the concentrations where they modify bilayer material properties. Curcumin has been reported to improve  $\Delta F508$ -CFTR function in vivo (12), a result that could be due to improved trafficking of ΔF508-CFTR to the plasma membrane as well as to enhanced function of channels already in the plasma membrane. Whether or not curcumin improves

trafficking remains controversial (64, 65). That curcumin activates CFTR at the single-channel level is well established (13-15), although the changes in function depend on the experimental conditions. We find that the effect of curcumin, unlike the effect of capsaicin and genistein, is variable even when using robust gramicidin channels (Figure 5B). This variability could be due to curcumin's high lipid/electrolyte partition coefficient, taken together with curcumin's chemical instability (42-44). The variability is reduced by focusing on the curcumin-induced relative lifetime changes for two different gA channels, which eliminates the membrane-to-membrane variation in  $m_{\rm curc}$  (Figure 7).

In conclusion, we have shown that curcumin, in addition to its well-established antioxidant effects, is a general modifier of lipid bilayer material properties at the concentration where it modifies the function of many unrelated proteins. Curcumin's modification of bilayer material properties may provide insight into its ability to modify the function of structurally unrelated membrane proteins, by altering the energetic consequences of the hydrophobic coupling between the protein and the host bilayer.

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