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Theory of the effect of unsaturation on the main-chain transition

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We calculate the temperature of the main transition of lipids as a function of chain length for saturated lipids, and as a function of location of a *cis* double bond for lipids with one or two monounsaturated chains. We employ an extension of Marcelja's self-consistent field method which contains only two interaction parameters, and include many more chain orientations. Agreement with experiment on both the variation with chain length and with location of the double bond is satisfactory.

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I. INTRODUCTION

The main-chain transition of saturated phospholipids has been a subject of a great amount of theoretical study [1] particularly because of its relevance to biology. In the disordered, or liquid crystalline state, the chains are characterized by thermal excitation of several gauche bonds. This causes the chains to be packed somewhat loosely, which permits a diffusion of transmembrane proteins within the lipid bilayer characteristic of a two-dimensional fluid. Such diffusion is necessary for proper cell function. In the ordered, or gel, phase, the number of gauche bonds is reduced, the chains pack more tightly, and the diffusion times increase to a point at which the cell can no longer function. Thus, bilayer composition is regulated so that the chains are in the disordered state at biological temperatures.

The reason that the transition can occur is clear; entropic considerations favor the occurrence of many gauche bonds within the chains. Energetic considerations favor the elimination of such gauche bonds, not only because they are energetically unfavorable with respect to the trans configuration, but also because the van der Waals interaction between chains is enhanced if the chains have few gauche bonds and are therefore relatively well aligned. The competition between the entropy and the cooperative van der Waals interaction energy can produce a first-order transition with temperature in which, *inter alia*, the ensemble average number of gauche bonds changes discontinuously. Because the average lateral extent of the chains is related to the number of gauche bonds, and the volume occupied by the chains is relatively constant, the transition is also reflected in a jump in the average area occupied by each chain.

The importance of the van der Waals interaction is further manifested in several ways. As the chains are made longer, the experimental transition temperature increases, indicating that the ordering effect of the van der Waals interaction between the additional carbons outweighs the entropy arising from the additional configurations these new carbons permit. The dependence of the transition temperature T_m on the number of carbons in the saturated chain, N, is fit rather well by the phenomenological form $T_m(N) = T_m(\infty) - b/N, b > 0$. A further measure of the importance of the van der Waals interaction is the effect that a double bond has on the transition temperature. The presence of a double bond, which in biological systems is most often *cis*, introduces a kink into the chain which prevents the chains from packing as well as they would have in the absence of the double bond, and therefore lowers the transition temperature. The extent to which the transition is lowered depends on the location of the double bond. As might be expected, the effect is least when the double bond is near either end of the chain; if near the head, the kink simply results in initiating the remaining saturated carbon chain at a different point in space. Because the remainder of the chain has fewer carbons than the full chain, the transition temperature is lower according to the phenomenological formula given above. If the kink is near the end of the chain, the disorder introduced does not affect the saturated chain above it, so again the effect is similar to that of simply shortening the saturated chain. The depression of the transition temperature is largest when the double bond is near the middle of the chain [2,3]. A large fraction of membrane lipids are characterized by two chains, one of which is saturated, while the other has a single *cis* double bond near the middle of the chain. It is thought that the unsaturated chain is present to ensure that the membrane is in the disordered, liquid crystalline state at physiological temperatures. There are other lipids, however, which are completely saturated.

There has been renewed interest in packing problems presented by saturated and unsaturated lipids recently. This is due to the belief that lipids in the plasma membrane, which also contains a significant mole fraction of cholesterol, undergo a lateral phase separation into regions rich in cholesterol and saturated lipids which float like rafts in a sea of lipids containing one unsaturated chain [4–6]. It is well known that saturated and unsaturated lipids will phase separate when the former undergoes its main-chain transition [4], and that the presence of cholesterol lowers the transition temperature and weakens its strength [7,8]. All of these threads must be woven together in order to understand raft formation.

The difficulty in calculating the main-chain transition results from the large number of degrees of freedom which characterize the chain. The chains consist typically of 12–22 carbons and their associated hydrogens. Even if one restricts the bonds between carbons to the three states "trans," "gauche plus," and "gauche minus" of Flory's rotational isomeric states model [9], there are of the order of 3^N distinct configurations of a single chain. In addition for a given sequence of these bonds, there are also rotations of the chain about its own axis, specified by one angle, and the various spatial orientations of the chain, specified by two other angles. Additional degrees of freedom are introduced if one considers the headgroups to which the chains are attached.

One approach to the problem posed by such a large number of degrees of freedom is to consider only classes of such states. For example, one might consider only two kinds of states, ordered and disordered [10–12] which have different interactions. The number of states may be many more than just two, as in the ten-state Pink model [13], but it is orders of magnitude smaller than 3^N, and represents a radical reduction in the number of degrees of freedom. Another approach is to assume that the interaction energy between a given chain and other chains, and between a given chain and the aqueous environment is either independent of the chain configuration, or only depends on a few of the carbons [14,15]. This reduces enormously the work of calculating the partition function. Almost all such approximations lead to the introduction of numerous phenomenological parameters. Another way to make the problem tractable is to treat the chains as continuous elastic lines [16], which permits one to utilize the methods of polymer theory [17].

A different approach was taken by Marcelja [18] who considered, for a given value of the three angles which specify the overall orientation of the chain, all of its internal states permitted within the rotational isomeric states model. The interaction energy of a given configuration depended upon the complete specification of the configuration. The execution of this program was limited by the use of only three orientations of the chains.

Very little has been done to calculate the dependence of the transition temperature of a chain with one double bond on the position of that bond, particularly in the most biologically relevant systems in which the lipid has one saturated and one unsaturated chain [15].

In this paper, we extend the calculation of Marcelja to include a sufficient number of chain orientations so that the calculated transition temperature becomes relatively insensitive to additional orientations. There are essentially only two unknown parameters which specify the strength of the interactions of a chain with other chains, and with water. We also extend it to describe the transitions of chains with a single double bond at a location we specify, and the transition of lipids with both a saturated and an unsaturated chain. We compare our results for chains containing up to 16 carbons and find satisfactory agreement with experiment. Finally, we show that in a system with an unsaturated chain, the point at which the first-order main-chain transition ends depends not only on the chain length, but also on the location of the double bond. Thus, short chains with a double bond near either chain end may undergo a first-order transition, while a chain of the same length with the double bond near the center will not.

II. THEORY

We first consider a system of $\mathcal{N}$ saturated chains consisting of $N = n_s + 2$ carbons and their associated hydrogens. The chains are anchored at a planar membrane interface. All but the first and last carbon in the chain have associated with them two hydrogens, and we denote by $\theta_{i,\gamma}$ the angle between the normal to the interface and the normal to the ith plane of two hydrogens and a carbon in the γth chain. An order parameter $\hat{\psi}_\gamma$ is introduced which measures the order of the γth chain,

$$\hat{\psi}_\gamma = \frac{1}{n_s} \sum_{i=1}^{n_s} \left[\frac{3}{2} \cos^2 \theta_{i,\gamma} - \frac{1}{2} \right]. \tag{1}$$

Here, as throughout, the circumflex on $\hat{\psi}_\gamma$ denotes that this quantity depends on the chain configuration. The Hamiltonian of the system is

$$H = \sum_{\gamma=1}^{\mathcal{N}} \left[\sum_{i=1}^{n_s} e_{i,\gamma} + p \hat{a}(\hat{\psi}_\gamma) \right] - \frac{V_0}{2 n_s \mathcal{N}} \sum_{\gamma,\gamma'} \hat{n}_{tr,\gamma} \hat{\psi}_\gamma \hat{n}_{tr,\gamma'} \hat{\psi}_{\gamma'} . \tag{2}$$

The first term is simply the internal energy of the chains as $e_{i,\gamma}$ is the energy of the ith bond in a trans or gauche state. Although there are $n_s + 1$ bonds, rotation of the bond nearest the tail produces no new configuration. The second term represents an interaction between the water outside the membrane and the chains within. The area of the γth chain exposed to water is $\hat{a}(\hat{\psi}_\gamma)$ which depends, in a manner to be specified below, on the configuration of the chain. The strength of this interaction is p. The last term represents the effect of the van der Waals interaction between chains which causes the chains to align parallel to the normal of the membrane.

It might be expected that this term would simply be proportional to $\hat{\psi}_\gamma \hat{\psi}_{\gamma'}$ as in a Maier-Saupe interaction [19]. Marcelja adds to the order parameter the prefactor $\hat{n}_{tr,\gamma}$, which is defined as the number of trans bonds in the γth chain. As these factors are linear in the chain length, the presence of the $1/n_s$ ensures that the energy is extensive in the length of the chain. The effect of this additional factor is to make the chain interaction proportional not to the square of the order parameter but some effective, and larger, power [20]. Indeed, Gruen [21] takes the interaction to be proportional to the cube of the order parameter. The reasoning is that chains which are disordered and, thus, are characterized by a small order parameter, will be well separated. As the van der Waals interaction falls rapidly with distance, an expression for this interaction should depend on a large power of the order parameter.

Because the order parameter of the system, Eq. (1), is not a local one, but is an average over all carbons in the chain, effects arising from local chain interactions, such as occurs in the interdigitation of chains from the two leaves of a bilayer, are not described. However, as the chains in a bilayer are not appreciably interdigitated, we believe that this effect on the main-chain transition and its dependence on the location of a double bond can be ignored. It should also be noted that the Hamiltonian of Eq. (2) contains no variables representing the head groups, so interactions between such groups are ignored. As a result of this simplification, one cannot, for example, describe the difference in transition temperatures between phosphoethanolamines and phosphocholines [2,15].

As the area of the system is not fixed, the appropriate statistical ensemble is one in which the average area is fixed by a surface tension σ;

$$Z(\beta,\sigma)=\sum_{\{\mathcal{N}\}}\exp\left[-\beta\left\{H-\sigma\sum_{\gamma}\hat{a}(\hat{\psi}_{\gamma})\right\}\right], \tag{3}$$

where the sum is over all configurations of the $\mathcal{N}$ chains, and $\beta=1/k_BT$, with k_B Boltzmann's constant and T the temperature. We are actually interested in the ''tensionless state'' of the membrane in which $\sigma=0$, but will carry the functional dependence on σ for completeness.

We utilize the identity

$$\exp\left[\frac{a}{2\mathcal{N}}w^2\right]=\int_{-\infty}^{\infty}dX\left(\frac{\mathcal{N}a}{2\pi}\right)^{1/2}\exp\left[-\frac{\mathcal{N}a}{2}X^2+aXw\right], \tag{4}$$

with

$$w=\sum_{\gamma}\hat{n}_{tr,\gamma}\hat{\psi}_{\gamma}, \tag{5}$$

$$a=\beta V_0/n_s, \tag{6}$$

to obtain

$$Z(\beta,\sigma)=\sum_{\{\mathcal{N}\}}\exp\left[-\beta\left\{H-\sigma\sum_{\gamma}\hat{a}(\hat{\psi}_{\gamma})\right\}\right]$$

$$\equiv\int dX\left(\frac{\mathcal{N}\beta V_0}{2\pi n_s}\right)^{1/2}\exp[-\beta G(\beta,\sigma,X)] \tag{7}$$

$$=\int dX\left(\frac{\mathcal{N}\beta V_0}{2\pi n_s}\right)^{1/2}\exp\left(-\frac{\mathcal{N}\beta V_0X^2}{2n_s}\right)Q^{\mathcal{N}}(\beta,\sigma,X), \tag{8}$$

$$Q(\beta,\sigma,X)\equiv\sum_{\{\}}\exp\left\{-\beta\left[\sum_i e_i+(p-\sigma)\hat{a}-\frac{V_0}{n_s}X\hat{n}_{tr}\hat{\psi}\right]\right\}, \tag{9}$$

$$\frac{\beta G(\beta,\sigma,X)}{\mathcal{N}}=\frac{\beta V_0X^2}{2n_s}-\ln Q(\beta,\sigma,X). \tag{10}$$

Note that $Q(\beta,\sigma,X)$ is the partition function of a *single* chain in the external field X, and the sum in Eq. (9) is over all states of a *single* chain. Because the partition function is that of a single chain, the index γ can be dropped.

In the thermodynamic limit, the integral over X can be evaluated by steepest descents. The integral is dominated by that value of X which extremizes $G(\beta,\sigma,X)$. We denote this value by x. It satisfies

$$x(\beta,\sigma)=\frac{n_s}{\beta V_0}\frac{\partial\ln Q[\beta,\sigma,x(\beta,\sigma)]}{\partial x}, \tag{11}$$

$$=\langle\hat{n}_{tr}\hat{\psi}\rangle, \tag{12}$$

$$\equiv n_{tr}\psi, \tag{13}$$

which can be rewritten as a self-consistent equation for $n_{tr}\psi(\beta,\sigma)$;

$$n_{tr}\psi=\frac{\sum_{\{\}}\hat{n}_{tr}\hat{\psi}\exp\left\{-\beta\left[\sum_i e_i+(p-\sigma)\hat{a}-\frac{V_0}{n_s}n_{tr}\psi\hat{n}_{tr}\hat{\psi}\right]\right\}}{\sum_{\{\}}\exp\left\{-\beta\left[\sum_i e_i+(p-\sigma)\hat{a}-\frac{V_0}{n_s}n_{tr}\psi\hat{n}_{tr}\hat{\psi}\right]\right\}}. \tag{14}$$

In the thermodynamic limit, the exact free energy, $-\beta^{-1}\ln Z(\beta,\sigma)$, is given by $G[\beta,\sigma,x(\beta,\sigma)]\equiv\mathcal{N}\mu(\beta,\sigma)$. We get

$$\mu(\beta,\sigma)=\frac{V_0n_{tr}^2\psi^2}{2n_s}-\beta^{-1}\ln Q[\beta,\sigma,x(\beta,\sigma)]. \tag{15}$$

All the thermodynamic functions follow from the chemical potential. The average area per chain

$$a=-\frac{\partial\mu(\beta,\sigma)}{\partial\sigma}, \tag{16}$$

$$=\langle\hat{a}\rangle, \tag{17}$$

where the expectation value is calculated in the single chain ensemble governed by the partition function $Q[\beta,\sigma,x(\beta,\sigma)]$. The internal energy per chain $\epsilon(\beta,\sigma)$ is obtained from

$$\epsilon(\beta,\sigma)-\sigma a=\frac{\partial[\beta\mu(\beta,\sigma)]}{\partial\beta} \tag{18}$$

$$=\frac{\partial[\beta\mathcal{N}^{-1}G\{\beta,\sigma,x(\beta,\sigma)\}]}{\partial\beta} \tag{19}$$

$$=\left.\frac{\partial[\beta\mathcal{N}^{-1}G(\beta,\sigma,x)]}{\partial\beta}\right|_{x=x(\beta,\sigma)}+\left.\frac{\partial[\beta\mathcal{N}^{-1}G(\beta,\sigma,x)]}{\partial x}\frac{\partial x(\beta,\sigma)}{\partial\beta}\right|_{x=x(\beta,\sigma)} \tag{20}$$

$$=\frac{\partial[\beta\mathcal{N}^{-1}G(\beta,\sigma,x)]}{\partial\beta}\Big|_{x=x(\beta,\sigma)}, \tag{21}$$

as the second term vanishes because $G(\beta,\sigma,x)$ is extremized with respect to x.

Carrying out the partial differentiation of Eq. (15) with respect to β with x fixed, we obtain

$$\epsilon=\left\langle \sum_i e_i+p\hat{a}\right\rangle-\frac{V_0 n_{tr}^2\psi^2}{2n_s}. \tag{22}$$

The entropy per chain $s(\beta,\sigma)$ is obtained from

$$s=-\beta(\mu-\epsilon+\sigma a) \tag{23}$$

and the expressions for the chemical potential and internal energy, Eqs. (15) and (22), respectively.

For our calculations we have chosen $\hat{a}(\hat{\psi})=a_0L_0/\hat{L}(\hat{\psi})$, where a_0 is a constant, L_0 is the end-to-end length of the chain in the all trans configuration, and $\hat{L}(\hat{\psi})$ is the end-to-end length of the chain in the configuration characterized by the order parameter $\hat{\psi}$. Thus, the interaction with water depends on the configuration of the chain, but not on its orientation. The strength of the interaction with water depends on the product pa_0 which is taken to be $pa_0=4\times10^{-14}$ ergs, essentially the thermal energy k_BT of a biological system. The strength of the order parameter interaction is $V_0=6.81\times10^{-14}$ ergs$=980$ cal/mol. These constitute the two parameters of the system, and the first has little latitude. The second is not so constrained, and we could have taken it to be a function of the number of carbons in the tail, a procedure which would have shifted our results in temperature to obtain better average agreement with experiment. We have chosen, with one exception noted below, to keep V_0 fixed so that the theory has as few adjustable parameters as possible. The difference in energy between gauche and trans bonds was taken from the literature, 2.78×10^{-14} ergs$=400$ cal/mol. All calculations are carried out for the tensionless membrane, $\sigma=0$.

We have generated the states to be included in the partition function as follows. We generate all configurations consistent with the rotational isomeric states model. For each configuration, we look at the end-to-end vector and include the following orientations. We first rotate the configuration such that the end-to-end vector is normal to the membrane plane, an angle $\omega=0°$. We discretize the range $0\leqslant\omega\leqslant90°$ into s equal intervals, and then rotate the configuration into each interval, weighting each contribution to the partition function by a factor of $\sin\theta$ to account for orientations simply rotated about the normal to the membrane. For each configuration and value of θ, we discretize the rotations about the end-to-end vector, measured by the angle $0\leqslant\alpha\leqslant360°$ into t equal intervals. Any orientation of any configuration in which a carbon breaks the plane of the membrane is discarded. Thus, in contrast to the three orientations considered by Marcelja [18], or the single one of Gruen [21], we consider $s\times t$ orientations. For small values of this product, we find that the transition temperature varies greatly with it. By varying the number of intervals, we find that $s=10$ intervals of ω and $t=10$ intervals of α are sufficient to determine the transition temperature, in degrees Kelvin, of the model system to within 2%. Further, by examining the average statistical weight of configurations with given orientations, we can see that the configurations which are most important in the ordered state are those with ω less than, or of the order of, 40° while in the disordered state, there is little statistical difference in the average statistical weights of orientations of all angles.

It is straightforward to extend our calculations to chains with one *cis* double bond. The number of CH_2 planes is $n_s=N-4$, instead of $n_s=N-2$ for the saturated chains. The length L_0 is now that of the longest configuration. Further as discussed by Flory [9], the configurations and energies of the bonds adjoining the double bond are different from the others. There are no other changes in the calculation.

To describe lipids containing two chains of different lengths of which one is saturated and the other unsaturated, one must generalize the Hamiltonian of Eq. (2). This can be done in several ways. We choose the following to describe $\mathcal{L}$ lipids. We define an order parameter $\hat{\psi}_{\gamma,k}$ for the γth chain of type $k=1,2$,

$$\hat{\psi}_{\gamma,k}=\frac{1}{n_{s,k}}\sum_{i=1}^{n_{s,k}}\left[\frac{3}{2}\cos^2\theta_{i,\gamma,k}-\frac{1}{2}\right], \tag{24}$$

and the fraction f_k of the total number of CH_2 planes which are in the chain of type k

$$f_k=\frac{n_{s,k}}{n_{s,1}+n_{s,2}}. \tag{25}$$

The Hamiltonian is

$$H=\sum_{k=1}^{2}\sum_{\gamma=1}^{\mathcal{L}}\left[\sum_{i=1}^{n_{s,k}} e_{i,\gamma,k}+p\hat{a}(\hat{\psi}_{\gamma,k})\right]-\frac{V_0}{2\mathcal{L}}\sum_{\gamma,\gamma'}\left(\sum_{k=1}^{2}\frac{f_k\hat{n}_{tr,\gamma,k}\hat{\psi}_{\gamma,k}}{n_{s,k}^{1/2}}\right)\left(\sum_{k=1}^{2}\frac{f_k\hat{n}_{tr,\gamma',k}\hat{\psi}_{\gamma',k}}{n_{s,k}^{1/2}}\right). \tag{26}$$

When the chains are identical, the $f_k=1/2$. As the number of chains is twice the number of lipids, it is seen that the above Hamiltonian reduces to that of Eq. (2) as it should.

Proceeding as before, we obtain

$$\frac{G(\beta,\sigma)}{\mathcal{L}}=V_0\left(\sum_{k=1}^{2}\frac{f_k n_{tr,k}\psi_k}{n_{s,k}^{1/2}}\right)^2-\beta^{-1}\sum_{k=1}^{2}\ln Q_k[\beta,\sigma,x(\beta,\sigma)], \tag{27}$$

where the two, average, coupled, order parameters ψ_k satisfy the self-consistent equations

$$n_{tr,k}\psi_k=[Q_k\{\beta,\sigma,x(\beta,\sigma)\}]^{-1}\sum_{\{\}}\hat{n}_{tr,k}\hat{\psi}_k\exp\left\{-\beta\left[\sum_i \epsilon_{i,k}+(p-\sigma)\hat{a}(\hat{\psi}_k)-2V_0\frac{f_k}{n_{s,k}^{1/2}}\left(\sum_{k=1}^{2}\frac{n_{tr,k}f_k\psi_k}{n_{s,k}^{1/2}}\right)\hat{n}_{tr,k}\hat{\psi}_k\right]\right\}, \tag{28}$$

with

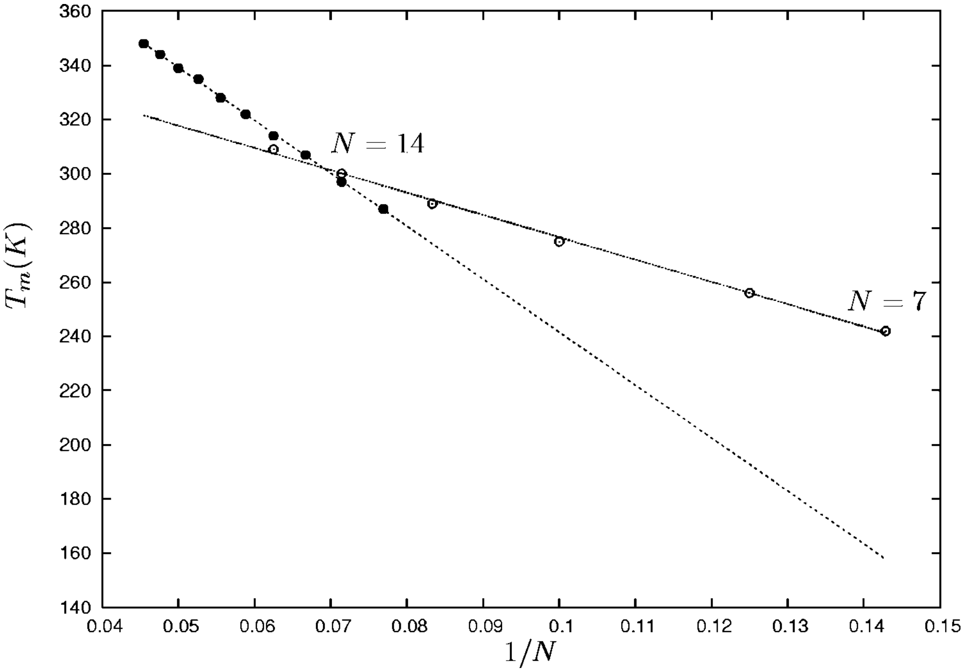

FIG. 1. Main-chain transition, $T_m(N)$, in degrees Kelvin for saturated chains as a function of chain length, N. Calculated results are shown as open circles; experimental phosphatidylcholine results as filled circles.

$$Q_k[\beta,\sigma,x(\beta,\sigma)]=\sum_{\{\}} \exp\left\{-\beta\left[\sum_i \epsilon_{i,k}+(p-\sigma)\hat{a}(\hat{\psi}_k) -2V_0\frac{f_k}{n_{s,k}^{1/2}}\left(\sum_{k=1}^{2}\frac{n_{tr,k}f_k\psi_k}{n_{s,k}^{1/2}}\right)\hat{n}_{tr,k}\hat{\psi}_k\right]\right\}. \tag{29}$$

III. RESULTS FOR SATURATED AND FOR UNSATURATED CHAINS

Our results for the chain melting temperature $T_m(N)$ in degrees Kelvin, as a function of the number N of carbons in the chain is shown in Fig. 1, where $T_m(N)$ is plotted $1/N$, as suggested phenomenologically.

We have calculated the melting temperature for $N \leqslant 16$. As the results are approximately a straight line, they do fit the form observed phenomenologically. Also shown are the experimental results for saturated phosphatidylcholines [2]. One sees that the magnitude of the slope of our results is too small by about a factor of 2. We find that there is a critical point between the value $N=6$, for which the chain does not have a first-order transition, and 7 for which it does. Experimentally, it is found that chains of length $N=8$ do not have a first-order main transition, while chains of length $N=9$ do

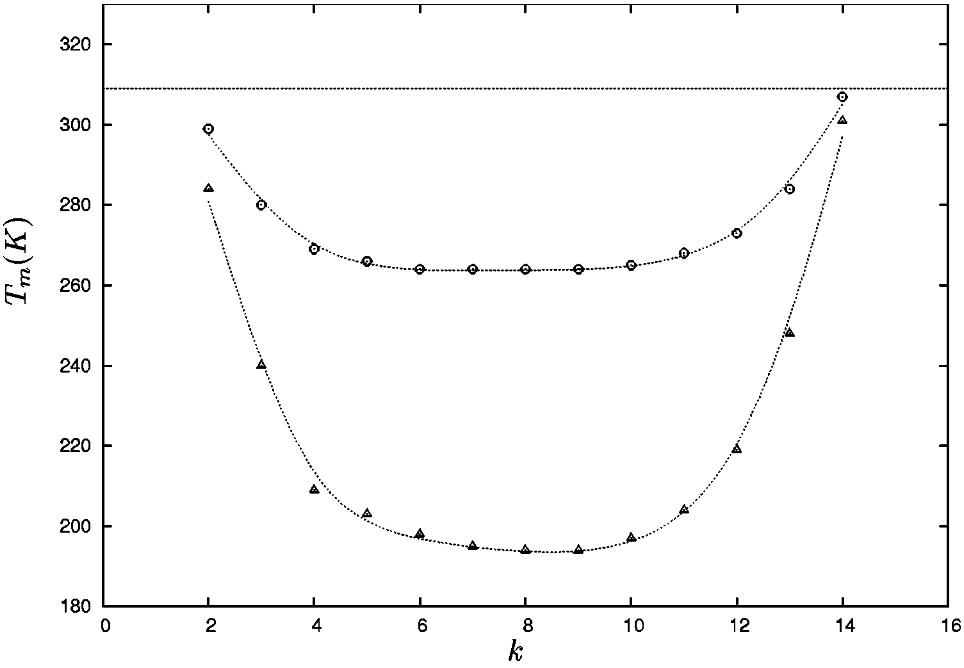

FIG. 2. Chain melting temperature T_m as a function of position of double bond, k, for a chain of length 16. The melting temperature for $C(16){:}C(16)$ is 308°. Triangles denote melting temperatures for $C(16{:}1\Delta^k){:}C(16{:}1\Delta^k)$; circles for $C(16){:}C(16{:}1\Delta^k)$. Dotted lines are guides to the eye.

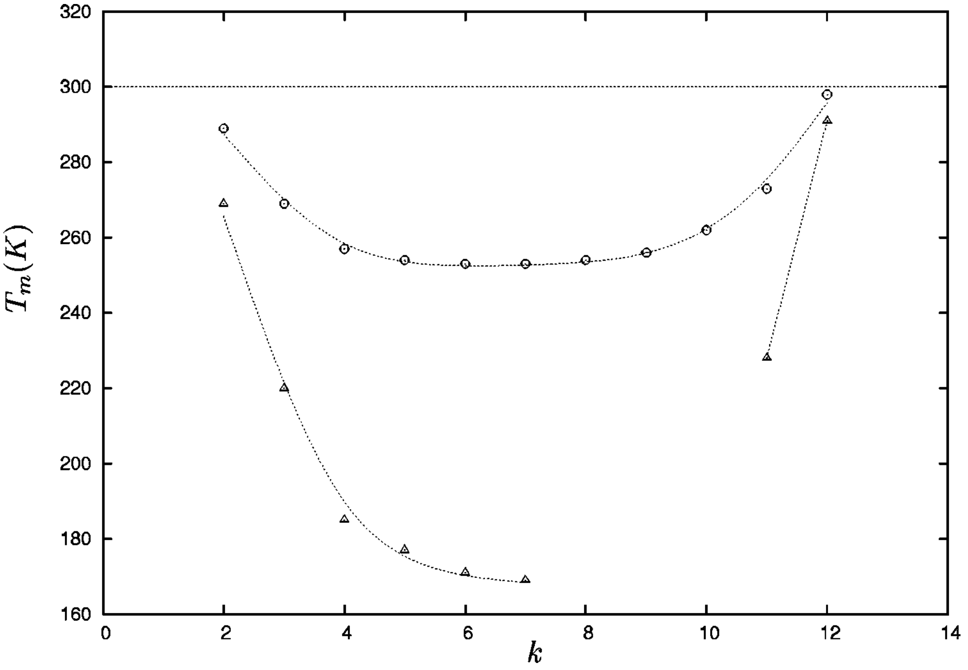

FIG. 3. Chain melting temperature T_m as a function of position of double bond, *k*, for a chain of length 14. The melting temperature for $C(14){:}C(14)$ is 300°. Triangles denote melting temperatures for $C(14{:}1\Delta^k){:}C(14{:}1\Delta^k)$; circles for $C(14){:}C(14{:}1\Delta^k)$. Dotted lines are guides to the eye.

[2]. Presumably, the first-order transition in lipids end at a tricritical point at which the transition becomes a continuous one to a hexatic phase [22]. This transition is not included in our theory, and so our first-order transitions terminate at critical points.

In Fig. 2, we show results for the main-chain transition of a chain of length $N=16$. If the chain is saturated, we obtain $T_m=308$ K which is to be compared to 336 K and 314 K for $C(16){:}C(16)$ phosphatidylethanolamine (PE) and phosphatidylcholine (PC), respectively [2]. The calculated transition temperature of $C(16{:}1\Delta^k){:}C(16{:}1\Delta^k)$ and of $C(16){:}C(16{:}1\Delta^k)$ is shown, with triangles and with circles, respectively, as a function of the location *k* of the double bond. The greatest reduction in transition temperature occurs when the bond is located near the middle of the chain, as is observed experimentally.

Figure 3 shows our results for chains of length 14. We obtain $T_m(14)=300$ K compared to 297 K for $C(14){:}C(14)$ PC. Note that there are no first-order transitions for $8\leqslant k\leqslant 10$.

It is reasonable to assume that, in analogy to the phenomenological equation for the melting temperature of saturated chains, the melting temperature of lipids $C(N){:}C(N{:}1\Delta^k)$ has the form

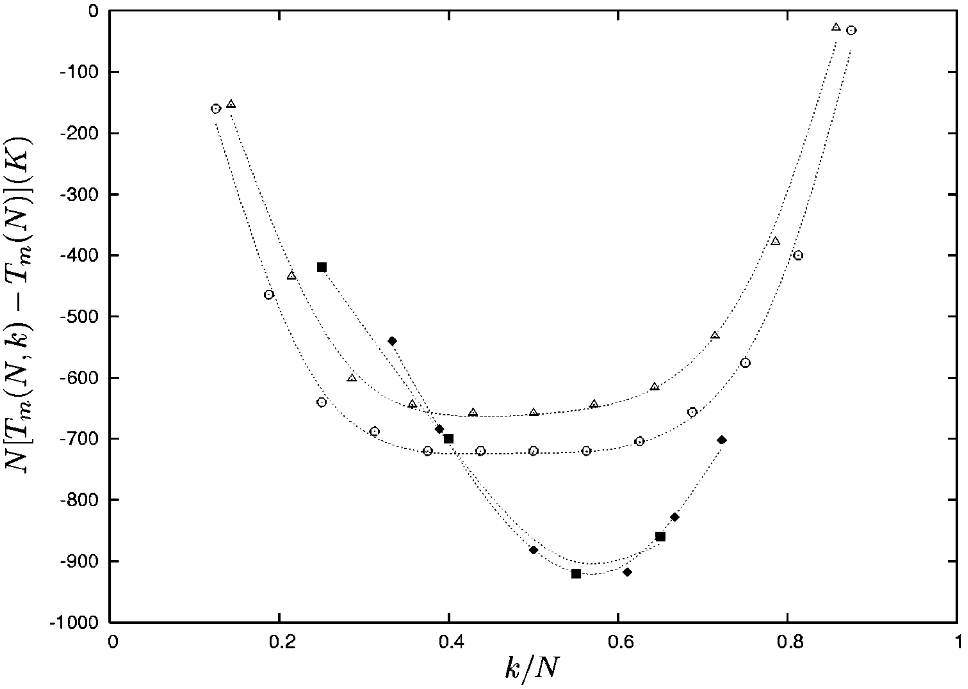

FIG. 4. Difference between transition temperatures of unsaturated and saturated chains of equal length vs position of double bond. Open triangles and circles, calculated results for $N=14$ and 16. Solid diamonds and squares, experimental results for $N=18$ and 20.

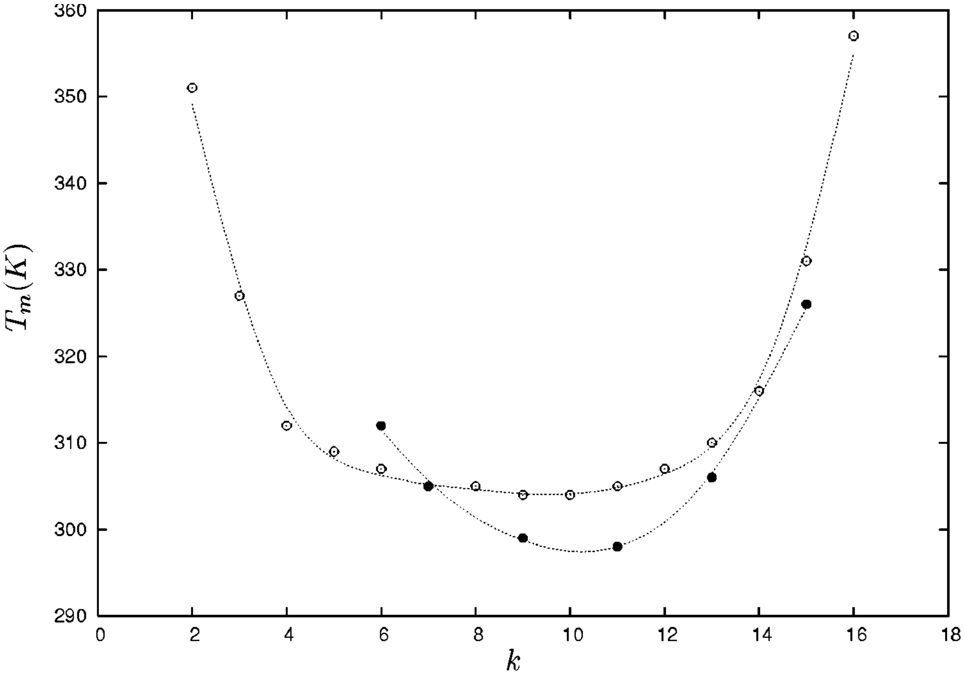

FIG. 5. Calculated (open circles) and experimental (filled circles) transition temperatures T_m for $C(16){:}C(18{:}\Delta^k)$ in degrees Kelvin as a function of double bond position k.

$$T_m(N,k)=T_m(\infty)-\frac{b'(k)}{N}, \quad b'>0. \tag{30}$$

Therefore, we have plotted, in Fig. 4, our results for $C(N){:}C(N{:}1\Delta^k)$ with $N=14$ (triangles), and 16 (circles) in the form of $N[T_m(N,k)-T_m(N)]$ vs k/N as well as experimental results [2] for PCs of $N=18$ (filled diamonds) and 20 (filled squares). While the experimental temperature differences vary somewhat more rapidly with position than do our calculated results, it is clear that the calculated results contain the essence of the effect of the double bond.

We show our results for $C(16){:}C(18{:}\Delta^k)$ in Fig. 5, where we also compare them with experimental results on PEs [2]. Here, we have used $V_0=1200$ cal/mol. The agreement is quite satisfactory.

We note an interesting result. As a saturated chain is shortened, the first-order transition disappears. Clearly this must also happen for a monounsaturated chain, but the temperature at which it disappears will depend on the location of the double bond as well as the chain length. We see from Fig. 3 that $C(14{:}1\Delta^k){:}C(14{:}1\Delta^k)$ has no first-order transition for $k=8,9$, or 10. As the chain is shortened, this region of k increases as is shown in Fig. 6.

In conclusion, we have extended the model of Marcelja [18] to include mixtures of chains of different length and

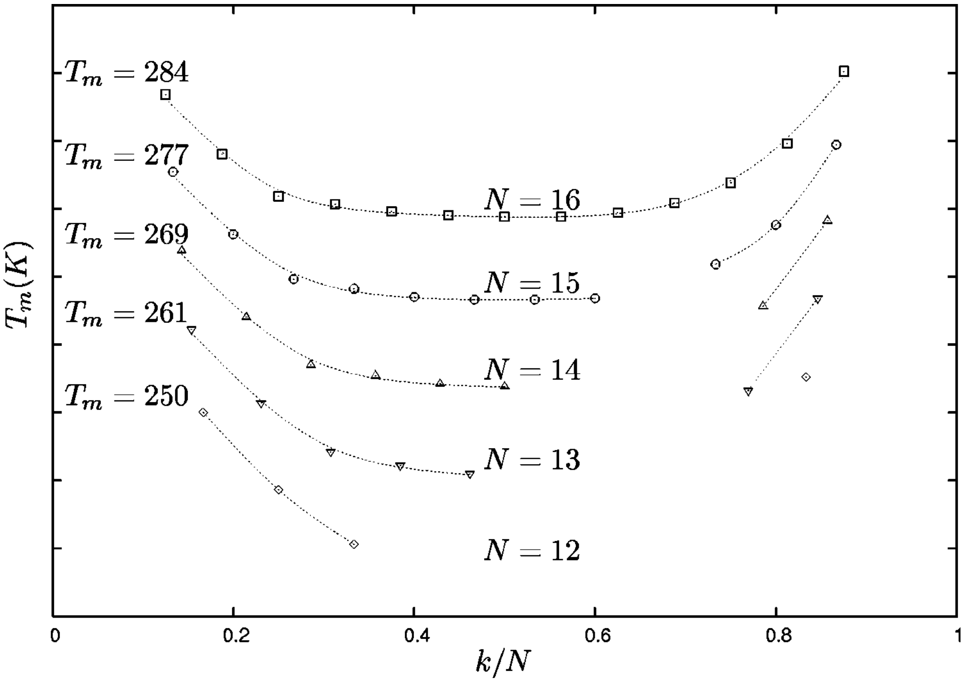

FIG. 6. Transition temperatures for chains of varying length as a function of double bond position. Results for each length have been displaced for clarity.

degree of unsaturation, and included a much larger number of chain orientations in the partition function. With only two unknown interaction parameters, the model captures the essence of the main-chain transition and its dependence on chain length and location of a double bond. The advantage and disadvantage of the model is that the interaction energy of a given chain configuration depends on the entire configuration, as might be expected. The disadvantage is that this makes it difficult to calculate the partition function of long chains which take many configurations and orientations. By direct enumeration, we have calculated results for chains up to $C(16){:}C(18{:}\Delta^k)$. It is possible to include longer chains by Monte Carlo sampling of the configurations. Another direction of improvement would be to incorporate an incompressibility constraint so that the hydrophobic region is liquidlike [23]. Were this possible, the phase separation of saturated and unsaturated lipids should follow and with that, much of the theory of raft formation.

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