

Accurate binding of calcium to phospholipid bilayers by effective inclusion of electronic polarization

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1. Abstract directly from Joe's conference abstracts. To be rewritten. Classical molecular dynamics simulations give detailed information about membrane structure and dynamics. However, there is still a room for improvements in current force fields it is known from the literature, that the binding of ions, especially cations, to phospholipid membranes is overestimated in all classical models [1]. We suggest that the membrane-ion interactions can be corrected by including implicit electronic polarizability into the lipid models through the electronic continuum correction (ECC) [2], which was already applied to monovalent and divalent ions yielding models that feature correct ion pairing [3]. Using the electrometer concept [3, 4] and x-ray scattering form factors, our simulations point out that our hypothesis is correct and ECC is indeed a missing important contribution in current classical lipid models. Moreover, the solid physical principles behind ECC are found not to hamper other relevant properties of a phospholipid bilayer. The new lipid model, "ECC-lipids", shows accurate binding affinity to sodium and calcium cations and head group order parameter response to bound charge. We also provide for the first time a realistic stoichiometry of bound calcium cations to a POPC membrane, and their binding sites. This work will continue as an open collaboration project NMRLipids VI (<http://nmrlipids.blogspot.fi>).

I. INTRODUCTION

Cation interactions with cellular membranes play a key role in several biological processes, like in signal propagation in neurons and vesicle fusion. **2.JOE: list more introductory examples, where it has interesting effects.** Zwitterionic phosphocholine (PC) lipid bilayers have been widely used as model systems to understand molecular level details of specific cation interactions with cellular membranes by using experimental [1–5] and theoretical methods [6? –8] **3.PAVEL: introduce previous theoretical work that discusses cation binding to POPC w.r.t. its specific moieties, e.g. Lukas' paper.** While relative binding affinity of different ions is agreed to follow Hoffmeister series, the molecular details of binding and binding energetics are not agreed in the literature [1–3, 9? , 10]. Non-invasive spectroscopic methods, like nuclear magnetic resonance (NMR), scattering and infrared spectroscopy, give accurate information about ion binding in lipid bilayers [3, 11–15]. Molecular level interpretation of the results, however, requires assumptions about binding models and is often not fully conclusive [?]. On the other hand, the accuracy of the state of the art atomistic resolution lipid and ion models have turned out insufficient for the detailed interpretation of cation binding details [10]. The overestimated specific cation binding observed in current lipid models [10] may lead to artificially positively charged membranes and significant artefacts in MD simulations (e.g. divalent cation-induced charge inversion of bacterial membranes [16] **4.JOE: this may be a too daring statement.**

SAMULI: I think that the divalent cation induced charge inversion is not an artefact, but it might happen with too small concentrations. On the other hand, it is not a new observation either, see e.g. literature cited in NMRLipids IV project.).

In this work we show that the accuracy of ion binding, especially calcium, in zwitterionic PC lipid bilayer can be significantly improved for classical MD simulation models of zwitterionic lipids by including electronic polarizability in the polar region of lipid molecules using the electronic continuum correction (ECC) [17]. This approach has been previously shown to improve performance of ion models against neutron scattering data in concentrated solutions and ab-initio simulations [18? , 19]. The realistic structure of ions in a bulk solvent was not, however, sufficient to correct binding in lipid bilayers [10]. To fix it, we propose a classical fixed-charge MD simulation model of 1-Palmitoyl-2-oleoylphosphatidylcholine (POPC) lipid that accounts for electronic polarizability by using ECC. We will validate such a model by comparing its lipid bilayer structure to x-ray scattering data and its head group structure to NMR experiments. We will then quantify the accuracy of the head group order parameter response to the bound charge and compare it to the experimental NMR data of sodium and calcium binding in PC lipid bilayers. In addition, we will quantify relative binding affinities of different moieties in POPC to such cations. This will be discussed in terms of binding modes, stoichiometry and binding isotherms and their models used in experiments. The proposed POPC model, ECC-lipids, and the approach to obtain it is, hence, highly useful for future MD simulations with physiological salt conditions, and for effects where membrane electrostatics play a major role.

II. METHODS

A. Electronic continuum correction for lipid bilayers

The lack of electronic polarizability in the standard MD simulation force fields has been considered highly relevant is-

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sue since the early days of lipid bilayer simulations. In this work we circumvent the rather demanding explicit inclusion of electronic polarization effects [20] by implicitly including electronic polarizability in lipid bilayer simulations by using the electronic continuum correction (ECC) [17]. Technically, it is a similar approach to the phenomenological charge-scaling as applied in the early studies where a scaling factor one half was used [21, 22]. However, the concept of ECC is physically well justified and rigorously derived [17, 23, 24], but significantly more simple than the explicit inclusion of electronic polarizability [20] both for derivation and application.

According to ECC, electronic polarizability can be included in classical MD simulations by placing all particles into a homogeneous dielectric continuum with a dielectric constant ϵ_{el} , which is the electronic part of the dielectric constant of the media [17]. Measurements of high frequency dielectric constant gives values of approximately $\epsilon_{el} \approx 2$ for almost any biomaterial [17]. Such a dielectric continuum can be easily included in standard MD simulation by a formal transformation of partial charges

$$Q^{ECC} = f_q \cdot Q \quad (1)$$

with a constant scaling factor $f_q = \epsilon_{el}^{-1/2}$ effectively representing the newly introduced electronic continuum. The value measured for water, $\epsilon_{el} = 1.78$, gives a scaling factor of $f_q = 0.75$ [17], which has been successfully used to improve the performance of force field for ions [18, 19].

While the scaling factor of $f_q = 0.75$ for ions in water is well justified and improves the model performance against experimental scattering data [18, 19, 25], it is not clear if the same factor should be used for partial charges in molecules, i.e., lipids in our case. Unlike the total charge of molecules, atomic partial charges within each molecule are not experimental observables. Although there have been proposed several schemes for the assignment of partial charges of molecules, methods targetting at fitting of electrostatic potentials are most popular among classical fixed charge force fields for biomolecules. [26] Currently the most commonly employed scheme is the RESP scheme [27, 28], which fits the electrostatic potential from quantum mechanical calculations. The resulting set of fixed partial atomic charges is hence the best fit to electrostatic potentials of an ensemble of conformations of a molecule. Such a physical meaning is especially well suited for the application of ECC, which targets at improving electrostatic interactions. Depending to the details, partial charge calculations may also partially include some of the solvent electronic polarizability effects. Thus, we expect that the correct ECC scaling factor, f_q , for molecular partial charges does not have to be strictly $f_q = \epsilon_{el}^{-1/2}$, but rather lies between this value (no electronic polarizability in the charge calculation) and 1 (full electronic polarizability already included in the charge calculation).

In this work, we empirically sample this parameter space $f_q \in [0.75, 1.0]$ to find an atomistic MD simulation force field parameters for lipids that accurately describe the lipid head group response to varying concentrations of cations when

compared to NMR data [14, 15, 29]. Such data can be used to accurately assess ion binding in PC bilayers, as discussed in Ref. 10 and in section II B. We chose Lipid14 [30] force field parameters as a starting point, because their response to bound ions was apparently most realistic against NMR data in recent work by NMRLipids project (see Fig. 5 in Ref. 10). Also glycerol backbone and head group structures in Lipid14 model were relatively realistic when compared with other state of the art lipid models [31]. The ECC correction was applied to Lipid14 parameters by scaling partial charges of the head-group, glycerol backbone and carbonyl regions, which are the most polar parts in lipids and are expected to have the largest contribution to the cation binding. The hydrocarbon chain parameters are not modified, because they are already highly optimized and give generally a good description for hydrophobic part of lipid bilayers in various conditions in most lipids models, including Lipid14 [32]. In contrast, improvements in glycerol backbone and headgroup parameters are required in all available lipid models [31].

Exploring different scaling factor values, applied to head-group, glycerol backbone and carbonyl charges of Lipid14 model, we found out that ion binding and related headgroup order parameter responses become weaker. The optimal behaviour of ion binding was observed with the scaling factor $f_q = 0.8$. Interestingly, this scaling factor is in line with the estimate given by “implicitly polarized charges” (IPolQ) [33] combined with RESP calculations in vacuum and implicit solvent reported in [34]. IPolQ charges are obtained as the average of partial charges given by RESP calculation [27] in vacuum and in a solvent. Applying the scaling factor of 0.75 to IPolQ charges calculated from the data in Ref. [34], gives similar partial charges to ones obtained by scaling Lipid14 charges with a factor 0.8.

While, the charge scaling improved the behaviour of lipid-ion interactions, it reduced the area per molecule of lipid bilayer without ions below experimental values. Simulations with Lipid14 parameters having partial charges of headgroup, glycerol backbone and carbonyls scaled with 0.8 gave the area per molecule value of $\approx 60 \text{ \AA}^2$, which is significantly smaller than the experimental value 64.3 \AA^2 ([5.missing REF for APL experiment]) and the original Lipid14 value $(65.6 \pm 0.5) \text{ \AA}^2$ [30]. The decrease of area was found to arise from a lower hydration of the lipid head group region, which can be explained by the decreased solvation free energy due to the lower polarity of molecules with scaled charges. The hydration can be increased by reducing the effective radius of atoms by changing the σ parameters in Lennard-Jones potential for the selected atoms similarly as done for free ions in solution [18, 19, 25]. This increases solvation free energy by allowing water molecules to approach closer to lipid atoms and have stronger electrostatic interactions with them. After reducing the σ parameters with a factor of $f_\sigma = 0.89$ for the same atoms for which charges were scaled, the area per molecule value was again in agreement with experimental value (see Table II).

B. Comparison of ion binding affinity to experiments by using the electrometer concept

Ion binding was compared between experiments and simulations by using lipid head group order parameters and "electrometer concept" [10, 36]. The concept is based on the experimental observation that the C-H bond order parameters of α and β carbons in lipid head group (see Fig. 1) are proportional to the amount of bound charge in a lipid bilayer [36]. This is rationalized as a change of lipid head group dipole tilt to more vertical orientation with bound positive charge and *vice versa* for negative charge [36]. More recent analysis in the NMRlipids project concluded that the order parameters decrease with bound positive charge and increase with bound negative charge when the signs are taken in account [10, 32]. The concept was also shown to be suitable for the comparison of ion binding affinity in lipid bilayers between simulations and experiments [10].

The order parameters for α and β segments in headgroup, as well as for all C-H bonds in lipid molecules, can be accurately measured by using ^2H NMR or ^{13}C NMR techniques. The order parameters can be calculated from MD simulations by using the definition

$$S_{\text{CH}} = \frac{3}{2} \langle \cos^2 \theta - 1 \rangle, \quad (2)$$

where θ is the angle between the bond and membrane normal and average is taken over all sampled configurations [32].

According to the electrometer concept, the change of the head group order parameters as a function of the amount of bound charge per lipid X^\pm can be written as [37]

$$\Delta S_{\text{CH}}^i = S_{\text{CH}}^i(X^\pm) - S_{\text{CH}}^i(0) = \frac{4m_i}{3\chi} X^\pm, \quad (3)$$

where $S_{\text{CH}}^i(0)$ denote the order parameter in the absence of bound charge, i refers to either α or β carbon, m_i is an empirical constant depending on the valency and position of bound charge, and the value of the quadrupole coupling constant is $\chi \approx 167 \text{ kHz}$. Atomic absorption spectra and ^2H NMR data gave $m_\alpha = -20.5$ and $m_\beta = -10.0$ for Ca^{2+} binding to POPC bilayer (in the presence of 100 mM NaCl) [10, 15, 32]. Before using electrometer concept to analyze cation binding, we calibrate the response of headgroup order parameters to the bound charge in the simulation models. This is done by comparing the slope m_i in Eq. 3 between simulations and experiments of cationic surfactants in POPC bilayer [29]. Since essentially all surfactants locate in bilayer, the molar ratio directly gives the amount of bound charge per lipid X^\pm is these systems.

C. Ion concentrations and binding affinity

The experimental headgroup order parameter data used in this work is reported as a function of cation concentration remaining in the bulk solvent [14, 15]. To determine the same concentration from simulations, we use large enough

box to ensure that the ion concentration reaches a clear plateau and the electroneutrality is satisfied at the edge of simulation box. It should be noted that the recent work by NMR-lipids project compared simulations to the same experimental data by using the relative molar concentration in water $[\text{salt}] = N_c \times [\text{water}] / N_w$, where $[\text{water}] = 55.5 \text{ M}$ [10]. This is not exactly the same as the concentration reported in the used experimental data, because the binding of ions in bilayer reduces the bulk concentration. The difference slightly moves points towards lower concentrations but do not affect the conclusions in the previous study [10].

The ion binding affinities between different models were compared by calculating the relative surface excess of ions with respect to water, Γ_i^w , as [38]

$$\Gamma_i^w = \Gamma_i - \Gamma_w \frac{C_i - C'_i}{C_w - C'_w} \quad (4)$$

$$\Gamma_a = \frac{n_a - C_a V - C'_a V'}{A}; \quad a = i, w, \quad (5)$$

where index i and w denote ions and water respectively, prime accent denotes the phase inside bilayer, whereas non-prime symbols account for bulk water phase, n is the total amount of water or ions, C denotes bulk concentrations, V is the volume of the respective phase separated by the Gibbs dividing plane, A is the area of the interface, and Γ_a is the surface excess of water or ions. As Γ_i^w does not depend on the definition of the interfacial region and the position of the Gibbs dividing plane [38], we consider the whole simulation box as an interface. Note that phospholipid membranes are bilayers, and hence the interface occurs in the simulation box twice providing a surface area $2A$. The concentrations of water and ions inside the bilayer can be expected to vanish, thus $C'_{i,w} = 0$. This provides us a simplified relation for the relative surface excess of lipid bilayers in simulations

$$\Gamma_i^w = \frac{1}{2A} \left(n_i - n_w \frac{C_i}{C_w} \right), \quad (6)$$

where the bulk concentrations, C_w and C_i , can be determined from the concentration plateau at the edge of the simulation box.

D. Comparison of lipid bilayer structure to experiments

Lipid bilayer structure without ions was validated against NMR experiments by order parameters for C-H bonds and x-ray scattering experiments by using form factors. The former validates the structures sampled by individual lipid molecules in simulations with segmental resolution, while the latter validates the dimensions of the lipid bilayer (thickness and area per molecule) [32].

The order parameters were calculated from simulations for all C-H bonds in lipid molecule by using Eq. 2. Form factors

TABLE I: Simulation parameters

| simulation property | parameter |
|---------------------------|--|
| time-step | 2 fs |
| equilibration time | 100 ns |
| simulation time | 200 ns |
| temperature | 313 K |
| thermostat | v-rescale [50] |
| barostat | Parrinello-Rahman, semi-isotropic [51] |
| long-range electrostatics | PME [52] |
| cut-off scheme | Verlet [53] |
| Coulomb and VdW cut-off | 1.0 nm |
| constraints | LINCS, only hydrogen atoms [54] |
| constraints for water | SETTLE [55] |

7.This could be moved to SI. Only simulation lengths needs to be mentioned in the main paper.

TABLE II: Area per lipid (APL) from different models of POPC without ions

| model | APL (Å ²) | Temperature [K] |
|--|-----------------------|-----------------|
| Lipid14 [30] | 65.6 ± 0.5 | 303 |
| ECC-lipids | | |
| (4.6 · 5.1 nm ²), 72 lipids patch, OPC3 | 63.2 | 313 |
| (6.4 nm) ² , 128 lipids patch, OPC3 | 64.2 | 313 |
| (6.4 nm) ² , 128 lipids patch, SPC/E | 65.1 | 313 |
| (6.4 nm) ² , 128 lipids patch, OPC | 64.4 | 313 |
| (6.4 nm) ² , 128 lipids patch, TIP4p/2005 | 66.8 | 313 |
| experiment [60] 12.REF | 64.3 | 303 |
| experiment | 67.3 | 323 |

13.SAMULI: I would put here Lipid14 in 303K, ECC-lipid in 303K and experiment in 303K. Rest in SI. The best experimental value would be the one analyzed from the form factor shown in previous figure, if available.

were calculated from equation

$$F(q) = \int_{-D/2}^{D/2} \left(\sum_{\alpha} f_{\alpha}(q_z) n_{\alpha}(z) - \rho_s \right) \exp(izq_z) dz, \quad (7)$$

where $f_{\alpha}(q_z)$ is the density of atomic scattering length, ρ_s is the density of solvent scattering length, $n_{\alpha}(z)$ is the number density of atom α and z is the distance from the membrane centre along its normal spanning the membrane with thickness D .

E. Simulation details

1. Simulations with aqueous ions

The simulated systems consisted of 1-Palmitoyl-2-oleoylphosphatidylcholine (POPC) bilayer and an aqueous salt solutions of varying concentrations. In particular, the periodic orthorhombic simulation box contained 128 POPC molecules and approximately 50 water molecules per each lipid. Water molecules were described by OPC3 model [39] as it is currently the most accurate three site rigid water model. In order to test transferability of the newly developed ECC-lipids model, we also performed several additional simulations with water models OPC [40], SPC/E [41], TIP3p-FB and TIP4p-FB [42], and TIP4p/2005 [43] presented in Supporting Information (SI). We used ECC-ions model for ions [19, 25?]. Simulations with Lipid14 use ion models by Dang [44–46], and by Åqvist [47]. Classical molecular dynamics simulations were performed using the GROMACS [48] simulation package (version 5.1.4). The simulation settings used in this work are summarized in Table I, and they are based on previously used settings in [10] available at [49]. Simulation trajectories and parameters are available at [?]

6.To be uploaded to Zenodo.

2. Simulations with cationic surfactants

Automated topology builder [56] was first used to create the structure of dihexadecyldimethylammonium bromide, $C_{12}Cl_{16}^+N_2C_1Br^-$, molecule. AmberTools program [57] was then used to generate the Amber-type force field parameters. The parameters were converted to the Gromacs format by using acpype tool [58]. The partial charges were then manually modified to approximately correspond to their equivalent segments in Lipid14 [30]. The surfactants were randomly placed among the lipids to form bilayer structures with mole fractions 10%, 20%, 30%, 42% and 50% of surfactant in the POPC bilayer. All systems contained 50 POPC molecules per leaflet, 6340 TIP3P water molecules and 6, 14, 21, 35 or 50 surfactants per leaflet. The systems were simulated for 200 ns using Lipid14 model for POPC. First 20 ns was omitted from the analysis.

The same systems were also simulated with ECC-lipid model for POPC **8.How long?**. In these simulations the ECC correction was also applied to the cationic surfactant by scaling all **9.Were all scaled? Are there charges is tails? Were those scaled as well in this case?** charges with the same factor as for ECC-lipids, $f_q = 0.8$, and by using the atom types with reduced σ parameters from ECC-lipids.

III. RESULTS AND DISCUSSION

A. POPC membrane and its structure

In order to validate the newly developed model, ECC-lipids, we compared our simulation results without any ions to NMR order parameters measurements and x-ray scattering form factors (Fig. 1 and Table II). The tail order parameters being already highly optimized in the original Lipid14 model [30] are found to match the experimental values nicely. The head group and glycerol backbone order parameters accuracy is comparable to the state of art lipid models available in literature [32]. The agreement between the x-ray scattering

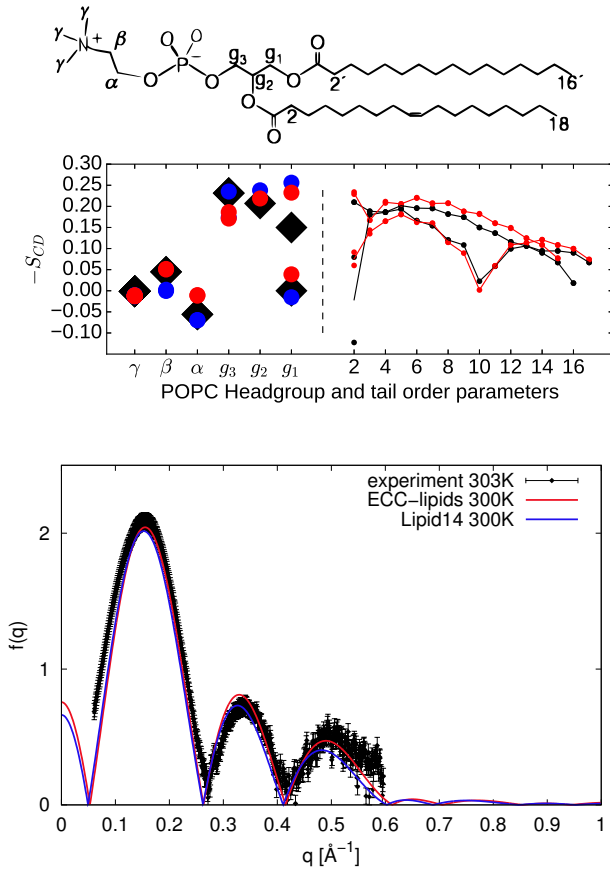


FIG. 1: X-ray scattering form factors from experiments [?] and simulations using Lipid14 [30] and ECC-lipids models. Order parameters of head group, glycerol backbone and sn-1 and sn-2 tails from simulations with Lipid14 [30] and ECC-lipids models compared with experimental order parameters from [59].

10. There seems to be a typo in experimental value for other order parameter for C2 carbon in sn-2 chain; it should be negative. The scale of the y-axis should be then zoomed when this is fixed.

11. x-axis scale in form factor figure from 0 to 0.6, until where experimental data is available.

form factors and the areas per molecule from simulations and experiments confirm that the membrane structural properties are well captured. A structural comparison of ECC-lipids with Lipid14 can be found in SI along with results with other water models.

B. Response of POPC headgroup to bound charge

Before proceeding to ion binding affinity studies, we quantify the response of headgroup order parameters to the amount of bound charge by using mixtures of monovalent cationic surfactants and POPC [29]. The amount of bound charge per PC in these systems is given by the molar fraction of cationic surfactants, because essentially all surfactants locate in the lipid bilayers. Comparison of headgroup order parameter changes between simulations and experiments as a function of mole

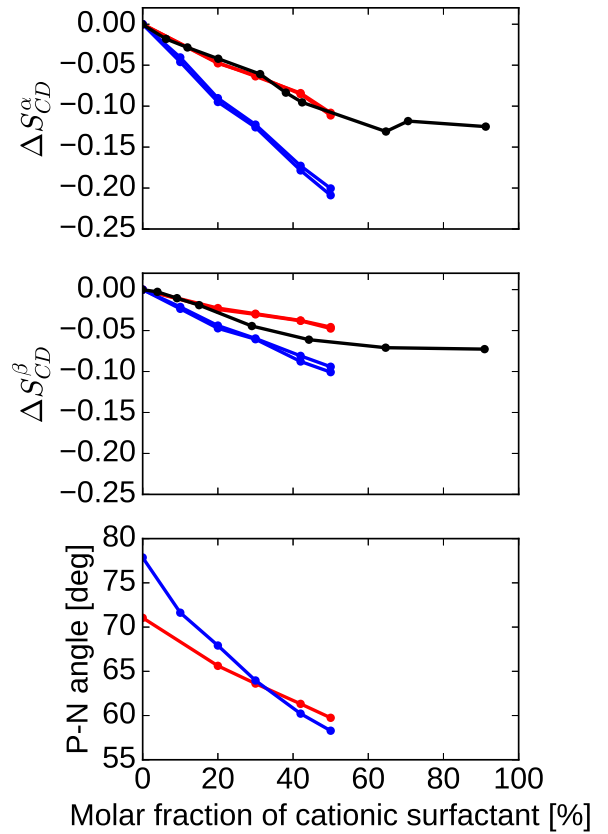


FIG. 2: Headgroup order parameter changes and P-N vector orientation as a function of cationic surfactant (dihexadecyldimethylammonium bromide, $C_{12}Cl_{16}^+N_2C_1Br^-$) in PC bilayer from simulations and experiments [29].

14. Labels are missing.

15. Order should be the same as in other figures, i.e., β segment on top.

16. I would put x-axis from 0 to 51 and maybe zoom y-axis little bit as well.

fraction of cationic surfactants can be then used to validate the sensitivity of lipid headgroup to bound charge in simulation models.

The headgroup order parameter changes as a function of mole fraction of cationic surfactant dihexadecyldimethylammonium bromide ($C_{12}Cl_{16}^+N_2C_1Br^-$) is compared between experiments [29] and simulations in Fig. 2. Approximately linear decrease of the order parameters is observed in simulations and experiments with increasing amount of cationic surfactants up to mole fractions of $\sim 50\%$, as expected from Eq. 3. The slope is, however, too steep in Lipid14 model indicating that the headgroup order parameters are too sensitive to a bound charge. The ECC-lipids model gives a slope in very good agreement with experiments for the α segment, while the slope is slightly underestimated for the β segment.

17. SAMULI: We could calculate the slopes from simulations, but I am not sure if we would actually learn anything useful from this.

Also the effect of bound cations on the headgroup P-N vector angle with respect to the membrane normal is shown in Fig. 2. The headgroup orients more parallel to the membrane normal with an increasing amount of bound cations, as ex-

pected [36]. The orientation effect is more pronounced in Lipid14 model than in ECC-lipids model, which is in line with the order parameter results and reduced charge–dipole interactions in the ECC-lipid model. Since the response of α -order parameter is in very good agreement with experiments in ECC-lipid model, we can suggest a relation between order parameter and P-N vector angle changes. The data gives $\Delta\Theta_{P-N} = \Delta S_{CH}$, which can be used to estimate P-N vector angle changes from experimental results for α order parameters. 18.SAMULI: I think that we should establish the relation between order parameter and P-N vector angle changes by using ECC-lipids model. This would be useful for people measuring alpha order parameter changes from experiments.

C. Cation binding affinity in POPC

The linear decrease of the headgroup order parameters, quantified in previous section, can be used to measure the amount of bound aqueous cations in lipid bilayers [10, 36]. The headgroup order parameter response to NaCl and CaCl₂ concentrations from experiments (DPPC [14] and POPC [15]) and different simulation models for POPC are shown in Fig. 3.

As already discussed previously [10], NaCl has a negligible effect on the headgroup order parameters with submolar concentrations due to the very weak binding in PC bilayers. In contrast to almost all the other simulation models, this behaviour is reproduced by Lipid14 model with Åqvist ions [10]. The headgroup order parameter response to CaCl₂ concentration was, however, overestimated with the same combination of force field parameters [10]. The results were not improved when ion models by Dang et al. [44–46] or ECC-ions [19, 25] with more realistic bulk behaviour were used, as seen in in Figs. 3 and ?? (in SI), respectively. 19.Add OP-response of Lipid14+ECC-ions plot in SI. Together with extensive data in previous work [10], the results suggest that CaCl₂ binding behaviour in PC bilayers cannot be corrected by only improving the ion models.

Significant improvement is achieved when the developed ECC-lipid model is used. The headgroup order parameter changes as a function of CaCl₂ concentration model show a good agreement between ECC-lipid model and experiments in Fig. 3. Ion binding affinity is quantified by using the relative surface excess between ions and water from Eq. 6 and density profiles along membrane normal shown in Fig. 4. The relative surface excess for ECC-lipid model with ECC-ions $\Gamma_i^w = 0.07nm^{-3}$ is significantly smaller than for Lipid14 with Åqvist $\Gamma_i^w = XXnm^{-3}$ and Dang ions $\Gamma_i^w = 0.3nm^{-3}$.

20.This paragraph is to be finalized when we have the surface excess analysis done by using Eq. 6.

The good agreement with experiments indicates that the ECC corrected lipid model has a sufficient accuracy for realistic studies of details of ions binding to lipid bilayers.

26.SAMULI: Maybe we should discuss the repeat distances and area per molecules measured at [4, 5, 61]

D. Binding stoichiometry

The good agreement of ECC-lipids model with experiments encourages us to analyse the molecular binding details from MD simulations. Direct analysis of contacts between ions and lipids from simulations suggest that the most abundant POPC:Ca²⁺ complex has stoichiometry of 2 POPC:1 Ca²⁺. As shown in Fig. 5 this is in agreement with the ternary complex model suggested based on head group order parameter experiments [15]. In addition to the ternary complexes, there also is a non-negligible probability of one Ca²⁺ cross-bridging three POPC molecules. Technical details of the analysis are in the SI.

In addition, we estimated the relative binding affinities of several moieties in POPC: phosphate moiety, side chain 1 carbonyl group and side chain 2 carbonyl group. Using the probability isodensity contours (see Fig. 6), we estimate that the largest contribution to the binding of Ca₂⁺ to POPC membranes likely comes from the phosphate group. Although the isodensity plots are relatively easy to interpret, the contours shown in Fig. 6 cannot conclusively tell on the details of Ca₂⁺ binding to any of the two carbonyl moieties.

27.JOE: Put details of the cation-binding stoichiometry analysis to SI.

28.JOE: Update the binding isotherm figure with new simulations

29.SAMULI: The same authors have also literature, where they say that ternary complex may not be the only option. I will recheck and come back to this. SAMULI: This is written in [62]: "Ca2+binding to POPC bilayers over the whole concentration range can be best described in terms of formation of a ternary complex involving complexation of two lipids to one calcium ion (Altenbach and Seelig, 1984). The addition of a sodium competition term has not changed this conclusion. However, if Ca2+ concentrations up to 100 mM are considered, the data can be equally well explained by a 1:1 binding mechanism (cf. Figure 7). In contrast, the Ca2+ binding to POPC-POPG mixtures can be best described by assuming a 1:1 stoichiometry regardless of the range of Ca2+concentrations." We might or might not want to discuss about this.

30.SAMULI: I would also analyze how much there is contact between ions and different parts of the lipid (phosphate, carbonyl, etc.). JOE: Pavel suggest using volumetric map (e.g. in VMD) to visualise the amounts of Ca, Na and Cl bound to different moieties.

31.SAMULI: I think we should quantify this, i.e. how much there are these. Maybe also the other possible complexes? Maybe also the correlation between complexes and binding sites, if it is not too much work. JOE: This looks like a careful work for the next paper to me. I'd only add a relatively simple analysis of binding sites and probably the propensity of 1-2-3 membered clusters. SAMULI: I agree that we should not use too much time on this now..

32.Finalize stoichiometry analysis for Na⁺, Ca²⁺, their interaction energies with the lipid membrane, etc, and finalize the discussion after these results.

IV. CONCLUSIONS

We show that the Na⁺ and Ca²⁺ binding in phospholipid bilayers can be accurately described with classical MD simulation models, where electronic polarization is effectively included by using electronic continuum correction (ECC) [17]. This is a significant improvement over other available lipid models, which all overestimate specific cation binding affinities [10]. The newly proposed model, which we denote as

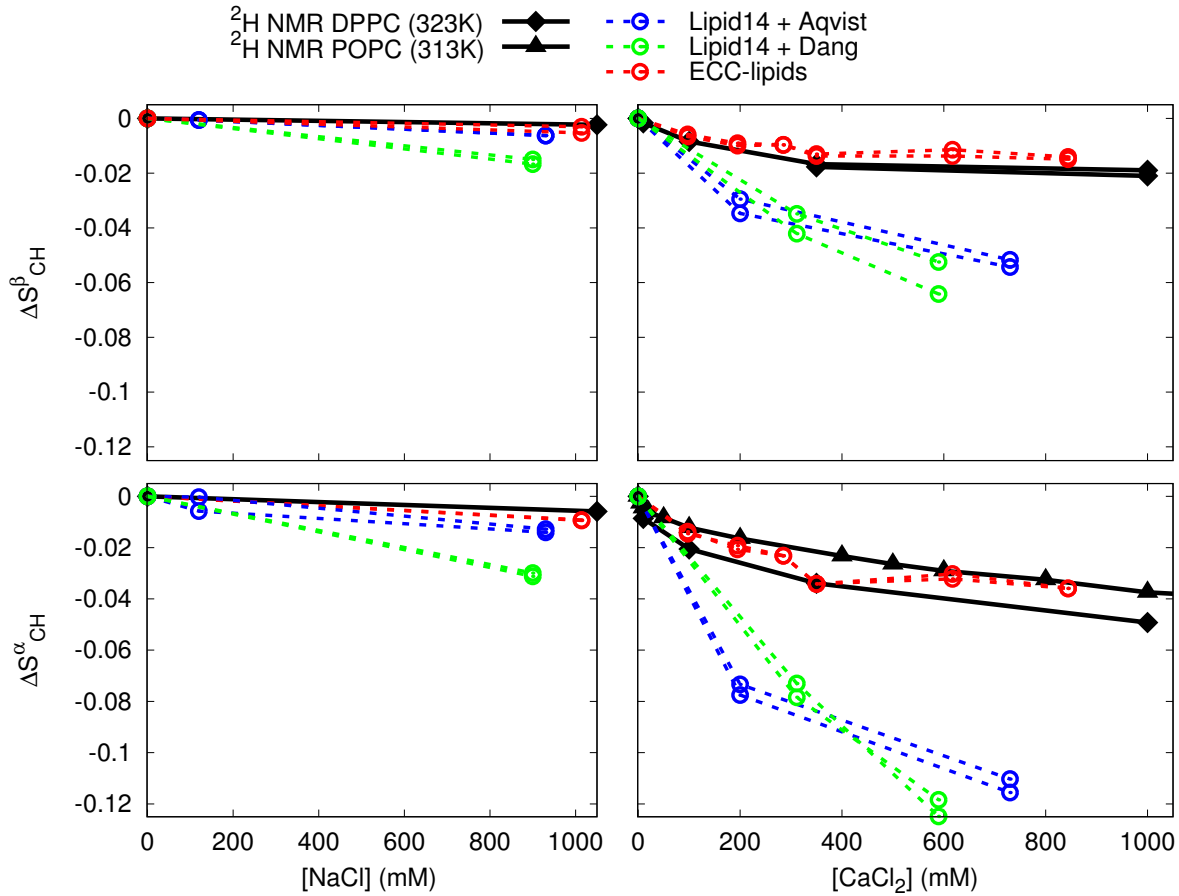


FIG. 3: Changes of headgroup order parameters of POPC bilayer as a function of NaCl and CaCl_2 concentrations are shown from simulations with different force fields together with experimental data (DPPC [14] and POPC [15]). Ion concentrations in bulk water are shown in x-axis. Values from simulations are calculated from the plateau of cation number density C_{np} at the box edge as $[\text{ion}] = C_{np}/0.602$. Simulation data with Lipid14 and Åqvist ion parameters is taken directly from Ref. [10].

”ECC-lipids 17”, exhibits accurate head group order parameter response to bound cations, monovalent Na^+ and cationic surfactant dihexadecyldimethylammonium bromide, and divalent Ca^{2+} also quantifying their binding affinities. Moreover, ECC-lipids 17 reproduce the lipid bilayer structural details with similar accuracy as other state of the art lipid models [10]. Several water models (OPC3[39], OPC [40], SPC/E [41] and TIP4p/2005 [43]) were used to exemplify the transferability of the parameters of the new ECC-lipids 17 force field.

Direct analysis of calcium binding details from MD simulations is in agreement with ternary complex model, which is suggested based on NMR data [15]. In this model 1 calcium binds to 2 POPC molecules, which together form a ternary complex. **33.Continue summary using previous section once it is finished.**

The electronic continuum correction is applied here on Lipid14 POPC model [30], but we expect that the correction can be generalized also for other lipids and force fields. The parameters can be used with existing standard nucleic acid and protein force fields, e.g. AMBER-FB15 [63]. We suggest us-

ing state of the art water models like OPC3[39] or OPC [40], which yield higher accuracy than the traditional TIP3p water model [64].

This work can be reached as a repository containing all data at [zenodo.org:\dots\dots\dots](https://zenodo.org/records/1234567) and as project NMRLipids VI in nmrlipids.blogspot.fi.

Acknowledgments

SUPPLEMENTARY INFORMATION

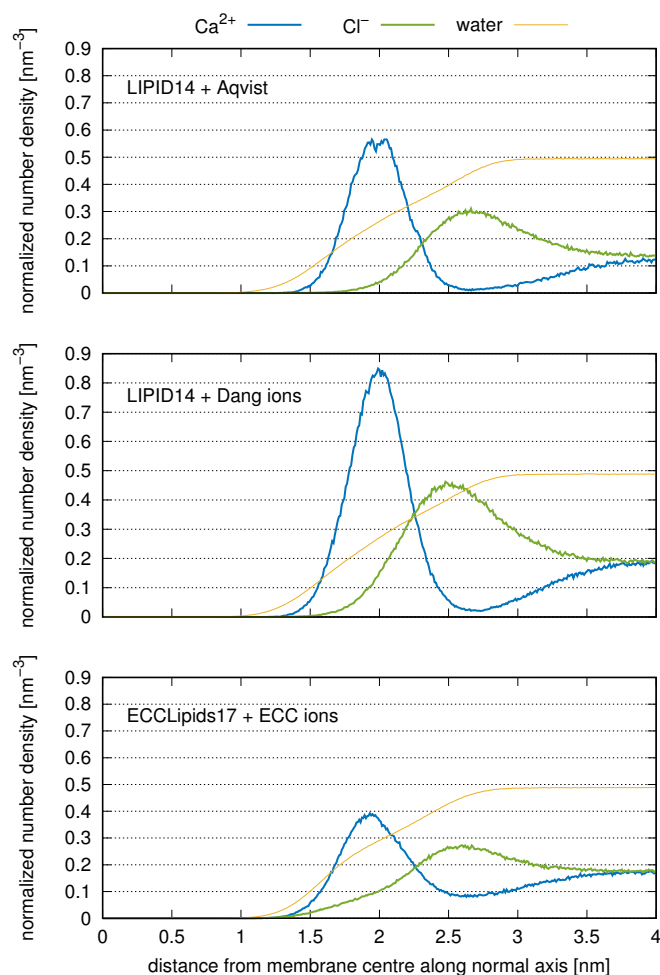


FIG. 4: Number density of Ca^{2+} and Cl^- as a function of membrane normal axis for different force fields. Data for Lipid14 with Åqvist ions are taken directly from Ref. 10. Densities of Cl^- and water are divided with 2 and 200, respectively, to visualize them with the same scale as Ca^{2+} . The molar concentration of the ions in water is 350 mM in all systems presented here.

21. Calculate the surface excess for L14+Åqvist sim.

22. PAVEL: draw phosphate position with its variance, add water density (scaled) and include the number of Γ -surface access.

23. JOE: Change the figure so that it contains a membrane background

24. Results with Lipid14+Dang to be added once done – running with larger box.

25. The current data for Dang simulation seems to contain more ions than others.

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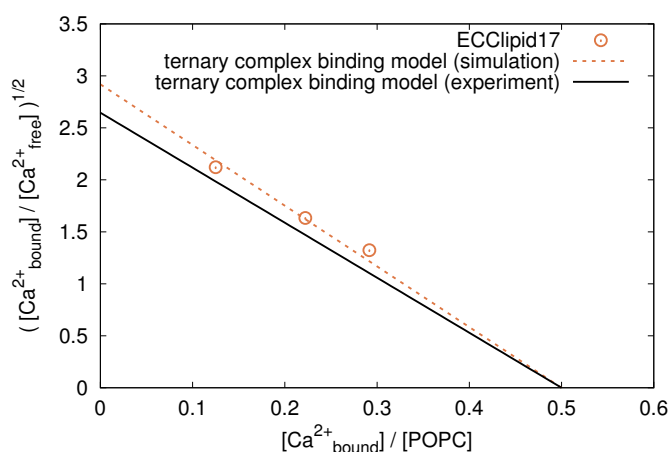


FIG. 5: Binding isotherm assuming stoichiometry of 2 POPC:1 Ca^{2+} as used in [15] fits our simulation data well.

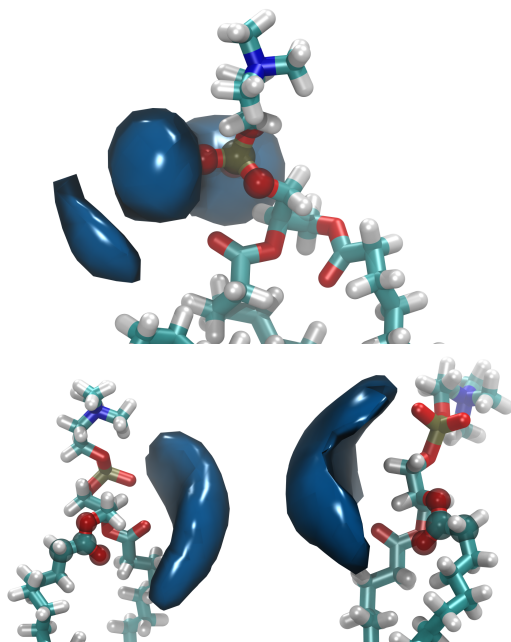


FIG. 6: Contours of probability isodensities of Ca_2^+ with respect to various moieties fixed in space (highlighted with transparent spheres): phosphate moiety, side chain 1 carbonyl group and side chain 2 carbonyl group. Shown contours suggest that the dominant contribution to Ca_2^+ binding likely comes from the phosphate group, but remain inconclusive on the details of the interactions with any of the two carbonyl groups.

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ToDo

- | | P. |
|--|-----------|
| 1. Abstract directly from Joe's conference abstracts. To be rewritten. | 1 |
| 2. JOE: list more introductory examples, where it has interesting effects. | 1 |
| 3. PAVEL: introduce previous theoretical work that discusses cation binding to POPC w.r.t. its specific moieties, e.g. Lukas' paper | 1 |
| 4. JOE: this may be a too daring statement. SAMULI: I think that the divalent cation induced charge inversion is not an artefact, but it might happen with too small concentrations. On the other hand, it is not a new observation either, see e.g. literature cited in NMRlipids IV project. | 1 |
| 5. missing REF for APL experiment | 2 |
| 7. This could be moved to SI. Only simulation lengths needs to be mentioned in the main paper. | 4 |
| 6. To be uploaded to Zenodo | 4 |
| 12. put original references, not Slipids param. paper. | 4 |
| 13. SAMULI: I would put here Lipid14 in 303K, ECC-lipid in 303K and experiment in 303K. Rest in SI. The best experimental value would be the one analyzed from the form factor shown in previous figure, if available. | 4 |
| 8. How long? | 4 |
| 9. Were all scaled? Are there charges in tails? Were those scaled as well in this case? | 4 |
| 10. There seems to a typo in experimental value for other order parameter for C2 carbon in sn-2 chain; it should be negative. The scale of the y-axis should be then zoomed when this is fixed. | 5 |
| 11. x-axis scale in form factor figure from 0 to 0.6, until where experimental data is available. | 5 |
| 14. Labels are missing. | 5 |
| 15. Order should be the same as in other figures, i.e. β segment on top. | 5 |
| 16. I would put x-axis from 0 to 51 and maybe zoom y-axis little bit as well. | 5 |
| 17. SAMULI: We could calculate the slopes from simulations, but I am not sure if we would actually learn anything useful from this. | 5 |

| | |
|---|---|
| 18. SAMULI: I think that we should establish the relation between order parameter and P-N vector angle changes by using ECC-lipids model. This would be useful for people measuring alpha order parameter changes from experiments. | 6 |
| 19. Add OP-response of Lipid14+ECC-ions plot in SI . | 6 |
| 20. SAMULI: Maybe we should discuss the repeat distances and area per molecules measured at [4, 5, 61] . | 6 |
| 21. This paragraph is to be finalized when we have the surface excess analysis done by using Eq. 6. | 6 |
| 26. JOE: Put details of the cation-binding stoichiometry analysis to SI. | 6 |
| 27. JOE: Update the binding isotherm figure with new simulations | 6 |
| 28. SAMULI: The same authors have also literature, where they say that ternary complex may not be the only option. I will recheck and come back to this. SAMULI: This is written in [62]: "Ca2+-binding to POPC bilayers over the whole concentration range can be best described in terms of formation of a ternary complex involving complexation of two lipids to one calcium ion (Altenbach and Seelig, 1984). The addition of a sodium competition term has not changed this conclusion. However, if Ca2+ concentrations up to 100 mM are considered, the data can be equally well explained by a 1:1 binding mechanism (cf. Figure 7). In contrast, the Ca2+ binding to POPC-POPG mixtures can be best described by assuming a 1:1 stoichiometry regardless of the range of Ca2+-concentrations." We might or might not want to discuss about this. | 6 |
| 29. SAMULI: I would also analyze how much there is contact between ions and different parts of the lipid (phosphate, carbonyl, etc.). JOE: Pavel suggest using volumetric map (e.g. in VMD) to visualise the amounts of Ca, Na and Cl bound to different moieties. | 6 |
| 30. SAMULI: I think we should quantify this, i.e. how much there are these. Maybe also the other possible complexes? Maybe also the correlation between complexes and binding sites, if it is not too much work. JOE: This looks like a careful work for the next paper to me. I'd only add a relatively simple analysis of binding sites and probably the propensity of 1-2-3 membered clusters. SAMULI: I agree that we should not use too much time on this now. | 6 |
| 31. Finalize stoichiometry analysis for Na ⁺ , Ca ²⁺ , their interaction energies with the lipid membrane, etc, and finalize the discussion after these results. | 6 |
| 32. Continue summary using previous section once it is finished. | 7 |
| 22. Calculate the surface excess for L14+Aqvist sim. . | 8 |
| 23. PAVEL: draw phosphate position with its variance, add water density (scaled) and include the number of T-surface access. | 8 |
| 24. JOE: Change the figure so that it contains a membrane background | 8 |
| 25. Results with Lipid14+Dang to be added once done – running with larger box. | 8 |