SUPPLEMENTARY INFORMATION:

Improved Cation Binding to Lipid Bilayer with Negatively Charged POPS by Effective Inclusion of Electronic Polarization

Josef Melcr,[*,†] Tiago Ferreira,[‡] Pavel Jungwirth,[†] and O. H. Samuli Ollila[*,†,¶]

†*Institute of Organic Chemistry and Biochemistry, Czech Academy of Sciences, Prague 6, Czech Republic*

‡*NMR group - Institut for Physics, Martin-Luther University Halle-Wittenberg*

¶*Institute of Biotechnology, University of Helsinki*

E-mail: melcr@marge.uochb.cas.cz; samuli.ollila@helsinki.fi

Simulation details

Table S1: Simulation parameters

simulation property	parameter
time-step	2 fs
equilibration time	50 ns
total simulation time	$\geq 1\mu$s
temperature	298 K
thermostat	v-rescale[1]
barostat	Parrinello-Rahman, semi-isotropic[2]
long-range electrostatics	PME[3]
cut-off scheme	Verlet[4]
Coulomb and VdW cut-off	1.0 nm
constraints	LINCS, only hydrogen atoms[5]
constraints for water	SETTLE[6]

NMR experiments

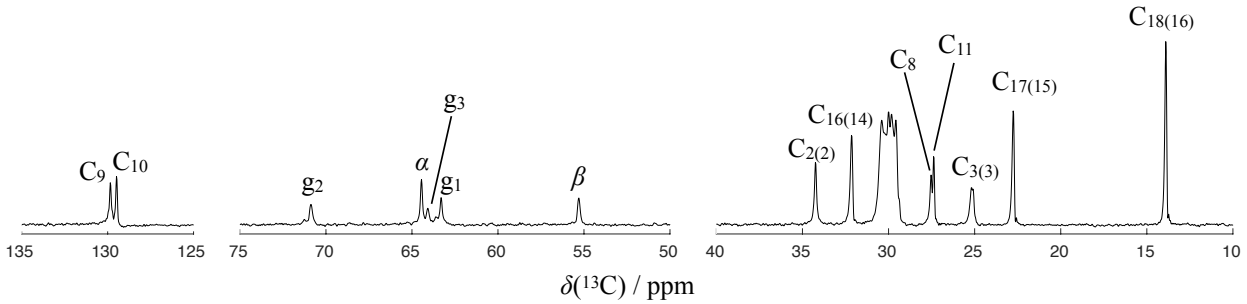

Figure S1: Refocused-INEPT ^{13}C spectrum of multilamellar POPS vesicles at 298 K with peak assignments for non–crowded spectral region (*sn*-1 chain in parenthesis).

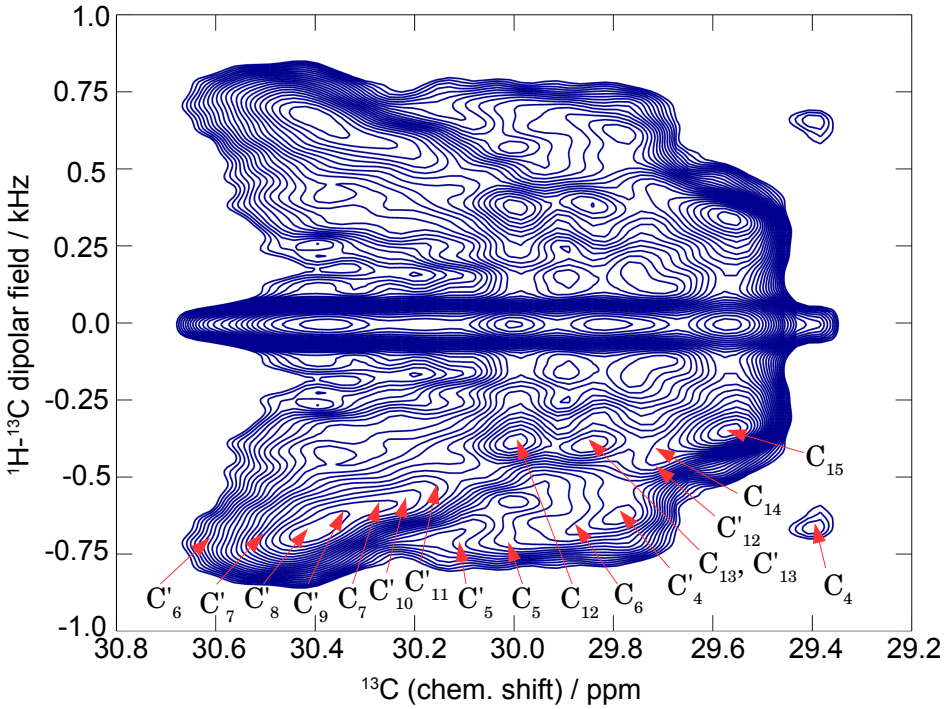

Figure S2: 2D-NMR R-PDLF spectra from the crowded spectral region of multilamellar POPS vesicles with the peak assignment. Apostrophes refer to the palmitoyl (*sn*-1) chain.

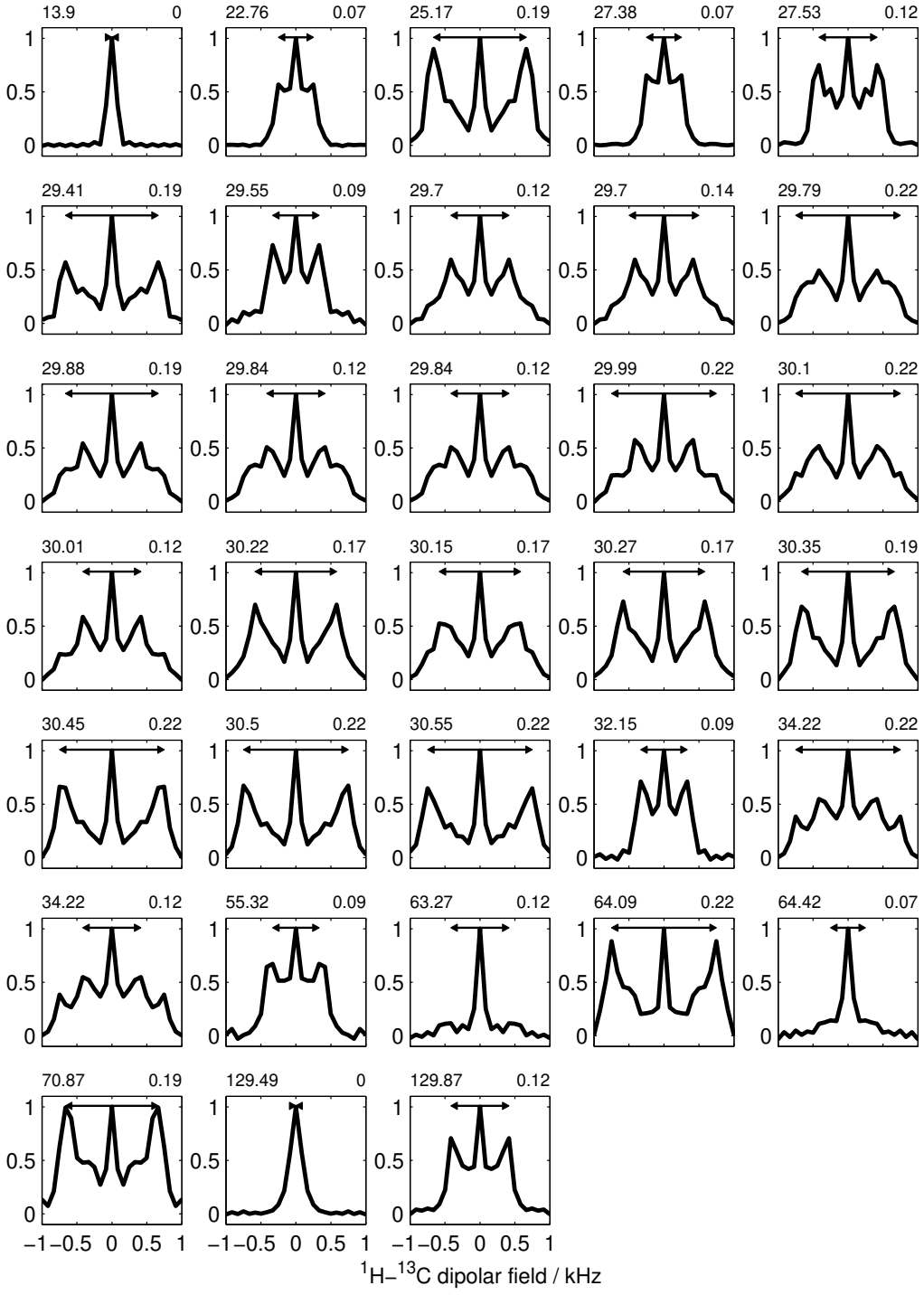

Figure S3: Dipolar slices from the R-PDLF spectra of multilamellar POPS vesicles used to determine the acyl chain order parameters. Numbers of on top of figures refer to the chemical shift (left) and order parameter value (right).

Interactions of POPS with K^+ and Na^+ counterions and POPC

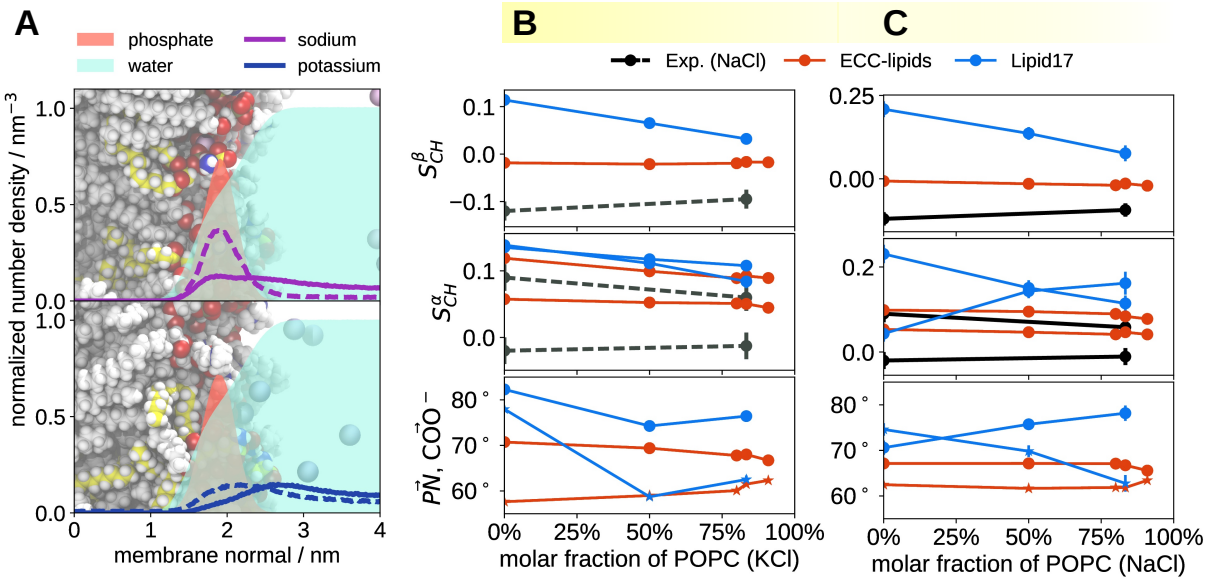

Figure S4: **(A)** Number density profiles of K^+ and Na^+ counterions along the membrane normal axis in ECC-lipids (solid lines) and Lipid17/Dang (dashed lines) simulations of POPC:POPS (5:1) bilayers. The density profiles of phosphate groups and water are divided by 4 and 100, respectively. **(B, C)** The POPS head group order parameters, the P–N (circles) and C_β–C_γ vector angles (stars) with respect to the membrane normal as a function of POPC content in a bilayer from ECC-lipids and Lipid17/Dang simulations with Na^+ (C) and K^+ (B) counterions. Experimental order parameter values are from Ref. 7 and the signs from Ref. 8 (only Na^+ counterions, but shown also in the left plots (B) for K^+ with dashed lines). Error bars are not visible for most of the simulation points because they are smaller than the point size. Chemical structure and labelling of carbon segments of POPC is shown in Fig. 3 in the main text.

Density profiles of additional monovalent cations in POPC:POPS (5:1) mixtures

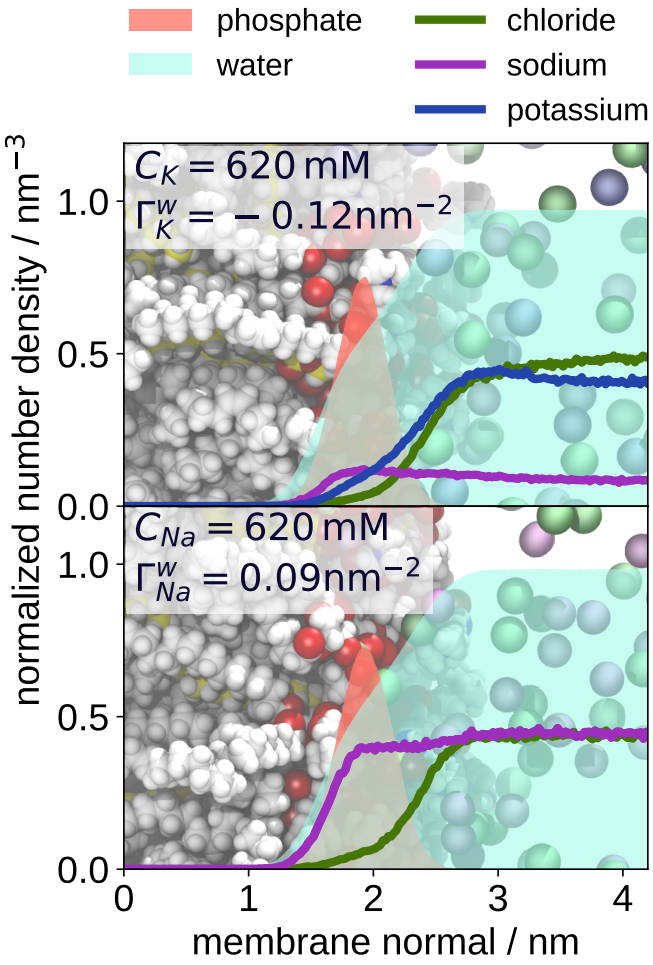

Figure S5: Number density profiles of K^+, Na^+ and Cl^- along the membrane normal axis from ECC-lipid simulation of POPC:POPS (5:1) mixture with Na^+ counterions and additional KCl (top) and NaCl (bottom) concentrations. The additional Na^+ are not distinguished from the counterions in bottom plot. The density profiles of phosphate groups and water are divided by 4 and 100, respectively.

Populations of bound Ca^{2+} cations to the PC:PS (5:1) bilayer

Table S2: Percentages of the population of bound Ca^{2+} to various lipid moieties in a pure POPC bilayer with 350 mM $CaCl_2$ and in a POPC:POPS (5:1) mixture with 409 mM $CaCl_2$. The threshold for counting a contact was set to 0.3 nm, which encompasses the first peak of the radial distribution function between the cations and the oxygen atoms of the lipids.

exclusive interacting moiety	percentage of bound Ca^{2+}	
	5 POPC:1 POPS	POPC
PC	59	100
PO_4 in PC	41	67
carbonyls in PC	<1	1
PS	8	
PO_4 in PS	2	
COO^- in PS	4	
carbonyls in PS	<1	
both PC and PS	33	
PC and PO_4 in PS	9	
PC and COO^- in PS	17	
PC and carbonyls in PS	<1	

Residence times of cations

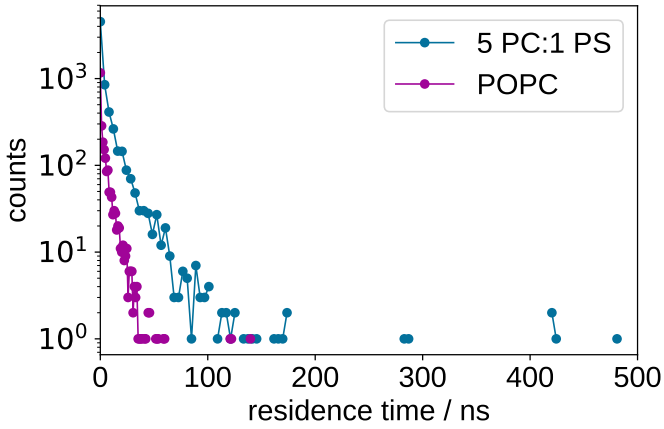

Figure S6: Histograms of Ca^{2+} residence times in a pure POPC with 350 mM $CaCl_2$ and in a POPC:POPS (5:1) mixture with 400 mM $CaCl_2$ from ECC-lipid simulations. Previously published simulation data[9] for pure POPC bilayers was taken directly from Ref. 10.

References

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