Sopporting Information for Interface Counterions Localization Induces Switch Between Tight and Loose Configurations of Knotted Weak Polyacid Rings Despite Intermonomer Coulomb Repulsion

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Methods and model

Our system consists of a single ring polyelectrolyte simulated in a cubic simulation box of length L, the latter value chosen in order to have a concentration of monomers $C_{\text{mono}} = 10^{-2}$ M, with periodic boundary conditions in all the three dimensions. The polyelectrolyte is simulated via a coarse–grained "beads and springs" primitive model, and it consists in $N_{\text{mono}} = 120$ weak acidic (hence, titratable) monomers bonded together to form a circular chain via finitely extensible nonlinear elastic (FENE) potentials,

$$u_{\text{FENE}}(r_{ij}) = -\frac{1}{2}k_{\text{FENE}}\Delta r_{\text{max}}^2 \ln\left[1 - \left(\frac{r_{ij}}{\Delta r_{\text{max}}}\right)^2\right],\tag{1}$$

where r_{ij} is the distance between two bonded monomers *i* and *j*, $k_{\text{FENE}} = 30\epsilon$ is the depth of the potential, $\Delta r_{\text{max}} = 3\sigma$ is the maximum allowed displacement, and $\sigma = 3.55$ Å. Monomers are treated as soft spheres, their excluded volumes simulated via a purely repulsive shifted and truncated Lennard–Jones potential,

$$u_{LJ}(r_{ij}) = \begin{cases} 0 & \text{if } r_{ij} \ge 2^{\frac{1}{6}}\sigma \\ 4\epsilon \left[\left(\frac{\sigma}{r_{ij}}\right)^{12} - \left(\frac{\sigma}{r_{ij}}\right)^6 + 1 \right] & \text{if } r_{ij} < 2^{\frac{1}{6}}\sigma; \end{cases}$$
(2)

here, r_{ij} is the distance between two monomers i and j and $\epsilon = 1$. Polyelectrolyte conformations are sampled via Langevin dynamics, integrating the trajectories via a velocity Verlet algorithm with a time step $\delta t = 0.01 \sqrt{\sigma(m/\epsilon)}$.

In order to take into account the weak acidic nature of the monomers, beside the Langevin dynamics we implemented the constant–pH method^{1–3}, which assumes the system in equilibrium with an implicit infinite reservoir at a fixed chemical potential of H⁺ ions, the latter defined by the value assumed by the control parameter pH - p K_a . In details, the state of a monomer *i*, that is neutral ($q_i = 0$) or charged ($q_i = -1$), can be switched using a Monte Carlo scheme with a modified Metropolis–Hastings acceptance probability that take into account also the chemical potential of the protons in solution; that is

$$P_{\rm acc} = \min\left\{1, e^{-\frac{\Delta E'}{k_B T}}\right\},\tag{3}$$

$$\Delta E' = \Delta E \pm k_B T (\text{pH} - \text{p}K_a) \ln (10), \qquad (4)$$

where ΔE is the change in the total potential (i.e., the change in Coulomb and Lennard-Jones interactions) due to the reaction attempt. The plus sign is used when a monomer is protonated (association), while the minus sign is used when a monomer dissociates. Notice that in order to maintain the system electroneutral, a counterion (CI, $q_{\rm CI} = +1$) is inserted in the simulation cell every time a monomer dissociates, whereas a randomly chosen CI is eliminated every time a protonation reaction takes place. In a few simulations, we also added a certain amount of mono– and di–valent salt (z = 1, $q_{\rm S} = \pm 1$ and z = 2, $q_{\rm S} = \pm 2$, respectively) in order to simulate the system in presence of a background ionic force. As the monomers, also CIs and salt ions are treated as soft spheres, and, hence, they're subjected to the same Lennard–Jones potential. Coulomb interactions are simulated via the P3M method and implicit solvent, the latter assumed to be water at room temperature unless otherwise indicated. Hence, the Bjerrum length of the system is $l_B = 2.0\sigma = 7.10$ Å. All simulations have been performed with the software package ESPResSo⁴.

Simulation protocol

For each pH - p K_a value investigated, the system has been warmed up for a time $t = 5 \cdot 10^4$, attempting $10N_{\text{mono}}$ dissociation/protonation reactions every 10^3 integration steps. Then, the system has been integrated for $t = 5 \cdot 10^5$, attempting N_{mono} reactions every 10^3 integration steps. System properties have been collected every 10^3 integration step. We performed a blocking analysis in order to verify that samples were uncorrelated.

Simulations without the insertion of counterions

Simulations without the insertion of CIs have been performed disabling the electroneutrality checks in ESPReSso⁴ and replacing the insertion/deletion of CIs with the insertion/deletion of neutral dummy particles with a negligible excluded volume.

Simulations of polyelectrolytes with quenched charges

We performed a few simulations with polyelectrolytes with various dissociation degrees α but quenched charges, so that they behave as strong polyacids with a certain amount of non-tritratable neutral monomers, the latter uniformly distributed along the chain.

Investigated properties

Dissociation degree α

A weak polyelectrolyte is a polymer whose monomers carry weak acidic or basic groups. Let us briefly discuss polyacids as an example. In such a case, a monomer HA can dissociate releasing a proton H^+ and forming the conjugate base A^- :

$$HA \rightleftharpoons A^- + H^+.$$
 (5)

We define the mean dissociation degree α of the polyelectrolytes as

$$\alpha \equiv \langle \alpha(\mathrm{pH} - \mathrm{p}K_a, \mathrm{X}_n) \rangle = \frac{\langle [\mathrm{A}^-] \rangle}{\langle [\mathrm{HA}] + [\mathrm{A}^-] \rangle} = \frac{\langle \sum_i^{N_{\mathrm{mono}}} |q_i| \rangle}{N_{\mathrm{mono}}};$$
(6)

here, X_n represents the knot topology, [HA] and [A⁻] are the (istantaneous) molar concentrations of dissociated and undissociated monomers, respectively, and the average is taken over all the sampled configurations. The ionization behavior of an isolated acidic monomer with a certain pK_a (that is the ideal case described by the Henderson–Hasselbalch equation) differ from the one observed for monomers belonging to polyelectrolyte, the latter showing a $pK_{a,eff}$ which is, in the most of the case, higher than pK_a . Thus, we can define the shift in pK units due to the polymeric nature as

$$\Delta p K_a = p K_{a,\text{eff}} - p K_a = \log_{10} \left(\frac{\alpha}{1 - \alpha} \right).$$
(7)

Noticeably, we found that species able to form chemical specific interactions, such as charged hydrogen bonds, may show a negative $\Delta p K_a^{5-8}$. Let us point out that in linear polyacids, but also in other heterogeneous system like branched species, nanogels or polymer networks, $\Delta p K_a$ is also a function of the monomer position along the chain, due to the fact that the latter influences the beads neighborhood. At contrary, in a ring polyelectrolyte all monomers are identical and, hence, they show the same ionization behavior. In a knotted circular polyelectrolyte, the presence of the knot (especially if the latter is tight, hence localized over a small portion of the chain) is expected to induce a modification in the dissociation behavior of the monomers that take part to it. Nevertheless, if the knot is not impeded to move along the whole chain and simulations are long enough to ensure an ergodic sampling of the system at the equilibrium, also in this case $\Delta p K_a$ can be considered independent to the monomer position.

Radius of gyration $R_{\rm g}^2$

We define the average radius of gyration of the polyelectrolyte as

$$R_{\rm g}^2 \equiv \langle R_{\rm g}^2(\alpha, \mathbf{X}_{\rm n}) \rangle = \frac{\langle \sum_i^{N_{\rm mono}} (\mathbf{r}_i - \mathbf{r}_{\rm CoM})^2 \rangle}{N_{\rm mono}},\tag{8}$$

where \mathbf{r}_i and \mathbf{r}_{CoM} represents the positions of the *i*-th monomer and the center of mass, respectively. The average is taken over all the sampled configurations. R_g^2 distributions have been generated by collecting the instantaneous R_g^2 value of each sampled configurations, generating histograms with a bin width equal to 0.1775 Å² and rescaling perform normalization.

Fraction of condensed counterions $\varphi_{\rm CI}$

We define the mean fraction of CIs localized at the interphase (i.e., "condensed") φ_{CI} as the number of CIs that lies at a distance equal or less than $2\sigma = 7.10$ Å to at least one monomer over the total number of counterions in the simulation box averaged over all the configurations sampled during the simulation. We arbitrary set $\varphi_{\text{CI}} = 0$ in case of no CIs in solution (fully undissociated polyelectrolyte). In a few simulations we added monovalent salts in solution, and we calculated the mean fraction of condensed cations φ_{tot} , which is defined as φ_{CI} but including both CIs and monovalent salt ions in the count.

Debye length $\lambda_{\rm D}$

The Debye length of the solution at a certain pH - pK_a value (and, hence, at a certain degree of ionization α of the polyelectrolyte ring), $\lambda_D(\alpha) \cong \lambda_D = \kappa^{-1}$, is computed using the canonical formula

$$\kappa = \sqrt{4\pi l_{\rm B} \sum_{i} C_i q_i^2},\tag{9}$$

where C_i is the concentration of the *i*-th species, while the index *i* runs over mobile species (CIs and salt ions).

Results



Figure S1: Radius of gyration R_g^2 as a function of pH - p K_a for polyelectrolytes presenting different knots.



Figure S2: Probability density of the radius of gyration R_g^2 as a function of pH - p K_a for the 0_1 polyelectrolyte.



Figure S3: Fraction of "condensed" CIs, φ_{CI} , as a function of pH - p K_a for polyelectrolytes presenting different knots.



Figure S4: (a) $\Delta p K_a$ as a function of α , and (b) α as a function of pH - p K_a for polyelectrolytes presenting different knots. Notice the curve crossing at high pH and α .



Figure S5: Monomer–monomer pair distribution functions g(r) as a function of pH - p K_a for the four topologies investigated: (a) 0_1 , (b) 3_1 , (c) 4_1 , (d) 5_1 .



Figure S6: Monomer–CI pair distribution functions g(r) as a function of pH - p K_a for the four topologies investigated: (a) 0_1 , (b) 3_1 , (c) 4_1 , (d) 5_1 .



Figure S7: CI–CI pair distribution function g(r) as a function of pH - p K_a for the four topologies investigated: (a) 0_1 , (b) 3_1 , (c) 4_1 , (d) 5_1 .

Simulation without counterions (CIs)



Figure S8: Radius of gyration R_g^2 as a function of pH - p K_a for the 3₁ case: a comparison between simulations with and without the insertion of CIs.



Figure S9: Probability density for the radius of gyration R_g^2 as a function of pH - p K_a for the 3_1 topology in absence of CIs.



Figure S10: Monomer–monomer pair distribution functions g(r) as a function of pH - p K_a for the simulation of the 3_1 ring in absence of CIs.

Impact of Bjerrum length l_B



Figure S11: Radius of gyration R_g^2 as a function of pH - p K_a for the 3₁ topology and various l_B values.



Figure S12: Probability density for the radius of gyration R_g^2 and selected trajectory snapshots are shown as a function of pH - p K_a for the 3_1 case and various l_B values: (a) $l_B = 3.55$ Å, (b) $l_B = 7.10$ Å, (c) $l_B = 10.65$ Å, (d) $l_B = 14.20$ Å.



Figure S13: Fraction of "condensed" CIs, φ_{CI} , as a function of (a) α and (b) pH - p K_a for the 3_1 case and various l_B values. Notice the absence of "kinks" in φ_{CI} for $l_B \geq 3\sigma$



Figure S14: (a) ΔpK_a as a functions of α , and (b) α as a function of pH - p K_a for the 3₁ case and various l_B values.



Figure S15: Monomer–monomer pair distribution functions g(r) as a function of pH - p K_a for various l_B values: (a) $l_B = 3.55$ Å, (b) $l_B = 7.10$ Å, (c) $l_B = 10.65$ Å, (d) $l_B = 14.20$ Å.



Figure S16: Monomer–CI pair distribution functions g(r) as a function of pH - p K_a for various l_B values: (a) $l_B = 3.55$ Å, (b) $l_B = 7.10$ Å, (c) $l_B = 10.65$ Å, (d) $l_B = 14.20$ Å.



Figure S17: CI–CI pair distribution functions g(r) as a function of pH - p K_a for various l_B values: (a) $l_B = 3.55$ Å, (b) $l_B = 7.10$ Å, (c) $l_B = 10.65$ Å, (d) $l_B = 14.20$ Å.

Impact of salt valency and concentration



Figure S18: Radius of gyration R_g^2 as a function of pH - p K_a for the 3₁ polyelectrolyte in solution with various salt valences and concentrations.



Figure S19: Probability density for the radius of gyration R_g^2 and selected trajectory snapshots as a function of pH - p K_a for the 3_1 case and various salt valencies z and concentrations C_S : (a) $C_S = 0$ M, (b) $C_S = 10^{-2}$ M, z = 1, (c) $C_S = 2.5 \cdot 10^{-3}$ M, z = 2, (d) $C_S = 10^{-2}$ M, z = 2.



Figure S20: Fraction of "condensed" CIs φ_{CI} and fraction of total "condensed" cations φ_{tot} as a function of (a) α and (b) pH - p K_a for the 3₁ polyelectrolyte and various salt conditions.



Figure S21: (a) ΔpK_a as a functions of α , and (b) α as a function of pH - p K_a for the 3₁ case and various salt conditions.



Figure S22: Monomer–monomer pair distribution functions g(r) as a function of pH - p K_a for various salt valencies z and concentrations $C_{\rm S}$: (a) $C_{\rm S} = 0$ M, (b) $C_{\rm S} = 10^{-2}$ M, z = 1, (c) $C_{\rm S} = 2.5 \cdot 10^{-3}$ M, z = 2, (d) $C_{\rm S} = 10^{-2}$ M, z = 2.



Figure S23: Monomer–CI pair distribution functions g(r) as a function of pH - p K_a for various salt valencies z and concentrations $C_{\rm S}$: (a) $C_{\rm S} = 0$ M, (b) $C_{\rm S} = 10^{-2}$ M, z = 1, (c) $C_{\rm S} = 2.5 \cdot 10^{-3}$ M, z = 2, (d) $C_{\rm S} = 10^{-2}$ M, z = 2.



Figure S24: CI–CI pair distribution functions g(r) as a function of pH - p K_a for various salt valencies z and concentrations $C_{\rm S}$: (a) $C_{\rm S} = 0$ M, (b) $C_{\rm S} = 10^{-2}$ M, z = 1, (c) $C_{\rm S} = 2.5 \cdot 10^{-3}$ M, z = 2, (d) $C_{\rm S} = 10^{-2}$ M, z = 2.

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