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Evidence for water structuring forces between surfaces

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ABSTRACT

Structured water on apposing surfaces can generate significant energies due to reorganization and displacement of water as the surfaces encounter each other. Force measurements on a multitude of biological structures using the osmotic stress technique have elucidated commonalities that point toward an underlying hydration force. In this review, the forces of two contrasting systems are considered in detail: highly charged DNA and nonpolar, uncharged hydroxypropyl cellulose. Conditions for both net repulsion and attraction, along with the measured exclusion of chemically different solutes from these macromolecular surfaces, are explored and demonstrate common features consistent with a hydration force origin. Specifically, the observed interaction forces can be reduced to the effects of perturbing structured surface water.

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1. Introduction

Hydration energies of charges and polar molecules are large, and the displacement of water in the binding or folding reactions of macromolecules has significant energetic consequences [1]. Water organized by these groups generally has preferred orientations. Additionally, nonpolar surfaces seem to structure water [2] and their interaction with water is considered to underlie the hydrophobic force [1,3]. Since water forms hydrogen-bonded networks, the structuring of water by charges, polar, and nonpolar groups on a macromolecular surface will likely perturb adjacent water layers. What happens when two surfaces are brought into close proximity, such that the last few water layers on each surface are in contact? Can water still optimally hydrate each surface? As surfaces approach, the change in hydration energy defines a hydration force. There is significant experimental and theoretical evidence that water in tight spaces is far different from bulk water [4–7]. How much water is perturbed by surfaces is still a much debated question. The range of water perturbation seems dependent on technique. Estimates vary from indicating that only the first layer is different from bulk water [8,9] to a perturbation that extends several layers into solution [10–16]. Extended surfaces seem to order water better than small molecules [11,12]. Water structuring is additionally convoluted with electrostatics through nonlocal dielectrics [17,18] and dielectric saturation [19]. Enough uncertainty exists in modeling water that there is not a definitive expectation for hydration forces as for Van der Waals interactions or electrostatics. An interaction of molecules acting through water structuring has been advocated by several others [20–25].

Our basic approach has been to look for commonalities among measured forces for many different classes of macromolecules. We measure forces using the osmotic stress technique [26,27]. Ordered arrays of macromolecules are equilibrated against a polymer solution, very typically polyethylene glycol, PEG. The polymer chosen is excluded from the macromolecular array and applies an osmotic pressure on it. PEG is a particularly useful polymer since it is excluded from many macromolecules. Salts, water, and small solutes equilibrate between the polymer solution and condensed array. The average interaxial spacing between macromolecules, D_{int}, can be determined by X-ray scattering to good accuracy. The resulting osmotic pressure Π vs D_{int} curves are thermodynamic force measurements. Combined measurement of the osmotic pressure and volume V (obtained through D_{int}) gives a convenient entry into many thermodynamic expressions based on the Gibbs–Duhem equation [28–31].

Fig. 1 shows the dependence of osmotic pressure on surface to surface separations for a variety of biologically relevant macromolecules ranging from highly charged DNA and didodecylphosphate bilayers to net neutral, zwitterionic PC bilayers to completely uncharged carbohydrates schizophyllan and hydroxypropyl cellulose. The striking feature is the common exponential dependence of the force on distance with an apparent decay length of ~3–4 Å. This common force characteristic for these very different systems suggests a common origin that we have concluded is due to water structuring. The range of interaction is ~15–20 Å, which corresponds to about

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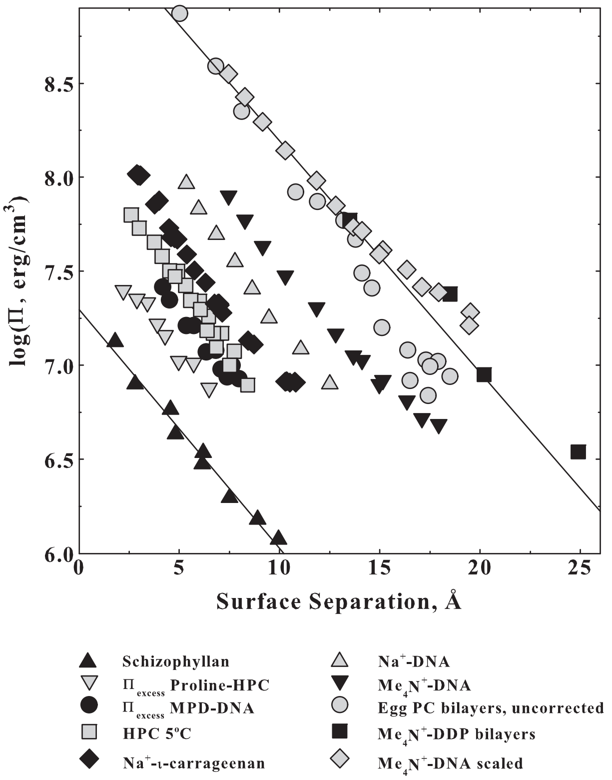

Fig. 1. A comparison of forces measured for several different systems in ordered arrays. Π is the osmotic pressure applied by the excluded polymer in the bulk solution acting on the condensed macromolecular phase. Distances are given as approximate surface-to-surface separations of macromolecules. Schizophyllan [55] and hydroxypropyl cellulose (HPC) [30] are completely uncharged. DNA in NaBr and TMABr, tetramethyl ammonium, (unpublished data) and ι-carrageenan in NaCl (unpublished data) are highly charged linear double helices. DDP (didodecyl phosphate) in TMA$^+$ salt is a highly charged planar bilayer (data from [56]). Egg PC is a zwitterionic planar bilayer that has the phosphate and quaternary amine of the head group covalently linked (data from [57]). The TMA$^+$–DNA force has also been corrected to planar packing and to the same surface area/phosphate as DDP. The close overlap of the corrected TMA$^+$–DNA, egg PC (that has about the same surface area/molecule as DDP) and TMA$^+$–DDP forces illustrates the striking similarity of these homologous systems. The salt concentrations for the charged surfaces are high enough that forces are insensitive to ionic strength. The excess pressures due to solute exclusion are also shown for the nonpolar alcohol methylpentane diol (MPD) at 1 molal interacting with DNA and for zwitterionic proline at 1 molal interacting with uncharged HPC. The straight lines show a decay length of ~4 Å. The force amplitudes span a range greater than 100-fold.

three to four water layers on each surface. The chemical potential change of a water molecule at $\Pi = 10^6$ erg/cm^3, the osmotic pressure at the large separations, is quite small, only ~10^{-3} kT. When summed over the many water molecules separating the surfaces, however, the integrated energies can be large. The pre-exponential factors or force amplitudes vary more than 100-fold for this set of macromolecules. These force curves smoothly change, not at all like the oscillatory forces seen experimentally and predicted theoretically between hard, fixed surfaces [22]. Biological surfaces are soft and compliant.

An order parameter theory was initially developed to account for the forces first seen between zwitterionic lipid bilayers [32,33]. It is based on a surface structuring of water on the macromolecular surface that propagates into solution characterized by a water–water correlation length, λ. Correlation lengths of 3–5 Å have been observed for density fluctuations in pure water [34,35]. Two exponential forces are expected from the order parameter theory [36] — one from the direct interaction of hydration structures on apposing macromolecular surfaces characterized by a decay length λ. This term can be either attractive or repulsive depending on the mutual structuring of water on the two surfaces; the hydrogen bonding of the intervening water can be either disrupted or reinforced as surfaces approach [29,36,37]. Attraction will occur when complementary water structures on apposing surfaces are correlated. A second order term that gives rise to an exponential force with a λ/2 decay length reflects a disruption of the stabilizing water structure extending out into solution from one surface simply due to the presence of another surface. This force is always repulsive and resembles in form electrostatic image charge repulsion. The magnitude of the force depends on the strength of water structuring on the surface. In spite of its simplicity, this formalism provides a good first order description of the forces between divergent macromolecular systems.

In the rest of this review, we will focus on two specific and divergent systems, highly charged DNA and nonpolar uncharged hydroxypropyl cellulose (HPC). The ~4 Å decay length force is prominent in both systems not only as a repulsion but also, under appropriate conditions, as an attraction that drives spontaneous assembly. Furthermore, the exclusions both of nonpolar alcohols from DNA and of salts and polar solutes from HPC are also characterized by this 4 Å decay length force. Hydration forces measured between lipid bilayers have been extensively reviewed [27,38–40].

2. DNA

Fig. 2 shows NaDNA force curves as dependent on NaBr concentration. Forces converge to a salt concentration insensitive interaction at high osmotic pressures. At low osmotic pressures, two force regimes are apparent. The force is salt concentration dependent for ionic strengths less than ~0.8 M as would be expected for an electrostatic interaction. The apparent decay length at low pressures is close to the expected Debye–Huckel shielding length for these ionic strengths. At salt

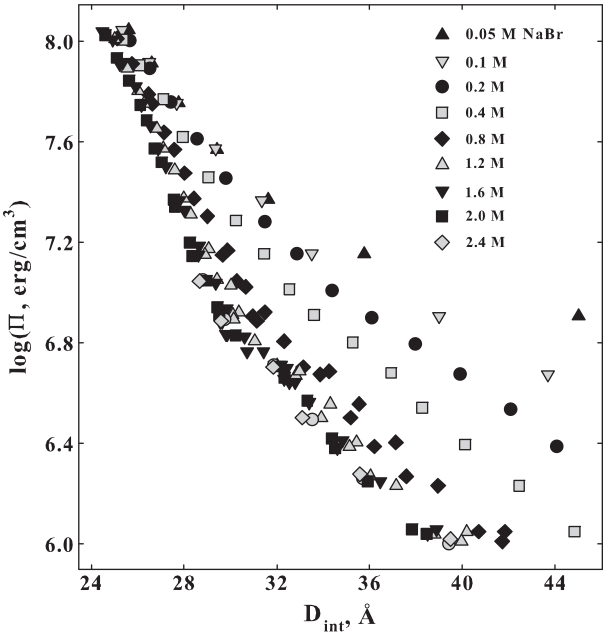

Fig. 2. The dependence of DNA–DNA forces on NaBr concentration is shown. The diameter of DNA is ~20 Å. Forces converge at high pressures for all salt concentrations. For ionic strengths less than ~0.8 M, an electrostatic interaction dominates at low pressures. The decay length of the apparent exponential in this regime is consistent with the Debye–Huckel shielding length. At higher ionic strengths, the forces at low pressures converge. The apparent exponential decay length is ~4.2 Å. The decay length of the high pressure force obtained after subtracting the low pressure forces is ~2 Å and has an amplitude independent of salt concentration.