SUPPORTING INFORMATION FOR

Molecular dynamics simulation of strong interaction mechanisms at wet interfaces in clay-polysaccharide nanocomposites

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**Molecular dynamics simulation details**

The cutoff for the non-bonded van der Waal’s interaction was set to 1.0 nm. The non-bonded van der Waal’s force was computed by a switching function starting at 0.9 nm and ending at 1.0 nm. The long-range van der Waal’s interactions beyond the cutoff were recovered using a dispersion correction. Moreover, long-range electrostatic interactions were calculated using the particle mesh (PME) method\(^1\)\(^,\)\(^2\) with a real-space cutoff of 1.2 nm and a grid order of 4.

All simulations were carried out in the isothermal-isobaric (NpT) ensemble at \(T = 300\) K and \(p = 1\) atm using the Nosé-Hoover thermostat\(^3\)\(^,\)\(^4\) and the Parrinello–Rahman barostat\(^5\)\(^,\)\(^6\), respectively. All bonds were constrained with the P-LINCS constraint algorithm\(^7\). The equations of motion were integrated using the leap-frog algorithm with a time step of 2 fs\(^8\). Frames containing all atomic positions were saved every 2 ps for analysis.

**Method of estimating the equilibrated state**

It is difficult to determine an absolute equilibrated adsorption state from a simulation. However, after a sufficiently long simulation, it is highly likely that a quasi-equilibrated state has been achieved. For this to apply, one generally demands that the adsorbed state should be dynamically stable with regard to both structures and energies\(^9\). Structural stability can be measured by, e.g., the root-mean-square deviation (RMSD) which describes the deviation of a conformation from an initial structure:

\[
RMSD = \sqrt{\frac{1}{M} \sum_{i=1}^{N} m_i [r_i(t) - r_i(0)]^2}
\]

where \(m_i\) is the mass of atom \(i\), \(M\) is the total mass, \(r_i(t)\) is the position of atom \(i\) at time \(t\) and \(r_i(0)\) is initial position of atom \(i\) taken from the starting structure of the XG molecule \((t=0)\). The summation is over all \(N\) XG atoms.
Energy stability is judged by the total instantaneous interaction energy between the XG and MTM, which is defined as:

\[ E_{\text{int}}(t) = E_{XG+MTM}(t) - E_{XG}(t) - E_{MTM}(t) \]  

where \( E_{\text{int}} \) means the interaction energy between the XG and MTM, \( E_{XG+MTM} \) refers to the total energy of the XG and MTM, and \( E_{XG} \) and \( E_{MTM} \) are the internal energies of XG and MTM, respectively. The energy terms on the right side of Eq. (2) were calculated from the corresponding trajectories. Each system was simulated for 100 ns and data from the final 20 ns was used for analysis.

**Method for evaluating the binding affinity**

In computer simulation studies, free energy profiles are commonly calculated as potentials of mean force, PMF’s, which can be calculated from MD simulations in several ways. In this work, the free energy profile for the desorption of XG from a MTM surface is evaluated by the Umbrella sampling method, which has become a mature and widely used method for evaluating free energies.\(^{10}\) The choice of Umbrella Sampling is to overcome the limitation of sampling problems suffered by a great many techniques.\(^{10}\) The simulations of the desorption process were carried out on each XG-MTM system with the lowest interaction energy (Native XG (B [180°]) and Modified XG (B [180°])).

A pulling MD simulation was first run to get the desorbed path, where the center of mass (COM) of the XG backbone was set as the pulling group. The whole pulling process was conducted along the direction of the z axis, which is perpendicular to the MTM surface. The harmonic force constant was set to \( k = 2000 \) and the pulling velocity \( v = 0.001 \text{ nm·ps}^{-1} \). Forces and atomic coordinates were saved every 1 ps.
The reaction coordinate, \( \xi \), for the umbrella sampling was chosen as the distance between the MTM and the center of mass of the XG fragment, perpendicular to the MTM surface. Different configurations along this coordinate were generated by dynamically pulling the XG fragments off the surface during the course of a 3 ns simulation mentioned above. Great effort was made to determine how many windows would be enough for a trustworthy umbrella sampling calculation. In this study, the number of umbrella windows was 250. Starting configurations for each window were taken as snapshots from the 3 ns pulling trajectory with the frequency of 10 ps to ensure sufficient overlap between adjacent windows, and with the initial 0.5 ns of the trajectory discarded. Each window was then simulated for 500 ps with an applied umbrella potential according to Eq. (3).

\[
\omega_i(\xi) = \frac{k_i}{2} (\xi - \xi_i)^2
\]  

(3)

Where \( \omega_i(\xi) \) is the biased potential of window \( i \), \( \xi \) is the reaction coordinate, \( k_i \) specifies the strength of biasing potential, and \( \xi_i \) are the reference points, uniformly distributed along \( \xi \). From the simulation of each separate window, an umbrella histogram was recorded. In this way, the unbiased probability distribution along the reaction coordinate was by the weighted histogram analysis method (WHAM) as implemented in the GROMACS suit. The statistical uncertainties were evaluated by the bootstrap analysis technique with Bayesian bootstrapping using 100 bootstraps. The simulation data were saved every 2ps.

**Method for calculating the quasiharmonic entropy**

Assuming that \( \Delta S_{XG} \) is dominated by the conformational entropy of the XG, thus neglecting any contributions from COM (the center of mass) translations and rotations, we can estimate \( \Delta S_{XG} \) using a quasiharmonic (QH) approximation. Using four trajectories representing the
adsorbed and the free state of Native XG and Modified XG respectively, the mass-weighted covariance matrix $C$ of all $N$ XG coordinates (excluding non-polar hydrogens) in cartesian space was calculated after superposition on an average structure to remove COM translations and rotations. The matrix $C$ was further diagonalized. There are now $M = N - N_{\text{constr}} - 6$ non-zero eigenvalues which corresponds to the variances of the $M$ eigenmodes, and where $N_{\text{constr}}$ is the number of hard constraints present in the model. In the case of native XG, $M = 411$, and for the modified version $M = 383$. The QH entropy $S_{\text{QH}}$ is now calculated by assuming that the system can be approximated as a collection of $M$ quantum mechanical harmonic oscillators with variances as above. The simulations included in the analysis were 60 ns in length for all for sufficient time to converge well.

It is possible to calculate corrections to $S_{\text{QH}}$ by estimating the deviation from the exact classical entropy $S_{\text{cl}}$. To do that, the eigenvectors were projected on the original trajectory to get the time evolution of the eigenmodes. These were used to create histograms that approximate the one- and two-dimensional probability distributions $p(r)$ of the eigenmodes from which the classical entropy $S_{\text{cl}}$ is given by Eq. (4), as usual. The bin widths of $p(r)$ were chosen according to Ref. The integrals were evaluated using numerical integration. In this manner, corrections up to second order were calculated, accounting for anharmonicity and pair-wise correlations of the eigenmodes, respectively (see Refs for details).

$$S_{\text{cl}} = \int p \log(p) \, dr$$

(4)

**Analysis of adsorbed state**

Evaluation of the quasi-equilibrated state was made by the instantaneous interaction energy between the XG fragment and MTM, and the root-mean-square deviation (RMSD) of the XG
fragment. Fig. S1 shows the instantaneous interaction energy between the native XG fragment and MTM, and between the modified XG fragment and MTM, calculated from all 8 different starting orientations, as function of simulation time. Fig. S2 shows the time evolution of the RMSDs of each XG fragment, for all 8 different starting orientations. From both figures, we see that after approximately 80 ns the system seems to have reached equilibrium. The strongest interaction between each XG and MTM was found for the B[180°] starting orientation, and it is therefore of interest to discuss the adsorption process and conformational properties based on this starting orientation.
Figure S1. Time evolution of $E_{\text{int}}$ for the native XG (black line), and the modified XG (red line), respectively in A orientation: (a)-(d) corresponding to A$[0^\circ]$-A$[270^\circ]$ and B orientation (e)-(h) corresponding to B$[0^\circ]$-B$[270^\circ]$. 
Figure S2. Time evolution of the RMSDs for native XG (black line) and modified XG (red line), respectively, in A orientation (a)-(d) corresponding to A[0°]-A[270°] and B orientation (e)-(h) corresponding to B[0°]-B[270°].
Analysis of conformational properties of the XG fragments in free states

Calculated values of the dominant dihedral angles of the free XG fragments are shown in Table S1. Snapshots (t=60ns) of the free XGs are displayed in Fig. S3.

Table S1 The glycosidic linkage and side chain dihedral angles (°) of the native and modified XG fragments in the free states, only water and XGs.

<table>
<thead>
<tr>
<th>Glycosidic linkage</th>
<th>Native XG</th>
<th>Modified XG</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>( \Phi )</td>
<td>( \Psi )</td>
</tr>
<tr>
<td>G3</td>
<td>49.3±12.7</td>
<td>-0.7±11.7</td>
</tr>
<tr>
<td>G4</td>
<td>38.6±17.3</td>
<td>-9.0±14.6</td>
</tr>
<tr>
<td>G5</td>
<td>42.7±29.9</td>
<td>-1.8±18.2</td>
</tr>
<tr>
<td>G6</td>
<td>47.8±11.8</td>
<td>-1.6±17.9</td>
</tr>
</tbody>
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Figure S3. Snapshots of the free state XG (t=60 ns) after removing MTM, Native XG, (a); Modified XG, (b). Water molecules and sodium ions are not shown for clarity. Color scheme is
as follows: glucan backbone residues (magenta), side chain xylosyl residues (cyan), galactosyl residue (red). The drawing method of XG molecular is licorice.

References
