

# Molecular Dynamics Simulation and Quantum Chemical Calculations of Surfactant Having Suppression Effect on Water Trees

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Polyethylene (PE) is a hydrophobic polymeric insulating material. It has been found that adding hydrophilic additives can enhance the water tree resistance of PE. Such additives are most often surfactants that contain both hydrophobic and hydrophilic groups within their molecular structures. It is considered that a surfactant added to PE surrounds water molecules and stabilizes them. Hence, it is highly plausible that the solubilization of moisture in a supersaturated state leads to the suppression of water tree initiation in PE. In this study, we investigated the aggregation of water molecules and the orientation of surfactants toward water clusters by molecular dynamics (MD) simulation. In addition, quantum chemical calculations were performed to reveal the mechanism by which a surfactant suppresses water tree initiation. A comparison of the computational results with experiments suggests that the addition of a surfactant is extremely effective in suppressing bow-tie water trees.

**Keywords :** molecular dynamics simulation, quantum chemical calculation, polyethylene, surfactant, suppression effect, water tree

## 1. Introduction

Water treeing occurs when an electric field is applied to an insulating material in contact with water<sup>(1)</sup>. Water trees occur at the interface between the insulating layer and an electrode, void, or contaminant in the insulating material. Polyethylene (PE), used widely as an insulating material for power cables, is a hydrophobic polymeric insulating material. On the other hand, a surfactant contains both hydrophobic and hydrophilic groups in its molecular structure. It is considered that a surfactant added to PE surrounds water molecules and stabilizes them. Sekii, et al. experimentally revealed that hydrophilic additives can enhance the water tree resistance of PE<sup>(2)(3)</sup>. They also confirmed that the addition of a surfactant suppresses bow-tie water trees (BTTs)<sup>(2)(3)</sup>. Molecular dynamics (MD) simulations have been conducted for systems including polymers and water molecules<sup>(4)(8)</sup>. However, few studies have been conducted on the suppression effect of water trees by performing MD simulations and quantum chemical calculations<sup>(9)</sup>.

In this study, we investigated the aggregation of water molecules and the orientation of surfactants toward water clusters in PE chains by MD simulation. Furthermore, quantum chemical calculations

were performed for the case of a surfactant in proximity to a small water cluster with reference to experimental results.

## 2. Simulation Method

**2.1 PE and Surfactant** Figure 1 shows the molecular structure of PE and the surfactant considered in this study<sup>(2)(3)</sup>. We used PE as a base material, as shown in Fig. 1 (a). We also used an amphiphilic surfactant having both a hydrophobic group and a hydrophilic group in its molecular structure, as shown in Fig. 1 (b).

In a surfactant, the hydrophobic group is a nonpolar group with strong affinity to oil and low affinity to water. The hydrophobicity increases if there are many hydrocarbon chains such as alkyl groups or cyclic structures such as aryl groups. In contrary, the hydrophilic group has a large polarity and strong affinity to water. The hydrophilic group forms weak bonds with water molecules by electrostatic action or hydrogen bonding. Representative hydrophilic groups are the hydroxyl group, amino group, and carboxyl group.

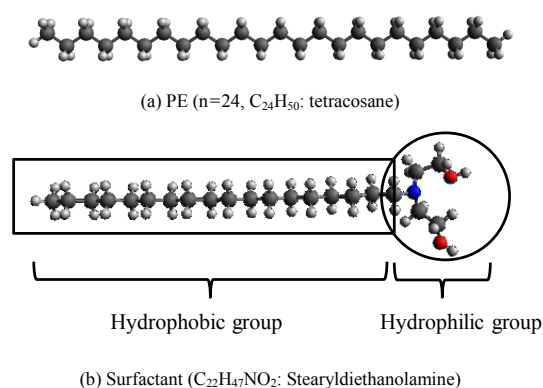


Fig. 1. Molecular structure of PE and surfactant

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When surfactants are added to hydrophobic polymers such as cross-linked polyethylene (XLPE), water molecules aggregate to form water clusters, and the surfactants and water clusters in XLPE are considered to form micelles in the amorphous region of the XLPE in the presence of water, as shown in Fig. 2<sup>(2)(3)</sup>. Such micelle structures comprising a water cluster surrounded by surfactants are thermodynamically stable. Hence, it is highly plausible that the solubilization of moisture in the supersaturated state will lead to the suppression of water tree initiation in XLPE.

**2.2 Reference Experimental Results** Figure 3 shows the volume density of BTTs in XLPE with and without surfactants obtained by Sekii and co-workers<sup>(2)(3)</sup>. We can clearly see that the volume density of BTTs in the case with surfactants is smaller than that without surfactants. Therefore, it is considered that the surfactants suppress BTT initiation.

**2.3 Quantum Chemical Calculations** In this study, we used the Gaussian 09 quantum chemical program to obtain the electric dipole moments, energy levels, molecular orbitals, and three-dimensional (3D) electrostatic potential distributions of the PE, surfactants, water molecules, water clusters, and combined water clusters and surfactants<sup>(10)</sup>. More specifically, we applied B3LYP as the exchange-correlation functional and 6-31g\* as the basis set<sup>(11)(12)</sup>. High-precision second-order Møller–Plesset perturbation theory (MP2), an improvement over the Hartree–Fock (HF) *ab initio* method<sup>(13)(14)</sup>, is often used for quantum chemical calculations of water molecules or water clusters. However, its practicality strongly depends on the performance of the computer and can be time demanding. Therefore, we used density functional theory (DFT) to perform highly accurate calculations in a relatively short time.

**2.4 MD Simulation** MD simulation is used to investigate the physical motion of atoms and molecules<sup>(4)(9)</sup>. First, the initial arrangement of atoms or molecules is determined. After that, the forces exerted by one atom or molecule on another are calculated. The forces acting between atoms or molecules comprise the chemical bonding forces when atoms form molecules, the

electrostatic forces generated by positively or negatively charging atoms or molecules, and the intermolecular forces acting between molecules. Then, these forces are summed. Next, the motion of atoms or molecules subjected to these forces is calculated in accordance with Newton's laws of motion. This reveals how the arrangement of atoms or molecules has changed from the initial arrangement after a certain time.

In this study, we used Gromacs 5.0.7 as the software for MD simulation to determine the molecular structure and to clarify the effect on the diffusion and aggregation of PE, the surfactant, and water molecules. Here, the four-point transferable intermolecular potential (TIP4P) was used for the water molecules<sup>(15)</sup>. TIP4P improves the electrostatic distribution around the water molecules by slightly shifting the charge of the oxygen atom toward the hydrogen atom.

The general Amber force field<sup>(16)</sup> (GAFF) and 3D periodic boundary conditions were employed in the x, y, and z directions. Furthermore, the Lennard–Jones potential was used to approximate the interaction between the combination of neutral atoms or molecules in this simulation. The particle-mesh Ewald (PME) summation was used for the Coulombic interaction<sup>(17)</sup>. All bonds including hydrogen were employed using a linear constraint solver (LINCS) algorithm<sup>(18)</sup>. A fixed time step of 2 fs was used throughout all MD simulations.

The procedure of the MD simulation was as follows. First, PEs, surfactants, and water molecules were randomly arranged in a cell. After that, the energy of the cell was minimized using the method of steepest descent. In this steepest descent method, the energy minimization calculation is terminated when the system becomes 100 kJ mol<sup>-1</sup> nm<sup>-1</sup> or less. Next, an NVT ensemble with a constant volume and constant temperature of 300 K, controlled by a Nosé–Hoover thermostat<sup>(19)(20)</sup>, was applied to the system for 250,000 steps (500 ps). Then, an NPT ensemble with a constant temperature of 300 K and a constant pressure of 100 kPa, controlled by the Parrinello–Rahman barostat<sup>(21)</sup>, was conducted for 5,000,000 steps (10 ns). Finally, an NPT production run under the same conditions as the NPT ensemble was conducted for 5,000,000 steps (10 ns). During the production run, the molecular trajectory was recorded every 1,000 steps.

### 3. Results and Discussion

**3.1 Aggregation of Water Molecules and Orientation of Surfactant toward Water Cluster by MD Simulation** Figure 4 shows the initial structure, final structure, and an enlarged view of the final structure near a water cluster for each MD simulation model, whose parameters are summarized in Table 1. To emphasize the water molecules and surfactants, the PE molecules in Fig. 4 are indicated by wire-type structures. It can be seen that the water molecules aggregate and form a water cluster. Moreover, the hydrophilic groups of surfactants are oriented toward the water cluster in PE chains, as shown in Figs. 4 (b) and (c). Figure 5 shows the density of PE chains as a function of time during the 10 ns NPT production run for each model. These values are in good agreement with the literature<sup>(4)(5)(22)</sup>.

Here, we used the radial distribution function (RDF) to analyze the structure of the formed water cluster. The RDF in a system of atoms or molecules describes how the density varies as a function of distance from a reference atom or molecule. The RDF of water molecules was calculated from the molecular trajectory obtained during the 10 ns NPT production run.

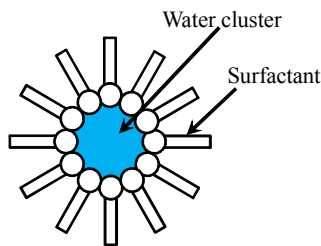


Fig. 2. Micelle formed in amorphous region of XLPE

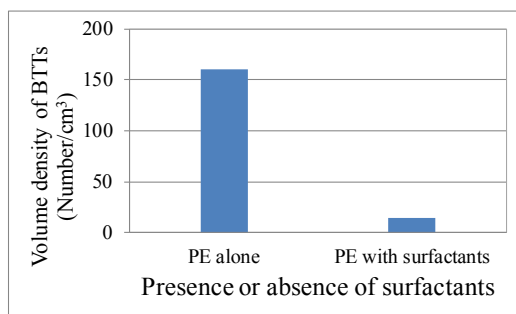


Fig. 3. Volume density of BTTs in XLPE with and without surfactants<sup>(2)(3)</sup>

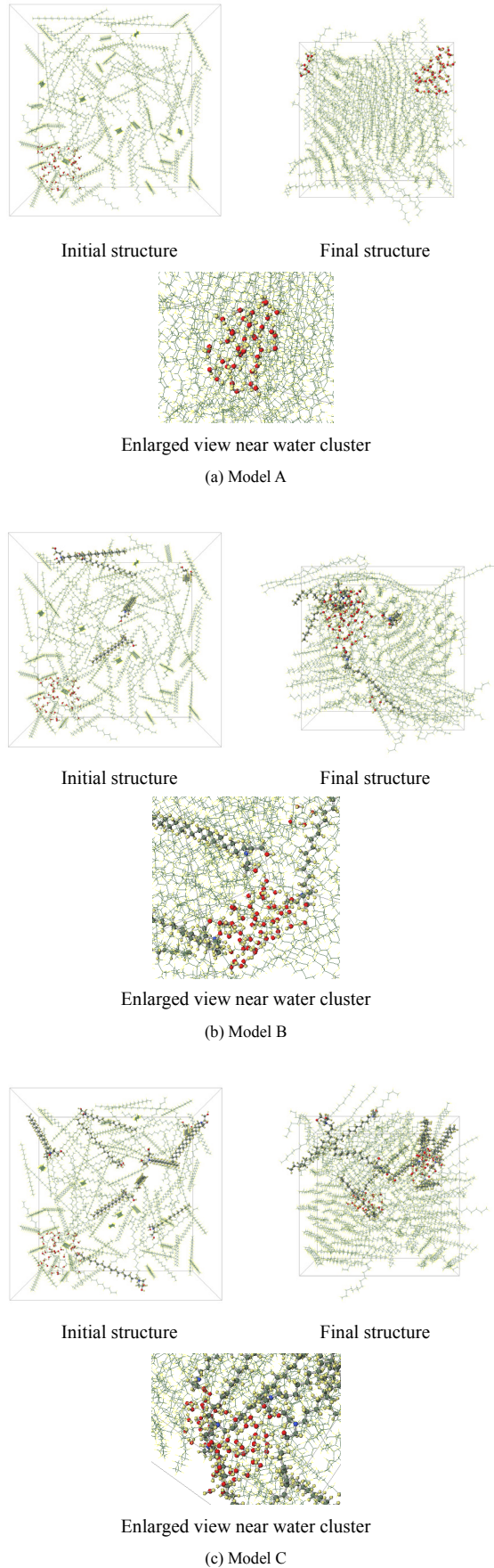


Fig. 4. Initial structure, final structure, and enlarged view of final structure near water cluster for each MD simulation model

Table 1. Parameters of MD simulation models

Model	A	B	C
Number of PEs	100	100	100
Number of surfactants	0	5	10
Number of water molecules	50	50	50
wt% of PEs	97.4	92.6	88.3
wt% of surfactants	0	4.9	9.3
wt% of water molecules	2.6	2.5	2.4
Density of initial structure (kg/m <sup>3</sup> )	200	200	200
Density of final structure (kg/m <sup>3</sup> )	872	847	862

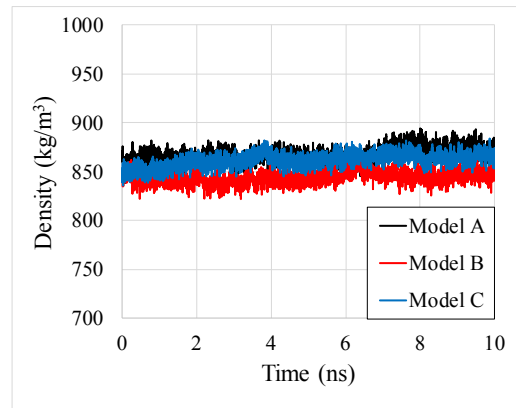


Fig. 5. Density of PE chains as a function of time during 10 ns NPT production run for each model

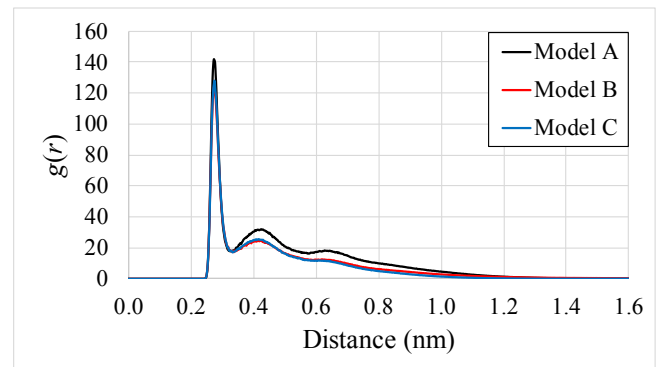


Fig. 6. RDF between oxygen atoms of water molecules for each MD simulation model

Figure 6 shows the RDF between the oxygen atoms of water molecules for each MD simulation model. Here,  $g(r)$  is the probability that another oxygen atom of a water molecule exists at a distance  $r$  from the reference oxygen atom of a water molecule. At distance  $r$  from the reference oxygen atom, with the number of oxygen atoms between two spherical shells with radii  $r$  and  $r+dr$  represented as  $n(r)$ , the density of oxygen atoms in the spherical shell is

$$\frac{n(r)}{4\pi r^2 dr} \dots \dots \dots (1)$$

Dividing Eq. (1) by the average density  $\rho$  of the system yields the RDF  $g_i(r)$  of oxygen atom  $i$ .

$$g_i(r) = \frac{n(r)}{4\pi r^2 dr \rho} \quad (2)$$

The average of Eq. (2) is taken as the RDF  $g(r)$  of the system.

$$g(r) = \langle g_i(r) \rangle = \frac{\langle n(r) \rangle}{4\pi r^2 dr \rho} \quad (3)$$

In Fig. 6, the first sharp peak is at 0.28 nm and the second broad peak is at 0.42 nm. Although the value of  $g(r)$  is zero at 0.24 nm or less, this means that the oxygen atoms of water molecules do not overlap each other. The first sharp peak at 0.28 nm indicates the high probability of oxygen occupancy of adjacent water molecules<sup>(4)(9)(23)-(25)</sup>. Since the distance between adjacent oxygen atoms exhibiting hydrogen bonding between is 0.272 nm, the sharp peak is considered to correspond to the interaction due to hydrogen bonding. The second broad peak at 0.42 nm represents the distance to second-neighbor oxygen atoms.

Since whole pairs between oxygen atoms of water molecules are averaged and divided by the density as shown in Eqs. (1) to (3),  $g(r)$  is considered that there is no contradiction even if it becomes extremely large. Although the RDF is originally used to describe the structure of clusters and liquid containing water, we focused on the distance between oxygen atoms in water molecules instead of clusters in this MD simulation.

On the other hand, it is difficult for the whole system after MD simulation to distinguish between crystalline and amorphous. It is also difficult to consider from the gauche-trans (anti) conformation in terms of current PE length, the number of PE molecules and the calculation time<sup>(22)(26)(27)</sup>. The influence of the structure determined by the initially placed molecular position and subsequent NVT ensemble should remain in the production run.

Figure 7 shows the RDF between the carbon atoms at the left end ( $C_0$ - $C_0$ ), central part ( $C_{12}$ - $C_{12}$ ) and right end ( $C_{23}$ - $C_{23}$ ) of the PE shown in Fig. 1 (a) for each MD simulation model. In the RDF in the crystals, sharp peaks such as the delta function exist discretely up to large interatomic distances. Moreover,  $g(r)$  does not converge to 1<sup>(27)</sup>. On the other hand, in the RDF obtained by this MD simulation,  $g(r)$  is 0 until 3.2 Å because PE chains cannot approach each other within about 3.2 Å due to the repulsive force resulting from the overlap of electrons<sup>(27)</sup>. After that, the largest and sharp peak appeared at around 4.2 Å at the left end and right end, and around 5.2 Å at the central part of PE as shown in Fig. 1 (a). This

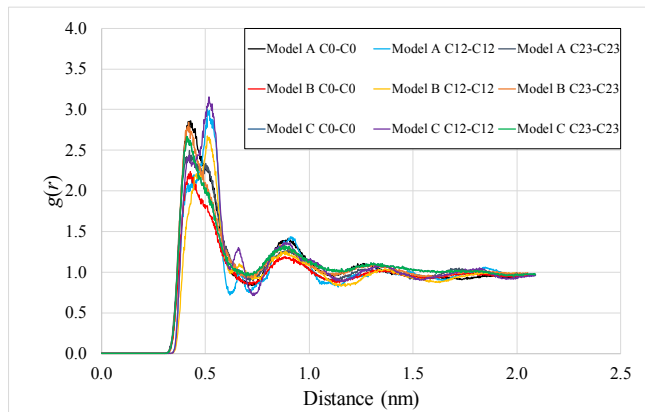


Fig. 7. RDF between the carbon atoms at the left end ( $C_0$ - $C_0$ ), central part ( $C_{12}$ - $C_{12}$ ) and right end ( $C_{23}$ - $C_{23}$ ) of the PE shown in Fig. 1 (a) for each MD simulation model

sharp peak corresponds to the first solvation layer. Then, the second peak and third peak gradually decrease in height. Finally,  $g(r)$  converges to 1. That is, the structure disappears. These are features that are not crystalline but amorphous<sup>(27)</sup>.

### 3.2 Quantum Chemical Calculation of $H_2O$ and $5H_2O$ by DFT

Figure 8 shows one water molecule ( $H_2O$ ) and five water molecules ( $5H_2O$ ) considered in this investigation<sup>(13)(14)</sup>. Although water clusters should be extracted from MD simulation results, we could not successfully extract them by employing periodic boundary conditions. For  $5H_2O$ , a simple structure optimization based on molecular mechanics was carried out in advance. From the RDF in Fig. 6, the average distance between oxygen atoms in adjacent water molecules was found to be 0.28 nm. As a result, the distances between oxygen atoms in  $5H_2O$  were set to about 0.28 nm, as shown in Table 2.

Figure 9 shows the electric dipole moments, energy levels, and molecular orbitals for  $H_2O$  and  $5H_2O$ . The electric dipole moment

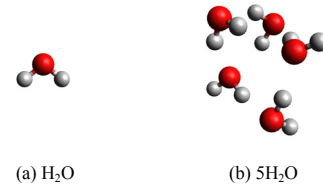


Fig. 8.  $H_2O$  and  $5H_2O$  considered in this investigation

Table 2. Distances between oxygen atoms in  $5H_2O$

Combination	Distance (nm)
O <sub>1</sub> -O <sub>2</sub>	0.2856
O <sub>1</sub> -O <sub>3</sub>	0.2.819
O <sub>1</sub> -O <sub>4</sub>	0.3469
O <sub>1</sub> -O <sub>5</sub>	0.2703
O <sub>2</sub> -O <sub>3</sub>	0.2752
O <sub>2</sub> -O <sub>4</sub>	0.2955
O <sub>2</sub> -O <sub>5</sub>	0.4160
O <sub>3</sub> -O <sub>4</sub>	0.2667
O <sub>3</sub> -O <sub>5</sub>	0.3983
O <sub>4</sub> -O <sub>5</sub>	0.2710

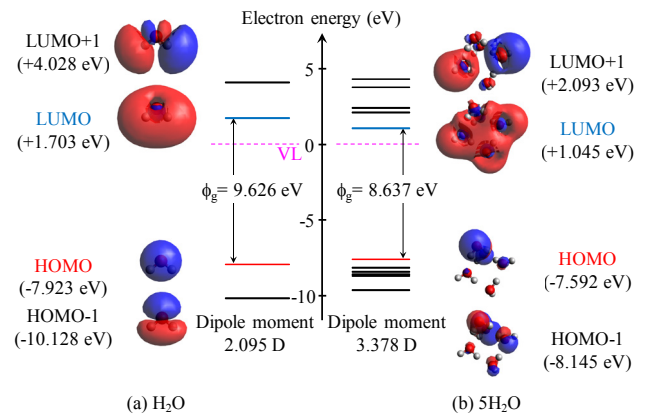


Fig. 9. Dipole moments, energy levels, and molecular orbitals for  $H_2O$  and  $5H_2O$



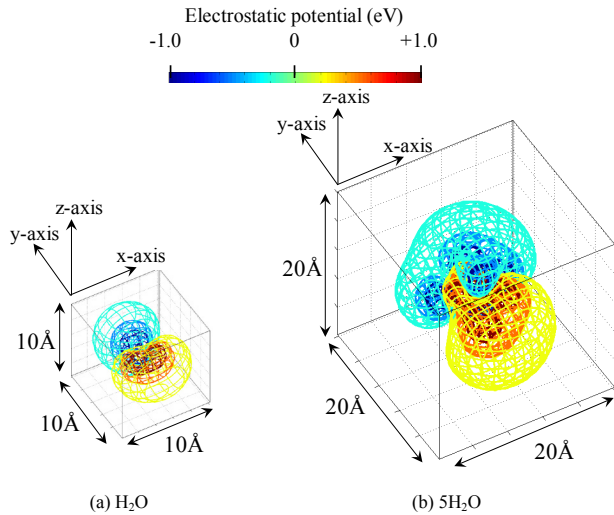


Fig. 10. 3D electrostatic potential distributions for  $\text{H}_2\text{O}$  and  $5\text{H}_2\text{O}$

of  $5\text{H}_2\text{O}$  was about 1.6 times larger than that of  $\text{H}_2\text{O}$ . Therefore, charge trapping by  $5\text{H}_2\text{O}$  is easier than that by  $\text{H}_2\text{O}$ <sup>(28)</sup>. Moreover, the energy gap between the highest occupied molecular orbital (HOMO) and lowest unoccupied molecular orbital (LUMO) levels is narrow in  $5\text{H}_2\text{O}$ . This is due to the presence of four oxygens with high electronegativity near  $\text{H}_2\text{O}$ .

Figure 10 shows the 3D electrostatic potential distributions for  $\text{H}_2\text{O}$  and  $5\text{H}_2\text{O}$ . Warm colors represent positively charged regions and cold colors represent negatively charged regions. We can see that the hydrogen side is positively charged and the oxygen side is negatively charged in  $\text{H}_2\text{O}$ , as shown in Fig. 10 (a). On the other hand, in  $5\text{H}_2\text{O}$ , a pair of positively charged and negatively charged regions larger than those in  $\text{H}_2\text{O}$  were formed, as shown in Fig. 10 (b).

### 3.3 Quantum Chemical Calculation of Surfactant Alone and Surfactant in Proximity to $5\text{H}_2\text{O}$ by DFT

As shown in Fig. 2, when a surfactant having a hydrophobic group and hydrophilic group is added to a hydrophobic polymer such as PE or XLPE, the surfactant forms a micelle in the amorphous region of the polymer. Therefore, it is considered that the surfactant surrounds a water cluster, stabilizing the cluster.

Here, we performed a quantum chemical calculation of the surfactant alone and the surfactant in proximity to  $5\text{H}_2\text{O}$  (surfactant +  $5\text{H}_2\text{O}$ ). That is, we calculated part of a micelle containing  $5\text{H}_2\text{O}$  using DFT, as shown in Fig. 11. The closest distance between an oxygen atom of the water cluster and an oxygen atom of the surfactant is 0.2736 nm.

Figure 12 shows the electric dipole moments, energy levels, and molecular orbitals for the surfactant alone and surfactant +  $5\text{H}_2\text{O}$ . The electric dipole moment of surfactant +  $5\text{H}_2\text{O}$  is about 2.5 times larger than that for the surfactant alone. Since water tree initiation is related to electron transfer under an electric field<sup>(1)</sup>, the much larger electric dipole moment of surfactant +  $5\text{H}_2\text{O}$  is considered to be more effective in electron trapping<sup>(28)</sup> and contribute more to the suppression of water tree initiation. Moreover, the energy gaps became narrower with the addition of the surfactant, particularly surfactant +  $5\text{H}_2\text{O}$ . While there is almost no fluctuation in the HOMO level, the LUMO level is further reduced by the addition of four water molecules. This is considered due to the effect of oxygen with high electronegativity. From the molecular orbitals,

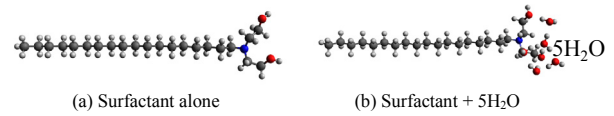


Fig. 11. Surfactant alone and surfactant +  $5\text{H}_2\text{O}$  as part of micelle

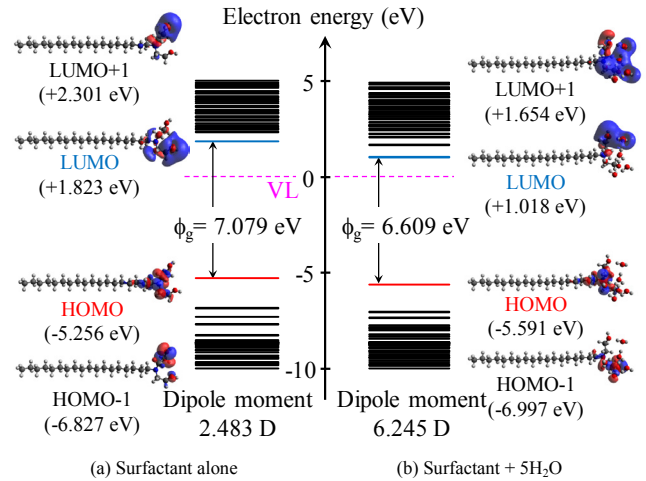


Fig. 12. Dipole moments, energy levels, molecular orbitals for surfactant alone and surfactant +  $5\text{H}_2\text{O}$

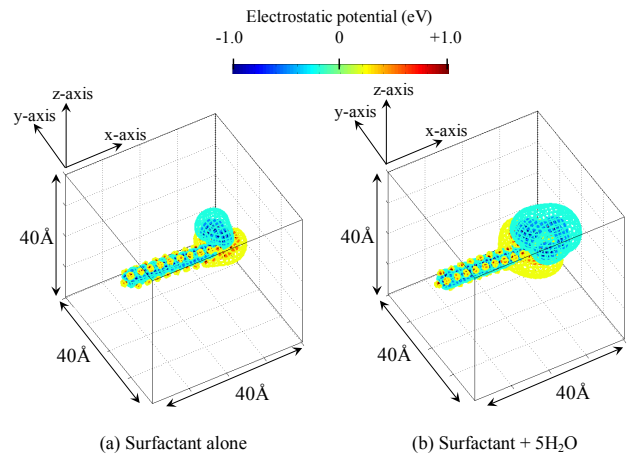


Fig. 13. 3D electrostatic potential distributions for surfactant alone and surfactant +  $5\text{H}_2\text{O}$

it can also be seen that the trapping sites are concentrated in the vicinity of nitrogen and oxygen, which have high electronegativity.

Figure 13 shows the 3D electrostatic potential distributions for the surfactant alone and surfactant +  $5\text{H}_2\text{O}$ . Since five oxygens having an electronegativity of 3.5 are located close to the surfactant in surfactant +  $5\text{H}_2\text{O}$ , it can be seen that the 3D electrostatic potential distribution is spread over a wide area, particularly in the hydrophilic group region of the surfactant. In contrast, there is no significant change in the hydrophobic group in the surfactant alone and surfactant +  $5\text{H}_2\text{O}$ . Since the surfactant contains one nitrogen and two oxygens with high electronegativity in the molecular structure, it is considered that hydrogen bonding occurs.

**3.4 Effect of Surfactant on Suppression of BTT** A BTT is caused by a defect such as a void or contaminant in an insulating material, as shown in Fig. 14. Moreover, there may be moisture present inside the insulating material or external moisture may

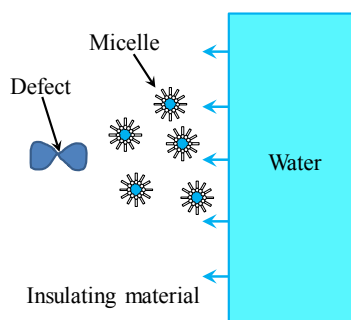


Fig. 14. Effect of surfactant on Suppression of BTT

penetrate through the insulating material to reach a defect and generate a BTT. However, when the surfactant was added, the initiation of a BTT was suppressed to less than 20% of the case without the surfactant, as shown in Fig. 3<sup>(2)(3)</sup>.

We now consider the model shown in Fig. 14. First, moisture pre-existed inside the insulating material and/or external moisture penetrated through the insulating material form water clusters owing to hydrogen self-bonding and aggregation. Then, the amphiphilic surfactant added to the insulating material surrounds each water cluster with the hydrophilic groups oriented toward the water cluster. Hence, micelles are formed to solubilize the moisture presented in the supersaturated state in the insulating material. These micelles suppress water trees by delaying the supply of water to the defect.

#### 4. Conclusions

In this study, we performed MD simulation and DFT quantum chemical calculations to reveal the mechanism by which water tree initiation is suppressed by amphiphilic surfactants. Our comparison of the computational results with experiments suggests that the addition of a surfactant is extremely effective in suppressing BTT. Our main findings related to the mechanism of such water tree suppression are as follows.

(1) Water molecules form a water cluster mainly by hydrogen bonding.

(2) The electric dipole moment of surfactant + 5H<sub>2</sub>O is larger and the energy gap is narrower than those for the surfactant alone.

(3) We successfully modeled part of a micelle by combining a surfactant and a small water cluster.

Moreover, future tasks are as follows.

(1) The additive amount of the surfactant in which suppression of BTT was confirmed was 0.2 wt% in the experiment. However, in this MD simulation, the additive amount of the surfactant was 25 or 50 times as 4.9 wt% or 9.3 wt%, as shown in Table 1. Therefore, it is important to make a large scale simulation by increasing the length of the PE chains and to match with the actual additive amount of the surfactant.

(2) We are aware that the convergence in the basis set of 6-31g\* is not suitable and this DFT calculation is sensitive to basis set. Therefore, we have a plan to use a more appropriate basis set. Although the structure optimization was performed in this DFT calculation, the self-consistent field (SCF) calculation was not set regarding the convergence condition.

(3) Although we showed that the water cluster locally has a large electric dipole moment depending on the oxygen atoms in water molecules with large electronegativity, we are now considering that this widely spread electrostatic potential

distribution reduces the LUMO level of surrounding surfactant.

(4) In this study, a micelle after MD simulation could not be extracted due to periodic boundary conditions. Therefore, DFT calculation was performed by simulating a part of the micelle. In the future, we would like to extract the micelle from the final structure after MD simulation and perform DFT calculation. Thereby, we would like to seek the mechanism of initiation and propagation of BTT.

(5) We will consider the case in which an electric field is applied as well as the molecular interactions between PE, surfactants, and water molecules.

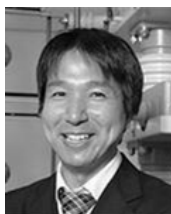
#### Acknowledgment

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