

Sugar-Induced Stabilization Effect of Protein Structure

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Abstract : Sugars and polyols are known to be bioprotectants preventing such as protein denaturation and enzyme deactivation and widely used as a nontoxic additive in various industrial and medical products. The mechanism of their protective actions has been explained by specific bindings between biological components and additives, changes in solvent viscosities, and surface tension and free energy changes upon transfer of those components into additive solutions. On the other hand, some organisms having tolerances against extreme environment produce stress proteins and/or accumulate sugars in cells, which is called cryptobiosis. In particular, trehalose has been drawing attention relevant to cryptobiosis under external stress such as high or low temperature, drying, osmotic pressure, and so on. The function of cryptobiosis by trehalose has been explained relevant to the restriction of the intra-and/or-inter-molecular movement by vitrification or from the replacement of water molecule by trehalose. Previous results suggest that the structure and interaction between sugar and water are a key determinant for understanding cryptobiosis. Recently, we have shown direct evidence that the protein hydration (solvation) and structural stability against chemical and thermal denaturation significantly depend on sugar species and glycerol. Sugar and glycerol molecules tend to be preferentially or weakly excluded from the protein surface and preserved the native protein hydration shell. Due to the protective action of the protein hydration shell by those molecules, the protein structure is stabilized against chemical (guanidinium chloride) and thermal denaturation. The protective action depends on sugar species. To understand the above trend and difference in detail, it is essentially important to clarify the characteristics of solutions containing those additives. In this study, by using wide-angle X-ray scattering technique covering a wide spatial region (~3-120 Å), we have clarified structures of sugar solutions with the concentration from 5% w/w to 65% w/w. The sugars measured in the present study were monosaccharides (glucose, fructose, mannose) and disaccharides (sucrose, trehalose, maltose). Due to observed scattering data with a wide spatial resolution, we have succeeded in obtaining information on the internal structure of individual sugar molecules and on the correlation between them. Every sugar gradually shortened the average inter-molecular distance as the concentration increased. The inter-molecular interaction between sugar molecules was essentially showed an exclusive tendency for every sugar, which appeared as the presence of a repulsive correlation hole. This trend was more weakly seen for trehalose compared to other sugars. The intermolecular distance and spread of individual molecule clearly showed the dependence of sugar species. We will discuss the relation between the characteristic of sugar solution and its protective action of biological materials.

Keywords : hydration, protein, sugar, X-ray scattering

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