Long-Range Protein-Water Dynamics Role in Understanding Insect Antifreeze Proteins

Yao Xu, David M. Leitner

Short Abstract —

We examine dynamics of water molecules and hydrogen bonds at the water-protein interface of antifreeze proteins by all-atom molecular dynamics simulations and THz spectroscopy. Water dynamics in the hydration layer around the protein is analyzed by calculation of velocity autocorrelation functions and their power spectra, and hydrogen bond time correlation functions are calculated for hydrogen bonds between water molecules and the protein. Both water and hydrogen bond dynamics from sub-picosecond to hundred picosecond time scales are sensitive to location on the protein surface and appear correlated with protein function.

***Keywords* — Protein-Water Dynamics, Antifreeze Proteins, THz Spectroscopy, Molecular Dynamics Simulation**

THE antifreeze proteins (AFPs) are proteins which are characterized by their ability to lower the freezing point compared to the melting point. Thermal Hysteresis (TH) is the difference between both points and is a measure for freezing point suppression. The magnitude of the thermal hysteresis depends on the specific activity and concentration of the AFP as well as on the presence of co-solutes [1-3].

Hyperactive AFPs, identified in insects give rise to thermal hysteresis values up to 5-6°C which exceeds that of other AFPs by far. In previous studies [4, 5] we speculated that the activity of AFP can be attributed to two distinct molecular mechanisms: a) short range direct interaction of a protein site with the growing ice face and b) long range via changes in the water dynamics by the solute-solvent interaction exceeding up to 20 Ä from the protein surface.

In the present talk we combine terahertz spectroscopy and molecular dynamics to show that long-range-protein-water interactions are essential contribution to the high antifreeze activity of insect proteins. We support our assumption by studying the effect of the addition of the osmolyte sodium citrate.

REFERENCES

[1] Duman, J. G. Antifrezze and Ice Nucleator Proteins in Terrestrial Arthropods *Annual Review of Physiology* **2001**, *63*, 327.

[2] DeVries, A. and Wohlschlag, D. Freezing resistance in some Antarctic Fishes *Science* **1969**, *163*, 1073.

[3] Yeh, Y. and Feeney, R. E. Antifreeze Proteins: Structures and Mechanisms of Function *Chemical Reviews* **1996**, *96*, 601.

[4] Ebbinghaus, S. et al. Antifreeze Glycoprotein Activity Correlates with Long-range Protein-water Dynamics *Journal of the American Chemical Society* **2010**, *132*, 12210.

[5] Ebbinghaus, S. et al. An Extended Dynamical Hydration Shell Around Proteins *Proceedings of the National Academy of Sciences* **2007**, *104*, 20749.

Acknowledgement: This work was funded by Volkswagen Foundation.

Department of Chemistry and Chemical Physics Program, University of Nevada, Reno. E-mail: xuy3@unr.edu