QUANTUM–CLASSICAL PATH INTEGRAL SIMULATION OF PROTON TRANSLOCATION IN BIOLOGICAL CHANNELS

Allocation: Illinois/75 Knh
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EXECUTIVE SUMMARY

The PI uses the quantum–classical path integral (QCPI) methodology, along with the modular decomposition of the path integral, to perform highly accurate simulations of proton translocation dynamics in water chains embedded in biological channels. These methods allow an accurate treatment of important quantum mechanical effects, accounting for the effects of the protein environment in full atomistic detail.

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RESEARCH CHALLENGE

Understanding the mechanism of the proton translocation along water chains embedded in biological channels continues to attract much theoretical and experimental effort. An interesting question is related to whether the dynamic is sequential or concerted. The accurate treatment of quantum effects, along with a faithful treatment of phase interference in the interaction of the protons with the environment, is critically important for reaching definitive conclusions in this regard. Unfortunately, quantum mechanical calculations scale exponentially with the number of coupled degrees of freedom.

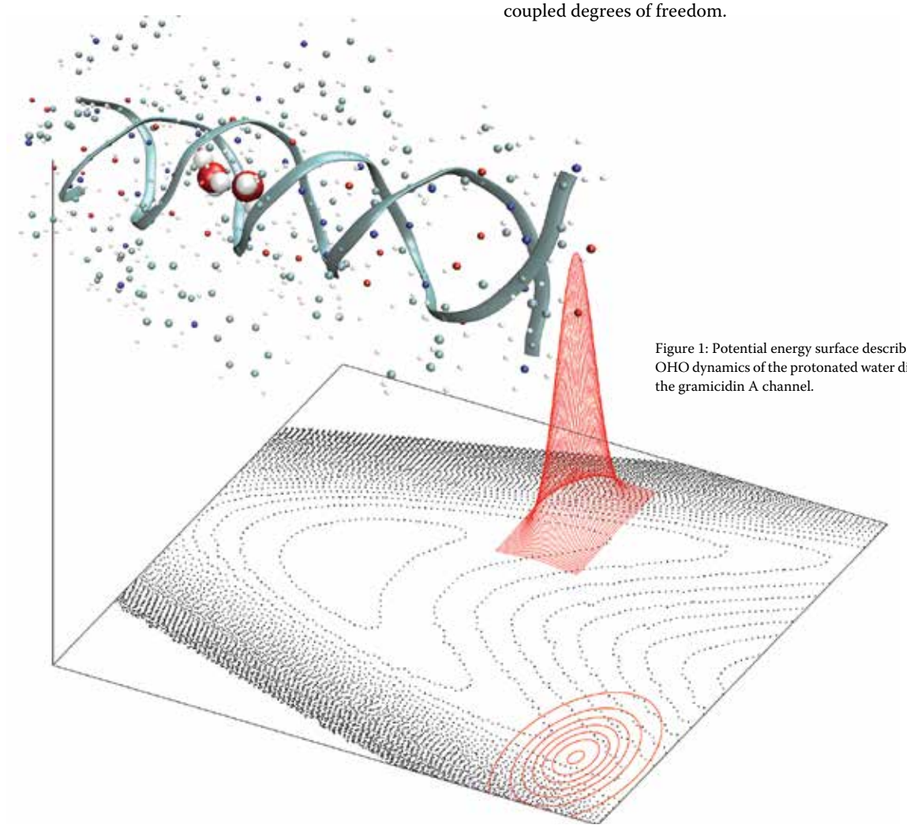

Figure 1: Potential energy surface describing the OHO dynamics of the protonated water dimer in the gramicidin A channel.

METHODS & CODES

The PI's initial calculations on a protonated water dimer are based on the QCPI [1–7] methodology she developed, with several recent advances to her code. Specifically, its ability to describe solvents has been increased with the addition of a molecular dynamics package, developed by her for QCPI, that contains an implementation of the CHARMM force field for protein environments along with accurate potentials for water clusters as well as the ability to simulate various subsystems, each with its own force field. Another development of the methods is the flexibility of augmenting the system Hamiltonian with matrix elements that depend on time through select solvent coordinates. The extension of this work to treat longer chains with multiple transferring protons will utilize the modular decomposition of the path integral [8–10] developed recently by the PI.

RESULTS & IMPACT

This project involves the simulation of the dynamics of the protonated water dimer in the gramicidin A protein channel. The problem of the translocation of a proton along a water chain has fascinated scientists for decades. Since the discovery of water chains in protein channels, such a system has been considered a model for a proton pump that helps maintain osmotic pressure between a cell and its environment. The diffusivity of the proton is in fact a fast process that can be accounted for if one considers not only quantum tunneling but also its interplay with the thermal fluctuations of the oxygen atoms of the chain and the coupling to the protein that surrounds it.

Using the QCPI code, the PI has simulated the transfer dynamics of the excess proton injected in a neutral water dimer, from which she estimates a population decay on a timescale of shorter than 0.1 picosecond. This process is driven in great part by the strengthening of the hydrogen bond that pulls the oxygen atoms closer. This picture becomes more complicated in longer chains, where the motion of the oxygen atoms is correlated, and there are more reaction pathways for the proton diffusion that may correspond to a shuttling motion or a concerted displacement of multiple hydrogen atoms. The researcher plans to address these questions by simulating the dynamics of proton translocation in longer chains, taking into account the quantum mechanical character of multiple transferring protons using the modular decomposition of the path integral methodology.

WHY BLUE WATERS

The QCPI calculations require a multilevel parallelism. Blue Waters provides the ideal platform for the implementation of the algorithm.