

THERMODYNAMIC CHARACTERIZATION OF CONFORMATIONAL LANDSCAPE IN PROTON-COUPLED OLIGOPEPTIDE TRANSPORTERS

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PI: Mahmoud Moradi¹

¹University of Arkansas, Fayetteville

EXECUTIVE SUMMARY

Proton-coupled oligopeptide transporters (POTs) use the inwardly directed proton flow to uptake small peptides and peptide-like molecules. The human POT transporters PepT1 and PepT2 provide the main route through which the body absorbs and retains dietary proteins. Human POTs also recognize several important families of peptide-like drug compounds such as β -lactam antibiotics. In order to function, POTs undergo large-scale conformational changes, whose characterization is the key in understanding the mechanism of transport by these proteins. The inward- (IF) to outward-facing (OF) structural transition of POTs, however, has remained elusive despite many experimental and computational efforts. We have employed all-atom molecular dynamics (MD) simulations along with novel enhanced sampling techniques to, for the first time, characterize the large-scale conformational changes of a bacterial POT transporter, namely GkPOT. By employing novel loosely coupled multiple-copy (LCMC) algorithms, our simulations provide a detailed description of the GkPOT conformational landscape, which sheds light on the structure–function relationship in POTs.

RESEARCH CHALLENGE

Membrane transporters provide the machinery to intimately couple active transport of materials to various forms of cellular energy. POT transporters couple the energy from proton flow to the transport of dipeptides, tripeptides, and their analogs [1]. A key feature of POTs is their substrate promiscuity [2], which is of great interest from a biomedical perspective. Human POT transporters PepT1 and PepT2, which play a key role in absorbing and retaining dietary proteins (in the small intestine and kidney, respectively) [3] recognize several important families of peptide-like drugs such as β -lactam antibiotics [4] and can improve the uptake of poorly absorbed/retained medications if attached to amino acids or dipeptides (prodrugs) [5]. Recent structural studies have resulted in several crystal structures of bacterial POTs [6–10], among which GkPOT, the POT transporter found in the bacterium *Geobacillus kaustophilus*, has the highest resolution (1.9 Å) [10]. These crystal structures, which are all in the IF state, provide the basis of our understanding of POTs' transport mechanism at the structural level. However, in order to function as active transporters, POTs are known to alternate between distinct IF and OF states. The conformation of the OF state and the transition pathway between the two functional states have remained elusive.

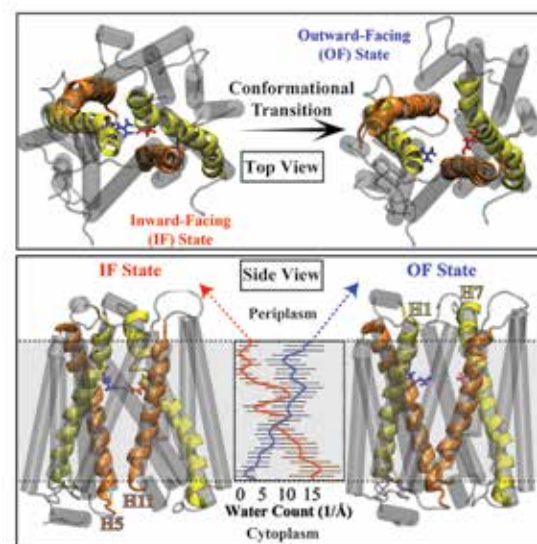


Figure 1: Top and side views of GkPOT transporter (cartoon representation) in its IF state (PDB: 4IKV [1]) and OF state (our model generated using enhanced sampling techniques), along with the water count along the pore as measured from equilibrium simulations of each model.

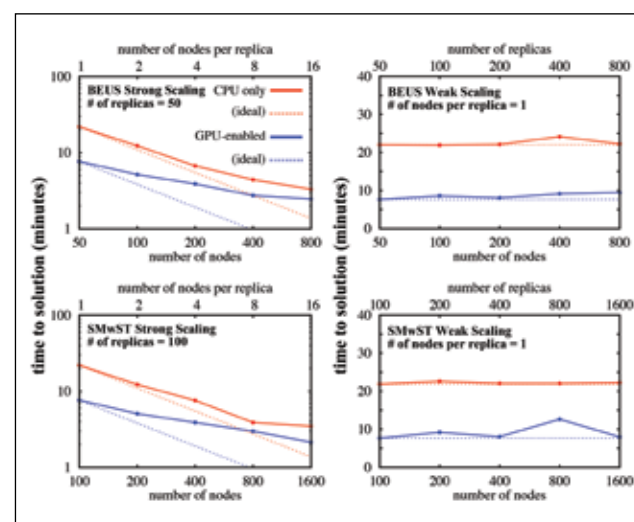


Figure 2: Strong and weak scaling of the Riemannian BEUS and SMwST algorithms [2] implemented in NAMD 2.10. Time-to-solution is reported for 40 ps of GkPOT simulations in explicit membrane and water (~85,000 atoms).

Previous MD simulations that relied on equilibrium simulations have failed to reliably characterize large-scale conformational changes such as those involved in POTs [10–11]. While the conventional MD can provide information on local conformational changes of a protein upon binding or unbinding of a substrate, ion, or proton, the global conformational changes observed are not often statistically significant. Functionally important conformational changes such as the IF–OF transition in membrane transporters typically occur on timescales beyond those accessible to conventional all-atom MD. The large-scale conformational changes, on the other hand, are typically studied using simplified modeling techniques such as coarse-graining, which could completely ignore or misrepresent the role of chemical events in the transport process. The main challenge in characterizing the large-scale conformational changes of proteins such as those associated with GkPOT is to reach the functionally relevant timescales without compromising the chemical details.

METHODS & CODES

We used a novel ensemble-based simulation approach [12–15] to reconstruct the entire transport cycle of GkPOT. Bias-Exchange Umbrella Sampling (BEUS) and String Method with Swarms of Trajectories (SMwST) are two independent LCMC algorithms employed. Both methods require parallel execution of hundreds of MD simulations of large protein systems with explicit representation of water and membrane, which requires hundreds of nodes. Our methodology was partly based on the techniques developed and used to investigate the thermodynamic cycle of the glycerol-3-phosphate transporter (GlpT) [14]. This is a rigorous and practical approach in characterizing large-scale conformational changes of proteins and their coupling to chemical events, which efficiently takes advantage of petascale computing. An important modification to the methodology to increase the accuracy of the results was introduced that involves a Riemannian formulation of free energy calculation and path-finding algorithms [15].

The software engine used for the simulations is NAMD: a highly scalable MD code implemented in Charm++, an object-based message-driven execution system based on C++. NAMD has been enhanced to support extremely scalable LCMC algorithms on massively parallelized computers of CPUs and GPUs. Multiple concurrent NAMD instances are launched with internal partitions of Charm++ and are located continuously within a single communication world. Messages between NAMD instances are passed by low-level point-to-point communication functions, which are accessible through NAMD's Tcl scripting interface.

RESULTS & IMPACT

The OF structure shown in Fig. 1 represents the first OF model of POT transporters, generated using our all-atom MD simulations in combination with LCMC algorithms discussed above. Our model is verifiably a stable OF structure since the subsequent equilibrium simulations show a water accessibility

consistent with an OF state (see the water profiles in Fig. 1). Our simulations also suggest that the full IF–OF transition requires the binding of both proton and substrate (data not shown). The pathways generated using parallel SMwST [14] and modified using our recently introduced Riemannian formalism [15] reveal that the proton-bound GkPOT cannot transition to the OF state (data not shown). Unlike the common simulation studies, which either rely on unbiased equilibrium simulations or simple representations (e.g., coarse-graining), our approach combines the accuracy of all-atom MD with the accessibility of long timescales provided by enhanced sampling techniques. The successful employment of these cutting-edge multiple-copy algorithms using Blue Waters resources opens a new window to structural biology of membrane transporters that bypasses the limitations of computational approaches to study structure–function relationships in these proteins.

WHY BLUE WATERS

We have explicitly shown that the unbiased all-atom MD, which is routinely used in the field, could be quite misleading in deciphering mechanistic features of membrane transporters due to the great gap in the timescales associated with the conventional simulations and the function of these proteins [11]. On the other hand, we have shown that the LCMC algorithms such as BEUS and SMwST [14–15] can be used to reconstruct unknown conformational transitions of membrane transport proteins. Unlike the conventional all-atom or coarse-grained MD that can be performed on sub-petascale machines, LCMC MD simulations of membrane transporters are well suited for large petascale computational resources such as Blue Waters as they require hundreds of nodes for a single job. We note that the “weak scaling” of these algorithms (Fig. 2) makes them particularly attractive for large petascale machines, as they can utilize hundreds of compute nodes with almost perfect efficiency.

PUBLICATIONS AND DATA SETS

Immadietty, K., J. Hettige, and M. Moradi. What can and cannot be learned from molecular dynamics simulations of bacterial proton-coupled oligopeptide transporter GkPOT? *J. Phys. Chem. B.*, 121:15 (2017), pp. 3644–3656, DOI: 10.1021/acs.jpcc.6b09733.

Moradi, M., K. Immadietty, and J. Hettige, Couplings between local and global conformational changes in proton-coupled oligopeptide transporters. *Biophysical Society Meeting*, New Orleans, La., February 11–15, 2017.