Exploring transmembrane potential

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Transmembrane potential is a driving force for multiple biological processes including the conductance of ionic channels or in nerve cells, the somatic and axonal action potentials, or the translocation of homeodomains such as engrailed protein. In cells, this potential is generated from the ion imbalance between the intracellular and the extracellular compartments. Protein-membrane interactions are also dependant on this potential as it constitutes an attracting force for the protein (such as engrailed) to get into or pass through the plasma membrane. To understanding how important this factor is for proteins and peptides able to cross the membrane such as antimicrobial peptide (AMP) or cell-penetrating peptides (CPP), some active research is ongoing [1,2]. In this work, molecular dynamic (MD) simulations were employed to get the atomic details of this phenomenon. However, most computational works on this subject used so far an external field to mimic the transmembrane potential, instead of a more realistic ion imbalance approach, mainly for its lower computational cost and easiness of implementation. This limitation has made the research on this topic very limited and a lot of questions remain. Here, we used a special technique using flat-bottomed potential [3] to limit the computational cost to explore transmembrane potential with ion imbalance and how it can be evaluated. We tested multiple approaches to compute the value of the potential in MD simulations as well as its role on the interaction of the CPP penetratin with membranes. This exploratory work has shown that it is still difficult to completely assess the potential value but it is an important factor for understanding penetratin translocation.

Bibliography :

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