Modeling Enzymatic Pathways in Giant Lipid Vesicles

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Abstract

Giant vesicles (GVs) are artificial chemical systems largely used as cell models [1-3], since they are micrometer-sized closed compartments bounded by a semi-permeable membrane, which in turn is composed by self-assembling amphiphiles. By opportunely engineering the lipid membrane and by entrapping cascade-reaction enzymes inside GVs, it comes possible to design micro-sized reactors where metabolic pathways of biotechnological interest can take place sustained by external substrate feeding.

Modeling these supramolecular reacting systems is of great interest both to better understand the dynamics of enzymatic reactions in confined space, but also to improve the design and the implementation of new metabolic micro-reactors. In previous theoretical works [4-8], we studied the time behavior of nanosized reacting vesicles by using a stochastic approach in order to elucidate the role of intrinsic fluctuations, i.e. fluctuations in the reactions occurring time (intrinsic stochasticity). In this contribution, instead, a deterministic 3D approach based on the COMSOL Multiphysics® platform will be presented and discussed. The 3D approach describes individual GVs giving also morphological 3D-space details and allows to take into account explicitly the diffusion of substrates, through the external solution and in the internal vesicle water core, along with the molecular transport across the lipid membrane. It assumes that intrinsic noise is negligible in first approximation and that random fluctuations observed in the time behavior of a vesicle population are mainly due to extrinsic stochasticity, i.e. due to the different composition of the reacting comportments.
In this contribution, the deterministic 3D modeling approach is applied to a three-enzyme metabolic pathway as a case study and the theoretical outcomes are contrasted with confocal microscopy analysis.

Reference

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