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細胞性粘菌の蛍光顕微単一細胞代謝測定

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The energy metabolism monitoring of single cell ameba

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Living things appeared on the earth as a unicellular organism and evolved into multicellular one. A reason for this evolution attracts interests. In order to investigate the advantages in the energy metabolism of the malticellular organism, we employed Dictyostelium cells and measured cellular NADH, which could be an indicator of ATP synthesis. We have find that the NADH level in the cells decreases as forming multicellular structure and that high density of cells declines the NADH level much quickly. In this article, the effect of cell-cell contact and/or adhesion on the NADH level will be discussed. A fluorescence microscope was used to quantify NADH fluorescence by UV-irradiation. A serious damage induced by long term irradiation required to optimize the protocol of irradiation. The protocol was established to monitor NADH level in the single cell without any critical damage. Results: Our monitoring system could detect the difference of NADH level between single cell amebas. The intensity of motionless cells was constant, however the individual cells have their own value. These results suggested that the system could detect the peculiarity of the individual cells. The migrating ameba showed fluctuating in fluorescence intensity. We further observed that the NADH level increased by addition of cyanide in time lapse analysis. These results strongly suggest that our method is a powerful tool for detecting the energy metabolism in single cell ameba.

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Escherichia coli が作り出す同心円状パターンにおける界面揺らぎの解析

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Analysis of interface fluctuations in concentric ring-like pattern of *Escherichia coli*

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Formation of spatial patterns of cells from a mass of initially identical cells is a recurring theme in biophysics. The dynamics that direct pattern formation in biological systems often involve collective cell movements. An example is growing colony formation in the bacterium *Escherichia coli* in which an unstructured population of identical cells rearranges into a beautiful, stable pattern depending on nutrient environment and softness of agar substrate. Recently, we have identified novel concentric ring-like pattern of E.coli colony, whose interface is rough but exhibits protrusive structures. These protrusions propagate like solitary waves and create the periodic pattern of height in bacterial colony. We therefore propose that the interfacial dynamics is important for pattern formation. However, how such dynamics is accomplished is not fully understood. To address this issue, we investigate collective cell movement at the interface. We find that bacteria do not swim but swarm near the interface. Furthermore, the swarming behavior is not affected by concentrated amino acids. Although this result suggests that chemotaxis is not essential for collective cell movement, we unexpectedly find that more than 1.0M glycine specifically flattens the protrusive structure and causes the loss of spatial pattern in growing bacterial colony. Our finding implicates that concentrated glycine suppresses long-range correlation near interface.

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ショウジョウバエ胚においてBicoidの確率的拡散と協同的結合が*hunchback*の発現に及ぼす影響

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Effects of stochastic diffusion and cooperative binding of Bicoid on expression of *hunchback* in *Drosophila* embryo

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Embryonic pattern formation in *Drosophila* starts with the formation of a spatial gradient of the maternal morphogen Bicoid (Bcd). Bcd diffuses through embryo after translated from bcd mRNA which is localized at the anterior tip of the embryo and binds cooperatively to the hunchback (*hb*) enhancer element to induce *hb* expression in the anterior half of the embryo. Although both Bcd diffusion and its downstream activation of *hb* gene are stochastic processes, it has been shown experimentally that fluctuation in the Hb level along the anterior-posterior axis is much smaller than that of the Bcd level [1]. How can noisy input of Bcd produce more precise output of Hb early in development? By extending our previous mean-field method [2], which describes single-cell dynamics of gene expression, we analytically describe the 1-dimensional spatial dynamics of Bcd and *hb* to investigate how stochastic fluctuation in Bcd diffusion and cooperativity in binding of Bcd to *hb* enhancer affect the hb expression.

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ショウジョウバエの初期胚におけるBicoidとHunchbackの3次元確率シミュレーション

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Stochastic three-dimensional simulation of Bicoid and Hunchback in the early *Drosophila* embryo

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The maternal morphogen Bicoid (Bcd) plays an important role in patterning the anterior-posterior axis of the early *Drosophila* embryo. Translated from the maternal mRNA which is localized at the anterior tip of the embryo, Bcd diffuses through embryo to form an exponential distribution along the anterior-posterior axis. Expression of Zygotic *hunchback (hb)* is activated by Bcd at the anterior half of the embryo where Bcd concentration exceeds a threshold. The expressed Hb has a precise spatial distribution, which has only 4% embryo-to-embryo positional variation at its threshold concentration. The upstream Bcd distribution, however, fluctuates by 30% of embryo length at its threshold concentration, implying that the fluctuation in the positional information is reduced drastically at the step from Bcd to Hb.

To investigate how fluctuation in the Hb distribution is controlled against stochastisity of Bcd, we perform a Monte Carlo simulation of translation, diffusion, and *hb* activation using the Gillespie algorithm. *Drosophila* embryo is modeled by a cylinder by assuming that the *bcd* mRNA molecules are localized on the cylinder head. Translated Bcd diffuses through the cylinder and binds cooperatively to the *hb* enhancer located at the side surface of the cylinder. With this model, we discuss how extrinsic fluctuation in Bcd diffusion and intrinsic fluctuation in *hb* expression are related.