3P-274 多細胞の条件指標と最大多様性指標の関係式は、楕円曲線を含んでいる

Algebraic relations between high cell-type diversity and cell-type ratio of multicells

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The development of a multicellular organism is a dynamic process. Starting from one or a few cells, the organism becomes a set of cells with different types that form well-determined patterns. In this sheet, we have constructed a model for generalized Anabaena, which is one of green algae, using a stochastic Lindenmayer system (sL-system). An L-system is a parallel rewriting system that was originally introduced for modelling the development of multicellular organisms. Over this L-system model, first, we have derived the exact algebraic equations between the measure of cell-type diversity and the ratio of cell-types on representative branching/linear cell lineage with the aid of quantifier elimination method. Surprisingly and interestingly, these algebraic equations include elliptic curves which may shed profound insights into the structure of multicells. Second, we have surveyed the rational points and quadratic irrational points of the algebraic equations which are deeply related to the periodic and self-similar structures, respectively. Last, we discuss the relevance of these points to the cell lineage of developmental process of multicells. This talk is supported in part by the Program for Improvement of Research Environment for Young Researchers from Special Coordination Funds for Promoting Science and Technology (SCF) commissioned by the Japan Science and Technology Agency (JST).

3P-275 細胞サイズリポソーム内における内封反応システムと脂質膜の相互作用の定量的解析

Quantitative analysis of interactions between the phospholipid membrane and encapsulated reaction systems in cell-sized liposomes

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In cell-sized compartments, interactions between the enclosed molecules and the membrane boundary become inevitably significant due to the large surface-to-volume ratio. To elucidate the effect of compartmentalization, we developed a measurement system to quantify the progress of biochemical reactions encapsulated in cell-sized liposomes in correlation to liposome volumes using a fluorescence-activated cell sorter. It was done by simultaneously measuring the internal aqueous volume and the concentration of reaction product generated by the transcription and translation of enzyme followed by the hydrolysis of fluorogenic substrate, in individual liposomes. The internal aqueous volume was quantified from the intensity of red fluorescent protein encapsulated with the reaction mixture. Similarly, the amount of reaction product was quantified from the green fluorescence signal emitted upon hydrolysis of the substrate. The effects of the liposome membrane on enzyme reaction and protein synthesis systems encapsulated, which vary in proportion to the power of surface-to-volume ratio, were elicited by kinetic analysis of 100,000 liposome populations. We revealed that encapsulation efficiency of biochemical molecules (enzyme or DNA) and their reaction (substrate hydrolysis or protein synthesis) rate were altered with different compositions of liposome membrane. The present technique and analysis method will aid the quantitative understanding of the molecular interactions between internal components and membrane in reconstituted cell models.

3P-276 非平衡熱水環境におけるプロテノイド代謝系分子の出現

The emergence of catalytic activities of a complex from five kinds of amino acids by non-equilibrium hydrothermal environments

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We have been attempted to observe a glimpse of chemical evolutions in mixtures of five kinds of amino acids, glycine, L-alanine, L-valine, L-aspartic acid and L-glutamic acid. These amino acids were assumed to be a potential evolutionarily minimal set for making peptides having a tertiary structure. The mixture was circulated through a flow reactor simulating seawater circulation in the vicinity of hydrothermal vents in the primitive ocean. We have already reported that certain types of reaction products had a DNA-binding activity.

The flow reactor we used was constructed for simulating both the pressure and temperature conditions of hydrothermal vents. In the flow reactor, a high-temperature high-pressure fluid at 220 degree and at 24 MPa was injected into a low temperature (0 degree) chamber at the same pressure. A steep temperature gradient would exist at the near interface between high and low temperature chambers. The reacted solution was consisted of five kinds of amino acids as described each at 20 mM in pure water. The products were analyzed by HPLC profiles.

The profiles clearly suggest that variety of complexed molecules were synthesized. Among them was more hydrophobic compound than original amino acids with approximated molecular weight of about 3000 dalton. From the molecular weight and the hydrophobicity of the compound, we are speculating that the compounds could have some kinds of catalytic properties, and are trying to identify the nature of their functions.

3P-277 細胞の成長・分裂を模したマイクロエマルジョン制御プラットフォーム

Platform for controlling micro-emulsions as a model of growth and division cycle of the cell

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Living cells autonomously replicate themselves as they grow. By this way the volume, the number of genomic DNA, and the metabolic reaction system of the offspring are kept identical with the originals. Recently, the use of artificial microcompartments (lipid vesicle, water-in-oil (W/O) emulsion, and microchambers) has been proposed to model the biochemical reaction in a cell-sized volume. However, as such artificial compartments are yet static, the encapsulated reaction terminates as a result of saturation of the products or exhaustion of the substrates. We are developing a microfluidic system for dynamically controlling the growth and division of W/O emulsions with a droplet size of 30-50 μm to imitate replicating cycle of living cells. In this microchannels system, emulsion droplets were electrically fused with other droplets and then split by the T-shaped bifurcation; the former process imitated the cell growth as well as feeding, and the latter imitated cell division. A variety of solutions, such as pure water, salt buffer, and cell culture medium, could be successfully used for the water phase (=droplets), indicating that various biological reactions can be tested in this platform. We will report the realization of continuous reactions in microcompartments sustained by the repeated fusion-division cycles.

3P-278 遺伝情報の自己複製システムを作って理解する

Requirements for the efficient self-replication system of genetic information

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We attempted to gain insight into the basic characters of self-replication system, in which the genetic information is replicated by self-encoded replicase by the constructive approach. Recently, we constructed a system in which the Q β RNA replicase was translated from sense strand RNA by the reconstituted translation system, resulting in synthesis of complementary strands to replicate the genetic information. This artificial self-replication system has much lower replication efficiency than natural systems, such as that of RNA viruses. Therefore, we tried to identify requirements for efficient self-replication system by comparing to natural systems. Previously, we demonstrated that the balance between translation and replication was critical for efficient self-replication because of the inhibitory effects of translation on RNA replication. Here, we reported that compartmentalization of self-replication reaction into femto liter sized water-in-oil emulsion enhanced the replication efficiency because of the repression of "parasite RNA" propagation. The "parasite RNA" is a short highly replicable RNA, however, does not have an ability of self-replication, which is produced by RNA recombination at low frequency. The compartmentalization was found to confine the parasite RNA within a few compartments, and majority of compartments were free from the parasites. This result indicated that compartmentalization of the self-replication system is important not only for genotype-phenotype linkage, but also for repressing parasites.

3P-279 同じ制御下の異なる遺伝子の環境変化に対する発現応答

Identical regulatory mechanisms, diverse expression patterns-- A study on the adaptive response to environmental changes

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Living cells respond to a variety of harsh environments by adjusting their gene expressions, mostly mediated by the signal transduction systems. However, it is observed that bacterial cells could optimize their gene expression without using such signal transduction system, when the nutrient starvation occurred. The mechanism of such adaptive response is unknown. Here, we design an artificial gene expression network to examine how such adaptive response is induced and whether the corresponding gene is specifically expressed. Two different genes (proteins), responsible for various biological activities, such as, drug resistance, biosynthesis, etc., are employed in two separated gene expression networks, but are downstream of the same promoter (Ptet) under the same regulatory mechanism. The two fragments (networks) are integrated into the genome of *E. coli*, and the expression of the two genes is detected by flow cytometry (FACS), and quantitatively analyzed according to the fluorescence intensity of the co-expressed fluorescent proteins, GFP and RFP, respectively. We find that the different conditions (environments) induce the distinct responses, that is, varied stresses result in different gene expression patterns, even under the identical regulatory mechanism. Further analysis and details will be reported.

3P-280 タンパク質合成活性に因子間相互作用が与える影響の定量的解析

Quantifying contributions of inter-component interactions on the activity of protein translation system

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The protein translation reaction, one of the most important regulators of cell