2PT206 枯葉に擬態した蛾・蝶の翅模様に実装された正確な擬態をもたらすモジュールデザイン**Modular spatial stabilization of leafy moth/butterfly wing patterns for precise mimesis**Takao K. Suzuki, Hideki Sezutsu (*NIAS TG_SilkwormUnit*)

In nature, where *yuragi* is pervasive, many features of animal's structures are assumed to be so perfectly suited to their function that they seem unlikely to have arisen by chance. Among these features, mimetic patterns, resemblance to natural objects such as leaves, seem to be a typical example implementing a specific design to deal with *yuragi*. However, how the mimetic leafy patterns are established to manage *yuragi* has been poorly understood. Here, we developed a novel method, morphometrical network analysis, to reveal how the leafy moth/butterfly wing patterns are spatially coordinated. As model organisms, we used two leafy wing patterns: a moth, *Oraesia excavata*, and a butterfly, *Kallima inachus*. Our quantitative analysis indicated that in both organisms the constituent components of the leafy patterns are tightly coupled as modules, each of which corresponds to each component of the leaf venation pattern (i.e., the main, right-hand, and left-hand venation patterns). Interestingly, phylogenetic analysis showed that the modules detected in two organisms evolved independently, strongly suggesting that the modules of two leafy patterns were needed for mimetic performance. The establishment of modules allows within-module components to be put together, suggesting that the leafy pattern is precisely stabilized by implementing the spatially-synchronized arrangement of its subordinate leaf-venation components. Our results may suggest that the modular design likely improve the visual trick of leafy mimesis for predator avoidance.

2PT207 巨大化大腸菌(GP)からの大腸菌再生過程の観察**Observation of reproducing process the *E. coli* bacterium from a giant protoplast**Kazuhiro Tabata¹, Takao Sogo¹, Shoji Takeuchi², Hiroyuki Noji¹ (¹*App. chem. Univ. Tokyo*, ²*IIS Univ. Tokyo*)

We report to reproduce into the original bacteria from a giant protoplast (GP), having a diameter in excess of 10 μm and prepared from a single *Escherichia coli* bacterium. Bacteria have long been known to be capable of gigantism. When ampicillin is added after a lysozyme treatment in an isotonic solution for culturing *E. coli*, cell wall synthesis is inhibited and division does not occur; this results in gigantism and the relatively easy formation of a GP with a diameter larger than 10 μm . A GP formed through such abnormal gigantism is believed to have already lost the ability to divide and proliferate. However, when this GP was confined in a microchamber and observed for more than 10h, we found that the spherical GP deformed and divided. This result may indicate that *E. coli* maintains its life system and is in a functional state even after becoming a GP and experiencing an extreme change in its intracellular environment. We showed that the GP have an ability to divide and return to its original bacteria cell using the microchamber. We investigated the extent to which the gene expression system inside the GP was stable with respect to the duration of GP transformation culturing and found that protein expression ceased approximately 10 h after culturing. This finding is consistent with the fact that *E. coli* also stopped increasing in size in approximately 10 h, suggesting that 10 h is the critical line for the *E. coli* life system.

2PT208 天然のタンパク質のアミノ酸配列における隠れた局所的な反復性についての考察**An investigation on local pseudo-periodicity in the amino-acid sequences of native proteins**Koji Inai, Masahito Oka (*Osaka Prefecture University*)

In the previous work, we tried to investigate the repetitive amino-acid sequences in proteins by using currently available protein data base. A total of 8286132 proteins have the repetitive amino-acid sequences among whole 12619557 proteins, suggesting that repetitive amino-acid sequences are generally found in the native proteins. Then, using autocorrelation function method, we also tried to investigate the cryptic periodicity of amino-acid sequence, which cannot be found in the usual method aimed at the strict amino-acid sequence. It was shown that many proteins have quasi-repetitive sequences by these analyses. In this work, it is further tried to investigate on local pseudo-periodicity which was failed to notice in the full sequence analysis because its autocorrelation

coefficient is usually underestimated. It was shown that many quasi-repetitive sequences were locally found in proteins in addition to those found in the previous work. These results would be a supporting data for our hypothesis on the amino-acid sequences of the earliest proteins.

2PT209 人工共生系の実験進化**Experimental evolution of a synthetic symbiosis**Kazufumi Hosoda¹, Akihiro Asao², Shingo Suzuki¹, Tetsuya Yomo^{1,2,3} (¹*IST, Osaka-u*, ²*FBS, Osaka-u*, ³*ERATO, JST*)

Most organisms belong to some mutually beneficial symbioses (mutualisms) in nature. Despite their ubiquity, mutualisms are evolutionarily vulnerable, because they are based on cooperative behaviors which do not necessarily provide direct benefit to the own fitness. Roughly speaking, if organisms only optimize their own fitness, mutualisms seem to collapse due to the emergence of "selfish" one that abandons the cooperative behavior. Various theories based on the natural selection (ultimate factor) have been proposed to fill the gap between the ubiquity and the vulnerability, but little is known about the insight into the physical/structural property of organisms (proximate factor) that affects the evolution of mutualism. As it is very challenging to follow the evolution of natural mutualisms at the molecular level, studying experimental evolution of a synthetic symbiosis, which is composed of previously non-interacting different populations, is effective to gain an understanding of the structural insight (Momeni et al. 2011). Here we show that a synthetic mutualism composed of two genetically engineered *Escherichia coli* strains did not collapse but developed in ~1,000 generation. The strains actually increased their own growth ability in the evolution, but they did not lose their cooperative ability. With the results of comprehensive analyses showing how their intracellular state changed, we want to discuss why they developed, not being too selfish.

2PT210 束論を用いた種の遷移における頑健性と最適性の研究**The robust and the optimal adaptation in species-transition network from the perspective of the lattice theory**Takayuki Niizato, Yukio Gunji (*Grad. Sch. Sci., Univ. Kobe*)

We investigate the adaptive behavior of species to a given environment. We here focus on two contradictory aspects of the adaptive process in evolution. The one is the optimization implying that species increase their own fitness as much as possible in a given environment. The other one is robustness implying that species sustain the inherent diversity despite changing environments. We address this issue to construct a model by using a lattice theory. A crucial point in our model relies on the novel idea of "multiplicity of fitness" which can cover malfunctioned individuals. This idea is partly taken in nature of exaptation. The multiplicity of fitness, in our model, would emerge as an overestimation of the fitness (each individual tends to overestimate own fitness compared with underlying fitness). This overestimation is not random, but context-dependent, represented by a lattice structure. We here show that species in our model demonstrate the power law of the lifespan distribution and 1/f fluctuation for the adaptive process without any parameter tuning. We also discuss essential difference between the behavior for adapting process and stochastic parameter-tuned process. Using a lattice theory enables us to construct a simple model of the adaptation equipped with the multiplicity of fitness, because we can address a complex fitness landscape by an algebraic ordered set. Furthermore, we provide new approach to the network theory by using lattice theory.

2PT211 Study on competitive reaction between enzymes with different diffusivityKenta Yashima¹, Jun Nakabayashi², Akira Sasaki³ (¹*Meiji Univ.*, ²*Yokohama City Univ.*, ³*The Graduate University for Advanced Studies*)

Diffusion process of molecules within heterogeneous medium shows a peculiar behavior termed anomalous diffusion. Here the motions of molecules are hindered by the obstacles, which constitute the heterogeneity of the environment. Accordingly, compared to homogeneous medium, the area that a molecule moves for a given time is smaller for heterogeneous medium. This affects the reaction process deeply (especially for diffusion limited reactions) and the classical formulation based on mass action law fails to describe the process and a formulation based on the Fractal reaction theory is necessary [Kopelman, Science 1988]. In this study we analyzed the competitive reaction between enzymes with different sizes. We assume that for larger enzymes obstruction due to molecular crowding makes the environment heterogeneous to it. On the other hand for smaller enzymes the environment is assume to be