- 1P234 大腸菌と細胞性粘菌の実験室内共生系における大腸菌の遺伝子発現ダイナミクス解析
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The gene expression transition dynamics of *E.coli* in the symbiotic system with *D.discoideum*.
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We established the experimental symbiotic system with *E.coli* and *D.discoideum* to examine how symbiosis emerges. The two species achieve a state of stable coexistence within mucoid colonies, we named it "Symbiotic colony", after several weeks of co-cultivation, although *E.coli*-*D.discoideum* is the prey-predator relationship. In our previous report, we observed the local distribution of each cell in that colony. In addition, we investigated population dynamics and intracellular condition during the establishment of symbiotic relationship by flow cytometry, and so on. These physiological changes of the *E.coli* cells are thought to be induced through a interaction with *D.discoideum* cells. To gain a better understanding of how they change their relationship, we need to learn about their intracellular changes. In this study, we compared the *E.coli* all gene expression time series of symbiotic cells with non-symbiotic cells and found several interesting changes with customized DNA tiling array that could measure the precise level of *E.coli* gene expression covering its all ORF expression, antisense expression and non-coding RNA expression. As a result, we found that, at first, the distribution of gene expression levels exhibited a power-law distribution, then it was collapsed and got out of shape in the process of forming symbiosis, but it was recovered with emerging the symbiotic colony. We would like to discuss about how to transit symbiotic relationship from the point of view of the transient dynamics analysis of *E.coli* gene expression.

- 1P236 タンパク質翻訳系のネットワークロジーとその進化
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Network topology of protein translation system and its evolution
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We investigated the effects of each 4192 *Escherichia coli* open reading frame (ORF) product on the GFP synthesis reaction *in vitro*. Comprehensive analysis indicated that at least 12% of the *E. coli* ORF products modulated the yield of synthesized functional GFP. We mapped the ribosomal proteins, core proteins, and beneficial and deleterious components on the previously obtained *E. coli* PPI network in order to investigate the topology of the translation system in the network. As a measure of the location of each proteins in the network, we calculated closeness centrality (C), which is defined by the inverse of the average distance from protein i toward all other nodes (proteins). The distribution of C showed that ribosomal proteins and core components are located close to the center, core components being located slightly outside than the ribosomal proteins, whereas beneficial and deleterious components were distributed evenly in the entire network. Furthermore, by elucidating the orthologs of the components involved in the translation system in bacteria species, we found that majority of beneficial and deleterious components are an evolutionary late-comer. From these observations, we propose that the beneficial and deleterious components evolved to attach not directly to the center of translation machinery but rather to the outside from the surrounding area in the PPI network.

- 1P235 タンパク質翻訳反応に影響する大腸菌 ORF 産物の網羅探索
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Comprehensive analysis on the effect of *Escherichia coli* ORFs on protein translation reaction
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We investigated the effects of each of the 4192 *Escherichia coli* open reading frame (ORF) products on the protein translation reaction. Each of the ORF products was first synthesized using an *in vitro* translation system, followed by synthesizing green fluorescent protein (GFP) in the same test tube. By detecting the GFP fluorescence intensity, we estimated the effect of each ORF on the *in vitro* translation system. Comprehensive analysis indicated that at least 3.8% or 8.2% of the *E. coli* ORF products decreased or raised the yield of functional GFP, respectively. In addition, a 2.44-fold increase in GFP fluorescence intensity was observed when the synthesis reaction was performed in the presence of a mixture of six purified ORF products found to be beneficial through comprehensive analysis. We investigated the correlation between the increase in the observed fluorescence intensity by adding one of the six proteins to the translation reaction and the decrease in the observed fluorescence intensity by omitting one of the six proteins from the translation reaction containing the six proteins. We found that there is no or only very little interdependency among the five proteins identified (HrpA, Orn, Tig, PhuH, and TrxC). Our data may be useful in designing *in vitro* translation systems with significantly higher performance than those available at present.

- 1P237 アレルゲンユニーク断片スコアとアレルゲンタンパク質構造の温度因子との相関
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1aD04 Allergen unique fragment score correlates with fluctuated structure of allergen protein
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Allergen proteins contain IgE epitopes which interact directly with immunoglobulin E. IgE epitopes are small part of protein structure, consisting of sequential or divided segments of amino acid sequence, which are useful for allergy medication. The difficulties of experimental identification of IgE epitopes are reflected in small number of allergens with known epitopes. Current prediction systems are based on identical sequence match or high homology with known allergens, and the essential drawback of such methods is that new IgE epitopes or allergen proteins cannot be predicted. In this research, we compared the sequences of allergen(ALG) and non-allergen(NEG) proteins, focusing on recurring 3~8aa sequence fragments in each dataset. Then, allergen unique fragment pairs(AUF) were extracted by combining the fragments existing in only ALG with the other fragments in only ALG or both ALG and NEG. The distributions of amino acid residues around the center of AUF revealed that the shape of the wavelet-like distributions was common to all amino acids and only the amplitude of the wavelet changed among the amino acids. These distributions were converted to score index, the AUF score was developed. Applying to allergens, AUF score peaks were not only at large part of IgE epitopes but also at many non epitope regions. Interestingly, AUF score peaks in 3D-structures were located at the segments with high temperature factor or interface of IgC-allergen complex. The correlations of AUF score and segments with large fluctuation will be discussed.