average phenotype change by genetic mutation, the observed restoration of phenotypic fluctuation works as an evolutionary strategy to produce an extreme phenotype, which works at the individual level selection.

3P-287 表現型ゆらぎ存在下での多細胞性の進化

Evolution of multicellularity under phenotypic noise

Masashi Tachikawa (JST, ERATO Complex Systems Biology Project)

Does the phenotypic noise affect the evolution? Phenotypic noise caused by stochasticity in cellular processes affects the developmental dynamics, which can give the large phenotype variety even for a genetically homogeneous population. The phenotype variety is thought to be related with the evolvability of the organisms. To investigate the impact of phenotypic noise on the evolution of multicellularity, we performed evolutionary simulations. We present several gene regulatory network models for developmental dynamics of a cell group, and design the evolutionry tasks to acquire the spontaneous cell differentiation. We found that the evolutionary processes of all models are classified into two types, one is accelerated by the increase of phenotypic noise, the other is not. Using dynamical systems theory, we found that difference of bifurcation structures involved in these evolutionary processes generates the two types. The bifurcation structures are determined by the given evolutionary tasks.

3P-288

講演取消

3P-289 植物オルガネラにおけるRNAエディティング部位とタンパク質立体構造との相関関係

Correlation between RNA editing sites on amino acid residues and protein three-dimensional structures in plant organelles

Mitiko Go (1,2,3) and Kei Yura (4).(1: Ochanomizu Univ; 2: Dept Bio-Science, Nagahama Inst Bio-Science and Technology; 3: Tokyo Medical and Dental Univ; 4. Graduate School of Humanities and Sciences, Ochanomizu Univ)

In plant organelles, RNA editing, a process that converts a nucleotide of mostly a codon and hence of the encoded amino acid, is often observed. Some of the editing events have been shown to be required for the proteins to function, yet no systematic patterns in converted sites were found on RNAs, and the role and origin of RNA editing in plant organelles remain to be elucidated. Here we studied the relationship between amino acid residues encoded by edited codons and the structural characteristics of these residues within proteins, such as protein-protein interfaces, elements of secondary structure, and protein structural cores. We found that the residues encoded by edited codons were significantly biased toward involvement in protein structural cores. RNA editing converts codons for hydrophilic to hydrophobic amino acids, hence only the edited form of an mRNA was likely translated into a polypeptide with core-forming residues at the appropriate positions, which is required for a protein to form a functional three-dimensional structure. This study provides the first observation that RNA editing sites are related to positions important for structure formation of the protein. Since the editing enzymes were known to be encoded by a nuclear genome, our findings suggest that gene expression in plant organelles is regulated by nuclear genes through adjusting residues important for protein folding.

3P-290 ナンジャモンジャゴケ葉緑体のＲＮＡエディティング部位の同定と予測

Prediction of RNA editing sites solely from the newly characterized DNA sequences of the moss *Takakia lepidozioides* chloroplast

Kei Yura(1), Yuki Miyata(2), Tomotsugu Arikawa(3), Masanobu Higuchi(4), Mamoru Sugita(2). (1: Graduate School of Humanities and Sciences, Ochanomizu Univ.; 2: Center for Gene Research, Nagoya Univ.; 3: Dept Biology, Keio Univ.; 4: Dept Botany, National Museum of Nature and Science)

RNA editing in land plant organelles is a process primarily involving the conversion of cytidine to uridine in pre-mRNAs. The process is required for gene expression in plant organelles, because this conversion alters the encoded amino acid residues and improves the sequence identity to homologous proteins. Proteins encoded in the nuclear genome are known to be essential for editing site recognition in chloroplasts, yet the mechanisms by which this recognition occurs remain to be elucidated. We determined the genomic and cDNA sequences of moss *Takakia lepidozioides* chloroplast genes and computationally analyzed the putative recognition regions of *trans*-factors, namely sequences with 41 nucleotides around RNA editing sites, to gain clues for the recognition mechanisms of RNA editing sites. *T. lepidozioides* chloroplast has been expected to have many RNA editing sites and analysis of these sequences provides a unique opportunity to perform statistical analyses of chloroplast RNA editing sites. We divided the 302 newly obtained sequences into eight groups based on sequence similarity to identify group-specific patterns, and the patterns were applied to predict novel RNA editing sites in *T. lepidozioides* transcripts. The predictions were verified by experiments and approximately 60 percent of these predicted sites turned out to be true editing sites. The success of this prediction suggests that the obtained patterns are indicative of key sites recognized by *trans*-factors around editing sites of *T. lepidozioides* chloroplast genes.

3P-290 ドメイン配列を用いたタンパク質間相互作用予測

Prediction of protein-protein interactions using domain sequences

Masanori Kakuta (1), Kazuya Sumikoshi (1), Shugo Nakamura (1), Kentaro Shimizu (1). (1: Dept of Biotechnology, Graduate School of Agricultural and Life Sciences, Univ of Tokyo)

Protein-protein interactions play an important role in various biological functions. Interaction networks are useful to grasp relations between biological function and to predict protein functions. Therefore, various prediction methods for protein-protein interactions have been developed. These methods are largely divided into two groups: domain-based methods and sequence-based methods. Domain-based methods use domain compositions and learn the propensities of domain-domain interactions from training data of protein-protein interaction. Sequence-based methods use protein sequences and predict protein-protein interactions based on the similarity of sequence pairs. Domain-based methods recognize domain regions, but do not consider the sequence difference between domain regions. In contrast, sequence-based methods consider differences between sequences, but deal with whole sequence without domain information. Here, we developed a prediction method of protein-protein interactions considering domain sequences, which incorporate the advantages of both domain-based methods and sequence-based methods. This method is based on the support vector machine and uses a novel kernel function which calculates the similarity of protein sequence pairs based on the similarity of domain sequence pairs. We applied the method to human protein-protein interaction dataset.

3P-292 物理化学的性質を用いた１本型膜タンパク質の高精度予測法の開発

Development of a high performance prediction method for single spanning membrane proteins

Toshiyuki TSUJI(1) and Shigeki MITAKU(1). (1: Dept Applied Physics, Graduate School of Engineering, Nagoya Univ

Membrane proteins constitute 20-25% of open reading frames in a biological genome. Previously we developed a membrane protein predictor SOSUI and a signal peptide predictor SOSUIsignal. However, the accuracy of those systems is low for the prediction of single spanning (TM1) membrane proteins which is a common problem to all membrane protein prediction tools.In this study, we prepared a non redundant dataset of membrane and soluble proteins from Swissprot, focusing on TM1 membrane proteins with a signal peptide (SP). First, we classified the dataset into soluble proteins, single spanning proteins with and without a SP and multi spanning proteins by SOSUI ver.3. It was elucidated that many single spanning proteins with a SP have a transmembrane helix near the carboxyl terminus and a SP at the amino terminus. Therefore, using the physicochemical properties of hydrophobic segments around the amino and carboxyl termini, a novel prediction system for membrane proteins with TM1 with SP was developed whose accuracy was 86% for TM1 with SP and 72% for TM1 without SP. The result was better than the previous prediction tools by 20% in prediction of TM1 with SP.

3P-293 Ｎ末端シグナル配列に基づく植物及び動物タンパク質の細胞内局在予測

Prediction of protein intracellular localization based on N-terminal sequences for plants and animals

Noriyuki Sakiyama (1,2) and Shigeki Mitaku (1). (1: Dept. of Applied Physics, Graduate School of Engineering, Nagoya Univ; 2: Venture Business Laboratory, Nagoya Univ)

The intracellular localization of proteins from amino acid sequences is one of the most important issues of the classification of total proteins from biological genomes. Among various organelles, chloroplast and mitochondria have very similar biochemical functions and protein import processes into the two organelles are also similar. In fact, proteins targeted to chloroplast and mitochondria have signal sequences at the N-terminus. In this work, we first developed a system for classifying proteins in plant cells among chloroplast, mitochondria, endoplasmic reticulum (ER), and other localization, and then a