S10-1
Development of an integrated analysis system for metagenomics and a global microbial database MicrobeDB.jp

Ken Kurokawa
Grad. Sch. of Biosci. Biotechnol., TITECH

メタゲノム統合解析システムおよび微生物統合 DB 「MicrobeDB.jp」 の開発
○黒川 顕
東工大・生命理工

Key word: metagenome, database

Microbes are essential for every part of life on Earth. Numerous microbes inhabit the biosphere, many of which are uncharacterized or uncultivable. They form a complex microbial community that deeply affects against surrounding environments. Metagenome analysis provides a radically new way of examining such complex microbial community without isolation or cultivation of individual bacterial community members. However, metagenome analysis is more complex than common genome analysis, because an analysis target is composed of enormous bacterial strains instead of a single strain. Moreover, the enormous amounts of sequencing data produced by next generation sequencers are difficult to effectively analyze using existing computational tools. To untangle the complexity of metagenome analysis procedures, we developed an integrated analysis system for metagenomics with metagenome database, visualizing tools for massive metagenomic data, HumanMetaBodymap, Body-BLAST, and also developed an analysis pipelines for metagenomics by integrating with all the developed tools. Recently, we have been developing a global microbial database integrated by microbe genomics and metagenomics database named "MicrobeDB.jp". In the meeting, I will present about our metagenome analysis pipelines and an integrated database "MicrobeDB.jp".

S10-2
On the relationship between growth environments and metabolic network modularity in prokaryotes

Kazuhiro Takemoto¹²
¹Grad. Sch. of Compt. Sci. and Syst. Eng., Kyushu Inst. Tech., ²JST-PRESTO

原核生物における生育環境と代謝ネットワークのモジュール構造の関係について
○竹本 和広¹²
¹ 九州大・院側工、 ²JST さきがけ

Key word: metabolic networks, modularity, network analysis, environment, mathematical model

Modularity is an important structural feature in metabolic networks, and it is might be acquired through the network transformation with changing environments in evolutionary history. A previous study suggested that the variability in natural habitat promotes network modularity in bacteria inspired by a theoretical study that has qualitatively demonstrated that changes in the evolutionary goal, which is interpreted as variability in the natural habitat, promote network modularity. However, since many factors influence the structure of the metabolic network, this phenomenon might be limited and there may be other explanations for the change in metabolic network modularity. Therefore, we focus on archaea because they belong to another domain of prokaryotes and show variability in growth conditions, but not in habitats because of their specialized growth conditions. We show the absence of a relationship between network modularity and habitat variability, and find that growth conditions affect metabolic network modularity. In an attempt to suggest an alternative explanation, we propose a model for metabolic networks. Our model can be reproducibly applied, in qualitative as well as quantitative terms, to instances of metabolic network modularity in both bacteria and archaea. Our findings suggest that metabolic network modularity can be more simply determined than previously thought.