

BGI セミナー (9/27, 13:00~, 慶應大学湘南藤沢キャンパス) の ご案内

9月27日に神奈川県藤沢市の慶應 SFC にて4名の BGI の研究者を招きセミナーを行います。BGI はご存知の通り NGS 分野で世界をリードする研究を次々に発表しておりますが、今回はその中でもさまざまな生物のシーケンシングから、トランスクリプトーム解析やエピゲノム解析、またそれらのバイオインフォマティクスなど多岐に渡る内容に関してご講演いただく予定です。東京・神奈川近辺の方はよろしければ是非お越しください。

このセミナーは山形県鶴岡市の慶應義塾大学先端生命科学研究所にも中継いたします。また、これに加えて私も先日公開いたしました当研究所所長のゲノム配列の決定及びそれを利用したパーソナルゲノム教育に関しまして発表をさせていただきます予定です。

日時：9月27日(木)13:00
場所：慶應義塾大学湘南藤沢キャンパス メディアセンター B1 階 AV ホール
(山形県鶴岡市の慶應義塾大学先端生命科学研究所にも遠隔中継しますので鶴岡市の方にもご参加いただけます)
湘南藤沢キャンパスの方は直接ご来場いただいて構いませんが、鶴岡キャンパスの方は入館手続きが必要となりますので事前にご連絡をお願いします。
アクセス：http://www.sfc.keio.ac.jp/files/892/map_j.pdf
連絡先：gaou@sfc.keio.ac.jp (荒川和晴)

Speaker: Xiaodong FANG

Title: Genome assembly and functional analysis of oyster

Abstract: The Pacific oyster *Crassostrea gigas* belongs to one of the most species-rich but genomically poorly explored phyla, the Mollusca. We report the sequencing and assembly of the oyster genome using short-reads and a fosmid-pooling strategy, along with transcriptomes of development and stress response, and proteome of shell. The oyster genome is highly polymorphic and rich in repetitive sequences, with some transposable elements still actively shaping variation. Transcriptome studies reveal an extensive set of genes responding to environmental stress. Expansion of heat shock protein 70 and of inhibitors of apoptosis is likely central to the oyster's adaptation to sessile life in the highly stressful intertidal zone. Our analyses also show shell formation in molluscs is more complex than currently understood and involves extensive participation of cells and their exosomes. The oyster genome sequence fills a void in our understanding of the Lophotrochozoa.

Speaker: Likai MAO

Title: The power of phylogeny analysis based on transcriptome data

Abstract: Figuring out evolutionary relationship has been playing important roles in varieties of biological fields. Evolutionary scientists have been building phylogenetic trees using a handful of genetic sequences. However, this often produced controversial trees with low support especially in deep nodes. Next-generation sequencing has brought great hope to accomplish this daunting task. However, it needs a big-enough budget to perform whole-genome sequencing. In contrast, transcriptome sequencing produces comparable amount of gene data with much lower expenses which are affordable for most researchers. In this talk, we will present some work, including ourselves', of creating robust phylogenies revealing deep relationships in various species, showing the power of phylogeny analysis based on transcriptome data.

Speaker: Zhiyong HUANG

Title: The evolution of bats

Abstract: Bats represent about 20% of all classified mammal species worldwide, with about 1,240 bat species divided into two suborders: megabat and microbat. Bats feature some of nature 's most extreme ecological adaptations, such as flight, echolocation and hibernation, and have recently come under increasing scrutiny relating to their proposed role as 'reservoir hosts' in maintaining and spreading of some of the world 's most alarming viral diseases including Ebola, Nipah, Hendra and SARS. By genomic comparison and virus infected transcriptome analysis, we identified features in the bat genomes that provide insight into biological traits including flight, immunity, echolocation and hibernation, revealing the unique evolution process of the two major chiropteran suborders.

Speaker: Guangliang YIN

Title: Epigenomics and Transcriptomics Studies in Cancer Researches

Abstract: Next generation sequencing (NGS) provides promising means to study human personal genomes and human diseases, like cancers. Although cancers are widely recognized to be an accumulative process with somatic mutations, the epigenetics alterations in last decades are becoming clear that has an important role involved in various stages of cancer development. In addition, dysregulations of gene expression as well as structural variations in cancer cells were identified to be as biomarkers for diagnosing and classification of subtypes of cancers. Many experimental approaches and analytical tools were developed for epigenetics studies and transcriptome studies. BGI, as a leading genomics institute in multidisciplines research in world, is also focusing on these fields in cancer studies. We believed that epigenomics and transcriptomics analyses in cancer studies are indispensable for not only tumorigenesis studies, but personalized treatments for cancer patients by using NGS as well.