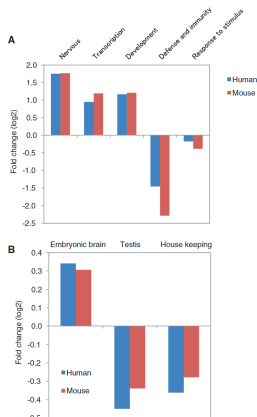


Hidden connection between CNSs and macroscopic phenotypes of eukaryotes



Enrichment of CNS-associated genes (Babarinde and Saitou 2016).

Speaker: Dr. Naruya Saitou
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17th July 2018, 16:00 - 17:00 p.m.
Lab1, Level C, C016

Preface of my textbook “Introduction to Evolutionary Genomics Second Edition” (2018, Springer, in press) starts from these sentences:

Organisms on the earth are rich in diversity. Each organism also contains its own genome with many genes. These complex genetic systems have been generated and constantly modified through eons of evolution since the origin of life. Evolutionary study is thus indispensable for gaining the unified view of life. Because even a single-cell bacterium is so complex, we have to study its genetic entity, that is, its genome, to acquire a comprehensive view of the organism.

Study of natural history goes back to search of nature conducted in hunter-gatherer cultures for more than one million years, while evolutionary studies were initiated only 200 years ago. Nowadays, evolutionary studies and natural history studies are essentially synonyms. Because biodiversity develops through evolution of genomes, genome diversity is central to natural history studies. However, classic natural history studies mostly relied on morphological characters, while there were difficulty for DNA and amino acid sequences to explain those morphological diversity. This gap between molecules and morphologies is now closing. I would like to summarize our recent studies on possible roles of evolutionarily conserved noncoding sequences (CNSs) for macroscopic phenotypes of eukaryotes.

All Welcome

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