



CDB SEMINAR

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Friday, December 20, 2013

13:30~14:30 A7F Seminar Room

New protist models elucidating the origin of metazoan multicellularity: ichthyosporeans and filastereans

Summary

How animals evolved their complex multicellularity? Towards answering this long-standing question, we are studying on unicellular (or colonial) protists that are the closest relatives to multicellular animals (metazoans) besides choanoflagellates. Two such lineages are known to date: filastereans and ichthyosporeans. The genomes of a filasterean, *Capsaspora*, and two ichthyosporeans, *Creolimax* and *Sphaeroforma* are sequenced. Analyses on their genomes revealed an unexpectedly rich gene repertoire that were previously considered to be metazoan-specific, for example, those for cell-adhesion, transcription factors involved in metazoan development, tyrosine kinases controlling intercellular signaling, and the organ size control system. Only a limited number of genes, which are mostly involved in cell-cell communication, turned out to be a metazoan-specific innovation. We thus consider that the acquisition of these metazoan-specific developmental systems and the co-option of pre-existing genes drove the evolutionary transition from unicellular protists to metazoans.

In order to know the gene co-option process at the origin of metazoans, the functions of these "multicell-relevant" genes in unicellular organisms have to be elucidated. We have recently succeeded in transforming our model organisms, which has not yet been achieved in choanoflagellates. Our attempts to illuminate the origin of multicellularity using these new models will be introduced.

Host:

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