

医工薬融合 GCOE Seminar Series

Center for Medical System Innovation
through Multidisciplinary Integration
The University of Tokyo

Chemical and biochemical evolution written in the genomes of sunflower family

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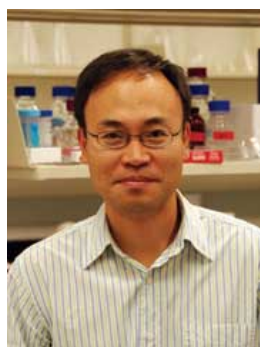
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Date: Monday, October 22, 2012

Time: 16:00 - 18:00

Venue: 10F. Conference Room, Faculty of Pharmaceutical Science Research Bldg., the University of Tokyo



A recent development in next-generation sequencings (NGS) broke the boundary between “model” and “non-model” organisms, presenting opportunities to investigate the untapped metabolisms in plants. Sunflower (or Asteraceae) family is one of the under-studied plant families, albeit it constitutes ~8% of all angiosperms (~24,000 species). Asteraceae has evolved from the South America at about 50 million years ago and has rapidly radiated to other continents to become a dominant plant family on earth. One characteristic compound, sesquiterpene lactone (STL), is commonly found in Asteraceae, and it has enormously diversified in parallel with Asteraceae speciation. Therefore, we conjectured that the studies of STL metabolism in 50 million years of time-frame provide an insight into how specialized metabolisms evolve and diversify in plant. Using the NGS data, the genes coding for the central oxidizing enzymes in the STL biosynthesis were identified from several sub-families of Asteraceae, including a fossil plant *Barnadesia spinosa* and a recently evolved species, *Artemisia annua*. Comparative studies of their catalytic activities have shown that the primordial enzyme from *B. spinosa* displays promiscuous activities whereas the recently emerged enzyme shows a very narrow substrate-specificity. By pairing the primordial enzyme with various sesquiterpene substrates, unnatural terpene compounds could be synthesized in engineered microbes. This result agrees with the theory of enzyme evolution that catalytic promiscuity drives rapid acquisitions of new functions. In addition to STL, lettuce and sunflower can also synthesize terpene-polymer, natural rubber, with different degree of polymer lengths. Since lettuce is an annual, transformable, and self-pollinating plant, classical genetics and reverse genetics can be used to understand the natural rubber metabolism. Our recent data of natural rubber metabolism in lettuce will be also discussed in this seminar.

Organizer: GCOE Program Center for Medical System Innovation through Multidisciplinary Integration, the University of Tokyo

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