Targeted Genome Modification Technologies and Their Applications in Crop Improvements

Precise genome modification with engineered nucleases is a powerful tool for studying basic biology and applied biotechnology. Recent advances in genome engineering indicate that innovative crops developed by targeted genome modification using site-specific nucleases (SSNs) have the potential to avoid the regulatory issues raised by genetically modified organisms (GMO). These powerful SSNs tools, comprising zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and clustered regulatory interspaced short palindromic repeats (CRISPRs)/Cas systems, enable precise genome engineering by introducing DNA double strand breaks (DSBs) that subsequently trigger DNA repair pathways involving either non-homologous end joining (NHEJ) or homologous recombination (HR). Our recent studies prove the versatility of TALEN and the CRISPR/Cas system to modify the genomes of crop plants (i.e. rice and wheat) and establish a new strategy for plant genome modification.

Speaker 1: Dr. Caixia Gao
Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China

Language: English
Date: Wednesday, Mar. 12  14:00～15:00 (part1)
Location: East Building 717/719 (7F), Yokohama Campus
   ◆Live telecast from Yokohama  <Wako: Bioscience Building, 3F S310>
   <Tsukuba: Informatics and JCM Building 4F Conference Room>
Host: CSRS, Gene Discovery Research Group & Plant Genomic Network Research Team
Contact: Tel 045-503-9587  (ext.) 94-8248
Mammalian genome engineering with the CRISPR/Cas system

The ability to introduce targeted modifications into genomes and engineer model organisms holds enormous promise for biomedical and technological applications, and has driven the development of tools such as zinc finger nucleases (ZFNs) and transcription activator-like effector nucleases (TALENs). To facilitate genome engineering in mammalian cells, we engineered two CRISPR (clustered regularly interspaced short palindromic repeats) programmable nuclease systems from Streptococcus pyogenes SF370 and S. thermophilus LMD–9 through heterologous expression of the minimal protein and RNA components in mouse and human cells. We have demonstrated that Cas9 nucleases can be guided by short RNAs (sgRNAs) to introduce double stranded breaks (DSB) in the mammalian genome, which can be used to induce multiplexed gene knockout or homology-directed repair. Furthermore, we have engineered Cas9 into a nicking enzyme to minimize mutagenic DNA repair processes, and show that Cas9 nickases can likewise be guided by pairs of appropriately offset sgRNAs to mediate DSBs with high efficiency and specificity. Finally, I will discuss our recent work on SpCas9 structure and functional analysis.

Speaker 2: Dr. Fei Ann Ran
Broad Institute of MIT and Harvard, USA

Language: English
Date: Wednesday, Mar. 12  15:00～16:00 (part2)
Location: East Building 717/719 (7F), Yokohama Campus
  ●Live telecast from Yokohama  <Wako: Bioscience Building, 3F S310>)
  <Tsukuba: Informatics and JCM Building 4F Conference Room>
Host: CSRS, Gene Discovery Research Group & Plant Genomic Network Research Team
Contact: Tel 045–503–9587  (ext.) 94–8248