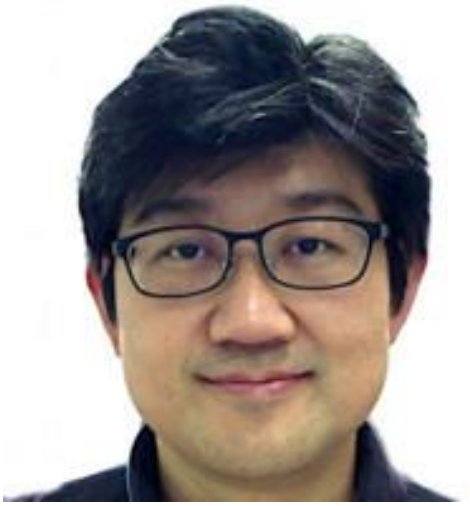
NUS National University of Singapore | Department of Biological Sciences, Faculty of Science

SEMINAR

Mon 1 April 2019 | 2 pm | DBS Conference Room 1

Hosted by Dr Chae Eunyoung

CRISPR-Cas9 mediated base editing in plant research



By Sang-Tae Kim

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Sang-Tae Kim is a senior research fellow at the Center for Genome Engineering, Institute for Basic Science (IBS) in South Korea.

He obtained his Ph.D. in Ecology and Evolutionary Biology at Yale University during which he explored allopolyploid speciation in Polygonaceae using molecular phylogenetic approach. During a postdoctoral training at the Max Planck Institute, Tuebingen, he carried out population genomics research on Arabidopsis thaliana and Arabidopsis lyrata. His current research interests lie in developing genome-editing platforms and post editing bioinformatic tools in plants to eventually investigate natural genetic variation and their contribution to trait evolution.

CRISPR-Cas9 mediated genome editing is one of the most important and versatile technologies in modern biological research. Recently, base-editing tools targeting nucleotide substitution has been developed using the fusion of CRISPR-Cas9 and deaminase. Cytosine or adenine base editors (C/G to T/A or A/T to G/C conversion; CBE, ABE) are expected to broaden the road to the goal as we can introduce various types of base substitution mutations leading to amino-acid change or splicing modifications. Base editor can induce a neo-function to the target gene as well as non-sense mutations with much more predictable manner. Base editor has been applied in plant research but it is still challenging in the choice of promoter relating to germ line transmission. In my talk I will briefly address the recent big advances in genome editing by touching the practical issues in genome editing such as designing, targeting, delivery, and analysis. I will also introduce our recent studies on CBE and ABE applications on Arabidopsis, including 1) non-sense mutations on the LFY gene, a transcription factor regulating the floral initiation, 2) a decoding of natural variation in green revolution gene, GA20ox1, 3) induced mis-splicing by adenine base editing. Our results will give more insights to the future studies incorporating base editing tools in functional assay of natural variations and trait improvement in crop research with intensive screening of base editing.

Artwork by Ann Nee, DBS, NUS