



Akihiko Kondo

Kobe University

Tuesday, October 22, 2019; 1:15 PM

Akihiko Kondo received his Ph.D. from Kyoto University in Chemical Engineering (1988). He was appointed as full professor of Kobe University in 2003 and also appointed as a team leader of the cell factory research team at RIKEN Center for Sustainable Resource Science (Yokohama) in 2012. He was also appointed as a program officer of Advanced Low Carbon Technology Research and Development Program by Japan Science and Technology Agency (JST) in 2011. He became a member of Science Council Japan in 2017.

A. Kondo has developed various platform technologies such as cell surface display systems, metabolic pathway design tools, metabolic analysis technologies, genome editing and long chain DNA synthesis technologies. He also has applied these platform technologies for construction of various microbial cell factories for production of biofuels and various chemicals from biomass, and cyanobacteria and microalgae for production of starch, oil and chemicals from CO₂. Based on these studies, he founded 4 startup companies such as, Bio-energy (Biofuel company in 2001), BioPalette (Genome editing company in 2018), Synprogen (Genome synthesis company in 2018) and Algal Nexus (Microalgae company in 2019).

A. Kondo has been appointed as editor or editorial board members of many Journals such as Journal of Biotechnology, Metabolic Engineering, Biotechnology for Biofuels, Bioresource Technology, etc. He has published more than 600 peer reviewed international papers.

Abstract: Genome Editing with Base Editing Systems from Bacteria to Plants

In place of nuclease activity of conventional genome editing, DNA base-modifying reactions allow direct introduction of point mutations (base editing, BE). By tethering the DNA deaminase activity to nuclease-deficient CRISPR/Cas9 system, we have developed a genome editing tool that enables targeted point mutagenesis. An AID orthologue PmCDA1 was attached to nuclease-deficient mutant of Cas9 (D10A and H840A) to perform highly efficient and target-specific nucleotide editing. This base editing system, termed Target-AID, induced cytosine point mutation in 3-5 bases range at the distal site within target sequence. Use of nickase Cas9 (D10A), which retains single-strand cleaving activity, greatly increase the efficiency.

The toxicity associated with Cas9 has been greatly diminished, enabling application of this technique to wider range of organisms including yeast, bacteria, animals and plants. The tools are now applicable to various organisms with modifications. In mammals and plants, use of nickase Cas9 (D10A), which retains single-strand cleaving activity, greatly increased the efficiency, although it also occasionally induced insertion/deletion (indel). Co-expression of Uracil-DNA glycosylase inhibitor (UGI) further boosted the efficiency and reduced the indel formation. In *E.coli*, dCas9 is preferred and the use of UGI allows multiplex editing of up to 41 loci of multicopy elements. Endogenous deaminases in human cells can also be recruited for base editing and might provide better delivery and safer option. Several modifications and improvements have been made available for highest efficiency and mitigating unwanted effects, depending on the applications.