<table>
<thead>
<tr>
<th>Title</th>
<th>A Powerful CRISPR/Cas9-Based Method for Targeted Transcriptional Activation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Author(s)</td>
<td>Katayama, Shota; Moriguchi, Tetsuo; Ohtsu, Naoki; Kondo, Toru</td>
</tr>
<tr>
<td>Citation</td>
<td>Angewandte Chemie. International Edition, 55(22): 6452-6456</td>
</tr>
<tr>
<td>Issue Date</td>
<td>2016-05-23</td>
</tr>
<tr>
<td>Doc URL</td>
<td><a href="http://hdl.handle.net/2115/65578">http://hdl.handle.net/2115/65578</a></td>
</tr>
<tr>
<td>Rights</td>
<td>This is the peer reviewed version of the following article: S. Katayama, T. Moriguchi, N. Ohtsu, T. Kondo, Angew. Chem. Int. Ed. 2016, 55, 6452, which has been published in final form at <a href="http://dx.doi.org/10.1002/anie.201601708">http://dx.doi.org/10.1002/anie.201601708</a>. This article may be used for non-commercial purposes in accordance with Wiley Terms and Conditions for Self-Archiving.</td>
</tr>
<tr>
<td>Type</td>
<td>article (author version)</td>
</tr>
<tr>
<td>File Information</td>
<td>main_manuscript_file_angewandte_final.pdf</td>
</tr>
</tbody>
</table>
A Powerful CRISPR/Cas9-Based Method for Targeted Transcriptional Activation

Shota Katayama*, Tetsuo Moriguchi, Naoki Ohtsu, and Toru Kondo*

Abstract: The targeted transcriptional activation of endogenous genes is an important tool for understanding physiological transcriptional networks, synthesizing genetic circuits, and inducing cellular phenotype changes. The CRISPR/Cas9 system has a great potential to achieve this purpose, however it has not yet succeeded to activate endogenous genes and induce cellular phenotype changes, efficiently. We herein show a powerful method for transcriptional activation by the CRISPR/Cas9-based system. Replacement of the methylated promoter with unmethylated one by the CRISPR/Cas9-based system was sufficient to activate the expression of the neural cell-specific gene OLIG2 and the embryonic stem cell-specific gene NANOG in HEK293T cells. Moreover, CRISPR/Cas9-based OLIG2 activation induced embryonic carcinoma cell line NTERA-2 to express neuronal marker βIII-tubulin. Thus, these data provide a novel method to handle genetic circuits and phenotype changes.

Technologies for editing the epigenetic marks of targeted genes are required to understand complex transcriptional networks, accurately. Small molecules, such as DNA methylation inhibitors, alter the epigenetic state globally, but cannot target any specific loci. The CRISPR/Cas9 (clustered, regularly interspaced, short palindromic repeat/CRISPR-associated protein 9) system has been shown to target specific genomic locus and induce the site-directed DNA break, when combined with a single-guide RNA (sgRNA) that contains the complementary 20 nucleotides of the target sequence and the protospacer-adjacent motif (PAM), NGG [17]. Recent studies have demonstrated that the nuclease-null Cas9 (dCas9), which was fused with transcription activation domains (e.g. VP16 or VP64), functioned as a transcriptional activator [8][18], suggesting that the CRISPR/Cas9-based system can be used to control the expression of specific genes. Since the transcriptional activity of the dCas9 activators was not high [8][16], however, the efficacy of the cell-fate changes was still very low (~10%) [17]. In addition, it was concerned that the dCas9 activators may trigger non-targeted transcriptional activation with unknown transcription regulators and their transcriptional activity may not be a physiological level. It was, therefore, required to establish new system that activates the target gene expression at physiological level and induces cell-fate changes.

In order to achieve this, we have focused on the microhomology-mediated end-joining (MMEJ)-dependent integration of donor DNA using CRISPR/Cas9 (Fig. 1). MMEJ is a DNA double-stranded break (DSB) repair mechanism that utilizes microhomologous sequences (5-25 bp) for error-prone end-joining [21]. Using the MMEJ-recombinant CRISPR/Cas9 system, here we show a powerful method that activates the silenced gene by replacing its methylated promoter with unmethylated one. This system can be used for the analysis of transcriptional networks, cell-fates and genetic circuits in various types of cells.

We designed a CRISPR/Cas9-based epigenome editing system (Fig. 1a). The methylated promoter in the targeted gene is cut off by two sgRNA-Cas9 complexes and replaced with the microhomology arms (HA)-harboring DNA fragment, which contains unmethylated promoter, luciferase and the foot-and-mouth disease virus 2A self-cleaving peptide (2A), by MMEJ-dependent integration, thereby we can monitor the transcriptional activity by measuring Luciferase activity. To examine our hypothesis, we targeted the OLIG2 gene (Fig. 1b), which encodes a basic helix-loop-helix type transcription factor regulating neuronal and oligodendrocyte differentiation [22][23]. Since 700 bp upstream sequence from human OLIG2 transcription start site (TSS), which has been registered as its promoter by the Transcriptional Regulatory Element Database (TRED), is reported as essential region for gene expression [24], we constructed two vectors, the 0-bp OLIG2 vector, which is for the insertion of the Luciferase gene and 2A into the OLIG2 TSS, and the 700-bp OLIG2 vector, which is for replacing the methylated OLIG2 promoter with the unmethylated 700bp OLIG2 promoter, the Luciferase gene and 2A, and transfected them into HEK293T cells. Five days after transfection, we found strong Luciferase activity (approximately 270-fold) in the 700-bp OLIG2 vector transfected cells but not in the control cells (Fig. 1c). We also found the induction of OLIG2 expression in the 700-bp OLIG2 vector transfected cells by the endo-point reverse transcriptase-PCR (RT-PCR) (Fig. 1d) and quantitative PCR (qPCR, approximately 140-fold compared with 0-bp OLIG2 cells, Fig. 1e). Using western blotting analysis, we confirmed the accumulated OLIG2 protein in the 700-bp OLIG2 vector transfected cells (Supplementary fig. 1). Furthermore, FACS analysis revealed that OLIG2 was expressed in the edited HEK293T cells (18.2% in total) at a same level as in human glioblastoma-initiating cell E6 (GBM6) (Supplementary fig. 7a left panels). We corrected that the 700-bp and 0-bp OLIG2 were precisely integrated into the targeted genomic locus (Fig. 1f). These results revealed that our CRISPR/Cas9-based epigenome editing system can activate the transcription of an endogenous gene.

To address whether OLIG2 induction by the epigenome editing system is sufficient to induce the cell-fate change, we applied this system to human embryonic carcinoma (EC) cells (NTERA-2). Four days after transfection, we found strong OLIG2 expression in the 700-bp OLIG2 cells by RT-PCR (Fig. 1g).

[1] M.Sc. S. Katayama, Dr. T. Moriguchi, Dr. N. Ohtsu, Prof. T. Kondo* Graduate School of Medicine, Hokkaido University Division of Stem Cell Biology, Institute for Genetic Medicine, Hokkaido University Sapporo, Hokkaido 060-0815 (Japan) E-mail: shotakatayama.bio@gmail.com, tkondo@igm.hokudai.ac.jp

Supporting information for this article is given via a link at the end of the document.
2A and qPCR (approximately 120-fold compared with 0-bp OLIG2 cells, Fig. 2d). FACS analysis revealed that OLIG2 was expressed in the edited NTERA-2 cells (19.1% in total) at a same level as in GBME6 (Supplementary fig. 7b). We corrected that the 700-bp and 0-bp OLIG2 were precisely integrated into the targeted genomic locus (Fig. 2e). We observed morphological changes with axonal shapes in the 700-bp OLIG2-transfected cells at 7 days after transfection (Fig. 2a, Supplementary fig. 2a). These cells were immunolabeled for an early neuronal marker βIII-tubulin (Fig. 2a) and a late neuronal marker neurofilament 160 (NF160, Supplementary fig. 2a), whereas neither 0-bp OLIG2 transfected cells nor untransfected cells were positive for these markers.

**Figure 1.** Activation of endogenous OLIG2 gene expression by the CRISPR/Cas9-based epigenome editing system. (a) Schematic design of the CRISPR/Cas9-based epigenome editing system. (b) Schematic model of the OLIG2 (700-bp and 0-bp) epigenome editing systems. Arrows indicate primer sites for genomic PCR. (c) Induced luciferase activity in the 700-bp OLIG2 cells at 5 days after transfection. Error bars indicate SD (n=3). *p<0.01  (d) RT-PCR analysis of OLIG2 transcription. (e) qPCR analysis of OLIG2 transcription. Error bars indicate SD (n=3). *p<0.01  (f) PCR evaluation of OLIG2 epigenome editing using primers shown in (b).

FACS analysis further revealed that the approximately 20% of 700-bp OLIG2 cells were positive for βIII-tubulin and 10% of them were NF160-positive, although none of the 0-bp OLIG2 cells were positive for these markers (Fig. 2b, Supplementary fig. 2b). These results apparently indicated that the epigenome editing of OLIG2 promoter was sufficient to induce NTERA2 cells to differentiate into neurons.
transfected with the 700-bp OLIG2 vector, proliferated, similarly (Supplementary fig. 3b). Taken together, these data suggested that the knock-in frequency of the editing system was about 40%.

In order to evaluate whether the epigenome editing can activate other methylated promoters, we focused on NANOG that is an essential transcription factor required for the maintenance of pluripotency in embryonic stem (ES) cells and early embryos [26, 27]. Deb-Rinker et al. have shown the critical role of maintenance of pluripotency in embryonic stem (ES) cells and that is an essential transcription factor required for the differentiation in human pluripotent stem cells. On the other hand, expression of target genes but has not succeeded to induce cell fate conversion. Hilton et al. have combined CRISPR/Cas9 system [8]. To construct vectors with unmethylated target promoter, we have extensively used E. Coli DH5 strain (hsdR17(rk-,mk+), recA1, relA1, supE44, thi-1, endA1, gyrA96) [37] competent cells. Although most of competent strains contain three DNA methyltransferases, Dam (methylates adenine in GATC), Dcm (methylates internal cytosine in CCAGG and CCTGG) and EcoK1 (methylates adenine in AAC(N6)GTGC and GCAC(N6)GTT), none of these methyltransferases target CpG islands. Therefore, we targeted 700 bp upstream sequences from human NANOG TSS [28], therefore we targeted 700 bp upstream sequences from human NANOG TSS, which has been registered by the TRED, for the editing. We constructed two vectors, the 0-bp NANOG vector, which is for the insertion of the Luciferase gene and 2A into the NANOG promoter sequence

Figure 3. Activation of NANOG gene in HEK 293T cells by the CRISPR/Cas9-based epigenome editing system. (a) Schematic model of the 700-bp NANOG and 0-bp NANOG epigenome editing systems. Arrows indicate primer sites for genomic PCR. (b) Induced luciferase activity by the 700-bp NANOG editing. Error bars indicate SD (n=3), *p<0.001 (c) qPCR analysis of NANOG transcription. (d) qPCR analysis of NANOG transcription. Error bars indicate SD (n=3), *p<0.001 (e) PCR evaluation of NANOG epigenome editing using primers shown in (a).

To clarify whether our epigenome editing system induced off-target mutations, we selected two highest potential off-target sites of each gRNA, which were ranked by the CRISPR design tool (http://crispr.mit.edu/). We amplified the target sites by PCR (Supplementary fig. 4a) and evaluated their sequences. There was no mutation in the potential off-target sites (Supplementary fig. 4b).

Cas9-mediated genome editing has been used to various types of cells and model organisms [29]. In particular, the application of this system to human cells including pluripotent stem cells is useful for making disease models and finding therapeutic methods [30]-[33]. These indicate that the CRISPR/Cas9 system has great potential for broad applications.

Since the finding of dCas9, a number of transcribed/silenced expression in the 700-bp NANOG transfected cells by RT-PCR (Fig. 3c) and qPCR (approximately 280-fold compared with 0-bp NANOG cells, Fig. 3d), Western blotting analysis further verified the induction of NANOG protein in the 700-bp NANOG vectored transfected cells (Supplementary fig. 1). A genomic PCR analysis indicated that the 700-bp and 0-bp NANOG were precisely integrated into the genomic locus (Fig. 3e). Together all, these data suggested that the epigenome editing can be used to activate silenced promoters.
As we have demonstrated, replacement of the methylated promoter with unmethylated one was sufficient to activate the target gene expression. However, this raised a question of how long the unmethylated status was kept in the cells. Both Dnmt3a and 3b were shown to induce de novo methylation at CpG sites, therefore methylation kinetics in the edited promoter seems to depend on their expression level. In the mouse ES cells that highly express both Dnmt3a and 3b [59], it has been shown to take 11 days until de-methylated locus by 5-Aza has been remethylated to a steady-state [40]. The Human Protein Atlas data (http://www.proteinnlasis.org/) indicated that the expression of Dnmt3a and 3b is relatively low in HEK293T, whereas NTERA2 strongly expresses both genes. Since we have detected OL/G2 expression in NTERA2 at 7d after transfection (Supplementary fig. 5), then, our epigenome editing system activates target gene expression transiently, depending on the expression level of Dnmt3a and 3b. However, it may be possible to achieve a long-lasting active state of the specific promoter by coupling our epigenome editing system with a DNA demethylase, such as TET1 hydroxylase [41].

The DNA demethylating drug 5-aza-2-deoxycytidine (5-Aza) is broadly used to erase DNA methylation in the genome [42] and to activate genes that are silenced by their promoter methylation. We have used 5-Aza to induce OL/G2 expression in HEK293T and NTERA2, however we could not detect the expression in these cells (Supplementary fig. 6), indicating that 5-Aza does not always activate any gene expression.

Altogether, these indicate that our epigenome editing system is suitable for understanding complex transcriptional networks at a physiological level, synthesizing genetic circuits, and engineering cell.

Acknowledgments

We are grateful to Dr. Atsuo Kawahara for pCS2P-krtt1c19e-linker-eGFP-mut.

Keywords: Synthetic Biology • Gene technology • DNA methylation • Gene expression • mRNA