

Characterization & Comparison of CRISPR-Derived Editing Methods for Human Pluripotent Stem Cells (hPSCs)

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Research Question

What are the advantages and disadvantages of the CRISPR-derived gene editing methods for specific engineering applications of hPSCs?

Introduction

The Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) system is a vital tool for modifying genomic DNA. When used in conjunction with human pluripotent stem cells (hPSCs), CRISPR enables researchers to perturb gene function, model diseases, and develop therapeutics [2]. Initial CRISPR systems utilized a Cas9 endonuclease and sgRNA to generate double-stranded breaks at a target loci. The breaks are then repaired with either non-homologous end joining (NHEJ) or homology-directed repair (HDR) [2]. Since then, the technology has been modified for specific applications. There are currently four classes of CRISPR-derived editing agents: nucleases, base editors, transposases/recombinases, and prime editors (Figure 1) [3]. Each class has its strengths and limitations, and many factors (such as the edit type) should be considered when choosing an editing agent [3]. The purpose of this project is to determine the most optimal editing method for different engineering applications. Furthermore, the feasibility of each class will be evaluated when employed on hPSCs.

Methods

Research data was collected from multiple peer-reviewed literatures on CRISPR technology and hPSCs. The data was organized based on the editing agent class and the intended gene editing application. To conduct the data analysis, a list of metrics were generated to evaluate the viability of each class. For each editing objective (generating indels, mutations, etc. of varying size), the methods were ranked from most to least optimal (or not applicable) based on their editing efficiency, off-target editing, and other metrics.

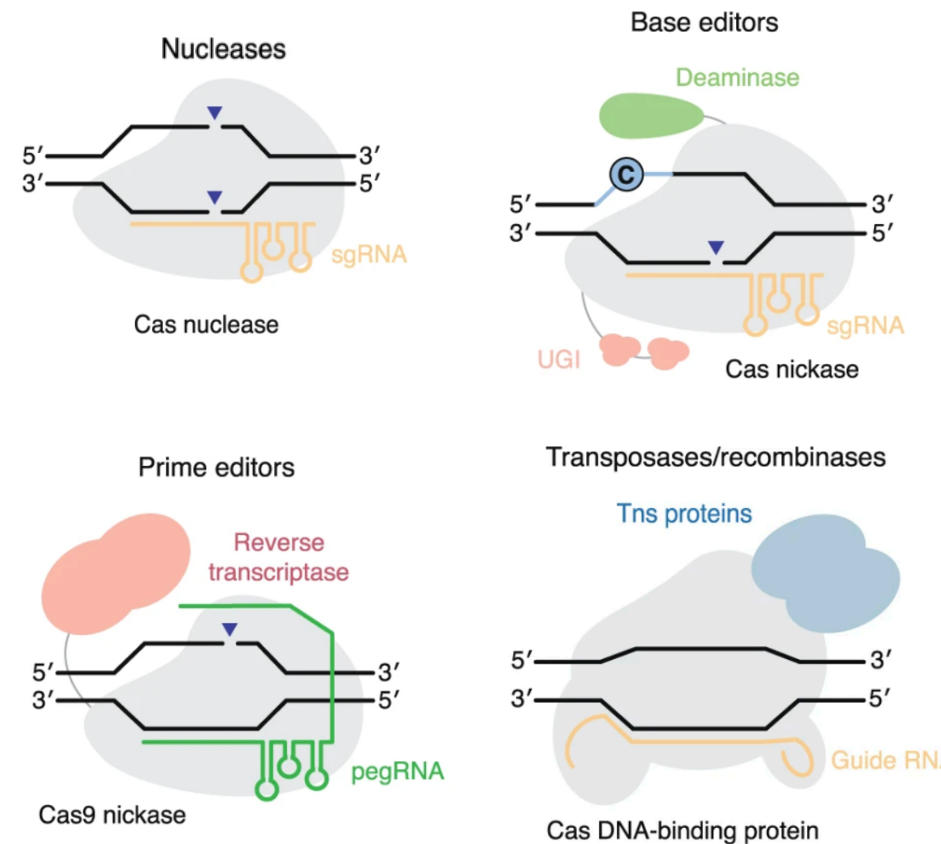


Figure 1. Visual overview of the four classes of CRISPR-derived systems. Source: Anzalone et al. 2020.

Edit type	Starting sequence	Desired product	Reagent(s), method(s)	Byproducts
Stochastic indels	5' PAM 3' 3' 1 20 5'	5' Indel PAM 3' 3' Indel 5'	Cas nuclease	Diverse indels (predictable, but not controllable)
PAM-distal transition point mutations	5' C PAM 3' 3' G 20 5'	5' T PAM 3' 3' A 20 5'	Base editors (CBEs, ABEs)	Possibility of bystander mutations
PAM-proximal point mutations	5' G PAM 3' 3' C 20 5'	5' T PAM 3' 3' A 20 5'	Cas nuclease HDR Prime editors	Indel byproducts, especially from nucleases
Small insertions (e.g., 1-40 bp)	5' PAM 3' 3' 1 20 5'	5' 1 bp PAM 3' 3' 21 5'	Cas nuclease HDR Prime editors	Indel byproducts, especially from nucleases
Small deletions (e.g., 1-80 bp)	5' PAM 3' 3' 1 20 5'	5' PAM 3' 3' 18 5'	Cas nuclease HDR Prime editors	Indel byproducts, especially from nucleases
Large insertions (>30 bp)	5' PAM 3' 3' 1 20 5'	5' 1 kb PAM 3' 3' 5' 5'	Cas nuclease HDR Cas nuclease EJ Cas transposases/recombinases	Indel byproducts, wrong insert orientation, multiple inserted fragments, vector insertion
Large deletions (>40 bp)	5' PAM 200 bp PAM 3' 3' 1 20 5'	5' PAM PAM 3' 3' 5' 5'	Cas nuclease EJ Cas nuclease HDR	Indels at individual cut sites, inverted intervening sequence

Figure 3. Method per editing type. Source: Anzalone et al. 2020.

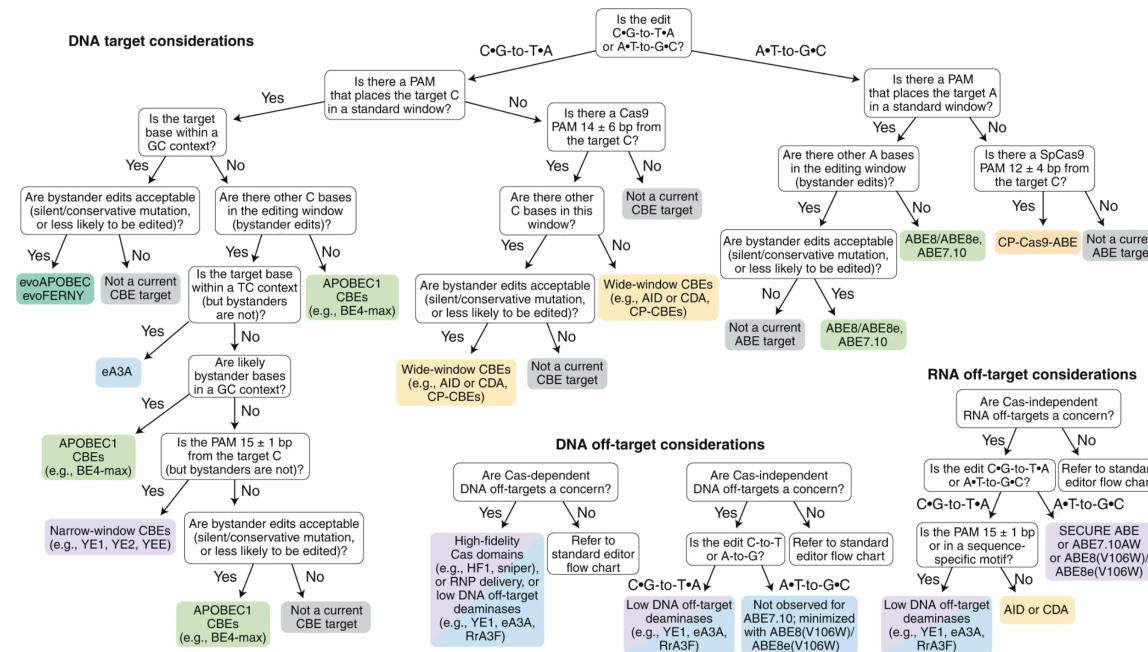


Figure 2. Decision tree for base editors. Source: Anzalone et al. 2020.

References

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