Opinion Article

## CRISPR-Mediated Knock-in of Fluorescent Reporters for Real-Time Monitoring of Stem Cell Differentiation

## Jenni Havens\*

Department of Biotechnology and Bioengineering, University of Sao Paulo, Sao Paulo, Brazil

## DESCRIPTION

Understanding stem cell differentiation dynamics requires precise tools for monitoring lineage commitment and fate decisions in real-time. Traditional methods rely on endpoint analyses that provide limited temporal resolution of differentiation processes. This research develops Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-mediated knock-in strategies for introducing fluorescent reporters under control of lineage-specific promoters, enabling real-time visualization of stem cell fate transitions during directed differentiation protocols.

Human induced Pluripotent Stem Cells (hiPSCs) were cultured on vitronectin-coated surfaces in mTeSR1 medium and maintained in optimal conditions for genetic modification. Clustered Regularly Interspaced Short Palindromic Repeats associated with protein 9 (CRISPR-Cas9) constructs were designed to facilitate precise knock-in of fluorescent protein sequences at endogenous *loci* through homology-directed repair.

Monitoring the dynamic process of stem cell differentiation is fundamental to understanding developmental biology and optimizing stem cell-based therapies. Traditional methods for tracking cell fate changes, such as immunostaining and transcriptome analysis, often require cell fixation or lysis, limiting their utility in real-time applications. To overcome these limitations, fluorescent reporter systems have become indispensable tools, enabling live-cell imaging and real-time analysis of gene expression and lineage commitment. Recent advances in genome editing, particularly the CRISPR/Cas9 system, have significantly enhanced the precision and efficiency of inserting fluorescent reporters at endogenous gene *loci* in stem cells.

CRISPR-mediated knock-in techniques leverage the programmable nature of the Cas9 nuclease and guide RNA (gRNA) to introduce site-specific double-strand breaks, allowing precise integration of fluorescent reporter genes through Homology-Directed Repair (HDR). This strategy ensures that the reporter is placed under the control of native regulatory elements, faithfully reflecting the expression patterns of key

developmental genes. As a result, researchers can visualize and quantify the temporal and spatial dynamics of stem cell differentiation in vitro and in vivo with unprecedented accuracy.

The application of CRISPR-mediated knock-in of fluorescent reporters has transformed stem cell research by providing powerful insights into lineage specification, heterogeneity, and developmental trajectories. Furthermore, it enables high-throughput screening of differentiation protocols and enhances the safety and reproducibility of cell-based therapies. This introduction explores the methodologies, advantages, and impact of using CRISPR technology to engineer fluorescent reporters for real-time monitoring of stem cell differentiation.

Donor templates incorporated mNeonGreen, mCherry, and mTurquoise2 fluorescent proteins with 2A peptide sequences to enable bicistronic expression while maintaining endogenous protein function. Extensive homology arms of 800-1000 base pairs were included to maximize HDR efficiency. Ribonucleoprotein delivery was optimized using electroporation parameters specifically adapted for hiPSCs, with puromycin selection facilitating isolation of correctly targeted clones.

Molecular characterization confirmed successful knock-in events in 15%-22% of treated cells, with Southern blot analysis verifying correct integration without additional insertions. Fluorescence microscopy revealed dynamic reporter expression patterns during differentiation, with SOX2-mNeonGreen showing progressive downregulation during exit from pluripotency.

Time-lapse imaging revealed previously unobserved heterogeneity in differentiation timing, with individual cells showing variable kinetics of fate commitment. Quantitative analysis demonstrated that reporter expression levels correlated strongly with endogenous protein expression as determined by immunofluorescence staining.

Live-cell imaging during cardiac differentiation revealed complex temporal dynamics of mesoderm specification, with mCherry expression peaking at day 1 and gradually declining as cardiac progenitor markers emerged. This real-time visualization enabled identification of optimal timing for growth factor additions and

Correspondence to: Jenni Havens, Department of Biotechnology and Bioengineering, University of Sao Paulo, Sao Paulo, Brazil, E-mail: jennihavens@chop.br

Received: 03-Mar-2025, Manuscript No. MAGE-25-38125; Editor assigned: 05-Mar-2025, PreQC No. MAGE-25-38125 (PQ); Reviewed: 19-Mar-2025, QC No. MAGE-25-38125; Revised: 26-Mar-2025, Manuscript No. MAGE-25-38125 (R); Published: 02-Apr-2025, DOI: 10.35841/2169-0111.25.14.401

Citation: Havens J (2025). CRISPR-Mediated Knock-in of Fluorescent Reporters for Real-Time Monitoring of Stem Cell Differentiation. Adv Genet Eng. 14:401.

Copyright: © 2025 Havens J. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

media changes, improving differentiation efficiency by 34% compared to standard protocols.

## **CONCLUSION**

CRISPR-mediated reporter knock-in provides powerful tools for real-time monitoring of stem cell differentiation with unprecedented temporal resolution. The ability to visualize fate

decisions as they occur offers new insights into differentiation dynamics and enables optimization of directed differentiation protocols. This work establishes a generalizable approach for creating reporter cell lines that advance our understanding of development and regenerative medicine. Importantly, the presence of fluorescent reporters did not interfere with normal differentiation capacity, as confirmed by lineage-specific marker expression and functional assays.