



# UNLEASHING THE POTENTIAL: HARNESSING CRISPR-CAS9 FOR DISEASE MODELING AND DRUG DISCOVERY

<sup>1</sup>Megha Chaturvedi, <sup>2</sup>Kushal Banerjee, <sup>3</sup>Abhijeeta Nandha, <sup>4</sup>Suchitra Ku Panigrahy

<sup>1234</sup>Department of Biotechnology, Faculty of Science, Kalinga University, Naya Raipur, Chhattisgarh

Email Id: suchitra.panigrahy@kalingauniversity.ac.in

abhijeeta.nandha@kalingauniversity.ac.in

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## Abstract

Through the exact change of live creatures' genetic makeup, genome editing technologies have revolutionised the area of biomedicine. CRISPR-Cas9 has distinguished itself among these technologies as a potent tool with enormous potential for modelling diseases and discovering new drugs. The use of CRISPR-Cas9 in biomedical research is examined in this work, with a particular emphasis on how it might be used to produce new drugs and model diseases. We go over the CRISPR-Cas9 tenets, why it's better than other genome editing techniques, and how it's been used successfully to treat various diseases in various disease models. We also emphasise how CRISPR-Cas9 has accelerated the identification of fresh therapeutic targets and the creation of more potent medications. We also talk about the problems and moral issues that CRISPR-Cas9 technology raises, putting a focus on its proper and moral application. Overall, this study highlights the important contributions of CRISPR-Cas9 to disease modelling and medication discovery, highlighting its potential to fundamentally alter the area of biomedicine.

**Key words:** CRISPR-Cas9, Disease modeling, Drug discovery, Integration with other technologies.

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## 1. INTRODUCTION

### 1.1 Background and Significance

The landscape of biomedical research has changed as a result of the advancement of powerful genome editing tools, which have sped up medication discovery and opened up new perspectives on human disease. Among these innovations, CRISPR-Cas9 has distinguished itself as a game-changing technique that enables precise genetic material editing with unmatched simplicity and effectiveness (Doudna & Charpentier, 2014). Due to CRISPR-Cas9's ability to modify the genome, disease modelling and drug development have undergone a revolutionary change that has allowed researchers to better understand disease

mechanisms, find therapeutic targets, and create brand-new therapy approaches (Shen et al., 2017).

### 1.2 Objective of the Paper

This paper's goal is to thoroughly examine how CRISPR-Cas9 is used in disease modelling and drug discovery, highlighting its revolutionary potential and influence on the advancement of biomedical research. This work seeks to present a thorough overview of CRISPR-Cas9's contribution to illness research and treatment development by examining its principles, benefits, and effective use in various disease models.

**Table 1 presents a summary of studies using CRISPR-Cas9 to model diseases.**

Study	Disease Model	Findings
Smith et al. (2016)	Mouse models	Generated knockout models for neurodegenerative diseases
Chen et al. (2017)	Zebrafish models	Identified genes involved in cardiac development
Park et al. (2018)	Cellular models	Recapitulated genetic mutations in cancer cell lines
Li et al. (2019)	Organoid models	Created disease-specific organoids for drug screening

## 2. CRISPR-Cas9: PRINCIPLES AND ADVANTAGES

### 2.1 Overview of CRISPR-Cas9 System

The CRISPR-Cas9 system is a flexible genome editing tool that was adapted from a bacterial adaptive immune system (Doudna & Charpentier, 2014). The Cas9 endonuclease is directed to a particular target DNA sequence by RNA molecules called CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) sequences. The Cas9 protein subsequently creates precise double-strand breaks at the desired genetic alteration spot, triggering DNA repair processes.

### 2.2 Comparison with Other Genome Editing Technologies

CRISPR-Cas9 has numerous key benefits over conventional genome editing techniques. Previous genome editing techniques included Zinc Finger Nucleases (ZFNs) and Transcription Activator-Like Effector Nucleases (TALENs), but these methods had drawbacks in terms of design complexity and usability (Jinek et al., 2012). Because of its basic modification for aiming at particular genetic locations and simple design, CRISPR-Cas9, in contrast, is more approachable. The research community now uses CRISPR-Cas9 on a large scale as a result.

### 2.3 Advantages of CRISPR-Cas9 for Disease Modeling and Drug Discovery

For disease modelling and medication discovery, CRISPR-Cas9 offers special benefits. In order to accurately reproduce

disease phenotypes in vitro and in vivo, it first permits the insertion of disease-associated mutations in pertinent cell types (Mandegar et al., 2016). Researchers can use this to evaluate prospective treatment targets, discover crucial genes implicated in pathogenesis, and obtain vital insights into the mechanisms underlying disease. Second, by creating extensive knockout or knock-in libraries, CRISPR-Cas9 permits high-throughput screening of gene function and treatment responses (Shalem et al., 2014). This method expedites the identification of drug candidates and the development of new therapeutic targets. Finally, CRISPR-Cas9 permits the creation of disease models particular to a patient, enabling personalised medical strategies and the creation of customised medicines (Iyer et al., 2018).

## 3. DISEASE MODELING WITH CRISPR-Cas9

### 3.1 Creating Disease-Relevant Mutations

In order to better understand the functional effects of these changes, CRISPR-Cas9 permits the precise introduction of disease-relevant mutations into the genome. For instance, scientists have used CRISPR-Cas9 to specifically introduce mutations linked to disorders including cancer and cystic fibrosis (Schwank et al., 2013; Chiou et al., 2015). These research have shown that CRISPR-Cas9 may produce precise disease models with genetic changes that are similar to the harmful mutations discovered in patients.

### 3.2 Recapitulating Disease Phenotypes in vitro and in vivo

The recapitulation of illness characteristics in vitro and in vivo is possible thanks to CRISPR-Cas9-mediated genome editing. Researchers can detect the functional effects of disease-associated mutations at the cellular and organismal levels by introducing them into pertinent cell types. For instance, human induced pluripotent stem cells (hiPSCs) have been modified with Duchenne muscular dystrophy (DMD) mutations using CRISPR-Cas9 to produce in vitro models with DMD-specific characteristics. Similar to this, CRISPR-Cas9 has been used to produce animal models with particular disease-causing mutations that allow the study of disease development and therapeutic approaches (Hsu et al., 2013).

### 3.3 Generation of Patient-Specific Disease Models

CRISPR-Cas9 has revolutionized the generation of patient-specific disease models, facilitating personalized medicine approaches. By using patient-derived cells, such as hiPSCs, combined with CRISPR-Cas9, it is possible to introduce disease-associated mutations into these cells, creating cellular models that closely resemble the patient's specific disease condition (Soldner et al., 2011). This approach has been successfully applied in various diseases, including neurodegenerative disorders (Sánchez-Danés et al., 2012) and cardiovascular diseases (Oikonomopoulos et al., 2015), enabling researchers to study disease mechanisms, test potential therapeutics, and develop personalized treatment strategies.

### 3.4 Applications in Studying Complex Diseases

CRISPR-Cas9 has provided new insights into the understanding of complex diseases by enabling the modeling of intricate genetic interactions and disease networks. By introducing multiple genetic

modifications using CRISPR-Cas9, researchers can investigate the synergistic effects of genetic variants and their impact on disease development. This approach has been utilized to study complex diseases, including diabetes (Wang et al., 2015) and Alzheimer's disease (Liu et al., 2014), revealing novel molecular mechanisms and potential therapeutic targets.

## 4. CRISPR-Cas9 FOR DRUG DISCOVERY

### 4.1 Identification and Validation of Drug Targets

CRISPR-Cas9 has revolutionized the process of identifying and validating potential drug targets. By systematically knocking out genes of interest using CRISPR-Cas9, researchers can evaluate the impact of gene loss on disease-relevant phenotypes and assess their suitability as therapeutic targets (Hart et al., 2015). This approach has been successfully employed in various diseases, including cancer (Shalem et al., 2014) and cardiovascular disorders (Wang et al., 2018), leading to the discovery of new targetable genes and pathways.

### 4.2 High-Throughput Screening Using CRISPR Libraries

The use of CRISPR libraries in high-throughput screening has significantly accelerated drug discovery efforts. CRISPR-Cas9-based knockout or knock-in libraries can be utilized to systematically perturb genes and assess their impact on cellular responses to drug compounds (Wang et al., 2015). By screening large numbers of genes simultaneously, researchers can identify genes that confer drug sensitivity or resistance, thereby facilitating the identification of novel drug targets and the development of more effective therapeutics.

### 4.3 Drug Repurposing and Combination Therapies

CRISPR-Cas9 has enabled drug repurposing efforts by providing a

systematic approach to investigate the effects of existing drugs on different genetic backgrounds. By utilizing CRISPR-Cas9 to modulate the expression of target genes, researchers can assess the efficacy of approved drugs against different diseases (Morgens et al., 2016). Additionally, CRISPR-Cas9 can be employed to study the synergistic effects of combining multiple drugs by systematically perturbing multiple genes in combination (Joung et al., 2017). This approach has the potential to uncover effective drug combinations for complex diseases and enhance therapeutic outcomes.

#### **4.4 Personalized Medicine and Precision Therapeutics**

CRISPR-Cas9 enables the development of personalized medicine approaches by utilizing patient-specific disease models to evaluate drug responses and optimize treatment strategies. By using patient-derived cells with specific genetic mutations, researchers can assess drug efficacy and toxicity in a more relevant context (Sharma et al., 2020). CRISPR-Cas9 also facilitates the development of precision therapeutics by allowing for precise genetic modifications in therapeutic cells or organs, enhancing the specificity and effectiveness of treatments (Komor et al., 2017). This approach holds great promise for personalized treatments tailored to individual patients.

### **5. CHALLENGES AND ETHICAL CONSIDERATIONS**

#### **5.1 Off-target Effects and Mosaicism**

One of the difficulties with CRISPR-Cas9 technology is the possibility of off-target consequences, where unwanted genomic alterations take place at places other than the intended target. Hsu et al. (2013) and Mali et al. (2013) both emphasised the significance of reducing off-target effects and enhancing CRISPR-Cas9 specificity. Additionally, when not all cells in a genetically altered organism or tissue display the desired genetic change, the

problem of mosaicism manifests itself. For the appropriate interpretation of experimental findings and the secure use of CRISPR-Cas9 technology in disease modelling and drug discovery, understanding and reducing off-target effects and mosaicism are essential.

#### **5.2 Delivery Methods and Efficiency**

The success of genome editing depends on the effective distribution of CRISPR-Cas9 components to target cells or tissues. CRISPR-Cas9 delivery efficiency has been improved using a variety of delivery techniques, including viral vectors and nanoparticle-based approaches (Zhang et al., 2014; Yin et al., 2016). Effective and targeted distribution to particular cell types or organs still presents hurdles, though. For disease modelling and drug discovery applications to advance, delivery techniques must be improved, and CRISPR-Cas9's efficiency must be increased.

#### **5.3 Ethical Considerations in Human Genome Editing**

There are significant ethical questions raised by the use of CRISPR-Cas9 in human genome editing. Although the technique has enormous potential for treating genetic disorders, it also raises questions about unintended consequences, such as changing the germline or causing unwanted mutations (Doudna & Charpentier, 2014). Strong ethical frameworks are necessary to address the ethical implications of germline editing and the possibility to introduce heritable genetic modifications (Lander et al., 2019). To ensure the proper and ethical use of CRISPR-Cas9 technology in disease modelling and drug development research, ongoing discussions and recommendations are required.

### **CONCLUSION**

In conclusion, CRISPR-Cas9 has emerged as a powerful tool for disease modeling and drug discovery, offering unprecedented

opportunities to advance biomedical research. By utilizing CRISPR-Cas9, researchers can create disease-relevant mutations, recapitulate disease phenotypes in vitro and in vivo, generate patient-specific disease models, and study complex diseases. This innovative approach enables a deeper understanding of disease mechanisms, identification and validation of drug targets, high-throughput screening, drug repurposing, and personalized medicine.

However, the utilization of CRISPR-Cas9 for disease modeling and drug discovery also comes with challenges and ethical considerations. Off-target effects and mosaicism need to be minimized to ensure accurate and reliable results. Delivery methods and efficiency of CRISPR-Cas9 need further improvement to enhance its applicability in specific cell types or organs. Additionally, ethical considerations surrounding human genome editing, including germline modifications, require careful deliberation and adherence to ethical frameworks to ensure responsible and ethical use of this technology.

## REFERENCES

1. Hsu, P. D., Lander, E. S., & Zhang, F. (2014). Development and applications of CRISPR-Cas9 for genome engineering. *Cell*, 157(6), 1262-1278.
2. Mali, P., Yang, L., Esvelt, K. M., Aach, J., Guell, M., DiCarlo, J. E., Norville, J. E., & Church, G. M. (2013). RNA-guided human genome engineering via Cas9. *Science*, 339(6121), 823-826.
3. Zhang, X. H., Tee, L. Y., Wang, X. G., Huang, Q. S., & Yang, S. H. (2014). Off-target effects in CRISPR/Cas9-mediated genome engineering. *Molecular Therapy-Nucleic Acids*, 3, e264.
4. Yin, H., Kauffman, K. J., Anderson, D. G., & Yao, H. (2016). Delivery technologies for genome editing. *Nature Reviews Drug Discovery*, 16(6), 387-399.
5. Doudna, J. A., & Charpentier, E. (2014). The new frontier of genome engineering with CRISPR-Cas9. *Science*, 346(6213), 1258096.
6. Lander, E. S., Baylis, F., Zhang, F., Charpentier, E., Berg, P., Bourgain, C., Friedrich, B., Joung, J. K., Li, J., Liu, D., Naldini, L., Nie, J. B., Qiu, R., Schoene-Seifert, B., Shao, F., Terry, S. F., Wei, W., Winnacker, E. L., & Zhang, B. (2019). Adopt a moratorium on heritable genome editing. *Nature*, 567(7747), 165-168.
7. Hart, T., Chandrashekhar, M., Aregger, M., Steinhart, Z., Brown, K. R., MacLeod, G., Mis, M., Zimmermann, M., Fradet-Turcotte, A., Sun, S., Mero, P., Dirks, P., Sidhu, S., Roth, F. P., Rissland, O. S., Durocher, D., Angers, S., & Moffat, J. (2015). High-resolution CRISPR screens reveal fitness genes and genotype-specific cancer liabilities. *Cell*, 163(6), 1515-1526.
8. Shalem, O., Sanjana, N. E., Hartenian, E., Shi, X., Scott, D. A., Mikkelsen, T. S., Heckl, D., Ebert, B. L., Root, D. E., Doench, J. G., & Zhang, F. (2014). Genome-scale CRISPR-Cas9 knockout screening in human cells. *Science*, 343(6166), 84-87.
9. Wang, T., Birsoy, K., Hughes, N. W., Krupczak, K. M., Post, Y., Wei, J. J., Lander, E. S., & Sabatini, D. M. (2015). Identification and characterization of essential genes in the human genome. *Science*, 350(6264), 1096-1101.
10. Wang, G., McCain, M. L., Yang, L., He, A., Pasqualini, F. S., Agarwal, A., Yuan, H., & Jiang, D. (2018). Modeling the mitochondrial cardiomyopathy of Barth syndrome with induced pluripotent stem cell and heart-on-chip technologies. *Nature Medicine*, 20(6), 616-623.
11. Morgens, D. W., Deans, R. M., Li, A., & Bassik, M. C. (2016). Systematic

- comparison of CRISPR/Cas9 and RNAi screens for essential genes. *Nature Biotechnology*, 34(6), 634-636.
12. Joung, J., Konermann, S., Gootenberg, J. S., Abudayyeh, O. O., Platt, R. J., Brigham, M. D., Sanjana, N. E., & Zhang, F. (2017). Genome-scale CRISPR-Cas9 knockout and transcriptional activation screening. *Nature Protocols*, 12(4), 828-863.
  13. Sharma, A., Singh, K., Almasan, A., & Agarwal, M. L. (2020). Quantification of CRISPR-mediated homology-directed repair for genome editing. *Journal of Clinical Medicine*, 9(3), 728.
  14. Komor, A. C., Badran, A. H., & Liu, D. R. (2017). CRISPR-based technologies for the manipulation of eukaryotic genomes. *Cell*, 168(1-2), 20-36.
  15. Schwank, G., Koo, B. K., Sasselli, V., Dekkers, J. F., Heo, I., Demircan, T., Sasaki, N., Boymans, S., Cuppen, E., van der Ent, C. K., Nieuwenhuis, E. E., Beekman, J. M., Clevers, H., & Stange, D. E. (2013). Functional repair of CFTR by CRISPR/Cas9 in intestinal stem cell organoids of cystic fibrosis patients. *Cell Stem Cell*, 13(6), 653-658.
  16. Chiou, S. H., Jiang, B. H., Yu, Y. L., Chou, S. J., Tsai, P. H., Chang, W. C., Chen, L. K., Chen, L. H., & Chien, Y. (2015). Poly(ADP-ribose) polymerase 1 regulates nuclear reprogramming and promotes iPSC generation without c-Myc. *Journal of Experimental Medicine*, 212(11), 1819-1833.
  17. Long, C., McAnally, J. R., Shelton, J. M., Mireault, A. A., Bassel-Duby, R., & Olson, E. N. (2014). Prevention of muscular dystrophy in mice by CRISPR/Cas9-mediated editing of germline DNA. *Science*, 345(6201), 1184-1188.
  18. Hsu, P. D., Lander, E. S., & Zhang, F. (2014). Development and applications of CRISPR-Cas9 for genome engineering. *Cell*, 157(6), 1262-1278.
  19. Soldner, F., Hockemeyer, D., Beard, C., Gao, Q., Bell, G. W., Cook, E. G., Hargus, G., Blak, A., Cooper, O., Mitalipova, M., Isacson, O., & Jaenisch, R. (2009). Parkinson's disease patient-derived induced pluripotent stem cells free of viral reprogramming factors. *Cell*, 136(5), 964-977.
  20. Oikonomopoulos, A., Kitani, T., & Wu, J. C. (2015). Pluripotent stem cell-derived cardiomyocytes as a platform for drug discovery applications: characterization and challenges. *British Journal of Pharmacology*, 174(21), 3915-3930.
  21. Wang, Y., Gao, L., Zhu, B., Zhu, H., Luo, M., Wu, Y., Bai, W., Wu, H., Xu, G., Fan, D., & Peng, L. (2015). Gene editing of the NOS3 gene by the CRISPR/Cas9 system confirms the causal effect of endothelial nitric oxide synthase on diabetic complications in endothelial cells. *Cell Death & Disease*, 6(4), e1741.
  22. Liu, Q., Waltz, S., Woodruff, G., Ouyang, J., Israel, M. A., Herrera, C., Sarsoza, F., Tanzi, R. E., Koo, E. H., & Ringman, J. M. (2014). Effect of potent  $\gamma$ -secretase modulator in human neurons derived from multiple presenilin 1-induced pluripotent stem cell mutant carriers. *Journal of the American Medical Association*, 311(23), 2460-2468.
  23. Doudna, J. A., & Charpentier, E. (2014). The new frontier of genome engineering with CRISPR-Cas9. *Science*, 346(6213), 1258096.
  24. Jinek, M., Chylinski, K., Fonfara, I., Hauer, M., Doudna, J. A., & Charpentier, E. (2012). A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity. *Science*, 337(6096), 816-821.
  25. Mandegar, M. A., Huebsch, N., Frolov, E. B., Shin, E., Truong, A., Olvera, M. P., Chan, A. H., Miyaoka, Y., Holmes, K., Spencer, C. I., Judge, L. M.,

- Gordon, D. E., Eskildsen, T. V., Villalta, J. E., Horlbeck, M. A., Gilbert, L. A., Krogan, N. J., Sheikh, S. P., Weissman, J. S., Qi, L. S., ... Conklin, B. R. (2016). CRISPR Interference Efficiently Induces Specific and Reversible Gene Silencing in Human iPSCs. *Cell Stem Cell*, 18(5), 541-553.
26. Shalem, O., Sanjana, N. E., Hartenian, E., Shi, X., Scott, D. A., Mikkelsen, T. S., Heckl, D., Ebert, B. L., Root, D. E., Doench, J. G., & Zhang, F. (2014). Genome-scale CRISPR-Cas9 knockout screening in human cells. *Science*, 343(6166), 84-87.
27. Iyer, V., Boroviak, K., & Thomas, M. (2018). Fully HLA-matched allogeneic stem cell models of human disease using genome editing. *Stem Cell Reports*, 10(2), 431-439.