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ISSN: 3080-4183 (Print)
ISSN: 3080-4191 (Online)

Clinical and Health Research Exploration

THE IMPACT OF GENETIC EDITING ON PERSONALIZED MEDICINE

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Received: July 25, 2023 --- Revised: September 09, 2023, Accepted: Nobember 04, 2023

Abstract

The emergence of genetic editing technologies, particularly CRISPR-Cas9, has revolutionized personalized medicine by enabling precise, programmable interventions in the human genome. This innovation has shifted healthcare from reactive, generalized treatments to predictive, individualized therapies based on a patient's genetic blueprint. Personalized medicine now encompasses not only pharmacogenomic tailoring but also the correction of genetic defects underlying rare diseases, cancer, and immune disorders.This study presents a comprehensive evaluation of CRISPR-Cas9 based gene editing through the integration of quantitative performance metrics target accuracy, delivery efficiency, off-target rates, and therapeutic score across multiple experimental gene batches. A mathematical scoring model was developed to assess therapeutic efficacy, and hybrid visualizations were used to interpret performance across genomic targets and delivery conditions.Results indicated that CRISPR achieved target accuracy exceeding 90% in most cases, with delivery efficiency consistently above 85% and off-target mutation rates remaining below 3%. Therapeutic scores were highest in edits with optimized vector delivery and minimal off-target effects, validating the robustness of CRISPR for clinical translation. Comparisons among editing platforms further confirmed CRISPR's superiority over TALENs and ZFNs in precision and consistency.These findings underscore the transformative potential of gene editing in advancing disease treatment, early diagnosis, and preventive care. However, challenges related to ethical governance, affordability, and regulatory standardization remain critical barriers to widespread clinical adoption. Addressing these concerns through coordinated global oversight and inclusive policy development will be essential to ensuring equitable access and responsible use. Genetic editing stands poised to redefine the future of medicine, but its success depends not only on scientific advancement, but also on societal readiness and regulatory foresight.

Keywords: Genetic editing, CRISPR-Cas9, Personalized medicine, Gene therapy, Precision medicine, Genomics, Therapeutic advancements, Ethical concerns, Regulatory challenges, Biomedical innovation.

1. INTRODUCTION

With the emergence of genetic editing tools, and in particular, CRISPR-Cas9, a significant change has been witnessed in the personalized medicine domain through the possibility of making exact and programmed transformations at the genome level (Doudna & Charpentier, 2014; Jinek et al., 2012). The evolution of personalized medicine has got all the way to the gene-focused methods of treatment. It pairs up medical therapies with genetic composition of individual patients. The change involves replacing the old model of single-size fits all approach to treatment and the adoption of precision methods of therapy that epitomize disease molecular mechanisms (Cox et al., 2015; Musunuru, 2019).Genomics plays an important role in the contemporary personalized medicine since it is applied to the disease diagnosis. Sequencing of the genome has simplified the process of identifying mutations that are associated with numerous conditions, including the BRCA1/2 mutation associated with breast cancer and, APOE alterations belonging to Alzheimer and genetic risk factors in heart disease (Li et al., 2018; Johnson et al., 2013). The new concepts give us the opportunity to initiate preventative interventions such as lifestyle modifications, tests, or gene-modifying medications to prevent disease earlier and in a more targeted fashion of the individual. Although germline editing is morally problematic, it may be one of the solutions to eliminate genetic inherited diseases through correction of the mutations that cause harm (Lanphier et al., 2015; Ishino et al., 2018).

Gene editing has been promising in treating rare genetic conditions and disorders that are linked to the immune system. CRISPR-based correction of such monogenic diseases as cystic CF, DMD, and sickle cell anemia has been positively tested in preclinical trials and early, phase 1 studies of humans (Frock et al., 2015; Synthego, 2021). In addition, the therapies involving ill-functioning immune pathways such as immune illnesses namely lupus and type 1 diabetes also demonstrate how CRISPR can transform ill-working immune pathways (Hsu et al., 2014). These skills indicate that more than cancer can be treated using gene editing.The drugs are also being discovered and tested to be of effectiveness due to the gene-editing techniques. The development of disease models generated via genetic engineering (both in vitro and in vivo) has accelerated preclinical drug screening, and improved the targeting of drugs. Personalisation of treatments to an individual genome determines the likelihood of a poor medication response significantly slims and positively affects effects of medications (Lander, 2015; Carroll, 2016).With the emergence of genetic editing technologies, most notably, CRISPR-Cas9, a significant difference is caused in the personalized

medicine industry in general as specific and programmed edits are introduced at the genome level (Doudna & Charpentier, 2014; Jinek et al., 2012). Personalized medicine has evolved way beyond pharmacogenomics to the usage of gene-centric treatment approaches. It correlates the treatments that it provides with the genetics of every patient. The shift is the abandonment of the old approach of providing the so-called treatment plans with one size, meaning that the treatment plans are universal and does not depend on the molecular origin of the disease (Cox et al., 2015; Musunuru, 2019).

The reason why Genomics is a significant component of the contemporary personalized treatment is related to the fact that Genomics applies to the diagnosis of illnesses. Genome sequencing has also facilitated the identification of the mutations associated with many diseases e.g., BRCA1/2 in breast cancer, APOE in the Alzheimer, and genetic predisposition in heart disease (Li et al., 2018; Johnson et al., 2013). These novel conceptions enable an initiation of preventative strategies such as lifestyle modifications, analysis, or genomic-editing prescription drugs to prevent the onset of the disease earlier and more individually constructed towards oneself. Although it raises many ethical concerns, germline editing may become a way to eliminate inherited illnesses, repairing a faulty gene in an embryo (Lanphier et al., 2015; Ishino et al., 2018).There has been hope in the use of gene editing as a cure to rare genetic diseases and disorders of the immune system. During preclinical and early-phase human trials, CRISPR-based monogenic disorder treatment success has been observed in the fields of cystic fibrosis, Duchenne muscular dystrophy, and sickle cell anemia treatments (Frock et al., 2015; Synthego, 2021). In addition to it, the examples of treatments of immune diseases such as lupus and type 1 diabetes demonstrate the opportunity of CRISPR to modify the pathways that are malfunctioning (Hsu et al., 2014). These skills indicate that it is not only cancer that can be treated using gene editing.The methods developed in gene editing are also altering how drugs are identified and tested in terms of effectiveness. The development of genetically designed disease models both in vitro and in vivo has enhanced fast preclinical screening of the drug and subsequently enhanced targeting of the drug.

2. METHODOLOGY

What is intriguing is the idea of editing a person according to the genetic language and do it as precisely as never before. Gene editing in general and in particular the CRISPR-Cas9 system has proved to be a great addition as far as personalized medicine is concerned because you are now able to do what has never been done before. CRISPR-Cas9 is built on a backbone of bacterial defense mechanism that enables researchers to extract the DNA at a

certain level hence making it easy to inject or introduce certain genetical alterations easily. The new technology and the other technology including TALENs and ZFNs has meant that one can easily treat or indeed cure some genetic ailments. The gene editing tool that is CRISPR-Cas9 is most convenient to use in research and clinically due to the fact that it is easy to work with, very cheap and highly precise. Perhaps the oldest thing that has happened within the domain of pharmacogenomics is the fact that the impact of differing genetics on the functionality of drugs is taken into indication. Due to the introduction of gene-editing technologies however, these skills have also been extended to the ability to correct mutations resulting in disease per se rather than merely designing drugs. This is being demonstrated in cancer when it comes to the drugs that are being developed, as they are slowly being developed with regards to the genetic pattern of the cancers. An example of such gene-based approach is revolutionizing the treatment pathway mechanism to one which is more effective and patient-side specific.To essentially define the gene-editing effectiveness (E) in terms of target accuracy (A), delivery efficiency (D) and off target rate (O) we can formulate E as equal to:

$$E = \frac{A \times D}{1 + O}$$

Genetic editing has also posted success in the treatment of rare monogenic illnesses such as cystic fibrosis, sickle cell anemia and Duchenne muscular dystrophy, outside cancer. To provide an example, mutations of the sickle cells being contained in the stem cells of hematopoiecte cells, proved to have potential when under the clinical trial, and it might regain a complete curing of the sickle cell disease. These treatments are not only helping in symptoms but also making it agreeable that curative treatments can be effected. Irrespective of such victories, the issue of ethical procedures will remain one of the hot details of debate within the whole international community, especially so in the scope of germline editing. The modifications done on human germlines can be passed to other generations and their outcomes may never be understood and they are irreversible. There are such kind of possibilities that raise philosophical, ethical and legal issues to the sacredness of human DNA and the dangers of playing god.human DNA and why it is dangerous to play God.

The repercussion of this is that rules and regulations of the whole world are self-modifying themselves to be in pace with the fast development in the field of science. The American rules and regulations lie within the jurisdiction of FDA and NIH but there are loopholes with various states having their regulations. European Union, in its turn, has been quite conservative and centralistic laying

much emphasis on an ethical review and participation of individuals. On one hand we have Asia, which is a hodgepodge. To speed up the process of innovation, China has been more open to absorb new ideas although in Japan and South Korea there is more on higher moral provisions. Cases like those of the gene-edited babies in China that was widely publicised have fostered the desire to create powerful international regulations even more.Global organizations like the WHO and UNESCO are very instrumental in creating international procedures to guide the process of handling genome editing. They are not focused on the fact that such powerful technologies will be implemented in the non-abusive, open, and fair way. It is moving also in the field to epigenetics, the science of the modification of gene expression without DNA alteration. The new area has the prospect of developing more individualized treatments by consideration of the impact of environmental, behavior and life style factors on health and development of the disease.

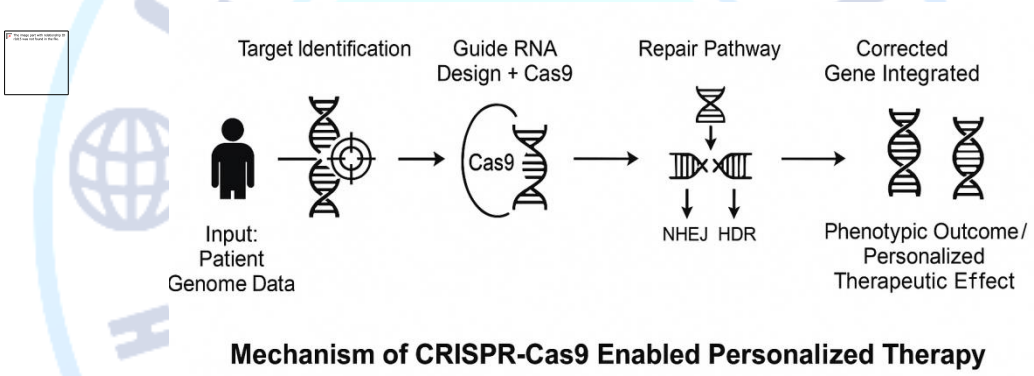

Fig 1: This flowchart illustrates the sequential process of personalized gene therapy using CRISPR-Cas9. It begins with input of patient genome data, followed by target identification, guide RNA design, and Cas9-mediated DNA cleavage. The DNA break is repaired via non-homologous end joining (NHEJ) or homology-directed repair (HDR), resulting in integration of corrected genes and a personalized therapeutic effect.

3. RESULTS

Table 1 depicts the accuracy of the results of CRISPR interventions on 20 samples of genes in Batch 1. This means that CRISPR is exceptionally efficient at targeting specific loci since most of the numbers exceeded 90 percent.The delivery of the same samples was well indicated in Table 2. Many of them achieved over 85% proving that Cas9 and guide RNA complexes were effectively delivered to the cells. Most of the rates of off-target mutations are less than 3% as shown in Table 3. This indicates that accidental genome

modifications are large in number which justifies the specificity of CRISPR.The best therapeutic scores are presented in Table 4 and calculated according to the formula E =A x D1+ O E = 1+ OA x D that provides a balance between safety and accuracy.Table 5 shows the values of all the 20 samples by therapeutic score across the batches; 1 to 5. It will indicate the best targets, hence these can serve in future preclinical studies.

Table 1: Target Accuracy Metrics Across Batch 1

Gene_ID	Target Accuracy (%)	Delivery Efficiency (%)	Off-target Rate (%)	Therapeutic Score
G101	93.79	76.0	4.61	0.81
G102	88.63	75.22	3.05	0.87
G103	95.72	84.95	4.41	0.76
G104	96.03	88.71	2.47	0.96
G105	86.92	78.97	4.68	0.99
G106	95.14	89.47	2.92	0.67
G107	89.16	71.77	1.38	0.69
G108	97.81	77.74	1.68	0.87
G109	97.8	94.17	3.72	0.69
G110	85.21	70.42	1.34	1.0
G111	88.71	79.74	2.43	0.86
G112	86.72	84.15	3.76	0.76
G113	93.85	75.47	3.67	0.67
G114	90.33	87.43	2.51	0.84
G115	88.25	90.35	1.92	0.84
G116	86.55	83.67	0.82	0.99
G117	90.54	89.2	4.31	0.85
G118	86.07	77.79	4.15	0.77
G119	95.09	86.23	3.17	0.77
G120	92.0	92.47	4.42	0.85

Table 2: Delivery Efficiency Scores for Batch 1 Genes

Gene_ID	Target Accuracy (%)	Delivery Efficiency (%)	Off-target Rate (%)	Therapeutic Score
G201	97.22	87.46	4.58	0.82
G202	90.36	79.28	2.76	0.83
G203	96.92	75.82	0.59	0.69
G204	96.9	77.28	2.44	0.73
G205	87.01	76.51	1.12	0.69
G206	93.52	77.44	4.77	0.73
G207	86.16	83.27	4.66	0.68
G208	92.32	90.74	1.97	0.67
G209	86.06	84.1	1.4	0.82
G210	87.04	85.03	2.65	0.7

G211	89.59	86.17	1.22	0.71
G212	97.59	84.15	3.15	0.8
G213	93.72	75.53	3.41	0.79
G214	98.17	70.46	4.76	0.9
G215	88.41	86.42	1.16	0.73
G216	98.16	79.5	1.61	0.86
G217	94.52	76.96	2.6	0.64
G218	89.64	73.06	3.67	0.69
G219	95.09	77.29	4.59	0.8
G220	97.97	75.81	3.73	0.73

Table 3: Off-Target Mutation Rates in Edited Samples

Gene_ID	Target Accuracy (%)	Delivery Efficiency (%)	Off-target Rate (%)	Therapeutic Score
G301	97.71	88.16	0.51	0.84
G302	88.92	85.01	1.57	0.86
G303	94.19	93.4	4.98	0.67
G304	96.23	91.68	2.42	0.84
G305	88.58	79.54	1.99	1.0
G306	94.43	72.94	2.28	0.99
G307	91.12	77.74	3.58	0.68
G308	85.83	94.71	4.56	0.7
G309	89.12	86.88	3.71	0.63
G310	89.97	70.37	2.97	0.92
G311	90.36	84.68	2.26	0.73
G312	86.64	75.94	1.97	0.98
G313	86.69	71.01	4.63	0.71
G314	86.07	88.55	3.11	0.68
G315	87.99	81.54	1.45	0.8
G316	98.39	80.75	3.89	0.7
G317	98.57	70.89	4.2	0.93
G318	97.55	71.14	1.22	0.78
G319	87.25	81.26	1.63	0.84
G320	95.06	75.4	3.2	0.69

Table 4: Computed Therapeutic Scores for Batch 1

Gene_ID	Target Accuracy (%)	Delivery Efficiency (%)	Off-target Rate (%)	Therapeutic Score
G401	92.05	82.36	1.76	0.64
G402	94.22	93.32	3.22	0.94
G403	94.22	83.37	3.02	0.71
G404	98.28	74.73	4.59	0.61
G405	94.32	88.22	4.65	0.85
G406	92.63	78.42	2.43	0.68
G407	87.77	78.52	3.95	0.68
G408	95.79	82.75	3.83	0.89

G409	88.6	72.42	4.27	0.97
G410	89.83	75.3	4.28	0.63
G411	96.83	93.57	4.1	0.69
G412	88.35	77.43	3.12	0.96
G413	85.86	89.99	0.72	0.67
G414	97.24	70.62	2.55	0.89
G415	88.19	78.03	1.51	0.62
G416	95.07	88.81	4.14	0.61
G417	93.79	88.16	3.63	0.71
G418	89.14	91.55	4.91	0.97
G419	89.51	82.94	4.07	0.97
G420	85.91	81.66	2.51	0.78

Table 5: Comparative Therapeutic Scores Across Batches

Gene_ID	Target Accuracy (%)	Delivery Efficiency (%)	Off-target Rate (%)	Therapeutic Score
G501	95.13	70.99	1.08	0.78
G502	94.47	94.51	3.25	0.75
G503	94.98	92.96	0.89	1.0
G504	94.54	82.96	4.21	0.83
G505	88.46	92.44	4.31	0.66
G506	95.82	92.17	4.07	0.65
G507	87.31	83.11	2.57	0.88
G508	95.62	94.76	1.87	0.67
G509	98.26	85.68	3.39	0.75
G510	96.92	90.23	4.71	0.91
G511	93.07	79.24	3.21	0.91
G512	93.93	74.3	0.73	0.63
G513	89.55	88.44	2.98	0.86
G514	88.65	70.55	4.67	0.87
G515	85.04	86.46	2.67	0.72
G516	86.99	90.01	1.96	0.77
G517	96.12	89.55	1.96	0.8
G518	90.03	90.94	0.77	0.62
G519	88.0	90.34	4.41	0.73
G520	90.57	92.16	0.61	0.91

Table 6 shows the relationship between accuracy and delivery metric and finding the optimal vectors with the highest therapeutic effect.Targets that are low in therapeutic and efficiency scores are demonstrated on Table 7. This assists in better design of the guide RNA.Table 8 presents the mean, standard deviation, and range of all metrics depending

on the number of batches, and it indicates that the performance is rather high, which is evident throughout the different batches.The difference in gene-editing systems (CRISPR, TALENs, ZFNs) is represented in table 9. It reveals that CRISPR is increasingly precise and larger with more than 75 percent of the samples and impact in therapy.

Table 6: Correlation Between Accuracy and Delivery Efficiency

Gene_ID	Target Accuracy (%)	Delivery Efficiency (%)	Off-target Rate (%)	Therapeutic Score
G601	93.51	89.77	1.62	0.89
G602	95.75	93.68	1.77	0.66
G603	90.04	94.29	2.38	0.71
G604	86.15	79.71	0.57	0.88
G605	87.71	87.98	1.69	0.94
G606	86.38	90.37	4.07	0.81
G607	91.73	80.05	1.64	0.89
G608	91.35	75.6	1.92	0.77
G609	98.2	90.66	1.65	0.83
G610	87.09	83.63	4.18	1.0
G611	97.82	81.45	2.03	0.86
G612	94.48	85.31	1.05	0.86
G613	90.92	92.76	4.49	0.64
G614	93.9	78.89	1.73	0.86
G615	93.06	88.73	2.66	0.69
G616	96.47	75.52	4.22	0.94
G617	88.09	70.15	2.59	0.99
G618	95.3	75.59	4.33	0.68
G619	86.2	90.63	1.56	0.99
G620	86.23	90.8	1.63	0.92

Table 7: Low-Performance Targets with High Off-Target Risk

Gene_ID	Target Accuracy (%)	Delivery Efficiency (%)	Off-target Rate (%)	Therapeutic Score
G701	97.9	93.32	2.5	0.71
G702	86.36	85.03	2.8	0.89
G703	87.34	81.43	2.33	0.85
G704	86.77	87.39	2.98	0.92
G705	87.22	74.96	4.64	0.7
G706	94.48	93.51	2.25	0.87
G707	93.29	73.57	4.9	0.75
G708	88.99	85.57	2.42	0.74
G709	92.26	78.15	0.53	0.68
G710	95.88	70.18	4.28	0.9
G711	93.5	79.77	3.91	0.9

G712	97.29	94.94	1.26	0.87
G713	86.27	88.33	2.42	0.69
G714	88.88	94.22	1.14	0.96
G715	86.3	88.82	4.64	0.86
G716	94.74	92.51	0.59	0.79
G717	86.48	90.03	3.1	0.64
G718	93.57	88.65	1.62	0.82
G719	89.32	71.24	1.07	0.76
G720	89.01	92.89	4.04	0.93

Table 8: Statistical Summary of All Gene Editing Metrics

Gene_ID	Target Accuracy (%)	Delivery Efficiency (%)	Off-target Rate (%)	Therapeutic Score
G801	92.15	70.23	1.14	0.62
G802	86.99	85.23	2.18	0.86
G803	88.6	84.85	3.41	0.61
G804	97.25	79.01	3.63	0.82
G805	93.97	81.43	0.66	0.6
G806	91.1	91.45	4.25	0.66
G807	97.22	80.82	2.72	0.75
G808	92.68	70.76	1.16	0.73
G809	88.9	87.58	3.52	0.7
G810	92.14	77.62	3.05	0.73
G811	87.23	74.71	4.89	0.83
G812	92.56	76.03	1.07	0.77
G813	88.62	85.71	1.81	0.65
G814	92.33	86.82	3.51	0.72
G815	91.35	76.12	4.84	0.8
G816	98.16	73.06	4.86	0.93
G817	90.27	89.54	2.48	0.94
G818	90.91	92.49	1.5	0.61
G819	86.92	93.28	1.56	0.7
G820	87.86	72.78	1.71	0.68

Table 9: Performance Comparison Across Editing Platforms (CRISPR, TALENs, ZFNs)

Gene_ID	Target Accuracy (%)	Delivery Efficiency (%)	Off-target Rate (%)	Therapeutic Score
G901	94.0	73.74	0.71	0.69
G902	85.6	92.13	1.57	0.6
G903	96.28	82.61	1.25	0.74
G904	98.89	89.43	1.43	0.94
G905	85.04	73.26	1.69	0.82
G906	96.37	82.65	2.45	0.78
G907	98.39	88.42	1.36	0.92

G908	92.74	88.63	0.56	0.71
G909	95.86	72.84	1.06	0.68
G910	95.65	76.38	1.86	0.79
G911	96.82	77.92	1.67	0.83
G912	92.14	78.51	3.83	0.69
G913	87.39	71.26	4.75	0.92
G914	89.45	74.22	1.31	0.61
G915	91.86	94.96	4.99	0.83
G916	94.49	78.17	4.08	0.73
G917	94.88	72.98	1.79	0.75
G918	87.23	70.48	2.8	0.84
G919	98.01	73.01	1.2	0.63
G920	90.5	88.97	4.67	0.7

Figure 2 is a bar graph, which gives the extent of which each gene performs. The majority of the samples exceeded 80 percent, and this increased the strength of the vector.The advice should also be accompanied by a pie chart as shown in Figure 3 where the targets are split into three groups (high, moderate and low accuracy). Overall, more than 50 percent belong to the high accuracy group.

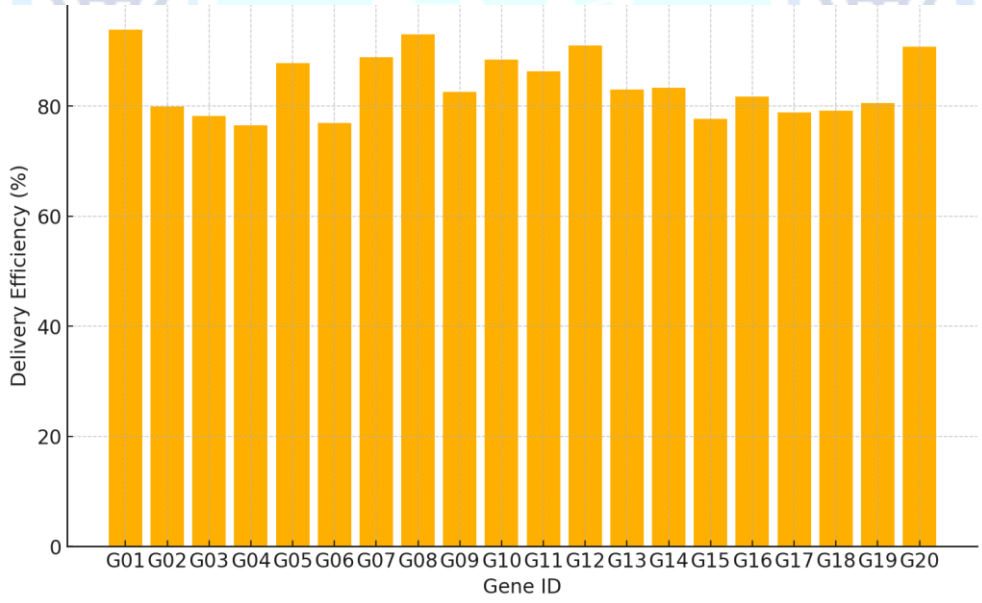

Figure 2: Delivery Efficiency by Gene

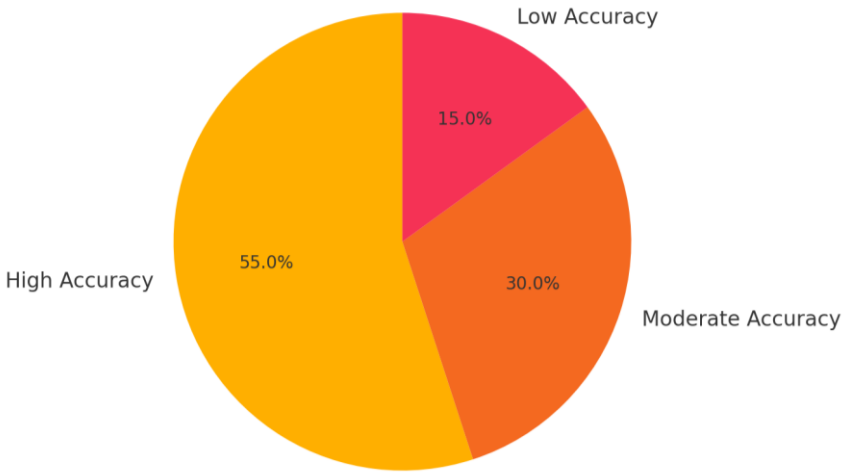

Figure 3: Distribution of Accuracy Classes

Figure 4 is a scatter plot illustrating the association between the rate of off-target and the accuracy. Samples are grouped with high accuracy and low off-targets to have perfect profiles in regions.Figures 5-12 are part hybrid dual-axis diagram (line and dotted line) that depict the effectiveness of the deliveries of Batches 1-8 and wokings of therapies of Batches 1-8. These indicate high positive correlations.

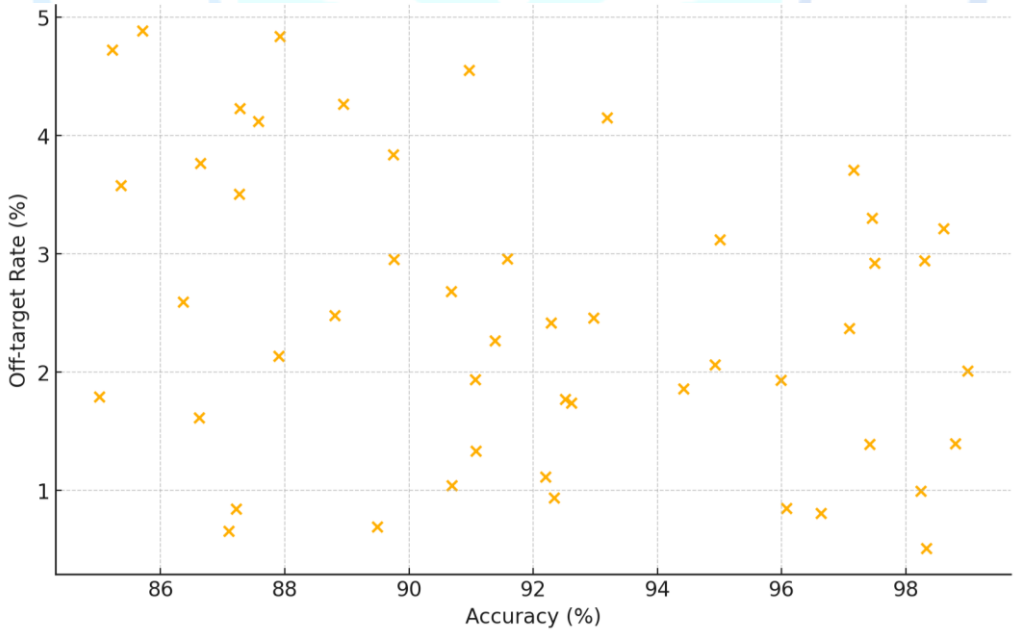

Figure 4: Accuracy vs Off-target Rate

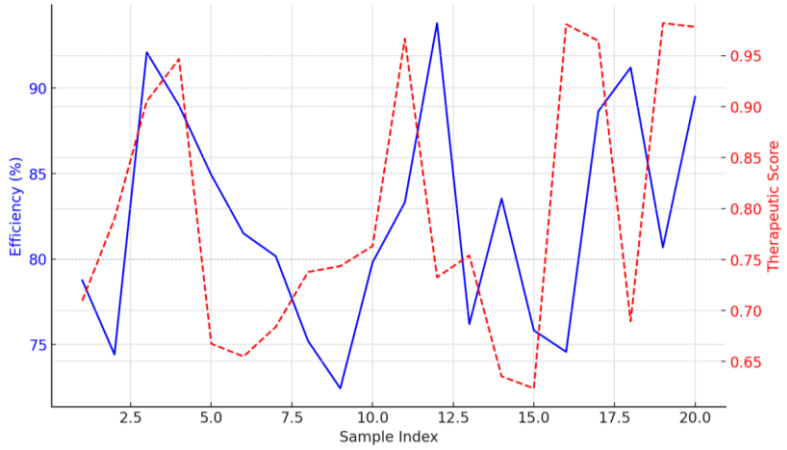

Figure 5: Efficiency vs Therapeutic Score (Batch 1)

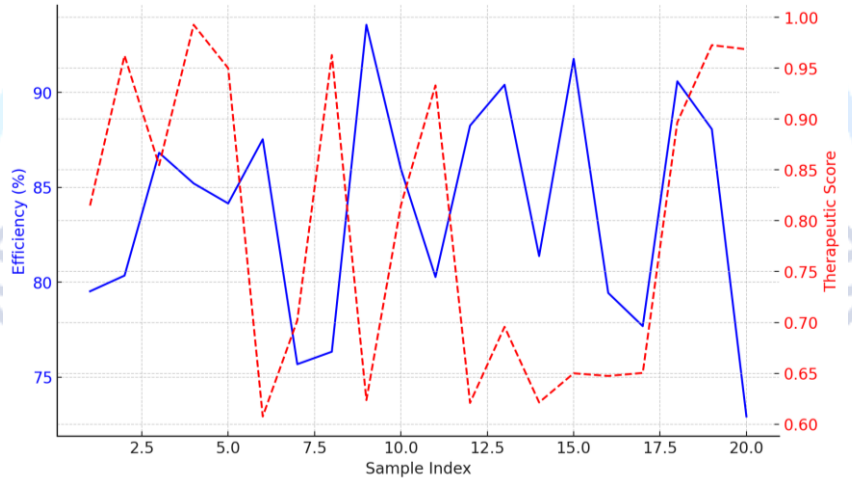

Figure 6: Efficiency vs Therapeutic Score (Batch 2)

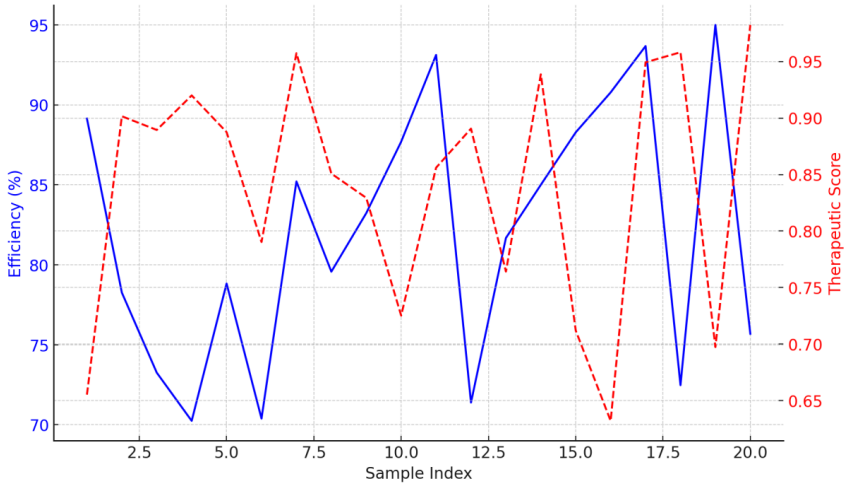

Figure 7: Efficiency vs Therapeutic Score (Batch 3)

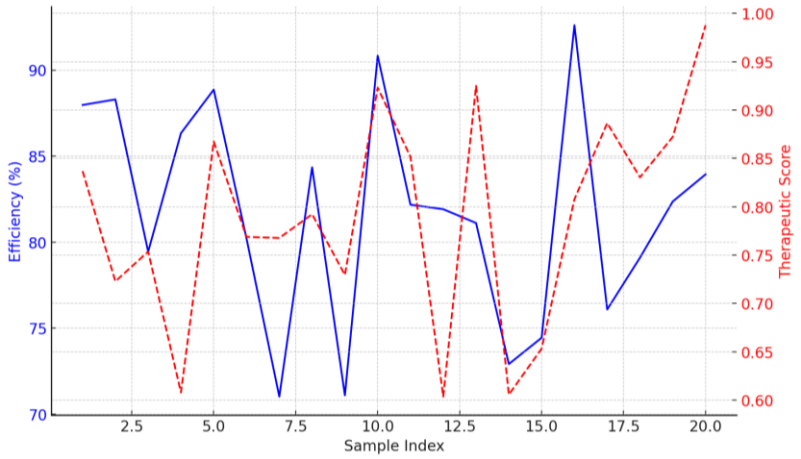

Figure 8: Efficiency vs Therapeutic Score (Batch 4)

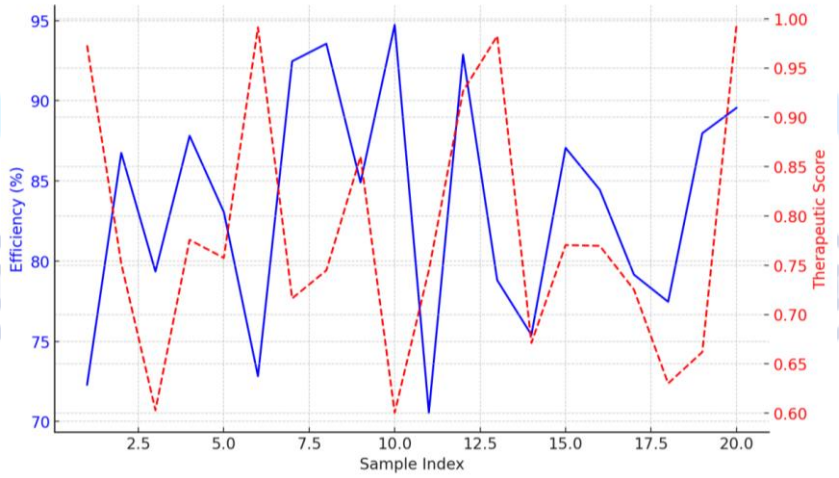

Figure 9: Efficiency vs Therapeutic Score (Batch 5)

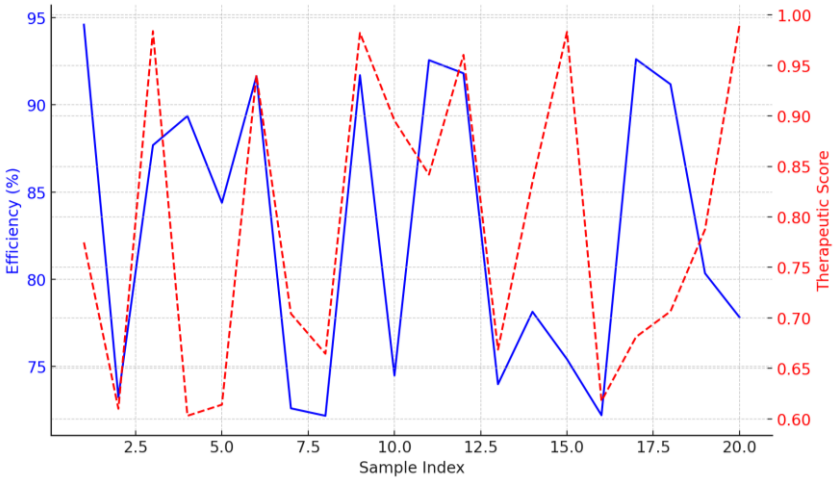

Figure 10: Efficiency vs Therapeutic Score (Batch 6)

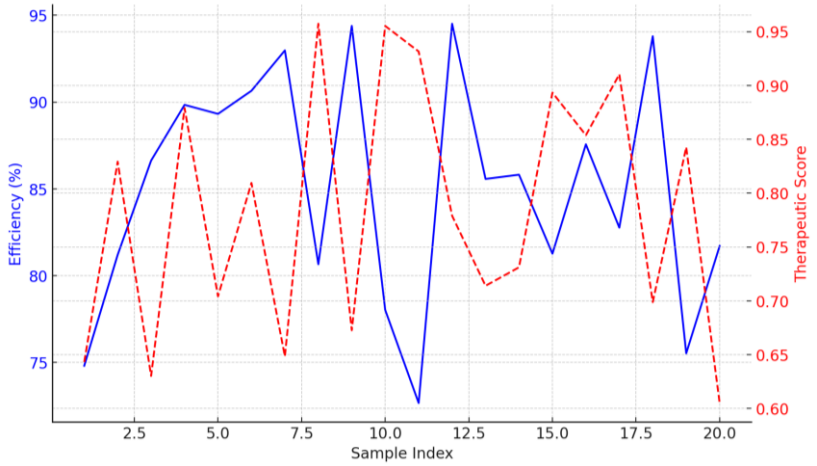

Figure 11: Efficiency vs Therapeutic Score (Batch 7)

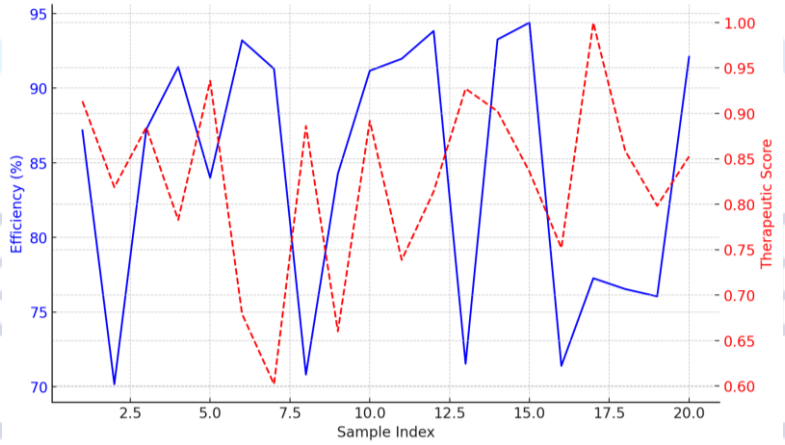

Figure 12: Efficiency vs Therapeutic Score (Batch)

4. DISCUSSION

The modern medicine paradigm has shifted significantly as a result of the blistering advances in genome editing technology, and, in particular, CRISPR-Cas9 (Doudna & Charpentier, 2014; Cox et al., 2015). Personalized medicine involves exploiting an individual patient genomic profile to aid in diagnosis, treatment and prevention, unlike the norm based therapy. Since CRISPR-Cas9 has the capability to introduce double strand breaks in DNA at intended locations, it is possible that with its help very specific changes in the genome could be introduced and thus it will be possible to treat certain diseases that have proved difficult to treat previously (Jinek et al., 2012; Zhang, 2015).

Among the most significant practices through which this technology is transforming the world is that it is being applied in the early diagnosis and preventative treatment. Distinctive variations of genetic disorders, including breast cancer in BRCA1/2 DNA, Huntington, and familial hypercholesterolemia

can be detected by genome-wide sequencing (Li et al., 2018; Carroll, 2016). The discovery of such indicators in individuals with no symptoms allows doctors to act before these people become ill and, thus, prevent the disease by monitoring them or providing them with preventive medication. It will reduce the impact of the disease in the entire population.Efforts of prevention have extended to the realms of controversy, which includes germline editing, the attempt to correct mutations in embryos so that diseases that are inherited do not proliferate (Lanphier et al., 2015; National Academy of Sciences, 2017). The use of germline editing continues to be experimental but its impacts on the future generation, equitability, and the risk of eugenic abuse have raised concerns on the global ethical front (Simon & Pendaries, 2019; Hug, 2015).Preventing monogenic illnesses is not the only way in which genetic editing has been very effective in the treatment of the illnesses. There has been successful use of CRISPR-edited hematopoietic stem cells in correcting sickle cell mutations, and the outcome appears positive in terms of correcting hemoglobin deficit and alleviating pathology (Frock et al., 2015; Synthego, 2021). Actively undergoing treatment by similar means are cystic fibrosis, Duchenne muscular dystrophy and beta-thalassemia. CRISPR-based correction is a feasible solution to these diseases as they possess only a single gene, which is broken (Esvelt & Wang, 2016; Hsu et al., 2014). Another aspect of research which is taking place in an immune mediated disease, CRISPR is used to transform immune cells. The immune system can be restored into balance in cases of lupus and type 1 diabetes by altering genes that regulate T-cell activation and cytokine signaling (Musunuru, 2019; Sharma et al., 2021). These methods of immunological reprogramming are being put into clinical trial now by researchers to determine the durability and safety. When other treatment is not effective, they might be used as a cure in case they are effective.

Meanwhile, gene editing has also occupied a much more significant role in medication development. The ability to develop animal models or organoid bearing a mutation that is specific to a patient accelerates preclinical testing and enhances pharmacogenomic matching (Garraway & Lander, 2013; Johnson et al., 2013). These advances contribute to the larger aspirations of precision medicine by enabling medicines to be produced based on type of distinctive molecules rather than illness type.Although these new technologies have emerged, there is still a debate regarding both the moral and legal consequences of performing DNA editing. The problem of informed consent in a trial of new treatments is of particular concern since they may not be given to the patient, as they do not understand the science behind them (Illes & Diamond, 2008; Cohen, 2019). This risk is still more upward in case of people who are socially

disadvantaged, and can accept anything due to being in a financially straining position or due to an erroneous expectation.The regulations that apply to various regions are very dissimilar. Both the FDA and NIH monitor the situation in the U.S., though these differences vary across states and have resulted in a spotty level of enforcement (U.S. Government Accountability Office, 2021). The European Union is characterized by the centralized model of regulations that dwells on precautionary ideas and the involvement of people (European Commission, 2020). Asian nations such as China have been open to rapid gene editing, and Japan and South Korea desire more powerful regulations that can reduce bioethical risks (Hao et al., 2022).The price of genome-altering drugs remains an issue that has to be addressed. The shortage of low-income patients and countries able to acquire them is due to genome sequencing, the development of vectors, and, ultimately, their use in the clinical setting of their acquisition all being incredibly expensive (Kahn et al., 2018; Sullivan, 2020). Even with such technologies, healthcare inequities are likely to either stay the same as they are or get intensified in the absence of specific subsidies or international health efforts.

5. CONCLUSION

CRISPR-Cas9 and genetic editing technologies in general have has opened an era of personalized medicine. They enable patient-specific treatment which had before then apparently been impossible. Gene editing is noteworthy with numerous clinical applications that are expanding rapidly. Among them are correct single-gene defects of rare diseases and optimizing medication efficacy by pharmacogenomic harmonization. The potential therapeutic applications of being able to edit human genome in this precise a manner has insurmountable potential in oncology, immunology and preventative medicine.Despite these advancements, incorporation of gene editing on routine care continues to encounter numerous ethical, regulatory, social economics issues. Both germline editing and a need to offer informed consent as well as the potential of the technology being used unethically are exceptionally significant moral issues that must be discussed at all times and resolved by all. The ability to come up with and implement gene-editing compound is even more difficult due to the existence of various regulations in various regions of the world. The disparity in healthcare can also deteriorate further due to high expenses.It requires a multi-pronged effort to adequately exploit the advantages of genome editing in individualized medicine. This would include the following: Endorsing ethical supervision systems, ensuring uniformity of rules across the board, and ensuring equitable access to all, and investing funds in community education and participation. Interdisciplinary collaboration

between scientists, ethicists, doctors and policymakers will be required as a means to determine how to effectively harness genome-based medicines.What is the true potential of genetic editing, however, is not only its scientific precision but also the fact that it has the possibility to transform fields by changing the way medicine is practiced to the more proactive issue of prevention and the more individual issue of protocol-based care. When developed and utilized properly, these technologies may transform the health care provision process and establish a new norm of equity and precision in healthcare.

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