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Inherited arrhythmias and gene therapy: Are there any ethical considerations to take into account?

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Abstract

Interventional electrophysiology represents a relatively recent subspecialty within the field of cardiology. In the past half-century, there has been significant advancement in the development and implementation of innovative ablation treatments and approaches. However, the treatment of arrhythmias continues to be inadequate. Several arrhythmias, such as ventricular tachycardia and atrial fibrillation, pose significant challenges in terms of therapeutic efficacy, whether through interventional procedures or the administration of antiarrhythmic drugs. Cardiologists are engaged in ongoing research to explore innovative methodologies, such as genome editing, with the purpose of effectively managing arrhythmias and meeting the growing needs of patients afflicted with rhythm disturbances. The field of genome editing has significant promise and has the potential to serve as a highly effective personalized therapy for rhythm disorders in patients. However, several ethical issues must be considered.

Key Words: Arrhythmia; Sudden cardiac death; Genome editing; Long QT; Channelopathies; Mutation

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Core Tip: The use of genome editing to treat rhythm disturbances at the substrate level could provide a revolutionary treatment for disorders that the current standard of care is inadequate. Our knowledge of the disease is the only limit in identifying a perfect genome editing tool for several rhythm disturbances. As our understanding of gene vectors and transfer techniques progress, a novel therapy approach will be upon us, where cardiac muscles are altered to be impervious to rhythm disturbances, enhancing patients' quality of living and relieving the burden on healthcare organizations. Ethical issues will eventually arise, as the treatments will be expensive.

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INTRODUCTION

Inherited cardiac arrhythmias syndromes are a cluster of diverse disorders that predispose to life-threatening rhythm disturbances and abrupt cardiac death[1]. Due to inadequate penetrance and genetic variability, their detection is not invariably straightforward[2]. Additionally, current therapies are typically invasive and only preventative[1,2]. While often effective in relieving or preventing symptoms, current pharmacological or interventional treatments do not specifically address the underlying genetic defect or the key intermediary pathways implicated in the development of these disorders[3]. Clustered regularly interspaced short palindromic repeats (CRISPR)/Cas9 techniques, in particular, have the ability to modify the genetic electrophysiologic substrate, hence enabling treatment for many lethal disorders[4]. So far, gene therapy has enabled the *in vitro* replication of rhythm disturbances, offering a consistent framework for variable pathogenesis, pathophysiological, and drug-testing research[1-4]. Nevertheless, *in vivo* procedures still require further investigation into the techniques' reliability, precision, and efficacy.

GENOME EDITING FOR INHERITED ARRHYTHMIAS

Inherited cardiac arrhythmia syndromes are disorders characterized by one or more genetic abnormalities that enhance the incidence of rhythm disturbance and culminate in a life-long risk of unexpected death[1]. Inherited arrhythmias can be categorized as electrophysiologic equilibrium abnormalities (long QT syndrome, catecholaminergic polymorphic ventricular tachycardia), organic disorders linked to rhythm disturbances (hypertrophic cardiomyopathy), or a combination involving both a proclivity for rhythm disturbances and organic heart disease (arrhythmogenic cardiomyopathy)[5]. Certain compounds that modify agonists (beta-blockers) or ion channels (sodium channel blockers) have shown effectiveness in specific forms of familial rhythm disturbances, although individuals are often only partially shielded[5,6]. Several types of familial rhythm disturbances have a gradual course, and thus no presently known treatment effectively slows disease advancement[7]. Current research has suggested that genetic treatment for people with familial rhythm disturbances might be developed to prevent harmful rhythm disturbances as well as hinder disorder development by addressing core disorder processes[6-9]. These upcoming treatments have the ability to decrease adverse reactions significantly while also improving clinical results[10].

Because gene variability is widespread in channelopathies, additional genetic variants are being found and included in the prospective catalog of variations amenable to genetic analysis[1,11]. Even though both patient-dependent and patient-independent *in vitro* techniques could corroborate a variant's pathogenic potential, more compelling data and statistical validation of disorder etiology are required before they could be included in commonly utilized medical testing[1-4]. Furthermore, despite significant advances in comprehending the pathophysiology of familial rhythm disturbances, guidelines for treatment approaches, such as beta-blockers, left cardiac sympathetic denervation, or implantable cardioverter-defibrillator, have not altered in the previous 40 years[1-4]. The ability to incorporate unique disease-causing variants while maintaining the same genetic origin allows for an impartial assessment of different mutations[1-4]. This comparison research revealed that various variants in the same gene could be the result of unique genetic pathways, strengthening the viewpoint that the therapy of familial rhythm disturbances must shift toward targeted therapy and patient-specific treatments[2,12].

Precision Medicine emerged as a novel approach to disease treatment and prevention, which considers the unique interplay between an individual's genetic profile, environmental factors, and lifestyle factors[13]. The primary objective of this technique is to predict appropriate interventions and preventive measures that may yield greater efficacy for individual patients or, more feasibly, for cohorts of patients sharing common attributes[13]. The present method stands in opposition to the prevailing one-size-fits-all paradigm, wherein illness treatment and prevention strategies are formulated solely on the basis of randomized trials without taking into account individual variations[13].

While missense mutations are generally straightforward to edit using CRISPR/Cas9, addressing complex variants, including double heterozygosity, could present further barriers that must be overcome[1,2]. Furthermore, CRISPR/Cas9 has various disadvantages that have slowed the use of *in vivo* gene therapy in the management of rhythm disturbances[1, 2]. The homologous recombination *cellular* mechanism, downregulated in terminally differentiated cell types such as

cardiac myocytes, reduces the odds of success[1,2]. Moreover, correcting a minor amount of molecules may result in pro-arrhythmic episodes, worsening the individuals' medical conditions[1,2].

Pro-arrhythmia is a potential concern of treatments that modify heart rhythm[2,4]. This issue is particularly significant in the context of adeno-associated viruses (AAV) genome editing, which could lead to myocardial heterogeneities due to cardiac myocytes that have and have not been transfected by AAV[2,4]. A rigorous assessment of pro-arrhythmic potential necessitates screening in bigger animals with pulse rate, anatomy, and heart physiology similar to humans[2,4].

Another field of ongoing research is the immunological reaction to genome editing[1,2]. In big animals given massive AAV loads, the intrinsic immunity mechanism was activated, culminating in a possibly deadly inflammatory process[4]. The formation of neutralizing antibodies following one AAV treatment presently precludes subsequent vector dosage, which might promote high-level transmission or increase genetic engineering longevity[4]. Even though AAV transduction of cardiac myocytes causes minor inflammation, the possibility of adverse immunity reactions must be addressed when the therapy carrier expresses a foreign protein[4].

Overall, current investigations of inherited arrhythmia disorders and gene therapy have revealed that these disorders may be effectively replicated in the laboratory, revealing deficient ion currents and enabling a suitable framework for molecular, analytical, and drug-testing research[2]. Even though immensely attractive, this technique remains in its infancy, and transitioning from the lab to the patient may require more study to increase the procedures' reliability, effectiveness, and accuracy. Future *in vivo* CRISPR/Cas9 investigation in heart channelopathies could eventually enable us to realize its promise to treat these disorders and make personalized medicine a reality[6-8].

Over the past decade, there have been significant developments in genome editing and its applicability to familial rhythm disturbances. Genome editing with AAV vectors has shown outstanding outcomes for non-cardiac disorders[1]. The obstacles for viral vector-based heart genome editing entail demonstrating effectiveness at transduction efficiencies feasible in individuals, as well as demonstrating safety at these dosages. Off-target complications, the formation of pro-arrhythmia, the durability of treatment, and the limitation of reversibility following therapy continue to pose major challenges for translation[6-8]. Creating techniques to counteract innate immunity and allow for recurrent doses will significantly increase the therapeutic value of viral vectors, increase safety, and resolve issues about treatment durability [1,2]. To render viral genome editing cost effective, the tremendous cost of medical-grade AAV development must be reduced. The discovery of technologies for effective and specific myocardial distribution for oligonucleotides and altered mRNAs would be a game changer.

CONCLUSION

The notion of a pathogenic genetic mutation within a gene that encodes a cardiac ion channel, resulting in a substrate extremely prone to arrhythmias, has emerged as the fundamental framework for understanding the pathophysiology of all these syndromes[14]. According to current guidelines, it is recommended that individuals diagnosed with hereditary cardiomyopathies and arrhythmia syndromes have genetic testing as a standard component of their medical management[15]. The use of genome editing to treat rhythm disturbances at the substrate level could provide a revolutionary treatment for disorders that the current standard of care is inadequate. Our knowledge of the disease is the only limit in identifying a perfect genome editing tool for several rhythm disturbances. As our understanding of gene vectors and transfer techniques progress, a novel therapy approach will be upon us, where cardiac muscles are altered to be impervious to rhythm disturbances, enhancing patients' quality of living and relieving the burden on healthcare organizations. Ethical issues will eventually arise, as the treatments will be expensive. Who will cover the cost? Will there be an accurate risk stratification and patient selection tool, or will existing disparities in access to healthcare interventions increase?

FOOTNOTES

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