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The Role of Genomics in the Prevention of Cardiovascular Diseases

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Abstract With the rapid development of high-throughput sequencing technology and the continuous progress of data analysis methods, genomics provides new perspectives and tools for the prevention of cardiovascular diseases. This study elaborates on the important role and potential impact of genomics in the prevention of cardiovascular diseases. Research has found that genomics not only helps guide drug selection and dosage adjustment, but also provides guidance for lifestyle interventions, thereby helping individuals reduce the risk of cardiovascular disease. By conducting in-depth research on the association between genes and cardiovascular disease, it is possible to accurately identify high-risk individuals and develop targeted prevention strategies. However, the application of genomics also faces ethical, privacy, technological, and legal challenges. In the future, with the continuous innovation of technology and the reduction of costs, genomics is expected to play a greater role in the prevention of cardiovascular diseases and make important contributions to human health.

Keywords Genomics; Cardiovascular disease; Prevention; Risk assessment; Personalized drug selection

Cardiovascular diseases, including coronary heart disease, stroke, hypertension, etc., have become a global health issue. With the aggravation of population aging, the change of lifestyle and the impact of environmental factors, the incidence rate and mortality of cardiovascular diseases are rising. According to the latest data from the World Health Organization (WHO), cardiovascular disease causes nearly 18 million deaths annually, accounting for more than one-third of the total global deaths (Roth et al., 2020). In addition, cardiovascular disease also brings enormous economic burden to patients and society, including medical expenses, loss of productivity, and decreased quality of life.

In the face of this severe situation, preventing the occurrence of cardiovascular diseases has become a crucial task. Traditional cardiovascular disease prevention strategies mainly focus on lifestyle adjustment, control of risk factors (such as hypertension, hyperlipidemia, diabetes, etc.), and early screening and intervention (Becheva et al., 2023). However, these methods vary significantly among individuals, and some individuals may still develop cardiovascular disease despite following a healthy lifestyle. This indicates that in addition to traditional risk factors, there are other unknown genetic and environmental factors that affect the occurrence of cardiovascular disease.

In order to gain a deeper understanding of the pathogenesis of cardiovascular disease and explore more precise and personalized prevention strategies, genomics research is particularly important. Genomics is a science that studies the structure, function, and evolution of the genome of living organisms. It utilizes advanced technologies such as high-throughput sequencing and bioinformatics analysis to comprehensively analyze the genetic information of the human genome (Pérez-Losada et al., 2020), revealing genetic variations and mechanisms related to cardiovascular diseases. Abraham et al. (2021) found through genomics research that using genomics can more accurately predict an individual's risk of cardiovascular disease, providing scientific basis for developing personalized prevention and treatment plans.

The purpose of this study is to review the role of genomics in the prevention of cardiovascular disease, explain the importance of genomics in the research of cardiovascular disease by introducing the global status and impact of cardiovascular disease, and deeply discuss the application and challenges of genomics in the prevention of cardiovascular disease, hoping to provide useful reference and enlightenment for researchers and relevant

practitioners, promote the further development of genomics in the field of cardiovascular disease prevention, and make contributions to reducing the incidence rate and mortality of cardiovascular disease and improving human health.

1 The Relationship Between Genomics and Cardiovascular Disease

1.1 Overview of the genetic basis of cardiovascular diseases

Cardiovascular disease is a complex disease that often involves the interaction of multiple genetic and environmental factors in its occurrence and development. Genetic factors play an important role in the occurrence of cardiovascular diseases, which has been widely studied and clinically proven. With the rapid development of genomics technology, the understanding of the genetic basis of cardiovascular diseases is also constantly deepening.

Genetic basis refers to genes and their variations associated with specific diseases or traits. In cardiovascular diseases, many genes and their variations have been found to be closely related to susceptibility, age of onset, disease progression, and prognosis. For example, Hopewell et al. (2017) found that certain gene variants, such as PCSK9, increase the risk of coronary heart disease, stroke or hypertension, because they affect atherosclerosis and coronary heart disease by regulating cholesterol metabolism. PCSK9 affects cholesterol metabolism, leading to an increase in LDL cholesterol levels and may exacerbate the development of coronary heart disease by promoting thrombosis and inflammatory response.

Yin et al. (2013) found that different allele variations in the Apolipoprotein E gene, particularly ε The 4-allele gene is associated with an increased risk of cardiovascular disease, as ε The 4 alleles have adverse effects on cholesterol metabolism and lipid transport. In existence ε In the case of 4-allele genes, energy supply may decrease and support for neurons may weaken, which may exacerbate the development of cardiovascular disease.

Ference et al. (2016) found that HMGCR has similar, independent and cumulative effects on reducing cardiovascular events and diabetes risk per unit of low density lipoprotein cholesterol level. 3-hydroxy-3-methylglutaryl CoA reductase (HMG-CoA reductase) is a key enzyme in cholesterol synthesis, and therefore, mutations in the HMGCR gene affect its activity or are associated with cholesterol levels and cardiovascular disease risk.

Genomic technologies, particularly genome-wide association studies (GWAS) and single gene genetic disease studies, provide powerful tools for revealing the genetic basis of cardiovascular diseases. GWAS can identify multiple gene regions associated with cardiovascular disease risk by detecting single nucleotide polymorphisms (SNPs) and other variations in the genome on a large scale. Defesche (2017) discussed that single gene genetic disease research focuses on cardiovascular diseases caused by single gene mutations, such as familial hypercholesterolemia and Marfan's syndrome.

It is worth noting that although genomics has revealed many genetic variations related to cardiovascular disease, the genetic mechanisms of cardiovascular disease are still far from fully understood. This is mainly because cardiovascular disease is a polygenic genetic disease, which involves the synergistic effects of multiple genes and complex interactions with environmental factors (Figure 1). Therefore, future research needs to explore the interaction between genes and the environment on a broader scale in order to gain a deeper understanding of the genetic basis of cardiovascular disease.

1.2 How genomics reveals the genetic mechanisms of cardiovascular diseases

Genomics can deeply reveal the genetic mechanisms of cardiovascular diseases through various methods such as GWAS, sequence analysis, comprehensive genetic and epigenetic data, single gene genetic disease research, gene expression analysis, and genome-environment interaction research. GWAS is a powerful tool for identifying genetic variations associated with specific diseases or traits. By extensively detecting variations such as single nucleotide polymorphisms (SNPs) in the genome, GWAS can identify multiple gene regions associated with cardiovascular disease risk, disease progression, and prognosis. McPherson et al. (2006) reported an association between the 9p21.3 region and the risk of coronary artery disease, which is an early example of using the GWAS method.

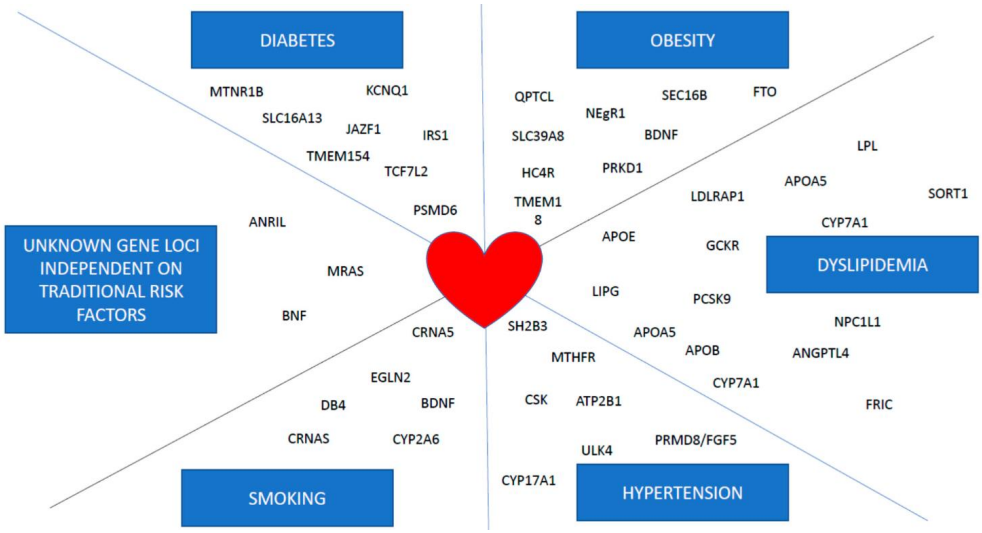

Figure 1 The influencing factors of cardiovascular disease and the selected genes of its SNPs (Vrablík et al., 2021)

Note: The different divisions indicate the genes closely related to the occurrence and development of cardiovascular diseases through SNPs under traditional risk factors such as obesity, smoking, diabetes, etc

Sequence analysis is an important analytical method primarily used to discover consecutive events that occur within a certain time interval, forming a sequence that should have universal significance. Hopewell et al. (2017) investigated the association between PCSK9 gene mutations and low LDL levels and reduced risk of coronary heart disease, demonstrating the application of sequence analysis in identifying cardiovascular disease risk factors. In the field of biology, sequence analysis is widely used in alignment, pattern recognition, gene prediction, evolutionary analysis, and protein structure prediction of DNA, RNA, and protein sequences.

The integration of genetic and epigenetic data provides a more comprehensive and in-depth perspective to understand the genetic characteristics and gene expression patterns of organisms. Bjorklund et al. (2017) demonstrated in their study of the effects of arsenic exposure on epigenetics how genetics can be combined with epigenetics to investigate how environmental factors increase disease risk by altering gene expression patterns. This comprehensive analysis not only helps to reveal the pathogenesis of genetic diseases and complex phenotypes, but also helps to discover new treatment strategies and personalized medical plans.

Although cardiovascular disease is often regarded as a polygenic inherited disease, there are also some monogenic inherited diseases closely related to cardiovascular disease (Table 1). Studying these single gene inherited diseases can help better understand the genetic basis of cardiovascular disease. For example, Defescher et al. (2017) found that familial hypercholesterolemia is caused by mutations in the LDLR gene, which impair LDL receptor function, leading to elevated cholesterol levels and an increased risk of cardiovascular disease.

Gene expression analysis can study the expression levels of specific genes in different tissues and physiological states. By comparing the gene expression profiles between normal and diseased states, changes in gene expression related to cardiovascular disease can be discovered, thereby revealing the genetic mechanisms of the disease. For example, certain genes may have abnormal expression in the myocardium or vascular tissue of patients with cardiovascular disease, which may be related to the occurrence and development of the disease.

In addition to studying the variation and expression of genes themselves, genomics can also study the interaction between genes and environmental factors (such as lifestyle, dietary habits, environmental factors, etc.). This interaction may have a significant impact on the occurrence and development of cardiovascular diseases. For example, Jeong et al. (2020) found that certain genetic variations may make individuals more sensitive to certain environmental factors, such as smoking and a high salt diet, thereby increasing the risk of cardiovascular disease.

Table 1 Selected examples of monogenic cardiovascular diseases (Vrablík et al., 2021)

Gene(s)	CVD	Manifestation
LDLR, APOB, PCSK9	Familial hypercholesterolemia	High concentrations of LDL and total cholesterol; xanthomas; arcus lipoides cornae; xanthalesmas; coronary heart disease
ABCG5, ABCG8	Sitosterolemia	High plasma sitosterol, campesterol; hypercholesterolemia; premature coronary heart disease; xanthomas
MYH7, MYBPC3, TNNT2, TPM1, MYL2, MYL3, PLN	Hypertrophic cardiomyopathy	Hypertrophy of left ventricle, shortness of breath, diastolic dysfunction, left ventricular outflow ischemia
PKP2, DSP, DSG2, JUP, TMEM43	Arrhythmogenic right ventricular cardiomyopathy	Ventricular arrhythmias, right ventricular cardiomyopathy
MYH7, MYBPC3, TNNT2, MYH6, MYPN, ANKRD1, RAF1, DES, DMD	Familial dilated cardiomyopathy	Diastolic dysfunction, left ventricular hypertrophy, atrial fibrillation, congestive heart failure
FBN1, TGFBR1, TGFBR2, SMAD3, TGFB2, TGFB3, SKI	Marfan's syndrome	Aortic aneurysm or dissection, valvular heart disease, enlargement of the proximal pulmonary artery, congestive heart failure, arrhythmias
ACTA2, FBN1, MYH11, TGFBR1/2, LOX, COL3A1, TGFB2/3	Thoracic aortic aneurysm and dissection	Chest pain, renal cysts, thumb-palm sign, temporal arteritis, bicuspid aortic valve, abdominal aneurysm, intracranial aneurysm
BMPR2, BMPR1B, CAV1, KCNK3, SMAD9, ACVRL1, ENG, EIF2AK4	Pulmonary arterial hypertension	Right ventricular failure, impaired brachial artery flow-mediated dilation, increased pulmonary vascular resistance
KCNQ1/H2/E1/J2, SCN5A, CAV3, CALM1/2	Long QT syndrome	Malignant arrhythmia, palpitations, syncope, anoxic seizures secondary to ventricular arrhythmia
KCNH2	Short QT syndrome	Abbreviated QTc interval on the ECG, propensity for atrial and ventricular arrhythmias
SCN5A	Brugada syndrome	Elevation of the ST, ventricular fibrillation, syncope, arrhythmia

1.3 Known genes and variations related to cardiovascular disease

Genomics has revealed some important mechanisms in this field by delving deeper into the association between genetic variation and cardiovascular disease. Through genome-wide association studies (GWAS) and other technologies, scientists have discovered multiple genes and variations associated with cardiovascular disease risk, disease progression, and prognosis. Among them, Hopewell et al. (2017) found that the APOE gene ε The 4-allele gene is associated with an increased risk of coronary heart disease and stroke, while the PCSK9 gene mutation may lead to an increase in low-density lipoprotein (LDL) cholesterol levels in the blood, thereby increasing the risk of cardiovascular disease.

Variations in the ANGPTL gene family can affect blood lipid levels and angiogenesis (Oldoni et al., 2016), while variations in the LPL gene are associated with triglyceride metabolism (Young et al., 2019). Wang et al. (2018) found that variations in the CETP gene may affect cholesterol levels in HDL and LDL. The mechanisms of action of these genes and mutations in cardiovascular disease are complex and diverse, involving multiple aspects such as cholesterol metabolism, angiogenesis, and inflammatory response. In addition, Heshmatzad et al. (2023) discussed the role of non coding region variations in cardiovascular disease, including promoters/enhancers, introns, miRNAs, and 5'/3' UTRs, which account for 90% of all identified single nucleotide polymorphisms associated with cardiovascular features and diseases.

Understanding these genetic variations is of great significance for the prevention, diagnosis, and treatment of cardiovascular diseases, as they can help us identify high-risk individuals and develop personalized intervention strategies. However, it is worth noting that genetic variation is only one of the many factors that contribute to the occurrence and development of cardiovascular diseases, while environmental factors, lifestyle factors, and others also play important roles.

2 The Application of Genomics in the Prevention of Cardiovascular Diseases

2.1 Application of genomics in risk assessment

Genomics plays an important role in the prevention of cardiovascular diseases, especially in the field of risk assessment. By utilizing advanced genomic technologies, scientists can more accurately assess an individual's risk of cardiovascular disease, providing strong support for early prevention and intervention measures.

In terms of risk assessment, genomic technology can analyze individual genetic information and identify genetic variations related to cardiovascular disease. These genetic variations may involve multiple aspects such as heart structure, function, and metabolic pathways, providing in-depth insights into individual cardiovascular disease risk. By analyzing this genetic information, doctors can develop more personalized prevention strategies.

Liu et al. (2018) believe that adjusting lifestyle, improving dietary habits, and increasing physical exercise can reduce the incidence and mortality of cardiovascular disease. Abraham et al. (2016) studied the Genomic Risk Score (GRS) of 49310 SNPs generated from a meta-analysis of coronary heart disease (CHD) based on the CARDIoGRAMplusC4D Consortium, and independently tested it in five prospective population cohorts. Benes et al. (2018) outlined the progress in genomic medicine, particularly in improving cardiovascular disease (CVD) risk prediction through gene risk scoring.

Genomic technology can also be used to construct animal models and simulate the occurrence and development of human cardiovascular diseases. These animal models can help researchers delve deeper into the interrelationships between genes and diseases, further revealing the genetic mechanisms of cardiovascular disease. By understanding these mechanisms, more effective drugs and treatment methods can be developed, providing more comprehensive support for the prevention and treatment of cardiovascular diseases.

The application of genomics in risk assessment is still in its developmental stage, and there are still some challenges and limitations. For example, the function and impact of many genetic variations are still not fully understood, which may affect the accuracy and reliability of risk assessment. In addition, the application of genomic technology also needs to consider ethical, privacy, and legal issues to ensure its reasonable and safe use in cardiovascular disease prevention.

2.2 Personalized drug selection and dosage adjustment

Genomics can not only be used for risk assessment in cardiovascular disease prevention, but also guide personalized drug selection and dosage adjustment. By understanding individual genetic variations, doctors can accurately select drugs targeting specific genetic variations, thereby improving drug efficacy and reducing adverse reactions. Musunuru (2014) explored how the ability to obtain personalized genomes can transform patient care, enabling doctors to more accurately predict disease risk and tailor treatment based on individual circumstances. Special emphasis was placed on the application of pharmacogenetics in determining drug or dose selection.

In terms of drug selection, genomic technology can help doctors determine which drugs are more effective for specific individuals. Rysz et al. (2020) found that certain genetic variations may lead to changes in the metabolism and efficacy of certain drugs in the body. Therefore, by detecting these genetic variations, doctors can choose the most effective drugs for individuals. For example, in the treatment of hypertension, certain genetic variations may lead to poor efficacy of certain antihypertensive drugs, while others may be more effective. Through genomic testing, doctors can select the most suitable antihypertensive drugs for patients, thereby improving treatment effectiveness.

Genomics can also provide important guidance in adjusting drug dosage. Different individuals may have different reactions to drugs, so adjusting drug dosage based on individual genetic variations can better balance drug efficacy and side effects. Rysz et al. (2020) discussed that increasing or decreasing drug doses may help improve efficacy or reduce adverse reactions in certain situations. Through genomic testing, doctors can more accurately predict an individual's response to drugs and adjust drug dosage accordingly, thereby achieving personalized drug treatment.

2.3 Genomics guided lifestyle interventions

Genomics also plays an important role in guiding lifestyle interventions for cardiovascular disease prevention. Everyone's genome is unique, so understanding individual genetic variations can tailor more suitable lifestyle recommendations for them, thereby more effectively reducing the risk of cardiovascular disease.

In terms of nutrition and diet, genomics can help individuals choose a diet that is more suitable for them. Ouzounian et al. (2007) discussed the applications of genomics and proteomics in cardiovascular medicine, including predictive prevention and personalized treatment of diseases. These methods may provide support for preventing and treating cardiovascular disease by optimizing individual dietary intake. For example, Cha et al. (2018) found that certain genetic variations may affect an individual's metabolism of fat, carbohydrates, or certain nutrients. By detecting these genetic variations, individuals can be provided with personalized dietary recommendations, such as reducing the intake of certain foods or increasing the intake of certain nutrients, to improve cardiovascular health.

In terms of exercise, genomics can also provide guidance for individuals. Certain genetic variations may affect an individual's exercise tolerance, muscle strength, and recovery ability. By understanding these genetic variations, individuals can develop more appropriate exercise plans, such as selecting the appropriate type, intensity, and frequency of exercise, to improve cardiovascular health.

In addition, genomics can provide individuals with personalized advice on unhealthy habits such as smoking and drinking. Certain genetic variations may increase an individual's sensitivity to these bad habits, thereby increasing the risk of cardiovascular disease. By understanding these genetic variations, individuals can be provided with more specific advice on smoking cessation, alcohol restriction, etc., helping them improve their lifestyle and reduce risks.

2.4 Early screening and diagnostic strategies

By utilizing advanced genomic technologies, it is possible to detect signs of cardiovascular disease earlier, thereby achieving early intervention and treatment, and improving the cure and survival rates of the disease. Genomic techniques can help identify genetic variations associated with cardiovascular disease. These genetic variations may involve multiple aspects such as heart structure, function, and metabolic pathways. By detecting these genetic variations, high-risk individuals can be screened and targeted screening and diagnosis can be carried out. This helps to detect signs of cardiovascular disease earlier, thus achieving early intervention and treatment.

Schnabel et al. (2012) discussed how new sequencing techniques, epigenetics, and transcriptomics methods can be used for large-scale screening and follow-up of CVD, and how these advances can enhance understanding of the genetic basis of CVD. Ginsburg et al. (2005) discovered new "omics" technologies that allow for "whole genome" querying of sequence variations, transcription, proteins, and metabolites, collectively providing tools for the transformation of cardiovascular gene medicine.

Genomic technology can also be used to develop new diagnostic methods and biomarkers. Berger and Mardis (2018) discovered specific gene variations or expression patterns through in-depth research on the relationship between gene variations and cardiovascular disease, which can serve as new biomarkers for disease diagnosis. In addition, genomic technology can also help doctors understand the pathogenesis and progression of diseases, thereby providing ideas for the development of new diagnostic methods.

2.5 Success case analysis

In recent years, genomics has made significant progress in the prevention of cardiovascular diseases, with one famous successful case being the development and application of PCSK9 inhibitors. PCSK9 (pre protein converting enzyme Bacillus subtilisin 9) is a gene closely related to cardiovascular disease. Research has found that mutations in the PCSK9 gene increase the level of low-density lipoprotein cholesterol (LDL-C) (Figure 2), thereby increasing the risk of cardiovascular disease (Hopewell et al., 2017).

SNP	Effect/other allele	Effect allele frequency	LDL-C reduction	
			mmol/L (95% CI)	*P*
rs11591147	T/G	1.5%	0.50 (0.47–0.54)	9×10^{-143}
rs505151	A/G	96.5%	0.09 (0.07–0.11)	4×10^{-17}
rs11206510[a]	C/T	18.8%	0.08 (0.07–0.09)	2×10^{-53}
rs2479409[a]	A/G	65.5%	0.06 (0.06–0.07)	3×10^{-50}
rs562556[a]	G/A	18.3%	0.06 (0.05–0.08)	6×10^{-21}
rs11583680[a]	T/C	14.1%	0.03 (0.02–0.05)	1×10^{-8}

Figure 2 Effects of PCSK9 variants on low-density lipoprotein cholesterol (Hopewell et al., 2017)

Based on this discovery, researchers have successfully developed PCSK9 inhibitor drugs, such as ilozumab and Aliciumab (Iqbal et al., 2019). These drugs can specifically inhibit the function of PCSK9, thereby reducing LDL-C levels and effectively preventing the occurrence of cardiovascular diseases. Multiple clinical trials have confirmed that PCSK9 inhibitors perform well in reducing the risk of cardiovascular events, providing a new powerful weapon for cardiovascular disease prevention.

This successful case fully demonstrates the important role of genomics in the prevention of cardiovascular diseases. By delving into the association between genes and cardiovascular disease, researchers can not only discover new drug targets, but also provide scientific basis for drug development, ultimately bringing good news to patients.

3 Challenges and Prospects

3.1 Ethical, privacy, and legal issues faced

The application of genomics in the prevention of cardiovascular diseases faces numerous ethical, privacy, and legal issues. From an ethical perspective, genomics involves the acquisition and use of individual genetic information. This requires doctors to respect individual autonomy and privacy in research and application, ensuring that their genetic information is not abused or leaked. We also need to consider the issue of genetic discrimination, which refers to unfair treatment in employment, insurance, and other aspects due to differences in individual genetic information. Therefore, it is necessary to establish corresponding ethical norms and regulatory mechanisms to ensure the fairness and impartiality of genomic research.

Privacy protection is an important issue that needs to be addressed in genomics applications. Individual genetic information belongs to highly sensitive personal data, and once leaked or abused, it may cause serious physical and mental harm to the individual. Therefore, strict data protection measures need to be taken to ensure the security and privacy of genetic information. At the same time, it is necessary to formulate and improve relevant regulations at the legal and regulatory level, clarify the requirements for the collection, storage, use, and sharing of genetic information, and protect the legitimate rights and interests of individuals.

From a legal perspective, genomics involves the protection and utilization of individual genetic information, and corresponding laws and regulations need to be formulated to regulate it. For example, it is necessary to clarify the ownership, usage rights, and distribution of benefits of genetic information to avoid disputes and conflicts (Clayton et al., 2019). In addition, it is necessary to establish a sound regulatory mechanism to severely crack down on illegal and irregular behaviors, and ensure the legality and standardization of genomic research.

3.2 Technical challenges and limitations

The technical challenges and limitations faced in the application of genomics in the prevention of cardiovascular diseases mainly include the following aspects:

Although genome sequencing technology has made significant progress, there are still some technical challenges. Rego and Snyder (2018) found that high-throughput sequencing is not suitable for longer DNA sequences, and there are significant difficulties in handling chimeric genes and multicopy sequences. This means that scientists may encounter some technical obstacles when obtaining and analyzing genetic information related to cardiovascular diseases.

With the continuous advancement of technology, the amount of data generated by genome sequencing technology is also increasing, which poses great challenges to data processing and analysis. Thanassoulis et al. (2013) discussed hundreds of new genetic variations in heart disease and other cardiovascular diseases and their risk factors identified through large-scale genetic research over the past decade. Despite successfully identifying new genomic loci, genomic research has been criticized for its high cost, slow translation into clinical care, and many unfulfilled promises. At present, many institutions and laboratories are searching for more efficient and accurate data analysis methods to better solve the problems of gene sequencing data processing and analysis.

The application of genomics in medical research still faces technological and cost limitations. Katsanis et al. (2013) discussed the point that genomic technology is reaching, which can detect genetic variations in patients with high precision and reduced cost, potentially fundamentally changing medicine. However, despite these technological breakthroughs, the challenge of interpreting and processing large amounts of genomic data still exists. At present, the technology of genome sequencing is not mature enough, and the accuracy and reliability of sequencing need to be improved. In addition, the cost of genome sequencing remains high, which limits its widespread application in clinical practice.

Although genomics provides scientists with a wealth of genetic information about cardiovascular diseases, the occurrence and development of diseases are often the result of multiple factors working together, and genes are only a part of it. Therefore, when using genomics for disease prediction and diagnosis, it is necessary to approach the results with caution and avoid over interpretation and over treatment.

3.3 Future development direction and potential impact

The future development direction and potential impact of genomics in cardiovascular disease prevention are very broad. With the continuous progress and innovation of technology, we can expect more breakthroughs and achievements.

The future genome sequencing technology will be more efficient, precise, and cost-effective. This will make large-scale genome sequencing possible, providing stronger support for early screening, diagnosis, and prevention of cardiovascular diseases. By conducting in-depth research on the relationship between genes and cardiovascular disease, it is possible to more accurately predict disease risk and tailor prevention strategies for individuals.

The application of technologies such as artificial intelligence and machine learning in genomic data analysis will become increasingly widespread. Heil et al. (2021) analyzed the increasing integration of human genomics and its applications in biomedicine with artificial intelligence, as well as how these associated artificial intelligence methods are associated with causal knowledge needs in biomedical research and development and medical practice. Benes et al. (2018) summarized the progress and expected future directions of genomic medicine to improve cardiovascular risk reduction. Mendelian randomization and genome-wide association studies provide

important insights into the role of genetics in dyslipidemia and cardiovascular disease. These technologies can help scientists better process and analyze large amounts of genomic data, uncover more genetic information and potential value. By constructing predictive models and optimizing algorithms, the accuracy and reliability of genomics in cardiovascular disease prevention can be improved.

The integration of genomics with other omics such as transcriptomics and proteomics will also become an important direction in the future. Through the joint analysis of multiple omics data, a more comprehensive understanding of the pathogenesis and pathological processes of cardiovascular diseases can be obtained, providing deeper insights for the development of new treatment methods and drugs.

With the increasing application of genomics in the prevention of cardiovascular diseases, it is also necessary to pay attention to its impact on society and economy. Pasipoularides (2018) suggests that genomics may change the understanding and treatment of cardiovascular diseases, promoting personalized and precise healthcare services. At the same time, the development of genomics may also bring about ethical, privacy, and legal issues that require us to formulate corresponding norms and policies for management and guidance.

4 Suggestions and Outlook

Genomics plays an important role in the prevention of cardiovascular diseases. By utilizing advanced genomic technologies, individuals can more accurately assess their cardiovascular disease risk, providing strong support for developing personalized prevention strategies (Benes et al., 2018). In addition, genomics can guide personalized drug selection and dosage adjustment, as well as lifestyle interventions, in order to more effectively reduce the risk of cardiovascular disease.

In the process of using genomics for cardiovascular disease prevention, it is also necessary to face relevant ethical, privacy, and legal issues, as well as technological challenges and limitations. These issues require continuous research and exploration by scientists, establishing corresponding norms and mechanisms to ensure the safe, effective, and widespread application of genomics in cardiovascular disease prevention.

With the continuous progress and innovation of technology, the application prospects of genomics in the prevention of cardiovascular diseases are very broad. In the future, we can look forward to more efficient, accurate, and low-cost genome sequencing technology, as well as more advanced data analysis methods and algorithms, to provide more precise and personalized support for early screening, diagnosis, and prevention of cardiovascular diseases.

In addition, multi omics integration research will become an important direction in the future. Through the joint analysis of multi omics data, a more comprehensive understanding of the pathogenesis and pathological processes of cardiovascular diseases can be obtained (Joshi et al., 2020), providing deeper insights for the development of new treatment methods and drugs. At the same time, it is necessary to pay attention to the social and economic impact of genomics in the prevention of cardiovascular diseases, formulate corresponding policies and norms, and ensure that it makes greater contributions to the healthy development of society and humanity.

In summary, genomics has enormous potential and value in the prevention of cardiovascular diseases. Through continuous research and innovation, it is expected to better utilize genomics to prevent and treat cardiovascular diseases, and make greater contributions to the development of human health.

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