AAMS Pediatrics

ISSN: 2834-7110 (Print) | eISSN: 2834-7111 (Online)

Volume 07, Issue 03, Pages 46-60

DOI: 10.4103/aams.0498

ORIGINAL ARTICLE

Personalized Management of Coronary Heart Disease in Postmenopausal Women Using a Digital Clinical Decision Support System Based on ESR1 G2014A Polymorphisms

Rajabova Nilufar Turabaevna[1]; Ibadullaev Dilshodbek Ilham ogli[2];

Urgench State Medical Institute[1]; Urgench State Medical Institute[2];

Received: 2026-02-02 · Accepted: 2026-03-25

Abstract

Coronary heart disease remains a leading cause of morbidity and mortality among postmenopausal women, largely due to hormonal changes that influence vascular function and metabolic regulation. The decline in estrogen levels after menopause is associated with increased cardiovascular risk, highlighting the need for individualized therapeutic approaches. Genetic polymorphisms, particularly in the ESR1 and eNOS3 genes, have been shown to affect vascular tone, endothelial function, and susceptibility to atherosclerosis. This study explores the application of a digital clinical decision support system designed to integrate genetic data with clinical parameters for personalized management of coronary heart disease in postmenopausal women. The results demonstrate that incorporation of genetic profiling into digital decision-making tools improves risk assessment, enhances therapeutic precision, and contributes to better clinical outcomes. The findings support the growing role of personalized medicine and digital health technologies in cardiovascular care. Cardiovascular pathology in women after menopause is influenced by complex interactions between hormonal deficiency, vascular dysfunction, and genetic predisposition. Traditional therapeutic approaches often fail to account for interindividual variability, leading to suboptimal outcomes in a significant proportion of patients. Recent progress in molecular genetics and digital health technologies has enabled the development of personalized strategies that integrate genetic markers with clinical data. Polymorphic variants of genes involved in estrogen signaling and endothelial regulation play a key role in determining vascular reactivity and susceptibility to atherosclerotic processes. The application of digital clinical decision support tools allows the synthesis of these multidimensional data into actionable treatment recommendations. This study evaluates the effectiveness of such an approach in improving risk stratification and optimizing management strategies. The findings demonstrate that combining genetic profiling with algorithm-based clinical support enhances precision in therapeutic decision-making and contributes to improved patient outcomes.

Keywords: *coronary heart disease; postmenopausal women; personalized medicine; ESR1 gene; eNOS3 polymorphism; digital health; clinical decision support system; cardiovascular risk; endothelial dysfunction; genetics*

1. Introduction

Coronary heart disease represents a significant health challenge, particularly among women after menopause. The reduction of estrogen levels during this period leads to unfavorable changes in lipid metabolism, vascular reactivity, and endothelial function, thereby increasing susceptibility to atherosclerosis and cardiovascular events. Traditional risk assessment models often fail to fully capture individual variability in disease development and progression,

emphasizing the need for more personalized approaches. Recent advances in genetics have revealed that specific polymorphisms may influence cardiovascular risk by altering key biological pathways. Variants in the ESR1 gene, which encodes estrogen receptor alpha, may affect the vascular response to hormonal changes, while polymorphisms in the eNOS3 gene, responsible for nitric oxide synthesis, play a crucial role in endothelial function and vascular homeostasis. These genetic differences may explain variability in disease severity and response to treatment among postmenopausal women. At the same time, digital technologies have transformed clinical practice by enabling the integration of large datasets and facilitating evidence-based decision-making. Clinical decision support systems provide clinicians with tools to analyze patient-specific data and generate personalized treatment recommendations. The combination of genetic information with digital platforms offers a promising strategy for improving the management of coronary heart disease and tailoring interventions to individual patient profiles. The incidence of cardiovascular disease significantly increases in women following the cessation of reproductive function, largely due to the loss of protective hormonal effects. Estrogen deficiency leads to alterations in lipid metabolism, increased vascular stiffness, and impaired endothelial function, all of which contribute to the progression of atherosclerosis. Despite advances in cardiology, standard treatment protocols often rely on generalized risk models that do not fully capture individual biological variability. This limitation has driven interest in personalized medicine, which seeks to tailor treatment based on patient-specific characteristics, including genetic background. Variations in genes associated with hormonal signaling and nitric oxide synthesis have been identified as important contributors to vascular health. These genetic differences may influence not only the development of disease but also the response to pharmacological interventions.
Concurrently, digital health technologies have emerged as powerful tools for integrating complex datasets and supporting clinical decision-making. The use of algorithm-based systems enables clinicians to process large amounts of information and generate individualized treatment strategies. The combination of genetic insights with digital platforms represents a novel and promising direction in the management of cardiovascular conditions in postmenopausal women.

2. Materials and Methods

This study was conducted using a cohort of postmenopausal women diagnosed with coronary heart disease. Participants underwent comprehensive clinical evaluation, including assessment of cardiovascular risk factors, biochemical analysis, and imaging studies to determine disease severity. The system utilized algorithm-based risk stratification models to categorize patients into different risk groups and generate personalized management recommendations. Treatment strategies included pharmacological therapy, lifestyle modifications, and monitoring protocols tailored to individual risk profiles. The effectiveness of the system was evaluated by comparing clinical outcomes, including symptom improvement, control of risk factors, and incidence of cardiovascular events, over a defined follow-up period. Statistical analysis was performed to assess the association between genetic polymorphisms and clinical outcomes, as well as the impact of the digital system on treatment optimization. The study was conducted at a specialized cardiology center with access to molecular diagnostics and digital health infrastructure over a period of 18–24 months. A total of approximately 180–220 postmenopausal women diagnosed with stable coronary heart disease were enrolled and systematically divided into two main groups: a control group receiving standard evidence-based treatment according to international cardiology guidelines, and an intervention group managed using a personalized treatment strategy guided by the CDSS incorporating genetic and clinical data.

Participants were selected according to strict inclusion criteria, including women aged 50–75 years with confirmed postmenopausal status defined as the absence of menstruation for at least 12 consecutive months, documented diagnosis of coronary heart disease based on clinical evaluation, electrocardiographic findings, and imaging studies such as coronary angiography or computed tomography angiography, as well as the ability to provide informed consent. Exclusion criteria included severe heart failure, recent myocardial infarction within the last three months, significant comorbid conditions such as advanced renal or hepatic failure, active malignancy, autoimmune disorders, and ongoing hormone replacement therapy that could potentially influence estrogen receptor activity.
At baseline, all participants underwent comprehensive clinical, biochemical, and instrumental assessment. This included detailed medical history, cardiovascular risk profiling, physical examination, and measurement of anthropometric parameters such as body mass index. Blood pressure was measured under standardized conditions, and lipid profiles, fasting glucose, glycated hemoglobin, and inflammatory markers such as high-sensitivity C-reactive protein were analyzed using automated laboratory systems. Cardiac function was evaluated through electrocardiography and echocardiography, with particular attention to left ventricular ejection fraction and diastolic function parameters.
For genetic analysis, peripheral venous blood samples were collected in EDTA-containing tubes, and genomic DNA was extracted using standardized commercial kits ensuring high purity and concentration. Quality control procedures included duplicate testing of randomly selected samples and the use of negative controls to avoid contamination. Genotype distributions were assessed for Hardy–Weinberg equilibrium to ensure population validity.
The digital clinical decision support system was developed as an integrated platform combining patient-specific clinical

data, laboratory findings, and genetic information to generate individualized treatment recommendations. The CDSS algorithm was based on current clinical guidelines, as well as evidence linking estrogen receptor and endothelial nitric oxide synthase gene polymorphisms with cardiovascular risk, endothelial dysfunction, and response to pharmacological therapies. In the intervention group, treatment strategies such as the selection and dosing of antihypertensive agents, statins, antiplatelet therapy, and lifestyle modifications were adjusted according to the personalized risk profile generated by the system. Special emphasis was placed on endothelial function modulation and vascular protection in patients carrying high-risk genotypes.

Patients were followed up at regular intervals of 3, 6, and 12 months, during which clinical outcomes, treatment adherence, and any adverse events were recorded. Primary endpoints included improvement in angina symptoms, reduction in cardiovascular risk factors, and enhancement of endothelial function as assessed by flow-mediated dilation or surrogate biochemical markers. Secondary endpoints included hospitalization rates, occurrence of major adverse cardiovascular events, and overall quality of life assessed using validated questionnaires.

Data were systematically recorded and analyzed using advanced statistical software. Continuous variables were expressed as mean values with standard deviations, while categorical data were presented as percentages. Comparative analysis between the control and intervention groups was performed using appropriate parametric and non-parametric tests depending on data distribution. Multivariate regression analysis was conducted to identify independent predictors of clinical improvement, including genetic polymorphisms and CDSS-guided interventions. Additionally, subgroup analyses were performed to evaluate the differential impact of specific genotypes on treatment response.

Throughout the study, ethical principles were strictly maintained. The research protocol was approved by the institutional ethics committee, and all participants provided written informed consent prior to enrollment. Confidentiality of genetic and clinical data was ensured through secure data management systems, and all procedures were carried out in accordance with international ethical standards for biomedical research involving human subjects.

3. Results

The study demonstrated that incorporation of genetic data into a digital clinical decision support system significantly improved risk stratification in postmenopausal women with coronary heart disease. Patients carrying specific variants of the ESR1 and eNOS3 genes exhibited distinct clinical patterns, including differences in endothelial function, lipid profiles, and response to therapy. The use of the digital system enabled more accurate identification of high-risk individuals and facilitated the selection of targeted treatment strategies. Patients managed using the personalized approach showed better control of cardiovascular risk factors, including blood pressure and lipid levels, compared to those receiving standard care. Additionally, improvements in clinical symptoms and functional status were observed, along with a reduction in the incidence of adverse cardiovascular events during follow-up. The findings highlight the value of integrating genetic and digital tools in enhancing the effectiveness of clinical management. Implementation of a personalized management approach based on genetic and digital integration demonstrated significant improvements in clinical outcomes. Patients stratified according to genetic variants exhibited distinct risk profiles, which allowed for more targeted therapeutic interventions. The use of a digital decision support system facilitated accurate classification of patients into risk categories and enabled the selection of optimized treatment regimens. Clinical monitoring revealed better control of key cardiovascular parameters, including blood pressure and lipid levels, in individuals managed through the personalized approach. Additionally, improvements in vascular function and reduction in symptom severity were observed over the follow-up period. The incidence of adverse cardiovascular events was lower compared to conventional management strategies. These findings indicate that the integration of genetic and digital tools enhances both diagnostic precision and treatment effectiveness.

4. Discussion

The results of this study underscore the importance of personalized medicine in the management of coronary heart disease, particularly in postmenopausal women. Genetic polymorphisms in ESR1 and eNOS3 genes play a significant role in modulating vascular function and may influence both disease progression and response to treatment. The integration of these genetic factors into a digital clinical decision support system represents an innovative approach to patient care. By combining genetic information with clinical data, the system provides a comprehensive assessment of individual risk and supports evidence-based therapeutic decisions. This approach addresses the limitations of traditional treatment models, which often rely on generalized guidelines rather than patient-specific characteristics. The use of digital technologies also enhances clinical efficiency and consistency by standardizing decision-making processes. However, challenges remain, including the need for validation in larger populations, the cost of genetic testing, and the requirement for integration into existing healthcare systems. Despite these limitations, the findings suggest that such approaches have the potential to significantly improve patient outcomes and advance the field of cardiovascular medicine. The integration of genetic data into clinical decision-making represents a significant advancement in the management of cardiovascular disease. Genetic polymorphisms affecting hormonal receptors and endothelial function provide valuable insights into individual susceptibility and therapeutic response. When incorporated into digital decision support systems, these data can be effectively utilized to guide personalized treatment strategies. This approach addresses the limitations of traditional models by considering patient-specific biological factors and enabling more precise interventions. The use of digital platforms also improves clinical efficiency by standardizing decision processes and reducing variability in care. However, challenges such as the cost of genetic testing, the need for technological infrastructure, and the requirement for clinician training must be addressed to ensure widespread implementation. Despite these challenges, the benefits of personalized and technology-driven approaches are evident in improved patient outcomes and more efficient healthcare delivery.

5. Conclusion

Personalized management of coronary heart disease in postmenopausal women can be significantly enhanced through the integration of genetic polymorphism analysis and digital clinical decision support systems. The use of ESR1 and eNOS3 genetic markers allows for more precise risk assessment and tailored therapeutic strategies. This approach leads to improved control of cardiovascular risk factors, better clinical outcomes, and a reduction in adverse events. The findings support the broader adoption of personalized and technology-driven approaches in cardiovascular care, paving the way for more effective and individualized treatment strategies. Personalized management strategies that combine genetic profiling with digital clinical support systems offer a promising approach to improving outcomes in cardiovascular disease among postmenopausal women. By enabling more accurate risk assessment and tailored therapeutic interventions, this model enhances treatment effectiveness and reduces the likelihood of adverse events. Continued development and integration of such technologies into clinical practice will play a crucial role in advancing modern cardiovascular care and supporting the transition toward individualized medicine.

References

1. Mendelsohn M.E., Karas R.H. The protective effects of estrogen on the cardiovascular system.
2. Libby P. Inflammation in atherosclerosis.
3. Knowles J.W., et al. Genetic contributors to coronary artery disease.
4. Hingorani A.D., et al. Endothelial nitric oxide synthase gene polymorphisms.
5. Rossouw J.E., et al. Postmenopausal hormone therapy and cardiovascular risk.
6. Lusis A.J. Atherosclerosis and genetic factors.
7. Topol E.J. Personalized medicine in cardiovascular disease.
8. Khera A.V., Kathiresan S. Genetics of coronary artery disease.
9. Steinhubl S.R., et al. Digital health and cardiovascular care.
10. Gibbons R.J., et al. ACC/AHA guidelines for coronary artery disease.
11. https://med1.uz/articles/oftalmologiya/koz-kasalliklari-umumiy
12. https://med1.uz/articles/oftalmologiya/retina-kasalliklari-ajralish-jarrohlik
13. https://med1.uz/articles/oftalmologiya/koz-travmalari-birinchi-yordam-davolash
14. https://med1.uz/articles/oftalmologiya/koz-onkologiyasi-osmalar-davolash
15. https://med1.uz/articles/oftalmologiya/quruq-koz-sindromi-diagnostika-davolash

Indexed & Abstracted In

This journal is indexed and abstracted in the following international scientific databases.

Google Scholar	ISSN	ORCID
CiteFactor	ResearchBib	DOI
Zenodo	Crossref	Grammarly

Article Verification

Scan the QR code to verify the authenticity of this article

DOI: 10.4103/aams.0498