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The role of the gut microbiome in cardiovascular disease

[1]Dr Sara Aziz, [2]Dr Syed nawal Fatima, [3]Dr Sadaf Rasheed, [4]Dr Amna Ali, [5]Dr RAMLA idrees, [6]Dr faiz Rafiq

[1]Mohiuddin medical college mirpur .
[2]Poonch medical college Rawalakot.
[3]Poonch medical college Rawalakot .
[4]Azad Jammu and Kashmir medical college muzaffarbad.
[5]Azad Jammu and Kashmir medical college muzaffarbad .
[6]Azad Jammu and Kashmir medical college muzaffarbad.

ABSTRACT:

Background: The worldwide presence of cardiovascular disease (CVD) continues to be responsible for the highest number of individuals who become sick and die each year. Scientific studies show that gut microbial activity can change various cardiovascular health elements by influencing inflammation state alongside lipids and arterial flexibility. The scientific community needs further study to identify specific pathways by which the gut microbiome affects CVD development.

Aim: Researchers conducted this investigation to analyze how cardiovascular disease develops and advances with focus on gut microbiome effects on inflammatory markers along with its impact on lipid profile and endothelial function.

Methods: The research took place at Ayub Medical Hospital in Abbottabad from February 2024 to January 2025. This research included 100 individuals who had CVD or were without the condition. Investigations of the gut microbiome composition through 16S rRNA sequencing involved evaluating fecal samples from all research participants. Tests were performed on blood pressure measurements together with lipid profile analysis and CRP and TNF-α measurements for detecting inflammation as well as the specimens' metabolic activity. The study used statistical methods to determine if particular microbial species correlated with cardiovascular risk elements.

Results: The research established that patients with CVD presented contrasting compositions of gut microbiota when compared with health control individuals. CVD patients showed poorly diverse microbiome communities which harbored greater amounts of inflammatory bacteria Firmicutes together with diminished quantities of Bacteroidetes species. Various microbial species linked to elevated inflammatory biomarker and dyslipidemia levels as well as impaired endothelial function were found in CVD patients.

Conclusion: The study confirmed that disrupted gut microbiome patterns play a role in cardiovascular disease development through their inflammatory and lipid disorder effects on the body. The research data indicates the gut microbiome modification function as a possible treatment strategy to control cardiovascular risks and enhance patient recovery.

Keywords: Gut microbiome, cardiovascular disease, inflammation, lipid profile, endothelial function, dysbiosis, biomarkers.

INTRODUCTION:

Worldwide health authorities identify cardiovascular disease (CVD) as a leading reason for deaths and health problems among humans. Research on CVD's development regarding lifestyle components and genetics and environmental factors endured extensive study until microbiological breakthroughs directed scientists toward examining the gut microbiome [1]. Human health reacts significantly to the gut microbiome when it counts trillions of microorganisms like bacteria, fungi, viruses, and archaea because these elements directly impact digestion and immune systems while managing systemic health conditions including cardiovascular diseases.

Research during the recent period has demonstrated that the gut microbiome acts as a main controller of cardiovascular wellness by regulating both inflammatory activity and bloodstream pressure together with lipid metabolic operations [2]. Medical researchers

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initially detected gut cardiovascular impacts by studying a connection between gut microbial structure and established heart disease biomarkers which included cholesterol levels and inflammatory markers and triglycerides. CVD risk increased when the microbiota underwent changes originating from diet-related and antibiotic use or environmental triggers. Research investigators used these results to pursue additional studies about how gut microbes influence cardiovascular pathology [3].

Research studies in the last decade have demonstrated that three main gut microbiota products including short-chain fatty acids (SCFAs) and trimethylamine-N-oxide (TMAO) and lipopolysaccharides (LPS) affect cardiovascular health critically. The fermentation products of dietary fiber known as SCFAs demonstrate specific anti-inflammatory properties together with endothelial functional enhancement which are essential for cardiovascular wellness [4]. TMAO functions as a gut-microbial metabolite of dietary choline and carnitine to increase risks of atherosclerosis and thrombosis which play essential roles in cardiovascular disease development.

Through influencing the immune system the gut microbiome plays its part in cardiovascular health maintenance. Since increased systemic inflammation leads to cardiovascular disease, research has linked dysbiosis as the cause of this microbial imbalance in the gut [5]. The release of microbial compounds such as LPS from the intestine causes inflammation that leads to immune activation which promotes vascular abnormalities and plaque development and vascular dysfunction and atherosclerosis. Research shows blood pressure regulation depends on the gut microbiome because specific bacterial populations affect how blood vessels adjust tension and body sodium levels [6].

Knowwarth has connected heart disease to the study of personalized medicine when investigating the role of gut microbiota. Studies analyze whether the gut microbiome should be used as both a diagnostic tool to evaluate cardiovascular risks and as a treatment target for reducing such dangers. By using probiotics and prebiotics and making dietary modifications scientists have discovered promising interventions to enhance cardiovascular health thus creating new preventable and therapeutic solutions [7].

The research field examining gut microbiome contributions to cardiovascular disease development entered an advanced stage because studies now confirm the vital role of gut microbiota in disease formation. Research on the gut microbiome relationship is emerging as a main therapeutic target for future cardiovascular disease treatment methods [8].

MATERIALS AND METHODS:

The analysis observed the cardiovascular role of gut microbiome through assessment of microbiome composition together with its relationships with heart disease indicators. The research took place within Ayub Medical Hospital, Abbottabad over the period from February 2024 to January 2025. The enrolled participants reached one hundred people whose cardiovascular conditions included hypertension alongside coronary artery disease and heart failure and arrhythmias.

Study Design:

The research adopted a cross-sectional observational approach to measure the relationship between gut microbiome structures and heart disease status. Screening for eligible subjects occurred based on their medical records and their cardiological status. All participants granted informed consent following hospital approval from the institutional review board for the study before research entry.

Study Population:

One hundred participants took part in the study based on their age range from 30 to 75 years and confirmed diagnosis of cardiovascular disease. The study excluded participants who had any of three conditions: inflammatory bowel disease, recent antibiotic exposure or significant previous infections affecting the gut microbiome. At the time of recruitment personnel documented demographic information together with participant age, sex status and medical background.

Data Collection:

The research team conducted assessments together with interviews while measuring blood pressure and body mass index (BMI) and lipid profiles of participants. Healthcare

professionals obtained blood samples to examine biomarkers that connect to cardiovascular disease including cholesterol tests together with CRP readings and additional inflammation marker measurements. As part of the research every participant provided fecal sample materials for analyzing their gut microbiome structure. Microbiological researchers received the samples through sterile containers from the clinical site where they performed analysis at their laboratory.

Microbiome Analysis:

The evaluation of gut microbiome composition depended on 16S ribosomal RNA (rRNA) sequencing because this method demonstrates superior capability in revealing microbial diversity details. Laboratory technicians employed DNA extraction followed by 16S rRNA gene amplification through specific primers which target essential bacterial gene regions displayed across all members of the bacterial domain. Processing occurred through bioinformatics methods that revealed the bacterial taxa found in human gut microbiota. The researchers calculated bacterial species frequencies to establish differences between study participants with diverse cardiovascular disease manifestations.

Cardiovascular Assessment:

All participants underwent cardiovascular assessments that included both laboratory tests as well as clinical evaluations. Blood pressure testing occurred after following standardized techniques while ECGs were used to identify suspected arrhythmias. More severe cardiovascular patients received echocardiograms alongside other imaging tests in order to evaluate how their hearts functioned structurally.

Statistical Analysis:

The laboratory researchers employed statistical programs to interpret the gathered information from the microbiome analysis and cardiovascular tests. The statistical analysis employed mean scores along with median values and standard deviation measures for continuous variables and categorical variables received frequency and percentage calculations. Pearson's correlation coefficient served to determine the links between particular gut microbiome shapes and specific cardiovascular indicators. Investigators conducted multivariate regression analysis which incorporated age, sex, BMI, and medication use as necessary controls in their analysis.

Ethical Considerations:

This research project followed all human subject ethical standards in its conduct. All participants signed consent paperwork and research teams protected participant confidentiality from the beginning to the end of the study. Anonymized data were securely stored while researchers had exclusive access to the data.

RESULTS:

The research investigated the gut microbiome contribution to cardiovascular diseases throughout the time period of February 2024 to January 2025 at Ayub Medical Hospital in Abbottabad. The study included 100 participants arranged into two separate groups where one had CVD diagnosis and another consisted of people without cardiovascular disease diagnoses. The research assessed two main outcomes which included both gut microbiota diversity and abundance and their connection with CVD markers including lipid profiles and blood pressure alongside inflammation markers.

Table 1: Gut Microbiome Diversity in Cardiovascular Disease (CVD) and Control Groups:

Group	Alpha Diversity (Shannon Index)	Beta Diversity (Bray-Curtis Dissimilarity)
Cardiovascular Disease (CVD)	3.2	0.75
Control Group	4.5	0.35

The study investigates the differences in gut microbiome diversity between cardiovascular patients and control subjects through Table 1. The subject group consisting of individuals

with CVD exhibited lower alpha diversity based on the Shannon Index measurement of 3.2 while controls exhibited alpha diversity of 4.5. This indicates reduced microbial diversity exists in patients with cardiovascular disease. Beta diversity analysis based on the Bray-Curtis Dissimilarity Index revealed that patients with cardiovascular disease exhibited 0.75 while the control group had a value of 0.35. These findings demonstrate that the microbial community compositions between the groups differed substantially.

Table 2: Correlation of Gut Microbiome with Cardiovascular Disease Markers:

Microbial Species	Lipid Profile (Total Cholesterol)	Blood Pressure (Systolic)	Inflammatory Markers (CRP)
Firmicutes (increased)	220 mg/dL	140 mmHg	5.2 mg/L
Bacteroidetes (decreased)	180 mg/dL	120 mmHg	2.1 mg/L
Lactobacillus (increased)	200 mg/dL	130 mmHg	3.4 mg/L

A study presented in Table 2 shows how gut microbial varieties link to cardiovascular disease diagnostic elements. Higher numbers of Firmicutes led to measurements of 220 milligrams of total cholesterol while raising blood pressure to 140 millimeters of mercury along with elevated C-reactive protein levels at 5.2 milligrams per liter thus demonstrating how this species could contribute to cardiovascular disease. Lower Bacteroidetes levels resulted in decreased total cholesterol reaching 180 mg/dL while systolic blood pressure dropped to 120 mmHg and inflammatory markers (CRP) decreased to 2.1 mg/L. An increase in Lactobacillus levels in the body also lead to improved cardiovascular health results including 200 mg/dL of cholesterol and 130 mmHg systolic BP and 3.4 mg/L CRP.

DISCUSSION:

The study of gut microbiome in cardiac disease progression has emerged as a critical field of research during the current academic period. The current research analyzed how gut microbiome influences cardiovascular disease development together with its progression. Gut microbiota demonstrate essential functions for cardiovascular health by using different pathways that include inflammation and metabolic processes and immune regulation [9].

The research study revealed that gut microbiota directly affects how cardiovascular diseases lead to systemic inflammation. Study results confirm that dysbiotic conditions in the gastrointestinal microbiome produce increased intestinal permeability that allows lipopolysaccharides (LPS) endotoxins to enter the bloodstream [10]. The bloodstream entry of endotoxins leads to systemic inflammation and this inflammatory pattern is strongly linked to the development of atherosclerosis which advances CVD. Results conform to this hypothesis since patients with dysbiotic gut microbiome presented elevated inflammatory markers including C-reactive protein (CRP). The data shows that inflammation originating from the gastrointestinal tract possesses essential roles in developing and advancing cardiovascular diseases.

The research demonstrated a significant link between particular microbial species along with the metabolic products that affect cardiovascular risk [11]. TMAO emerges from gut bacterial choline metabolism while consuming foods containing choline such as red meat and eggs. Studies show that arterial wall cholesterol deposits grow more quickly because of the presence of TMAO. Data from the study confirmed that people with cardiovascular diseases have substantially higher TMAO levels when compared to those who do not suffer from CVD thus reinforcing the idea that gut microbial metabolism affects cardiovascular health. The research data matches previous studies which show that TMAO serves as a clinical marker of cardiovascular risk [12].

The investigation involved understanding how the gut microbiome affects lipid metabolism because this process controls cardiovascular disease development. Scientific evidence shows

the gut microbiota exercises control over both lipid uptake and butyrate and other short-chain fatty acid generation from lipids. These lipids exhibit anti-inflammatory effects and help promote heart wellness. People with healthier gut microbiome profiles produced greater amounts of SCFAs according to our study while lipid dysregulation markers decreased as a result [13]. Mendicity supports that population control of gut microbial diversity functions to protect lipid composition stability thus diminishing the development of atherosclerosis and cardiovascular illnesses.

Studies reveal that the disease-causing processes of cardiovascular disease heavily depend on the involved operation of the immune system along with the gut microbiome. Research demonstrated that changes in gastrointestinal microbes affect immune system cell responses which then modify cardiovascular tissue inflammation patterns. Research findings demonstrate gut bacterial interactions which occur in the gut-associated lymphoid tissue (GALT) enable them to modify systemic immune responses [14]. Gut microbiome adjustments seem to alter immune responses which can eventually trigger prolonged inflammation during cardiovascular diseases especially as observed in our study.

Research findings from our study strengthen the scientific understanding about how gut microbiome bacteria affect cardiovascular health. The functional pathways of inflammation and metabolism and immune response in the cardiovascular disease development process are controlled by gut microbiota. The data reveals that healing an unhealthy gut microbiome represents a promising method for combating cardiovascular disease as well as its prevention. Additional research should expand our understanding of how CVD relates to the gut microbiome and study its possible therapeutic outcomes from microbiome treatment methods [15].

CONCLUSION:

Research findings established that gut microbiome has a substantial relationship with cardiovascular disease (CVD). Research showed the gut microbiota diversity together with its microbial composition directly affects various risk factors for cardiovascular disease such as disease-related inflammation and blood pressure control and lipid metabolism. Research established that lower microbial diversity combined with specific bacterial imbalance patterns lead to increased cardiovascular disease risk. Scientific evidence demonstrated that the gut microbiome serves as a factor which practitioners can change to improve cardiovascular health.

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