KMANPUB | Health Nexus Vol. 4 No. 4 (2026): 1-9

Article history:
Received 10 May 2026
Revised 21 May 2026
Accepted 10 June 2026
Initial Publication 31 July 2026
Final Publication 01 October 2026

Aerobic Interval Training and Probiotic Supplementation Modulate Intrinsic Apoptosis-Related Gene Expression in the Myocardium of Rats with Myocardial Infarction

Sayed Touraj Miri Reykandeh[1], Elham Eftekhari Gheinani[1*], Jamshid Banaei Borojeni[1]

1. Department of Sport Sciences, Na.C., Islamic Azad University, NajafAbad, Iran

*** Corresponding author email address:** Elhameftekhari@iau.ac.ir

A r t i c l e I n f o

Article type:
Original Research

How to cite this article:
Miri Reykandeh, S. T., Eftekhari Gheinani, E., & Banaei Borojeni, J. (2026). Aerobic Interval Training and Probiotic Supplementation Modulate Intrinsic Apoptosis-Related Gene Expression in the Myocardium of Rats with Myocardial Infarction. *Health Nexus, 4*(4), 1-9.
https://doi.org/10.61838/kman.hn.5842

A B S T R A C T

Myocardial infarction (MI) promotes mitochondrial dysfunction, oxidative stress, and cardiomyocyte loss, partly through activation of the intrinsic apoptotic pathway. Exercise training and probiotics may each influence these processes, but evidence concerning their combined effects is limited. This controlled animal study examined the effects of aerobic interval training (AIT), Lactobacillus acidophilus supplementation, and their combination on myocardial expression of Apaf1, Bax, Bcl2, Casp9, and Casp3 and on the Bax/Bcl2 expression ratio. Forty-eight male Wistar rats (250 ± 30 g) were allocated to six groups (n = 8 each): healthy control, sham surgery, MI, MI + AIT, MI + probiotic, and MI + AIT + probiotic. MI was induced by permanent ligation of the left anterior descending coronary artery. The interventions continued for 10 weeks; AIT was performed five sessions per week, and the probiotic was administered daily at 10^9 colony-forming units/mL. Left ventricular tissue was collected 48 h after the final intervention. Relative mRNA expression was quantified by real-time polymerase chain reaction and analyzed using one-way analysis of variance followed by Tukey testing. Significant group effects were detected for all outcomes ($P < 0.001$; $\eta^2 = 0.79–0.89$). Compared with healthy controls, MI increased Apaf1, Bax, Casp9, and Casp3 expression, reduced Bcl2 expression, and markedly increased the Bax/Bcl2 ratio. Both interventions attenuated these changes. The combined intervention produced the values closest to control levels, reducing Apaf1, Bax, Casp9, Casp3, and the Bax/Bcl2 ratio by approximately 62%, 63%, 62%, 63%, and 87%, respectively, relative to untreated MI, while increasing Bcl2 expression. These findings indicate that AIT and probiotic supplementation, particularly when combined, are associated with a less pro-apoptotic myocardial gene-expression profile after experimental MI. Because only mRNA outcomes were assessed, protein-level, functional, and clinical confirmation is required.

Keywords: *myocardial infarction; aerobic interval training; probiotic; intrinsic apoptosis; Bax/Bcl2 ratio; Wistar rat*

1. Introduction

Myocardial infarction remains a major cause of irreversible cardiomyocyte loss and subsequent ventricular dysfunction. Interruption of coronary blood flow rapidly reduces oxygen and substrate delivery, impairs adenosine triphosphate production, disrupts ion homeostasis, and initiates inflammatory and oxidative responses. The injury is not limited to the initial ischemic region. Mitochondrial dysfunction, reactive oxygen species accumulation, calcium imbalance, and altered cell-death signaling can expand tissue damage and contribute to adverse left ventricular remodeling. Apoptosis has therefore been identified as one of the mechanisms linking acute ischemic injury to progressive structural and functional deterioration after MI (1, 2).

The intrinsic apoptotic pathway is closely regulated by mitochondrial membrane integrity. Within the B-cell lymphoma-2 family, Bax promotes mitochondrial outer-membrane permeabilization, whereas Bcl2 opposes this process. An increase in Bax relative to Bcl2 favors cytochrome-c release and formation of the apoptosome. Apoptotic protease-activating factor 1 (Apaf1) then recruits and activates initiator caspase-9, which contributes to activation of executioner caspase-3. The Bax/Bcl2 ratio is commonly interpreted as an index of the balance between pro- and anti-apoptotic signaling, although transcript abundance does not necessarily correspond to protein activity or completed cell death. Accordingly, simultaneous assessment of Apaf1, Bax, Bcl2, Casp9, and Casp3 can provide a molecular profile of the intrinsic pathway, but such findings require confirmation using protein expression, caspase activity, and tissue-level apoptosis assays (3-5).

Exercise is a potentially useful nonpharmacological strategy for limiting secondary cardiac injury. Appropriately prescribed aerobic interval training can improve oxidative capacity, endothelial function, antioxidant defense, and mitochondrial quality control. In experimental MI, interval training has been associated with improved mitochondrial network dynamics and reduced myocardial oxidative and apoptotic disturbances (6, 7). Exercise-related adaptations may reduce the mitochondrial signals that favor Bax activation and caspase recruitment, thereby shifting the cellular environment toward survival. Nevertheless, exercise after MI is highly dependent on timing, intensity, progression, and clinical stability. Findings from animal models cannot be translated into unsupervised recommendations for human patients.

The gut–heart axis provides a complementary biological target. Intestinal microorganisms and their metabolites can influence systemic inflammation, oxidative status, vascular function, and myocardial responses to ischemic injury. Probiotic supplementation may modify these signals by supporting intestinal barrier integrity and altering microbial metabolic activity. Experimental work has reported that probiotic or Lactobacillus-based interventions can reduce inflammatory and oxidative injury and modify apoptosis-related markers in cardiometabolic and ischemic conditions (8-10). However, effects are strain-specific and dose-dependent; the term probiotic should not be treated as a uniform intervention.

Exercise and probiotics may influence partly distinct but interacting processes. Exercise primarily induces systemic and myocardial adaptations through repeated metabolic and mechanical stimuli, whereas probiotics may operate through intestinal, immune, and metabolic pathways. A combined intervention could therefore produce a broader response than either strategy alone. Previous studies have generally examined exercise or probiotics separately, and relatively little evidence is available regarding their concurrent influence on the mitochondrial apoptosis-related gene network after MI. The present study addressed this gap by examining AIT, L. acidophilus supplementation, and their combination in a rat model of permanent coronary artery occlusion. The primary objective was to compare relative myocardial mRNA expression of Apaf1, Bax, Bcl2, Casp9, and Casp3 and the Bax/Bcl2 ratio across healthy, sham, untreated MI, and intervention groups. It was hypothesized that MI would produce a pro-apoptotic expression profile and that both interventions would attenuate this pattern, with the combined condition showing the greatest overall modulation.

2. Methods and Materials

2.1. Study Design and Ethical Approval

This controlled post-test animal experiment used 48 male Wistar rats. The study was approved by the Research Ethics Committee of the Najafabad Branch, Islamic Azad

Health Nexus
E-ISSN: 2981-2569

University (IR.IAU.NAJAFABAD.REC.1405.097). The work was conducted under institutional animal-care requirements, with attention to minimizing pain, stress, and unnecessary animal use. Reporting was prepared with reference to the ARRIVE 2.0 recommendations and the principles of the Guide for the Care and Use of Laboratory Animals (11, 12).

2.2. *Animals, Housing, and Experimental Groups*

The rats weighed approximately 250 ± 30 g and were housed under controlled laboratory conditions at 22 ± 2 °C, 50%–60% relative humidity, and a 12-h light/12-h dark cycle. An acclimation period was provided before experimental procedures. Animals were allocated to six groups (n = 8 per group): healthy control, sham surgery, MI, MI + AIT, MI + probiotic, and MI + AIT + probiotic. The healthy control group did not undergo thoracotomy or coronary ligation. The sham group underwent the operative procedures without coronary occlusion. The remaining four groups underwent MI induction before the assigned intervention.

2.3. *Induction of Myocardial Infarction*

MI was induced through permanent ligation of the left anterior descending coronary artery. Rats were anesthetized with ketamine and xylazine, thoracotomy was performed, and the coronary artery was tied using nonabsorbable suture material. Successful local ischemia was judged intraoperatively from reduced perfusion and color change in the anterior left ventricular region. Sham-operated animals underwent the same surgical exposure without ligation. Animals were monitored during postoperative recovery before beginning the intervention phase.

2.4. *Aerobic Interval Training*

Before formal training, rats assigned to exercise were familiarized with treadmill running and completed an incremental performance assessment. Exercise intensity was prescribed relative to the measured maximal capacity and progressed across the 10-week program. Training was performed five days per week. Each session consisted of repeated moderate-to-vigorous running intervals separated by active-recovery periods. This structure was selected to provide repeated cardiovascular stimulation while allowing recovery between work bouts, consistent with interval-training approaches used in experimental post-MI research (6, 7).

2.5. *Probiotic Supplementation*

The probiotic intervention contained a standardized L. acidophilus preparation at a concentration of 10^9 colony-forming units/mL. It was administered daily at a consistent time for 10 weeks to the MI + probiotic and MI + AIT + probiotic groups. Control groups did not receive the active probiotic intervention. The protocol was intended to influence gut–heart signaling and systemic inflammatory or oxidative processes that may contribute to myocardial injury.

2.6. *Tissue Collection*

Forty-eight hours after the final exercise or supplementation exposure, animals were deeply anesthetized and euthanized. Hearts were rapidly excised, and left ventricular tissue was separated, frozen in liquid nitrogen, and stored at −80 °C until molecular analysis. The 48-h interval was used to reduce the influence of the immediate acute response to the final exercise session and to emphasize the accumulated intervention effect.

2.7. *RNA Extraction and Real-Time PCR*

Total RNA was extracted from left ventricular tissue, and RNA quality and concentration were assessed using spectrophotometric and electrophoretic procedures. Complementary DNA was synthesized by reverse transcription. Real-time polymerase chain reaction was used to quantify relative mRNA expression of Apaf1, Bax, Bcl2, Casp9, and Casp3. Relative expression was calculated using the 2^−ΔΔCt method after normalization to an internal reference transcript. The Bax/Bcl2 ratio was calculated from the relative expression values. All reported molecular outcomes therefore represent transcript-level measurements rather than protein abundance or enzyme activity.

2.8. *Statistical Analysis*

Data were analyzed using SPSS version 26 and are presented as mean ± standard deviation. Normality was

Health Nexus
E-ISSN: 2981-2569

evaluated with the Shapiro–Wilk test, and homogeneity of variance was assessed with Levene's test. Each outcome was compared across the six independent groups using one-way analysis of variance, followed by Tukey's post hoc procedure when the omnibus test was significant. Statistical significance was set at $P < 0.05$. Eta squared (η^2) was reported as the omnibus effect-size estimate. Because the design included healthy and sham reference groups in addition to the four MI-related conditions, the reported one-way analysis establishes group differences but does not formally test an exercise-by-probiotic interaction. Consequently, the combined condition is described as producing the greatest observed modulation, rather than as proving statistical synergy.

3. Findings and Results

The analysis included 48 animals, with eight rats in each group. The normality and homogeneity assumptions for parametric analysis were satisfied. The sham group remained close to the healthy control group across the measured transcripts, whereas the untreated MI group showed a pronounced shift toward a pro-apoptotic expression profile.

The omnibus group effect was significant for Apaf1 ($F(5, 42) = 48.72$, $P < 0.001$, $\eta^2 = 0.85$), Bax ($F(5, 42) = 55.34$, $P < 0.001$, $\eta^2 = 0.87$), Bcl2 ($F(5, 42) = 32.18$, $P < 0.001$, $\eta^2 = 0.79$), the Bax/Bcl2 ratio ($F(5, 42) = 64.51$, $P < 0.001$, $\eta^2 = 0.89$), Casp9 ($F(5, 42) = 46.85$, $P < 0.001$, $\eta^2 = 0.84$), and Casp3 ($F(5, 42) = 52.40$, $P < 0.001$, $\eta^2 = 0.86$). These values indicate large between-group effects for all molecular outcomes, with the largest effect observed for the Bax/Bcl2 ratio.

Table 1

Relative myocardial mRNA expression and Bax/Bcl2 ratio across experimental groups

Group	Apaf1	Bax	Bcl2	Bax/Bcl2	Casp9	Casp3
Healthy control	1.00 ± 0.12	1.00 ± 0.15	1.00 ± 0.13	1.00 ± 0.14	1.00 ± 0.16	1.00 ± 0.15
Sham	1.08 ± 0.18	1.12 ± 0.20	0.95 ± 0.12	1.17 ± 0.19	1.10 ± 0.18	1.15 ± 0.21
MI	3.85 ± 0.52	4.20 ± 0.61	0.42 ± 0.09	10.00 ± 1.45	3.75 ± 0.48	4.05 ± 0.55
MI + AIT	2.10 ± 0.34	2.20 ± 0.39	0.82 ± 0.13	2.68 ± 0.42	2.05 ± 0.31	2.15 ± 0.37
MI + probiotic	2.45 ± 0.41	2.55 ± 0.44	0.74 ± 0.11	3.44 ± 0.53	2.35 ± 0.40	2.50 ± 0.43
MI + AIT + probiotic	1.45 ± 0.25	1.55 ± 0.28	1.15 ± 0.18	1.35 ± 0.24	1.42 ± 0.22	1.50 ± 0.27

Values are mean ± standard deviation (n = 8 per group) and are expressed as fold change. AIT, aerobic interval training; MI, myocardial infarction.

Table 2

One-way analysis of variance for myocardial gene-expression outcomes

Outcome	F(5, 42)	P	η^2
Apaf1	48.72	< 0.001	0.85
Bax	55.34	< 0.001	0.87
Bcl2	32.18	< 0.001	0.79
Bax/Bcl2	64.51	< 0.001	0.89
Casp9	46.85	< 0.001	0.84
Casp3	52.40	< 0.001	0.86

All omnibus tests used six groups and had 5 and 42 degrees of freedom for the between-group and residual terms, respectively.

Relative to the healthy control mean, untreated MI was associated with approximately 3.85-fold Apaf1, 4.20-fold Bax, 3.75-fold Casp9, and 4.05-fold Casp3 expression. Bcl2 decreased to 0.42-fold, while the Bax/Bcl2 ratio increased to 10.00. This coordinated pattern is compatible with increased mitochondrial pro-apoptotic signaling at the transcript level.

Both AIT and probiotic supplementation shifted the outcomes toward control values. In the MI + AIT group, Apaf1, Bax, Casp9, and Casp3 values were 2.10, 2.20, 2.05, and 2.15, respectively; Bcl2 increased to 0.82, and the Bax/Bcl2 ratio fell to 2.68. In the MI + probiotic group, the corresponding values were 2.45, 2.55, 2.35, 2.50, 0.74, and

Health Nexus
E-ISSN: 2981-2569

3.44. The AIT group therefore showed slightly lower pro-apoptotic transcript means than the probiotic group, while both interventions produced a clear shift toward the healthy-control profile.

The combined group showed the most favorable observed molecular profile. Compared with untreated MI, Apaf1 decreased by 62.3%, Bax by 63.1%, Casp9 by 62.1%, Casp3 by 63.0%, and the Bax/Bcl2 ratio by 86.5%; Bcl2 increased from 0.42 to 1.15, corresponding to a 173.8% increase relative to the MI mean. The combined-group means were close to those of the healthy and sham groups, although not identical for every outcome.

Figure 1

Relative myocardial expression of pro-apoptotic pathway genes across groups. Bars show mean ± standard deviation (n = 8 per group). AIT, aerobic interval training; MI, myocardial infarction.

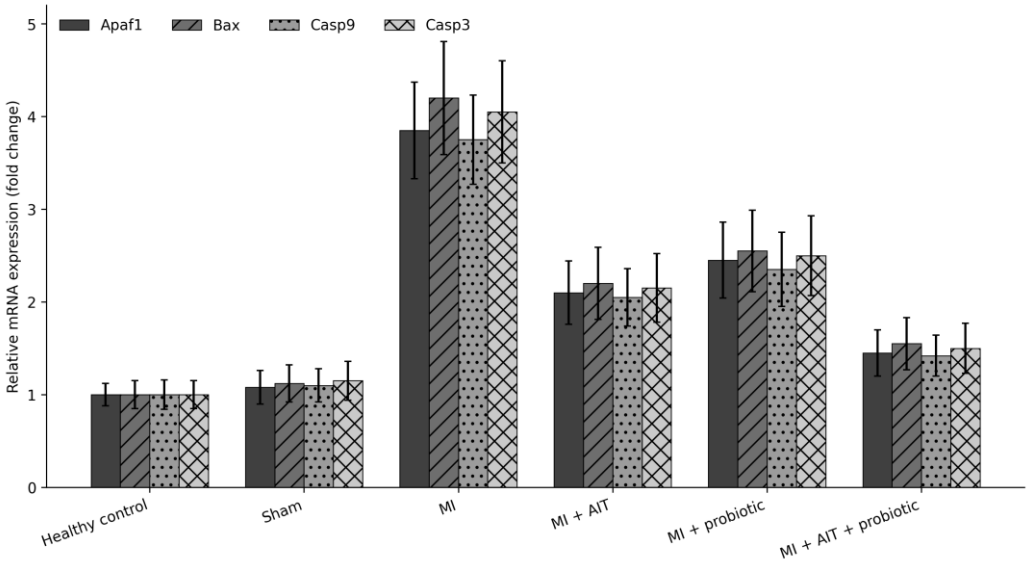
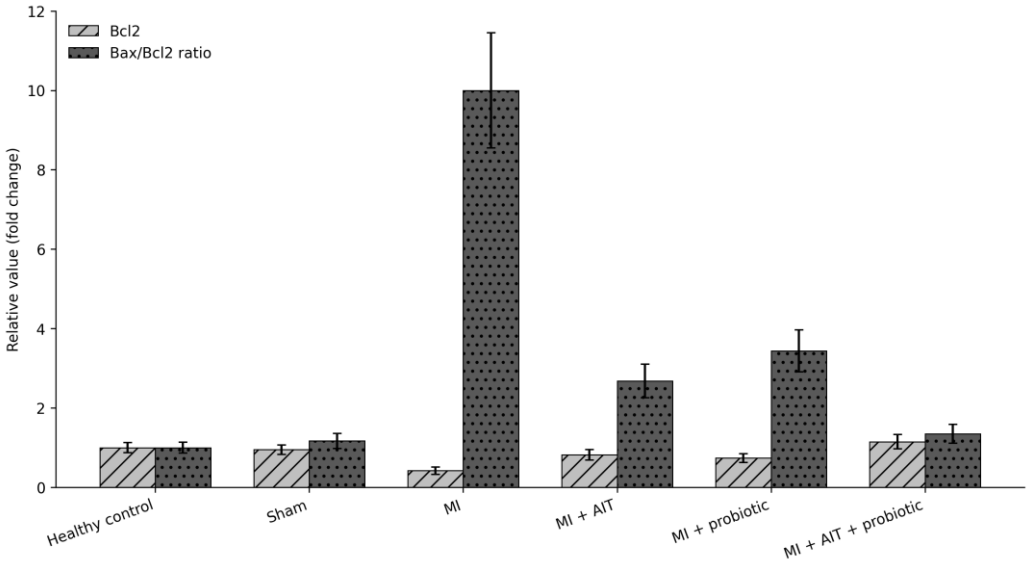


Figure 2

Relative Bcl2 expression and Bax/Bcl2 ratio across experimental groups. Bars show mean ± standard deviation (n = 8 per group). AIT, aerobic interval training; MI, myocardial infarction.



Health Nexus
E-ISSN: 2981-2569

4. Discussion

The principal finding was that experimental MI produced a coordinated increase in pro-apoptotic transcripts and a reduction in the anti-apoptotic transcript Bcl2, whereas AIT and probiotic supplementation attenuated this pattern. The combined intervention yielded the lowest Apaf1, Bax, Casp9, Casp3, and Bax/Bcl2 values among the MI intervention groups and the highest Bcl2 value. These results support the study hypothesis and suggest that the two interventions were associated with a myocardial gene-expression environment less favorable to activation of the intrinsic apoptotic pathway.

The untreated MI profile is biologically plausible. Ischemia limits oxidative phosphorylation, disrupts mitochondrial membrane potential, and increases reactive oxygen species production. These changes can favor Bax-mediated membrane permeabilization and reduce the relative influence of anti-apoptotic Bcl2. Cytochrome-c release enables Apaf1-dependent apoptosome formation and caspase-9 activation, followed by downstream caspase-3 signaling. Earlier work has linked apoptosis with adverse post-infarction remodeling and cardiomyocyte loss (1, 2). The present findings add a coherent transcript-level pattern across several points in the pathway rather than relying on a single marker.

The Bax/Bcl2 ratio showed the largest omnibus effect and the greatest proportional response to the combined intervention. This ratio can be useful because it summarizes opposing regulatory signals within the same molecular family. Nevertheless, it should not be treated as a direct count of apoptotic cells. Bax and Bcl2 are regulated post-transcriptionally, and their localization, conformation, binding partners, and protein abundance affect mitochondrial permeability. Likewise, increased Casp9 or Casp3 mRNA does not establish cleavage or catalytic activity. The current evidence therefore supports modulation of apoptosis-related gene expression, not definitive demonstration that apoptosis itself was reduced. Future work should include Western blotting or immunohistochemistry for Bax, Bcl2, cleaved caspase-9, and cleaved caspase-3, enzymatic caspase assays, TUNEL staining, and direct measures of mitochondrial function.

AIT reduced all four pro-apoptotic transcripts and increased Bcl2 relative to untreated MI. This pattern is consistent with evidence that interval training can improve mitochondrial network dynamics, oxidative metabolism, and antioxidant capacity in the post-infarction myocardium (6, 7). Repeated exercise can stimulate mitochondrial biogenesis and quality-control processes, improve endothelial and peripheral adaptations, and reduce chronic oxidative burden. Such adaptations may lower the stimuli that drive mitochondrial outer-membrane permeabilization. In Iranian experimental studies, interval or aerobic exercise has also been associated with modulation of Bax and Bcl2 expression in cardiac or skeletal muscle tissue (13-16).

The exercise findings require appropriate clinical restraint. The protocol was applied after experimental MI under controlled laboratory conditions, and the animals were selected, monitored, and exposed to a defined progression. Human patients differ substantially in infarct size, ventricular function, medication, comorbidities, arrhythmia risk, and exercise tolerance. The results should therefore be viewed as mechanistic support for further research rather than as a prescription. In clinical settings, interval training after MI must be individualized and supervised within cardiac rehabilitation.

Probiotic supplementation also reduced the pro-apoptotic profile. A plausible explanation involves the gut–heart axis. Ischemic cardiac injury and systemic stress may impair intestinal barrier function and alter microbial metabolites, potentially amplifying inflammation and oxidative stress. A suitable probiotic strain may support barrier integrity or alter immunometabolic signaling, indirectly reducing myocardial stress. Studies have reported cardioprotective effects of probiotic supplementation or Lactobacillus interventions in experimental models, including improvements in oxidative defense and regulation of Bax, Bcl2, or caspase-related expression (8-10, 17).

Probiotic effects cannot be generalized across products because strain identity, viability, dose, delivery route, treatment duration, baseline microbiota, diet, and antibiotic exposure can alter the response. The present findings are therefore specific to the L. acidophilus preparation and concentration used in this experiment. Future studies should measure microbiome composition, circulating microbial metabolites, intestinal permeability, inflammatory cytokines, and oxidative markers to determine whether the

Health Nexus
E-ISSN: 2981-2569

myocardial molecular effects are mediated through the gut–heart axis.

The combined intervention produced a greater observed normalization than either intervention alone. Exercise and probiotics could plausibly act through complementary pathways: exercise through direct myocardial and systemic adaptation, and probiotics through intestinal and immunometabolic signaling. Nevertheless, the study does not provide a formal test of synergy. A statistical interaction requires a factorial analysis restricted to comparable MI groups, with exercise and probiotic exposure represented as separate factors. The present one-way analysis demonstrates that the combined group differed in mean profile from the other groups, but it cannot determine whether the combined effect exceeded the sum of independent effects. Future experiments should use a factorial design, prespecified interaction testing, and sufficient power for that interaction.

The magnitude of the reported group effects was large, but several design considerations affect interpretation. The study used only male rats, so sex-specific responses remain unknown. It evaluated one exercise protocol and one probiotic preparation over 10 weeks, limiting dose–response inference. Outcomes were measured at a single post-intervention time point, and only the left ventricular mRNA profile was assessed. No echocardiographic, hemodynamic, infarct-size, histological, inflammatory, oxidative, mitochondrial-respiration, or protein-level endpoints were integrated into the analysis. The molecular findings therefore cannot establish improved cardiac function or reduced infarct burden.

Despite these limitations, the study has several strengths. It included healthy and sham reference groups, compared exercise and probiotic interventions separately and together, examined multiple genes spanning the intrinsic pathway, and reported effect sizes in addition to significance values. The consistent direction of Apaf1, Bax, Bcl2, Casp9, Casp3, and Bax/Bcl2 changes reduces the likelihood that the interpretation depends on an isolated biomarker. The results provide a clear rationale for studies that integrate transcript, protein, cellular, and functional outcomes.

5. Practical and Research Implications

From a translational perspective, the findings support a combined lifestyle-oriented research framework rather than an immediate treatment recommendation. Exercise-based cardiac rehabilitation already requires medical screening, individualized intensity, monitoring, and progression. Probiotic use is similarly dependent on strain, product quality, dose, and host condition. If subsequent studies confirm that the two interventions act through complementary pathways, a carefully supervised program combining exercise rehabilitation with a defined microbiota-directed intervention could be evaluated as an adjunct to standard post-MI care. Such evaluation should focus first on safety and feasibility and should not replace evidence-based pharmacological or interventional treatment.

A useful next experimental step would be a preregistered 2 × 2 factorial study among animals with comparable MI severity, with AIT and probiotic exposure as independent factors. The design should include an a priori power analysis for the interaction term, concealed allocation, blinded outcome assessment, and complete reporting of attrition. Serial echocardiography, infarct-size quantification, hemodynamic assessment, exercise capacity, and survival should be integrated with transcript and protein measurements. Measuring oxidative stress, inflammatory cytokines, mitochondrial respiration, membrane potential, cytochrome-c release, and caspase cleavage would clarify whether the observed transcript changes belong to a coherent causal pathway.

The probiotic mechanism should also be tested directly. Fecal microbiome sequencing, short-chain fatty acids, trimethylamine-N-oxide, intestinal permeability markers, and circulating endotoxin could determine whether changes in the gut environment precede myocardial effects. Including female animals and animals with common cardiometabolic comorbidities would improve biological relevance. Time-course sampling could distinguish early injury responses from long-term remodeling. Finally, data and analysis code should be made available where ethically and institutionally possible, and reporting should include individual data points in addition to group summaries. These measures would substantially strengthen reproducibility and provide a more defensible basis for later clinical trials.

6. Conclusion

In a rat model of permanent coronary artery occlusion, MI was associated with increased myocardial Apaf1, Bax,

Health Nexus
E-ISSN: 2981-2569

Casp9, and Casp3 mRNA expression, reduced Bcl2 expression, and a markedly elevated Bax/Bcl2 ratio. Ten weeks of AIT or L. acidophilus supplementation attenuated this pro-apoptotic transcript pattern, and the combined intervention produced the greatest observed shift toward control values. The data support further investigation of combined exercise and microbiota-directed strategies as adjunctive approaches to post-MI cardiac protection. They do not establish reduced apoptosis at the protein or cellular level, functional cardiac benefit, statistical synergy, or clinical efficacy. Confirmation requires rigorously reported animal experiments and controlled human studies incorporating molecular, structural, and functional endpoints.

Authors' Contributions

All authors contributed to the conception and design of the study, acquisition or interpretation of data, critical revision of the manuscript, approval of the final version, and accountability for the integrity of the work.

Declaration

Generative AI tools were used only for English-language refinement, organization, and editorial assistance during manuscript preparation. The authors reviewed, corrected, and verified all AI-assisted content and accept full responsibility for the scientific accuracy and final manuscript. No AI tool was used as an author or as a substitute for scientific judgment.

Transparency Statement

The data supporting the findings of this study are available from the corresponding author upon reasonable request, subject to institutional requirements.

Acknowledgments

The authors thank the participating centers, clinicians, adolescents, and guardians who made the study possible.

Declaration of Interest

The authors report no conflict of interest.

Funding

This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

Ethics Considerations

The study was approved by the Research Ethics Committee of the Najafabad Branch, Islamic Azad University (IR.IAU.NAJAFABAD.REC.1405.097). Animal procedures were conducted in accordance with institutional animal-welfare requirements and with reference to the Guide for the Care and Use of Laboratory Animals and ARRIVE 2.0 reporting principles.

References

1. Baldi A, Abbate A, Bussani R, Patti G, Melfi R, Angelini A, et al. Apoptosis And Post-Infarction Left Ventricular Remodeling. Journal of Molecular and Cellular Cardiology. 2002;34(2):165-74. [PMID: 11851356] [DOI]
2. Kunapuli S, Rosanio S, Schwarz ER. How Do Cardiomyocytes Die? Apoptosis And Autophagic Cell Death In Cardiac Myocytes. Journal of Cardiac Failure. 2006;12(5):381-91. [PMID: 16762802] [DOI]
3. Elmore S. Apoptosis: A Review Of Programmed Cell Death. Toxicologic Pathology. 2007;35(4):495-516. [PMID: 17562483] [PMCID: PMC2117903] [DOI]
4. Lossi L. The Concept Of Intrinsic Versus Extrinsic Apoptosis. Biochemical Journal. 2022;479(3):357-84. [PMID: 35147165] [DOI]
5. Sahoo G, Samal D, Khandayataray P, Murthy MK. A Review On Caspases: Key Regulators Of Biological Activities And Apoptosis. Molecular Neurobiology. 2023;60(10):5805-37. [PMID: 37349620] [DOI]
6. Jiang HK, Wang YH, Sun L, He X, Zhao M, Feng ZH, et al. Aerobic Interval Training Attenuates Mitochondrial Dysfunction In Rats Post-Myocardial Infarction: Roles Of Mitochondrial Network Dynamics. International Journal of Molecular Sciences. 2014;15(4):5304-22. [PMID: 24675698] [PMCID: PMC4013565] [DOI]
7. Lu K, Wang L, Wang C, Yang Y, Hu D, Ding R. Effects Of High-Intensity Interval Versus Continuous Moderate-Intensity Aerobic Exercise On Apoptosis, Oxidative Stress, And Metabolism Of The Infarcted Myocardium In A Rat Model. Molecular Medicine Reports. 2015;12(2):2374-82. [PMID: 25936391] [DOI]
8. Chen X, Zou X, Zhou Y, Peng C, Huang R. The Role Of Gut Microbiota In Myocardial Ischemia-Reperfusion Injury. Frontiers in Cardiovascular Medicine. 2025;12:1625299. [PMID: 41063836] [PMCID: PMC12500671] [DOI]
9. Liang Y, Zhao L, Zhang X, Liu S, Lu P, Wang J, et al. Lactobacillus Ameliorates Myocardial Ischemia-Reperfusion Injury By Attenuating Apoptosis, Inflammation, Oxidative Stress, And Ferroptosis. BMC Medicine. 2025;23(1):377. [PMID: 40598393] [PMCID: PMC12218948] [DOI]
10. Maherinia H, Peeri M, Azarbayjani MA, Delfan M. Aerobic Exercise Training Combined With Probiotic Supplementation Improves Antioxidant Defense Of Cardiomyocytes By Regulating Nrf2 And Caspase-3 Gene

Expression In Type 2 Diabetic Rats. Comparative Exercise Physiology. 2022;18(3):255-64. [DOI]
11. National Research Council. Guide For The Care And Use Of Laboratory Animals: National Academies Press; 2011. [DOI]
12. Percie Du Sert N, Hurst V, Ahluwalia A, Alam S, Avey MT, Baker M, et al. The Arrive Guidelines 2.0: Updated Guidelines For Reporting Animal Research. PLOS Biology. 2020;18(7):e3000410. [PMID: 32663219] [PMCID: PMC7360023] [DOI]
13. Asgharpour-Arshad M, Siahkouhian M, Bolboli L, Jafari A, Sheikhzadeh-Hesari F. Effects Of Three Months Of Aerobic Interval Training On The Expression Of Selected Mitochondrial Apoptosis-Pathway Genes In Rat Skeletal Muscle. Applied Exercise Physiology Research. 2017;13(25):211-21.
14. Ghahremani M, Azarbayjani MA, Peeri M, Raoofi A. Effect Of Aerobic Interval-Training Intensity On Bcl2 And Bax Gene Expression In Rats With Myocardial Infarction. Armaghane Danesh. 2017;22(6):781-91.
15. Kordi N, Azizi M, Samadi M, Tahmasbi V. Effect Of Aerobic Training On Selected Pro- And Anti-Apoptotic Myocardial Genes In Rats After Methamphetamine Withdrawal. Sport and Biokinetic Sciences. 2023;15(30):1-10.
16. Soori R, Zare-Shahneh M, Choobineh S, Ramezankhani A. Effect Of High-Intensity Interval Training On Pro- And Anti-Apoptotic Gene Expression In Cardiac Tissue Of Aged Male C57Bl/6 Mice. Journal of Exercise Physiology and Physical Activity. 2018;11(2):13-24.
17. Bonab SF, Tahmasebi S, Ghafouri-Fard S, Eslami S. Preventive Impact Of Probiotic Supplements On Heart Injury And Inflammatory Indices In A Rat Model Of Myocardial Infarction: Histopathological And Gene Expression Evaluation. APMIS. 2025;133(1):e13479. [PMID: 39415755] [DOI]

Health Nexus
E-ISSN: 2981-2569