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Original Research Abstracts

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The 12th Annual Scientific Meeting InaHRS 2025

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[12INAHRS-OR1]

The Effect of Single Dose and Intrapocket Prophylactic Antibiotic Administration on the Incidence of Infections Related to Implantable Cardiovascular Electronic Devices

M. H. Trisnawan[1], P. Ardhianto[1], N. Farhanah[2], I. Edward[3]
[1]Cardiovascular Department, Universitas Diponegoro, Semarang, Indonesia
[2]Internal Medicine Department, Universitas Diponegoro, Semarang, Indonesia
[3]Clinical Pathology Department, Universitas Diponegoro, Semarang, Indonesia

Background and aims: Antibiotic pre- and post-Cardiovascular Implantable Electronic Device (CIED) implantation using ampicillin sulbactam is the regional standard. This study aimed to evaluate whether a simplified single-dose antibiotic regimen is as effective as an extended regimen in preventing early infections and reducing implant-related rehospitalizations.

Materials and Methods: A double-blind RCT in subjects who underwent PPM implantation based on total sampling from April 2024 to January 2025. The treatment group received prophylactic antibiotics, ampicillin sulbactam 1.5 g IV 1 h pre-incision and 1.5 g intrapocket, while the control group received additional ampicillin sulbactam 1.5 g IV every 12 h for 3 days post-implantation. Patients were observed for up to 28 days and assessed for the incidence of infection and rehospitalization related to PPM infection. The non-inferiority margin using the fixed-margin method in this study was 5%.

Results: A total of 90 patients were included in the study. Most of them were women (58.9%). Forty subjects in the treatment group had one superficial infection event, while 50 subjects in the control group had three superficial infection events (total 4.4%). Rehospitalization after PPM infection was 3 subjects (3.3%). There was no significant difference in the incidence of infection and rehospitalization between the treatment and control groups [OR 0.42; (95% CI 0.05-3.85), p=0.816], with the lower limit of the CI not exceeding the non-inferiority margin of 5%.

Conclusion: Single-dose IV and intrapocket prophylactic antibiotic administration was non-inferior to the regional standard treatment.

Keywords: PPM, PPM infection, rehospitalization, prophylactic antibiotic

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[12INAHRS-OR2]

Prognostic Value of Short-Term Non-Invasive Sudden Cardiac Death Risk Stratification in Ischemic Cardiomyopathy

W. Kwandou[1], F.M. Yofrido[1], N.P. Labi[2], C.J. Hardi[3], S. Adiwinata[1], F.M. Halim[1], J. Julianus[1], B.M. Setiadi[1], A.L. Panda[1]

[1]Department of Cardiology and Vascular Medicine Sam Ratulangi University
Prof. Dr. R. D. Kandou General Hospital, Manado, Indonesia
[2]Faculty of Medicine, Sam Ratulangi University, Manado, Indonesia
[3]Manado City General Regional Hospital, Manado, Indonesia

Background and aims: Non-invasive sudden cardiac death (SCD) risk stratification, such as signal-averaged electrocardiogram (SAECG), heart rate variability (HRV), deceleration capacity (DC), QRS fragmentation, and spatial QRS-T angle, has been reported to predict both SCD and non-arrhythmic mortality in ischemic cardiomyopathy; however, the use of these parameters for predicting SCD is still contradictory. This study aimed to assess the prognostic value of short-term non-invasive SCD risk stratification in ICM.

Materials and methods: This single-center prospective study included 84 patients with ICM between January and June 2023. Short term 15 minutes non-invasive SCD risk stratification parameters were assessed, including SAECG, QRS fragmentation, HRV, DC, and spatial QRS-T angle. The primary endpoint was a composite of cardiac events, including all-cause mortality, sudden cardiac death, and non-arrhythmic death.

Results: The study population had a mean age of 63.9 ± 9.5 years, with males comprising approximately 71% of the cohort. During a median follow-up of 22 months, the overall mortality rate within this patient group was 42.8%, and the overall SCD rate was 28.5%. Individuals classified within the higher deceleration capacity (DC) risk category demonstrated a significantly elevated incidence of both sudden cardiac death (SCD) and all-cause mortality, as evidenced by a statistically significant log-rank test ($p < 0.001$). In contrast, other evaluated parameters, such as SAECG, QRS complex fragmentation, HRV, and spatial QRS-T angle, did not exhibit a statistically significant association with the occurrence of SCD events and all-cause mortality.

Conclusion: Among all short-term noninvasive SCD risk stratification parameters, low deceleration capacity is an independent predictor of sudden cardiac death and all-cause mortality in ischemic cardiomyopathy.

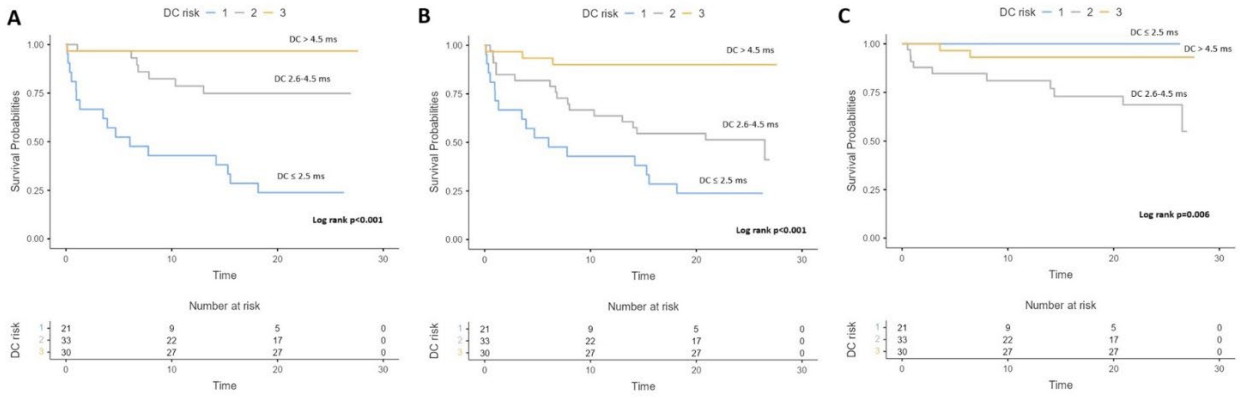

Figure 1. (A). Kaplan-Meier Curve of SCD from DC Risk Group (B). Kaplan-Meier Curve of All-Cause Mortality from DC Risk Group (C).Kaplan-Meier Curve of Non-Arrhythmic Mortality from DC Risk Group.

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[12INAHRS-OR3]

Survival Analysis of Heart Rate Variability Triangular Index for Predicting Sudden Cardiac Death in Ischemic Cardiomyopathy

D. Hadi[1], C. J. Hardi[1], W. Kwandou[1], F. M. Yofrido[1], A. N. Aristo[1], G. J Pangemanan[1], B. M. Setiadi[3]
[1]Department of Cardiology and Vascular Medicine, Faculty of Medicine, Sam Ratulangi University
[2]Manado City General Regional Hospital, Manado, Indonesia
[3]Department of Cardiology and Vascular Medicine, Prof. Dr. R. D. Kandou General Hospital, Manado, Indonesia

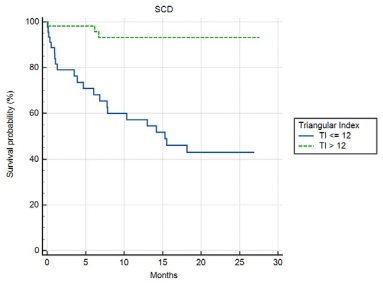
Background and aims: Sudden Cardiac Death (SCD) is a leading cause of cardiac death in patients with ischemic cardiomyopathy (ICM), despite substantial advancements over the past decades. Current guidelines recommend implantable cardioverter-defibrillator (ICD) implantation in patients with left ventricular ejection fraction (LVEF) <35% for the primary prevention of SCD. However, ICD is associated with high costs and is not readily available in many countries, such as Indonesia. It is important to stratify the risk in patients with ICM to determine who would benefit more from ICD implantation. Unfortunately, LVEF alone is insufficient to determine the risk. Therefore, this study aimed to assess heart rate variability as a parameter for deciding which patients would benefit more from ICD implantation.

Materials and methods: A total of 100 patients were enrolled in a hospital-based analytical observational study conducted between January 2023 and April 2025. Heart rate variability (HRV) parameters were derived from high-resolution short-term ambulatory ECG of patients with a history of ischemic cardiomyopathy. The primary endpoint was the occurrence of SCD during the study period. Survival analysis was performed using Kaplan-Meier curves.

Results: The study population consisted of 100 patients, including 75 male patients with a mean age of 63 ± 9.85 years. These patients were monitored for 26 months, and the overall SCD rate for the study population was 25 patients (25%), whereas the survival probability for patients with heart rate variability triangular index (HRV-TI) ≤ 12 was 45%. Patients with HRV-TI ≤ 12 demonstrated a significantly higher risk of SCD, with an HR of 7.34 (95% CI 3.29 – 16.36, p <0.0001). Thus, patients with HRV-TI of ≥ 12 were found to have higher survival rates and thus can be deferred from ICD implantation. Patients with HRV-TI ≤ 12 can be considered for further testing, such as an electrophysiological study, to further stratify the risk and indication for ICD implantation.

Conclusion: Patients with HRV-TI of 12 had higher survival rates, suggesting that ICD implantation may be deferred in these patients. Patients with HRV-TI ≤ 12 should be considered for further testing due to the potential need for ICD implantation

Keywords: Ischemic Cardiomyopathy, Heart Rate Variability Triangular Index, Sudden Cardiac Death



Comparison of survival curves (Logrank test)

Chi-squared	23,7380
DF	1
Significance	P < 0,0001

Hazard ratios[a] with 95% Confidence Interval

Factor	TI <= 12	TI > 12
TI <= 12	-	0,1363 0,06114 to 0,3039
TI > 12	7,3371 3,2911 to 16,3572	-

[a] Column/Row

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[12INAHRS-OR4]

Integrative in Silico and Bioinformatic Analysis Reveals Hub Genes and Novel Therapeutic Targets in Lone Atrial Fibrillation

A. R. Fadhlan[1], A. A. Wahyuning[2] Bidhari[3]
[1]Citra Husada Hospital, Jember, Indonesia
[2]Majenang General Hospital, Jember, Indonesia
[3]Faculty of Medicine, Gadjah Mada University, Yogyakarta, Indonesia

Background and aims: Atrial fibrillation (AF) is the most common sustained cardiac arrhythmia and is associated with adverse outcomes. Lone AF is a distinct subtype that occurs in individuals aged < 60 years without structural heart disease, hypertension, or other identifiable causes. The pathophysiology of this disease is complex, with genetic factors playing a pivotal role. This study aimed to identify key genes and their associated biological processes in AF and propose potential therapeutic targets using an in silico approach.

Materials and methods: Genes linked to lone AF were retrieved from the GeneCards database. A protein–protein interaction (PPI) network was constructed using the STRING database. Gene Ontology (GO) enrichment analyses for biological processes and molecular functions were performed using WebGestaltR. Hub genes were identified using the DMNC algorithm in the CytoHubba plugin of Cytoscape. Three-dimensional structures of key proteins were modeled using SWISS-MODEL and validated using ERRAT and PROCHECK software.

Results: Ninety-two lone AF-related genes were identified. PPI analysis revealed significant interactions (p < 1.0e-16). GO analysis highlighted "cardiac muscle cell action potential" and "cardiac muscle cell contraction" as the most significant biological processes, while "antioxidant activity" was the top molecular function (FDR p < 0.05). Of the 92 genes, 56 were enriched in these pathways. Ten hub genes were identified, among which *GPD1L, SCN1B, SCN4B,* and *KCNE2* emerged as critical and potentially novel therapeutic targets for DCM.

Conclusions: *GPD1L, SCN1B, SCN4B,* and *KCNE2* are key genes involved in the molecular pathogenesis of lone AF and may serve as promising therapeutic targets.

Keywords: Bioinformatic, In silico, Lone Atrial Fibrillation

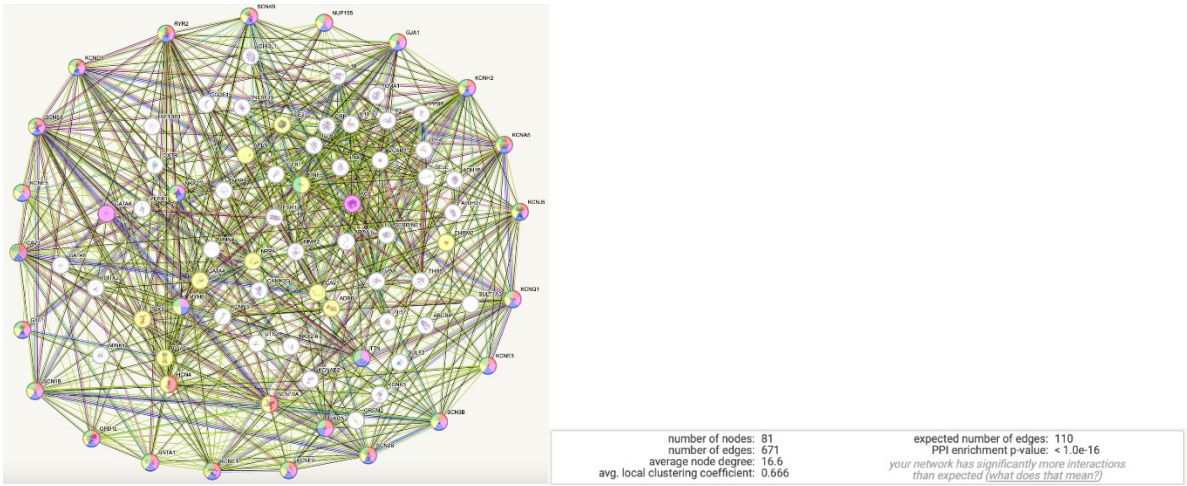

Figure 1. Protein-protein interaction network (PPIN) analysis. PPIN analysis using STRING tools of the hub-genes (81 genes with a high relevance score) related to Lone AF with PPI enrichment p-value showed a significant value (< 1.0e-16), indicating that the observed number of edges is significant, the nodes are not random, and the genes are related to each other. RED nodes: genes responsible for cardiac muscle cell action potential; PINK nodes: genes responsible for heart contraction; BLUE nodes: genes responsible for cardiac muscle contraction; yellow nodes: genes responsible for regulation of heart contraction; GREEN nodes: genes responsible for striated muscle contraction; WHITE nodes: not classified.

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[12INAHRS-OR5]

Differences of Biomarker Levels Related to Prophylactic Antibiotic Administration in Cardiac Implantable Electronic Devices Implantation

M.W. Hadi[1], I. Uddin[1], A.Y.A.B. Mochtar[1], N. Farhanah[2], I. Edward[3]
[1]*Cardiovascular Department, Diponegoro University, Kariadi Hospital, Semarang, Indonesia*
[2]*Internal Medicine Department, Diponegoro University, Kariadi Hospital, Semarang, Indonesia*
[3]*Clinical Pathology Department, Diponegoro University, Kariadi Hospital, Semarang, Indonesia*

Background: Infection is a serious complication of CIED implantation, 12-25% of CIED infections (CIEDI) are subclinical. Therefore, a highly sensitive and specific biomarker for infection can be used under these conditions. The use of postprocedural prophylactic antibiotics to prevent CIEDI remains controversial. This study aimed to determine the differences in biomarker levels in CIED patients who received pre- and intraprocedural prophylactic antibiotics compared to those who received pre-, intra-, and postprocedural antibiotics.

Methods: This double-blind RCT included patients who underwent permanent pacemaker (PPM) implantation. Subjects in the intervention group received prophylactic antibiotic ampicillin sulbactam 1.5 g IV 1 h pre- and intra-procedure, whereas subjects in the control group received additional ampicillin sulbactam 1.5 g IV twice a day for 3 days after implantation. Presepsin, IL-6, and procalcitonin were used as biomarkers of infection. Biomarkers were analyzed 1 d before and 24 h after implantation to obtain the delta value.

Results: Fifty-nine subjects were eligible for this study, of whom 27 were randomized into the intervention group and 32 into the control group. The median value of delta presepsin was -12.2 pg/mL in the intervention group and -9.9 pg/mL in the control group, IL-6 was -0.9 pg/mL in the intervention group and -0.3 pg/mL in the control group, and procalcitonin was -0.02 ng/mL in the intervention group as well as in the control group. The Mann-Whitney U test showed no differences in delta presepsin, IL-6, and procalcitonin levels between the intervention and control groups.

Conclusion: There were no significant differences in biomarker levels between CIED patients who received pre- and intraprocedural prophylactic antibiotics and those who received pre-, intra-, and postprocedural antibiotics.

Keywords: CIED infection, infection biomarker, presepsin, IL-6, procalcitonin

	Intervention (n=27) Median, SE (min-max)	**Control (n=32)** Median, SE (min-max)	**p value**
Delta presepsin (pg/mL)	-12.2, 14.0 (-325.6-84.1)	-9.9, 4.4 (-78.6-50.8)	0.548[a]
Delta IL-6 (pg/mL)	-0.9, 0.52 (-5.9-6.9)	-0.3, 1.06 (-20.3-15.4)	0.140[b]
Delta procalcitonin (ng/mL)	-0.02, 0.02 (-0.52-0.05)	-0.02, 0.02 (-0.26 -0.27)	0.951[b]

[a]Wilcoxon test
[b]Mann-Whitney test

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[12INAHRS-OR6]

Heart Rate Variability Triangular Index as a Predictor of Sudden Cardiac Death in Patients with Ischemic Cardiomyopathy

C. J. Hardi[1] , W. Kwandou[2] , F. M. Yofrido[2], B. M. Setiadi[3]
[1]Manado City General Regional Hospital, Manado, Indonesia
[2]Department of Cardiology and Vascular Medicine, Faculty of Medicine, Sam Ratulangi University
[3]Department of Cardiology and Vascular Medicine, Prof. Dr. R. D. Kandou General Hospital, Manado, Indonesia

Background and aims: Sudden Cardiac Death (SCD) accounts for 50% of cardiovascular deaths and the majority of deaths due to ischemic heart disease. Implantable cardioverter-defibrillators (ICDs) are indicated in patients with left ventricular ejection fraction (LVEF) <35% as primary prevention; however, their use in Indonesia is limited by cost and lack of insurance coverage. LVEF alone is insufficient for accurate risk stratification because of the risk of overtreatment in high-risk groups and undertreatment in low-risk groups. This study aimed to assess heart rate variability (HRV) parameters as additional noninvasive tools to improve primary prevention implantable cardioverter-defibrillator (ICD) selection in patients with ischemic cardiomyopathy (ICM).

Materials and methods: A total of 100 patients with a history of ischemic cardiomyopathy were enrolled in a hospital-based analytical observational study between January 2023 and April 2025. Heart rate variability (HRV) parameters were derived from high-resolution short-term ambulatory ECG. The primary endpoint was the occurrence of SCD during the study period. Comparative tests, regression analysis, ROC curve analysis, and diagnostic value evaluation were performed to assess the associations with SCD.

Results: A total of 100 patients (75% men, mean age 63.7 ± 9.9 years) were followed up, of whom 25 died suddenly. Of all the HRV parameters studied, the HRV triangular index (HTI) was independently associated with SCD. The area under the ROC curve (AUC) was 0.809 ($p < 0.001$), with a diagnostic performance of sensitivity of 88%, specificity of 69.3%, PPV of 48.9%, and NPV of 94.5% at a cutoff of ≤ 12. Multivariable analysis revealed that reduced HTI, SDNN, and SDaNN were significant predictors of sudden death. Decreased HTI may be caused by depressed vagal activity, which is strongly associated with the pathogenesis of ventricular arrhythmias and SCD.

Conclusion: In patients with ischemic cardiomyopathy, a severely decreased HRV triangular index from short-term ECG recordings was a significant predictor of SCD. HRV analysis in patients with ICM may be a valuable tool for further risk stratification to guide the management of patients.

Keyword: Heart rate variability triangular index, Sudden cardiac death

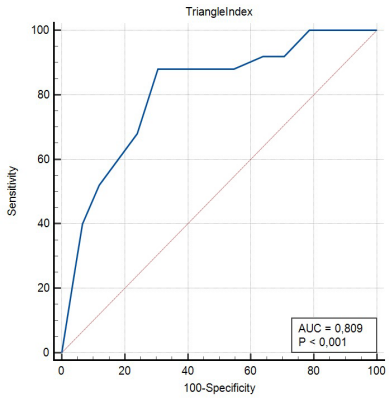

Figure 1. The area Under ROC Curve (AUC) of the HRV Triangle Index demonstrated good diagnostic performance (AUC = 0.809, $p < 0.001$).

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[12INAHRS-OR7]

Decoding the Molecular Blueprint of Atrial Fibrillation Recurrence Post-Ablation: Uncovering Novel Therapeutic Targets Through In Silico Network-Based Bioinformatic Analysis

N. Athoillah[1], P.A. Ardiani[1], Y.W. Febriyanti[1], P. Wulandari[2]
[1]Faculty of Medicine, University of Jember, Jember, Indonesia
[2]Departement of Cardiovascular, Faculty of Medicine, University of Jember - Dr. Soebandi General Hospital, Jember, Indonesia

Background and aims: Catheter ablation is an established therapy for symptomatic atrial fibrillation (AF), particularly in patients who are refractory to medical management. However, its long-term efficacy is limited by AF recurrence, which occurs in up to 50% of cases within the first year. This recurrence is driven by atrial remodeling, fibrosis, and electrical heterogeneity of the atria. Although genetic factors influence AF susceptibility and ablation outcomes, the specific hub genes and molecular networks underlying recurrence remain poorly characterized. Our study utilized in silico bioinformatic approaches to identify novel genetic targets for improving ablation durability.

Materials and methods: We used integrated bioinformatics tools to construct a protein-protein interaction network and performed functional enrichment analysis with STRINGS and WEBGSTALT, aiming to identify hub genes involved in atrial fibrillation recurrence post-ablation. Candidate genes were further validated using ERRAT and PROCHECK to assess their potential as therapeutic targets.

Results: Hub-gene analysis showed that 48 genes were the most contributing genes for the underlying pathomechanisms in atrial fibrillation after catheter ablation, with a significant PPI enrichment value ($p < 0.01$) and a significant false discovery rate (FDR) value ($p < 0.05$). High-level ERRAT and PROCHECK validation analyses also showed that the three best genes had stable, high-resolution, and non-degradable protein structures: SCN1B, SCN4B, KCNJ2, and ABCC9.

Conclusion: This study identified candidate for new therapeutic target genes with the greatest impact on atrial fibrillation recurrence post-ablation, namely SCN1B, SCN4B, KCNJ2, and ABCC9. It also highlights opportunities for future research to identify agents that could treat these therapeutic target genes in atrial fibrillation recurrence after catheter ablation.

Keywords: Atrial Fibrillation Recurrence, Bioinformatic, In silico, Post-Ablation

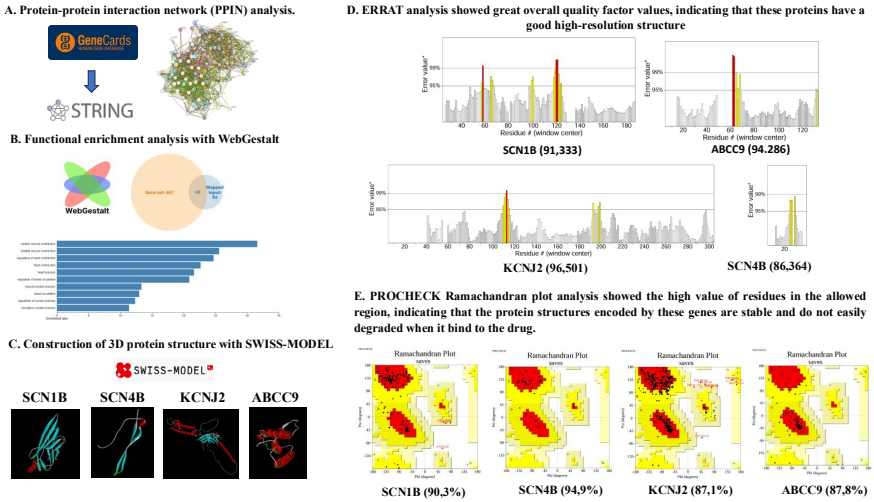

Figure 1. Graphical Abstract.

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[12INAHRS-OR8]

In Silico-based Multi-dimensional Bioinformatic Analysis of Brugada Syndrome: Decoding Hub Gene Networks, Gene Ontology, and Potential Therapeutic Targets

S. Larasati[1], M. I. Amien[1,2], S. Suryono[3,4]
[1]Faculty of Medicine, Universitas Jember, Jember, Indonesia
[2]BK Bokor Hospital, Malang, Indonesia
[3]Department of Cardiology and Vascular Medicine, Faculty of Medicine, Universitas Jember, Jember, Indonesia
[4]Department of Cardiology and Vascular Medicine, Dr. Soebandi General Hospital, Jember, Indonesia

Background: Brugada syndrome (BS) is a rare cardiac arrhythmia characterized by right bundle branch block and persistent ST-segment elevation, and is associated with a high risk of sudden cardiac death, predominantly in younger males with structurally normal hearts. This study aimed to identify critical genes, underlying gene ontology, and develop in silico-based therapeutic innovations targeting hub genes in BS.

Methods: Multiple bioinformatics tools were utilized to analyze the genes, such as protein–protein interaction networks (PPIN), functional enrichment analysis, cytoHubba, and ERRAT-PROCHECK, to determine the hub genes and gene ontology in terms of biological processes and molecular functions. Furthermore, we assessed the potential of the identified genes to serve as viable therapeutic targets.

Results: The PPIN, constructed using 410 genes retrieved from the GeneCards database, demonstrated statistical significance ($p < 1.0e-16$). Functional enrichment analysis identified 75 genes significantly associated with BS. Transmembrane transport binding (FDR <0.05) was the most significant pathway among the 16 enriched biological processes, and actin filament-based movement (FDR <0.05) was the most significant pathway among the 40 enriched molecular functions. The hub proteins involved in BS etiology were predicted based on the topological algorithms of CytoHubba, with the MCC approach represented in red to yellow, where red indicates the highest impact. ERRAT and PROCHECK were performed on the top ten genes identified by CytoHubba. ERRAT analysis was performed on ten genes and showed a standard overall quality factor value of GPD1L (98.08%), SCN5A (92.65%), CACNA2D1 (92.85%), and SCN1B (91.49%), suggesting that the protein structures have good resolution and are suitable as drug targets. PROCHECK Ramachandran plot analysis showed that GPD1L (98.08%), SCN5A (82.1%), CACNA2D1(90.2%), and SCN1B (93.7%) have a high number of residues in the allowed region, suggesting that the protein structures encoded by these genes are stable upon drug binding. This result showed that GPD1L, SCN5A, CACNA2D1, and SCN1B are critical genes with significant roles in biological processes and molecular functions related to BS, highlighting their potential as therapeutic targets.

Conclusion: Current evidence indicates that GPD1L, SCN5A, CACNA2D1, and SCN1B are critical genes in BrS and offer promising targets for therapeutic intervention.

Keywords: Brugada Syndrome, Bioinformatics, In silico

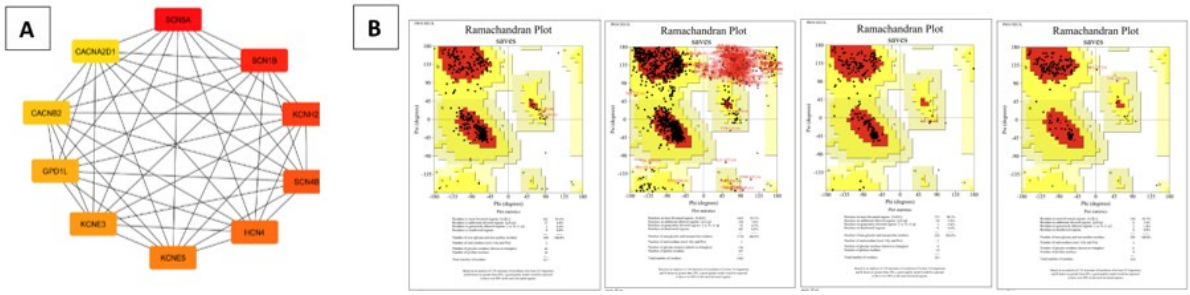

Figure 1. (A) CytoHubba analysis showing the top 10 hub genes. (B) PROCHECK analysis of GPD1L, SCN5A, CACNA21, SCN1B (left to right).

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[12INAHRS-OR9]

12-Lead Electrocardiography–Based Scoring System for Evaluating Eisenmenger Physiology in Adults with Atrial Septal Defect and Pulmonary Hypertension

C. E. Cipta[1], B. B. Bramantyo[1], L.K. Dinarti[1], A. B. Hartopo[1], D. W. Anggrahini[1]
[1]Department of Cardiology and Vascular Medicine, Sardjito General Hospital, Yogyakarta, Indonesia

Background and aims: Atrial septal defect (ASD) is the most prevalent congenital heart disease in adults and may lead to pulmonary arterial hypertension (PAH) and eventually progress to Eisenmenger syndrome if left uncorrected. Early identification of irreversible pulmonary vascular remodeling is challenging, particularly in resource-limited settings where access to right heart catheterization (RHC) is restricted. This study aimed to develop and validate a 12-lead ECG-based scoring system for predicting Eisenmenger physiology in adults with ASD.

Materials and Methods: We conducted a cross-sectional study using data from adult patients with unrepaired secundum ASD enrolled in the COHARD-PH registry. All patients underwent RHC to confirm PH and classify them into Eisenmenger and non-Eisenmenger groups. Eisenmenger syndrome was defined as a pulmonary vascular resistance index (PVRi) >8 WU·m² with bidirectional or right-to-left shunt. A diagnostic scoring model was developed using the Spiegelhalter-Knill-Jones method. The model performance was assessed using the area under the receiver operating characteristic curve (AUC), sensitivity, specificity, and overall accuracy.

Results: Of 197 adult ASD-PH patients, 63 (32%) met criteria for Eisenmenger syndrome. Four ECG parameters were identified as independent predictors and included in the scoring system: R wave in aVR > 4 mm, QRS amplitude in V1 > 6 mm, Negative T wave in V1–V3, and S wave in V5 > 10 mm. The scoring system produced cumulative values ranging from −11 to 9. A cut-off point of ≥3 demonstrated an AUC of 0.82 (95% CI: 0.761–0.878), with 80% specificity and 74.7% overall accuracy. Patients with a maximum score of 9 had an estimated 80% probability of Eisenmenger physiology, reflecting a strong discriminatory power in advanced disease.

Conclusion: We propose a clinically relevant, noninvasive ECG-based scoring system with strong diagnostic accuracy for identifying Eisenmenger physiology in adults with ASD-PH. Its high specificity and accuracy support its potential role in early risk stratification, particularly in settings where invasive hemodynamic assessment is limited or unavailable.

Keywords: Atrial septal defect, 12-leads electrocardiography, scoring system, Eisenmenger syndrome, pulmonary hypertension

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[12INAHRS-OR10]

The Role of QTc Interval in Early Detection of Cardiac Dysfunction Among Breast Cancer Patients Treated with Anthracycline-Based Regimens

M Lerista[1], F Soniya[1] , MR Felani[1], I Puspita[1] , NY Sari[1] , AE Tondas[1,2]

[1]*Department of Cardiology and Vascular Medicine, Dr Mohammad Hoesin General Hospital, Palembang, Indonesia*

[2] *Faculty of Medicine, Universitas Indo Global Mandiri (UIGM), Palembang, Indonesia*

Background

Cardiac dysfunction remains a major concern in patients with breast cancer undergoing anthracycline-based chemotherapy. Cancer therapy-related cardiac dysfunction (CTRCD) can lead to long-term morbidity and mortality if not detected early enough. Prolongation of the corrected QT interval (QTc) has been proposed as a potential early biomarker of cardiotoxicity. However, evidence of its predictive value for CTRCD remains underexplored in clinical settings. This study aimed to evaluate the association between QTcB and CTRCD incidence and to assess its value as a predictive marker in patients with breast cancer undergoing chemotherapy.

Methods

A retrospective cohort study was conducted involving female breast cancer patients receiving epirubicin, cyclophosphamide, and docetaxel (EC-Doc) chemotherapy at RSUP Dr. Mohammad Hoesin, Palembang. Pre-treatment QTc intervals were measured using Bazett's formula and were classified as normal or prolonged. CTRCD was identified within one year based on clinical and echocardiographic criteria. The predictive ability of QTc was evaluated using Receiver Operating Characteristic (ROC) analysis, and logistic regression was used to determine its association with CTRCD incidence.

Results

QTcB demonstrated moderate discriminatory ability (AUC = 0.717; 95% CI: 0.506–0.928; p = 0.040). Logistic regression revealed that QTcB was a strong independent predictor of CTRCD (OR = 296.701; p < 0.001), with the model explaining 64.5% of the variability (Nagelkerke R^2 = 0.645). The model achieved high sensitivity (100%) and accuracy (84.4%), although the specificity was moderate (61.5%).

Conclusion

QTc prolongation is significantly associated with CTRCD in patients with breast cancer receiving anthracycline-based chemotherapy. Given its simplicity and accessibility, QTc may serve as an early and cost-effective tool for identifying at-risk patients. Further studies with larger sample sizes and multivariate adjustments are required to confirm the role of routine cardio-oncology screening protocols.

Keywords: QTc, cardiotoxicity, breast cancer

Table 1. ROC Curve (AUC) and Regression Analysis between QTc and CTRCD.

Variable QTc (Bezzet)	Without CTRCD	With CTRCD	AUC (95% CI)	Std. Error	p – Value	Exp (B)	Nagelkerke R^2	Sensitivity	Spesifiticty	Accuracy
No	8 (36.4%)	14 (63.6%)	0.717 (0.506 – 0.928)	0.108	0.000	296.701	0.645	100%	61.5%	84.4%
Yes	5 (50%)	5 (50%)								

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[12INAHRS-OR11]

Potential Competitive Inhibition of Amiodarone Metabolism by Curcumin via CYP3A4: A Molecular Docking Study

P. K. Thios[1], N. I. U. Idris[1], G. Sabina[2], G. N. Uirianto[2], S. P. Nababan[2], N. H. Sakir[1], E. L. Febriyanti[1], H. K. Kaharuddin[1]

Faculty of Medicine, Hasanuddin University, Makassar, Indonesia[1]; Faculty of Medicine, Sam Ratulangi University, Manado, Indonesia[2]

Background: Curcumin, the primary polyphenolic compound in turmeric (Curcuma longa), is widely used for its anti-inflammatory, antioxidant, anticancer, and cardioprotective properties. Amiodarone is a first-line antiarrhythmic drug whose metabolism and clearance predominantly depend on hepatic cytochrome P450 3A4 (CYP3A4) enzyme activity. Emerging preclinical evidence indicates the concurrent use of curcumin and amiodarone in practice, with studies confirming curcumin's CYP3A4 modulation capability. Although both compounds are therapeutically beneficial, their interaction may significantly alter amiodarone biotransformation, potentially leading to therapeutic failure or dose-dependent toxicity. This in silico study employed molecular docking simulations to analyze the binding affinities and spatial configurations of both compounds within the CYP3A4 active site, providing crucial mechanistic insights for developing safer co-administration protocols.

Methods: Molecular docking simulations were conducted using SwissDock, a web-based docking platform, to explore the binding interactions between curcumin and amiodarone with CYP3A4, a key drug-metabolizing enzyme. The three-dimensional structure of CYP3A4 was obtained from the Protein Data Bank. Ligand structures were prepared using standard computational chemistry protocols, including energy minimization and geometric optimization. SwissDock allows flexible ligand docking within the active site of the enzyme, generating multiple binding poses. The key parameters analyzed included the estimated Gibbs free energy of binding (ΔG) and the spatial coordinates of the ligand-binding sites. The spatial overlap of curcumin and amiodarone binding poses was examined to assess the potential for competitive inhibition. The docking results were validated by comparing them with known CYP3A4 substrates and inhibitors.

Results and Discussion: Amiodarone exhibited a strong binding affinity for CYP3A4 (ΔG = -9.19 kcal/mol), indicating a stable interaction. Curcumin also demonstrated a substantial affinity (ΔG = -8.67 kcal/mol). The docking poses revealed significant spatial overlap within the CYP3A4 active site, suggesting that both ligands occupy closely adjacent or overlapping regions. This supports potential competitive inhibition, in which curcumin may interfere with amiodarone metabolism by competing for CYP3A4 binding sites.

Conclusion: This study highlights the potential for competitive interaction between curcumin and amiodarone at CYP3A4, which may alter the metabolism and clinical efficacy of amiodarone. Caution is advised when coadministering these compounds to avoid adverse herb-drug interactions and ensure optimal therapeutic outcomes.

Keywords: Curcumin, Amiodarone, CYP3A4, Molecular Docking, Herb-Drug Interaction

No.	Ligand	ΔG (kcal/mol)	Binding Location (x,y,z)	Estimated Overlap	Potential Notes
1	Amiodarone	-9.1906	(-15.7, -28.2, -8.8)	Yes	Strong Affinity
2	Curcumin	-8.6658	(-18.8, -32.1, -8.9)	Yes (Very Close)	Potential Competition

Figure 1. Table of Molecular Docking Results: Binding Affinity and Binding Site Analysis of the Ligands.

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[12INAHRS-OR12]

Comprehensive Predictor of Successful Ablation Site in Focal Idiopathic Right Ventricular Outflow Tract Arrhythmias

R. Karimah[1], C. Milla[2], R. Julario[2,3], B. Dharmadjati[2,3], R. Rosyadi[2,3], M. R. Amadis[2,3], R. I. Gunadi[2,3], M. J. Al-Farabi[2,3]

[1]Faculty of Medicine and Health, Institut Teknologi Sepuluh Nopember, Surabaya, Indonesia
[2]Faculty of Medicine, Universitas Airlangga, Surabaya, Indonesia
[3]Department of Cardiology and Vascular Medicine, Dr. Soetomo General Academic Hospital, Surabaya, Indonesia

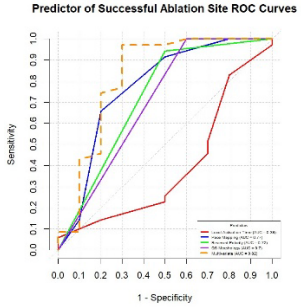
Background and Aims: In patients without structural heart disease, ventricular arrhythmias (VAs), such as premature ventricular contractions (PVCs) and ventricular tachycardia (VT), often originate from the right ventricular outflow tract (RVOT). Although the prognosis is generally favorable, a high arrhythmic burden can lead to serious consequences, including dilated cardiomyopathy and even sudden cardiac death. Radiofrequency catheter ablation (RFCA) is a widely used and effective treatment approach; however, complete elimination of arrhythmia is not always achieved. Therefore, standard techniques have been proposed, such as local activation time (LAT), pace mapping, unipolar QS morphology, and bipolar reversed polarities. This study aimed to assess the most reliable parameter for identifying successful ablation sites in focal idiopathic RVOT arrhythmias.

Materials and Methods: This retrospective cohort study evaluated patients with idiopathic RVOT VAs who underwent RFCA at a single center between January 2024 and February 2025. Demographic and electrophysiological data were analyzed using R software version 4.5.0, including the prediction accuracy.

Results: A total of 45 patients with idiopathic RVOT ventricular arrhythmias (VAs) were included in the study. Of these, 77.8% achieved successful ablation, whereas 22.2% had unsuccessful outcomes. Among the individual predictors, reversed polarity demonstrated the highest diagnostic performance (area under the curve [AUC] 0.721; sensitivity 94.3%; specificity 50%; Youden index [YJI] 1.443). QS morphology was effective in identifying successful ablation sites but tended to falsely indicate effectiveness at unsuccessful sites (AUC 0.700; sensitivity 100%; specificity 40%; YJI 1.400). Pace mapping performed reasonably well in detecting successful and unsuccessful sites (AUC 0.710, sensitivity 65.7%, specificity 70%, YJI 1.357). Local activation time (LAT) alone had limited diagnostic value, as it rarely identified true positives despite a low false-positive rate (AUC 0.394, sensitivity 5.7%, specificity 100%, YJI = 1.057). The optimal cut-off values were –39 ms for LAT and 97.5% for pace mapping (PM). When all four predictors were combined, the multivariate model achieved the highest predictive accuracy for successful ablation sites (sensitivity, 97.1%; specificity, 70%; YJI, 0.6714).

Conclusion: Overall, the use of all four parameters improved the accuracy of identifying ablation targets in idiopathic RVOT arrhythmias.

Keywords: Idiopathic Ventricular Arrhythmia; Local Activation Time; Pace Mapping; QS Morphology; Reversed Polarity



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[12INAHRS-OR13]

Precision Prediction of Atrial Fibrillation Progression via Integrated Inflammatory and ECG Signatures in a Multimodal Deep Learning–Bioinformatics Framework

M. A. Rafi[1], S. M. Rahim[1]
[1]*Faculty of Medicine, Universitas Indonesia, Jakarta, Indonesia*

Background and aims: Atrial fibrillation (AF) progression is associated with increased morbidity and mortality. Current predictive models have limited accuracy, leaving a significant gap in patient-risk stratification. This need is addressed using a validated multimodal deep learning–bioinformatics framework designed to enhance predictive performance and interpretability.

Materials and methods: A total of 847,332 individuals were analyzed using datasets from the UK Biobank, MIT-BIH AF Database, and PhysioNet Computing in Cardiology Challenges (2020–2025). ECG signals underwent preprocessing via NeuroKit2, BioSPPy, and HeartPy, yielding 248 features, including RMSSD, SDNN, LF/HF ratio, P-wave dispersion, PR intervals, and entropy measures. Serum biomarkers (CRP, IL-6, TNF-α, sTNFR1, and sIL-2Rα) were standardized and integrated with a deep neural network architecture, consisting of three convolutional layers, two bidirectional LSTM layers, and a atransformerr encoder with eight8 attention heads and two feed-forward layers), trained using Adam optimization (learning rate = 1e-4, batch size = 512, 100 epochs, early stopping). Hierarchical attention mechanisms facilitate multimodal fusion. Model interpretability employed SHAP (TreeExplainer), Grad-CAM, and t-SNE projection. The evaluation included 10-fold stratified cross-validation and external validation using the MIMIC-IV, ELSA-Brasil, and a prospective hospital cohort.

Results: The multimodal model achieved an AUC-ROC of 0.923 (95% CI: 0.918–0.928), accuracy of 88.5%, sensitivity of 87.3%, specificity of 84.1%, F1-score of 0.856, and PR-AUC of 0.901. External validation yielded AUCs of 0.917, 0.895, and 0.902, respectively, with Cohen's kappa exceeding 0.80 for all datasets. Feature attribution identified P-wave dispersion (SHAP, 0.102) and IL-6 (SHAP, 0.089) as the principal predictors. ECG-derived features contributed 69% to the prediction strength, with inflammatory biomarkers contributing 31%. Visual analytics revealed latent risk clusters and critical waveform segments associated with the risk of progression.

Conclusion: A high-precision deep learning–bioinformatics model integrating IL-6 and ECG dynamics enables robust prediction of AF progression. Its generalizability supports clinical adoption in precision cardiology settings.

Keywords: Atrial Fibrillation, Deep Learning, Bioinformatics, ECG Signal Processing, Inflammatory Biomarkers.

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[12INAHRS-OR14]

Predictors of Labile INR in HFpEF Patients with Atrial Fibrillation: An Observational Cohort Study

R. A. Manan[1] , P. S. Andjari[2] , K. Fahrurrozi[3], M. Akbar[4], W. Wita AS[2], B. Dwiatmojo[2], D. P. Andryan[2]

[1]Umar Wirahadikusumah General Hospital, Sumedang, West Java, Indonesia

[2] Department of Cardiology and Vascular Medicine, Umar Wirahadikusumah General Hospital, Sumedang, West Java, Indonesia

[3] Emergency Department, Klaten Islamic General Hospital, Klaten, Jawa Tengah, Indonesia

[4] Emergency Department, Al-Islam Hospital Bandung, Bandung, West Java, Indonesia

Background: Warfarin is widely used in many regions, necessitating stable INR control. Labile INR is associated with increased thromboembolic and bleeding risks, but its predictors in HFpEF-AF populations remain poorly understood.

Objective: To identify the clinical and biochemical predictors of labile INR in patients with HFpEF and AF undergoing warfarin therapy.

Methods: This was a prospective observational cohort study. We collected data from 87 patients with preserved EF from the AF local registry at our hospital. Patients with valvular AF were excluded from the study. Outcome of this study was to identify predictors of labile INR (defined as INR beyond therapeutic range) and 100% TTR

Results: Patients with CAD (HR 3.82, 95% CI 1.2– 11.5, p = 0.018) and functional mitral valve disease (HR 0.21, CI95% 0.–- 0.63, p = 0.005 were independent predictors of Labile INR. Chronic volume overload in MR can dilute serum proteins, such as albumin, to which warfarin binds. Several drugs used in CAD, especially statins and antiplatelets, can interact with warfarin metabolism (CYP450 enzymes) or increase the risk of bleeding, complicating warfarin dose adjustments. This leads to frequent INR fluctuations.

Conclusion: Labile INR is common in patients with HFpEF and AF undergoing warfarin therapy. Clinicians should consider these predictors when selecting and monitoring anticoagulant therapy.

Keywords: HFpEF, Atrial Fibrillation, Rehospitalization, Warfarin

Table 1. Multivariate Predictor of Labile INR.

Predictors	p- value	RR	95% CI	
			Min	Max
CAD	0,018*	3,82	1,26	11,5
Functional Mitral Regurgitation	0,005*	0,21	0,07	0,63

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[12INAHRS-OR15]

Predictors of 6 month Rehospitalization due to Acute Rapid Ventricular Response and EHRA Class Improvement in HFpEF Patients with Atrial Fibrillation: An Observational Cohort Study

P. S. Andjari[1] , R. A. Manan[2], K. Fahrurrozi[3], M. Akbar[4], W. Wita AS[1], B. Dwiatmojo[1], D. P. Andryan[1]

[1] *Department of Cardiology and Vascular Medicine, Umar Wirahadikusumah General Hospital, Sumedang, West Java, Indonesia*
[2] *Umar Wirahadikusumah General Hospital, Sumedang, West Java, Indonesia*
[3] *Emergency Department, Klaten Islamic General Hospital, Klaten, Jawa Tengah, Indonesia*
[4] *Emergency Department, Al-Islam Hospital Bandung, Bandung, West Java, Indonesia*

Background: Heart failure with preserved ejection fraction (HFpEF) frequently coexists with atrial fibrillation (AFib), complicating patient management. This study aimed to identify clinical, echocardiographic, and laboratory predictors of rehospitalization due to acute rapid ventricular episodes and Improvement in EHRA class over time.

Methods: This was a prospective observational cohort study. We collected data from 87 patients with preserved EF from the AF local registry at our hospital. Patients with valvular AF were excluded from the study. The aim of this study was to identify predictors of 6-month rehospitalization of RVR and improvement in mEHRA.

Results: Amiodarone (RR 0.02, CI 95% 0.00 – 0.32, p = 0.005), digoxin (RR 0.12, CI 95% 0.02 – 0.69, p = 0.017), and beta-blockers with digoxin (RR 0.02, CI 95% 0.02 – 0.32, p = 0.003) were independent predictors of Acute Rehospitalization due to Rapid Ventricular Episodes. This does not mean that antiarrhythmics increase rehospitalization but rather serves as a bailout strategy for patients who are already on beta-blockers but are rehospitalized due to acute RVR. Beta-blockers (RR 2.33, CI 95% 1.41 – 3.86, p = 0.01) and RAS vasodilators (RR 2.16, CI 95% 1.27 – 3.67, p = 0.01) were predictors of improved mEHR classification.

Conclusion: Rehospitalization due to acute RVR and AFib-related symptoms, quantified by the EHRA (European Heart Rhythm Association) classification, remain key outcomes. However, predictors of these outcomes in patients with HFpEF-AFib are not well established. These findings highlight the importance of comprehensive risk assessment and tailored management strategies to reduce recurrent hospitalizations and improve the symptom burden in this population.

Keywords: HFpEF, Vasodilator, Atrial Fibrillation, Rehospitalization

Table 1. Result AF HFPEF 1.

	Rehospitalization – Acute RVR			
Variables	**No (n=77)**	**Yes (n=10)**	**p-value**	**RR (95% CI)**
Functional Valve Regurgitation	33 (42.9%)	7 (70%)	0.18	1.14 (0.97 – 1.33)
Amiodarone	1 (2.6%)	2 (20.0%)	0.03*	2.71 (0.54 – 13.5)
Beta-Blockers	68 (88.%)	6 (60.0%)	0.04*	0.75 (0.52 – 1.09)
Digoxin	8 (10.4%)	3 (30.0%)	0.11*	1.25 (0.86 – 1.81)
BB-Digoxin	1 (1.3%)	2 (20%)	0.03	2.71 (0.55 – 13.5)
No Vasodilator	4 (5.2%)	2 (20.0%)	0.14	1.35 (0.76 – 2.39)

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[12INAHRS-OR16]

Predictors of Labile INR and TTR 100% in HFpEF Patients with Atrial Fibrillation: An Observational Cohort Study

R. A. Manan[1], P. S. Andjari[2] , K. Fahrurrozi[3], M. Akbar[4], W. Wita AS[2], B. Dwiatmojo[2], D. P. Andryan[2]

[1] *Umar Wirahadikusumah General Hospital, Sumedang, West Java, Indonesia*
[2] *Department of Cardiology and Vascular Medicine, Umar Wirahadikusumah General Hospital, Sumedang, West Java, Indonesia*
[3] *Emergency Department, Klaten Islamic General Hospital, Klaten, Jawa Tengah, Indonesia*
[4] *Emergency Department, Al-Islam Hospital Bandung, Bandung, West Java, Indonesia*

Background: Warfarin is widely used in many regions, necessitating stable INR control. Labile INR is associated with increased thromboembolic and bleeding risks, but its predictors in HFpEF-AF populations remain poorly understood. This study aimed to identify predictors of labile INR and 100% TTR in patients with HFpEF and AF on warfarin therapy.

Methods: This was a prospective observational cohort study. We collected data from 80 patients with non-valvular AF and HFpEF from the local registry at our hospital. The outcome of this study was to identify predictors of labile INR (defined as INR beyond the therapeutic range) and 100% TTR from the last three INR measurements.

Results: Patients with CAD, digoxin use, and CHA2DS2-VA scores ≥ 2 were independent predictors of Labile INR. Functional mitral regurgitation was a predictor of TTR 100%. Functional MR kinetics may play a role in promoting stable INR. Digoxin itself does not cause labile INR. Instead, instability likely arises from concomitant comorbidities (heart failure and infection, which leads to RVR) in patients requiring digoxin. Several CAD medications, especially statins and antiplatelets, can interact with warfarin metabolism or increase the risk of bleeding, complicating warfarin dose adjustment. CHA_2DS_2-VA scores and labile INR are interconnected through shared pathophysiology and dynamic risk progression (age, renal dysfunction, and hepatic congestion).

Conclusion: Several factors may promote or stabilize Labile INR. Nevertheless, this is a common problem among patients with HFpEF and AF on warfarin therapy, and clinicians should be aware of it.

Keywords: Atrial Fibrillation, Rehospitalization, Warfarin, INR, HFpEF

Table 1. Multivariate analysis of Labile INR & TTR 110%.

Labile INR	P value	RR	IK 95%	
			Min	Max
CAD	0,038*	3.38	1.07	10.7
Functional Mitral Regurgitation	0,016*	0.26	0.09	0.78
Digoxin	0.012*	19.8	1.95	201
CHA_2DS_2-VA Score >=2	0.024*	3.53	1.18	10.5
TTR 100% last 3 measurements				
CAD	0.038*	0.30	0.09	0.93
Functional Mitral Regurgitation	0.016*	3.87	1.29	11.6
Digoxin	0.012*	0.05	0.00	0.51
CHA_2DS_2-VA Score >=2	0.024*	0.28	0.10	0.85

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[12INAHRS-OR17]

The PRIME score: Padjadjaran predictive scoring model to predict prime hearts for recovery in atrioventricular block with reduced ejection fraction

W. Kamarullah[1], R. Pranata[1], G. Karwiky[1], C. Achmad[1], M. Iqbal[1]
[1]Department of Cardiology and Vascular Medicine, Faculty of Medicine, Universitas Padjadjaran, Hasan Sadikin General Hospital, Bandung, Indonesia

Background and aims: Left bundle branch area pacing (LBBAP) has emerged as a physiological pacing strategy for patients with atrioventricular block (AVB) and reduced ejection fraction (LVEF); however, predictors of left ventricular (LV) recovery remain unclear, particularly among those not meeting standard cardiac resynchronization therapy (CRT) criteria. This study aimed to develop and validate the **P**adjadjaran P**R**edictive Scor**I**ng Model for Left Ventricular Recovery (PRIME) score to identify patients most likely to experience LVEF improvement following LBBAP.

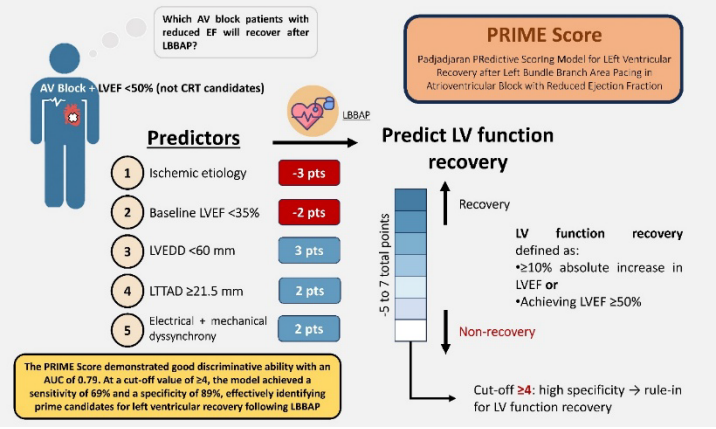
Materials and methods: We prospectively enrolled 48 patients with AVB and LVEF <50% who underwent de novo LBBAP between June 2020 and June 2024 at Dr. Hasan Sadikin General Hospital. Patients with prior RV pacing or CRT were excluded from the study. Echocardiographic and ECG data were collected at baseline and 12-month follow-up. LVEF improvement was defined as an absolute increase of ≥10% or normalization (LVEF ≥50%). Predictors were identified using logistic regression, and a scoring model was constructed using B/SE weighting. The model performance was assessed using ROC analysis.

Results: Among 48 patients (mean age 54.4±18.8 years, 43.8% male), 60.4% met the criteria for LVEF improvement. Responders more frequently had non-ischemic cardiomyopathy, smaller LVEDD, longer lead-tip to tricuspid annulus distance (LTTAD), and both electrical and mechanical dyssynchrony (all P<0.05). Five variables were selected for the PRIME Score: ischemic etiology (–3), baseline LVEF <35% (–2), LVEDD <60 mm (+3), LTTAD ≥21.5 mm (+2), and combined dyssynchrony (+2). The score showed good discriminative ability (AUC 0.79, 95% CI: 0.62–0.98), with a cutoff of ≥4 yielding 69% sensitivity and 89% specificity. Higher PRIME Scores were strongly associated with an increasing probability of LVEF recovery, from 5.3% (score -5) to 92.5% (score 7).

Conclusion: The PRIME Score offers a simple yet robust tool for predicting LV functional recovery after LBBAP in patients with AVB and LVEF <50%. By integrating structural, electrical, and procedural factors, individualized pacing decisions can be facilitated, especially in patients who are not traditionally eligible for CRT. Prospective validation in larger cohorts is required.

Keywords: left bundle branch area pacing; atrioventricular block; left ventricular recovery; predictive scoring model; heart failure with reduced ejection fraction

Graphical Abstract



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[12INAHRS-OR18]

Enhancing Cardiac Arrhythmia Complexities Detection with Electrocardiogram Signal Data Using Convolutional Neural Networks (CNNs)-Based Model

A.P. Wulandari[1,2], A. Rizal[2], S. Mandala[3,4], W. Jatmiko[5], S. Nurmaini[6], Adiwijaya[3,4]
[1]Faculty of Medicine, Universitas Brawijaya, Malang, East Java, Indonesia
[2]Department of Cardiology and Vascular Medicine, Universitas Brawijaya, Saiful Anwar General Hospital, Malang, East Java, Indonesia
[3]Human Centric (HUMIC) Engineering, Telkom University, Bandung 40257, Indonesia
[4]School of Computing, Telkom University, Bandung 40257, Indonesia
[5]Fakultas Ilmu Komputer Universitas Indonesia, Depok 16425, Indonesia
[6]Intelligent System Research Group, Universitas Sriwijaya, Palembang, South Sumatra 30139, Indonesia

Background and aims: Cardiac arrhythmias are significant cardiovascular health issues. Early arrhythmia detection is crucial and may lower mortality and morbidity. The rapid growth in digital technology has provided opportunities for arrhythmia screening, risk assessment, and diagnosis, enabling the initiation of appropriate therapeutic interventions in patients with arrhythmias. Diagnostic technology has been enhanced by artificial intelligence (AI) algorithms, and it has increasing potential for large-scale populations. Electrocardiogram (ECG) signals are commonly used to diagnose arrhythmias owing to their ability to identify abnormalities in morphology and rhythm. This study aims to demonstrate the deep learning complexities of arrhythmia classification from ECG signal data using a Convolutional Neural Network (CNN) model.

Materials and methods: We evaluated the performance of CNNs with Long Short-Term Memory (LSTM) for optimizing cardiac arrhythmia risk prediction and detection. This study focuses on detecting four common arrhythmia types from ECG records: premature atrial contractions (PACs), premature ventricular contractions (PVCs), left bundle branch block (LBBB), and right bundle branch block (RBBB). Modified lead II (MLII) and one of the following leads, V1-V5, were focused solely on ECG signal segments around the R-peak and addressed the hyperparameter tuning of the arrhythmia dataset.

Results: Our study showed an accuracy, sensitivity, and specificity, and an F1-score of 99.97%, 99.97%, 99.97%, 99.99%, and 99.97%, respectively.

Conclusion: This study successfully developed a deep learning model for arrhythmia classification from ECG signal data using a Convolutional Neural Network (CNN) model with significant sensitivity and specificity.

Keywords: Cardiac Arrhythmia Complexities Detection, Artificial Intelligence, Electrocardiogram, Convolutional Neural Networks, Long Short-Term Memory

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[12INAHRS-OR19]

Atrial Myopathy as a Key Predictor of Cryptogenic Stroke The Role of CHA_2DS_2-VASc Score and Atrial Fibrillation

C. Kahadi[1], I. Rakhmadhani[1], A. Rizal[1]

[1]Brawijaya Cardiovascular Research Centre, Department of Cardiology and Vascular Medicine, Faculty of Medicine, Universitas Brawijaya, Malang, Indonesia.

Background: Cryptogenic stroke (CS) accounts for a significant proportion of ischemic strokes, with atrial fibrillation (AF) being the primary thromboembolic source. Emerging evidence suggests that atrial myopathy (AM), an architectural, structural, electrophysiological, or contractile atrial abnormality, may contribute to stroke independently of AF. This study evaluated the association of AM, with and without AF, with CS risk and explored the predictive value of combining AM with CHA_2DS_2-VASc scoring.

Methods: A retrospective analysis was conducted on 112 patients admitted to Saiful Anwar Hospital, Malang (January 2023–December 2024). Univariate, bivariate (chi-square, t-test, and Mann-Whitney U-test), and multivariate logistic regression analyses were performed to assess the predictors of CS.

Results: AM was a strong independent predictor of CS (OR 6.41, 95% CI: 2.37-27.36, $p<0.001$). The combination of CHA_2DS_2-VASc ≥2 and AM significantly improved CS prediction (OR 7.95, 95% CI: 2.63-24.03, $p<0.001$) compared with CHA_2DS_2-VASc ≥2 alone (OR 1.91, 95% CI: 0.65-5.60, $p=0.239$) or CHA_2DS_2-VASc ≥2 with AF and AM (OR 3.60, 95% CI: 0.99–13.16, $p=0.050$).

Conclusion: Atrial myopathy, irrespective of AF, is strongly associated with cryptogenic strokes. Integrating AM into stroke risk stratification, particularly with CHA_2DS_2-VASc ≥2, enhances predictive accuracy, suggesting a potential shift in risk assessment paradigms

Keywords: Cryptogenic Stroke, Atrial Myopathy, Atrial Fibrillation, CHA_2DS_2-VASC score

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[12INAHRS-OR20]

Investigating Rare Coding and Structural Variants in Atrial Fibrillation: A Bioinformatics Approach

S. L. Xius[1], M. A. Fatih[1], N. P. Lesmana[1], S. D. Syofyan[1], S. Salim[1,2]
[1]Faculty of Medicine, Universitas Indonesia, Jakarta, Indonesia
[2]Cardiology Division, Department of Internal Medicine, Faculty of Medicine, Universitas Indonesia, Dr. Cipto Mangunkusumo Hospital, Jakarta, Indonesia.

Background: Atrial fibrillation (AF), the most common arrhythmia worldwide, affects over 59 million people and is increasing due to the aging population. Identifying disease-related genes involves various approaches. Bioinformatics analyses, such as Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment, and protein-protein interaction (PPI) networks, help to clarify gene functions and key molecular mechanisms. This study used these methods to identify rare coding sequences and structural variants that significantly contribute to AF susceptibility.

Methods: We collected a gene expression dataset (GSE22590) from the GEO database. Differentially expressed genes (DEGs) between diseased and control samples were identified using GEO2R. Overlapping DEGs were further analyzed to investigate each biological function and associated pathway through GO and KEGG pathway enrichment analysis, which was conducted using the Enrichr platform. PPI network was constructed using the Cytoscape Search Tool for the Retrieval of Interacting Genes database (STRING) with a confidence cutoff of 0.9. The top 10 hub genes were identified using the maximal clique centrality (MCC) via the CytoHubba plugin.

Results: Analysis of the two groups revealed 701 common DEGs, including 440 upregulated and 261 downregulated genes. The upregulated genes were associated with processes such as aminoacyl-tRNA biosynthesis ($_{adj}$ p: 0.0001) and products such as low-density lipoprotein particles ($_{adj}$ p: 0.7611) and chylomicrons ($_{adj}$ p: 0.7611). In contrast, the downregulated genes were involved in protein digestion and absorption ($_{adj}$ p: 0.00002042), extracellular matrix organization ($_{adj}$ p: 0.00002870), and cell adhesion mediator activity ($_{adj}$ p: 0.03129). The downregulated products included intracellular organelle lumen ($_{adj}$ p = 0.001050). Additionally, 89 DEGs out of 701 were screened into the PPI, which consisted of 89 nodes and 110 edges. Key hub genes by MCC are ranked as follows: FN1 (score=207), COL1A1 (score=175), FBN1 (score=174), DCN (score=168), BGN (score=150), COL1A2 (score=135), ELN (score= 43), COL3A1 and TLR4 (score=24), POSTN (score=10).

Conclusion: This study identified key pathways and hub genes that are differentially expressed in atrial fibrillation and may contribute to its pathogenesis. However, as with all bioinformatic analyses, false positives may occur, and these findings require experimental validation to confirm their functional relevance, suggesting further investigation.

Keywords: Atrial fibrillation, bioinformatics

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[12INAHRS-OR21]

Decoding Incomplete Penetrance in Arrhythmogenic Cardiomyopathy: A Bioinformatics Analysis of Symptomatic and Asymptomatic Carriers

M. A. Fatih[1], S. L. Xius[1], N. P. Lesmana[1], S. D. Syofyan[1], S. Salim[2]
[1]Faculty of Medicine, Universitas Indonesia, Jakarta, Indonesia
[2]Cardiology Division, Department of Internal Medicine, Faculty of Medicine, Universitas Indonesia, Dr. Cipto Mangunkusumo Hospital, Jakarta, Indonesia.

Background: Arrhythmogenic cardiomyopathy (ACM) is a rare inherited disorder with incomplete penetrance, in which carriers of the same mutation may differ in symptom presentation. To understand the molecular basis of this variability, gene expression profiling combined with functional enrichment analyses, such as Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG), can be used to highlight the affected pathways. Protein-protein interaction (PPI) network analysis may further reveal the central hub genes that drive disease expression. This study used these approaches to compare symptomatic and asymptomatic ACM carriers.

Methods: Gene expression data (GSE222793) were extracted from the Gene Expression Omnibus (GEO) database. Differentially expressed genes (DEGs) were derived from stem cell-derived cardiomyocytes between two groups (symptomatic and asymptomatic carriers) from the same family, detected using GEO2R. Enrichment analyses (GO and KEGG) were conducted using Enrichr. PPI networks were constructed using Cytoscape with the Search Tool for the Retrieval of Interacting Genes (STRING) using a confidence cutoff of 0.9, and the top hub genes were identified using degree and maximal clique centrality (MCC) via the CytoHubba plugin.

Results: We identified 85 DEGs (53 upregulated and 32 downregulated) in symptomatic carriers. Upregulated genes enriched in pathways including hypertrophic cardiomyopathy (p.adj=0.005607), dilated cardiomyopathy (p.adj=0.005607), and products such as sarcolemma (p.adj=0.1157) and calcium channels (p.adj=0.1557). Downregulated genes included products such as cell adhesion molecules (p.adj=0.07909) and cytoskeleton (p.adj=0.03624), and processes such as intermediate filament bundle assembly (p.adj=0.00005276) and vascular morphogenesis (p.adj=0.007482). PPI analysis included 17 DEGs (17 nodes and 43 edges). Key hub genes by degree were ranked as follows: USP9Y and ZFY (node degree=9), DDX3Y, KDM5D, UTY, and EIF1AY (node degree=8), PRKY, and RPS4Y1 (node degree=7), with other genes having node degrees ≤5. The key hub genes by MCC were ranked as follows: USP9Y and ZFY (score=5166), DDX3Y, KDM5D, and UTY (score=5160), EIF1AY (score=5046), PRKY, and RPS4Y1 (score=5040), with other genes having scores ≤120.

Conclusion: This study identified pathways and hub genes that are differentially expressed in ACM carriers and potentially contribute to incomplete penetrance in ACM. Our high cutoff value suggests the robustness and accuracy of our methods. However, the need for experimental validation should be considered, necessitating further studies.

Keywords: Arrhythmia, cardiomyopathy, bioinformatics

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[12INAHRS-OR22]

One-Day vs. Three-Day Antibiotic Prophylaxis for Prevention of Pocket Infection in Permanent Pacemaker Implantation: A Non-Inferiority Randomized Controlled Trial

I. D. Rochmawati[1], S. S. Baskoro[2], A. Rizal[2,3], Y. Waranugraha[2,3], A. P. Wikananada[2,3]
[1]Department of Cardiology, Urip Sumoharjo General Hospital, Bandar Lampung, Indonesia
[2]Cardiovascular Research Center, Faculty of Medicine, Brawijaya University, Malang, Indonesia
[3]Department of Cardiovascular Medicine, Saiful Anwar General Hospital, Malang, Indonesia

Background and aims: The optimal duration of antibiotic prophylaxis for Permanent Pacemaker (PPM) implantation remains controversial. Although extended antibiotic regimens are widely used to prevent device-related infections, they may contribute to increased antimicrobial resistance, higher healthcare costs, and adverse drug events. Recent studies have questioned the necessity of prolonged prophylaxis in low-risk patients, highlighting the need to reassess the current practices. To evaluate whether a one-day antibiotic prophylaxis regimen is non-inferior to the standard three-day regimen in preventing superficial pocket infections following PPM implantation.

Materials and methods: An ongoing single-center, open-label, randomized controlled trial was conducted at Saiful Anwar General Hospital, Malang, Indonesia, in June 2023 (ClinicalTrials.gov Identifier: NCT06355115). A total of 103 patients who underwent PPM implantation were enrolled: 55 received a one-day antibiotic prophylaxis regimen, and 48 received the standard three-day regimen. The primary outcome was the incidence of superficial pocket infections. The non-inferiority margin was assessed using an odds ratio (OR) margin of 0.77, based on prior literature.

Results: Superficial pocket infection rates were similar between the two groups. Bivariate analysis did not demonstrate a significant difference in pocket infection between the one-day group compared to the three-day group, RR 0.520 (95% CI: 0.430–0.629, p = 0.122). Non-inferiority was established based on a predefined non-inferiority margin.

Conclusion: One-day antibiotic prophylaxis is non-inferior to the standard three-day regimen in preventing superficial pocket infections in patients undergoing PPM implantation. These findings support the potential for shorter antibiotic use without an increased infection risk, contributing to antimicrobial stewardship efforts.

Keywords: PPM, antibiotic prophylaxis, pocket infection, non-inferiority, randomized controlled trial, superficial infection

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[12INAHRS-OR23]

Prioritizing Metabolic Risk for Atrial Fibrillation Reduction in Indonesia: Socio-Demographic Index (SDI) Targeted Interventions to Address Nationwide Disparities

I. Rakhmadhani[1], V. Mayangsari[1], A. Rizal[1]
[1]*Department of Cardiology and Vascular Medicine, Faculty of Medicine, Universitas Brawijaya, Malang, Indonesia*

Background: Indonesia has the second-highest prevalence of atrial fibrillation (AF) in Southeast Asia. Provincial heterogeneity in metabolic determinants remains unexamined despite widening socioeconomic inequities, a critical knowledge deficit that this investigation resolves through socio-demographic index (SDI) stratification.

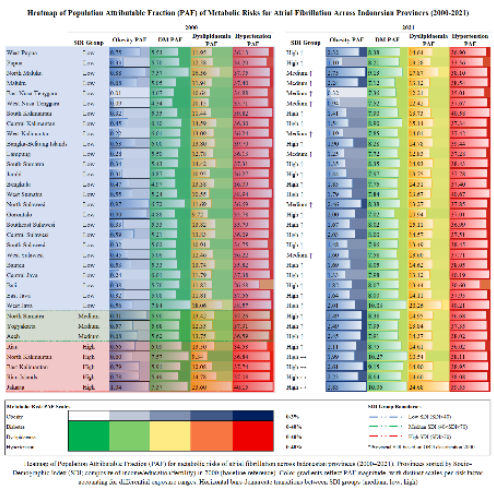
Methods: We analyzed Global Burden of Disease data (2000-2021) to compute population attributable fractions (PAF) for four metabolic risks across 34 Indonesian provinces: hypertension, obesity, dyslipidemia, and diabetes mellitus (DM). Provinces were annually classified into low, medium, and high SDI groups. We used three analytical approaches: (1) ANOVA with Tukey post-hoc tests for SDI group comparisons; (2) mixed-effects models incorporating provincial heterogeneity; and (3) EAPC calculation to assess trends in AF prevalence, DALYs, and mortality.

Results: Hypertension demonstrated national dominance (median PAF 36.4-37.4%), attaining maximal influence in medium-SDI provinces. SDI-stratified disparities were statistically significant for all metabolic risks ($p<0.001$). Key provincial patterns emerged

1. Low-SDI provinces sustained dyslipidemia burden (median PAF: 11.84% [IQR 9.72–18.69]) while experiencing Indonesia's most rapid AF mortality progression (EAPC +1.59%/yr). Mixed models confirmed dyslipidemia's provincial heterogeneity (variance 0.0396) and a national upward trend (+0.059%/yr, $p<0.001$).
2. Urban metabolic crisis: High-SDI provinces showed dual DM/obesity drivers (median PAF: DM 7.89%, obesity 1.82%), steepest AF prevalence growth (EAPC +0.28%/year), and highest dyslipidemia burden (14.58% PAF; Tukey $\Delta >0.035$ vs. low-SDI, $p<0.001$).
3. Hypertension acceleration: Hypertension risks increased most rapidly in low-SDI regions (mixed model: +0.0385%/yr acceleration, $p<0.001$), while obesity surged fastest in high-SDI areas (national trend +0.103%/yr; low-SDI deceleration: −0.056%/yr, $p<0.001$).
4. Indonesia had Southeast Asia's second-highest AF mortality growth (EAPC +1.44%/yr), with low-SDI provinces driving deaths (EAPC +1.59%/yr) and high-SDI provinces driving prevalence.

Conclusion: While hypertension uniformly contributes to preventable AF nationwide (36-38% PAF), SDI-specific priority interventions emerge: high-SDI provinces (e.g., Jakarta) necessitate integrated obesity/diabetes management complementing hypertension control to address multifactorial metabolic pathology; medium-SDI regions (e.g., North Sumatra) demand singular hypertension focus given their 37.4% peak burden; and low-SDI provinces (e.g., Papua) require urgent lipid-centric interventions to mitigate 11.8% of preventable deaths while countering hypertension acceleration. Such stratified public health measures—tailoring metabolic complexity resolution in urban centers, hypertension prioritization in transitional economies, and dyslipidemia reduction in resource-limited settings— have the potential to avert thousands of annual AF cases across socioeconomic strata.

Keywords: Atrial fibrillation, metabolic syndrome, population attributable fraction, EAPC, health disparities



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[12INAHRS-OR24]

Ventricular Arrhythmias in Hemodialysis Patients: Prevalence and Predictors from a Non-Referral Indonesian Hospital

G. S. E. Pambudi[1], F. Siddiq[2]
[1]*Jenderal Soedirman University*
[2]*Cardiologist at Nur Hidayah General Hospital, Bantul, Yogyakarta, Indonesia*

Background: Ventricular arrhythmias (VAs) significantly contribute to morbidity and mortality in patients undergoing chronic hemodialysis (HD), with a high risk of sudden cardiac death (SCD). However, few data are available regarding their prevalence and risk factors in non-referral healthcare settings, particularly in low- and middle-income countries (LMICs).

Objective: This study aimed to determine the prevalence and clinical predictors of VAs in maintenance HD patients at a non-referral Indonesian hospital using prospective ECG monitoring and comprehensive clinical data.

Methods: We conducted a single-center, prospective, observational study between January and December 2023. Adult patients with end-stage renal disease (ESRD) undergoing chronic HD at Nur Hidayah General Hospital were enrolled. Continuous ECG monitoring was performed throughout each HD session and during a 60-minute post-HD recovery period. VAs were defined and classified according to the standard cardiology guidelines. Demographic, laboratory, echocardiographic, and dialysis-related data were collected. Multivariate logistic regression analysis was performed to identify the independent predictors of VA occurrence.

Results: Of the 158 patients (mean age 52.3 ± 10.4 years; 55.1% male), 55 (34.8%) exhibited one or more forms of VA. PVCs were the most frequent (28.5%), followed by NSVT (6.3%). No cases of sustained VT or ventricular fibrillation (VF) were observed. Multivariate analysis identified three independent predictors: serum potassium fluctuation ≥1.0 mmol/L between pre- and post-dialysis (OR 2.41; 95% CI: 1.32–4.39; p = 0.004), intradialytic hypotension (OR 1.98; 95% CI: 1.15–3.42; p = 0.014), and echocardiographic evidence of LVH (OR 2.87; 95% CI: 1.52–5.41; p = 0.001).

Conclusion: Ventricular arrhythmias are common and clinically significant in patients undergoing chronic HD at non-referral centers. Key modifiable risk factors include electrolyte imbalance, hemodynamic instability, and structural cardiac abnormalities. Targeted risk stratification and protocolized monitoring may reduce the incidence of arrhythmic events in resource-constrained settings.

Keywords: ventricular arrhythmia; hemodialysis; low-resource setting; Indonesia; cardiovascular risk; predictors; sudden cardiac death; non-referral hospital

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[12INAHRS-OR25]

AI Copilot for the Heart: Real-Time Arrhythmia Alert System in Autonomous and Semi-Autonomous Vehicles

A. A. Jasmine[1], A. N. Putri[1], N. K. Ryanto[1]
[1]Faculty of Medicine Universitas Indonesia, Jakarta, Indonesia

Background: Sudden arrhythmic events pose a critical risk to drivers by causing syncope, cardiac arrest, and even death. This risk is especially pronounced among aging and cardiovascular high-risk populations, many of whom are driving autonomous or semi-autonomous vehicles. While ECG-based in-vehicle monitoring has been explored, existing systems lack real-time arrhythmia classification and automatic safety responses. This study aims to develop and evaluate an integrated, AI-based cardiac monitoring and response system that enhances driver safety by detecting arrhythmias in real time and activating autonomous in-vehicle protocols.

Methods: We developed an integrated, AI-based in-vehicle cardiac monitoring and safety response system, named "Copilot for the Heart." The system combines three biosensing modalities: wearable single-lead ECG sensors, PPG-based steering-wheel sensors, and seat-embedded ballistocardiography. A hybrid deep learning model using Convolutional Long Short-Term Memory (ConvLSTM) architecture was implemented for real-time arrhythmia detection and classification. Upon detection of abnormal cardiac rhythms, three automatic safety responses were triggered depending on severity: (1) audio-visual driver alert, (2) gradual lane-centering and braking, and (3) simulated emergency dispatch transmitting ECG and geolocation data. Behavioral and physiological responses were recorded simultaneously to evaluate system performance.

Results: The system achieved ~95% overall arrhythmia classification accuracy, with atrial fibrillation sensitivity and specificity of 96–97% and 97–98%, respectively. Ventricular arrhythmias were detected with ~95% accuracy; bradyarrhythmias ~92%. The mean time from arrhythmia onset to system alert was 2.0 ± 0.5 seconds, with AI inference latency under 50 ms. False-alarm rate was <5%. In 90–92% of arrhythmic events, automated maneuvers successfully stabilized the vehicle and prevented simulated collisions. Participant adherence and comfort were high, but variability in wearable usage was noted.

Conclusion: The AI Copilot system demonstrates promising feasibility for real-time arrhythmia detection and in-vehicle response activation. While simulation data are encouraging, real-world implementation faces challenges, including motion artifacts, signal fidelity, varying levels of vehicle autonomy, and inconsistent wearable usage. Biometric monitoring also raises some concerns related to ethics and data privacy. The upcoming challenges will target clinical validation, cost analysis, and multi-sectional integration for real-world adaptation of smart mobility.

Keywords: Arrhythmia, Artificial Intelligence, Autonomous Vehicles, ECG Monitoring, Cardiovascular Safety System

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[12INAHRS-OR26]

Comparative Effectiveness of Adjunctive Digoxin vs Amiodarone in Atrial Fibrillation Patients under Rate Control Experiencing Recurrent Rapid Ventricular Response: A Single-Centre Observational Analysis Study

D.P. Andryan[1], P.S. Andjari[1] , R.A. Manan[2], K. Fahrurrozi[3], M. Akbar[4], C. Parameswari[5], W.W.A Shariefuddin[1], B. Dwiatmojo[1]

[1] Department of Cardiology and Vascular Medicine, Umar Wirahadikusumah General Hospital, Sumedang, West Java, Indonesia
[2]Umar Wirahadikusumah General Hospital, Sumedang, West Java, Indonesia
[3] Emergency Department, Klaten Islamic General Hospital, Klaten, Jawa Tengah, Indonesia
[4] Emergency Department, Al-Islam Hospital Bandung, Bandung, West Java, Indonesia
[5] Faculty of Medicine, Universitas Padjadjaran, Bandung, Indonesia

Background: Patients with atrial fibrillation (AF) under rate control may still experience recurrent Rapid Ventricular Response (RVR) episodes. Adjunctive antiarrhythmic therapy, such as digoxin or amiodarone, is often considered in this setting. However, real-world data comparing clinical outcomes are limited.

Objective: To compare clinical outcomes and the incidence of recurrent RVR in patients with AF receiving adjunctive digoxin or amiodarone despite ongoing rate control therapy.

Methods: This study was 6 month prospective observational cohort study conducted from November to May 2025. We collected data from 203 patients from the AF local registry at our hospital. Patients who developed recurrent tachyarrhythmia were grouped based on adjunctive therapy: digoxin or amiodarone. The outcome was the comparison of recurrent tachyarrhythmia within six months after adjunctive therapy.

Results: A total of 203 patients were included in this study, and most of them (197 patients, 97%) were under rhythm control management with a beta blocker. Recurrent tachyarrhythmia occurred in 29 (14.3%) patients. Recurrent atrial fibrillation with rapid ventricular response occurred more frequently in the group receiving adjunctive digoxin (n = 18, RR 3.93, CI 95% 1.4 – 10.7, p=0.016) than ino the amiodarone group (n = 1, RR 0.21, CI 95% 0.08 – 0.55, p=0.005).

Conclusion: In patients with atrial fibrillation on rate-control therapy who experienced recurrent tachyarrhythmia, adjunctive digoxin was associated with a nearly fourfold higher 6-month risk of recurrent AF with a rapid ventricular response. In contrast, amiodarone use was associated with a 79% reduction in the 6-month risk of recurrent AF with a rapid ventricular response.

Keywords: Digoxin, Amiodarone, Atrial Fibrillation, Rehospitalization, Tachyarrhythmia

	Recurrence of RVR after additional AAD			
Predictors	**No (n=9)**	**Yes (n=20)**	**p-value**	**RR (95% CI)**
Add. Digoxin	4 (44.4%)	18 (90%)	0.016*	3.93 (1.44 – 10.7)
Add. Amiodarone	5 (55.6%)	1 (5.0%)	0.005*	0.21 (0.08 – 0.54)

*p<0.05

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[12INAHRS-OR27]

A Machine Learning Approach to Idiopathic PVC Localization: Integrating ECG, 3D Geometry, and Local Activation Time Data

D.E. Tambunan[1], A,Rizal[1]

[1]Cardiovascular Department, Saiful Anwar General Hospital, Universitas Brawijaya, Malang, Indonesia

Background: Catheter ablation is an effective therapy for patients with symptomatic idiopathic premature ventricular contractions (PVC). Determining the precise etiology of cardiac arrhythmias to enable suitable treatment is one of the most formidable issues.

Materials and Methods: This study presents a novel machine learning approach to determine the precise etiology of idiopathic PVCs. Our approach employs three extensive data types: 12-lead ECG recordings, detailed 3D models of the patient's heart, and local activation time (LAT) measurements acquired during treatment. We analyzed data from patients who underwent successful PVC ablation, creating a solid foundation for identifying the sources of arrhythmias. We extracted important information from each dataset in these cases and used it to train a machine learning model to identify the complex, often non-straightforward connections between the data and the actual PVC locations.

Results: Our methodology enhanced the accuracy and dependability of PVC localization compared with previous techniques that heavily depended on the operator's expertise. This arises from the integration of information from all three sources. The preliminary outcomes were encouraging.

Conclusions: The findings indicate that the ablation technique could be optimized, the duration of therapy potentially reduced, patient radiation exposure minimized, and the likelihood of problems diminished. This technology could enhance the efficacy and safety of PVC ablation procedures by offering a more precise, patient-centered approach.

Keywords: 3D Ablation, Machine Learning, Premature Ventricular Contractions (PVC)

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[12INAHRS-OR28]

Correlation Between β-Angle and r′ Triangle Base Duration at Right Precordial Leads and Brugada Provocation Test Results

I. Posangi[1], S. B. Raharjo[1,2], D. A. Hanafy[1,2], D. Y. Hermanto[1,2], R. R. Waliyuddin[1,2]
I. A. Balqis[1], Y. Yuniadi[1,2]
[1]National Cardiovascular Center Harapan Kita, Jakarta, Indonesia
[2]Faculty of Medicine, Universitas Indonesia, Jakarta, Indonesia

Background and Aims: Brugada Syndrome (BrS) is a cardiac channelopathy typically diagnosed by the presence of a type 1 Brugada ECG pattern. In cases of type 2 and 3 patterns, a positive provocation test using sodium channel blockers (SCB) is required. However, SCB agents are not universally available in all hospitals. This study aimed to evaluate whether the β-angle and r′-wave triangle base duration at right precordial leads can serve as non-invasive alternatives to SCB provocation testing.

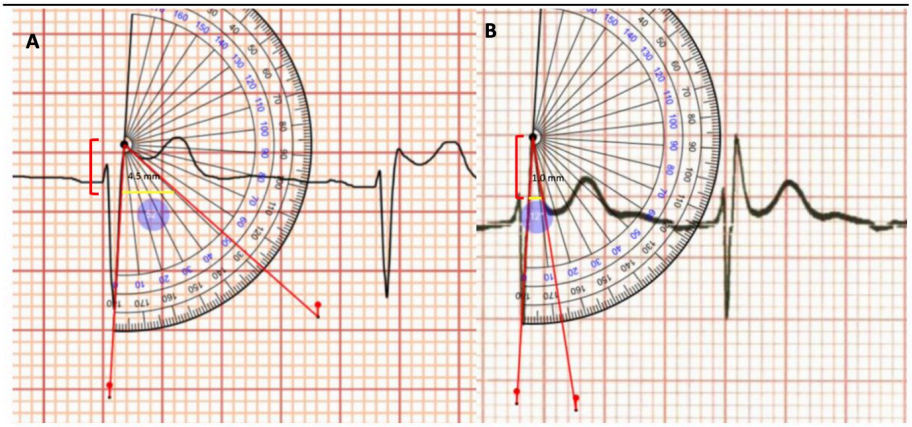
Materials and Methods: We conducted a cross-sectional study of 35 patients with suspected BrS (types 2 or 3) who underwent SCB provocation testing with flecainide. The β-angle and r′ triangle base duration were measured in leads V1 or V2 from the baseline ECGs. The data were analyzed to compare the ECG parameters between the provocation-positive and-negative groups. A subgroup of 19 patients underwent electrophysiological studies to assess the inducibility of ventricular tachycardia (VT) and fibrillation (VF).

Results: The study cohort consisted of 85.7% males. SCB provocation was positive in 71.4% of the patients (n=25). The mean β-angle was significantly higher in the provocation-positive group than in the negative group (35.12 ± 16.40° vs. 22.20 ± 11.48°, p = 0.030). Similarly, the r′ triangle base duration was significantly greater in the positive group (4.02 ± 2.44 mm vs. 2.08 ± 1.00 mm, p= 0.002). Among those who underwent EP studies, VT/VF was induced in 31.6% of the cases.

Conclusion: Both the β-angle and r′-wave triangle base duration were significantly higher in patients with positive SCB provocation, suggesting their potential as simple, non-invasive ECG markers to support BrS diagnosis when provocation testing is not feasible.

Keywords: Brugada Syndrome, ECG, β-angle, r′ wave, sodium channel blocker, provocation test

	Positive provocation (n=25)	Negative provocation (n=10)	p-value
Mean B-angle	35.12 ± 16.40	22.20 ± 11.48	0.030
Mean R'triangle base duration	4.02 ± 2.44	2.08 ± 1.00	0.002



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[12INAHRS-OR29]

Postoperative Atrial Fibrillation as an Independent Predictor of Impaired Functional Capacity After Coronary Artery Bypass Graft (CABG) Surgery: Insights From the First Large-Scale Cohort Study in Indonesia

R. E. Intan[1], R. Julario[1], B.B. Dharmadjati[1], M.R. Amadis[1], R.N. Rosyadi[1], R.I. Gunadi[1], M. Jibril[1], M. Ardiana[1], B. Radi[2], A. M. Ambari[2], B. Dwiputra[2], A. Santoso[2]

[1]Department of Cardiology and Vascular Medicine, Faculty of Medicine, Universitas Airlangga, Surabaya, Indonesia

[2]National Cardiovascular Center Harapan Kita, Jakarta, Indonesia

Background and aim: Postoperative atrial fibrillation (POAF), a common complication after coronary artery bypass grafting (CABG), is increasingly recognized not only for its association with adverse clinical outcomes but also for its potential impact on functional recovery. The six-minute walk test (6-MWT) is a validated submaximal test widely used to assess postsurgical functional capacity. This study aimed to evaluate the influence of POAF on early post-CABG functional capacity.

Materials and methods: A cross-sectional analysis was conducted on 1,509 post-CABG patients enrolled in a cardiac rehabilitation registry program between 2019-2021 at a national referral cardiac center. All 6-MWTs were performed before the early phase II cardiac rehabilitation program, within one week of discharge. POAF was defined as new-onset atrial fibrillation detected postoperatively without a history of pre-existing AF. Patients were stratified into two groups: POAF and SR. A comparative analysis of the 6-minute walk distance (6-MWD) was performed, followed by a multivariate regression analysis to identify the independent predictors of 6-MWD immediately after CABG.

Results: Of the 1,509 patients who underwent CABG, 34 (2.3%) developed POAF. The mean 6-MWD in the POAF group was significantly lower than that in the SR group (278.4 ± 70.2 m vs. 314.9 ± 75.6 m, p = 0.031)(Figure1). Multivariate regression analysis identified POAF as an independent negative predictor of 6-MWD (B = -28.36, p = 0.027), along with older age (B = -1.62, p < 0.001), female sex (B = -30.47, p < 0.001), and diabetes (B = -12.68, p < 0.001). Body height remained a positive predictor (B = +1.09 per cm, p < 0.001). The formula for predicting 6-MWD after surgery was as follows: 6-MWD (meters) = 212.57 + 30.47 (if male) – 1.62 (age in years) + 1.09 (body height in cm) – 12.68 (if with diabetes) – 28.36 (if with POAF). The model explained 15.3% of the variance in the 6-MWD (adjusted R^2 = 0.153).

Conclusion: POAF significantly impairs early functional recovery after CABG, as reflected by a reduced 6-MWD, and should be considered a modifiable target in post-CABG management. Early detection, prevention, and management strategies for POAF may enhance recovery outcomes and should be prioritized in the perioperative care protocols.

Keywords: POAF, 6MWD, CABG

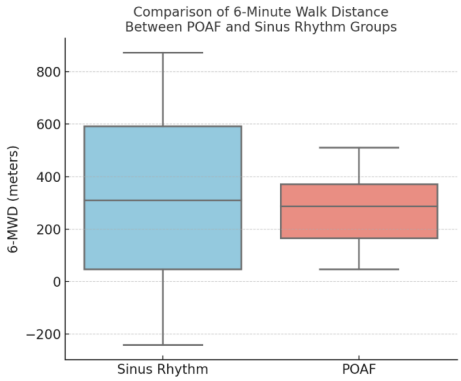

Figure 1. Distribution of 6-Minute Walk Distance in Post-Coronary Artery Bypass Graft Patients With and Without Postoperative Atrial Fibrillation (POAF).

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[12INAHRS-OR30]

Association and Performance of CHA_2DS_2VASc Score to Measure Stroke Risk in Rhumatic Mitral Stenosis in North Sumatera

Y. C. R. Napitupulu, T. W. A. T. B. Haykal, C. A. Andra, A. C. Lubis

Background: Stroke is a leading cause of death worldwide. Atrial Fibrillation (AF) is one of the most common global arrhythmias and is considered a risk factor for stroke. Rheumatic heart disease (RHD) causes mitral stenosis, leading to AF, and is predominantly found in developing countries. The majority of studies on the risk of stroke and CHA_2DS_2VASc score have not included patients with RHD, because most of them were performed in developed countries, where RHD has become rare. This study was conducted to evaluate the relationship between the CHA2DS2VASc score and stroke occurrence in a primary referral hospital in North Sumatra, Indonesia.

Methods: This retrospective cohort study used total sampling. The study was conducted at the outpatient clinic of Adam Malik Hospital between January 2023 and January 2024. The inclusion criteria were patients diagnosed with AF and moderate-to-severe rheumatic MS. The primary outcome was hemorrhagic and ischemic stroke.

Results: A total of 140 patients with AF and moderate-to-severe rheumatic MS were included. During the 12-month follow-up period, 12.1% of the patients experienced a stroke, and 7.9% died. The median CHA_2DS_2VASc score was 2 (IQR 1-4). The median CHA_2DS_2VASc score in the stroke group was higher than that in the non-stroke group ($p<0.05$) and was associated with stroke occurrence. CHA_2DS_2VASc score sensitivity and specificity were 82.4% and 47.2%, respectively, for measuring stroke risk at 1-year follow-up, with an AUC of 0.52 ($p = 0.707$).

Conclusion: The CHA2DS2VASc score was associated with stroke after 1-year of follow-up. However, in our study, the CHA_2DS_2VASc score could not be used to measure stroke risk in patients with rheumatic mitral stenosis with AF during a 1-year follow-up.

Keywords: Mitral stenosis, Atrial Fibrillation, Stroke.

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[12INAHRS-OR31]

Higher Normal Serum Potassium Level is Protective to Sudden Cardiac Death in Patients with Ischemic Cardiomyopathy with Impaired Autonomic Balance

Maradjabessy FH[1], Setiadi BM[1], Rampengan SH[1], Joseph V[1], Yofrido FM[1], Thengker AAA[1], Kalyanavati[1], Setiawan C[1]

[1]Departement of Cardiology and Vascular Medicine
Faculty Medicine of Sam Ratulangi University, Manado, Indonesia

Background: Sudden cardiac death (SCD) is the leading cause of mortality in patients with ischemic cardiomyopathy. Ventricular arrhythmias and SCD in ischemic cardiomyopathy are complex interactions between scar-related substrates, modulating factors (autonomic and metabolic), and triggers.

Methods: This hospital-based, observational, analytical study was conducted from January 2023 to April 2025. All participants underwent laboratory panels, echocardiography, and short-term ECG Holter monitoring. Comparative tests, regression analyses, ROC curve analyses, and diagnostic value calculations were performed to assess the association between deceleration capacity and potassium level with SCD incidence.

Results: Of the 100 participants, 23 % had high-risk DC, and SCD occurred in 25%. A lower DC value was significantly correlated with SCD (AUC = 0.823). Potassium levels did not differ between the SCD and non-SCD groups. However, among patients with high-risk DC, potassium levels were significantly lower in the SCD group (4.11 +/- 0.63, compared to 4.84 +/- 0.88 in the non-SCD group.

Discussion: Potassium levels act as an independent electrophysiological factor and modulator, amplifying the arrhythmogenic effects of impaired parasympathetic tone. A DC value <2.5 ms indicates severe parasympathetic tone impairment or sympathetic nervous system dominance, which indicates increased susceptibility to excessive sympathetic activity. Even in mild hypokalemia, ventricular conduction and repolarization are unstable, inhibiting the activity of IKr and IKs channels involved in phase 3 repolarization, prolonging the action potential, and increasing the risk of EAD development. Excess intracellular calcium ions due to β-adrenergic stimulation cause DAD. These are highly arrhythmogenic and can trigger PVCs with cardiac remodeling or fibrosis and can progress to VT/VF. A decrease in the action potential threshold occurs under conditions of increased oxidative stress and excitability in hypokalemia.

Conclusion: In patients with ischemic cardiomyopathy, a higher serum potassium threshold than that in the normal population may be required as a protective factor against SCD.

Keywords: short-term deceleration capacity, Ventricular late potentials, spatial QRS-T angle, potassium, Sudden cardiac death

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[12INAHRS-OR32]

Radiofrequency Catheter Ablation in Pediatric SVT Patients: Consistent Outcomes Regardless of Body Weight or Cardiac Anatomy

D. P. Dewanti[1], D. Y. Hermanto[1], D. A. Hanafy[1], S. B. Raharjo[1], Y.Yuniadi[1], R. R. Waliyuddin[1]
[1]National Cardiovascular Center Harapan Kita, Jakarta, Indonesia

Background: Radiofrequency ablation is the treatment of choice for pediatric SVT. However, previous studies have suggested that a lower body weight (<30 kg) is associated with increased procedural risks. This study aimed to present the characteristics, procedural means, and outcomes of pediatric patients who underwent ablation at the National Cardiovascular Center Harapan Kita.

Methods: This retrospective study analyzed pediatric patients (≤17 years) who underwent RF catheter ablation for SVT between January 2021 and May 2025. Regarding vascular access, we added the diameter of each sheath inserted into each vessel to illustrate the relationship between the sheath and vessel diameters. The primary endpoints were vascular complications and acute procedural success.

Results: This study evaluated the outcomes of 75 pediatric patients (median age: 13 years, IQR: 10–14; median weight: 43 kg, IQR: 35–54) who underwent RF catheter ablation for SVT.
Vascular complications did not occur in any of the patients who underwent ablation, even in the patient with the lowest body weight of 13.8 kg. The median diameter of the vascular access was 14F (IQR: 12–19) in the right femoral vein. The procedure demonstrated a high success rate of 90.6%, with 9.4% of patients requiring re-ablation. No significant differences were observed in age, weight, vascular access, or echocardiographic findings between patients with successful and unsuccessful ablation outcomes (p>0.05 for all comparisons). Patients with congenital heart disease (25.4%) had no difference in success rates compared to those with normal cardiac structures.

Conclusions: Radiofrequency catheter ablation is highly effective and safe in pediatric patients with SVT, regardless of body weight.

Keywords: Supraventricular Tachycardia, Ablation, Pediatrics

	Ablation Result		P Value
	Success n, % (68, 90.6)	Unsuccessful n, % (7, 9.3)	
Age (years), median (IQR)	12.5 (10-14)	14 (12-17)	0.322*
Gender			
Male	27 (39.7)	2 (28.6)	0.565
Female	41 (60.3)	5 (71.4)	
Body weight (kg), n (%), median (IQR)			
<30 kg	9 (13.2)	1 (14.3)	0.938
≥ 30kg	59 (86.8)	6 (85.7)	
Puncture Access (F), median (IQR)			
Right Jugular Vein	5 (0-6)	6 (0-6)	0.815*
Right Femoral Artery	0 (0-5)	0 (0-7)	0.747*
Left Femoral Artery	0 (0-0)	0 (0-0)	0.563*
Right Femoral Vein	14.5 (12-19)	14 (14-21)	0.217*
Left Femoral Vein	0 (0-6)	0 (0-12)	0.563*
Type of ablation, n (%)			
Conventional Ablation – AFL	1 (1.5)	0 (0)	0.486
Conventional Ablation – AVNRT	18 (26.5)	0 (0)	
Conventional Ablation – WPW	42 (61.8)	5 (71.4)	
3D Ablation – AFL	1 (1.5)	0 (0)	
3D Ablation – AT	2 (2.9)	1 (14.3)	
3D Ablation – WPW	3 (4.4)	1 (14.3)	
3D Ablation – PAC	1 (1.5)	0 (0)	
Echocardiographic findings, n (%)			
Normal Heart Structure & Function	39 (57.4)	4 (57.1)	0.569
Normal Heart Structure & Decreased Function	4 (5.9)	0 (0)	
Abnormal Heart Structure & Normal Function	14 (20.6)	3 (42.9)	
Abnormal Heart Structure & Decreased Function	2 (2.9)	0 (0)	
Not Done	9 (13.2)	0 (0)	
Complication, n (%)			
None	65 (95.6)	7 (100)	0.851
TAVB	2 (2.9)	0 (0)	
Death	1 (1.5)	0 (0)	
Vascular	0 (0)	0 (0)	

*p-value using the Mann-Whitney test

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[12INAHRS-OR33]

Uncovering Therapeutic Targets in Brugada Syndrome: Insights from Bibliometric and In Silico-Bioinformatic Analysis

A. D. Saputra[1], S. Suryono[2], M. I. Amien[1] A. I. Tohari[1], M. R. F. Hidayat[1]
[1]Faculty of Medicine, Universitas Jember, Jember, Indonesia
[2]Department of Cardiology and Vascular Medicine, dr. Soebandi General Hospital – Faculty of Medicine, Universitas Jember, Jember, Indonesia

Background: Brugada syndrome (BrS) is an uncommon inherited cardiac channelopathy characterized by a distinctive electrocardiographic pattern and an elevated risk of ventricular arrhythmias and sudden cardiac death (SCD), particularly in young adults. To date, over 40 genes have been implicated in its pathogenesis, with *SCN5A* being the most frequently mutated gene, accounting for approximately 30% of diagnosed cases. This study aimed to elucidate the key genetic determinants of BrS through an integrated bibliometric analysis and a multilevel in silico bioinformatics approach.

Methods: A total of 4,089 Brugada syndrome-related articles were obtained from the Scopus database and analyzed using RStudio (version 4.5.0), employing the Bibliometrix package (via the Biblioshiny interface) and VOSviewer (version 1.6.20) for bibliometric visualization. A total of 385 candidate genes associated with BrS were identified using GeneCards Suite. Subsequent in silico analyses were performed using WebGestaltR, STRING, Cytoscape-CytoHubba v3.10.3, and SAVES v6.1 to explore potential gene targets through protein–protein interaction network (PPIN) construction, three-dimensional protein structure modeling, and structural validation using ERRAT, and Ramachandran plot evaluation via PROCHECK.

Results: Bibliometric analysis of Brugada syndrome (BrS) genetics showed an increasing trend since 1998, with a publication peak in 2021. Keyword mapping revealed frequent associations with the terms *genetic*, *sudden cardiac death*, *ventricular fibrillation*, *arrhythmia*, and *SCN5A*. Building on these findings, a PPIN analysis focused on genes regulating membrane potential was conducted, guided by the biological process and KEGG pathway data. Among the 94 BrS-related genes, SCN1B, SCN4B, and KCNE3 emerged as potential therapeutic targets, supported by significant PPI enrichment. Structural validation using ERRAT and Ramachandran plot analyses confirmed their suitability as candidate drug targets.

Conclusion: Genetic factors play a crucial role in BrS. SCN1B, SCN4B, and KCNE3 are promising candidate genes for targeted therapy in BrS.

Keywords: Brugada Syndrome, Bibliometric, Bioinformatics, Genetic factor, Target therapy

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[12INAHRS-OR34]

Integrative Bioinformatics Analysis of Hub Gene Networks and Functional Enrichment Reveals Potential Therapeutic Targets in Lenegre-Lev Disease

S. Larasati[1], R. N. Erisadana[1]
[1]Faculty of Medicine, Universitas Jember, Jember, Indonesia

Background: Lenegre-Lev disease (LLD) is characterised by progressive fibrosis of the cardiac conduction system, resulting in a complete heart block, extremely slowed heart rate until sudden cardiac death. Despite its clinical significance, current therapies are limited to symptomatic management using cardiac pacing. This study aimed to identify potential therapeutic targets for LLD by targeting hub genes.

Methods: Multiple bioinformatics tools were utilized to analyze the genes, including Protein-Protein Interaction Networks (PPIN), functional enrichment analysis, cytoHubba, webgesult, and ERRAT-PROCHECK, to characterize hub genes, examine their gene ontology in biological processes, and investigate the potential of identified genes to serve as viable candidates for therapeutic targets.

Results: The GeneCards-derived PPIN showed highly significant statistical results ($p<1.0e-16$). Functional enrichment analysis revealed that 70 genes were significantly associated with LLD. Positive regulation of cell adhesion (FDR 1.6798e-23) was the most significant pathway among the biological processes. Hub proteins implicated in LLD pathogenesis were identified using the CytoHubba topological algorithms. The maximal clique centrality (MCC) approach was applied with color coding from red to yellow, where red signifies the most significant impact. ERRAT analysis was performed and showed a standard overall quality factor value of SRC (97.89%), JAK2 (98.03%), AKT1 (95.5%), ACTB (96.90%), and MTOR (97.06%), suggesting that the protein structures have good resolution and are suitable as drug targets. PROCHECK Ramachandran plot analysis showed that SRC (91.3%), JAK2 (91.6%), AKT1 (92.85%), ACTB (95.7%), and MTOR (90.9%) had a high number of residues in the allowed region, suggesting that the protein structures encoded by these genes are stable upon drug binding.

Conclusion: This study highlights the significant contribution of SRC, JAK2, AKT1, ACTB, and MTOR to LLD-associated biological processes, demonstrating their potential as prospective therapeutic targets.

Keywords: Lenegre-Lev Disease, Bioinformatics, In silico, arrhythmia

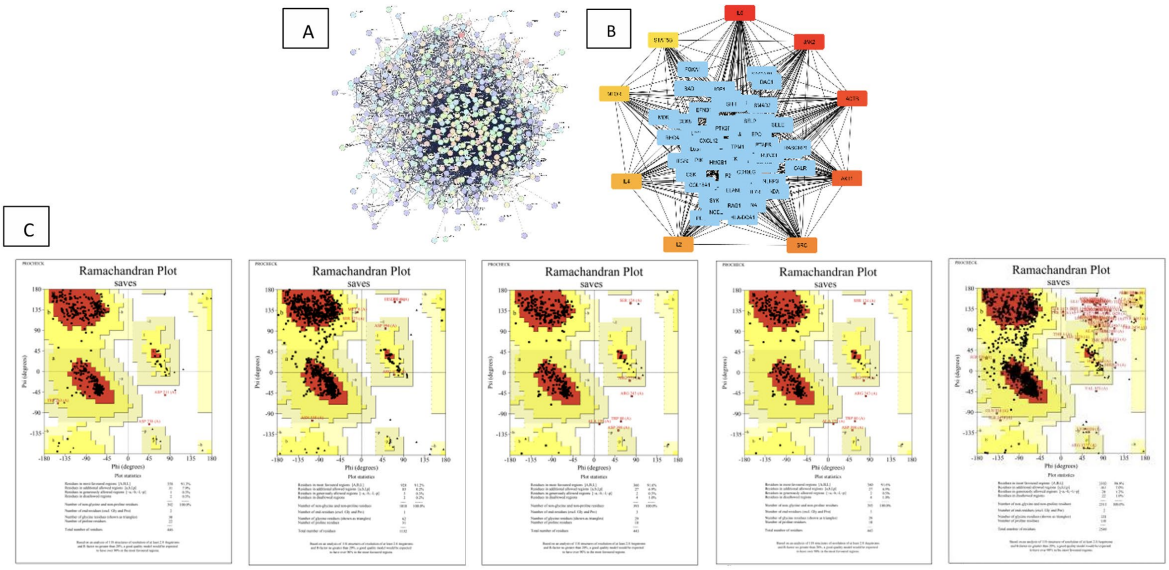

Figure 1. (A) PPIN analysis (B) CytoHubba analysis showing the top 10 hub genes (C) PROCHECK analysis of SRC, JAK2, AKT1, ACTB, and MTOR (left to right).

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[12INAHRS-OR35]

P-Wave Dispersion And P-Wave Terminal Force V1 as a Predictor of Diastolic Dysfunction Improvements in Patients Undergoing Percutaneous Coronary Intervention

A.M. Purnomo[1], V.B. Untu[1], V. Suryan[1], A.S. Japanto[1], B.M. Setiadi[1], A.L. Panda[1], G.E.H. Reppi[1]

[1]Department of Cardiology and Vascular Medicine, Prof. Dr. R. D. Kandou General Hospital - Sam Ratulangi University, Manado, Indonesia

Background and aims: Left ventricular diastolic dysfunction (LVDD) is a critical prognostic factor in patients with Coronary Artery Disease (CAD) after percutaneous coronary intervention (PCI). Worsening LVDD is a predictor of poor prognosis in patients with CAD. Emerging electrocardiographic markers, P-wave dispersion (PWD) and P-wave terminal force in lead V1 (PTFV1), may offer noninvasive insights into LVDD improvements after revascularization.

Methods: This prospective observational study enrolled 41 Chronic Coronary Syndrome (CCS) patients (75.6% male, mean age 57.73±7.57 years) with normal left ventricular systolic function (LVEF ≥ 50%) undergoing PCI at Prof. Dr. R. D. Kandou General Hospital, Manado, between May and July 2024. PWD and PTFV1 were measured pre- and post-intervention, along with 10 echocardiographic LVDD parameters. The collected data were analyzed using SPSS version 29.

Results: PWD and PTFV1 showed significant post-PCI improvements (ΔPWD: 15.36±13.05ms, $p < 0.001$; ΔPTFV1:9.36±10.07 mm.ms, $p < 0.001$). PWD reductions correlated strongly with Mitral E-wave enhancements ($p < 0.001$) but not with other LVDD indices. PTFV1 normalization was linked to improvements in tissue Doppler parameters: e'-septal ($p < 0.001$), e'-lateral ($p = 0.001$), average E/e' ($p < 0.001$), and E-wave deceleration time ($p < 0.001$).

Conclusion: PWD and PTFV1 are dynamic markers of LVDD recovery post-PCI, with PTFV1 demonstrating broader associations with LVDD parameters and providing prognostic value in this population. These findings support their utility in non-invasive and cost-effective monitoring of hemodynamic improvements, potentially guiding post-revascularization management in patients with CAD, especially in areas with limited resources.

Keywords: P-wave dispersion, P-wave terminal force V1, diastolic dysfunction, percutaneous coronary intervention