

A Multidomain Atrial Damage Index for Atrial Fibrillation Recurrence

Leire Moriones¹, Blas Echevarria², Javier Ibero³, Ignacio García-Bolao³, Susana Ravassa⁴, Pablo Lamata⁵, Jean Bragard¹

¹Universidad de Navarra, Pamplona, Spain

²Universitat Politècnica de Catalunya, Barcelona, Spain

³CUN, Universidad de Navarra, Pamplona, Spain

⁴CIMA, Universidad de Navarra, Pamplona, Spain

⁵King's College London, London, United Kingdom

Background and Aim: AF recurrence after ablation is a significant clinical challenge driven by heterogeneous atrial remodeling not fully captured by single-domain predictors. Current models often evaluate structural or electrical parameters in isolation, limiting predictive accuracy and interpretability. We propose a multidomain Atrial Damage Index (ADI 4D) to provide a structured clinical phenotyping framework and evaluate its association with one-year AF recurrence.

Methods: In a retrospective cohort of 143 patients undergoing first-time AF ablation, ADI 4D (composite score 0–8) integrated four domains: electrical substrate (Q2 healthy tissue >0.5 mV via high-density mapping), geometric remodeling (CT-derived volume tertiles), metabolic status (diabetes), and temporal status (AF type). Patients were stratified into three clinical stages representing increasing combined remodeling burden: Stage 1 (0–2), Stage 2 (3–4), and Stage 3 (≥ 5).

Results: Recurrence exhibited a non-monotonic distribution across stages: 26.2% in Stage 1 (n=17/65), 50.9% in Stage 2 (n=28/55), and 34.8% in Stage 3 (n=8/23). While overall predictive performance was modest (ROC-AUC 0.58; OR 1.23, 95% CI 1.02–1.49), ADI 4D successfully identified highly vulnerable substrates. Notably, the intermediate E1+G2 phenotype—characterized by early electrical alteration with advanced geometric dilation—yielded an 80% observed recurrence rate (n=5).

Conclusions: The ADI 4D enables interpretable, multidomain phenotyping of AF patients. Our findings reveal a non-linear risk structure driven by complex domain interactions rather than isolated structural burden. This proof-of-concept system highlights specific high-risk intermediate phenotypes that warrant further validation in larger prospective multi-center cohorts.