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ANALYSIS OF lncRNA EXPRESSION PROFILES AND CORRELATIONS WITH CLINICAL AND ECHOCARDIOGRAPHIC PARAMETERS IN SUBJECTS WITH PREDIABETES AND NEWLY DIAGNOSED TYPE 2 DIABETES MELLITUS

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Introduction and Aim. Type 2 diabetes mellitus (T2DM) is associated with early structural and functional cardiac alterations. Some long non-coding RNAs (lncRNAs) are markers of cardiac damage in diabetic cardiomyopathy; data in prediabetics remain unknown. This study aimed to evaluate the expression of lncRNAs related to myocardial fibrosis, epicardial adipose tissue (EAT) accumulation, and heart failure (HF) risk in subjects with prediabetes or newly diagnosed T2DM, and to explore correlations with clinical and echocardiographic parameters.

Materials and Methods. Thirty-three subjects with prediabetes or newly diagnosed T2DM, asymptomatic for HF, were enrolled. All participants underwent clinical evaluation, blood sampling, and transthoracic echocardiography. lncRNA expression was measured by real-time PCR using actin as reference gene. The analyzed lncRNAs were CCDC68-2: 1, ARL4C-2: 3, RNF145-1: 1, NOS2P3, and MALAT1.

Results. Subjects were divided according to median NT-proBNP levels into Group 1 (n=16, <75 pg/mL) and Group 2 (n=17, ≥ 75 pg/mL). BMI did not differ between groups. Group 2 showed higher C-reactive protein levels, greater prevalence of E/A ratio <0.7, and increased EAT thickness (all $p=0.05$). No differences were observed in indexed left atrial volume, E/E′ ratio, or isovolumic relaxation time. Expression of CCDC68-2: 1, ARL4C-2: 3, RNF145-1: 1, and MALAT1 was significantly higher in Group 2.

Conclusions. lncRNAs, combined with laboratory and echocardiographic parameters, may enable very early identification of individuals at increased risk of diabetic cardiomyopathy.