MicroRNA profile analysis in pericoronary adipose tissue of diabetic patients with significant coronary artery disease

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Background: Pericoronary adipose tissue (PCAT) regulates arterial homeostasis, is considered to act in paracrine manner,and plays a role in the pathogenesis of atherosclerosis. PCAT may be a source of microRNAs (miRs) that target other tissues and act as messengers for intercellular communication. In this study, we investigated whether the PCAT surrounding coronary occlusive atherosclerotic lesions shows specific miRs expression patterns in patients with diabetes type 2 compared to non-diabetic patients.

Methods: We enrolled 43 patients (29 men, aged 63±12 years old) with 3-vessel coronary artery disease who underwent elective coronary bypass surgery with and without diabetes type 2. The PCAT samples were received from all participants. miR-133a, miR-21, miR-26b, miR-9 and miR-143 expression levels in PCAT cells were quantified by real-time reverse transcription polymerase chain reaction.

Results: Twenty-one patients with diabetic type 2 (14 men, 64±10 years old) and twenty=two non-diabetic patients (15 men, 62±15 years old) were included in the study. PCAT analysis showed a significant upregulation of miR-21 levels in diabetic compared to non-diabetic patients (181±76 versus 21±15, p=0.04). Diabetic patients also revealed a significant increase of miR-26b and miR-143 expression in PCAT samples compared to on-diabetics (33±22 versus 16±13, p=0.02, 93±42 versus 16±23, p=0.01). No significant differences between the two sites were observed in PCAT expression of miR-133a and miR-9 (73±12 versus 130±143, 56±44 versus 34±33, respectively, p =NS for both).

Conclusions: miRs expression in PCAT from diabetic patients with significant coronary disease show a distinct expression profile. Our study opens new perspectives in the pathophysiologic role of PCAT in atherosclerotic complications of diabetes and should be further investigated.