

Relationship Among the Presence of Metabolic Syndrome, Weight Status and Plasma miRNA Expression in Older Adults From the Healthy Survey of São Paulo: A Population-Based Study

Gabrielli Carvalho,¹ Tanyara Payolla,¹ Paula Brandão-Lima,¹ Flavia Sarti,² Regina Fisberg,¹ and Marcelo Rogero¹

¹School of Public Health, University of São Paulo and ²School of Arts, Sciences and Humanities, University of São Paulo

Objectives: To evaluate the plasma expression of miR-30a, miR-130b, miR-376a and miR-let7c according to the presence of metabolic syndrome (MetS) and body mass index (BMI) in older adults and assess their association with metabolic biomarkers.

Methods: Data from 193 older adults (68.0 ± 11.0 years; 52.3% female) of the 2015 Health Survey of São Paulo with focus on Nutrition were used for this cross-sectional study. Participants with acute inflammatory diseases and in use of medication that can influence in this outcome were excluded from analysis. The presence of MetS was defined according to American Heart Association/National Heart, Lung, and Blood Institute criteria (2005). Overweight and obese individuals were grouped. The miRNAs were quantified by qRT-PCR, using a Fluidigm chip. The miRNA expression according to the BMI was assessed using the Kruskal-Wallis test followed by the Dunn test, while the miRNA expression according to the presence of MetS was

determined by the Mann-Whitney test. Spearman correlation between miRNA and metabolic biomarkers was performed.

Results: A total of 44.6% of the participants were overweight/obese and 61% of them had MetS. Plasma expression of miR-130b and miR-376a was lower in overweight individuals compared to non-overweight individuals. MiR-let7c, miR-122 and miR-30a showed greater expression in individuals with MetS compared to those without MetS. MiR-30a showed positive correlations with fasting blood glucose ($r = 0.100$; $P = 0.016$), total cholesterol (CT) ($r = 0.091$; $P = 0.028$), LDL-c ($r = 0.083$; $P = 0.047$), no HDL-c ($r = 0.101$; $P = 0.015$) and triacylglycerols (TG) ($r = 0.133$; $P = 0.001$). The expression of miR-let7c showed positive correlations with fasting glucose ($r = 0.0113$; $P = 0.006$), CT ($r = 0.100$; $P = 0.016$), LDL-c ($r = 0.102$; $P = 0.002$), not HDL-c ($r = 0.143$; $P < 0.001$), TG ($r = 0.201$; $P < 0.001$) and negative correlation with HDL-c ($r = -0.124$; $P = 0.002$). The expression of miR-130b correlated with TG ($r = 0.099$; $P = 0.018$) and miR-376a with CT ($r = 0.085$; $P = 0.042$) and TG ($r = 0.116$; $P = 0.005$).

Conclusions: Plasma expression of miRNA in older adults varied according to the presence of MetS and weight status, presenting correlations with metabolic biomarkers.

Funding Sources: Grant 2017/05125-7 | 2020/03104-5; 2019/22934-1, São Paulo Research Foundation (FAPESP) | 150834/2020-9, National Council for Scientific and Technological Development (CNPq).