Relationship Between Metabolic Syndrome and Circulating microRNA Expression in Adults

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Objectives: To verify the relationship between circulating miRNA (16, 363, 375, 486, and let7c) expression and risk factors for metabolic syndrome (MetS) in adults.

Methods: A cross-sectional population-based study including 192 adults without acute inflammatory diseases, cancer, or using medication that would affect the main outcomes. The BioMark^{TM} Fluidigm Dynamic Array for real-time qPCR was used to quantify miRNA expression levels in plasma. The miRNA expression levels categorized by the MetS status were analyzed by the Mann-Whitney test. The Kruskal-Wallis with post hoc Dunn's tests were used to compare miRNA expression levels categorized by the number of MetS risk factors (0, 1–2, and ≥3). Spearman's correlation between miRNA expression and MetS risk factors was performed.

Results: The sample included individuals with median age of 41 (20–59) years, 54.7% were women, and 58.3% overweight/obesity. MetS was observed in 33.9% of individuals (15.6% men, and 18.2% women), being increased waist circumference (WC) (67.7%), and reduced plasma HDL-c levels (52.1%) the most prevalent risk factors. Individuals with MetS showed reduced plasma expression of miR-16, −363, −375, and −486, but increased miR-let7c expression compared to the group without MetS ($P < 0.05$). Analysis of miRNA expression levels categorized according to the number of MetS risk factors demonstrated that individuals without risk factors did not differ from those with 1–2 risk factors. Individuals with 3 or more risk factors differed from all groups, except for the miR-16, which presented difference only in comparison to the group without risk factors. The miR-16 expression correlated negatively with body mass index (BMI) ($r = -0.169$; $P = 0.019$), WC ($r = -0.153$; $P = 0.034$), diastolic blood pressure ($r = -0.144$; $P = 0.046$), and glucose levels ($r = -0.171$; $P = 0.017$). The miR-let7c correlated positively with triacylglycerol ($r = 0.306$; $P < 0.001$), and negatively with HDL-c ($r = -0.173$; $P = 0.016$) levels. The miR-375 correlated negatively with BMI ($r = -0.203$; $P < 0.001$), WC ($r = -0.187$; $P < 0.001$), and positively with HDL-c levels ($r = 0.261$; $P < 0.001$). The miR-486 and −363 correlated negatively with BMI ($r = -0.155$; $P = 0.031$ | $r = -0.142$; $P = 0.049$, respectively).

Conclusions: The circulating miRNA evaluated were associated with the risk factors for MetS in adults.