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Identifying a microRNA fingerprint to predict QT prolongation

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Torsade de pointes (TdP) is a ventricular arrhythmia associated with QT interval prolongation that can be induced by several drugs. The objective was to identify circulating microRNA (miR) as potential biomarkers for risk stratification of susceptibility to QT interval prolongation. In a single center cohort study, whole blood was collected from 58 patients with coronary artery disease. Corrected QT intervals were measured by Fridericia's method (QTc). Patients were categorized according to QTc risk. Genome-wide next generation miR sequencing was performed. Multivariate regression analysis (additive model) was used to predict miRs associated with QTc risk. MiRs associated with QT interval risk were further assessed for potential functional significance using TargetScan with a context score < -0.4. 320 miRs were identified and 16 miRs were associated with QTc interval risk from the multivariate analysis ($p<0.05$; Figure). 11 of those miRs were previously related to cardiovascular function. Target scan analysis revealed 3 of the miRs may regulate cardiac ion channel gene targets associated with QTc prolongation. A profile of circulating miR has been identified that correlated with QT prolongation. The potential for a miR fingerprint to predict the susceptibility to drug induced QT prolongation warrants further investigation.

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