

Association between circulatory microRNAs in plasma and atrial fibrillation among men and women from the general population

Geurts S.; Mens MMJ; Bos MM.; Ikram MA.; Ghanbari M.; Kavousi M.

Erasmus University Medical Centre, Rotterdam, Netherlands (The)

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Background: MicroRNAs (miRNAs) are small non-coding RNAs that regulate gene expression. They have shown to play an important role in cardiovascular disease, but there is limited population-based data regarding the relationship between circulatory miRNAs in plasma and atrial fibrillation (AF). Moreover, it remains unclear if the associations between miRNAs with AF differ by sex.

Purpose: To determine the association of miRNAs with the risk of prevalent and incident AF among men and women from the general population.

Methods: Plasma levels of circulatory miRNAs were measured in 858 men and 1141 women from a large prospective population-based cohort study. Logistic regression and Cox Proportional Hazards models were used to assess the associations of 591 well-expressed miRNAs with the prevalence and incidence of AF. Models were adjusted for age and cardiovascular risk factors. We further examined the link between predicted target genes of identified miRNAs and AF.

Results: The mean age was 71.7 years (57.1% women), 58 men and 40 women had prevalent AF at baseline. Moreover, 96 men and 100 women developed AF during a median follow-up of 9.0 years. After adjusting for multiple testing, miR-4798-3p was significantly associated with prevalent AF among men; odds ratio: 0.39 (95% CI 0.24-0.66). No miRNAs were significantly associated with incident AF. MiR-4798-3p could potentially regulate the expression of AF-related genes, including genes involved in calcium and potassium handling in myocytes, protection of cells against oxidative stress, and cardiac fibrosis.

Conclusions: Plasma levels of miR-4798-3p were significantly associated with prevalent AF among men. Various target genes in relation to AF pathophysiology could potentially be regulated by miR-4798-3p that warrant further investigations in future experimental studies.