MicroRNA differential expression shared between rheumatoid arthritis and acute myocardial infarction: an exploratory study

Sirs,

Accumulating evidence indicates that a major cause of death among rheumatoid arthritis (RA) patients is cardiovascular disease (CVD). In fact, the risk of CVD is 1.5 times higher in RA compared with the general population (1). MicroRNAs (miRs) are small, non-coding RNA molecules of 21-24 base pairs that can control the expression of multiple gene posttranscriptional level. Abnormal expression of miRs in patients with RA are well documented. Some miRs have been associated with clinical variables of RA (tender joint and disease activity score-erythrocyte sedimentation rate) (DAS28-ESR) and with a higher risk and progression to RA (2, 3). Furthermore, reports indicate that some specific miRs might be helpful in the early detection of acute myocardial infarction (AMI) and differential expression of miRs has been identified in patients with coronary artery disease and atherosclerosis (4, 5). However, the association of those miRs with cardiovascular disease in patients with RA remains unclear. The aim of the study was to identify plasma miRs in RA patients that can facilitate earlier diagnosis of CVD and provide insight regarding the increase risk for CVD in these patients. We compared the plasmatic profiles of miRs (miRNome) in RA patients without CVD, in patients with early AMI but without RA, and in healthy controls, with the objective to find miRs commonly expressed in the two groups of patients but at different levels from the controls. RA patients were selected according to the criteria established by the American College of Rheumatology of 1987 and early AMI was defined as having an acute myocardial infraction before the age of 55. We recruited male subjects who were matched for age and for classical cardiovascular risk factors.

In accordance with our Institution's guidelines and the Helsinki Declaration, the subjects were informed of the research nature of the study and gave written consent prior to participation. The study was approved by the clinical research Ethics Committee of the University Hospital Sant Joan.

miRNome was analysed by real time PCR using validated TaqMan® OpenArray® MicroRNA panels which enables the quantification of 754 human miRNAs. Quantitative

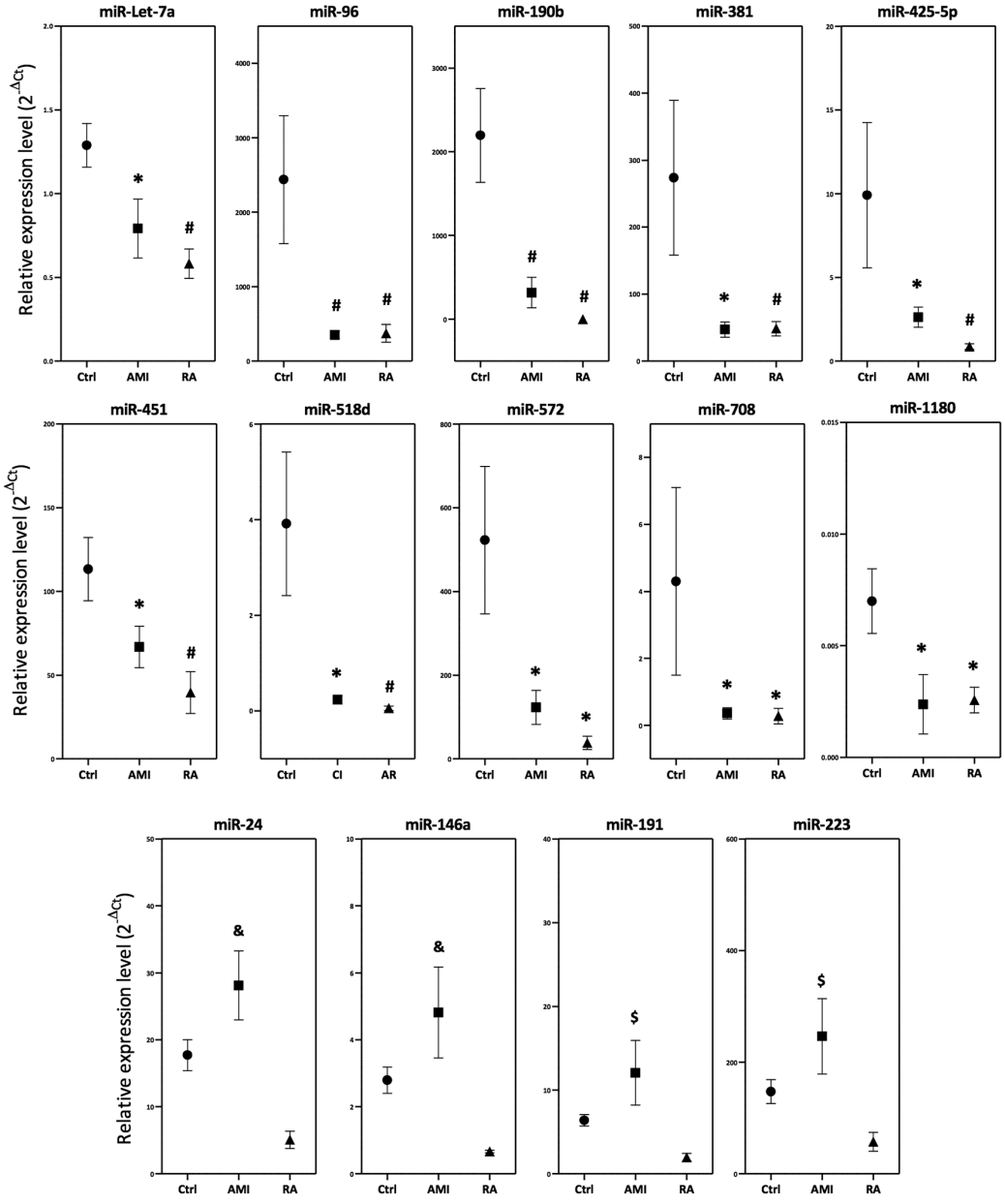

Fig. 1. Differential expression of miRs significantly downregulated in rheumatoid arthritis patients (RA) and in patients with cardiovascular disease (AMI) compared with healthy controls (Ctrl). $^{*}p<0.05$ *vs.* controls, $^{\#}p<0.01$ *vs.* controls, $^{\&}p<0.05$ *vs.* RA, and $^{\$}p<0.01$ *vs.* RA

changes in expression levels between groups (differential expression) were analysed with Expression Suite software. Selected miRs were further analysed with 2^{-Dct} method. Kruskal-Wallis test and Dunns post-test were used for the statistical analyses. Carotid intima-media thickness (cIMT) was also measured using a My Lab 50 X-Vision sonograph (Esaote SpA, Barcelona, Spain) with a linear array ultrasound probe small parts broadband transducer (5-12MHz). Statistical analyses were performed using SPSS software, v. 23. Continuous variables are presented as the mean (standard deviation).

The expression levels of 754 miRs were studied in 7 RA patients, 7 AMI patients and 7 healthy controls. The mean age of the population studied was 46.01(1.63), the body mass index was 26(2.7) and none of them were smokers, nor suffering from diabetes, hypertension or dyslipidaemia. In RA patients 71% and 57% were positive for anti-citrullinated peptide antibodies (ACPA) and rheumatoid factor antibodies (RF), respectively. The mean disease duration was 8.4 (8.0) years. We did not find any differences in cIMT between RA patients and controls. As for miRNome analysis, we detected 50% (379) of the miRs represented in the array in plasma of the three groups of patients. Circulating miRNome in RA and AMI patients were different from the controls. Plasma miRs that were expressed at the same level in RA and AMI patients but expressed significantly different compared with controls were: miRLet-7a, miR96, miR381, miR451, miR518d, miR425-5p, miR572, miR190b, miR708 and miR1180 (Fig. 1). Interestingly, all 10 miRs were down-regulated compared with controls. Moreover, 9 miRs were differentially expressed in AMI patients and 16 miRs in RA patients compared with controls. We observed carotid plaques in three of RA patients but we did not observe plaques in any of the controls. Interestingly, compared with RA patients without plaque, the RA patients with plaque have 23.6%, 34.8%, 25.7%, 4.7% and 0.6% less expression of miRlet-7a, miR96, miR381, miR451, miR425-5p, respectively. In RA patients, two of these miRs were significantly associated with inflammatory parameters. Specifically, the miR425-5p with C-reactive protein and miR381 with fibrinogen ($p<0.046$ and $p<0.042$, respectively). Furthermore, the figure also shows that miR24, miR146a, miR191, and miR223, which had been previously associated with CVD (6, 7) were upregulated in AMI patients but not in RA and controls, suggesting an association with elevated risk of CVD independently of inflammation.

Overall, we have identified 10 miRs sharing a similar expression pattern in RA patients and in individuals with early AMI, suggesting that these miRs could be epigenetic biomarkers of increased CVD in RA patients. A bigger clinical study is necessary to validate the role of these miRs.

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