Differential expression of micro RNAs from amniotic fluid-derived mesenchymal stem cell proliferation

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Objective

Human amniotic fluid mesenchymal stem cells (AF-MSCs) have become an attractive stem cell source for potential applications in regenerative medicine. Recent studies indicate that microRNAs (miRNAs) have a crucial role in self-renewal, in maintenance of stemness and differentiation. Our aim in this study was to determine the expression of miRNAs during proliferation and differentiation in AF-MSCs at normal and pathological pregnancy.

Methods

AF-MSCs from normal and fetus-affected gestations were expanded and induced for adipogenic, osteoblastic, myogenic and neurogenic differentiation. Typical cell surface and stem markers were detected by flow cytometry. We evaluated stemness gene expression and miRNA expression by using qRT-PCR method.

Results

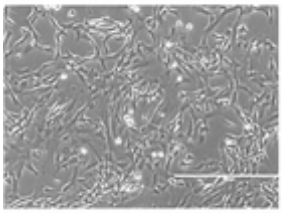
The results showed that MSCs from AF of normal and fetus-affected gestations maintained similar cell morphology, the expression of specific cell surface (CD44, CD90, CD105) and stemness (Oct4, Nanog, Sox2, Rex1) markers, and differentiation potential to adipogenic, osteogenic, neurogenic and myogenic lineages. We focused on the expression analysis of selected miR-17, miR-21, miR-34a, miR-148b and miR152 using RT-q-PCR to evaluate the role of those miRNA's in the fate of MSCs during cultivation at passage 3, 5 and 8. We observed significant down-regulation of miR-17 and miR-21and up-regulation of miR-34a and miR148b in cultures from two cell sources at late passage. The comparison of the expression of those miRNAs between normal and fetus-pathological samples revealed lower levels of all miRNAs selected except miR-21. In MSCs undergoing differentiation to four different lineages, miR-17 and miR-21 were down-regulated with nonsignificant changes between normal and fetus-pathological samples. miR-34a and miR146a were differently expressed during adipogenic and osteoblastic differentiation, while both were upregulated in myoblasts and neurogenic cells, showing that different phenotypes were associated with the differential expression of those miRNAs.

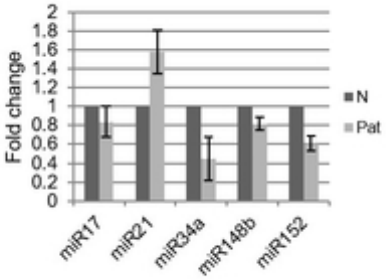
Conclusion

The results of this study demonstrate that the differences in miRNAs and their regulated functions exist in AF-MSCs from healthy pregnant women and patients with fetal abnormalities. These findings may have important implications on revealing the pathological state of fetus.

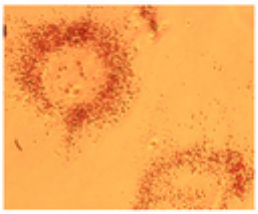
Differentiation

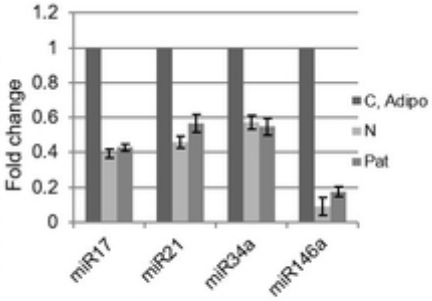
AF-MSC

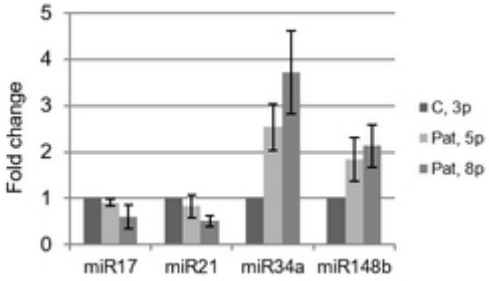




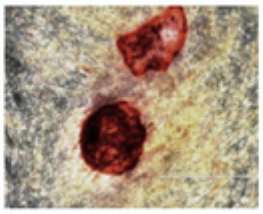
Adipo

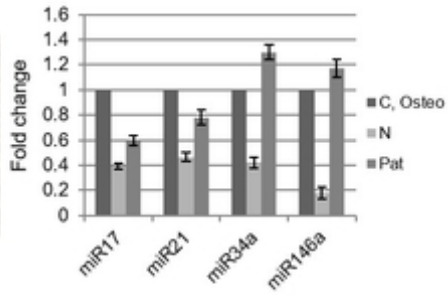




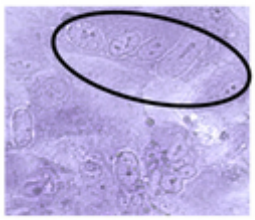


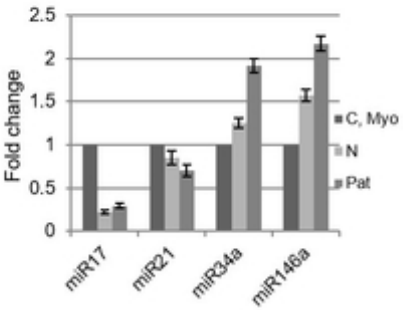
Osteo





Myo





Neuro