Differential Expression of Peripheral Blood and Synovial fluid-derived Exosomal-miRNAs in Osteoarthritis

Lai, Hwa-Yu; [1]Goh, Tuan-Xin; [1]Tan, Sik-Loo, [1]Teo, Seow-Hui; [1]Abbas, Azlina Amir & [1]Kamarul, Tunku.
[1]Tissue Engineering Group (TEG), National Orthopaedic Center of Excellence for Research & Learning (NOCERAL), Department of Orthopaedic Surgery, Faculty of Medicine, University of Malaya, 50603 Kuala Lumpur, Malaysia.

INTRODUCTION:

Exosomes participate in many physiological and pathological processes by regulating cell-cell communication, which is involved in numerous diseases, including osteoarthritis (OA). Several miRNAs have been identified as in exosomal RNA that plays an important role in OA. Exosomes are detectable in the human articular cavity and were observed to change with OA progression[1]. This study aims to identify differentially expressed(DE) exosomal-miRNA in OA plasma and synovial fluid(SF).

METHODS:

Peripheral blood(plasma) and SF samples were collected from arthroplasty and arthroscopy subjects (MREC reference number: 20164-2398). Plasma and SF exosomal-total RNA(TR) were extracted using exoRNeasy kit and quantified using Nanodrop^{TM} 2000 spectrophotometer. A total of 50 ng of exosomal-TR were used for Illumina NovaSeq SE50 next-generation sequencing(NGS) analysis. Bioinformatics analysis was conducted to identify and analyzed the DE miRNA in OA plasma and SF.

RESULTS:

Exosomal total RNAs were extracted from plasma and SF samples. The quality of total RNA extracted (A260/A280 ratio) ranged between 1.7-1.8 and 1.8-2.0 for plasma and SF samples respectively.

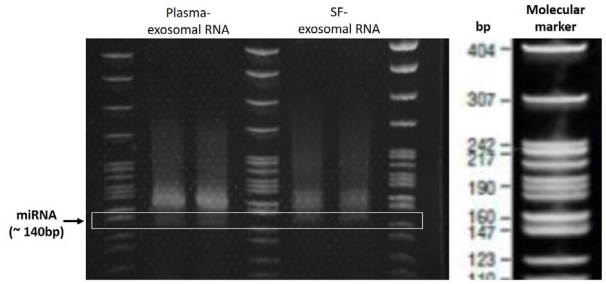

Figure 1: Representative agarose gel image of plasma and SF exosomal-total RNA NGS library. The 140 bp bands correspond to miRNAs (~20nt).

DISCUSSIONS:

The has-miR-125b-5p is down-regulated in chondrogenic mesenchymal stem cells[1]. The DE miRNAs identified are potential biomarkers for OA diagnosis.

CONCLUSION:

The study identified the DE miRNA in OA plasma and SF derived exosomes. Future studies shall investigate their roles in OA progression and further validation of these miRNAs as potential OA biomarkers.

REFERENCES:

1.Bella et al. 2019. *Cells* 9(2):398.