Single-cell RNA-seq analysis identifies meniscus progenitors and reveals the progression of meniscus degeneration

With the support by the National Natural Science Foundation of China and the Chinese Academy of Sciences, the research team led by Prof. Liao WeiMing (廖威明) and Zhang ZhiQi (张志奇) at the Joint Surgery Department, the First Affiliated Hospital of Sun Yat-sen University, uncovered the complex cell population of the meniscus, which was published in *Annals of the Rheumatic Diseases* (2019, Dec 23. pii: annrheumdis-2019-215926).

Osteoarthritis (OA) is the most common degenerative disease in joint surgery, among which knee joint lesions account for 85%. With the aging of China's population, the incidence of osteoarthritis is gradually increasing. Meniscus plays an important role in knee stability, shock absorption, contact force distribution, joint lubrication and proprioception. Meniscus degeneration is one of the important causes of osteoarthritis. However, due to the diversity of meniscus cell types and corresponding biomarkers, the specific mechanism of meniscus degeneration and corresponding biological targets are still unclear.

Single-cell RNA sequencing (scRNA-seq) is a well-established and powerful method to investigate transcriptomic cell-to-cell variation, which can be used to identify various cell types and provide insights into physiological and pathological processes. Therefore it is well suited to the study of complex cell populations in the meniscus. Through scRNA-seq, Zhang's group identified different subsets of cells and corresponding genes in the meniscus and analyzed the differentiation relationship between each subgro-up and the diversity characteristics of specific cell types. At the same time, the relatively unique cell groups with progenitor cell chara-cteristics were found in normal and osteoarthritis meniscus, and were named Fibrochondrocyte prog-enitor (FCP) and Degenerated men-iscus progenitor cells (DegP), respectively. Combined with bioi-nformatics analysis and molecular experiments, the differentiation of FCP to DegP was confirmed to be the abnormal differentiation process of meniscus degeneration, suggesting that this may be an important mechanism for meniscus degeneration. This study provides comprehensive census of human menis-cus cells, demonstrating FCP meniscus cells are progenitor cells and DegP could be a possible therapeutic target for meniscus degeneration.

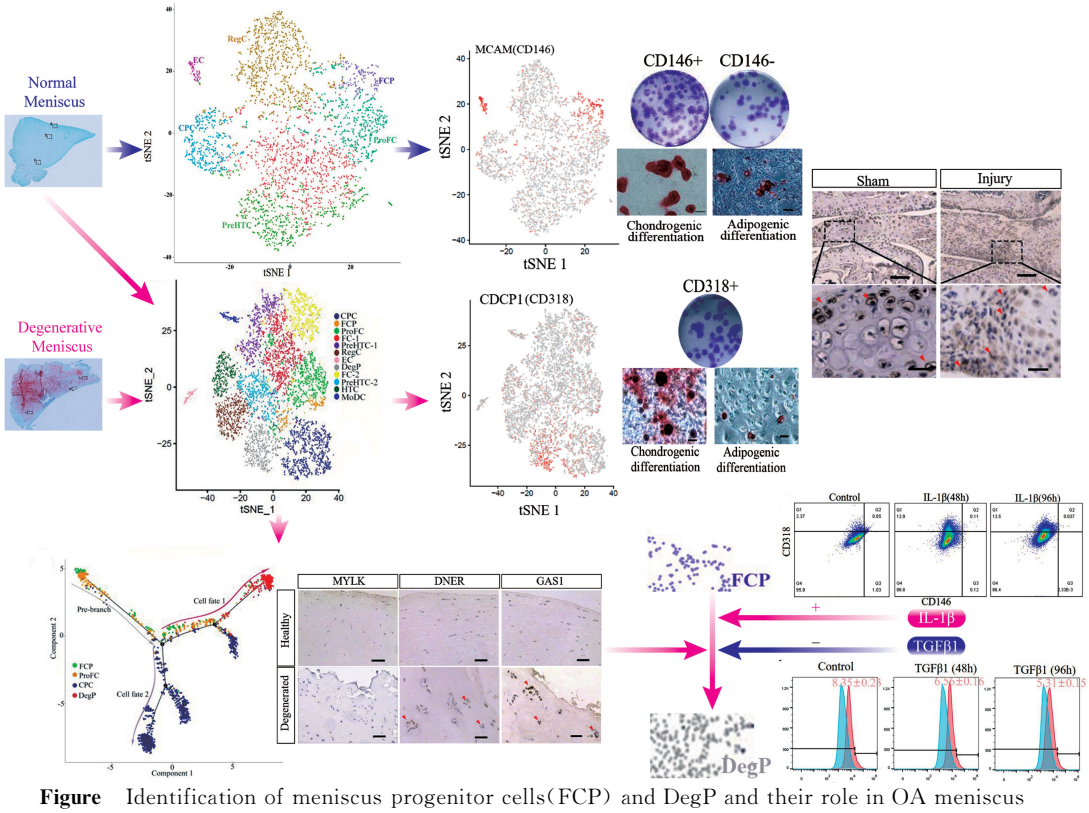

Figure Identification of meniscus progenitor cells(FCP) and DegP and their role in OA meniscus degeneration.