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Pig meniscus single-cell sequencing reveals highly active red zone chondrocyte populations involved in stemness maintenance and vascularization development

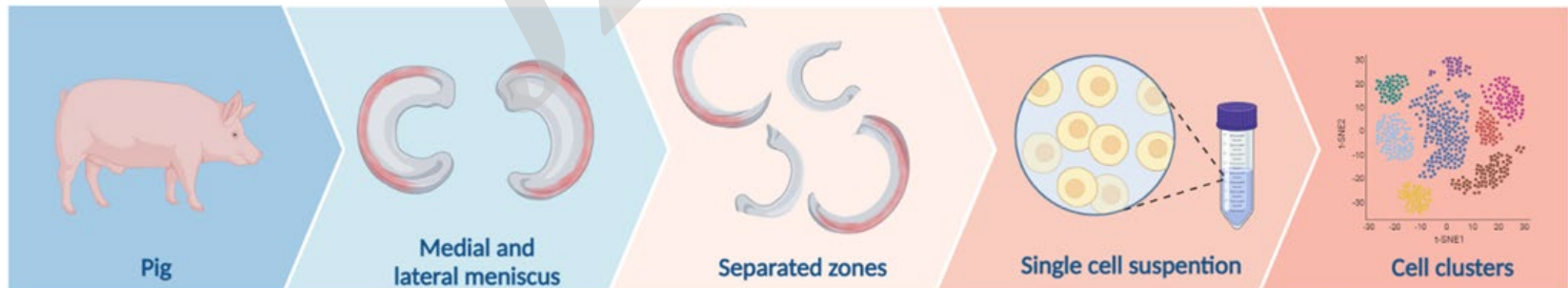
Key words: Single-cell sequencing; Transcriptome atlas; Meniscus; Chondrocyte; Pig model; Orthopedic

Research Summary

This research article summarizes our findings about porcine meniscus and its use as a potential novel therapeutical approach in orthopaedic therapy.

We present:

- a single-cell transcriptome atlas of the porcine meniscus, consisting of cell clusters corresponding to major cell types: chondrocytes, endothelial cells, smooth muscle cells, and immune cells
- detailed characterization of five distinct chondrocyte subclusters (Ch0-Ch4) in both red and white zones indicating a major difference in the cellular makeup of the zones and their different characteristics
- that the cellular makeup of the pig meniscus is comparable to that of humans, which supports the use of pigs as a model in orthopaedic therapy development



Innovation points

- Single-cell RNA sequencing revealed the presence of seven distinct cell populations
- Different subsets of chondrocytes are forming white and red zones of the porcine meniscus
- Single-cell trajectory analysis of chondrocyte subclusters reveals two distinct cell fates compliant with zonal composition

