Single-cell taxonomy of dorsal root ganglia reveals Gpr37l1 as a new analgesic target

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Dorsal root ganglia (DRGs) are the first gateway to the somatosensory system containing the cell bodies of primary sensory neurons and other numerous non-neuronal cells such as satellite glial cells (SGCs), macrophages and few T cells. Anatomical and functional evidence suggests that primary sensory neurons rely on interplays with these non-neuronal cells for maintenance of homeostasis and proper somatosensory functions. Conversely, dysfunctions of primary sensory neurons and non-neuronal cells in DRGs associated with tissue or nerve injury can result in somatosensory disorders, including chronic pain. Although high-throughput single-cell RNA sequencing (RNA-seq) have emerged as powerful tools to study the biology of cells in the brain, this approach has not been used yet to provide a comprehensive pictures of neuronal and non-neuronal cells in the DRGs. We have now established the use of Drop-seq, a high-throughput microfluidic technique that combining nucleic acid barcoding and RNA-seq, to analyze the transcriptome of thousands of individual DRG cells. We have identified and visualized 13 clusters of cells in DRGs according to their transcriptional profiling and expression of distinct marker genes, such as Tac1 for peptidergic nociceptors, Il31ra and MrgprA3 for pruriceptors, and Kcnj10 (i.e. Kir4.1) for SGCs. We are currently exploring new candidates in neuronal-glial signaling in the setting of chronic pain. This work provide the first comprehensive cellular census of DRG tissue and most importantly the identification of new neuronal and non-neuronal molecular signatures that may result in alternative therapeutic targets for the prevention and resolution of chronic pain.