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Smooth muscle genome/transcriptome browser offering genome-wide references and expression profiles of transcripts expressed in intestinal primary cells and tissues

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Transcriptome data on the quantitative numbers of transcriptional variants, expressed in primary cells offer essential clues in cellular functions and biological processes. We obtained transcriptomes from intestinal primary cells (smooth muscle cells, SMC; interstitial cells of Cajal, ICC; PDGFRα$^+$ cells, fibroblast-like cells) and tissues (jejunal and colonic smooth muscle and mucosa). We built "Smooth Muscle Transcriptome Browser" and "Smooth Muscle Genome Browser" that can offer genetic references and expression profiles of all transcripts expressed in SMC, ICC, PDGFRα$^+$ cells, associated jejunal and colonic tissues. Using these browsers, analyzing the transcriptomics, we have identified a unique set of cell signature genes for the three cell types including growth factors, transcription factors, epigenetic enzymes/regulators, protein kinases/phosphatases, cytokines/chemokines, receptors, and ion channels/transporters. We found that the cell signature genes are dysregulated in many gastrointestinal diseases and can serve as new pathological markers and therapeutic targets. Taken together, Smooth Muscle Transcriptome Browser and Smooth Muscle Genome Browser bring new insights into the cellular and biological functions of primary SMC, ICC, and PDGFRα+ cells in gastrointestinal smooth muscle biology and diseases.

Biography

Seungil Ro has obtained his Ph.D in Cell and Molecular Biology from the University of Nevada, Reno, USA in 2002, where he has been Associate Professor since 2015 in the Department of Physiology and Cell Biology in School of Medicine. His research interest includes the roles of microRNAs that regulate gastrointestinal smooth muscle motility and epigenetic remodeling. He has 35 papers published to his credit.

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