

## **Students' Annual Seminar**

### **Genes in the second nose: multilevel transcriptomics identifies cellular diversity and novel functional genes in the mouse vomeronasal neuroepithelium**

#### **Gubba Venkata Sai Devakinandan**

The vomeronasal organ (VNO), metaphorically called the second nose, is part of the vertebrate accessory olfactory system. It is an important sensory system model to understand how pheromones and kairomones elicit innate behaviours such as mating, aggression and predator avoidance. In similarity with the main olfactory system, VNO neurons regenerate throughout life, but they express completely different and diverse families of GPCRs, MHCs and other signalling components. I developed single cell transcription profiling to understand the diversity, gene co-expression patterns, and functional differences amongst neuronal subtypes. My analysis, performed in conjunction with spatial transcriptomics experiments, revealed: i) A diverse cell population map with distinct gene expression markers for each cell type, ii) Transient expression of transcription factors in immature neurons, which might be important for developmental divergence of neuronal subtypes and iii) specific co-expression patterns of GPCR and MHC gene families.

When comparing neuronal subtypes expressing V1 and V2-type GPCR families, I observed a significant enrichment of endoplasmic reticulum (ER) genes in neurons expressing V2-type GPCRs. Some of these hitherto un-characterised ER proteins seem to be expressed only in the VNO and not in other tissues, indicating a specific functional role. I will describe initial experiments to study a couple of VNO specific putative ER chaperones that reveal a non-compensatory role in VNO neuron function.

***Friday, Mar 24<sup>th</sup> 2023***

***02:00 PM (Tea / Coffee 1.45 PM)***

***Seminar Hall, TIFR-H***