Induction of Retinal Ganglion Cells through Transcription Factor Mediated Reprogramming

Manan Chopra

Department of Biological Sciences

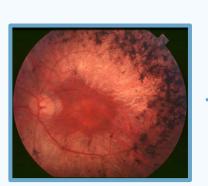
Mentor: Dr. Karl Wahlin Department of Ophthalmology

35th Annual URC Conference (Spring 2022)

285 MILLION

AFFECTED WORLDWIDE (2022)





Age-Related Macular Degeneration (AMD)

RETINAL DEGENERATION

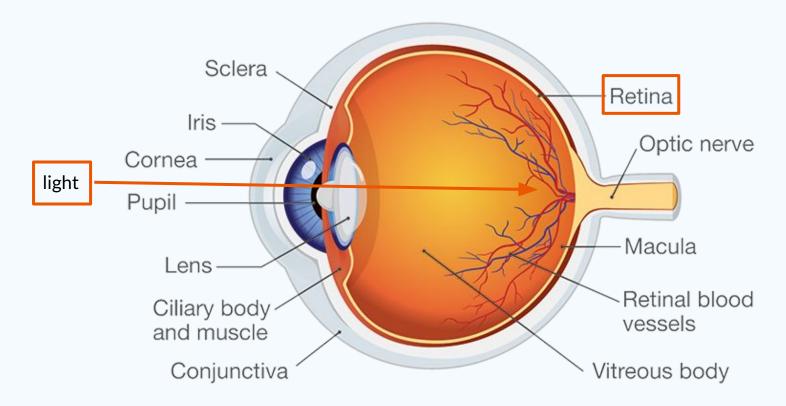
Retinitis Pigmentosa (RP)

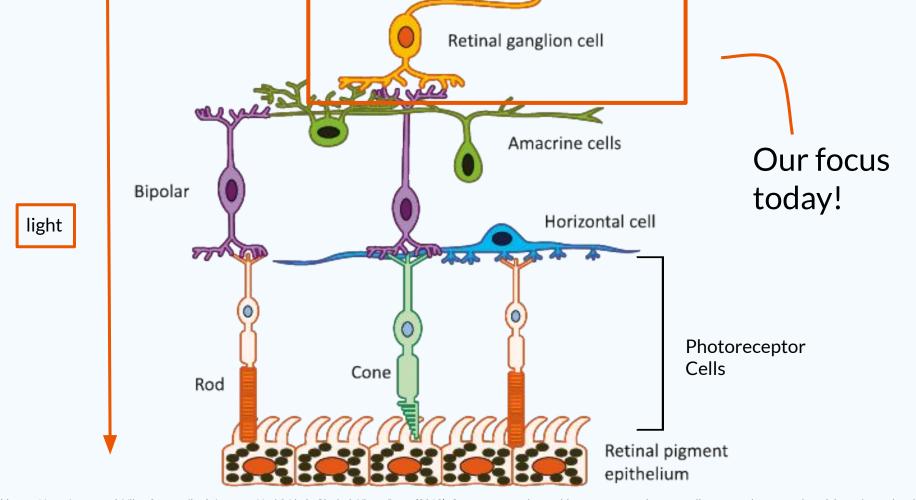
Glaucoma



The Retina & Retinal Ganglion Cells (RGCs)

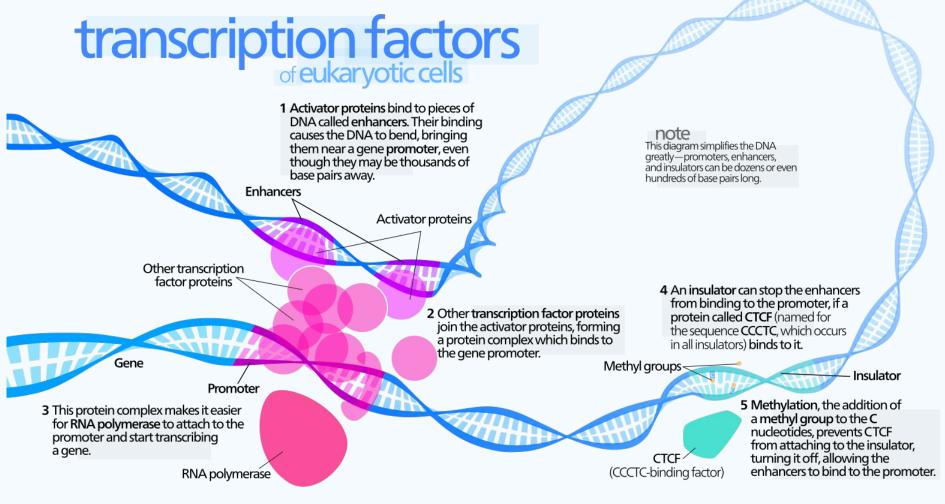
Human Eye Anatomy



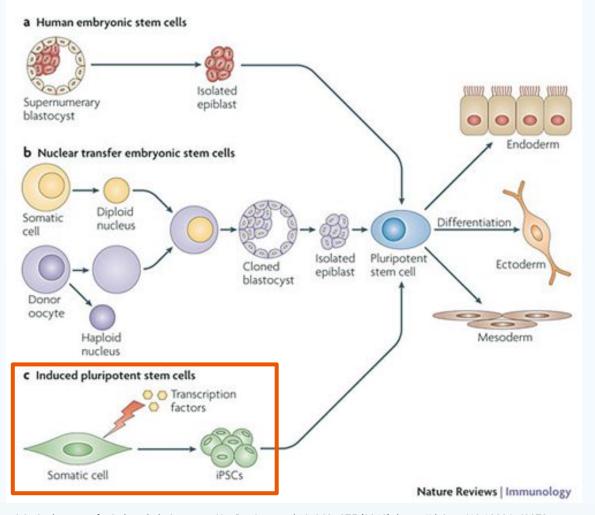


Dahlmann-Noor, Annegret & Vijay, Sauparnika & Jayaram, Hari & Limb, Gloria & Khaw, Peng. (2010). Current approaches and future prospects for stem cell rescue and regeneration of the retina and optic nerve. Canadian journal of ophthalmology. Journal canadien d'ophtalmologie. 45. 333-41. 10.3129/i10-077.

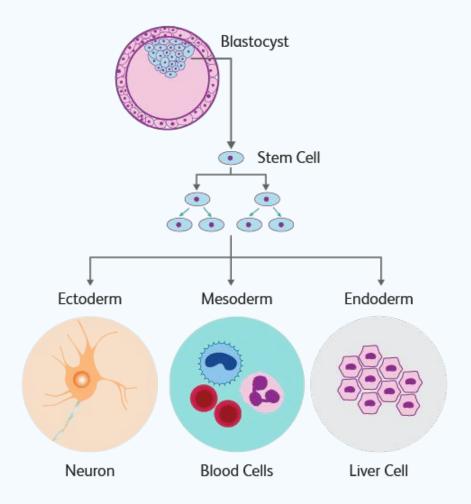
Transcription Factors (TFs)

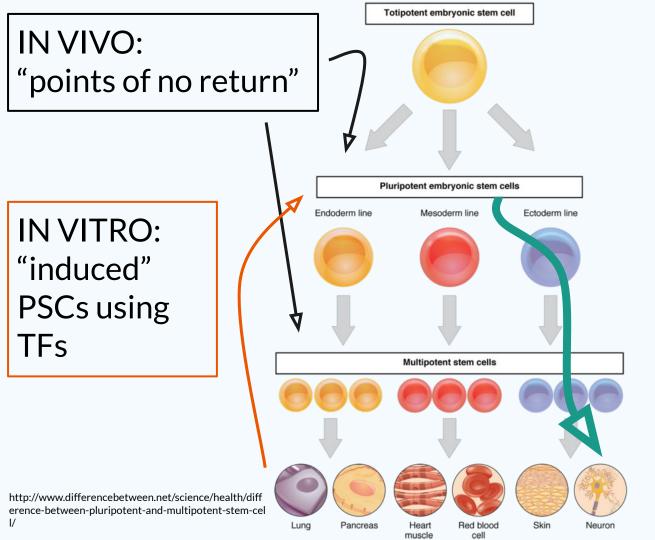


Pluripotent Stem Cells (PSCs) & 'Reprogramming'

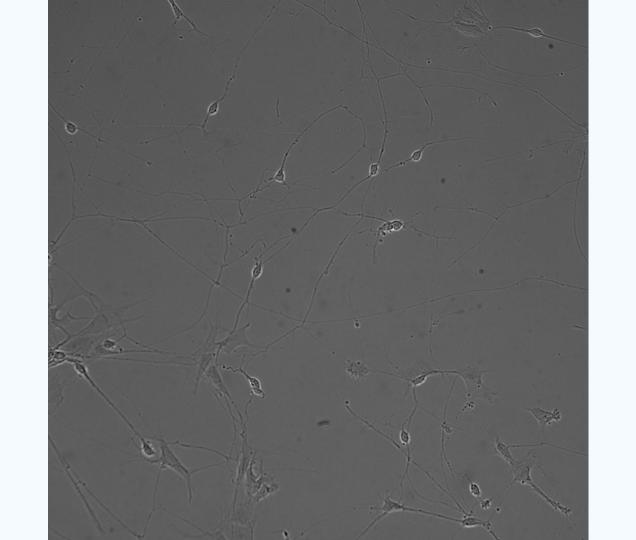


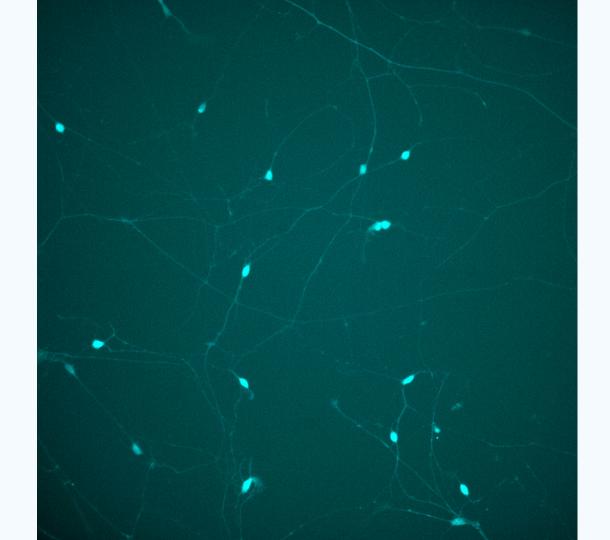
STEM CELLS IN VIVO

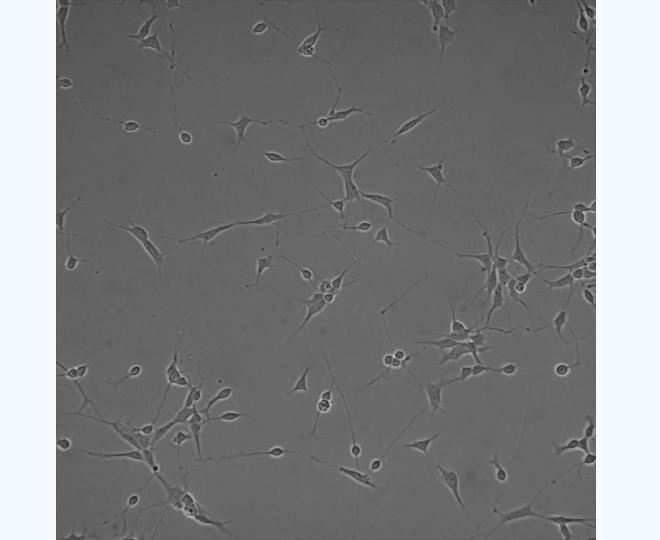


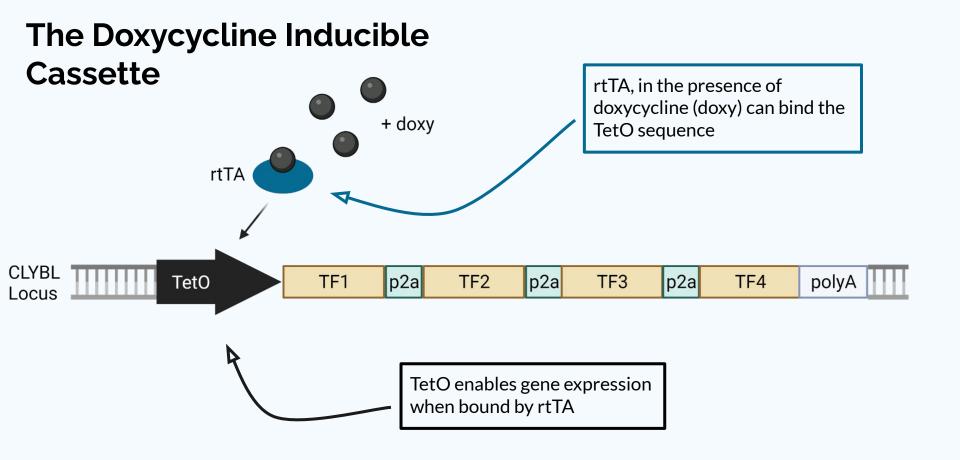


We want to take iPSCs and create "induced" RGCs We can use certain transcription factors to direct pluripotent stem cells into desired cell types (in our case, RGCs).

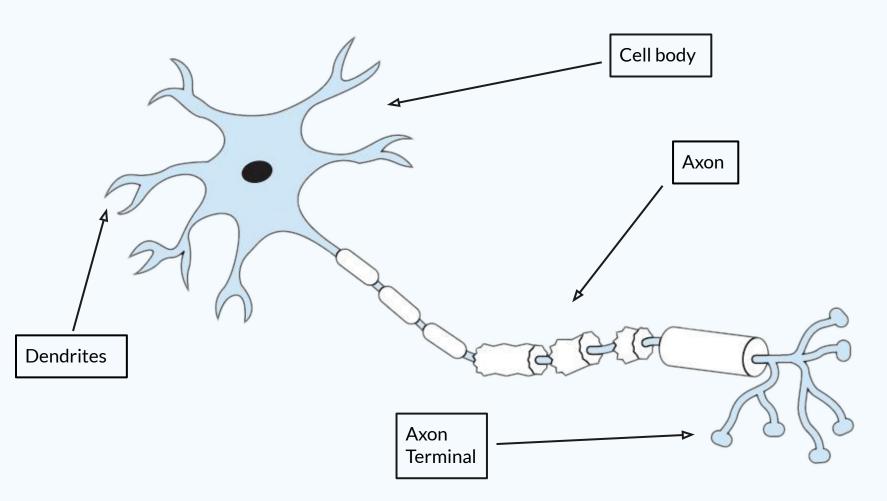








Insertion of the Cassette using CRISPR-Cas9 Editing Allows for very specific insertion of a desired insert Must provide a donor sequence which the cell will use to repair **gRNA** breaks induced by Cas9 Cas9 Complex crRNA Desired Insert **Donor DNA** (Template) Strand cuts 4111111111 Target DNA **DNA Containing PAM** Insert! Created with BioRender.com Sequence



Bioinformatics Analysis

Sequencing & Data Visualization

Summary of Transcriptomic Analysis



RNA Extraction

Take cells with the NAIP2 expression cassette (experimental group) and cells without NAIP2 expression cassette (CTL) and extract RNA.



RNAseq

Send RNA samples out to perform sequencing, obtain reads.



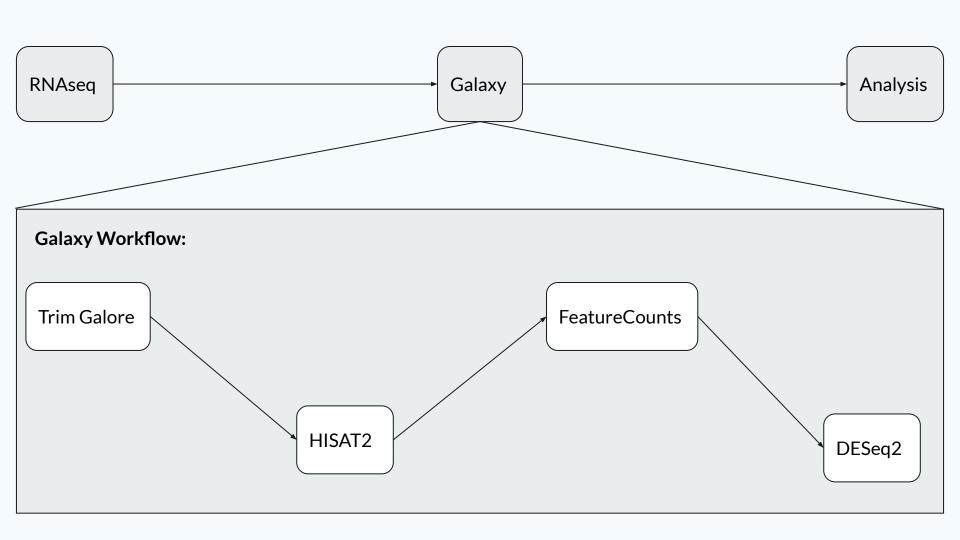
Galaxy Workflow

Process raw data from RNAseq so that we can interpret our results. Additionally, perform quality control checks on the data.

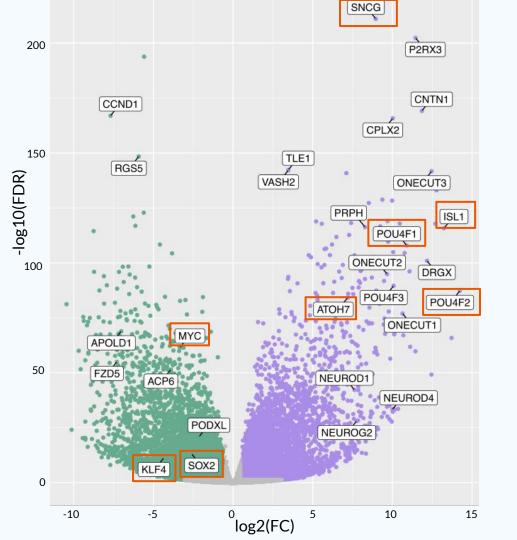


Data Visualization & Analysis

Using expression values outputted by the Galaxy workflow (specifically DESeq2), plot data with various methods to show trends and show an RGC-like expression profile in our experimental group.







Relative Expression Levels of Genes Expressed in CTL sample vs exp. sample

Showing upregulation of various RGC marker genes

Future Directions

- Redo bioinformatic analysis, this time comparing our induced RGCs to the transcriptome of known RGC cells
- Photoreceptor Cells (PRs) are another big area of cell death leading to retinal disorders
 - induced PRs
- Other areas of the brain
 - Regeneration of dopaminergic neurons for Parkinson's

Special Thanks!

- Dr Karl Wahlin
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- Samuel Levine