



ABSTRACT

Valproic acid (VPA) is a commonly used mood stabilizer and antiepileptic drug. In utero exposure to associated with increased risk for İS (NDDs). disorders Neural neurodevelopmental progenitor cells (NPCs) are crucial in neurodevelopment and may be vulnerable to VPA. We sought to determine VPA's effect on NPCs using cell viallges, a method which pools together cell lines in a shared in vitro environment. Stem-cell-derived NPCs from 12 donors were combined in equal proportions, then separated into two villages, treated with VPA or water control. Single-cell RNA sequencing and the Dropulation algorithm were used to profile gene expression and cell identity. We performed differential gene donor expression analysis using Voom and Dream and identified 356 differentially expressed genes that changed in response to VPA. Continued research into the effects of VPA can transform our understanding of improved healthcare, early NDDs, leading to interventions, and better outcomes for individuals with challenging neurodevelopmental conditions.



Figure 2. Experimental overview of the Cell Village used to treat samples with VPA and water

INTRODUCTION

- The purpose of this experiment was to test the effects of valproic acid on neural progenitor cells
- Statistical analysis was used to determine differential gene expression • VPA induces differentiation and
- inhibition of proliferation in NPCs







Figure 3. Voom mean-varience trend plot of differentially expressed genes as a result of VPA *before* filtering





Figure 5. Violin plot showing the density and distribution of genes

log2 fold change

Exploring the Impact of Valproic Acid on Neural Progenitor Cells through Cell Villages and Differential Gene Expression Analysis

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Experimental Methods

- 12 Donors Cells from Donors Pooled Togethe Freated w/ Water
- Village consisted of 12 donors
- One was treated with VPA and one with water
- Samples underwent single-cell RNA sequencing and **Dropulation analysis**





Figure 7. Volcano plot with Benjamini-Hochberg adjusted p-values of less than 0.01 and logFC threshold, represented by colors blue (downregulated and significant) and red (upregulated and significant)

Analysis Methods

Gene Expression Analysis

1. Preprocessing • Filtering the Genes



Figure 4. Voom mean-varience trend plot of differentially expressed genes as a result of VPA after filtering

2. Modeling Variables • Test - Treatment • Biological Variable - Sex "Random Effect" - Donor

> RawData FilteredData 0.0 .

Figure 6. Digital Gene Expression (DGE) graph representing frequency of genes before and after filtering











Upregulated Genes



Figure 9. Metascape bar graph created using the top 500 differentially expressed upregulated genes below adj. p-value of <0.01

Results



Figure 8. MDS plot of the effects of VPA on NPCs

Downregulated Genes



Figure 10. Metascape bar graph created using the top 500 differentially expressed downregulated genes below adj. p-value of <0.01

Genes of Interest Upregulated: GO:0007610: behavior R-HSA-195721: Signaling by WNT GO:0007420: brain development GO:0060071: Wnt signaling pathway, planar cell polarity pathway GO:0099170: postsynaptic modulation of chemical synaptic transmission **Downregulated:** R-HSA-2122947: NOTCH1 Intracellular Domain Regulates Transcription; GO:0021782: glial cell development; WP3584: MECP2 and associated Rett syndrome;

GO:0021872: forebrain generation of neurons

Future Directions

- Test NOTCH1 and other GO terms experimentally
- Compare to other ASD genes that were shown to be affected
- Aim to reproduce results from this experiment

ACKNOWLEDGEMENTS









7: negative regulation of extrinsic apoptotic signaling pathway 2: forebrain generation of neurons e of epithelial cell apical/basal pola

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