May 2nd, 11:00 AM - 1:00 PM

Effects of Chronic Stimulation of Nucleus Accumbens on Binge Drinking and Transcriptome

Dar'ya Pozhidayeva  
Portland State University

Evan Firsick  
Oregon Health & Science University

Kayla G. Townsley  
Oregon Health & Science University

Dan Iancu  
Oregon Health & Science University

Angela Ozbum  
Oregon Health & Science University

See next page for additional authors

Let us know how access to this document benefits you.

Follow this and additional works at: https://pdxscholar.library.pdx.edu/studentsymposium

Part of the Medicine and Health Sciences Commons

Pozhidayeva, Dar'ya; Firsick, Evan; Townsley, Kayla G.; Iancu, Dan; Ozbum, Angela; and Tran, A.T.D., "Effects of Chronic Stimulation of Nucleus Accumbens on Binge Drinking and Transcriptome" (2018). Student Research Symposium. 15.  
https://pdxscholar.library.pdx.edu/studentsymposium/2018/Poster/15

This Event is brought to you for free and open access. It has been accepted for inclusion in Student Research Symposium by an authorized administrator of PDXScholar. For more information, please contact pdxscholar@pdx.edu.
Presenter Information
Dar’ya Pozhidayeva, Evan Firsick, Kayla G. Townsley, Dan Iancu, Angela Ozbum, and A.T.D. Tran

This event is available at PDXScholar: https://pdxscholar.library.pdx.edu/studentsymposium/2018/Poster/15
Effects of Chronic Stimulation of Nucleus Accumbens on Binge Drinking and Transcriptome

D.Y. Pozhidayeva1,2,3, E.J. Firsick1,2, A.T.D. Tran1,2, K.G. Townsley1,2, O.D. Iancu1,2 and A.R. Ozburn1,2
1Department of Behavioral Neuroscience, Oregon Health & Science University, Portland, Oregon, 97239; 2Research and Development, Portland Veterans Affairs Medical Center, Portland, Oregon, 97239; 3Portland State University, Portland, Oregon, 97201.

Alignment

Workflow: How do we analyze changes in gene expression?

1. Quantifying Gene Expression Differences Between Groups

- Sequenced RNA from NAc tissue of mice from both CNO and VEH (Water and EtOH) treatment groups is aligned to the Mus musculus genome, and normalized.
- Regions of the sequenced genome in one sample cover regions of Mus musculus. Different samples between groups may have variability in alignment coverage.
- Based on this coverage between samples, we can see how genes are being expressed (Up-regulated/Down-regulated).
- How does CNO change gene expression? (What are the significant genes? What are their functions?)

2. How Do Differentially Expressed Genes Correlate?

- In gene co-expression networks, RNA-Seq data is transformed into a co-exist matrix. This matrix is used to compare gene expression between samples. Each gene (and its counts) correspond to a node; two nodes are connected if their expression values are highly correlated.
- The network is built on the basis of gene-gene correlations, which are collected in an adjacency matrix.
- The adjacency matrix is further processed and then clustered to detect gene modules (groups of genes that are coexpressed and often participate in the same biological processes).
- Genes that have many strong correlations are denoted as hubs. Our assumption is that they are important and potential targets for manipulation and/or therapy.
- Network properties in combination with differential expression can offer insights into molecular mechanisms.

Conclusions

- We found that chronically increasing NAc activity (via CNO/DREADD) can induce lasting reductions in binge-drinking and propose that molecular plasticity underlies this effect.
- By using these analyses, we are identifying changes in gene expression related to harmful binge-drinking and CNO/DREADD-induced reductions in binge-drinking.
- We plan to identify key hubs (WGCNA) for pharmacological manipulation of binge-drinking.

Acknowledgements

Many thanks to Dr. R. Jude Samulski at UNC Viral Vector Core for AAV prep. Supported by NIH grants [U01 AA10760 (JCC, ARO), US Department of Veterans Affairs Awards [IK2 BX002488 (ARO), Andrews Genomics Fund (ARO)].

Work reported in this poster was supported by the National Institutes of Health Common Fund and Office of Scientific Workforce Diversity under three award numbers UL1GM118964, R24LM118963, and 1UL1GM118965, administered by the National Institute of General Medical Sciences. The work is solely the responsibility of the authors and does not necessarily represent the official view of the National Institutes of Health.

This work was supported by the Ronald E. McNair Postbaccalaureate Achievement Program supported by grants from the U.S. Department of Education.

The authors gratefully acknowledge Sukhwant Jhaj, Dr. Tecuta Fiaeeva and staff.