

Temporal gene expression profiles and behavioral regression in children with ASD with post-synaptic density gene disruptions

Background

- Approximately one-third of children with an autism spectrum disorder (ASD) experience developmental regression within the first three years of life. However, the mechanisms underlying this behavioral phenotype remain unknown.
- Our group has identified higher rates of developmental regression in language and social engagement skills in children with de novo gene disrupting mutations to postsynaptic density (PSD) genes (Goin-Kochel et al., under review).
- PSD genes play a role in regulating synaptic function in human neocortex (Bayés) et al., 2011) and show differential timing in expression, with some genes preferentially expressed during synaptic formation and others during synaptic remodeling and differentiation (Swulius et al., 2010).
- Thus, disruptions in PSD genes preferentially expressed later in synaptic development may lead to normal initial behavioral development followed by onset of abnormal development and/or behavioral regression.
- Understanding the relationship between developmental gene expression timing and phenotypic ASD profiles may elucidate mechanisms of behavioral regression in ASD.

Objectives

The objectives are:

- To explore the relationship between gene expression timing and presence of behavioral regression in individuals with ASD who have PSD gene disruptions
- To explore regional differences in the relationship between gene expression timing and presence of behavioral regression in individuals with ASD who have PSD gene disruptions

Methods

- Participants were 40 children from the Simons Simplex Collection and The Autism Simplex Collection with PSD gene disruptions (as defined by lossifov et al., 2014) who met strict criteria for ASD.
- Timing of typical maximum expression for each PSD gene was extracted from the BrainSpan transcriptome exon microarray data (<u>http://www.brainspan.org</u>).
 - Expression data over three years post-birth was removed.
- For each gene, a t-test was performed to determine presence of significant differences between prenatal and postnatal expression levels. Genes were categorized in three groups based on changes in expression
- levels:
- Early: Prenatal expression was significantly greater than postnatal expression
- Late: Postnatal expression was significantly greater than prenatal expression
- No Change: Prenatal and postnatal expression levels were not significantly different
- Eight children with parentally reported history of developmental regression in language and social engagement skills were compared to 32 children without regression.

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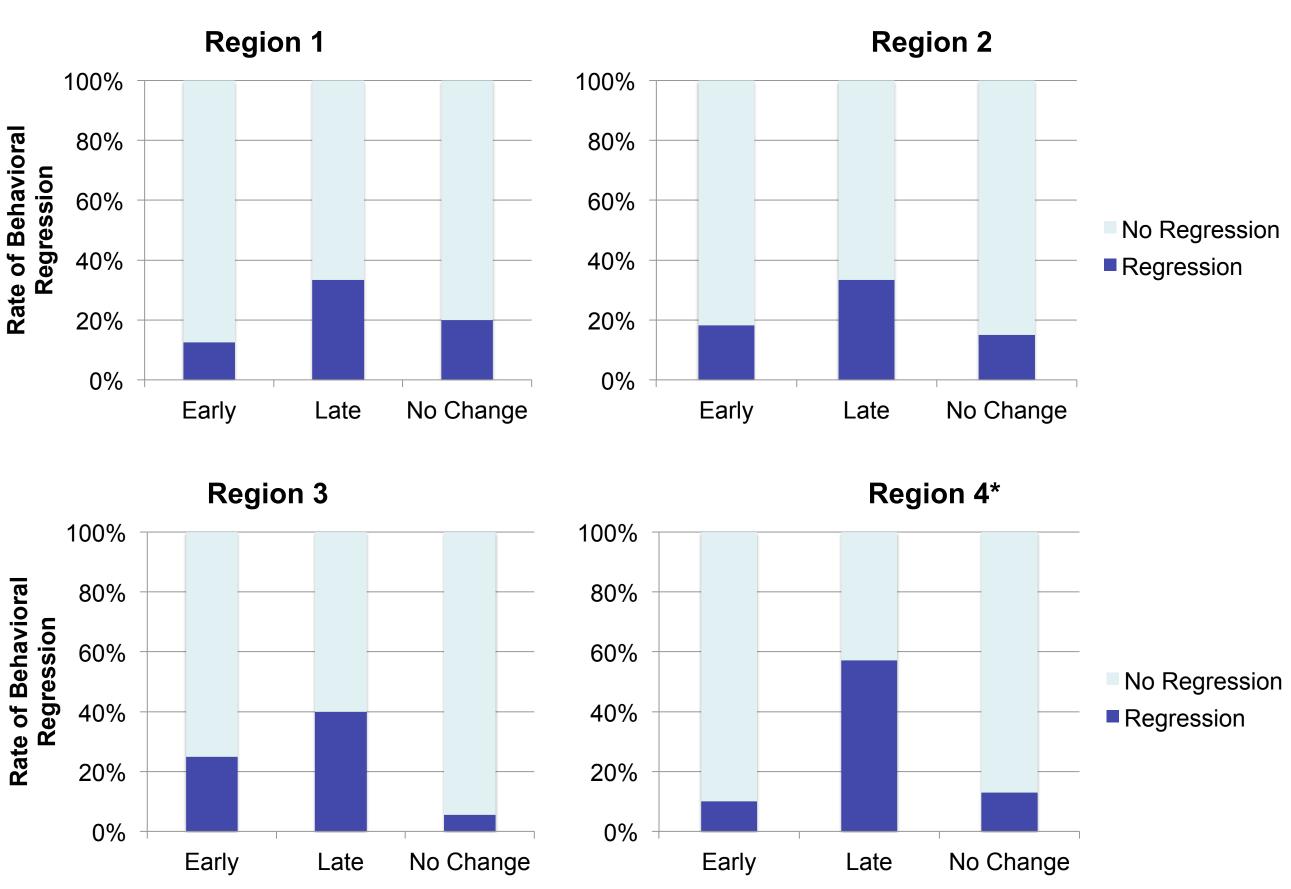
Results

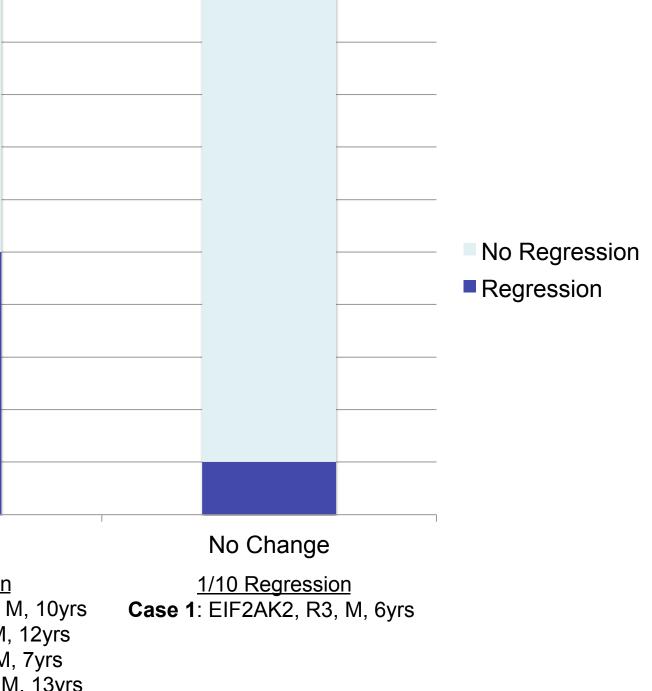
Rates of Regression in Individuals with Gene Disruptions in PSD Genes with Differential Typical Expression 100% 90% 80% 70% 60% 50% 40% **b** 30% 20% 10% 0% Early No Change Late <u>2/20 Regression</u> Case 1: GPRIN1, R1-4, M, 11yrs 5/10 Regression 1/10 Regression Case 1: DOCK5, R1-4, M, 10yrs **Case 1**: EIF2AK2, R3, M, 6yrs Case 2: DST, R1-4, M, 12yrs Case 2: KIF21A, R1-3, M, 6yrs

Case 3: PSD3, R4, M, 7yrs Case 4: RIMS1, R1-4, M, 13yrs **Case 5**: SORBS1, R3, M, 17yrs

Brain Regions (as identified by Willsey et al., 2013)

| Region 1 | Region 2 | Region 3 | Region 4 |
|---------------------------------------|-----------------------------------|-------------|--|
| Posterior inferior parietal cortex | Primary somatosensory cortex | Striatum | Mediodorsal nucleus of the thalamus |
| Primary auditory cortex | Primary motor cortex | Hippocampus | Cerebellar cortex |
| Primary visual cortex | Orbital prefrontal cortex | Amygdala | |
| Superior temporal cortex | Dorsolateral prefrontal cortex | | |
| Inferior temporal cortex | Medial prefrontal cortex | | |
| | Ventrolateral prefrontal cortex | | |





Rates of Regression by Brain Region

Results Continued

- cases (90%) did not report loss.
- nine cases (90%) did not report loss.
- five cases (50%) did not report loss.
- cerebellum (p=0.04).

- timing in symptom expression timing.
- impact symptom onset.

References Bayés, A., van de Lagemaat, L., Collins, M., Croning, M., Whittle, I., Choudhary, J., & Grant, S. (2011). Characterisation of the proteome, diseases and evolution of the human postsynaptic density. Nature Neuroscience, 14(1), 19–21. in Autism Spectrum Disorder.

coding mutations to autism spectrum disorder. Nature, 515, 216-21. Swulius, M. T., Kubota, Y., Forest, A., & Waxham, M. N. (2010). Structure and composition of the postsynaptic density during development. Journal of Comparative Neurology, 518(20), 4243-4260. Willsey, A. J., Sanders, S. J., Li, M., Dong, S., Tebbenkamp, A. T., Muhle, R. A., ... & Murtha, M. T. (2013). Coexpression networks implicate human midfetal deep cortical projection neurons in the pathogenesis of autism. Cell, 155(5), 997-1007.



For cases with gene disruptions in genes typically expressed in higher levels prenatally than postnatally, two cases (10%) reported loss, and 18

For cases with gene disruptions in genes typically expressed in similar levels prenatally and postnatally, one case (10%) reported loss, and

For cases with gene disruptions in genes typically expressed in greater levels postnatally than prenatally, five cases (50%) reported loss, and

Non-parametric analysis examining the relationship between the timing of gene expression levels and the presence of regression revealed differences in rates of loss: χ^2 (2, N = 40) = 7.500, p= 0.02.

When brain regions were examined separately, rates of loss remained significantly different only in Region 4, composed of the thalamus and

Discussion

The observed relationship between behavioral regression and period of maximum gene expression in individuals with likely gene-disrupting mutations to PSD genes suggests the importance of gene expression

Previous mouse model studies demonstrate preferential expression of PSD genes in different phases of synaptic development (Swulius et al., 2010); these findings suggest that the differential phases of expression can

 Specifically, our results suggest that differential timing of gene expression in the thalamic and cerebellar region may have an increased impact on rate of regression. Better understanding of the normal developmental timing of gene expression in genes disrupted in individuals with ASD may aid in explaining the phenotypic variability regarding symptom onset among children with ASD.

Goin-Kochel, R. P., Trinh, S., Barber, S., & Bernier, R. (under review). Gene disrupting mutations associated with regression

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