

Analysis on specific genetic pathways may uncover roots of autism

The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion and analysis.

The number of genetic variants implicated in autism is large and growing, but it's increasingly clear that identifying these variants is only the beginning of the quest to understand the biology of autism.

Although autism may affect large numbers of genes, their functions appear to converge on only a few biological pathways, including the development of the cerebral cortex. Ultimately, these findings suggest that, despite multiple genetic causes, we may need to target only a few pathways to effectively treat people with autism.

In one type of analysis, called weighted gene co-expression network analysis (WGCNA), researchers group genes based on the similarity of their expression patterns and then interpret the functional role of genes within each module.

Unfortunately, network analyses decipher only gene expression information. They are not designed to crunch data related to genetic variants, DNA modifications that affect gene expression, or information about the proteins themselves. Combining all of these datasets could provide an even more complete molecular understanding of autism.

Read full, original post: [Analyses of gene activity may yield clues to roots of autism](#)