**Untangling the spectrum: Using genetics to identify autism and co-occurring traits**

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**Background:** Autism represents a complex group of neurodevelopmental states. Whilst genetic variants linked to autism have been identified, little is known about how the genes these variants control interact with genes impacted by co-occurring traits. **Objectives:** To identify traits that co-occur with autism by analysing the interaction between genes controlled by autism-associated genetic variants and genes which play a role in the co-occurring traits. **Methods:** Genetic variants (single nucleotide polymorphisms [SNPs]) associated with autism were downloaded from the GWAS (genome-wide association studies) Catalogue. Potential co-occurring conditions were identified using the Multimorbid3D pipeline on adult and fetal cortical tissue separately. A protein-protein interaction network (PPIN) was developed to identify the proteins, and their genes, that interact with the proteins encoded by autism-associated expression quantitative trait loci (eQTLs). This network was expanded to four levels. At each level, traits associated with the proteins were identified using a modified phenome-wide association study (PheWAS) analysis. **Results:** Mood disorders, fatty acid levels, neurological conditions, and lung-related traits were identified as associated with autism. There were developmental stage-specific differences in the co-occurring traits and genes that were identified between the adult and fetal cortical tissue. **Discussion:** This study has identified traits that have a genetic risk of co-occurring with autism. Differences in genes identified in adult and fetal tissue offer insight into the development of different forms of autism. The identification of groups of co-occurring conditions linked by common genetic variants paves the way for future work improving understanding and diagnosis of autism and co-occurring traits.

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