Abstract: While we have recently seen major advances in our understanding of the complex genetic architecture of developmental neuropsychiatric disorders, etiologic heterogeneity remains a major obstacle. The study of highly penetrant genomic copy number variants (CNVs) can provide a window into disease pathophysiology. Here I will highlight our longitudinal and translational work focused on one such variant, 22q11.2 microdeletion syndrome (22qDel), a contiguous gene deletion disorder that is among the greatest known genetic risk factors for schizophrenia. Our findings reveal disruptions within specific developmental epochs, pointing to key periods for intervention. Further, across multiple levels of analysis, we find biological convergence with idiopathic (behaviorally defined) illness, suggesting that highly penetrant CNVs such as 22qDel can inform broader disease risk mechanisms.

Sponsored by: The UCLA Brain Research Institute, The David Geffen School of Medicine at UCLA, and The Semel Institute for Neuroscience & Human Behavior